
TEIL G: ANHANG

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Tab. 59: Liste der identifizierten Proteine von *S. aureus* RN1HG und RN1HG $\Delta sigB$ aus den Kulturüberständen von TSB und pMEM.

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
Toxine und Hämolsine (9)													
88194865	SAOUHSC_01121	Hla	alpha-hemolysin precursor	36 kDa	ez	10.00	Y		x	x	x	x	x
88194955	SAOUHSC_01219	LytN	cell wall hydrolase, putative	42 kDa	zw	9.18	Y			x			
88196641	SAOUHSC_03023	Drp35	Drp35	36 kDa	zyt	8.87	N					x	
88196348	SAOUHSC_02708	HlgA	gamma-hemolysin component A	35 kDa	ez	9.73	#NV				x	x	x
88196350	SAOUHSC_02710	HlgB	gamma-hemolysin component B	37 kDa	ez	9.73	Y				x		x
88196349	SAOUHSC_02709	HlgC	gamma-hemolysin component C	36 kDa	ez	9.73	Y				x	x	x
88193943	SAOUHSC_00130	IsdI	hypothetical protein SAOUHSC_00130	13 kDa	unb	2.50	N		x				x
88195915	SAOUHSC_02243		hypothetical protein SAOUHSC_02243	40 kDa	ez	9.73	Y				x		
88195647	SAOUHSC_01954	LukD	leukotoxin, LukD	37 kDa	ez	9.98	#NV		x		x		x
Virulenz-/Abwehrmechanismen (24)													
88193871	SAOUHSC_00051	Plc	1-phosphatidylinositol phosphodiesterase precursor, putative	37 kDa	ez	9.97	Y		x	x	x	x	x
88196592	SAOUHSC_02971	Aur	aureolysin, putative	55 kDa	ez	9.97	Y		x		x		x
88194572	SAOUHSC_00812	ClfA	clumping factor	96 kDa	zw	10.00	Y	x	x	x	x	x	x
88196585	SAOUHSC_02963	ClfB	clumping factor B, putative	94 kDa	zw	10.00	Y	x	x	x	x	x	x
88194744	SAOUHSC_00987	SspB	cysteine protease precursor, putative	45 kDa	ez	9.55	Y	x	x	x	x		x
88195217	SAOUHSC_01501	EbpS	elastin binding protein extracellular matrix and plasma binding protein, putative	53 kDa	zw	9.06	#NV		x	x	x	x	x
88194575	SAOUHSC_00816	Ssp,Empbp		38 kDa	unb	3.33	Y	x	x	x	x	x	
88194860	SAOUHSC_01114	Efb	fibrinogen-binding protein	19 kDa	ez	9.98	Y		x				
88196437	SAOUHSC_02802	FnbB	fibronectin binding protein B, putative	101 kDa	zw	10.00	N	x					
88194745	SAOUHSC_00988	SspA	glutamyl endopeptidase precursor, putative	36 kDa	ez	10.00	Y	x	x	x	x	x	x
88194063	SAOUHSC_00257		hypothetical protein SAOUHSC_00257	11 kDa	unb	2.50	N					x	
88196346	SAOUHSC_02706	Sbi	immunoglobulin G-binding protein Sbi, putative	50 kDa	unb	3.33	#NV	x	x	x		x	x

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88193965	SAOUHSC_00153	IpdC	indolepyruvate decarboxylase, putative	61 kDa	unb	2.50	N			x		x	x
88196625	SAOUHSC_03006	Lip	lipase	77 kDa	ez	9.73	Y			x	x	x	x
88194101	SAOUHSC_00300	Geh	lipase precursor	76 kDa	ez	10.00	Y	x	x	x	x	x	x
88196512	SAOUHSC_02883		LysM domain protein	28 kDa	ez	9.04	Y	x	x				
88193885	SAOUHSC_00069		protein A	56 kDa	zw	10.00	Y	x	x	x	x	x	x
88194325	SAOUHSC_00545		sdrD protein, putative	146 kDa	zw	10.00	Y	x	x	x	x	x	x
88195635	SAOUHSC_01941	SplB	serine protease SplB	26 kDa	ez	9.73	Y				x		x
88195630	SAOUHSC_01935	SplF	serine protease SplF, putative	26 kDa	ez	9.73	#NV		x		x		x
88195808	SAOUHSC_02127		staphopain thiol proteinase	44 kDa	ez	9.73	Y	x	x	x	x	x	x
88195848	SAOUHSC_02171	Sak	staphylokinase precursor, putative	19 kDa	ez	9.98	Y		x	x	x	x	
88194577	SAOUHSC_00818	Nuc	thermonuclease precursor	25 kDa	ez	10.00	Y				x	x	x
88195480	SAOUHSC_01779	Tig	trigger factor	49 kDa	zyt	8.87	N	x	x	x	x	x	x
Zellwandbiosynthese und -abbau (15)													
88194219	SAOUHSC_00427		autolysin precursor, putative	36 kDa	ez	9.98	Y	x	x	x	x	x	x
88194750	SAOUHSC_00994	Atl	bifunctional autolysin precursor, putative	137 kDa	ez	10.00	#NV	x	x	x	x	x	x
88195790	SAOUHSC_02108	Ftn	ferritin, putative	20 kDa	zyt	9.98	N	x	x	x	x	x	
88193909	SAOUHSC_00094		hypothetical protein SAOUHSC_00094	22 kDa	zw	9.93	Y	x	x	x	x	x	x
88196515	SAOUHSC_02887	IsaA	immunodominant antigen A, putative	24 kDa	ez	10.00	Y	x	x	x	x	x	x
88195840	SAOUHSC_02161		MHC class II analog protein	66 kDa	unb	3.33	Y				x		x
88194887	SAOUHSC_01145	PbpA	penicillin-binding protein 1	83 kDa	zm	9.82	Y	x	x	x		x	
88195184	SAOUHSC_01467	Pbp2	penicillin-binding protein 2	80 kDa	ez	9.55	N		x	x	x	x	x
88195360	SAOUHSC_01652	PbpF,Pbp3	penicillin-binding protein 3	77 kDa	zm	9.82	#NV		x	x	x	x	x
88194055	SAOUHSC_00248	LytM	peptidoglycan hydrolase, putative	34 kDa	ez	9.98	Y	x	x	x	x	x	x
88194324	SAOUHSC_00544		sdrC protein, putative	108 kDa	zw	10.00	Y	x	x	x	x	x	x
88196215	SAOUHSC_02571	SsaA	secretory antigen precursor, putative	29 kDa	ez	9.04	Y	x	x	x	x	x	x

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88194436	SAOUHSC_00671		secretory antigen SsaA-like protein	28 kDa	ez	9.73	Y	x	x	x	x	x	x
88194675	SAOUHSC_00918		truncated MHC class II analog protein	16 kDa	unb	3.33	Y	x	x	x	x	x	x
88196118	SAOUHSC_02466		truncated MHC class II analog protein	15 kDa	unb	3.33	Y		x	x	x	x	x
Zellumhüllung (19)													
88194626	SAOUHSC_00869	DltA	D-alanine-activating enzyme	55 kDa	zyt	9.98	N	x		x		x	
88194628	SAOUHSC_00871	DltC	D-alanyl carrier protein	9 kDa	zyt	8.87	N	x	x				
88194199	SAOUHSC_00405		hypothetical protein SAOUHSC_00405	29 kDa	unb	2.50	N			x	x	x	x
88194482	SAOUHSC_00717		hypothetical protein SAOUHSC_00717	16 kDa	unb	3.33	Y		x	x	x	x	x
88194518	SAOUHSC_00754		hypothetical protein SAOUHSC_00754	34 kDa	unb	6.46	Y				x		
88194829	SAOUHSC_01081	IsdA	hypothetical protein SAOUHSC_01081	39 kDa	zw	10.00	N	x	x	x	x	x	x
88194830	SAOUHSC_01082	IsdC	hypothetical protein SAOUHSC_01082	25 kDa	unb	3.33	Y		x		x		x
88195062	SAOUHSC_01332		hypothetical protein SAOUHSC_01332	34 kDa	unb	2.50	#NV				x	x	x
88195077	SAOUHSC_01349		hypothetical protein SAOUHSC_01349	11 kDa	zyt	8.87	N			x			
88195443	SAOUHSC_01739	LytH	hypothetical protein SAOUHSC_01739	33 kDa	unb	3.33	N		x		x		x
88195542	SAOUHSC_01843		hypothetical protein SAOUHSC_01843	101 kDa	zw	10.00	#NV				x		
88195590	SAOUHSC_01895		hypothetical protein SAOUHSC_01895	33 kDa	ez	9.55	Y		x	x	x	x	x
88195802	SAOUHSC_02121		hypothetical protein SAOUHSC_02121	45 kDa	unb	3.33	Y		x	x	x	x	x
88196433	SAOUHSC_02798		hypothetical protein SAOUHSC_02798	179 kDa	zw	10.00	N	x	x	x	x	x	x
88196599	SAOUHSC_02979		hypothetical protein SAOUHSC_02979	69 kDa	ez	9.73	Y	x	x	x	x	x	x
88196601	SAOUHSC_02982		hypothetical protein SAOUHSC_02982	71 kDa	zw	10.00	Y		x	x	x	x	x
88193889	SAOUHSC_00074	SirA	periplasmic binding protein, putative	37 kDa	unb	3.33	Y		x		x		x
88195460	SAOUHSC_01759	Mrec	rod shape-determining protein Mrec	31 kDa	unb	3.33	Y		x	x	x	x	x
88196468	SAOUHSC_02834	SrtA	sortase, putative	24 kDa	unb	3.33	Y				x		x

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Stressantwort (25)													
88194163	SAOUHSC_00365	AhpC	alkyl hydroperoxide reductase	21 kDa	zyt	9.98	N	x	x	x	x	x	x
88194162	SAOUHSC_00364	AhpF	alkyl hydroperoxide reductase, subunit F, putative	55 kDa	zyt	9.98	N	x		x		x	
88194551	SAOUHSC_00790	ClpP	ATP-dependent Clp protease, proteolytic subunit ClpP	22 kDa	zyt	9.65	N	x		x		x	
88196560	SAOUHSC_02933	BetB,CudA,GbsA	betaine aldehyde dehydrogenase	55 kDa	zyt	9.98	N				x		
88195057	SAOUHSC_01327	KatA	catalase	55 kDa	zyt	9.98	N	x	x	x	x	x	x
88195926	SAOUHSC_02255	GroES	chaperonin, 10 kDa, GroES, putative	10 kDa	zyt	10.00	N	x	x	x		x	
88195925	SAOUHSC_02254	GroL,GroEL	chaperonin, 60 kDa, GrpEL, putative	58 kDa	zyt	9.98	N	x	x	x		x	
88195129	SAOUHSC_01403	CspA	cold shock protein, putative	7 kDa	zyt	9.98	N	x	x	x	x	x	x
88196660	SAOUHSC_03045	CspB	cold shock protein, putative	8 kDa	zyt	9.98	N	x		x			
88194348	SAOUHSC_00573		hypothetical protein SAOUHSC_00573	29 kDa	unb	2.50	N			x	x	x	x
88194589	SAOUHSC_00831		hypothetical protein SAOUHSC_00831	15 kDa	unb	2.50	N					x	x
88194593	SAOUHSC_00835		hypothetical protein SAOUHSC_00835	14 kDa	zyt	8.87	N	x		x	x	x	x
88195014	SAOUHSC_01282	BsaA	hypothetical protein SAOUHSC_01282	18 kDa	unb	2.50	N			x		x	
88195522	SAOUHSC_01822	Tpx	hypothetical protein SAOUHSC_01822	18 kDa	unb	2.50	N	x	x	x	x	x	x
88196044	SAOUHSC_02381	Dps	hypothetical protein SAOUHSC_02381	17 kDa	unb	2.50	N	x	x	x	x	x	x
88196094	SAOUHSC_02441	Asp23	hypothetical protein SAOUHSC_02441	19 kDa	unb	2.50	N	x	x	x	x	x	x
88195155	SAOUHSC_01431	MsrB	methionine sulfoxide reductase, putative	16 kDa	zyt	8.87	N	x		x		x	
88196463	SAOUHSC_02829	Frp	NAD(P)H-flavin oxidoreductase, putative	25 kDa	zyt	8.87	N					x	
88195156	SAOUHSC_01432	MsrA2	peptide methionine sulfoxide reductase	21 kDa	unb	2.50	N			x		x	
88195361	SAOUHSC_01653	SodA	superoxide dismutase, Mn, putative	23 kDa	ez	9.55	N	x	x	x	x	x	x
88193908	SAOUHSC_00093	SodM	superoxide dismutase, putative	23 kDa	ez	9.55	N			x		x	x
88194846	SAOUHSC_01100	TrxA,Trx	thioredoxin	11 kDa	zyt	9.98	N	x	x	x	x	x	x
88194546	SAOUHSC_00785	TrxB	thioredoxin reductase	34 kDa	zyt	9.65	N	x		x		x	x
88194592	SAOUHSC_00834		thioredoxin, putative	12 kDa	zyt	8.87	N	x	x	x	x	x	x

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Regulation (12)													
88195548	SAOUHSC_01850	CcpA	catabolite control protein A	36 kDa	zyt	9.98	N			x			
88194239	SAOUHSC_00452		hypothetical protein SAOUHSC_00452	12 kDa	unb	2.50	N			x		x	x
88194421	SAOUHSC_00655		hypothetical protein SAOUHSC_00655	35 kDa	zyt	8.87	N			x		x	
88194459	SAOUHSC_00694		hypothetical protein SAOUHSC_00694	17 kDa	unb	2.50	N	x					x
88194477	SAOUHSC_00712		hypothetical protein SAOUHSC_00712	32 kDa	zyt	8.87	N	x					
88194753	SAOUHSC_00997		hypothetical protein SAOUHSC_00997	46 kDa	unb	3.33	Y		x	x	x		x
88194963	SAOUHSC_01228	CodY	hypothetical protein SAOUHSC_01228	29 kDa	zyt	8.87	N					x	x
88195657	SAOUHSC_01964	TRAP	hypothetical protein SAOUHSC_01964	20 kDa	zyt	8.87	#NV	x		x	x	x	x
88195154	SAOUHSC_01430	Crr	putative PTS system, mannitol-specific Iia	18 kDa	zyt	9.98	N	x		x	x	x	x
88196063	SAOUHSC_02402		component, putative staphylococcal accessory regulator T,	16 kDa	zyt	9.98	N			x		x	x
88194390	SAOUHSC_00620	SarA	putative	15 kDa	unb	2.50	N				x		
88196226	SAOUHSC_02583		transcriptional regulator, putative	34 kDa	unb	3.33	Y				x		x
Transport (36)													
88196546	SAOUHSC_02919	PanB	3-methyl-2-oxobutanoate hydroxymethyltransferase	28 kDa	unb	2.50	N	x		x	x	x	
88194087	SAOUHSC_00284		5'-nucleotidase, lipoprotein e(P4) family ABC transporter periplasmic binding	33 kDa	unb	3.33	Y			x			x
88196085	SAOUHSC_02430	HtsA	protein, putative ABC transporter, ATP-binding protein,	37 kDa	unb	3.33	Y		x				x
88194605	SAOUHSC_00847	SufC	putative ABC transporter, substrate-binding protein,	28 kDa	zm	9.49	N	x		x			
88194402	SAOUHSC_00634	MntC	putative enoyl-CoA hydratase/isomerase family	35 kDa	unb	3.33	Y		x	x	x	x	x
88194742	SAOUHSC_00985	MenB	protein, putative	30 kDa	zyt	8.87	N	x		x		x	x
88194761	SAOUHSC_01007	FolD	FolD bifunctional protein, putative glutamate-1-semialdehyde-2,1-	31 kDa	zyt	8.87	N			x	x	x	x
88195472	SAOUHSC_01771	HemL	aminomutase	46 kDa	zyt	8.87	#NV	x					
88194011	SAOUHSC_00201		hypothetical protein SAOUHSC_00201	53 kDa	zw	9.17	N				x		

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88194028	SAOUHSC_00220	IspD	hypothetical protein SAOUHSC_00220	25 kDa	zyt	8.87	N			x		x	
88194112	SAOUHSC_00311		hypothetical protein SAOUHSC_00311	10 kDa	zyt	8.87	N			x		x	x
88194606	SAOUHSC_00848	SufD	hypothetical protein SAOUHSC_00848	49 kDa	zyt	8.87	N	x		x		x	
88194608	SAOUHSC_00850		hypothetical protein SAOUHSC_00850	17 kDa	zyt	8.87	N	x		x			
88194609	SAOUHSC_00851	SufB	hypothetical protein SAOUHSC_00851	53 kDa	zyt	8.87	N	x		x		x	
88194831	SAOUHSC_01084	IsdD	hypothetical protein SAOUHSC_01084	41 kDa	unb	2.50	Y				x		x
88194832	SAOUHSC_01085	IsdE	hypothetical protein SAOUHSC_01085	32 kDa	zyt	8.87	N				x		x
88195556	SAOUHSC_01858		hypothetical protein SAOUHSC_01858	22 kDa	zyt	9.98	N	x	x	x		x	
88195571	SAOUHSC_01874		hypothetical protein SAOUHSC_01874	11 kDa	unb	2.50	N		x	x	x	x	x
88196199	SAOUHSC_02554	FhuD2	hypothetical protein SAOUHSC_02554	34 kDa	unb	3.33	Y		x	x		x	x
88196339	SAOUHSC_02699		hypothetical protein SAOUHSC_02699	29 kDa	unb	3.33	Y		x	x	x	x	x
88196600	SAOUHSC_02980		hypothetical protein SAOUHSC_02980	21 kDa	unb	2.50	N			x	x	x	x
88196194	SAOUHSC_02549	ModA	molybdenum ABC transporter, periplasmic molybdate-binding protein	29 kDa	unb	3.33	Y			x	x	x	x
88196188	SAOUHSC_02542	MoeA	molybdopterin biosynthesis protein moeA, putative	45 kDa	zyt	8.87	N			x		x	
88196190	SAOUHSC_02544	MoaB	molybdopterin precursor biosynthesis moaB, putative	19 kDa	zyt	8.87	N					x	
88195812	SAOUHSC_02132	NadE	NAD ⁺ synthetase	31 kDa	zyt	8.87	N			x		x	
88194828	SAOUHSC_01079	IsdB	neurofilament protein	72 kDa	zw	10.00	#NV				x		x
88194684	SAOUHSC_00927	OppA	oligopeptide ABC transporter, substrate-binding protein, putative	62 kDa	zw	9.18	Y		x				
88196403	SAOUHSC_02767	Opp-1A,Opp1A	peptide ABC transporter, peptide-binding protein, putative	60 kDa	zw	9.18	Y				x		x
88194781	SAOUHSC_01028	PtsH	phosphocarrier protein hpr, putative	9 kDa	zyt	10.00	N	x		x	x	x	x
88194341	SAOUHSC_00562	ThiD	phosphomethylpyrimidine kinase	30 kDa	unb	2.50	#NV	x	x				
88195475	SAOUHSC_01774	HemC	porphobilinogen deaminase	34 kDa	zyt	8.87	N			x		x	
88195473	SAOUHSC_01772	HemB	porphobilinogen synthase	37 kDa	zyt	8.87	N			x		x	
88195976	SAOUHSC_02310	KdpC	potassium-transporting ATPase, C subunit	21 kDa	unb	3.33	Y				x		x
88193967	SAOUHSC_00155	PtsG,GlcA	PTS system, glucose-spezifisch component	72 kDa	zm	10.00	#NV			x		x	

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88195582	SAOUHSC_01886	RibH	riboflavin synthase, beta subunit	16 kDa	zyt	8.87	N					x	
88194268	SAOUHSC_00483		S1 RNA binding domain protein	15 kDa	zyt	9.65	N					x	
zell. Prozesse (9)													
88194892	SAOUHSC_01150	FtsZ	cell division protein FtsZ	41 kDa	zyt	8.87	N	x		x		x	
88194891	SAOUHSC_01149	FtsA	cell division protein, putative	53 kDa	zyt	8.87	N		x				
88194886	SAOUHSC_01144	FtsL	hypothetical protein SAOUHSC_01144	15 kDa	zyt	8.87	N	x	x	x	x	x	x
88194898	SAOUHSC_01158		hypothetical protein SAOUHSC_01158	24 kDa	zyt	8.87	N		x				
88195179	SAOUHSC_01462		hypothetical protein SAOUHSC_01462	13 kDa	zyt	8.87	N	x	x	x	x	x	x
88195555	SAOUHSC_01857		hypothetical protein SAOUHSC_01857	145 kDa	ez	7.62	N			x		x	
88195846	SAOUHSC_02169	Chs,Chp	hypothetical protein SAOUHSC_02169	17 kDa	unb	3.33	Y		x		x		x
88194036	SAOUHSC_00229	ScdA	ScdA protein, putative signal recognition particle-docking protein	25 kDa	zyt	8.87	N			x		x	
88194942	SAOUHSC_01205	FtsY	FtsY	47 kDa	zyt	8.87	N					x	x
Energiemetabolismus (101)													
88195143	SAOUHSC_01418	SucA,OdhA	2-oxoglutarate dehydrogenase, E1 component	105 kDa	zyt	9.98	N			x		x	
88195142	SAOUHSC_01416	SucB,OdhB	2-oxoglutarate dehydrogenase, E2 component, dihydrolipoamide succinyltransferase	47 kDa	zyt	9.65	N			x		x	
88195324	SAOUHSC_01613	BfmBAA	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit, putative	36 kDa	unb	2.50	N	x		x		x	
88195323	SAOUHSC_01612	BfmBAB	2-oxoisovalerate dehydrogenase, E1 component, beta subunit, putative	36 kDa	zyt	8.87	N	x		x		x	
88193901	SAOUHSC_00086	ButA	3-ketoacyl-acyl carrier protein reductase, putative	27 kDa	zyt	9.65	N			x		x	x
88195507	SAOUHSC_01807	PfkA	6-phosphofructokinase, putative	33 kDa	zyt	8.87	N	x		x		x	
88195316	SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase, decarboxylating	52 kDa	zyt	8.87	N	x	x	x	x	x	x
88195520	SAOUHSC_01820	AckA	acetate kinase	44 kDa	zyt	9.98	N	x	x	x		x	
88195075	SAOUHSC_01347	CitB,AcnA	aconitate hydratase 1	99 kDa	zyt	9.98	N	x		x	x	x	

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88193983	SAOUHSC_00173	AcpD	acyl carrier phosphodiesterase	23 kDa	zyt	8.87	N	x		x		x	
88195518	SAOUHSC_01818	Ald1	alanine dehydrogenase	40 kDa	zyt	9.98	#NV			x		x	
88195172	SAOUHSC_01452	Ald2,Ald	alanine dehydrogenase	40 kDa	zyt	9.98	N					x	
88194378	SAOUHSC_00608	Adh,Adh1,AdhA	alcohol dehydrogenase I, putative	36 kDa	zyt	9.98	N			x		x	
88195822	SAOUHSC_02142	AldH,AldA2	aldehyde dehydrogenase, putative	52 kDa	zyt	9.98	#NV			x		x	
88193945	SAOUHSC_00132	AldA	aldehyde dehydrogenase, putative	54 kDa	zyt	9.65	N					x	
88196069	SAOUHSC_02409	RocF,Arg	arginase	33 kDa	zyt	8.87	N					x	
88196590	SAOUHSC_02969	ArcA	arginine deiminase	47 kDa	zyt	8.87	N			x		x	
88196009	SAOUHSC_02345	AtpA	ATP synthase F1, alpha subunit	55 kDa	zyt	8.87	N	x		x		x	
88196007	SAOUHSC_02341	AtpD	ATP synthase F1, beta subunit	51 kDa	zyt	8.87	N	x		x		x	
88194872	SAOUHSC_01129	ArcC	carbamate kinase	34 kDa	zyt	8.87	N			x		x	
88196587	SAOUHSC_02965		carbamate kinase	34 kDa	zyt	8.87	N			x		x	
88194665	SAOUHSC_00908	Cdr	coenzyme A disulfide reductase, putative	49 kDa	zyt	9.98	N	x		x		x	x
88195564	SAOUHSC_01867	Dat	D-amino acid aminotransferase delta-1-pyrroline-5-carboxylate dehydrogenase, putative	32 kDa	zyt	8.87	N	x		x		x	
88196500	SAOUHSC_02869	RocA		57 kDa	zyt	9.98	#NV			x		x	x
88196042	SAOUHSC_02379	DeoC2	deoxyribose-phosphate aldolase	23 kDa	zyt	9.98	#NV	x		x		x	x
88194795	SAOUHSC_01043	PdhD,LpdA	dihydrolipoamide dehydrogenase	49 kDa	zyt	9.98	N	x	x	x	x	x	x
88195325	SAOUHSC_01614	BfmBC	dihydrolipoamide dehydrogenase dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase complex E2, putative	51 kDa	zyt	9.65	N					x	
88194794	SAOUHSC_01042	PdhC	D-isomer spezific 2-hydroxyacid dehydrogenase, NAD binding domain protein	46 kDa	zyt	9.98	N	x		x		x	
88194623	SAOUHSC_00866			32 kDa	zyt	9.65	N			x			
88196464	SAOUHSC_02830	Ddh	D-lactate dehydrogenase, putative	35 kDa	zyt	9.98	N	x		x	x	x	x
88194559	SAOUHSC_00799	Eno	enolase	47 kDa	zyt	9.98	N	x	x	x		x	x
88194704	SAOUHSC_00947	FabI	enoyl-(acyl-carrier-protein) reductase	28 kDa	zyt	8.87	N	x					
88193997	SAOUHSC_00187	ÜflB	formate acetyltransferase	85 kDa	zyt	9.98	N			x		x	

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88193954	SAOUHSC_00142	Fdh	formate dehydrogenase, NAD-dependent, putative	38 kDa	zyt	9.98	N						x
88196252	SAOUHSC_02610	HutG	formiminoglutamase	35 kDa	zyt	8.87	N					x	
88194472	SAOUHSC_00707	FruB	fructose 1-phosphate kinase, putative	33 kDa	unb	2.50	N			x		x	
88196553	SAOUHSC_02926		fructose-bisphosphate aldolase class-I, putative	33 kDa	unb	2.50	N	x	x	x	x	x	x
88195674	SAOUHSC_01983	FumC,CitG	fumarate hydratase, class II	51 kDa	zyt	9.98	N			x		x	
88194014	SAOUHSC_00204		Globin domain protein	43 kDa	zyt	8.87	#NV			x			
88195354	SAOUHSC_01646	GlcK,Glk,GlkA	glucokinase, putative	35 kDa	zyt	9.98	N	x		x		x	
88195310	SAOUHSC_01599	Zwf	glucose-6-phosphate 1-dehydrogenase	57 kDa	zyt	8.87	N	x	x	x	x	x	
88194657	SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase	50 kDa	zyt	9.98	N	x	x	x	x	x	x
88194555	SAOUHSC_00795	Gap1,Gap	glyceraldehyde-3-phosphate dehydrogenase, type I	36 kDa	zyt	9.98	N	x	x	x	x	x	x
88195494	SAOUHSC_01794	GapB,Gap2	glyceraldehyde-3-phosphate dehydrogenase, type I	37 kDa	zyt	9.98	Y			x		x	
88195009	SAOUHSC_01276	GlpK	glycerol kinase	56 kDa	unb	2.50	N	x					
88194594	SAOUHSC_00836	GcvH	glycine cleavage system H protein	14 kDa	zyt	8.87	N	x	x	x	x	x	x
88195342	SAOUHSC_01633		glycine cleavage system P-protein subunit I, putative	50 kDa	zyt	8.87	N			x		x	
88195341	SAOUHSC_01632		glycine cleavage system P-protein subunit II, putative	55 kDa	zyt	8.87	N					x	
88195343	SAOUHSC_01634	GcvT	glycine cleavage system T protein	40 kDa	zyt	9.98	N					x	
88194312	SAOUHSC_00532	Kbl	hypothetical protein SAOUHSC_00532	43 kDa	zyt	8.87	N		x	x		x	
88194332	SAOUHSC_00553		hypothetical protein SAOUHSC_00553	22 kDa	zyt	8.87	N	x	x	x	x	x	x
88194493	SAOUHSC_00728		hypothetical protein SAOUHSC_00728	74 kDa	zm	9.99	Y	x	x	x	x	x	x
88194635	SAOUHSC_00878		hypothetical protein SAOUHSC_00878	44 kDa	zyt	8.87	N					x	
88194654	SAOUHSC_00897	GlpQ	hypothetical protein SAOUHSC_00897	35 kDa	unb	4.86	#NV			x	x	x	x
88194760	SAOUHSC_01005		hypothetical protein SAOUHSC_01005	11 kDa	unb	3.33	#NV	x	x	x	x	x	x
88195010	SAOUHSC_01278	GlpD	hypothetical protein SAOUHSC_01278	62 kDa	zyt	9.98	N			x			
88195141	SAOUHSC_01415		hypothetical protein SAOUHSC_01415	30 kDa	zyt	8.87	N	x		x		x	
88195558	SAOUHSC_01860		hypothetical protein SAOUHSC_01860	12 kDa	zyt	8.87	N	x	x	x	x	x	x

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88195596	SAOUHSC_01901		hypothetical protein SAOUHSC_01901	26 kDa	unb	2.50	N	x		x	x	x	x
88195678	SAOUHSC_01987		hypothetical protein SAOUHSC_01987	22 kDa	zyt	8.87	#NV	x		x	x	x	x
88195820	SAOUHSC_02140	PpaC	hypothetical protein SAOUHSC_02140	34 kDa	zyt	8.87	N	x	x	x		x	
88195823	SAOUHSC_02143		hypothetical protein SAOUHSC_02143	39 kDa	zyt	8.87	N	x	x	x	x	x	x
88195830	SAOUHSC_02150		hypothetical protein SAOUHSC_02150	22 kDa	unb	2.50	N	x	x	x	x	x	x
88196029	SAOUHSC_02366	FbaA,Fba	hypothetical protein SAOUHSC_02366	31 kDa	zyt	8.87	N	x	x	x	x	x	x
88196050	SAOUHSC_02387		hypothetical protein SAOUHSC_02387	24 kDa	unb	2.50	N					x	
88196098	SAOUHSC_02445		hypothetical protein SAOUHSC_02445	37 kDa	zyt	8.87	N			x			
88196099	SAOUHSC_02447		hypothetical protein SAOUHSC_02447	36 kDa	zyt	8.87	N					x	x
88196100	SAOUHSC_02448		hypothetical protein SAOUHSC_02448	33 kDa	unb	2.50	Y				x	x	x
88196112	SAOUHSC_02460		hypothetical protein SAOUHSC_02460	32 kDa	zyt	8.87	#NV				x		
88196246	SAOUHSC_02604		hypothetical protein SAOUHSC_02604	32 kDa	zyt	9.98	N					x	
88196428	SAOUHSC_02793		hypothetical protein SAOUHSC_02793	68 kDa	zyt	8.87	N					x	
88196528	SAOUHSC_02900		hypothetical protein SAOUHSC_02900	31 kDa	zyt	8.87	N	x		x	x	x	x
88196248	SAOUHSC_02606	HutI	imidazolonepropionase	45 kDa	zyt	8.87	N					x	
88196549	SAOUHSC_02922	Ldh2,Ldh	L-lactate dehydrogenase	34 kDa	zyt	9.65	N	x		x		x	x
88194016	SAOUHSC_00206	Ldh1,LctE	L-lactate dehydrogenase	29 kDa	zyt	9.98	#NV	x		x		x	
88196554	SAOUHSC_02927	Mqo2	malate:quinone-oxidoreductase mannitol-1-phosphate 5-dehydrogenase, putative	56 kDa	unb	4.05	N			x		x	
88196064	SAOUHSC_02403	MtlD		41 kDa	zyt	8.87	N	x		x		x	
88195408	SAOUHSC_01702	Pfs,MtnN	MTA/SAH nucleosidase	25 kDa	zyt	8.87	N					x	
88194475	SAOUHSC_00710	NagA	N-acetylglucosamine-6-phosphate deacetylase	43 kDa	zyt	8.87	#NV			x		x	
88195510	SAOUHSC_01810		NADP-dependent malic enzyme, putative	44 kDa	zm	7.63	N	x	x	x		x	
88196320	SAOUHSC_02680	NarH	nitrate reductase, beta subunit	55 kDa	zyt	9.98	N			x			
88194648	SAOUHSC_00891		peptidyl-prolyl cis-trans isomerase, cyclophilin-type, putative	22 kDa	zyt	9.98	N	x		x		x	
88194349	SAOUHSC_00574	Pta	phosphate acetyltransferase	35 kDa	zyt	8.87	N	x	x	x	x	x	x

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88195605	SAOUHSC_01910	PckA	phosphoenolpyruvate carboxykinase (ATP)	59 kDa	unb	2.50	N			x		x	x
88194782	SAOUHSC_01029	PtsI	phosphoenolpyruvate-protein phosphotransferase	63 kDa	zyt	10.00	N	x	x	x		x	
88196066	SAOUHSC_02405	GlmM(femD),GlmM	phosphoglucosamine mutase	49 kDa	zyt	8.87	N	x		x		x	
88194556	SAOUHSC_00796	Pgk	phosphoglycerate kinase, putative	43 kDa	zyt	9.91	N	x		x		x	x
88194558	SAOUHSC_00798	Pgm,GpmI	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	56 kDa	zyt	9.98	N	x		x		x	
88196343	SAOUHSC_02703	GpmA	phosphoglycerate mutase, putative	27 kDa	unb	2.50	N			x	x	x	x
88194813	SAOUHSC_01064	PycA,Pyc	pyruvate carboxylase	129 kDa	zyt	8.87	N			x		x	
88194792	SAOUHSC_01040	PdhA	pyruvate dehydrogenase complex, E1 component, alpha subunit, putative	41 kDa	zyt	8.87	N	x	x	x	x	x	
88194793	SAOUHSC_01041	PhdB,PdhB	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	35 kDa	zyt	8.87	N	x	x	x	x	x	
88195506	SAOUHSC_01806	PykA,Pyk	pyruvate kinase	63 kDa	zyt	8.87	N	x		x		x	
88194758	SAOUHSC_01002	QoxA	quinol oxidase AA3, subunit II, putative	42 kDa	zm	10.00	Y		x		x	x	x
88195604	SAOUHSC_01909	MetK	S-adenosylmethionine synthetase	44 kDa	zyt	9.98	N	x					
88194850	SAOUHSC_01104	SdhA	succinate dehydrogenase, flavoprotein chain TC0881, putative	66 kDa	zm	7.84	N					x	
88194954	SAOUHSC_01218	SucD	succinyl-CoA synthetase, alpha subunit, putative	32 kDa	zyt	8.87	N	x		x		x	
88194953	SAOUHSC_01216	SucC	succinyl-CoA synthetase, beta subunit, putative	42 kDa	zyt	8.87	N	x	x	x		x	
88195066	SAOUHSC_01337	Tkt	transketolase	68 kDa	unb	2.50	N	x	x	x	x	x	
88194557	SAOUHSC_00797	TpiA,Tpi	triosephosphate isomerase	27 kDa	unb	2.50	N	x	x	x	x	x	x
88196249	SAOUHSC_02607	HutU	urocanate hydratase	61 kDa	zyt	8.87	N			x		x	x
Proteinbiosynthese (61)													
88195210	SAOUHSC_01493	RpsA	30S ribosomal protein S1, putative	43 kDa	zyt	9.98	N	x	x	x		x	
88196150	SAOUHSC_02500	RplE	50S ribosomal protein L5, putative	20 kDa	zyt	8.87	#NV	x	x	x	x	x	x
88194381	SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	62 kDa	zyt	9.98	N	x	x	x	x	x	x
88195188	SAOUHSC_01471	AsnS	asparaginyl-tRNA synthetase, putative	49 kDa	zyt	10.00	N			x		x	

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88195441	SAOUHSC_01737	AspS	aspartyl-tRNA synthetase	67 kDa	zyt	10.00	#NV	x		x		x	
88195444	SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr) deacylase	17 kDa	unb	2.50	N		x		x		x
88194290	SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	56 kDa	zyt	9.65	N	x	x	x	x	x	x
88195799	SAOUHSC_02117	GatA	glutamyl-tRNA(Gln) amidotransferase, A subunit	53 kDa	zyt	8.87	N	x		x		x	
88195798	SAOUHSC_02116	GatB	glutamyl-tRNA(Gln) amidotransferase, B subunit	54 kDa	zyt	8.87	#NV	x		x		x	
88195800	SAOUHSC_02118		glutamyl-tRNA(Gln) amidotransferase, C subunit	11 kDa	zyt	8.87	N		x				
88195373	SAOUHSC_01666	GlyS	glycyl-tRNA synthetase	54 kDa	zyt	10.00	N	x	x	x		x	
88194708	SAOUHSC_00951		hypothetical protein SAOUHSC_00951	19 kDa	zyt	8.87	N	x		x		x	
88196138	SAOUHSC_02487	RpsM	hypothetical protein SAOUHSC_02487	14 kDa	zyt	8.87	N	x	x	x		x	
88196161	SAOUHSC_02511	RplD	hypothetical protein SAOUHSC_02511	22 kDa	unb	2.50	N	x	x	x		x	
88194899	SAOUHSC_01159	IleS	isoleucyl-tRNA synthetase	105 kDa	zyt	9.98	N			x		x	
88195572	SAOUHSC_01875	LeuS	leucyl-tRNA synthetase	92 kDa	zyt	9.65	N			x		x	
88194278	SAOUHSC_00493	LysS	lysyl-tRNA synthetase	57 kDa	zyt	10.00	#NV	x					
88194248	SAOUHSC_00461	MetS, MetG	methionyl-tRNA synthetase, putative	75 kDa	zyt	9.98	#NV			x		x	
88196022	SAOUHSC_02359	PrfA	peptide chain release factor 1	40 kDa	zyt	9.98	N	x		x		x	
88194839	SAOUHSC_01092	PheS	phenylalanyl-tRNA synthetase, alpha subunit	40 kDa	zyt	10.00	N			x		x	
88194840	SAOUHSC_01093	PheT	phenylalanyl-tRNA synthetase, beta subunit	89 kDa	zyt	9.98	N	x		x		x	
88194973	SAOUHSC_01240	proS	prolyl-tRNA synthetase	64 kDa	zyt	10.00	N	x					
88194261	SAOUHSC_00474	RplY	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	24 kDa	zyt	8.87	#NV	x	x	x	x	x	x
88194300	SAOUHSC_00519	RplA	ribosomal protein L1	25 kDa	zyt	8.87	N	x	x	x		x	
88194301	SAOUHSC_00520	RplJ	ribosomal protein L10	18 kDa	zyt	8.87	N	x		x		x	
88194299	SAOUHSC_00518	RplK	ribosomal protein L11	15 kDa	zyt	8.87	N	x		x	x	x	x
88196130	SAOUHSC_02478	RplM	ribosomal protein L13	16 kDa	unb	2.50	N	x	x	x		x	
88196143	SAOUHSC_02492	RplO	ribosomal protein L15	16 kDa	unb	2.50	N	x	x	x		x	
88196135	SAOUHSC_02484	RplQ	ribosomal protein L17	14 kDa	zyt	8.87	N	x		x		x	x

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88196146	SAOUHSC_02495	RplR	ribosomal protein L18	13 kDa	zyt	8.87	N	x	x	x		x	x
88196159	SAOUHSC_02509	RplB	ribosomal protein L2	30 kDa	zyt	8.87	N	x		x		x	
88195485	SAOUHSC_01784	RplT	ribosomal protein L20	14 kDa	zyt	8.87	#NV	x		x		x	
88195458	SAOUHSC_01757	RplU	ribosomal protein L21	11 kDa	unb	2.50	N	x	x	x		x	
88196157	SAOUHSC_02507	RplV	ribosomal protein L22	13 kDa	zyt	8.87	Y	x	x	x		x	
88195456	SAOUHSC_01755	RpmA	ribosomal protein L27	10 kDa	unb	2.50	N	x		x		x	
88196154	SAOUHSC_02504	RpmC	ribosomal protein L29	8 kDa	zyt	8.87	N		x	x		x	
88196144	SAOUHSC_02493	RpmD	ribosomal protein L30	7 kDa	unb	2.50	N	x	x	x	x	x	x
88196024	SAOUHSC_02361	RpmE	ribosomal protein L31	10 kDa	unb	2.50	N	x	x	x	x	x	x
88196147	SAOUHSC_02496	RplF	ribosomal protein L6, putative	20 kDa	zyt	8.87	N	x			x	x	x
88194302	SAOUHSC_00521	RplL	ribosomal protein L7/L12	13 kDa	zyt	8.87	N	x		x	x	x	x
88193838	SAOUHSC_00017	RplI	ribosomal protein L9	17 kDa	zyt	9.65	N	x	x		x		x
88196137	SAOUHSC_02486	RpsK	ribosomal protein S11, putative	14 kDa	unb	2.50	N	x		x		x	
88194945	SAOUHSC_01208	RpsP	ribosomal protein S16	10 kDa	unb	2.50	Y	x		x		x	
88194965	SAOUHSC_01232	RpsB	ribosomal protein S2	28 kDa	zyt	8.87	#NV	x	x	x		x	
88195529	SAOUHSC_01829	RpsD	ribosomal protein S4	23 kDa	zyt	8.87	N	x					
88196145	SAOUHSC_02494	RpsE	ribosomal protein S5	18 kDa	zyt	8.87	#NV	x	x	x		x	
88194147	SAOUHSC_00348	RpsF	ribosomal protein S6	12 kDa	zyt	9.98	#NV	x	x	x	x	x	x
88194308	SAOUHSC_00528	RpsG	ribosomal protein S7	18 kDa	zyt	8.87	N	x	x	x		x	
88196148	SAOUHSC_02498	RpsH	ribosomal protein S8, putative	15 kDa	zyt	8.87	N		x	x		x	
88196129	SAOUHSC_02477	RpsI	ribosomal protein S9, putative	15 kDa	unb	2.50	#NV	x	x	x		x	
88194969	SAOUHSC_01236	Rrf,Frr	ribosome recycling factor	20 kDa	zyt	9.98	N	x	x	x	x	x	x
88193832	SAOUHSC_00009	SerS	seryl-tRNA synthetase	49 kDa	zyt	10.00	N	x		x		x	x
88195489	SAOUHSC_01788	ThrS	threonyl-tRNA synthetase	74 kDa	zyt	10.00	N			x		x	
88194309	SAOUHSC_00529	FusA,Fus	translation elongation factor G	77 kDa	zyt	9.98	N	x	x	x		x	
88195335	SAOUHSC_01625	Efp	translation elongation factor P	21 kDa	zyt	9.98	N	x		x		x	

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88194967	SAOUHSC_01234	Tsf	translation elongation factor Ts	32 kDa	zyt	9.98	#NV	x	x	x	x	x	x
88194310	SAOUHSC_00530	Tuf	translation elongation factor Tu	43 kDa	zyt	9.98	N	x	x	x	x	x	x
88195487	SAOUHSC_01786	InfC	translation initiation factor IF-3	20 kDa	zyt	9.98	#NV						x
88194690	SAOUHSC_00933	TrpS	tryptophanyl-tRNA synthetase	37 kDa	zyt	9.98	N			x	x	x	x
88195539	SAOUHSC_01839	TyrS	tyrosyl-tRNA synthetase	48 kDa	zyt	9.98	N	x					
88195468	SAOUHSC_01767	ValS	valyl-tRNA synthetase	102 kDa	zyt	9.98	N			x		x	
Proteinmetabolismus (38)													
88194678	SAOUHSC_00921	FabF,Fab	3-oxoacyl- synthase, putative	44 kDa	zyt	9.98	N	x		x		x	x
88194937	SAOUHSC_01199	FabG	3-oxoacyl-(acyl-carrier-protein) reductase, putative	26 kDa	zyt	9.98	N	x		x		x	x
88194005	SAOUHSC_00195	FadA	acetyl-CoA acetyltransferase, putative	42 kDa	zyt	9.98	N					x	
88195334	SAOUHSC_01624	AccB	acetyl-CoA carboxylase, biotin carrier protein	17 kDa	zyt	8.87	N			x		x	
88195333	SAOUHSC_01623	AccC	acetyl-CoA carboxylase, biotin carboxylase	50 kDa	zyt	8.87	N	x		x		x	
88194939	SAOUHSC_01201	HmrB,AcpP	acyl carrier protein	9 kDa	zyt	8.87	#NV	x	x	x	x	x	x
88195479	SAOUHSC_01778	ClpX	ATP-dependent Clp protease, ATP-binding subunit ClpX	46 kDa	zyt	9.98	N	x					
88196002	SAOUHSC_02336	FabZ	beta-hydroxyacyl-ACP dehydratase, putative	16 kDa	zyt	8.87	N	x		x		x	
88195390	SAOUHSC_01684	GrpE	co-chaperone GrpE	24 kDa	zyt	8.87	N	x	x	x	x	x	x
88195388	SAOUHSC_01682	DnaJ	DnaJ protein	42 kDa	zyt	9.98	N	x		x		x	
88195389	SAOUHSC_01683	DnaK	DnaK protein, putative	66 kDa	zyt	9.98	N	x	x	x	x	x	x
88196491	SAOUHSC_02860	MvaS	HMG-CoA synthase, putative	43 kDa	zyt	8.87	N	x	x	x	x	x	x
88194006	SAOUHSC_00196	FadB	hypothetical protein SAOUHSC_00196	85 kDa	unb	2.50	N					x	
88194007	SAOUHSC_00197	FadD	hypothetical protein SAOUHSC_00197	45 kDa	zyt	8.87	N					x	
88194271	SAOUHSC_00486	FtsH	hypothetical protein SAOUHSC_00486	78 kDa	zm	10.00	Y	x		x		x	
88194272	SAOUHSC_00487		hypothetical protein SAOUHSC_00487	32 kDa	unb	2.50	N	x		x		x	
88194313	SAOUHSC_00533		hypothetical protein SAOUHSC_00533	32 kDa	unb	2.50	N	x	x	x	x	x	x

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88194677	SAOUHSC_00920	FabH	hypothetical protein SAOUHSC_00920	34 kDa	unb	2.50	#NV	x		x		x	
88194972	SAOUHSC_01239		hypothetical protein SAOUHSC_01239	44 kDa	zm	9.99	N		x		x		x
88194988	SAOUHSC_01255		hypothetical protein SAOUHSC_01255	49 kDa	zyt	8.87	N						x
88194989	SAOUHSC_01256		hypothetical protein SAOUHSC_01256	50 kDa	unb	2.50	N			x		x	x
88195092	SAOUHSC_01365		hypothetical protein SAOUHSC_01365	38 kDa	zyt	8.87	N	x		x		x	
88195110	SAOUHSC_01383		hypothetical protein SAOUHSC_01383	69 kDa	zyt	9.98	N			x	x	x	x
88195151	SAOUHSC_01427	CtpA	hypothetical protein SAOUHSC_01427	55 kDa	unb	2.50	N				x		x
88195516	SAOUHSC_01816		hypothetical protein SAOUHSC_01816	40 kDa	zyt	8.87	N					x	x
88195559	SAOUHSC_01861		hypothetical protein SAOUHSC_01861	40 kDa	zyt	8.87	N			x		x	
88195565	SAOUHSC_01868		hypothetical protein SAOUHSC_01868	53 kDa	zyt	8.87	N	x	x	x		x	
88196609	SAOUHSC_02990		hypothetical protein SAOUHSC_02990 malonyl CoA-acyl carrier protein transacylase	228 kDa	zw	10.00	N			x		x	
88194936	SAOUHSC_01198	FabD	hypothetical protein SAOUHSC_01198	34 kDa	zyt	8.87	N	x		x		x	
88195784	SAOUHSC_02102	Map	methionine aminopeptidase, type I	28 kDa	zyt	8.87	N	x	x	x	x	x	x
88194694	SAOUHSC_00937	PepF,PepB	oligoendopeptidase F	70 kDa	zyt	9.98	N	x	x	x	x	x	x
88194521	SAOUHSC_00757	PepT	peptidase T, putative	46 kDa	zyt	9.98	N			x		x	
88194790	SAOUHSC_01038	Def	polypeptide deformylase	21 kDa	zyt	8.87	#NV	x	x	x	x	x	x
88194636	SAOUHSC_00879	PepA,AmpA	probable zytosol aminopeptidase	54 kDa	unb	2.50	N			x		x	
88195336	SAOUHSC_01626		proline dipeptidase, putative	39 kDa	zyt	8.87	N	x		x		x	
88195663	SAOUHSC_01972	PrsA	protein export protein PrsA, putative	36 kDa	unb	3.33	Y		x	x	x	x	x
88194660	SAOUHSC_00903	SpsB	Signal peptidase IB, putative	18 kDa	unb	4.05	N					x	x
AS-Biosynthese (14)													
88195327	SAOUHSC_01617	ArgR,AhrC	arginine repressor branched-chain amino acid	17 kDa	zyt	8.87	N			x		x	
88194316	SAOUHSC_00536	IlvE	aminotransferase glutamate dehydrogenase, NAD-spezifisch, putative	40 kDa	zyt	8.87	N	x		x	x	x	x
88194652	SAOUHSC_00895	GudB	glutamate dehydrogenase, NAD-spezifisch, putative	46 kDa	zyt	9.98	N			x		x	
88195018	SAOUHSC_01287	GlnA	glutamine synthetase, type I	51 kDa	zyt	9.98	N	x	x	x	x	x	x

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88194273	SAOUHSC_00488	CysK	hypothetical protein SAOUHSC_00488	33 kDa	zyt	8.87	N	x	x	x		x	x
88195550	SAOUHSC_01852		hypothetical protein SAOUHSC_01852	41 kDa	zyt	8.87	#NV	x		x		x	
88195838	SAOUHSC_02158		hypothetical protein SAOUHSC_02158	48 kDa	unb	2.50	N			x			
88195928	SAOUHSC_02257	SdrH	hypothetical protein SAOUHSC_02257	47 kDa	zw	9.18	Y		x		x		x
88194651	SAOUHSC_00894		ornithine aminotransferase, putative	43 kDa	zyt	8.87	N			x		x	
88194871	SAOUHSC_01128	Otc,ArgF	ornithine carbamoyltransferase	38 kDa	zyt	9.98	N			x		x	
88196589	SAOUHSC_02968	ArcB	ornithine carbamoyltransferase	38 kDa	zyt	9.98	N			x		x	
88195308	SAOUHSC_01597	ProC	pyrroline-5-carboxylate reductase	29 kDa	unb	2.50	N			x		x	
88196017	SAOUHSC_02354	GlyA	serine hydroxymethyltransferase, putative	45 kDa	zyt	9.98	N	x	x	x	x	x	x
88195171	SAOUHSC_01451	TdcB,IlvA	threonine dehydratase	37 kDa	zyt	8.87	N			x		x	
Nukleotidbiosynthese (21)													
88196141	SAOUHSC_02490	Adk	adenylate kinase, putative	24 kDa	zyt	9.98	N	x	x	x	x	x	
88195807	SAOUHSC_02126	PurB	adenylosuccinate lyase	50 kDa	zyt	8.87	N		x	x		x	
88193840	SAOUHSC_00019	PurA	adenylosuccinate synthetase	48 kDa	zyt	8.87	N		x	x		x	
88194909	SAOUHSC_01170	PyrAB,CarB	carbamoyl-phosphate synthase, large subunit	117 kDa	zyt	8.87	N	x					
88196031	SAOUHSC_02368	PyrG,CtrA	CTP synthase	60 kDa	zyt	8.87	N	x	x				
88195213	SAOUHSC_01496	Zmk	zytidylate kinase	21 kDa	zyt	8.87	#NV	x		x		x	
88194907	SAOUHSC_01168	PyrC	dihydroorotase	46 kDa	zyt	8.87	N	x		x		x	
88195544	SAOUHSC_01845	Fhs	formate-tetrahydrofolate ligase, putative	60 kDa	zyt	8.87	#NV	x	x	x		x	x
88194270	SAOUHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	20 kDa	zyt	9.98	N	x			x	x	x
88195202	SAOUHSC_01485	Ndk	nucleoside diphosphate kinase, putative	16 kDa	zyt	9.98	#NV			x		x	
88193914	SAOUHSC_00101	Drm,DeoB	phosphopentomutase	44 kDa	zyt	8.87	N	x	x	x	x	x	x
88194772	SAOUHSC_01018	PurD	phosphoribosylamine-glycine ligase	46 kDa	zyt	8.87	N			x		x	
88194762	SAOUHSC_01008	PurE	phosphoribosylaminoimidazole carboxylase, catalytic subunit	15 kDa	unb	2.50	N			x		x	

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88194769	SAOUHSC_01015	PurM	phosphoribosylformylglycinamidine cyclo- ligase	37 kDa	unb	2.50	N			x		x	
88194766	SAOUHSC_01012	PurQ	phosphoribosylformylglycinamidine synthase I	25 kDa	zyt	8.87	N			x	x	x	x
88194765	SAOUHSC_01011	PurS	phosphoribosylformylglycinamidine synthase, PurS protein	10 kDa	zyt	8.87	N			x	x	x	x
88196043	SAOUHSC_02380	DeoD2	purine nucleoside phosphorylase	26 kDa	unb	2.50	N	x	x	x	x	x	x
88196040	SAOUHSC_02377	Pyn,Pdp	pyrimidine nucleoside phosphorylase, putative	46 kDa	unb	2.50	N					x	
88194508	SAOUHSC_00743	Rir2,NrdF	ribonucleotide-disphosphate reductase beta chain, putative	38 kDa	zyt	8.87	N	x		x		x	
88196016	SAOUHSC_02353	Upp	uracil phosphoribosyltransferase	23 kDa	zyt	8.87	N	x		x		x	x
88194968	SAOUHSC_01235	SmbA,PyrH	uridylate kinase, putative	26 kDa	zyt	8.87	N	x					
Transkription und Replikation (16)													
88193825	SAOUHSC_00002	DnaN	DNA polymerase III, beta subunit	42 kDa	zyt	8.87	N	x		x		x	
88195207	SAOUHSC_01490	Hup,Hu	DNA-binding protein HU, putative	10 kDa	unb	2.50	N	x	x	x	x	x	x
88196136	SAOUHSC_02485	RpoA	DNA-directed RNA polymerase alpha chain, putative	35 kDa	zyt	9.98	N	x		x		x	
88196032	SAOUHSC_02369	RpoE	DNA-directed RNA polymerase, delta subunit, putative	21 kDa	zyt	8.87	N	x	x	x	x	x	
88195365	SAOUHSC_01658		endonuclease IV, putative	33 kDa	zyt	8.87	N			x		x	
88193826	SAOUHSC_00003		hypothetical protein SAOUHSC_00003	9 kDa	zyt	8.87	N	x	x	x			
88194019	SAOUHSC_00211		hypothetical protein SAOUHSC_00211	34 kDa	zyt	8.87	N					x	
88194530	SAOUHSC_00767	YfiA	hypothetical protein SAOUHSC_00767	22 kDa	zyt	8.87	N			x		x	x
88194853	SAOUHSC_01107		hypothetical protein SAOUHSC_01107	21 kDa	zyt	8.87	N	x	x	x		x	
88195483	SAOUHSC_01782		hypothetical protein SAOUHSC_01782	23 kDa	zyt	8.87	N			x		x	
88194984	SAOUHSC_01251	PnpA	polyribonucleotide nucleotidyltransferase, putative	77 kDa	zyt	9.98	N	x		x		x	
88196427	SAOUHSC_02791		pyrophosphohydrolase, putative	15 kDa	unb	2.50	N	x		x		x	
88194995	SAOUHSC_01262	RecA	recombination protein RecA, putative	35 kDa	zyt	8.87	N	x		x			
88195369	SAOUHSC_01662	SigA,RpoD	RNA polymerase sigma factor, putative	42 kDa	zyt	9.98	N					x	

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88195419	SAOUHSC_01714	GreA	transcription elongation factor GreA	18 kDa	zyt	8.87	N	x	x	x	x	x	x
88194976	SAOUHSC_01243	NusA	transcription termination-antitermination factor, putative	44 kDa	zyt	8.87	N	x		x		x	
Unbekannte Funktion (140)													
88195119	SAOUHSC_01392		ABC transporter, ATP-binding protein, putative	60 kDa	zm	9.49	N	x		x		x	
88194218	SAOUHSC_00426		ABC transporter, substrate-binding protein, putative	30 kDa	unb	3.33	Y					x	x
88194136	SAOUHSC_00336	Thl	acetyl-CoA acetyltransferase, putative	42 kDa	zyt	9.98	#NV	x		x		x	
88195775	SAOUHSC_02092	PepS,AmpS	aminopeptidase PepS, putative	47 kDa	zyt	8.87	N	x	x	x	x	x	x
88195965	SAOUHSC_02299	RsbW	anti-sigma B factor, putative	19 kDa	zyt	8.87	N			x		x	
88196008	SAOUHSC_02343	AtpG	ATP synthase F1, gamma subunit	29 kDa	unb	2.50	Y			x		x	
88196493	SAOUHSC_02862	ClpL	ATP-dependent Clp protease, ATP-binding subunit ClpC, putative	78 kDa	zyt	9.98	N			x		x	
88194148	SAOUHSC_00349	Ssb	bacteriophage L54a, single-stranded DNA binding protein	19 kDa	unb	2.50	N	x	x	x		x	
88194292	SAOUHSC_00511	CysS	cysteinyI-tRNA synthetase	54 kDa	zyt	9.98	N			x		x	
88196221	SAOUHSC_02577		D-isomer spezifc 2-hydroxyacid dehydrogenase, NAD binding domain protein	35 kDa	zyt	9.98	N	x		x		x	x
88194305	SAOUHSC_00525	RpoC	DNA directed RNA polymerase beta-prime chain, putative	134 kDa	zyt	9.98	N			x		x	
88195741	SAOUHSC_02057		dUTP pyrophosphatase	19 kDa	zyt	8.87	N	x	x	x	x	x	x
88194286	SAOUHSC_00505	ClpC	endopeptidase, putative	91 kDa	zyt	9.98	N			x		x	
88195685	SAOUHSC_01997	PerR	ferric uptake regulator-like protein, putative	17 kDa	zyt	9.98	#NV	x		x		x	
88195654	SAOUHSC_01961	HemH	ferrochelataase	35 kDa	zyt	9.65	N			x			
88196060	SAOUHSC_02399	GlmS	glucosamine--fructose-6-phosphate aminotransferase, isomerizing	66 kDa	zyt	8.87	N					x	
88194173	SAOUHSC_00375	GuaA	GMP synthase, putative	58 kDa	zyt	8.87	N	x		x		x	x
88194808	SAOUHSC_01058	TypA	GTP-binding protein TypA, putative	69 kDa	zyt	9.98	N	x		x			
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025	83 kDa	zw	10.00	Y			x	x	x	
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025	83 kDa	zw	10.00	Y						

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88193948	SAOUHSC_00135		hypothetical protein SAOUHSC_00135	19 kDa	zyt	8.87	#NV			x		x	
88194032	SAOUHSC_00225		hypothetical protein SAOUHSC_00225	27 kDa	unb	2.50	N	x		x	x	x	x
88194062	SAOUHSC_00256		hypothetical protein SAOUHSC_00256	33 kDa	unb	3.33	Y				x		
88194074	SAOUHSC_00269		hypothetical protein SAOUHSC_00269	20 kDa	unb	2.50	N	x					
88194145	SAOUHSC_00346	YchF	hypothetical protein SAOUHSC_00346	41 kDa	zyt	8.87	#NV	x					
88194155	SAOUHSC_00356		hypothetical protein SAOUHSC_00356	21 kDa	unb	3.33	Y		x	x	x	x	x
88194160	SAOUHSC_00362		hypothetical protein SAOUHSC_00362	24 kDa	unb	3.33	Y		x	x	x		x
88194167	SAOUHSC_00369		hypothetical protein SAOUHSC_00369	36 kDa	zyt	8.87	#NV	x	x	x	x	x	x
88194169	SAOUHSC_00371		hypothetical protein SAOUHSC_00371	15 kDa	zyt	8.87	N			x	x	x	x
88194180	SAOUHSC_00383		hypothetical protein SAOUHSC_00383	26 kDa	unb	6.46	Y		x		x		x
88194187	SAOUHSC_00392		hypothetical protein SAOUHSC_00392	26 kDa	ez	9.98	Y		x				
88194194	SAOUHSC_00399		hypothetical protein SAOUHSC_00399	25 kDa	ez	9.98	Y	x	x	x	x	x	
88194195	SAOUHSC_00400		hypothetical protein SAOUHSC_00400	57 kDa	unb	3.33	Y	x	x	x		x	
88194196	SAOUHSC_00401		hypothetical protein SAOUHSC_00401	11 kDa	unb	3.33	Y		x				
88194234	SAOUHSC_00444		hypothetical protein SAOUHSC_00444	12 kDa	unb	2.50	N	x		x		x	
88194256	SAOUHSC_00469	SpoVG	hypothetical protein SAOUHSC_00469	11 kDa	zyt	8.87	N		x	x	x	x	x
88194281	SAOUHSC_00500		hypothetical protein SAOUHSC_00500	21 kDa	zyt	8.87	N	x					
88194322	SAOUHSC_00542		hypothetical protein SAOUHSC_00542	32 kDa	zyt	8.87	N	x		x			
88194328	SAOUHSC_00549		hypothetical protein SAOUHSC_00549	33 kDa	zyt	8.87	N			x			
88194387	SAOUHSC_00617		hypothetical protein SAOUHSC_00617	19 kDa	unb	3.33	Y	x		x	x	x	x
88194440	SAOUHSC_00675		hypothetical protein SAOUHSC_00675	26 kDa	zyt	8.87	N	x		x		x	
88194451	SAOUHSC_00686		hypothetical protein SAOUHSC_00686	11 kDa	zyt	8.87	N	x	x	x			
88194469	SAOUHSC_00704		hypothetical protein SAOUHSC_00704	17 kDa	unb	3.33	Y		x		x		x
88194519	SAOUHSC_00755		hypothetical protein SAOUHSC_00755	12 kDa	unb	2.50	N	x					
88194596	SAOUHSC_00838	truncated-SA	hypothetical protein SAOUHSC_00838	34 kDa	zyt	8.87	#NV			x			
88194602	SAOUHSC_00844		hypothetical protein SAOUHSC_00844	30 kDa	zm	9.87	Y		x	x	x	x	x

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88194603	SAOUHSC_00845		hypothetical protein SAOUHSC_00845	7 kDa	unb	2.50	N		x		x	x	x
88194622	SAOUHSC_00865		hypothetical protein SAOUHSC_00865	28 kDa	unb	2.50	N	x	x	x	x	x	x
88194634	SAOUHSC_00877		hypothetical protein SAOUHSC_00877	12 kDa	zyt	8.87	N			x			
88194663	SAOUHSC_00906		hypothetical protein SAOUHSC_00906	33 kDa	zyt	8.87	N	x		x		x	
88194666	SAOUHSC_00909		hypothetical protein SAOUHSC_00909	32 kDa	zyt	8.87	N	x					
88194674	SAOUHSC_00917		hypothetical protein SAOUHSC_00917	19 kDa	unb	2.50	N			x			
88194729	SAOUHSC_00972		hypothetical protein SAOUHSC_00972	11 kDa	zyt	8.87	N			x			
88194787	SAOUHSC_01035		hypothetical protein SAOUHSC_01035	63 kDa	zyt	8.87	#NV					x	
88194788	SAOUHSC_01036		hypothetical protein SAOUHSC_01036	9 kDa	zyt	8.87	N		x			x	x
88194802	SAOUHSC_01050		hypothetical protein SAOUHSC_01050	40 kDa	zm	9.99	Y			x			x
88194810	SAOUHSC_01061		hypothetical protein SAOUHSC_01061	19 kDa	unb	2.50	#NV	x		x		x	
88194858	SAOUHSC_01112		hypothetical protein SAOUHSC_01112	15 kDa	unb	3.33	#NV		x		x	x	x
88194877	SAOUHSC_01135		hypothetical protein SAOUHSC_01135	4 kDa	unb	2.50	#NV			x	x	x	x
88194878	SAOUHSC_01136		hypothetical protein SAOUHSC_01136	4 kDa	unb	2.50	N			x		x	
88194880	SAOUHSC_01138		hypothetical protein SAOUHSC_01138	17 kDa	unb	2.50	N		x	x	x	x	x
88194895	SAOUHSC_01154		hypothetical protein SAOUHSC_01154	21 kDa	unb	2.50	N	x	x	x		x	
88194931	SAOUHSC_01192		hypothetical protein SAOUHSC_01192	13 kDa	unb	2.50	#NV			x			
88194932	SAOUHSC_01193		hypothetical protein SAOUHSC_01193	61 kDa	unb	2.50	N	x					
88194985	SAOUHSC_01252		hypothetical protein SAOUHSC_01252	59 kDa	zyt	8.87	N					x	
88195001	SAOUHSC_01268		hypothetical protein SAOUHSC_01268	11 kDa	zyt	8.87	N				x		x
88195053	SAOUHSC_01323		hypothetical protein SAOUHSC_01323	30 kDa	zyt	8.87	N	x		x	x	x	
88195118	SAOUHSC_01391		hypothetical protein SAOUHSC_01391	34 kDa	zyt	8.87	N			x		x	
88195139	SAOUHSC_01413		hypothetical protein SAOUHSC_01413	29 kDa	zyt	8.87	N	x					
88195140	SAOUHSC_01414		hypothetical protein SAOUHSC_01414	13 kDa	unb	2.50	N	x	x	x		x	
88195160	SAOUHSC_01436		hypothetical protein SAOUHSC_01436	16 kDa	zyt	8.87	N	x	x	x	x	x	x
88195162	SAOUHSC_01438		hypothetical protein SAOUHSC_01438	9 kDa	unb	2.50	N		x				

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88195168	SAOUHSC_01447		hypothetical protein SAOUHSC_01447	1030 kDa	zw	9.38	Y	x		x		x	
88195193	SAOUHSC_01476		hypothetical protein SAOUHSC_01476	12 kDa	zyt	8.87	N			x			
88195197	SAOUHSC_01480		hypothetical protein SAOUHSC_01480	43 kDa	zyt	8.87	N	x					
88195315	SAOUHSC_01604		hypothetical protein SAOUHSC_01604	14 kDa	zyt	8.87	N			x		x	
88195321	SAOUHSC_01610		hypothetical protein SAOUHSC_01610	16 kDa	zyt	8.87	N	x	x	x			
88195356	SAOUHSC_01648		hypothetical protein SAOUHSC_01648	17 kDa	unb	2.50	#NV		x				
88195401	SAOUHSC_01695		hypothetical protein SAOUHSC_01695	13 kDa	zyt	8.87	N	x					
88195424	SAOUHSC_01719		hypothetical protein SAOUHSC_01719	12 kDa	zyt	8.87	N						x
88195426	SAOUHSC_01721		hypothetical protein SAOUHSC_01721	10 kDa	unb	2.50	N						x
88195435	SAOUHSC_01730	CsbD	hypothetical protein SAOUHSC_01730	7 kDa	unb	2.50	#NV		x			x	
88195462	SAOUHSC_01761		hypothetical protein SAOUHSC_01761	18 kDa	unb	2.50	#NV		x		x		x
88195514	SAOUHSC_01814		hypothetical protein SAOUHSC_01814	15 kDa	unb	2.50	N			x			x
88195515	SAOUHSC_01815		hypothetical protein SAOUHSC_01815	25 kDa	zyt	8.87	N	x		x	x	x	x
88195519	SAOUHSC_01819		hypothetical protein SAOUHSC_01819	18 kDa	zyt	8.87	N	x		x		x	x
88195566	SAOUHSC_01869		hypothetical protein SAOUHSC_01869	16 kDa	unb	2.50	Y		x			x	
88195602	SAOUHSC_01907		hypothetical protein SAOUHSC_01907	31 kDa	zyt	8.87	N			x	x	x	x
88195613	SAOUHSC_01918		hypothetical protein SAOUHSC_01918	25 kDa	unb	2.50	N		x	x		x	
88195660	SAOUHSC_01968	Hit	hypothetical protein SAOUHSC_01968	16 kDa	unb	2.50	N	x		x			
88195668	SAOUHSC_01977		hypothetical protein SAOUHSC_01977	13 kDa	zyt	8.87	#NV	x	x	x	x		x
88195670	SAOUHSC_01979		hypothetical protein SAOUHSC_01979	18 kDa	zyt	8.87	N	x		x		x	
88195687	SAOUHSC_01999		hypothetical protein SAOUHSC_01999	17 kDa	zyt	8.87	N			x	x	x	x
88195701	SAOUHSC_02013		hypothetical protein SAOUHSC_02013	19 kDa	zyt	8.87	N			x		x	x
88195723	SAOUHSC_02037		hypothetical protein SAOUHSC_02037	15 kDa	zyt	8.87	N						
88195729	SAOUHSC_02044		hypothetical protein SAOUHSC_02044	23 kDa	zyt	8.87	N		x		x		
88195757	SAOUHSC_02073		hypothetical protein SAOUHSC_02073	21 kDa	unb	2.50	N		x			x	x
88195845	SAOUHSC_02167		hypothetical protein SAOUHSC_02167	13 kDa	unb	3.33	Y	x	x	x	x		x

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88195892	SAOUHSC_02218		hypothetical protein SAOUHSC_02218	11 kDa	unb	2.50	N	x	x	x	x	x	x
88196058	SAOUHSC_02396		hypothetical protein SAOUHSC_02396	32 kDa	zyt	8.87	N			x		x	
88196065	SAOUHSC_02404	FmtB	hypothetical protein SAOUHSC_02404	263 kDa	zw	10.00	Y		x	x			
88196067	SAOUHSC_02406		hypothetical protein SAOUHSC_02406	35 kDa	unb	2.50	Y						x
88196081	SAOUHSC_02425		hypothetical protein SAOUHSC_02425	10 kDa	unb	2.50	N			x		x	
88196212	SAOUHSC_02568		hypothetical protein SAOUHSC_02568	13 kDa	zyt	8.87	#NV	x		x			x
88196237	SAOUHSC_02594		hypothetical protein SAOUHSC_02594	24 kDa	zyt	8.87	N	x					
88196330	SAOUHSC_02690		hypothetical protein SAOUHSC_02690	59 kDa	unb	3.33	Y				x		x
88196364	SAOUHSC_02724		hypothetical protein SAOUHSC_02724	26 kDa	unb	2.50	N						x
88196410	SAOUHSC_02774		hypothetical protein SAOUHSC_02774	16 kDa	zyt	8.87	N						x
88196513	SAOUHSC_02885		hypothetical protein SAOUHSC_02885	69 kDa	zm	9.99	N				x		x
88196527	SAOUHSC_02899		hypothetical protein SAOUHSC_02899	38 kDa	zyt	8.87	N					x	
88196540	SAOUHSC_02912		hypothetical protein SAOUHSC_02912	17 kDa	zyt	8.87	N	x		x		x	
88196593	SAOUHSC_02972	IsaB	hypothetical protein SAOUHSC_02972	19 kDa	unb	3.33	Y	x		x	x	x	x
88196640	SAOUHSC_03022		hypothetical protein SAOUHSC_03022	19 kDa	unb	2.50	N			x	x	x	x
88194172	SAOUHSC_00374	GuaB	inosine-5'-monophosphate dehydrogenase	53 kDa	zyt	8.87	N	x		x		x	
88196290	SAOUHSC_02650		lipoprotein, putative nicotinate phosphoribosyltransferase, putative	23 kDa	unb	4.05	Y		x	x	x	x	x
88195813	SAOUHSC_02133		putative	55 kDa	zyt	8.87	N			x		x	
88195317	SAOUHSC_01606		peptidase T, putative	40 kDa	zyt	9.98	N			x		x	
88195728	SAOUHSC_02043		phage head protein, putative	37 kDa	zyt	8.87	N	x	x	x	x	x	
88196598	SAOUHSC_02978		phage infektion protein, putative	109 kDa	zm	9.99	Y		x		x		x
88195722	SAOUHSC_02036		phage structural protein, putative	22 kDa	unb	2.50	N	x	x				
88195710	SAOUHSC_02022		phage tail fiber protein, putative	44 kDa	zyt	8.87	N		x				
88195727	SAOUHSC_02042		phi Mu50B-like protein	11 kDa	unb	2.50	N		x				
88195758	SAOUHSC_02074		phi PVL orf 39-like protein	13 kDa	unb	2.50	Y						x
88195715	SAOUHSC_02028		phiETA ORF57-like protein	67 kDa	unb	2.50	N		x				

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokali- sation ^B	PSort- Score ^B	SP ^B	TSB, expP	pMEM, expP	TSB, f-statP	pMEM, f-statP	TSB, s-statP	pMEM, s-statP
88194561	SAOUHSC_00801	SecG	preprotein translocase, SecG subunit	10 kDa	zm	9.75	N		x		x		x
88194280	SAOUHSC_00499		pyridoxine biosynthesis protein	32 kDa	zyt	8.87	N	x		x		x	
88194307	SAOUHSC_00527	RpsL	ribosomal protein S12	15 kDa	unb	2.50	N			x			
88194304	SAOUHSC_00524	RpoB	RNA polymerase beta chain, putative	128 kDa	zyt	9.98	N	x		x		x	
88195999	SAOUHSC_02333		sceD protein, putative single-strand DNA-binding protein, putative	24 kDa	ez	9.98	#NV	x	x	x	x	x	
88195755	SAOUHSC_02071			19 kDa	unb	2.50	N		x	x	x	x	x
88194333	SAOUHSC_00554		SIS domain protein	18 kDa	unb	2.50	N			x		x	x
88195714	SAOUHSC_02027		SLT orf 129-like protein	14 kDa	unb	2.50	#NV		x		x		x
88195966	SAOUHSC_02300	RsbV	STAS domain, putative transcription antitermination protein,	12 kDa	zyt	8.87	N	x		x		x	x
88194298	SAOUHSC_00517	NusG	putative UDP-N-acetylglucosamine	21 kDa	zyt	8.87	N			x	x	x	
88196079	SAOUHSC_02423		pyrophosphorylase, putative	45 kDa	zyt	8.87	N	x		x		x	

Für gelfreie Analysen wurden je 2 µg des bakteriellen Überstandes der exponentiellen Wachstumsphase, der frühen stationären und der späten stationären Phase in TSB und pMEM verdaut. Die Präparation erfolgte jeweils für drei Bioreplikate. Die Proteine wurden mit mindestens 2 Peptiden identifiziert (Scaffold) und in ihre biologische Kategorien eingeteilt (TigR).

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

^B Die Lokalisation und die Vorhersage eines Signalpeptides erfolgte über P-Sort. ez = extrazellulär, zw = Zellwand, zm = zytoplasmatische Membran, zyt = Zytoplasma, unb = unbekannt, SP = Signalpeptid, N = kein Signalpeptid, Y = Signalpeptid vorhanden, #NV = Vorhersage nicht möglich.

expP = exponentielle Wachstumsphase, f-statP = frühe stationäre Phase, s-statP = späte stationäre Phase.

Tab. 60: Ermittelte Intensitäten zur Quantifizierung für die in Tabelle 59 identifizierten Proteine.

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Intensität [TSB, exp] ^B	Intensität [pMEM, exp] ^B	Intensität [TSB, f-stat] ^B	Intensität [pMEM, f-stat] ^B	Intensität [TSB, s-stat] ^B	Intensität [pMEM, s-stat] ^B
Toxine und Hämolsine (9)									
88194865	SAOUHSC_01121	Hla	alpha-hemolysin precursor		7.38E+06	1.63E+08	2.37E+08	2.06E+08	6.25E+07
88194955	SAOUHSC_01219	LytN	cell wall hydrolase, putative			1.35E+06			
88196641	SAOUHSC_03023	Drp35	Drp35					1.31E+06	
88196348	SAOUHSC_02708	HlgA	gamma-hemolysin component A				6.90E+06	7.79E+06	7.84E+06
88196350	SAOUHSC_02710	HlgB	gamma-hemolysin component B				3.00E+07		2.68E+07
88196349	SAOUHSC_02709	HlgC	gamma-hemolysin component C				2.07E+07	9.05E+06	1.97E+07
88193943	SAOUHSC_00130	IsdI	hypothetical protein SAOUHSC_00130		6.59E+05				1.60E+07
88195915	SAOUHSC_02243		hypothetical protein SAOUHSC_02243				1.39E+06		
88195647	SAOUHSC_01954	LukD	leukotoxin, LukD		1.04E+06		8.01E+05		5.94E+05
Virulenz-/Abwehrmechanismen (24)									
88193871	SAOUHSC_00051	Plc	1-phosphatidylinositol phosphodiesterase precursor, putative		2.74E+06	9.84E+06	6.61E+06	7.26E+06	5.05E+06
88196592	SAOUHSC_02971	Aur	aureolysin, putative		2.12E+07		1.00E+07		1.34E+07
88194572	SAOUHSC_00812	ClfA	clumping factor	1.42E+07	6.07E+07	1.28E+07	1.89E+07	9.57E+06	1.83E+07
88196585	SAOUHSC_02963	ClfB	clumping factor B, putative	6.63E+07	5.83E+07	4.76E+07	1.15E+07	2.54E+07	9.54E+06
88194744	SAOUHSC_00987	SspB	cysteine protease precursor, putative	5.83E+06	3.69E+07	5.19E+06	2.39E+07		1.48E+07
88195217	SAOUHSC_01501	EbpS	elastin binding protein		4.66E+06	5.00E+06	1.28E+06	4.28E+06	1.74E+06
88194575	SAOUHSC_00816	Ssp,Empbp	extracellular matrix and plasma binding protein, putative	6.81E+05	2.47E+06	1.64E+06	8.81E+05	1.48E+06	
88194860	SAOUHSC_01114	Efb	fibrinogen-binding protein		5.08E+06				
88196437	SAOUHSC_02802	FnbB	fibronectin binding protein B, putative	4.17E+05					
88194745	SAOUHSC_00988	SspA	glutamyl endopeptidase precursor, putative	7.31E+06	1.08E+07	6.07E+06	1.19E+07	4.85E+06	1.06E+07
88194063	SAOUHSC_00257		hypothetical protein SAOUHSC_00257					1.89E+05	
88196346	SAOUHSC_02706	Sbi	immunoglobulin G-binding protein Sbi, putative	1.88E+07	1.34E+07	1.46E+07	1.41E+07	5.94E+06	1.41E+07

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Intensität [TSB, expP] ^B	Intensität [pMEM, expP] ^B	Intensität [TSB, f-statP] ^B	Intensität [pMEM, f-statP] ^B	Intensität [TSB, s-statP] ^B	Intensität [pMEM, s-statP] ^B
88193965	SAOUHSC_00153	IpdC	indolepyruvate decarboxylase, putative			8.24E+06		9.39E+06	1.11E+06
88196625	SAOUHSC_03006	Lip	lipase			1.02E+08	1.69E+09	2.04E+08	2.47E+09
88194101	SAOUHSC_00300	Geh	lipase precursor	1.15E+07	2.69E+07	9.81E+07	4.38E+09	2.39E+08	3.57E+09
88196512	SAOUHSC_02883		LysM domain protein	9.78E+05	6.52E+06				
88193885	SAOUHSC_00069		protein A	5.10E+08	1.30E+08	7.02E+08	1.20E+08	4.31E+08	1.20E+08
88194325	SAOUHSC_00545		sdrD protein, putative	6.60E+07	6.60E+07	1.53E+08	2.17E+07	1.12E+08	1.34E+07
88195635	SAOUHSC_01941	SplB	serine protease SplB				3.54E+06		3.66E+06
88195630	SAOUHSC_01935	SplF	serine protease SplF, putative		4.02E+06		2.63E+06		2.41E+06
88195808	SAOUHSC_02127		staphopain thiol proteinase	7.67E+06	7.31E+06	7.60E+06	1.28E+07	5.44E+06	1.65E+07
88195848	SAOUHSC_02171	Sak	staphylokinase precursor, putative		1.26E+07	5.44E+06	7.06E+06	5.74E+06	
88194577	SAOUHSC_00818	Nuc	thermonuclease precursor				5.15E+06	7.16E+05	7.59E+06
88195480	SAOUHSC_01779	Tig	trigger factor	1.84E+08	2.48E+07	1.52E+08	8.21E+06	1.02E+08	6.30E+06
Zellwandbiosynthese und -abbau (15)									
88194219	SAOUHSC_00427		autolysin precursor, putative	2.33E+06	2.21E+07	7.57E+06	7.75E+07	5.83E+06	4.96E+07
88194750	SAOUHSC_00994	Atl	bifunctional autolysin precursor, putative	4.71E+07	7.05E+08	1.84E+08	1.02E+09	1.71E+08	9.81E+08
88195790	SAOUHSC_02108	Ftn	ferritin, putative	4.83E+06	2.79E+06	9.97E+06	1.36E+06	1.36E+07	
88193909	SAOUHSC_00094		hypothetical protein SAOUHSC_00094	8.08E+07	5.53E+07	4.03E+08	1.61E+08	2.94E+08	2.03E+08
88196515	SAOUHSC_02887	IsaA	immunodominant antigen A, putative	4.47E+08	2.79E+09	1.21E+08	1.74E+09	4.94E+07	1.11E+09
88195840	SAOUHSC_02161		MHC class II analog protein				1.22E+06		1.14E+06
88194887	SAOUHSC_01145	PbpA	penicillin-binding protein 1	8.34E+05	1.90E+05	1.20E+06		1.03E+06	
88195184	SAOUHSC_01467	Pbp2	penicillin-binding protein 2		4.95E+06	1.90E+06	2.51E+06	1.78E+06	1.87E+06
88195360	SAOUHSC_01652	PbpF,Pbp3	penicillin-binding protein 3		1.36E+06	1.84E+06	2.06E+06	1.62E+06	2.08E+06
88194055	SAOUHSC_00248	LytM	peptidoglycan hydrolase, putative	1.61E+08	4.11E+09	3.74E+07	5.58E+08	2.05E+07	3.86E+08
88194324	SAOUHSC_00544		sdrC protein, putative	8.57E+06	1.42E+07	4.23E+07	1.12E+07	3.09E+07	8.63E+06
88196215	SAOUHSC_02571	SsaA	secretory antigen precursor, putative	3.86E+08	3.06E+08	3.72E+07	1.35E+08	2.03E+07	6.04E+07

Accession-Nummer	Locus Tag ^A	Protein-name ^A	Beschreibung	Intensität [TSB, expP] ^B	Intensität [pMEM, expP] ^B	Intensität [TSB, f-statP] ^B	Intensität [pMEM, f-statP] ^B	Intensität [TSB, s-statP] ^B	Intensität [pMEM, s-statP] ^B
88194436	SAOUHSC_00671		secretory antigen SsaA-like protein	7.74E+07	8.84E+08	5.12E+07	3.06E+08	5.22E+07	1.71E+08
88194675	SAOUHSC_00918		truncated MHC class II analog protein	7.49E+06	5.05E+07	1.25E+07	1.30E+08	1.88E+07	6.33E+07
88196118	SAOUHSC_02466		truncated MHC class II analog protein		5.55E+08	2.73E+07	1.57E+08	4.93E+07	1.32E+08
Zellumhüllung (19)									
88194626	SAOUHSC_00869	DltA	D-alanine-activating enzyme	1.68E+07		1.58E+07		1.59E+07	
88194628	SAOUHSC_00871	DltC	D-alanyl carrier protein	9.66E+06	1.28E+06				
88194199	SAOUHSC_00405		hypothetical protein SAOUHSC_00405			1.42E+06	1.80E+06	1.41E+06	2.29E+06
88194482	SAOUHSC_00717		hypothetical protein SAOUHSC_00717		4.08E+07	2.03E+06	2.27E+07	2.81E+06	3.75E+07
88194518	SAOUHSC_00754		hypothetical protein SAOUHSC_00754				9.41E+05		
88194829	SAOUHSC_01081	IsdA	hypothetical protein SAOUHSC_01081	1.39E+07	2.14E+07	1.12E+07	4.85E+07	6.19E+06	8.44E+07
88194830	SAOUHSC_01082	IsdC	hypothetical protein SAOUHSC_01082		3.67E+06		1.11E+07		2.22E+07
88195062	SAOUHSC_01332		hypothetical protein SAOUHSC_01332				8.32E+06	1.09E+06	9.37E+06
88195077	SAOUHSC_01349		hypothetical protein SAOUHSC_01349			8.00E+05			
88195443	SAOUHSC_01739	LytH	hypothetical protein SAOUHSC_01739		4.09E+06		2.06E+06		1.96E+06
88195542	SAOUHSC_01843		hypothetical protein SAOUHSC_01843				3.49E+05		
88195590	SAOUHSC_01895		hypothetical protein SAOUHSC_01895		9.10E+06	1.13E+06	5.06E+06	8.81E+05	3.54E+06
88195802	SAOUHSC_02121		hypothetical protein SAOUHSC_02121		8.35E+06	5.08E+06	7.63E+06	4.36E+06	7.64E+06
88196433	SAOUHSC_02798		hypothetical protein SAOUHSC_02798	1.57E+07	7.94E+05	3.78E+07	1.74E+06	2.18E+07	1.23E+06
88196599	SAOUHSC_02979		hypothetical protein SAOUHSC_02979	1.23E+08	3.20E+07	7.05E+07	1.69E+08	5.58E+07	1.40E+08
88196601	SAOUHSC_02982		hypothetical protein SAOUHSC_02982		5.29E+07	4.70E+06	4.59E+07	2.44E+06	4.27E+07
88193889	SAOUHSC_00074	SirA	periplasmic binding protein, putative		6.25E+06		7.32E+06		4.52E+07
88195460	SAOUHSC_01759	MreC	rod shape-determining protein MreC		4.72E+06	4.18E+06	7.66E+06	2.89E+06	5.74E+06
88196468	SAOUHSC_02834	SrtA	sortase, putative				4.50E+05		6.98E+05

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Intensität [TSB, exp] ^B	Intensität [pMEM, exp] ^B	Intensität [TSB, f-statP] ^B	Intensität [pMEM, f-statP] ^B	Intensität [TSB, s-statP] ^B	Intensität [pMEM, s-statP] ^B
Stressantwort (25)									
88194163	SAOUHSC_00365	AhpC	alkyl hydroperoxide reductase	1.70E+08	5.23E+07	2.31E+08	6.91E+07	2.66E+08	5.15E+08
88194162	SAOUHSC_00364	AhpF	alkyl hydroperoxide reductase, subunit F, putative	1.27E+07		1.38E+07		1.33E+07	
88194551	SAOUHSC_00790	ClpP	ATP-dependent Clp protease, proteolytic subunit ClpP	2.50E+07		3.24E+07		2.50E+07	
88196560	SAOUHSC_02933	BetB,CudA, GbsA	betaine aldehyde dehydrogenase				2.92E+05		
88195057	SAOUHSC_01327	KatA	catalase	2.11E+07	2.67E+07	8.90E+07	2.21E+07	1.42E+08	4.40E+07
88195926	SAOUHSC_02255	GroES	chaperonin, 10 kDa, GroES, putative	1.75E+07	5.19E+05	1.21E+07		1.12E+07	
88195925	SAOUHSC_02254	GroL,GroE L	chaperonin, 60 kDa, GrpEL, putative	7.50E+07	6.42E+06	9.13E+07		6.70E+07	
88195129	SAOUHSC_01403	CspA	cold shock protein, putative	1.38E+07	4.34E+07	1.08E+07	2.57E+07	5.52E+06	4.62E+07
88196660	SAOUHSC_03045	CspB	cold shock protein, putative	5.73E+07		4.25E+07			
88194348	SAOUHSC_00573		hypothetical protein SAOUHSC_00573			1.84E+06	8.25E+05	3.97E+06	2.61E+06
88194589	SAOUHSC_00831		hypothetical protein SAOUHSC_00831					5.69E+05	3.70E+06
88194593	SAOUHSC_00835		hypothetical protein SAOUHSC_00835	4.83E+06		6.24E+06	9.27E+05	4.91E+06	8.82E+06
88195014	SAOUHSC_01282	BsaA	hypothetical protein SAOUHSC_01282			2.16E+06		2.46E+06	
88195522	SAOUHSC_01822	Tpx	hypothetical protein SAOUHSC_01822	6.16E+07	3.43E+06	6.95E+07	3.94E+06	6.97E+07	5.98E+06
88196044	SAOUHSC_02381	Dps	hypothetical protein SAOUHSC_02381	8.72E+06	6.58E+06	8.98E+06	5.41E+06	1.54E+07	1.32E+07
88196094	SAOUHSC_02441	Asp23	hypothetical protein SAOUHSC_02441	1.28E+07	2.58E+07	3.88E+07	2.13E+07	8.64E+07	1.48E+08
88195155	SAOUHSC_01431	MsrB	methionine sulfoxide reductase, putative	1.15E+07		1.09E+07		9.20E+06	
88196463	SAOUHSC_02829	Frp	NAD(P)H-flavin oxidoreductase, putative					4.76E+05	
88195156	SAOUHSC_01432	MsrA2	peptide methionine sulfoxide reductase			5.29E+06		4.61E+06	
88195361	SAOUHSC_01653	SodA	superoxide dismutase, Mn, putative	6.64E+07	6.39E+06	4.76E+07	5.98E+06	4.96E+07	1.29E+07
88193908	SAOUHSC_00093	SodM	superoxide dismutase, putative			4.71E+06		6.04E+06	2.27E+07
88194846	SAOUHSC_01100	TrxA,Trx	thioredoxin	5.66E+07	3.58E+07	5.10E+07	5.24E+07	4.28E+07	1.52E+08
88194546	SAOUHSC_00785	TrxB	thioredoxin reductase	1.33E+07		1.74E+07		1.60E+07	3.24E+06
88194592	SAOUHSC_00834		thioredoxin, putative	3.24E+07	1.19E+07	2.49E+07	4.98E+06	2.23E+07	1.64E+07

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Regulatoren (12)									
88195548	SAOUHSC_01850	CcpA	catabolite control protein A			3.08E+06			
88194239	SAOUHSC_00452		hypothetical protein SAOUHSC_00452			3.92E+06		3.08E+06	3.41E+06
88194421	SAOUHSC_00655		hypothetical protein SAOUHSC_00655			6.71E+05		3.60E+06	
88194459	SAOUHSC_00694		hypothetical protein SAOUHSC_00694	1.05E+06					1.47E+06
88194477	SAOUHSC_00712		hypothetical protein SAOUHSC_00712	2.52E+06					
88194753	SAOUHSC_00997		hypothetical protein SAOUHSC_00997		2.13E+06	4.64E+06	3.18E+06		2.58E+06
88194963	SAOUHSC_01228	CodY	hypothetical protein SAOUHSC_01228					2.22E+06	1.77E+07
88195657	SAOUHSC_01964	TRAP	hypothetical protein SAOUHSC_01964	3.98E+06		3.64E+06	1.76E+07	1.00E+07	6.09E+07
88195154	SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA, putative	5.19E+07		6.99E+07	4.55E+06	7.29E+07	6.71E+06
88196063	SAOUHSC_02402		PTS system, mannitol-specific Ila component, putative			1.93E+06		2.18E+06	1.95E+06
88194390	SAOUHSC_00620	SarA	staphylococcal accessory regulator T, putative				3.29E+05		
88196226	SAOUHSC_02583		transcriptional regulator, putative				7.82E+05		1.22E+06
Transport (36)									
88196546	SAOUHSC_02919	PanB	3-methyl-2-oxobutanoate hydroxymethyltransferase	7.39E+06		1.32E+07	2.16E+06	1.11E+07	
88194087	SAOUHSC_00284		5'-nucleotidase, lipoprotein e(P4) family			1.97E+06			2.66E+06
88196085	SAOUHSC_02430	HtsA	ABC transporter periplasmic binding protein, putative		1.17E+06				4.76E+06
88194605	SAOUHSC_00847	SufC	ABC transporter, ATP-binding protein, putative	1.87E+07		1.97E+06			
88194402	SAOUHSC_00634	MntC	ABC transporter, substrate-binding protein, putative		8.41E+08	6.61E+07	7.92E+08	6.21E+07	7.85E+08
88194742	SAOUHSC_00985	MenB	enoyl-CoA hydratase/isomerase family protein, putative	1.48E+07		1.11E+07		1.58E+07	2.15E+05
88194761	SAOUHSC_01007	FolD	FolD bifunctional protein, putative			2.42E+07	1.16E+06	3.50E+07	3.80E+06
88195472	SAOUHSC_01771	HemL	glutamate-1-semialdehyde-2,1-aminomutase	3.30E+06					
88194011	SAOUHSC_00201		hypothetical protein SAOUHSC_00201				3.15E+05		
88194028	SAOUHSC_00220	IspD	hypothetical protein SAOUHSC_00220			5.76E+06		7.91E+06	

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88194112	SAOUHSC_00311		hypothetical protein SAOUHSC_00311			1.13E+06		1.32E+06	9.22E+05
88194606	SAOUHSC_00848	SufD	hypothetical protein SAOUHSC_00848	5.28E+06		4.77E+06		2.84E+06	
88194608	SAOUHSC_00850		hypothetical protein SAOUHSC_00850	1.70E+06		9.63E+05			
88194609	SAOUHSC_00851	SufB	hypothetical protein SAOUHSC_00851	5.63E+06		6.33E+06		4.61E+06	
88194831	SAOUHSC_01084	IsdD	hypothetical protein SAOUHSC_01084				6.46E+06		8.13E+06
88194832	SAOUHSC_01085	IsdE	hypothetical protein SAOUHSC_01085				1.11E+06		3.64E+06
88195556	SAOUHSC_01858		hypothetical protein SAOUHSC_01858	2.09E+07	8.86E+05	1.59E+07		1.49E+07	
88195571	SAOUHSC_01874		hypothetical protein SAOUHSC_01874		2.24E+06	3.22E+06	2.62E+06	3.24E+06	6.07E+06
88196199	SAOUHSC_02554	FhuD2	hypothetical protein SAOUHSC_02554		2.46E+06	3.75E+06		4.64E+06	7.65E+06
88196339	SAOUHSC_02699		hypothetical protein SAOUHSC_02699		2.52E+06	1.28E+07	3.67E+06	1.43E+07	5.11E+06
88196600	SAOUHSC_02980		hypothetical protein SAOUHSC_02980			4.43E+05	2.99E+06	1.19E+06	1.21E+06
88196194	SAOUHSC_02549	ModA	molybdenum ABC transporter, periplasmic molybdate-binding protein			1.82E+06	1.42E+06	3.16E+06	3.08E+06
88196188	SAOUHSC_02542	MoeA	molybdopterin biosynthesis protein moeA, putative			2.45E+06		3.16E+06	
88196190	SAOUHSC_02544	MoaB	molybdopterin precursor biosynthesis moaB, putative					1.09E+06	
88195812	SAOUHSC_02132	NadE	NAD ⁺ synthetase			1.61E+06		2.97E+06	
88194828	SAOUHSC_01079	IsdB	neurofilament protein				1.44E+06		2.77E+06
88194684	SAOUHSC_00927	OppA	oligopeptide ABC transporter, substrate-binding protein, putative		1.34E+06				
88196403	SAOUHSC_02767	Opp- 1A,Opp1A	peptide ABC transporter, peptide-binding protein, putative				1.43E+06		3.45E+06
88194781	SAOUHSC_01028	PtsH	phosphocarrier protein hpr, putative	4.49E+07		4.20E+07	2.71E+06	3.02E+07	8.47E+06
88194341	SAOUHSC_00562	ThiD	phosphomethylpyrimidine kinase	5.59E+06	1.79E+06				
88195475	SAOUHSC_01774	HemC	porphobilinogen deaminase			2.16E+06		2.79E+06	
88195473	SAOUHSC_01772	HemB	porphobilinogen synthase			2.38E+06		3.40E+06	
88195976	SAOUHSC_02310	KdpC	potassium-transporting ATPase, C subunit				8.68E+06		2.54E+06
88193967	SAOUHSC_00155	PtsG,GlcA	PTS system, glucose-specific component			1.47E+06		1.19E+06	
88195582	SAOUHSC_01886	RibH	riboflavin synthase, beta subunit					3.13E+06	

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88194268	SAOUHSC_00483		S1 RNA binding domain protein					1.56E+06		
zell. Prozesse (9)										
88194892	SAOUHSC_01150	FtsZ	cell division protein FtsZ	1.93E+07		9.66E+06		7.32E+06		
88194891	SAOUHSC_01149	FtsA	cell division protein, putative		3.17E+05					
88194886	SAOUHSC_01144	FtsL	hypothetical protein SAOUHSC_01144	1.50E+07	6.22E+07	3.03E+07	1.55E+07	2.35E+07	9.15E+06	
88194898	SAOUHSC_01158		hypothetical protein SAOUHSC_01158		2.13E+06					
88195179	SAOUHSC_01462		hypothetical protein SAOUHSC_01462	2.59E+06	1.91E+07	9.51E+06	2.47E+06	9.26E+06	7.91E+06	
88195555	SAOUHSC_01857		hypothetical protein SAOUHSC_01857			6.55E+05		6.36E+05		
88195846	SAOUHSC_02169	Chs,Chp	hypothetical protein SAOUHSC_02169		2.85E+07		1.60E+07		1.85E+07	
88194036	SAOUHSC_00229	ScdA	ScdA protein, putative			2.50E+06		3.39E+06		
88194942	SAOUHSC_01205	FtsY	signal recognition particle-docking protein FtsY					4.48E+05	1.01E+06	
Energiemetabolismus (101)										
88195143	SAOUHSC_01418	SucA,OdhA	2-oxoglutarate dehydrogenase, E1 component			2.12E+06		8.90E+06		
88195142	SAOUHSC_01416	SucB,OdhB	2-oxoglutarate dehydrogenase, E2 component, dihydroliipoamide succinyltransferase			4.04E+06		1.26E+07		
88195324	SAOUHSC_01613	BfmBAA	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit, putative	2.54E+06		2.24E+06		2.26E+06		
88195323	SAOUHSC_01612	BfmBAB	2-oxoisovalerate dehydrogenase, E1 component, beta subunit, putative	2.69E+06		1.48E+06		1.77E+06		
88193901	SAOUHSC_00086	ButA	3-ketoacyl-acyl carrier protein reductase, putative			1.85E+07		3.54E+07	1.04E+06	
88195507	SAOUHSC_01807	PfkA	6-phosphofruktokinase, putative	1.02E+07		4.34E+06		3.86E+06		
88195316	SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase, decarboxylating	4.18E+07	4.01E+06	7.50E+07	3.30E+06	1.17E+08	1.16E+07	
88195520	SAOUHSC_01820	AckA	acetate kinase	5.21E+06	1.82E+06	2.60E+06		1.13E+07		
88195075	SAOUHSC_01347	CitB,AcnA	aconitate hydratase 1	3.39E+07		7.84E+07	5.05E+05	1.04E+08		
88193983	SAOUHSC_00173	AcpD	acyl carrier phosphodiesterase	1.89E+06		1.44E+06		1.56E+06		
88195518	SAOUHSC_01818	Ald1	alanine dehydrogenase			2.88E+06		6.14E+06		

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88195172	SAOUHSC_01452	Ald2,Ald	alanine dehydrogenase					3.18E+06	
88194378	SAOUHSC_00608	Adh,Adh1, AdhA	alcohol dehydrogenase I, putative			2.19E+07		3.32E+07	
88195822	SAOUHSC_02142	AldH,AldA 2	aldehyde dehydrogenase, putative			6.08E+05		1.13E+06	
88193945	SAOUHSC_00132	AldA	aldehyde dehydrogenase, putative					8.65E+05	
88196069	SAOUHSC_02409	RocF,Arg	arginase					1.54E+06	
88196590	SAOUHSC_02969	ArcA	arginine deiminase			5.59E+05		5.93E+05	
88196009	SAOUHSC_02345	AtpA	ATP synthase F1, alpha subunit	1.39E+07		4.62E+07		4.48E+07	
88196007	SAOUHSC_02341	AtpD	ATP synthase F1, beta subunit	1.80E+07		5.49E+07		5.36E+07	
88194872	SAOUHSC_01129	ArcC	carbamate kinase			9.53E+05		6.19E+05	
88196587	SAOUHSC_02965		carbamate kinase						
88194665	SAOUHSC_00908	Cdr	coenzyme A disulfide reductase, putative	6.39E+06		1.42E+07		1.47E+07	2.67E+06
88195564	SAOUHSC_01867	Dat	D-amino acid aminotransferase	3.95E+06		1.66E+06		2.04E+06	
88196500	SAOUHSC_02869	RocA	delta-1-pyrroline-5-carboxylate dehydrogenase, putative			1.58E+07		4.58E+07	7.54E+06
88196042	SAOUHSC_02379	DeoC2	deoxyribose-phosphate aldolase						
88194795	SAOUHSC_01043	PdhD,LpdA	dihydrolipoamide dehydrogenase	5.26E+07	2.30E+07	8.35E+07	1.41E+07	7.42E+07	2.20E+07
88195325	SAOUHSC_01614	BfmBC	dihydrolipoamide dehydrogenase					1.42E+06	
88194794	SAOUHSC_01042	PdhC	dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase complex E2, putative	5.75E+07		1.01E+08		6.24E+07	
88194623	SAOUHSC_00866		D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain protein			2.20E+05			
88196464	SAOUHSC_02830	Ddh	D-lactate dehydrogenase, putative	2.38E+07		1.44E+08	1.54E+05	1.30E+08	2.31E+05
88194559	SAOUHSC_00799	Eno	enolase	2.80E+08	5.04E+07	3.45E+08		4.11E+08	3.99E+06
88194704	SAOUHSC_00947	FabI	enoyl-(acyl-carrier-protein) reductase	5.48E+06					
88193997	SAOUHSC_00187	ÜflB	formate acetyltransferase			1.21E+07		2.72E+07	
88193954	SAOUHSC_00142	Fdh	formate dehydrogenase, NAD-dependent, putative						1.44E+07
88196252	SAOUHSC_02610	HutG	formiminoglutamase					6.88E+05	
88194472	SAOUHSC_00707	FruB	fructose 1-phosphate kinase, putative			1.38E+06		1.26E+06	

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88196553	SAOUHSC_02926		fructose-bisphosphate aldolase class-I, putative	2.18E+08	3.17E+07	1.70E+08	8.04E+06	1.62E+08	2.86E+07
88195674	SAOUHSC_01983	FumC,CitG	fumarate hydratase, class II			2.22E+06		6.86E+06	
88194014	SAOUHSC_00204		Globin domain protein			5.68E+06			
88195354	SAOUHSC_01646	GlcK,Glk,GlkA	glucokinase, putative	2.51E+06		1.44E+06		1.74E+06	
88195310	SAOUHSC_01599	Zwf	glucose-6-phosphate 1-dehydrogenase	6.38E+06	5.29E+05	1.06E+07	3.82E+05	1.42E+07	
88194657	SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase	2.81E+07	5.54E+06	6.84E+07	1.71E+06	1.09E+08	4.14E+06
88194555	SAOUHSC_00795	Gap1,Gap	glyceraldehyde-3-phosphate dehydrogenase, type I	1.74E+08	1.16E+08	7.25E+07	4.51E+07	1.31E+08	2.25E+08
88195494	SAOUHSC_01794	GapB,Gap2	glyceraldehyde-3-phosphate dehydrogenase, type I			5.87E+05		6.95E+05	
88195009	SAOUHSC_01276	GlpK	glycerol kinase	5.06E+06					
88194594	SAOUHSC_00836	GcvH	glycine cleavage system H protein	2.39E+07	6.36E+06	1.40E+07	2.75E+06	2.42E+07	6.04E+06
88195342	SAOUHSC_01633		glycine cleavage system P-protein subunit I, putative			5.13E+05		1.32E+06	
88195341	SAOUHSC_01632		glycine cleavage system P-protein subunit II, putative					2.71E+06	
88195343	SAOUHSC_01634	GcvT	glycine cleavage system T protein					2.29E+06	
88194312	SAOUHSC_00532	Kbl	hypothetical protein SAOUHSC_00532		6.71E+05	6.68E+06		1.22E+07	
88194332	SAOUHSC_00553		hypothetical protein SAOUHSC_00553	2.06E+07	2.58E+06	1.78E+07	3.85E+06	1.48E+07	2.17E+07
88194493	SAOUHSC_00728		hypothetical protein SAOUHSC_00728	7.20E+07	7.89E+07	2.27E+08	4.14E+08	1.97E+08	2.06E+08
88194635	SAOUHSC_00878		hypothetical protein SAOUHSC_00878					2.18E+06	
88194654	SAOUHSC_00897	GlpQ	hypothetical protein SAOUHSC_00897			3.06E+07	2.15E+07	2.26E+07	3.04E+07
88194760	SAOUHSC_01005		hypothetical protein SAOUHSC_01005	4.05E+06	2.83E+07	4.65E+06	1.09E+07	4.23E+06	8.33E+06
88195010	SAOUHSC_01278	GlpD	hypothetical protein SAOUHSC_01278			8.48E+05			
88195141	SAOUHSC_01415		hypothetical protein SAOUHSC_01415	8.16E+06		7.81E+06		8.69E+06	
88195558	SAOUHSC_01860		hypothetical protein SAOUHSC_01860	1.13E+07	3.65E+06	1.45E+07	9.43E+06	1.58E+07	2.81E+07
88195596	SAOUHSC_01901		hypothetical protein SAOUHSC_01901	1.27E+07		2.00E+07	5.24E+06	2.02E+07	2.19E+07
88195678	SAOUHSC_01987		hypothetical protein SAOUHSC_01987	1.91E+07		2.34E+07	4.09E+06	2.22E+07	7.72E+06
88195820	SAOUHSC_02140	PpaC	hypothetical protein SAOUHSC_02140	2.46E+07	8.11E+05	1.45E+07		1.22E+07	

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88195823	SAOUHSC_02143		hypothetical protein SAOUHSC_02143	5.28E+06	2.08E+06	4.32E+06	6.14E+05	1.04E+07	1.09E+06
88195830	SAOUHSC_02150		hypothetical protein SAOUHSC_02150	1.42E+07	1.56E+06	1.45E+07	1.55E+06	1.39E+07	3.55E+06
88196029	SAOUHSC_02366	FbaA,Fba	hypothetical protein SAOUHSC_02366	1.86E+08	7.54E+06	2.44E+08	1.17E+07	2.11E+08	3.00E+07
88196050	SAOUHSC_02387		hypothetical protein SAOUHSC_02387					1.30E+06	
88196098	SAOUHSC_02445		hypothetical protein SAOUHSC_02445			1.42E+05			
88196099	SAOUHSC_02447		hypothetical protein SAOUHSC_02447					6.65E+05	1.60E+05
88196100	SAOUHSC_02448		hypothetical protein SAOUHSC_02448				5.53E+06	3.06E+06	1.05E+07
88196112	SAOUHSC_02460		hypothetical protein SAOUHSC_02460				1.33E+05		
88196246	SAOUHSC_02604		hypothetical protein SAOUHSC_02604					1.75E+06	
88196428	SAOUHSC_02793		hypothetical protein SAOUHSC_02793					1.56E+06	
88196528	SAOUHSC_02900		hypothetical protein SAOUHSC_02900	3.11E+06		4.91E+06	1.75E+05	9.10E+06	3.26E+05
88196248	SAOUHSC_02606	HutI	imidazolonepropionase					3.56E+06	
88196549	SAOUHSC_02922	Ldh2,Ldh	L-lactate dehydrogenase	4.63E+06		1.33E+07		1.66E+07	1.33E+06
88194016	SAOUHSC_00206	Ldh1,LctE	L-lactate dehydrogenase	2.28E+06		1.77E+07		2.29E+07	
88196554	SAOUHSC_02927	Mqo2	malate:quinone-oxidoreductase			1.02E+07		7.26E+06	
88196064	SAOUHSC_02403	MtlD	mannitol-1-phosphate 5-dehydrogenase, putative	8.96E+05		2.07E+06		3.17E+06	
88195408	SAOUHSC_01702	Pfs,MtmN	MTA/SAH nucleosidase					4.11E+05	
88194475	SAOUHSC_00710	NagA	N-acetylglucosamine-6-phosphate deacetylase			2.78E+06		3.34E+06	
88195510	SAOUHSC_01810		NADP-dependent malic enzyme, putative	1.28E+07	1.82E+06	1.00E+07		1.02E+07	
88196320	SAOUHSC_02680	NarH	nitrate reductase, beta subunit			4.12E+05			
88194648	SAOUHSC_00891		peptidyl-prolyl cis-trans isomerase, cyclophilin-type, putative	2.56E+07		2.28E+07		2.07E+07	
88194349	SAOUHSC_00574	Pta	phosphate acetyltransferase	6.81E+07	2.76E+06	1.17E+08	4.54E+06	1.04E+08	1.66E+07
88195605	SAOUHSC_01910	PckA	phosphoenolpyruvate carboxykinase (ATP)			1.61E+07		5.88E+07	3.75E+06
88194782	SAOUHSC_01029	PtsI	phosphoenolpyruvate-protein phosphotransferase	7.64E+07	1.23E+06	9.12E+07		9.99E+07	
88196066	SAOUHSC_02405	GlmM(fem D),GlmM	phosphoglucosamine mutase	8.84E+06		9.84E+06		3.93E+06	

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88194556	SAOUHSC_00796	Pgk	phosphoglycerate kinase, putative	7.01E+07		7.54E+07		8.23E+07	3.07E+05
88194558	SAOUHSC_00798	Pgm,Gpml	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	4.09E+07		4.65E+07		5.41E+07	
88196343	SAOUHSC_02703	GpmA	phosphoglycerate mutase, putative			1.70E+07	1.08E+06	3.04E+07	6.09E+06
88194813	SAOUHSC_01064	PycA,Pyc	pyruvate carboxylase			5.96E+06		1.35E+07	
88194792	SAOUHSC_01040	PdhA	pyruvate dehydrogenase complex, E1 component, alpha subunit, putative	7.50E+07	1.03E+07	1.28E+08	1.30E+06	8.04E+07	
88194793	SAOUHSC_01041	PhdB,PdhB	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	1.08E+08	1.58E+07	1.71E+08	1.86E+06	1.15E+08	
88195506	SAOUHSC_01806	PykA,Pyk	pyruvate kinase	4.26E+07		2.49E+07		3.57E+07	
88194758	SAOUHSC_01002	QoxA	quinol oxidase AA3, subunit II, putative		2.23E+06		1.60E+06	2.49E+06	2.02E+06
88195604	SAOUHSC_01909	MetK	S-adenosylmethionine synthetase	3.01E+06					
88194850	SAOUHSC_01104	SdhA	succinate dehydrogenase, flavoprotein chain TC0881, putative					1.26E+06	
88194954	SAOUHSC_01218	SucD	succinyl-CoA synthetase, alpha subunit, putative	5.24E+06		3.20E+07		5.55E+07	
88194953	SAOUHSC_01216	SucC	succinyl-CoA synthetase, beta subunit, putative	7.01E+06	9.17E+05	1.75E+07		4.74E+07	
88195066	SAOUHSC_01337	Tkt	transketolase	1.62E+08	5.31E+06	2.50E+08	2.13E+06	2.01E+08	
88194557	SAOUHSC_00797	TpiA,Tpi	triosephosphate isomerase	1.40E+08	3.78E+07	1.79E+08	2.52E+07	1.57E+08	9.69E+06
88196249	SAOUHSC_02607	HutU	urocanate hydratase			3.73E+06		1.57E+07	5.67E+07
Proteinbiosynthese (61)									
88195210	SAOUHSC_01493	RpsA	30S ribosomal protein S1, putative	6.39E+07	9.64E+06	7.88E+07		1.46E+08	
88196150	SAOUHSC_02500	RplE	50S ribosomal protein L5, putative	4.14E+07	3.98E+06	1.65E+07	1.32E+06	1.62E+07	2.75E+06
88194381	SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	6.64E+06	1.31E+06	8.21E+06	6.51E+05	1.50E+07	2.57E+06
88195188	SAOUHSC_01471	AsnS	asparaginyl-tRNA synthetase, putative			5.88E+05		8.45E+05	
88195441	SAOUHSC_01737	AspS	aspartyl-tRNA synthetase	2.46E+06		1.35E+06		1.75E+06	
88195444	SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr) deacylase		3.44E+05		5.51E+05		2.20E+06
88194290	SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	4.71E+06	7.55E+05	2.29E+07	1.15E+06	2.61E+07	6.96E+06
88195799	SAOUHSC_02117	GatA	glutamyl-tRNA(Gln) amidotransferase, A subunit	2.14E+07		5.01E+06		3.43E+06	

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88195798	SAOUHSC_02116	GatB	glutamyl-tRNA(Gln) amidotransferase, B subunit	2.71E+07		9.74E+06		6.08E+06	
88195800	SAOUHSC_02118		glutamyl-tRNA(Gln) amidotransferase, C subunit		6.92E+06				
88195373	SAOUHSC_01666	GlyS	glycyl-tRNA synthetase	1.61E+07	6.09E+05	3.48E+06		6.51E+06	
88194708	SAOUHSC_00951		hypothetical protein SAOUHSC_00951	2.60E+06		5.92E+06		1.49E+07	
88196138	SAOUHSC_02487	RpsM	hypothetical protein SAOUHSC_02487	7.40E+06	2.15E+06	9.12E+06		4.65E+06	
88196161	SAOUHSC_02511	RplD	hypothetical protein SAOUHSC_02511	3.70E+07	7.83E+06	1.01E+07		8.49E+06	
88194899	SAOUHSC_01159	IleS	isoleucyl-tRNA synthetase			3.63E+06		8.21E+06	
88195572	SAOUHSC_01875	LeuS	leucyl-tRNA synthetase			3.40E+06		6.63E+06	
88194278	SAOUHSC_00493	LysS	lysyl-tRNA synthetase	1.91E+06					
88194248	SAOUHSC_00461	MetS, MetG	methionyl-tRNA synthetase, putative			5.15E+06		1.05E+07	
88196022	SAOUHSC_02359	PrfA	peptide chain release factor 1	5.46E+06		3.91E+06		4.13E+06	
88194839	SAOUHSC_01092	PheS	phenylalanyl-tRNA synthetase, alpha subunit			4.54E+06		4.86E+06	
88194840	SAOUHSC_01093	PheT	phenylalanyl-tRNA synthetase, beta subunit	4.03E+06		6.48E+06		9.04E+06	
88194973	SAOUHSC_01240	proS	prolyl-tRNA synthetase	1.48E+06					
88194261	SAOUHSC_00474	RplY	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	4.99E+07	4.36E+06	1.96E+07	1.76E+06	2.98E+07	1.95E+06
88194300	SAOUHSC_00519	RplA	ribosomal protein L1	3.29E+07	3.88E+06	8.66E+06		1.01E+07	
88194301	SAOUHSC_00520	RplJ	ribosomal protein L10	6.85E+07		2.70E+07		1.91E+07	
88194299	SAOUHSC_00518	RplK	ribosomal protein L11	1.06E+08		1.14E+08	1.03E+07	8.19E+07	2.80E+07
88196130	SAOUHSC_02478	RplM	ribosomal protein L13	5.69E+07	1.89E+07	1.48E+07		2.05E+07	
88196143	SAOUHSC_02492	RplO	ribosomal protein L15	1.04E+07	8.61E+05	1.70E+07		1.17E+07	
88196135	SAOUHSC_02484	RplQ	ribosomal protein L17	7.04E+06		5.99E+06		9.80E+06	1.20E+06
88196146	SAOUHSC_02495	RplR	ribosomal protein L18	1.38E+07	1.10E+07	8.44E+06		6.93E+06	2.43E+06
88196159	SAOUHSC_02509	RplB	ribosomal protein L2	5.04E+06		9.95E+06		1.24E+07	
88195485	SAOUHSC_01784	RplT	ribosomal protein L20	2.91E+06		1.55E+06		1.14E+06	
88195458	SAOUHSC_01757	RplU	ribosomal protein L21	3.43E+07	8.75E+06	1.70E+07		2.41E+07	
88196157	SAOUHSC_02507	RplV	ribosomal protein L22	2.16E+07	1.39E+07	3.49E+07		2.68E+07	

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88195456	SAOUHSC_01755	RpmA	ribosomal protein L27	2.50E+07		1.97E+07		1.52E+07	
88196154	SAOUHSC_02504	RpmC	ribosomal protein L29		1.99E+06	1.22E+06		1.61E+06	
88196144	SAOUHSC_02493	RpmD	ribosomal protein L30	3.87E+07	1.76E+07	3.77E+07	2.65E+06	2.68E+07	8.32E+06
88196024	SAOUHSC_02361	RpmE	ribosomal protein L31	3.41E+07	4.13E+07	2.25E+07	1.39E+07	1.72E+07	3.11E+07
88196147	SAOUHSC_02496	RplF	ribosomal protein L6, putative	5.26E+06			1.48E+06	7.65E+06	2.85E+06
88194302	SAOUHSC_00521	RplL	ribosomal protein L7/L12	6.59E+07		7.83E+07	2.39E+07	5.13E+07	9.40E+07
88193838	SAOUHSC_00017	RplI	ribosomal protein L9	2.26E+06	1.64E+06		6.57E+05		3.54E+06
88196137	SAOUHSC_02486	RpsK	ribosomal protein S11, putative	4.66E+06		7.23E+06		4.16E+06	
88194945	SAOUHSC_01208	RpsP	ribosomal protein S16	2.07E+07		1.82E+07		1.21E+07	
88194965	SAOUHSC_01232	RpsB	ribosomal protein S2	1.14E+07	7.37E+05	6.23E+06		5.90E+06	
88195529	SAOUHSC_01829	RpsD	ribosomal protein S4	5.62E+06					
88196145	SAOUHSC_02494	RpsE	ribosomal protein S5	2.03E+07	2.02E+07	3.84E+06		3.22E+06	
88194147	SAOUHSC_00348	RpsF	ribosomal protein S6	5.73E+07	2.80E+07	4.45E+07	3.36E+06	3.17E+07	6.08E+06
88194308	SAOUHSC_00528	RpsG	ribosomal protein S7	4.65E+06	2.52E+06	5.36E+06		4.07E+06	
88196148	SAOUHSC_02498	RpsH	ribosomal protein S8, putative		1.21E+07	7.81E+06		7.57E+06	
88196129	SAOUHSC_02477	RpsI	ribosomal protein S9, putative	3.34E+07	1.78E+07	4.46E+07		2.88E+07	
88194969	SAOUHSC_01236	Rrf,Frr	ribosome recycling factor	3.90E+07	2.94E+07	2.76E+07	9.55E+06	1.49E+07	3.39E+07
88193832	SAOUHSC_00009	SerS	seryl-tRNA synthetase	1.96E+07		4.78E+07		5.28E+07	3.39E+05
88195489	SAOUHSC_01788	ThrS	threonyl-tRNA synthetase			7.42E+05		3.28E+06	
88194309	SAOUHSC_00529	FusA,Fus	translation elongation factor G	2.19E+08	4.35E+06	5.73E+07		8.39E+07	
88195335	SAOUHSC_01625	Efp	translation elongation factor P	2.65E+07		2.17E+07		1.82E+07	
88194967	SAOUHSC_01234	Tsf	translation elongation factor Ts	1.21E+08	1.05E+07	7.61E+07	5.48E+07	1.75E+08	2.06E+08
88194310	SAOUHSC_00530	Tuf	translation elongation factor Tu	6.16E+08	1.84E+07	2.20E+08	1.12E+07	1.97E+08	1.86E+07
88195487	SAOUHSC_01786	InfC	translation initiation factor IF-3						1.63E+06
88194690	SAOUHSC_00933	TrpS	tryptophanyl-tRNA synthetase			5.37E+06	3.76E+05	6.50E+06	2.40E+06
88195539	SAOUHSC_01839	TyrS	tyrosyl-tRNA synthetase	2.47E+06					

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88195468	SAOUHSC_01767	ValS	valyl-tRNA synthetase			1.26E+06		3.08E+06		
Proteinmetabolismus (38)										
88194678	SAOUHSC_00921	FabF,Fab	3-oxoacyl- synthase, putative	8.83E+07		5.70E+07		4.45E+07	3.66E+06	
88194937	SAOUHSC_01199	FabG	3-oxoacyl-(acyl-carrier-protein) reductase, putative	3.41E+07		1.89E+07		1.66E+07	1.49E+05	
88194005	SAOUHSC_00195	FadA	acetyl-CoA acetyltransferase, putative					3.74E+06		
88195334	SAOUHSC_01624	AccB	acetyl-CoA carboxylase, biotin carboxyl carrier protein			2.38E+06		3.36E+06		
88195333	SAOUHSC_01623	AccC	acetyl-CoA carboxylase, biotin carboxylase	4.61E+06		4.64E+06		3.88E+06		
88194939	SAOUHSC_01201	HmrB,Acp P	acyl carrier protein	4.08E+07	3.36E+07	2.96E+07	3.40E+07	2.07E+07	9.26E+07	
88195479	SAOUHSC_01778	ClpX	ATP-dependent Clp protease, ATP-binding subunit ClpX	8.48E+06						
88196002	SAOUHSC_02336	FabZ	beta-hydroxyacyl-ACP dehydratase, putative	7.51E+06		1.05E+07		1.12E+07		
88195390	SAOUHSC_01684	GrpE	co-chaperone GrpE	6.69E+07	1.70E+07	6.88E+07	7.03E+06	4.69E+07	1.57E+07	
88195388	SAOUHSC_01682	DnaJ	DnaJ protein	1.83E+06		4.47E+06		4.51E+06		
88195389	SAOUHSC_01683	DnaK	DNAk protein, putative	3.82E+08	1.21E+07	2.90E+08	6.02E+06	2.51E+08	5.87E+06	
88196491	SAOUHSC_02860	MvaS	HMG-CoA synthase, putative	4.39E+07	5.90E+06	6.24E+07	3.83E+06	6.23E+07	1.09E+07	
88194006	SAOUHSC_00196	FadB	hypothetical protein SAOUHSC_00196					1.25E+07		
88194007	SAOUHSC_00197	FadD	hypothetical protein SAOUHSC_00197					5.68E+06		
88194271	SAOUHSC_00486	FtsH	hypothetical protein SAOUHSC_00486	3.38E+06		5.51E+06		6.31E+06		
88194272	SAOUHSC_00487		hypothetical protein SAOUHSC_00487	3.08E+06		3.73E+06		3.46E+06		
88194313	SAOUHSC_00533		hypothetical protein SAOUHSC_00533	2.17E+07	3.59E+06	2.65E+07	3.05E+06	2.21E+07	1.18E+07	
88194677	SAOUHSC_00920	FabH	hypothetical protein SAOUHSC_00920	2.73E+07		2.49E+07		2.27E+07		
88194972	SAOUHSC_01239		hypothetical protein SAOUHSC_01239		5.22E+06		2.89E+06		1.92E+06	
88194988	SAOUHSC_01255		hypothetical protein SAOUHSC_01255						1.11E+06	
88194989	SAOUHSC_01256		hypothetical protein SAOUHSC_01256			6.78E+05		9.36E+05	1.51E+06	
88195092	SAOUHSC_01365		hypothetical protein SAOUHSC_01365	5.48E+05		1.86E+06		3.78E+06		

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88195110	SAOUHSC_01383		hypothetical protein SAOUHSC_01383			9.39E+05	6.69E+05	1.46E+06	3.79E+06
88195151	SAOUHSC_01427	CtpA	hypothetical protein SAOUHSC_01427				6.22E+05		1.66E+06
88195516	SAOUHSC_01816		hypothetical protein SAOUHSC_01816					5.58E+06	3.61E+06
88195559	SAOUHSC_01861		hypothetical protein SAOUHSC_01861			2.11E+06		3.09E+06	
88195565	SAOUHSC_01868		hypothetical protein SAOUHSC_01868	2.55E+07	9.51E+05	3.70E+07		4.12E+07	
88196609	SAOUHSC_02990		hypothetical protein SAOUHSC_02990			5.89E+05		8.99E+05	
88194936	SAOUHSC_01198	FabD	malonyl CoA-acyl carrier protein transacylase	2.60E+07		4.75E+06		6.24E+06	
88195784	SAOUHSC_02102	Map	methionine aminopeptidase, type I	1.89E+07	2.89E+06	2.58E+07	3.97E+06	2.22E+07	2.33E+07
88194694	SAOUHSC_00937	PepF,PepB	oligoendopeptidase F	4.06E+06	2.83E+06	9.53E+06	4.80E+06	1.80E+07	3.02E+07
88194521	SAOUHSC_00757	PepT	peptidase T, putative			2.39E+06		3.27E+06	
88194790	SAOUHSC_01038	Def	polypeptide deformylase	1.12E+07	5.38E+06	1.28E+07	3.46E+06	8.30E+06	2.26E+07
88194636	SAOUHSC_00879	PepA,Amp A	probable cytosol aminopeptidase			2.34E+06		3.65E+06	
88195336	SAOUHSC_01626		proline dipeptidase, putative	2.49E+06		4.89E+06		1.03E+07	
88195663	SAOUHSC_01972	PrsA	protein export protein PrsA, putative		5.09E+06	1.16E+07	2.43E+07	1.26E+07	8.07E+07
88194660	SAOUHSC_00903	SpsB	Signal peptidase IB, putative					1.61E+06	2.43E+06
AS-Biosynthese (14)									
88195327	SAOUHSC_01617	ArgR,AhrC	arginine repressor			3.15E+05		1.03E+06	
88194316	SAOUHSC_00536	IlvE	branched-chain amino acid aminotransferase	2.93E+07		2.03E+07	7.45E+05	2.91E+07	3.39E+06
88194652	SAOUHSC_00895	GudB	glutamate dehydrogenase, NAD-specific, putative			5.16E+06		1.86E+07	
88195018	SAOUHSC_01287	GlnA	glutamine synthetase, type I	6.41E+07	2.06E+07	1.18E+08	2.96E+06	1.52E+08	3.42E+06
88194273	SAOUHSC_00488	CysK	hypothetical protein SAOUHSC_00488	6.43E+07	2.38E+06	6.08E+07		4.09E+07	4.13E+06
88195550	SAOUHSC_01852		hypothetical protein SAOUHSC_01852	2.24E+06		2.42E+06		5.53E+06	
88195838	SAOUHSC_02158		hypothetical protein SAOUHSC_02158			6.29E+05			
88195928	SAOUHSC_02257	SdrH	hypothetical protein SAOUHSC_02257		4.97E+06		1.44E+07		9.80E+06

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88194651	SAOUHSC_00894		ornithine aminotransferase, putative			5.23E+06		1.89E+07	
88194871	SAOUHSC_01128	Otc,ArgF	ornithine carbamoyltransferase			1.56E+06		2.97E+06	
88196589	SAOUHSC_02968	ArcB	ornithine carbamoyltransferase			2.14E+06		4.86E+06	
88195308	SAOUHSC_01597	ProC	pyrroline-5-carboxylate reductase			2.29E+06		2.76E+06	
88196017	SAOUHSC_02354	GlyA	serine hydroxymethyltransferase, putative	7.47E+06	2.46E+06	1.61E+07	1.73E+06	2.03E+07	5.35E+06
88195171	SAOUHSC_01451	TdcB,IlvA	threonine dehydratase			1.07E+06		1.59E+06	
Nukleotidbiosynthese (21)									
88196141	SAOUHSC_02490	Adk	adenylate kinase, putative	2.64E+07	4.09E+06	2.31E+07	2.37E+06	1.73E+07	
88195807	SAOUHSC_02126	PurB	adenylosuccinate lyase		3.22E+05	7.81E+06		1.48E+07	
88193840	SAOUHSC_00019	PurA	adenylosuccinate synthetase		3.93E+06	9.52E+06		1.20E+07	
88194909	SAOUHSC_01170	PyrAB,Car B	carbamoyl-phosphate synthase, large subunit	3.24E+06					
88196031	SAOUHSC_02368	PyrG,CtrA	CTP synthase	2.19E+06	7.11E+05				
88195213	SAOUHSC_01496	Cmk	cytidylate kinase	2.56E+06		1.40E+06		1.06E+06	
88194907	SAOUHSC_01168	PyrC	dihydroorotase	7.88E+06		1.28E+07		8.84E+06	
88195544	SAOUHSC_01845	Fhs	formate-tetrahydrofolate ligase, putative	1.12E+07	1.90E+06	8.54E+07		1.58E+08	8.60E+05
88194270	SAOUHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	3.58E+06			7.19E+05	9.02E+05	2.37E+06
88195202	SAOUHSC_01485	Ndk	nucleoside diphosphate kinase, putative			4.48E+06		4.84E+06	
88193914	SAOUHSC_00101	Drm,DeoB	phosphopentomutase	3.59E+07	1.30E+06	4.52E+07	3.29E+05	4.31E+07	4.41E+05
88194772	SAOUHSC_01018	PurD	phosphoribosylamine-glycine ligase			6.24E+05		1.37E+06	
88194762	SAOUHSC_01008	PurE	phosphoribosylaminoimidazole carboxylase, catalytic subunit			1.39E+07		1.25E+07	
88194769	SAOUHSC_01015	PurM	phosphoribosylformylglycinamide cyclo-ligase			5.47E+06		5.28E+06	
88194766	SAOUHSC_01012	PurQ	phosphoribosylformylglycinamide synthase I			1.67E+07	5.97E+05	1.50E+07	8.42E+05
88194765	SAOUHSC_01011	PurS	phosphoribosylformylglycinamide synthase, PurS protein			4.29E+06	2.26E+06	6.04E+06	3.87E+06
88196043	SAOUHSC_02380	DeoD2	purine nucleoside phosphorylase	7.98E+07	2.03E+07	9.76E+07	1.28E+07	9.68E+07	4.83E+07

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88196040	SAOUHSC_02377	Pyn,Pdp	pyrimidine nucleoside phosphorylase, putative					4.76E+06	
88194508	SAOUHSC_00743	Rir2,NrdF	ribonucleotide-disphosphate reductase beta chain, putative	3.43E+06		2.90E+06		5.39E+06	
88196016	SAOUHSC_02353	Upp	uracil phosphoribosyltransferase	3.57E+06		3.21E+06		6.12E+06	
88194968	SAOUHSC_01235	SmbA,PyrH	uridylylate kinase, putative	3.19E+06					
Transkription und Replikation (16)									
88193825	SAOUHSC_00002	DnaN	DNA polymerase III, beta subunit	1.32E+07		9.84E+06		4.39E+06	
88195207	SAOUHSC_01490	Hup,Hu	DNA-binding protein HU, putative	3.43E+07	1.74E+08	6.55E+07	2.67E+07	4.66E+07	1.27E+08
88196136	SAOUHSC_02485	RpoA	DNA-directed RNA polymerase alpha chain, putative	1.52E+07		1.18E+07		1.92E+07	
88196032	SAOUHSC_02369	RpoE	DNA-directed RNA polymerase, delta subunit, putative	3.71E+07	1.62E+07	1.32E+07	1.48E+06	1.09E+07	
88195365	SAOUHSC_01658		endonuclease IV, putative			5.75E+06		4.23E+06	
88193826	SAOUHSC_00003		hypothetical protein SAOUHSC_00003	2.13E+06	5.85E+05	2.18E+06			
88194019	SAOUHSC_00211		hypothetical protein SAOUHSC_00211					1.33E+06	
88194530	SAOUHSC_00767	YfiA	hypothetical protein SAOUHSC_00767			4.34E+06		1.18E+07	1.36E+06
88194853	SAOUHSC_01107		hypothetical protein SAOUHSC_01107	1.57E+06	2.24E+06	1.23E+06		8.86E+05	
88195483	SAOUHSC_01782		hypothetical protein SAOUHSC_01782			1.59E+06		2.53E+06	
88194984	SAOUHSC_01251	PnpA	polyribonucleotide nucleotidyltransferase, putative	3.50E+06		4.00E+06		8.63E+06	
88196427	SAOUHSC_02791		pyrophosphohydrolase, putative	1.25E+06		7.31E+05		1.57E+06	
88194995	SAOUHSC_01262	RecA	recombination protein RecA, putative	3.20E+06		1.02E+06			
88195369	SAOUHSC_01662	SigA,RpoD	RNA polymerase sigma factor, putative					9.47E+05	
88195419	SAOUHSC_01714	GreA	transcription elongation factor GreA	7.49E+07	1.81E+07	8.38E+07	1.17E+07	6.38E+07	3.84E+07
88194976	SAOUHSC_01243	NusA	transcription termination-antitermination factor, putative	6.15E+06		2.46E+06		3.91E+06	
unbekannte Funktion (140)									
88195119	SAOUHSC_01392		ABC transporter, ATP-binding protein, putative	9.16E+06		1.77E+06		1.90E+06	
88194218	SAOUHSC_00426		ABC transporter, substrate-binding protein, putative					1.84E+07	5.85E+06
88194136	SAOUHSC_00336	Thl	acetyl-CoA acetyltransferase, putative	9.43E+06		5.73E+06		8.37E+06	

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88195775	SAOUHSC_02092	PepS,AmpS	aminopeptidase PepS, putative	6.03E+06	5.89E+06	6.04E+06	5.93E+05	9.14E+06	6.47E+05
88195965	SAOUHSC_02299	RsbW	anti-sigma B factor, putative			6.93E+05		1.33E+06	
88196008	SAOUHSC_02343	AtpG	ATP synthase F1, gamma subunit			3.77E+06		4.80E+06	
88196493	SAOUHSC_02862	ClpL	ATP-dependent Clp protease, ATP-binding subunit ClpC, putative			1.42E+07		2.52E+07	
88194148	SAOUHSC_00349	Ssb	bacteriophage L54a, single-stranded DNA binding protein	9.65E+06	8.63E+05	1.15E+07		8.83E+06	
88194292	SAOUHSC_00511	CysS	cysteinyI-tRNA synthetase			4.56E+06		8.75E+06	
88196221	SAOUHSC_02577		D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain protein	4.66E+06		1.28E+07		1.45E+07	2.56E+06
88194305	SAOUHSC_00525	RpoC	DNA directed RNA polymerase beta-prime chain, putative			4.41E+06		1.04E+07	
88195741	SAOUHSC_02057		dUTP pyrophosphatase	1.90E+06	1.92E+06	2.27E+06	1.28E+06	3.79E+06	3.69E+06
88194286	SAOUHSC_00505	ClpC	endopeptidase, putative			3.77E+06		9.00E+06	
88195685	SAOUHSC_01997	PerR	ferric uptake regulator-like protein, putative	2.00E+06		1.72E+06		1.39E+06	
88195654	SAOUHSC_01961	HemH	ferrochelataase			1.16E+06			
88196060	SAOUHSC_02399	GlmS	glucosamine--fructose-6-phosphate aminotransferase, isomerizing					1.25E+06	
88194173	SAOUHSC_00375	GuaA	GMP synthase, putative	7.50E+06		1.04E+07		1.69E+07	2.69E+05
88194808	SAOUHSC_01058	TypA	GTP-binding protein TypA, putative	4.48E+06		1.42E+06			
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025			3.78E+06	1.27E+06	3.21E+06	
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025						
88193948	SAOUHSC_00135		hypothetical protein SAOUHSC_00135			3.69E+06		3.55E+06	
88194032	SAOUHSC_00225		hypothetical protein SAOUHSC_00225	6.89E+06		9.19E+06	4.14E+06	1.04E+07	1.90E+07
88194062	SAOUHSC_00256		hypothetical protein SAOUHSC_00256				5.13E+05		
88194074	SAOUHSC_00269		hypothetical protein SAOUHSC_00269	5.54E+05					
88194145	SAOUHSC_00346	YchF	hypothetical protein SAOUHSC_00346	1.54E+06					
88194155	SAOUHSC_00356		hypothetical protein SAOUHSC_00356		1.15E+08	1.01E+07	4.70E+07	1.48E+07	7.33E+07
88194160	SAOUHSC_00362		hypothetical protein SAOUHSC_00362		5.61E+05	6.10E+05	6.27E+05		1.21E+06
88194167	SAOUHSC_00369		hypothetical protein SAOUHSC_00369	6.31E+06	6.64E+06	1.69E+07	2.42E+06	1.89E+07	9.05E+06

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88194169	SAOUHSC_00371		hypothetical protein SAOUHSC_00371			2.44E+07	4.41E+06	4.42E+07	1.68E+07
88194180	SAOUHSC_00383		hypothetical protein SAOUHSC_00383		3.06E+07		3.27E+06		3.10E+06
88194187	SAOUHSC_00392		hypothetical protein SAOUHSC_00392		4.85E+06				
88194194	SAOUHSC_00399		hypothetical protein SAOUHSC_00399	2.59E+07	8.87E+06	4.13E+06	6.74E+05	2.94E+06	
88194195	SAOUHSC_00400		hypothetical protein SAOUHSC_00400	1.79E+07	9.98E+06	4.60E+06		3.30E+06	
88194196	SAOUHSC_00401		hypothetical protein SAOUHSC_00401		4.18E+07				
88194234	SAOUHSC_00444		hypothetical protein SAOUHSC_00444	6.33E+06		4.42E+06		4.43E+06	
88194256	SAOUHSC_00469	SpoVG	hypothetical protein SAOUHSC_00469		9.30E+06	8.26E+06	3.73E+06	9.06E+06	2.00E+07
88194281	SAOUHSC_00500		hypothetical protein SAOUHSC_00500	1.23E+06					
88194322	SAOUHSC_00542		hypothetical protein SAOUHSC_00542	3.79E+06		1.89E+06			
88194328	SAOUHSC_00549		hypothetical protein SAOUHSC_00549			5.61E+05			
88194387	SAOUHSC_00617		hypothetical protein SAOUHSC_00617	5.58E+07		1.90E+08	5.55E+08	1.57E+08	6.33E+08
88194440	SAOUHSC_00675		hypothetical protein SAOUHSC_00675	8.33E+06		2.01E+06		4.66E+06	
88194451	SAOUHSC_00686		hypothetical protein SAOUHSC_00686	2.08E+06	1.45E+06	3.78E+06			
88194469	SAOUHSC_00704		hypothetical protein SAOUHSC_00704		1.20E+08		1.87E+07		1.69E+07
88194519	SAOUHSC_00755		hypothetical protein SAOUHSC_00755	2.09E+06					
88194596	SAOUHSC_00838	truncated- SA	hypothetical protein SAOUHSC_00838			1.20E+06			
88194602	SAOUHSC_00844		hypothetical protein SAOUHSC_00844		3.71E+06	9.66E+05	2.41E+06	1.13E+06	6.08E+06
88194603	SAOUHSC_00845		hypothetical protein SAOUHSC_00845		7.86E+07		8.41E+06	1.80E+07	2.92E+07
88194622	SAOUHSC_00865		hypothetical protein SAOUHSC_00865	1.75E+07	1.36E+06	2.09E+07	1.12E+06	1.71E+07	2.45E+06
88194634	SAOUHSC_00877		hypothetical protein SAOUHSC_00877			2.28E+06			
88194663	SAOUHSC_00906		hypothetical protein SAOUHSC_00906	3.09E+07		3.77E+07		1.74E+07	
88194666	SAOUHSC_00909		hypothetical protein SAOUHSC_00909	1.21E+06					
88194674	SAOUHSC_00917		hypothetical protein SAOUHSC_00917			8.37E+05			
88194729	SAOUHSC_00972		hypothetical protein SAOUHSC_00972			1.27E+06			

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88194787	SAOUHSC_01035		hypothetical protein SAOUHSC_01035					2.40E+06	
88194788	SAOUHSC_01036		hypothetical protein SAOUHSC_01036		2.37E+06			2.34E+06	9.69E+06
88194802	SAOUHSC_01050		hypothetical protein SAOUHSC_01050			6.29E+05			5.24E+05
88194810	SAOUHSC_01061		hypothetical protein SAOUHSC_01061	3.21E+06		3.41E+06		3.46E+06	
88194858	SAOUHSC_01112		hypothetical protein SAOUHSC_01112		4.68E+06				
88194877	SAOUHSC_01135		hypothetical protein SAOUHSC_01135			5.67E+07	3.06E+08	7.27E+07	5.72E+08
88194878	SAOUHSC_01136		hypothetical protein SAOUHSC_01136			2.03E+07		2.23E+07	
88194880	SAOUHSC_01138		hypothetical protein SAOUHSC_01138		1.73E+06	5.48E+06	7.87E+05	1.09E+07	1.77E+06
88194895	SAOUHSC_01154		hypothetical protein SAOUHSC_01154	3.49E+06	1.65E+06	8.40E+06		4.46E+06	
88194931	SAOUHSC_01192		hypothetical protein SAOUHSC_01192			9.97E+05			
88194932	SAOUHSC_01193		hypothetical protein SAOUHSC_01193	1.89E+06					
88194985	SAOUHSC_01252		hypothetical protein SAOUHSC_01252					1.70E+06	
88195001	SAOUHSC_01268		hypothetical protein SAOUHSC_01268				1.56E+05		5.36E+05
88195053	SAOUHSC_01323		hypothetical protein SAOUHSC_01323	1.97E+07		1.80E+07	1.44E+05	1.67E+07	
88195118	SAOUHSC_01391		hypothetical protein SAOUHSC_01391			2.98E+06		2.87E+06	
88195139	SAOUHSC_01413		hypothetical protein SAOUHSC_01413	1.30E+06					
88195140	SAOUHSC_01414		hypothetical protein SAOUHSC_01414	2.69E+06	1.18E+06	2.64E+06		1.77E+06	
88195160	SAOUHSC_01436		hypothetical protein SAOUHSC_01436	3.51E+06	2.54E+06	2.12E+06	6.13E+05	1.56E+06	5.37E+05
88195162	SAOUHSC_01438		hypothetical protein SAOUHSC_01438		2.20E+06				
88195168	SAOUHSC_01447		hypothetical protein SAOUHSC_01447	2.65E+05		3.01E+05		2.28E+05	
88195193	SAOUHSC_01476		hypothetical protein SAOUHSC_01476			4.87E+05			
88195197	SAOUHSC_01480		hypothetical protein SAOUHSC_01480	2.41E+05					
88195315	SAOUHSC_01604		hypothetical protein SAOUHSC_01604			2.04E+06		2.37E+06	
88195321	SAOUHSC_01610		hypothetical protein SAOUHSC_01610	4.27E+06	1.01E+06	2.88E+06			
88195356	SAOUHSC_01648		hypothetical protein SAOUHSC_01648		8.48E+05				
88195401	SAOUHSC_01695		hypothetical protein SAOUHSC_01695	1.01E+06					

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88195424	SAOUHSC_01719		hypothetical protein SAOUHSC_01719						2.42E+06
88195426	SAOUHSC_01721		hypothetical protein SAOUHSC_01721						3.52E+06
88195435	SAOUHSC_01730	CsbD	hypothetical protein SAOUHSC_01730		2.75E+06			4.25E+05	
88195462	SAOUHSC_01761		hypothetical protein SAOUHSC_01761		2.18E+06		1.81E+06		2.21E+06
88195514	SAOUHSC_01814		hypothetical protein SAOUHSC_01814			1.61E+06			7.91E+05
88195515	SAOUHSC_01815		hypothetical protein SAOUHSC_01815	3.56E+06		9.13E+06	8.12E+05	1.05E+07	3.13E+06
88195519	SAOUHSC_01819		hypothetical protein SAOUHSC_01819	4.27E+06		2.42E+07		4.91E+07	3.17E+06
88195566	SAOUHSC_01869		hypothetical protein SAOUHSC_01869		6.27E+05			7.34E+05	
88195602	SAOUHSC_01907		hypothetical protein SAOUHSC_01907			5.86E+06	3.68E+05	7.57E+06	1.72E+06
88195613	SAOUHSC_01918		hypothetical protein SAOUHSC_01918		1.90E+05	2.28E+06		3.09E+06	
88195660	SAOUHSC_01968	Hit	hypothetical protein SAOUHSC_01968	4.85E+06		4.20E+06			
88195668	SAOUHSC_01977		hypothetical protein SAOUHSC_01977	4.19E+06	1.52E+07	4.03E+06	3.46E+06		1.23E+07
88195670	SAOUHSC_01979		hypothetical protein SAOUHSC_01979	1.09E+07		3.79E+06		3.44E+06	
88195687	SAOUHSC_01999		hypothetical protein SAOUHSC_01999			2.87E+06	3.96E+05	7.57E+06	1.10E+06
88195701	SAOUHSC_02013		hypothetical protein SAOUHSC_02013			4.83E+06		6.29E+06	5.37E+06
88195723	SAOUHSC_02037		hypothetical protein SAOUHSC_02037						
88195729	SAOUHSC_02044		hypothetical protein SAOUHSC_02044		1.91E+07		2.22E+06		
88195757	SAOUHSC_02073		hypothetical protein SAOUHSC_02073		1.05E+07			5.29E+06	2.75E+06
88195845	SAOUHSC_02167		hypothetical protein SAOUHSC_02167	2.38E+06	2.99E+07	2.49E+06	1.02E+07		6.44E+06
88195892	SAOUHSC_02218		hypothetical protein SAOUHSC_02218	2.60E+06	1.04E+06	5.42E+06	1.33E+06	4.87E+06	4.95E+06
88196058	SAOUHSC_02396		hypothetical protein SAOUHSC_02396			1.45E+06		1.30E+06	
88196065	SAOUHSC_02404	FmtB	hypothetical protein SAOUHSC_02404		2.59E+05	2.44E+05			
88196067	SAOUHSC_02406		hypothetical protein SAOUHSC_02406						1.50E+06
88196081	SAOUHSC_02425		hypothetical protein SAOUHSC_02425			1.83E+07		4.59E+07	
88196212	SAOUHSC_02568		hypothetical protein SAOUHSC_02568	2.02E+06		1.30E+06			3.66E+06
88196237	SAOUHSC_02594		hypothetical protein SAOUHSC_02594	4.83E+05					

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88196330	SAOUHSC_02690		hypothetical protein SAOUHSC_02690				1.77E+06		6.77E+06
88196364	SAOUHSC_02724		hypothetical protein SAOUHSC_02724						1.91E+06
88196410	SAOUHSC_02774		hypothetical protein SAOUHSC_02774						5.38E+05
88196513	SAOUHSC_02885		hypothetical protein SAOUHSC_02885				4.46E+06		6.31E+06
88196527	SAOUHSC_02899		hypothetical protein SAOUHSC_02899					2.77E+05	
88196540	SAOUHSC_02912		hypothetical protein SAOUHSC_02912	7.45E+06		5.22E+06		7.17E+06	
88196593	SAOUHSC_02972	IsaB	hypothetical protein SAOUHSC_02972	4.85E+06		4.14E+07	2.35E+07	5.26E+07	3.27E+07
88196640	SAOUHSC_03022		hypothetical protein SAOUHSC_03022			3.60E+06	4.44E+05	6.00E+06	2.66E+06
88194172	SAOUHSC_00374	GuaB	inosine-5'-monophosphate dehydrogenase	3.25E+07		8.81E+07		7.87E+07	
88196290	SAOUHSC_02650		lipoprotein, putative		6.77E+06	1.39E+06	1.01E+07	3.65E+06	2.05E+07
88195813	SAOUHSC_02133		nicotinate phosphoribosyltransferase, putative			7.19E+05		1.69E+06	
88195317	SAOUHSC_01606		peptidase T, putative			1.84E+06		2.04E+06	
88195728	SAOUHSC_02043		phage head protein, putative	1.01E+07	1.09E+08	7.85E+06	2.69E+06	5.73E+06	
88196598	SAOUHSC_02978		phage infection protein, putative		6.85E+06		4.73E+06		4.44E+06
88195722	SAOUHSC_02036		phage structural protein, putative	2.25E+06	8.13E+06				
88195710	SAOUHSC_02022		phage tail fiber protein, putative		3.57E+06				
88195727	SAOUHSC_02042		phi Mu50B-like protein		3.85E+06				
88195758	SAOUHSC_02074		phi PVL orf 39-like protein						2.49E+06
88195715	SAOUHSC_02028		phiETA ORF57-like protein		4.01E+05				
88194561	SAOUHSC_00801	SecG	preprotein translocase, SecG subunit		9.80E+05		2.05E+06		2.27E+06
88194280	SAOUHSC_00499		pyridoxine biosynthesis protein	4.01E+07		2.33E+07		2.90E+07	
88194307	SAOUHSC_00527	RpsL	ribosomal protein S12			2.74E+06			
88194304	SAOUHSC_00524	RpoB	RNA polymerase beta chain, putative	1.16E+07		1.07E+07		2.04E+07	
88195999	SAOUHSC_02333		sceD protein, putative	2.67E+07	2.15E+09	4.13E+06	4.94E+08	1.88E+06	
88195755	SAOUHSC_02071		single-strand DNA-binding protein, putative		2.00E+06	7.76E+06	3.23E+06	1.57E+07	3.69E+08
88194333	SAOUHSC_00554		SIS domain protein			9.22E+05		1.06E+06	1.29E+07

Accession- Nummer	Locus Tag ^A	Protein- name ^A	Beschreibung	Intensität [TSB, expP] ^B	Intensität [pMEM, expP] ^B	Intensität [TSB, f-statP] ^B	Intensität [pMEM, f-statP] ^B	Intensität [TSB, s-statP] ^B	Intensität [pMEM, s-statP] ^B
88195714	SAOUHSC_02027		SLT orf 129-like protein		1.86E+07		2.31E+06		1.44E+06
88195966	SAOUHSC_02300	RsbV	STAS domain, putative	1.26E+07		1.59E+07		1.44E+07	9.01E+06
88194298	SAOUHSC_00517	NusG	transcription antitermination protein, putative			1.30E+06	3.93E+05	2.56E+06	
88196079	SAOUHSC_02423		UDP-N-acetylglucosamine pyrophosphorylase, putative	4.56E+06		5.49E+06		6.80E+06	

Je 3 biologische Replikate wurden für gelfreie Analysen aufgearbeitet. Dazu wurden 2 µg des bakteriellen Überstandes der exponentiellen Wachstumsphase, der frühen stationären und der späten stationären Phase in TSB und pMEM verdaut. Die Proteine wurden identifiziert (Scaffold) und in ihre biologische Kategorien eingeteilt (TigR).

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

^B Die Intensitäten wurden mit Hilfe der Rosetta-Elucidator-Software ermittelt.

expP = exponentielle Wachstumsphase, f-statP = frühe stationäre Phase, s-statP = späte stationäre Phase.

Tab. 61: Identifizierte Proteine der exponentiellen Wachstumsphase von *S. aureus* RN1HG und RN1HG $\Delta sigB$ in pMEM.

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
Toxine und Hämolsine (4)														
88194865	SAOUHSC_01121	Hla	alpha-hemolysin precursor hypothetical protein	36 kDa	x	x	ez	10.00	Y	7.38E+06	3.22E+08	1.18E-07	38.462	2, 5, 6, 7
88193943	SAOUHSC_00130	IsdI	SAOUHSC_00130 hypothetical protein	13 kDa	x		unb	2.50	N	6.59E+05	2.26E+06	1.31E-04	3.378	
88195915	SAOUHSC_02243		SAOUHSC_02243	40 kDa		x	ez	9.73	Y	4.94E+05	4.77E+06	1.70E-02	11.765	7
88195647	SAOUHSC_01954	LukD	leukotoxin, LukD	37 kDa	x	x	ez	9.98	#NV	1.04E+06	1.37E+06	2.22E-01	1.462	5
Virulenz-/Abwehrmechanismen (24)														
88193871	SAOUHSC_00051	Plc	1-phosphatidylinositol phosphodiesterase precursor, putative	37 kDa	x	x	ez	9.97	Y	2.74E+06	1.11E+07	9.00E-03	4.878	7, 8
88196592	SAOUHSC_02971	Aur	aureolysin, putative	55 kDa	x	x	ez	9.97	Y	2.12E+07	3.59E+08	6.52E-10	17.857	7, 8
88194572	SAOUHSC_00812	ClfA	clumping factor	96 kDa	x	x	zw	10.00	Y	6.07E+07	9.97E+06	2.67E-36	-5.914	3, 7, 9, 10
88196585	SAOUHSC_02963	ClfB	clumping factor B, putative cysteine protease precursor, putative	94 kDa	x	x	zw	10.00	Y	5.83E+07	3.55E+07	6.48E-04	-1.599	
88194744	SAOUHSC_00987	SspB	putative	45 kDa	x	x	ez	9.55	Y	3.69E+07	4.47E+07	4.70E-02	1.294	7, 8
88195217	SAOUHSC_01501	EbpS	elastin binding protein extracellular matrix and plasma binding protein, putative	53 kDa	x	x	zw	9.06	#NV	4.66E+06	1.57E+06	6.90E-02	-2.374	
88194575	SAOUHSC_00816	Ssp,Empbp	binding protein, putative	38 kDa	x	x	unb	3.33	Y	2.47E+06	3.32E+06	3.01E-01	1.374	
88194860	SAOUHSC_01114	Efb	fibrinogen-binding protein glutamyl endopeptidase	19 kDa	x		ez	9.98	Y	5.08E+06	1.82E+06	1.50E-08	-2.344	
88194745	SAOUHSC_00988	SspA	precursor, putative	36 kDa	x	x	ez	10.00	Y	1.08E+07	2.41E+07	8.18E-04	2.695	5, 7, 8
88196115	SAOUHSC_02463	HysA	hyaluronate lyase hypothetical protein	92 kDa		x	ez	10.00	#NV	4.50E+05	2.49E+06	4.80E-02	6.849	
88194063	SAOUHSC_00257		SAOUHSC_00257 immunoglobulin G-binding protein Sbi, putative	11 kDa		x	unb	2.50	N	7.85E+05	3.66E+06	8.59E-04	5.263	
88196346	SAOUHSC_02706	Sbi	protein Sbi, putative	50 kDa	x	x	unb	3.33	#NV	1.34E+07	1.17E+08	7.47E-05	10.204	
88196625	SAOUHSC_03006	Lip	lipase	77 kDa		x	ez	9.73	Y	2.47E+07	4.40E+07	3.10E-02	2.237	1, 7, 8
88194101	SAOUHSC_00300	Geh	lipase precursor	76 kDa	x	x	ez	10.00	Y	2.69E+07	8.90E+07	2.00E-03	3.774	8
88196512	SAOUHSC_02883		LysM domain protein	28 kDa	x	x	ez	9.04	Y	6.52E+06	7.33E+06	2.64E-01	1.157	
88193885	SAOUHSC_00069		protein A	56 kDa	x	x	zw	10.00	Y	1.30E+08	7.66E+07	3.90E-02	-1.508	
88194325	SAOUHSC_00545		sdrD protein, putative	146 kDa	x	x	zw	10.00	Y	6.60E+07	5.42E+07	6.60E-02	-1.221	
88195635	SAOUHSC_01941	SplB	serine protease SplB	26 kDa		x	ez	9.73	Y	8.22E+05	4.09E+06	6.00E-03	5.747	7, 8
88195634	SAOUHSC_01939	SplC	serine protease SplC	26 kDa		x	ez	9.73	Y	3.66E+05	7.05E+05	3.60E-02	2.004	5, 7, 8

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195630	SAOUHSC_01935	SplF	serine protease SplF, putative	26 kDa	x	x	ez	9.73	#NV	4.02E+06	7.26E+06	1.30E-02	1.953	7, 8
88195808	SAOUHSC_02127		staphopain thiol proteinase staphylokinase precursor,	44 kDa	x	x	ez	9.73	Y	7.31E+06	3.20E+07	6.57E-04	5.181	5, 7, 8, 10
88195848	SAOUHSC_02171	Sak	putative	19 kDa	x	x	ez	9.98	Y	1.26E+07	8.71E+07	5.63E-04	7.407	7
88194577	SAOUHSC_00818	Nuc	thermonuclease precursor	25 kDa		x	ez	10.00	Y	9.11E+06	2.47E+07	2.25E-04	3.040	1, 5, 7, 10
88195480	SAOUHSC_01779	Tig	trigger factor	49 kDa	x	x	zyt	8.87	N	2.48E+07	5.54E+07	8.00E-03	2.488	
Zellwandbiosynthese und -abbau (14)														
88194219	SAOUHSC_00427		autolysin precursor, putative bifunctional autolysin precursor,	36 kDa	x	x	ez	9.98	Y	2.21E+07	2.50E+07	5.07E-01	1.148	8
88194750	SAOUHSC_00994	Atl	putative	137 kDa	x	x	ez	10.00	#NV	7.05E+08	1.01E+09	1.04E-01	1.447	10
88195790	SAOUHSC_02108	Ftn	ferritin, putative	20 kDa	x	x	zyt	9.98	N	2.79E+06	2.71E+06	7.75E-01	1.100	
88193909	SAOUHSC_00094		hypothetical protein SAOUHSC_00094 immunodominant antigen A,	22 kDa	x	x	zw	9.93	Y	5.53E+07	1.58E+08	1.50E-02	3.030	
88196515	SAOUHSC_02887	IsaA	putative	24 kDa	x	x	ez	10.00	Y	2.79E+09	2.54E+09	3.06E-01	-1.088	8
88194887	SAOUHSC_01145	PbpA	penicillin-binding protein 1	83 kDa	x	x	zm	9.82	Y	1.90E+05	5.82E+05	1.06E-04	3.125	
88195184	SAOUHSC_01467	Pbp2	penicillin-binding protein 2	80 kDa	x	x	ez	9.55	N	4.95E+06	1.06E+07	4.95E-08	2.183	
88195360	SAOUHSC_01652	PbpF,Pbp3	penicillin-binding protein 3 peptidoglycan hydrolase,	77 kDa	x	x	zm	9.82	#NV	1.36E+06	2.44E+06	2.83E-07	1.821	
88194055	SAOUHSC_00248	LytM	putative	34 kDa	x	x	ez	9.98	Y	4.11E+09	1.28E+09	1.62E-06	-2.749	
88194324	SAOUHSC_00544		sdrC protein, putative secretory antigen precursor,	108 kDa	x	x	zw	10.00	Y	1.42E+07	2.24E+07	7.53E-07	1.592	
88196215	SAOUHSC_02571	SsaA	putative secretory antigen SsaA-like	29 kDa	x	x	ez	9.04	Y	3.06E+08	9.89E+08	3.72E-24	3.195	7
88194436	SAOUHSC_00671		protein truncated MHC class II analog	28 kDa	x	x	ez	9.73	Y	8.84E+08	7.69E+08	3.78E-01	-1.109	
88196118	SAOUHSC_02466		protein truncated MHC class II analog	15 kDa	x		unb	3.33	Y	5.05E+07	7.71E+05	4.61E-13	-56.272	
88194675	SAOUHSC_00918		protein	16 kDa	x	x	unb	3.33	Y	5.55E+08	8.55E+08	6.85E-05	1.560	7, 10
Zellumhüllung (16)														
88194626	SAOUHSC_00869	DltA	D-alanine-activating enzyme	55 kDa		x	zyt	9.98	N	2.55E+05	8.24E+05	1.20E-02	3.546	
88194628	SAOUHSC_00871	DltC	D-alanyl carrier protein	9 kDa	x	x	zyt	8.87	N	1.28E+06	4.92E+06	2.00E-03	3.937	
88194199	SAOUHSC_00405		hypothetical protein SAOUHSC_00405	29 kDa		x	unb	2.50	N	1.47E+06	2.52E+06	5.00E-03	1.718	
88194482	SAOUHSC_00717		hypothetical protein	16 kDa	x	x	unb	3.33	Y	4.08E+07	1.02E+08	1.54E-06	2.475	

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
			SAOUHSC_00717											
88194829	SAOUHSC_01081	IsdA	hypothetical protein SAOUHSC_01081	39 kDa	x	x	zw	10.00	N	2.14E+07	6.86E+07	1.97E-04	3.436	7
88194830	SAOUHSC_01082	IsdC	hypothetical protein SAOUHSC_01082	25 kDa	x	x	unb	3.33	Y	3.67E+06	1.55E+07	2.90E-02	5.155	10
88195443	SAOUHSC_01739	LytH	hypothetical protein SAOUHSC_01739	33 kDa	x	x	unb	3.33	N	4.09E+06	4.42E+06	9.70E-01	-1.016	
88195590	SAOUHSC_01895		hypothetical protein SAOUHSC_01895	33 kDa	x	x	ez	9.55	Y	9.10E+06	8.82E+06	9.98E-01	1.001	
88195802	SAOUHSC_02121		hypothetical protein SAOUHSC_02121	45 kDa	x	x	unb	3.33	Y	8.35E+06	1.04E+07	1.40E-02	1.256	
88196419	SAOUHSC_02783		hypothetical protein SAOUHSC_02783	31 kDa		x	unb	2.50	#NV	1.41E+06	2.33E+06	2.40E-02	1.658	
88196425	SAOUHSC_02789		hypothetical protein SAOUHSC_02789	28 kDa		x	zyt	8.87	N	1.45E+05	2.46E+05	8.90E-02	1.761	
88196433	SAOUHSC_02798		hypothetical protein SAOUHSC_02798	179 kDa	x	x	zw	10.00	N	7.94E+05	5.63E+05	4.69E-01	-1.271	
88196599	SAOUHSC_02979		hypothetical protein SAOUHSC_02979	69 kDa	x	x	ez	9.73	Y	3.20E+07	1.65E+08	1.00E-02	6.289	
88196601	SAOUHSC_02982		hypothetical protein SAOUHSC_02982	71 kDa	x	x	zw	10.00	Y	5.29E+07	9.23E+07	2.00E-03	1.953	
88193889	SAOUHSC_00074	SirA	periplasmic binding protein, putative	37 kDa	x	x	unb	3.33	Y	6.25E+06	2.57E+07	5.60E-29	4.065	10
88195460	SAOUHSC_01759	Mrec	rod shape-determining protein Mrec	31 kDa	x	x	unb	3.33	Y	4.72E+06	1.22E+07	5.54E-23	2.558	
Stressantwort (13)														
88194163	SAOUHSC_00365	AhpC	alkyl hydroperoxide reductase	21 kDa	x	x	zyt	9.98	N	5.23E+07	1.24E+08	2.00E-03	2.577	
88194162	SAOUHSC_00364	AhpF	alkyl hydroperoxide reductase, subunit F, putative	55 kDa		x	zyt	9.98	N	1.15E+06	3.53E+06	3.20E-02	3.774	
88195057	SAOUHSC_01327	KatA	catalase	55 kDa	x	x	zyt	9.98	N	2.67E+07	1.92E+07	2.87E-01	-1.372	6, 10
88195926	SAOUHSC_02255	GroES	chaperonin, 10 kDa, GroES, putative	10 kDa	x		zyt	10.00	N	5.19E+05	6.68E+05	4.23E-01	1.357	
88195925	SAOUHSC_02254	GroL,GroEL	chaperonin, 60 kDa, GrpEL, putative	58 kDa	x	x	zyt	9.98	N	6.42E+06	1.57E+07	4.00E-03	2.618	
88195129	SAOUHSC_01403	CspA	cold shock protein, putative	7 kDa	x	x	zyt	9.98	N	4.34E+07	7.68E+07	1.92E-05	1.789	
88195522	SAOUHSC_01822	Tpx	hypothetical protein SAOUHSC_01822	18 kDa	x	x	unb	2.50	N	3.43E+06	7.94E+06	3.50E-02	2.519	
88196044	SAOUHSC_02381	Dps	hypothetical protein SAOUHSC_02381	17 kDa	x	x	unb	2.50	N	6.58E+06	1.41E+07	1.04E-01	2.433	

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88196094	SAOUHSC_02441	Asp23	hypothetical protein SAOUHSC_02441	19 kDa	x		unb	2.50	N	2.58E+07	8.73E+05	2.33E-20	-24.235	4, 7, 10
88195361	SAOUHSC_01653	SodA	superoxide dismutase, Mn, putative	23 kDa	x	x	ez	9.55	N	6.39E+06	4.72E+06	1.93E-01	-1.266	
88193908	SAOUHSC_00093	SodM	superoxide dismutase, putative	23 kDa		x	ez	9.55	N	3.82E+06	1.75E+07	6.67E-07	5.025	7, 10
88194846	SAOUHSC_01100	TrxA,Trx	thioredoxin	11 kDa	x	x	zyt	9.98	N	3.58E+07	5.32E+07	7.80E-02	1.610	
88194592	SAOUHSC_00834		thioredoxin, putative	12 kDa	x	x	zyt	8.87	N	1.19E+07	1.53E+07	2.36E-01	1.449	
Regulation (3)														
88194753	SAOUHSC_00997		hypothetical protein SAOUHSC_00997	46 kDa	x		unb	3.33	Y	2.13E+06	2.14E+06	8.34E-01	1.025	
88195657	SAOUHSC_01964	TRAP	hypothetical protein SAOUHSC_01964	20 kDa		x	zyt	8.87	#NV	3.64E+06	4.72E+06	3.79E-04	1.420	
88195154	SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA, putative	18 kDa		x	zyt	9.98	N	3.24E+06	9.09E+06	1.20E-02	3.135	
Transport (16)														
88194087	SAOUHSC_00284		5'-nucleotidase, lipoprotein e(P4) family	33 kDa		x	unb	3.33	Y	8.67E+05	8.24E+06	2.00E-03	11.236	7
88196085	SAOUHSC_02430	HtsA	ABC transporter periplasmic binding protein, putative	37 kDa	x		unb	3.33	Y	1.17E+06	2.52E+06	4.20E-02	2.110	
88194402	SAOUHSC_00634	MntC	ABC transporter, substrate- binding protein, putative	35 kDa	x	x	unb	3.33	Y	8.41E+08	1.03E+09	4.90E-01	1.248	
88194742	SAOUHSC_00985	MenB	enoyl-CoA hydratase/isomerase family protein, putative	30 kDa		x	zyt	8.87	N	4.62E+04	1.42E+05	4.40E-02	2.933	
88194831	SAOUHSC_01084	IsdD	hypothetical protein SAOUHSC_01084	41 kDa		x	unb	2.50	Y	1.40E+06	7.38E+06	5.90E-02	8.264	10
88194832	SAOUHSC_01085	IsdE	hypothetical protein SAOUHSC_01085	32 kDa		x	zyt	8.87	N	4.86E+05	1.51E+06	1.20E-02	3.165	
88195556	SAOUHSC_01858		hypothetical protein SAOUHSC_01858	22 kDa	x	x	zyt	9.98	N	8.86E+05	1.75E+06	2.20E-02	2.075	
88195571	SAOUHSC_01874		hypothetical protein SAOUHSC_01874	11 kDa	x		unb	2.50	N	2.24E+06	3.43E+06	1.12E-01	1.689	
88195914	SAOUHSC_02241		hypothetical protein SAOUHSC_02241	39 kDa		x	ez	9.73	Y	8.93E+05	1.04E+07	4.12E-04	11.905	7
88196199	SAOUHSC_02554	FhuD2	hypothetical protein SAOUHSC_02554	34 kDa	x	x	unb	3.33	Y	2.46E+06	4.70E+06	1.00E-03	2.058	
88196339	SAOUHSC_02699		hypothetical protein SAOUHSC_02699	29 kDa	x	x	unb	3.33	Y	2.52E+06	4.42E+06	4.30E-02	1.972	
88196194	SAOUHSC_02549	ModA	molybdenum ABC transporter,	29 kDa		x	unb	3.33	Y	1.15E+06	2.32E+06	1.70E-02	2.237	

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194828	SAOUHSC_01079	IsdB	periplasmic molybdate-binding protein	72 kDa		x	zw	10.00	#NV	4.21E+05	8.14E+05	1.62E-01	3.175	
88194684	SAOUHSC_00927	OppA	neurofilament protein	62 kDa	x	x	zw	9.18	Y	1.34E+06	2.35E+06	3.60E-02	2.358	
88196403	SAOUHSC_02767	Opp- 1A,Opp1A	oligopeptide ABC transporter, substrate-binding protein, putative	60 kDa		x	zw	9.18	Y	5.49E+05	3.56E+06	4.95E-04	6.897	10
88194781	SAOUHSC_01028	PtsH	peptide ABC transporter, peptide-binding protein, putative phosphocarrier protein hpr, putative	9 kDa	x	x	zyt	10.00	N	1.79E+06	2.77E+06	3.81E-01	1.462	
zell. Prozesse (6)														
88194892	SAOUHSC_01150	FtsZ	cell division protein FtsZ	41 kDa		x	zyt	8.87	N	7.45E+05	1.51E+06	3.00E-03	2.110	
88194891	SAOUHSC_01149	FtsA	cell division protein, putative	53 kDa	x	x	zyt	8.87	N	3.17E+05	2.30E+05	9.72E-01	1.010	
88194886	SAOUHSC_01144	FtsL	hypothetical protein SAOUHSC_01144	15 kDa	x	x	zyt	8.87	N	6.22E+07	5.11E+07	3.81E-01	-1.515	
88194898	SAOUHSC_01158		hypothetical protein SAOUHSC_01158	24 kDa	x	x	zyt	8.87	N	2.13E+06	5.35E+05	3.00E-02	-3.867	
88195179	SAOUHSC_01462		hypothetical protein SAOUHSC_01462	13 kDa	x	x	zyt	8.87	N	1.91E+07	7.53E+06	4.66E-04	-2.408	
88195846	SAOUHSC_02169	Chs,Chp	hypothetical protein SAOUHSC_02169	17 kDa	x	x	unb	3.33	Y	2.85E+07	3.75E+08	2.31E-18	12.658	
Energiemetabolismus (39)														
88195316	SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase, decarboxylating	52 kDa	x	x	zyt	8.87	N	4.01E+06	9.98E+06	3.00E-03	2.611	
88195075	SAOUHSC_01347	CitB,AcnA	aconitate hydratase 1	99 kDa	x	x	zyt	9.98	N	1.82E+06	2.99E+06	5.40E-02	1.848	
88196007	SAOUHSC_02341	AtpD	ATP synthase F1, beta subunit	51 kDa		x	zyt	8.87	N	7.76E+05	1.48E+06	7.00E-03	1.953	
88194795	SAOUHSC_01043	PdhD,LpdA	dihydrolipoamide dehydrogenase	49 kDa	x	x	zyt	9.98	N	2.30E+07	3.71E+07	2.90E-02	1.770	
88194794	SAOUHSC_01042	PdhC	dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase complex E2, putative	46 kDa		x	zyt	9.98	N	1.19E+06	3.43E+06	1.00E-03	2.882	
88196464	SAOUHSC_02830	Ddh	D-lactate dehydrogenase, putative	35 kDa	x	x	zyt	9.98	N	1.24E+06	1.18E+06	8.52E-01	1.057	
88194559	SAOUHSC_00799	Eno	enolase	47 kDa	x	x	zyt	9.98	N	5.04E+07	8.51E+07	5.20E-02	1.866	
88196553	SAOUHSC_02926		fructose-bisphosphate aldolase class-I, putative	33 kDa	x	x	unb	2.50	N	3.17E+07	8.99E+07	5.86E-05	2.967	

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195310	SAOUHSC_01599	Zwf	glucose-6-phosphate 1- dehydrogenase	57 kDa	x	x	zyt	8.87	N	5.29E+05	5.87E+05	6.83E-01	1.115	
88194657	SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase	50 kDa	x	x	zyt	9.98	N	5.54E+06	1.01E+07	4.00E-03	1.894	
88194555	SAOUHSC_00795	Gap1,Gap	glyceraldehyde-3-phosphate dehydrogenase, type I	36 kDa	x	x	zyt	9.98	N	1.16E+08	1.72E+08	5.50E-02	1.626	
88194594	SAOUHSC_00836	GcvH	glycine cleavage system H protein	14 kDa	x	x	zyt	8.87	N	6.36E+06	1.07E+07	9.00E-02	1.845	
88194312	SAOUHSC_00532	Kbl	hypothetical protein SAOUHSC_00532	43 kDa	x	x	zyt	8.87	N	6.71E+05	1.34E+06	4.40E-02	2.188	
88194332	SAOUHSC_00553		hypothetical protein SAOUHSC_00553	22 kDa	x	x	zyt	8.87	N	2.58E+06	3.52E+06	2.28E-01	1.527	
88194493	SAOUHSC_00728		hypothetical protein SAOUHSC_00728	74 kDa	x	x	zm	9.99	Y	7.89E+07	2.03E+08	1.00E-03	2.667	
88194654	SAOUHSC_00897	GlpQ	hypothetical protein SAOUHSC_00897	35 kDa		x	unb	4.86	#NV	5.62E+06	1.83E+07	6.85E-04	3.425	7, 8
88194760	SAOUHSC_01005		hypothetical protein SAOUHSC_01005	11 kDa	x	x	unb	3.33	#NV	2.83E+07	3.52E+07	1.52E-01	1.235	
88195141	SAOUHSC_01415		hypothetical protein SAOUHSC_01415	30 kDa		x	zyt	8.87	N	1.53E+05	5.69E+05	1.30E-02	3.984	
88195558	SAOUHSC_01860		hypothetical protein SAOUHSC_01860	12 kDa	x	x	zyt	8.87	N	3.65E+06	4.58E+06	9.90E-02	1.515	
88195596	SAOUHSC_01901		hypothetical protein SAOUHSC_01901	26 kDa		x	unb	2.50	N	2.35E+06	7.50E+06	1.80E-02	3.559	
88195678	SAOUHSC_01987		hypothetical protein SAOUHSC_01987	22 kDa		x	zyt	8.87	#NV	2.90E+06	3.90E+06	2.01E-01	1.456	
88195820	SAOUHSC_02140	PpaC	hypothetical protein SAOUHSC_02140	34 kDa	x	x	zyt	8.87	N	8.11E+05	1.88E+06	2.40E-02	2.660	
88195823	SAOUHSC_02143		hypothetical protein SAOUHSC_02143	39 kDa	x	x	zyt	8.87	N	2.08E+06	3.62E+06	8.18E-07	1.733	8
88195830	SAOUHSC_02150		hypothetical protein SAOUHSC_02150	22 kDa	x	x	unb	2.50	N	1.56E+06	4.20E+06	5.00E-03	2.967	
88196029	SAOUHSC_02366	FbaA, Fba	hypothetical protein SAOUHSC_02366	31 kDa	x	x	zyt	8.87	N	7.54E+06	2.19E+07	1.00E-03	3.205	
88196098	SAOUHSC_02445		hypothetical protein SAOUHSC_02445	37 kDa		x	zyt	8.87	N	1.33E+05	2.41E+05	1.53E-01	1.838	
88196112	SAOUHSC_02460		hypothetical protein SAOUHSC_02460	32 kDa		x	zyt	8.87	#NV	5.78E+05	1.10E+06	8.20E-02	2.212	
88196549	SAOUHSC_02922	Ldh2,Ldh	L-lactate dehydrogenase	34 kDa		x	zyt	9.65	N	8.55E+05	3.22E+06	1.01E-06	4.329	
88195510	SAOUHSC_01810		NADP-dependent malic enzyme, putative	44 kDa	x	x	zm	7.63	N	1.82E+06	4.49E+06	3.00E-03	2.584	
88194349	SAOUHSC_00574	Pta	phosphate acetyltransferase	35 kDa	x	x	zyt	8.87	N	2.76E+06	8.50E+06	3.00E-03	3.279	

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88194782	SAOUHSC_01029	PtsI	phosphoenolpyruvate-protein phosphotransferase	63 kDa	x	x	zyt	10.00	N	1.23E+06	3.13E+06	6.00E-03	2.732	
88194556	SAOUHSC_00796	Pgk	phosphoglycerate kinase, putative	43 kDa		x	zyt	9.91	N	1.48E+06	3.99E+06	6.00E-03	2.994	
88194792	SAOUHSC_01040	PdhA	pyruvate dehydrogenase complex, E1 component, alpha subunit, putative	41 kDa	x	x	zyt	8.87	N	1.03E+07	1.76E+07	7.00E-03	1.773	
88194793	SAOUHSC_01041	PhdB,PdhB	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	35 kDa	x	x	zyt	8.87	N	1.58E+07	3.05E+07	7.00E-03	2.092	
88195506	SAOUHSC_01806	PykA,Pyk	pyruvate kinase	63 kDa		x	zyt	8.87	N	1.07E+06	2.28E+06	8.00E-03	2.222	
88194758	SAOUHSC_01002	QoxA	quinol oxidase AA3, subunit II, putative	42 kDa	x	x	zm	10.00	Y	2.23E+06	2.87E+06	3.78E-01	1.289	
88194953	SAOUHSC_01216	SucC	succinyl-CoA synthetase, beta subunit, putative	42 kDa	x	x	zyt	8.87	N	9.17E+05	1.65E+06	2.20E-02	1.715	
88195066	SAOUHSC_01337	Tkt	transketolase	68 kDa	x	x	unb	2.50	N	5.31E+06	1.28E+07	5.00E-03	2.591	
88194557	SAOUHSC_00797	TpiA,Tpi	triosephosphate isomerase	27 kDa	x	x	unb	2.50	N	3.78E+07	5.85E+07	8.30E-02	1.792	
Proteinbiosynthese (36)														
88195210	SAOUHSC_01493	RpsA	30S ribosomal protein S1, putative	43 kDa	x	x	zyt	9.98	N	9.64E+06	2.41E+07	2.20E-02	2.915	
88196150	SAOUHSC_02500	RplE	50S ribosomal protein L5, putative	20 kDa	x	x	zyt	8.87	#NV	3.98E+06	4.94E+06	6.21E-01	1.126	
88194381	SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	62 kDa	x	x	zyt	9.98	N	1.31E+06	3.01E+06	6.21E-05	2.257	
88195444	SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr) deacylase	17 kDa	x		unb	2.50	N	3.44E+05	3.88E+05	2.20E-01	1.466	
88194290	SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	56 kDa	x	x	zyt	9.65	N	7.55E+05	8.38E+05	4.46E-01	1.513	
88195799	SAOUHSC_02117	GatA	glutamyl-tRNA(Gln) amidotransferase, A subunit	53 kDa		x	zyt	8.87	N	1.08E+05	3.34E+05	1.20E-02	3.115	
88195798	SAOUHSC_02116	GatB	glutamyl-tRNA(Gln) amidotransferase, B subunit	54 kDa		x	zyt	8.87	#NV	1.29E+06	5.41E+06	1.16E-12	4.608	
88195800	SAOUHSC_02118		glutamyl-tRNA(Gln) amidotransferase, C subunit	11 kDa	x	x	zyt	8.87	N	6.92E+06	3.98E+06	1.81E-01	-1.519	
88195373	SAOUHSC_01666	GlyS	glycyl-tRNA synthetase	54 kDa	x	x	zyt	10.00	N	6.09E+05	4.40E+05	1.53E-01	-1.363	
88196138	SAOUHSC_02487	RpsM	hypothetical protein SAOUHSC_02487	14 kDa	x	x	zyt	8.87	N	2.15E+06	1.90E+06	6.92E-01	-1.136	
88196161	SAOUHSC_02511	RplD	hypothetical protein SAOUHSC_02511	22 kDa	x	x	unb	2.50	N	7.83E+06	1.06E+07	6.60E-02	1.610	
88196022	SAOUHSC_02359	PrfA	peptide chain release factor I	40 kDa		x	zyt	9.98	N					

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194261	SAOUHSC_00474	RplY	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	24 kDa	x	x	zyt	8.87	#NV	4.36E+06	8.23E+06	6.20E-02	2.165	
88194300	SAOUHSC_00519	RplA	ribosomal protein L1	25 kDa	x	x	zyt	8.87	N	3.88E+06	5.92E+06	8.00E-03	1.580	
88194301	SAOUHSC_00520	RplJ	ribosomal protein L10	18 kDa		x	zyt	8.87	N	2.36E+06	5.88E+06	5.00E-03	2.801	
88194299	SAOUHSC_00518	RplK	ribosomal protein L11	15 kDa		x	zyt	8.87	N	2.63E+07	2.71E+07	6.31E-01	1.085	
88196130	SAOUHSC_02478	RplM	ribosomal protein L13	16 kDa	x	x	unb	2.50	N	1.89E+07	1.61E+07	4.38E-01	-1.170	
88196143	SAOUHSC_02492	RplO	ribosomal protein L15	16 kDa	x	x	unb	2.50	N	8.61E+05	3.63E+05	7.00E-03	-2.181	
88196146	SAOUHSC_02495	RplR	ribosomal protein L18	13 kDa	x	x	zyt	8.87	N	1.10E+07	7.03E+06	5.40E-02	-1.512	
88195458	SAOUHSC_01757	RplU	ribosomal protein L21	11 kDa	x	x	unb	2.50	N	8.75E+06	1.04E+07	1.06E-01	1.220	
88196157	SAOUHSC_02507	RplV	ribosomal protein L22	13 kDa	x	x	zyt	8.87	Y	1.39E+07	1.08E+07	2.39E-01	-1.328	
88196154	SAOUHSC_02504	RpmC	ribosomal protein L29	8 kDa	x		zyt	8.87	N	1.99E+06	1.12E+06	8.10E-02	-1.861	
88196144	SAOUHSC_02493	RpmD	ribosomal protein L30	7 kDa	x	x	unb	2.50	N	1.76E+07	6.47E+06	1.17E-05	-2.176	
88196024	SAOUHSC_02361	RpmE	ribosomal protein L31	10 kDa	x	x	unb	2.50	N	4.13E+07	1.95E+07	1.66E-01	-1.203	
88194302	SAOUHSC_00521	RplL	ribosomal protein L7/L12	13 kDa		x	zyt	8.87	N	5.13E+07	6.36E+07	2.24E-01	1.326	
88193838	SAOUHSC_00017	RplI	ribosomal protein L9	17 kDa	x		zyt	9.65	N	1.64E+06	9.05E+05	1.40E-02	-1.756	
88194965	SAOUHSC_01232	RpsB	ribosomal protein S2	28 kDa	x	x	zyt	8.87	#NV	7.37E+05	1.64E+06	4.64E-06	2.151	
88196145	SAOUHSC_02494	RpsE	ribosomal protein S5	18 kDa	x	x	zyt	8.87	#NV	2.02E+07	1.27E+07	8.90E-02	-1.586	
88194147	SAOUHSC_00348	RpsF	ribosomal protein S6	12 kDa	x	x	zyt	9.98	#NV	2.80E+07	2.33E+07	2.01E-01	-1.184	
88194308	SAOUHSC_00528	RpsG	ribosomal protein S7	18 kDa	x	x	zyt	8.87	N	2.52E+06	1.94E+06	3.31E-01	-1.366	
88196148	SAOUHSC_02498	RpsH	ribosomal protein S8, putative	15 kDa	x	x	zyt	8.87	N	1.21E+07	1.21E+07	8.01E-01	1.053	
88196129	SAOUHSC_02477	RpsI	ribosomal protein S9, putative	15 kDa	x	x	unb	2.50	#NV	1.78E+07	7.76E+06	9.75E-04	-2.282	
88194969	SAOUHSC_01236	Rrf,Frr	ribosome recycling factor	20 kDa	x	x	zyt	9.98	N	2.94E+07	2.99E+07	5.23E-01	1.215	
88194309	SAOUHSC_00529	FusA,Fus	translation elongation factor G	77 kDa	x	x	zyt	9.98	N	4.35E+06	1.22E+07	3.82E-05	2.924	
88194967	SAOUHSC_01234	Tsf	translation elongation factor Ts	32 kDa	x	x	zyt	9.98	#NV	1.05E+07	2.54E+07	0.00E+00	2.353	
88194310	SAOUHSC_00530	Tuf	translation elongation factor Tu	43 kDa	x	x	zyt	9.98	N	1.84E+07	5.79E+07	1.54E-05	3.413	
Proteinmetabolismus (18)														
88194678	SAOUHSC_00921	FabF,Fab	3-oxoacyl- synthase, putative 3-oxoacyl-(acyl-carrier-protein)	44 kDa		x	zyt	9.98	N	2.57E+06	7.15E+06	7.49E-04	2.959	
88194937	SAOUHSC_01199	FabG	reductase, putative	26 kDa		x	zyt	9.98	N	1.58E+05	2.16E+05	2.06E-01	1.799	
88194939	SAOUHSC_01201	HmrB,AcpP	acyl carrier protein	9 kDa	x	x	zyt	8.87	#NV	3.36E+07	5.27E+07	4.00E-02	1.661	
88195390	SAOUHSC_01684	GrpE	co-chaperone GrpE	24 kDa	x	x	zyt	8.87	N	1.70E+07	1.89E+07	4.15E-01	1.235	
88195389	SAOUHSC_01683	DnaK	DNAk protein, putative	66 kDa	x	x	zyt	9.98	N	1.21E+07	4.08E+07	1.77E-04	3.571	

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88196491	SAOUHSC_02860	MvaS	HMG-CoA synthase, putative	43 kDa	x	x	zyt	8.87	N	5.90E+06	1.31E+07	1.30E-02	2.433	
88194271	SAOUHSC_00486	FtsH	SAOUHSC_00486 hypothetical protein	78 kDa		x	zm	10.00	Y	2.46E+06	2.47E+06	6.04E-01	1.096	
88194313	SAOUHSC_00533		SAOUHSC_00533 hypothetical protein	32 kDa	x	x	unb	2.50	N	3.59E+06	1.81E+06	5.84E-04	-1.813	7, 10
88194677	SAOUHSC_00920	FabH	SAOUHSC_00920 hypothetical protein	34 kDa		x	unb	2.50	#NV	6.84E+05	1.70E+06	2.70E-04	2.591	
88194972	SAOUHSC_01239		SAOUHSC_01239 hypothetical protein	44 kDa	x	x	zm	9.99	N	5.22E+06	5.40E+06	9.07E-01	1.048	
88195110	SAOUHSC_01383		SAOUHSC_01383 hypothetical protein	69 kDa		x	zyt	9.98	N	6.86E+05	1.49E+06	2.00E-02	2.193	
88195565	SAOUHSC_01868		SAOUHSC_01868 malonyl CoA-acyl carrier	53 kDa	x	x	zyt	8.87	N	9.51E+05	2.01E+06	3.80E-02	2.500	
88194936	SAOUHSC_01198	FabD	protein transacylase	34 kDa		x	zyt	8.87	N	4.41E+05	1.73E+06	1.53E-05	4.444	
88195784	SAOUHSC_02102	Map	I	28 kDa	x	x	zyt	8.87	N	2.89E+06	3.64E+06	3.47E-01	1.252	
88194694	SAOUHSC_00937	PepF,PepB	oligoendopeptidase F	70 kDa	x	x	zyt	9.98	N	2.83E+06	2.65E+06	9.23E-01	1.031	
88194521	SAOUHSC_00757	PepT	peptidase T, putative	46 kDa		x	zyt	9.98	N	3.27E+05	3.82E+05	5.73E-01	1.193	
88194790	SAOUHSC_01038	Def	polypeptide deformylase	21 kDa	x	x	zyt	8.87	#NV	5.38E+06	4.74E+06	4.72E-01	-1.137	
88195663	SAOUHSC_01972	PrsA	protein export protein PrsA, putative	36 kDa	x	x	unb	3.33	Y	5.09E+06	1.57E+07	2.51E-20	3.049	
AS-Biosynthese (5)														
88194316	SAOUHSC_00536	IlvE	branched-chain amino acid aminotransferase	40 kDa		x	zyt	8.87	N	1.91E+06	4.88E+06	2.10E-02	2.941	
88195018	SAOUHSC_01287	GlnA	glutamine synthetase, type I	51 kDa	x	x	zyt	9.98	N	2.06E+07	2.10E+07	6.54E-01	1.098	
88194273	SAOUHSC_00488	CysK	SAOUHSC_00488 hypothetical protein	33 kDa	x	x	zyt	8.87	N	2.38E+06	2.70E+06	4.33E-01	1.233	
88195928	SAOUHSC_02257	SdrH	SAOUHSC_02257 serine hydroxymethyltransferase, putative	47 kDa	x	x	zw	9.18	Y	4.97E+06	6.77E+06	1.12E-01	1.372	
88196017	SAOUHSC_02354	GlyA		45 kDa	x	x	zyt	9.98	N	2.46E+06	3.70E+06	1.00E-03	1.493	
Nukleotidbiosynthese (11)														
88196141	SAOUHSC_02490	Adk	adenylate kinase, putative	24 kDa	x	x	zyt	9.98	N	4.09E+06	8.87E+06	6.00E-03	2.433	
88195807	SAOUHSC_02126	PurB	adenylosuccinate lyase	50 kDa	x	x	zyt	8.87	N	3.22E+05	8.44E+05	2.20E-02	2.801	
88193840	SAOUHSC_00019	PurA	adenylosuccinate synthetase	48 kDa	x	x	zyt	8.87	N	3.93E+06	7.42E+06	3.04E-05	2.075	

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88196031	SAOUHSC_02368	PyrG,CtrA	CTP synthase	60 kDa	x	x	zyt	8.87	N	7.11E+05	1.11E+06	3.40E-02	1.618	
88194907	SAOUHSC_01168	PyrC	dihydroorotase	46 kDa		x	zyt	8.87	N	9.21E+05	1.52E+06	2.90E-02	1.686	
88195544	SAOUHSC_01845	Geh	formate-tetrahydrofolate ligase, putative hypoxanthine	60 kDa	x	x	zyt	8.87	#NV	1.90E+06	7.50E+06	1.07E-12	3.984	
88194270	SAOUHSC_00485	Hpt	phosphoribosyltransferase	20 kDa		x	zyt	9.98	N	7.27E+05	1.20E+06	3.00E-03	1.773	
88193914	SAOUHSC_00101	Drm,DeoB	phosphopentomutase	44 kDa	x	x	zyt	8.87	N	1.30E+06	2.08E+06	8.00E-03	1.629	
88194765	SAOUHSC_01011	PurS	phosphoribosylformylglycinami dine synthase, PurS protein	10 kDa		x	zyt	8.87	N	1.23E+06	3.31E+06	9.00E-03	2.857	
88196043	SAOUHSC_02380	DeoD2	purine nucleoside phosphorylase	26 kDa	x	x	unb	2.50	N	2.03E+07	2.60E+07	2.29E-01	1.422	
88194508	SAOUHSC_00743	Rir2,NrdF	ribonucleotide-disphosphate reductase beta chain, putative	38 kDa		x	zyt	8.87	N	2.30E+06	4.51E+06	9.14E-10	1.961	
Transkription und Replikation (7)														
88195207	SAOUHSC_01490	Hup,Hu	DNA-binding protein HU, putative	10 kDa	x	x	unb	2.50	N	1.74E+08	7.37E+07	2.03E-04	-2.383	
88196136	SAOUHSC_02485	RpoA	DNA-directed RNA polymerase alpha chain, putative	35 kDa		x	zyt	9.98	N	1.09E+05	1.80E+05	2.00E-01	1.873	
88196032	SAOUHSC_02369	RpoE	DNA-directed RNA polymerase, delta subunit, putative	21 kDa	x	x	zyt	8.87	N	1.62E+07	1.75E+07	4.95E-01	1.143	
88193826	SAOUHSC_00003		hypothetical protein SAOUHSC_00003	9 kDa	x		zyt	8.87	N	5.85E+05	8.40E+05	7.90E-02	1.447	
88194916	SAOUHSC_01177	RpoZ	hypothetical protein SAOUHSC_01177	8 kDa	x		unb	2.50	N	2.24E+06	1.23E+06	2.40E-02	-1.820	
88195419	SAOUHSC_01714	GreA	transcription elongation factor GreA	18 kDa	x	x	zyt	8.87	N	1.81E+07	2.48E+07	1.06E-01	1.486	
88194976	SAOUHSC_01243	NusA	transcription termination- antitermination factor, putative	44 kDa		x	zyt	8.87	N	1.16E+05	2.79E+05	6.10E-02	2.710	
unbekannte Funktion (67)														
88194136	SAOUHSC_00336	Thl	acetyl-CoA acetyltransferase, putative	42 kDa		x	zyt	9.98	#NV	6.03E+05	7.64E+05	2.89E-01	1.335	
88195775	SAOUHSC_02092	PepS,AmpS	aminopeptidase PepS, putative bacteriophage L54a,	47 kDa	x	x	zyt	8.87	N	5.89E+06	8.37E+06	4.30E-02	1.499	
88195764	SAOUHSC_02080		antirepressor, putative bacteriophage L54a, single-	30 kDa		x	zyt	8.87	N	2.18E+05	4.55E+05	1.70E-02	2.045	
88194148	SAOUHSC_00349	Ssb	stranded DNA binding protein D-isomer spezific 2-hydroxyacid	19 kDa	x	x	unb	2.50	N	8.63E+05	1.10E+06	3.60E-01	1.397	
88196221	SAOUHSC_02577		dehydrogenase, NAD binding domain protein	35 kDa		x	zyt	9.98	N	8.79E+05	1.40E+06	1.37E-01	1.706	

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195741	SAOUHSC_02057		dUTP pyrophosphatase	19 kDa	x	x	zyt	8.87	N	1.92E+06	4.98E+06	2.05E-04	2.653	
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025	83 kDa		x	zw	10.00	Y	5.68E+05	2.32E+06	1.20E-02	4.505	7
88194032	SAOUHSC_00225		hypothetical protein SAOUHSC_00225	27 kDa		x	unb	2.50	N	1.94E+06	5.65E+06	2.00E-03	3.086	
88194059	SAOUHSC_00253		hypothetical protein SAOUHSC_00253	58 kDa		x	unb	3.33	Y	4.65E+05	3.26E+06	8.10E-26	6.173	
88194062	SAOUHSC_00256		hypothetical protein SAOUHSC_00256	33 kDa		x	unb	3.33	Y	3.23E+05	1.98E+06	1.25E-14	5.556	7
88194064	SAOUHSC_00258		hypothetical protein SAOUHSC_00258	115 kDa		x	zm	9.35	Y	2.71E+05	1.61E+06	1.52E-15	5.814	7
88194145	SAOUHSC_00346	YchF	hypothetical protein SAOUHSC_00346	41 kDa		x	zyt	8.87	#NV					
88194155	SAOUHSC_00356		hypothetical protein SAOUHSC_00356	21 kDa	x		unb	3.33	Y	1.15E+08	2.49E+06	0.00E+00	-38.809	7, 9, 10
88194160	SAOUHSC_00362		hypothetical protein SAOUHSC_00362	24 kDa	x		unb	3.33	Y	5.61E+05	1.13E+06	4.90E-02	2.320	
88194167	SAOUHSC_00369		hypothetical protein SAOUHSC_00369	36 kDa	x	x	zyt	8.87	#NV	6.64E+06	8.08E+06	1.91E-01	1.258	
88194180	SAOUHSC_00383		hypothetical protein SAOUHSC_00383	26 kDa	x	x	unb	6.46	Y	3.06E+07	1.20E+07	1.71E-09	-2.292	
88194187	SAOUHSC_00392		hypothetical protein SAOUHSC_00392	26 kDa	x	x	ez	9.98	Y	4.85E+06	2.90E+06	2.90E-01	-1.339	
88194194	SAOUHSC_00399		hypothetical protein SAOUHSC_00399	25 kDa	x	x	ez	9.98	Y	8.87E+06	2.13E+07	1.90E-04	2.358	
88194195	SAOUHSC_00400		hypothetical protein SAOUHSC_00400	57 kDa	x	x	unb	3.33	Y	9.98E+06	2.18E+07	1.90E-06	2.208	
88194196	SAOUHSC_00401		hypothetical protein SAOUHSC_00401	11 kDa	x	x	unb	3.33	Y	4.18E+07	5.29E+07	8.50E-02	1.464	
88194202	SAOUHSC_00408		hypothetical protein SAOUHSC_00408	12 kDa		x	zyt	8.87	N	2.27E+06	6.12E+06	6.85E-05	2.755	
88194256	SAOUHSC_00469	SpoVG	hypothetical protein SAOUHSC_00469	11 kDa	x		zyt	8.87	N	9.30E+06	3.43E+06	1.47E-04	-2.415	7
88194387	SAOUHSC_00617		hypothetical protein SAOUHSC_00617	19 kDa		x	unb	3.33	Y	4.54E+07	1.36E+08	1.56E-13	3.175	
88194451	SAOUHSC_00686		hypothetical protein SAOUHSC_00686	11 kDa	x		zyt	8.87	N	1.45E+06	5.40E+05	2.63E-05	-2.597	7
88194469	SAOUHSC_00704		hypothetical protein SAOUHSC_00704	17 kDa	x	x	unb	3.33	Y	1.20E+08	3.92E+07	7.08E-05	-2.648	
88194602	SAOUHSC_00844		hypothetical protein SAOUHSC_00844	30 kDa	x	x	zm	9.87	Y	3.71E+06	4.19E+06	3.51E-01	1.379	
88194603	SAOUHSC_00845		hypothetical protein	7 kDa	x		unb	2.50	N	7.86E+07	6.62E+05	6.93E-42	-66.183	4, 7, 9, 10

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
			SAOUHSC_00845											
88194622	SAOUHSC_00865		hypothetical protein SAOUHSC_00865	28 kDa	x	x	unb	2.50	N	1.36E+06	3.74E+06	2.20E-02	3.145	
88194663	SAOUHSC_00906		hypothetical protein SAOUHSC_00906	33 kDa		x	zyt	8.87	N	1.28E+06	3.87E+06	1.60E-02	3.425	
88194788	SAOUHSC_01036		hypothetical protein SAOUHSC_01036	9 kDa	x		zyt	8.87	N	2.37E+06	4.03E+06	9.60E-02	1.406	
88194858	SAOUHSC_01112		hypothetical protein SAOUHSC_01112	15 kDa	x	x	unb	3.33	#NV	4.68E+06	3.56E+06	1.68E-01	-1.263	
88194880	SAOUHSC_01138		hypothetical protein SAOUHSC_01138	17 kDa	x	x	unb	2.50	N	1.73E+06	3.06E+06	8.80E-02	2.096	
88194895	SAOUHSC_01154		hypothetical protein SAOUHSC_01154	21 kDa	x		unb	2.50	N	1.65E+06	1.83E+06	5.63E-01	1.127	
88195053	SAOUHSC_01323		hypothetical protein SAOUHSC_01323	30 kDa		x	zyt	8.87	N	3.73E+05	9.18E+05	3.50E-02	2.717	
88195140	SAOUHSC_01414		hypothetical protein SAOUHSC_01414	13 kDa	x	x	unb	2.50	N	1.18E+06	1.43E+06	9.58E-01	1.016	
88195160	SAOUHSC_01436		hypothetical protein SAOUHSC_01436	16 kDa	x	x	zyt	8.87	N	2.54E+06	3.02E+06	3.43E-01	1.230	
88195162	SAOUHSC_01438		hypothetical protein SAOUHSC_01438	9 kDa	x		unb	2.50	N	2.20E+06	2.24E+06	4.26E-01	1.433	
88195321	SAOUHSC_01610		hypothetical protein SAOUHSC_01610	16 kDa	x		zyt	8.87	N	1.01E+06	1.09E+06	5.95E-01	1.129	
88195356	SAOUHSC_01648		hypothetical protein SAOUHSC_01648	17 kDa	x	x	unb	2.50	#NV	8.48E+05	1.30E+06	7.90E-02	1.610	
88195424	SAOUHSC_01719		hypothetical protein SAOUHSC_01719	12 kDa		x	zyt	8.87	N	1.31E+06	3.34E+06	6.20E-02	2.445	
88195435	SAOUHSC_01730	CsbD	hypothetical protein SAOUHSC_01730	7 kDa	x		unb	2.50	#NV	2.75E+06	6.44E+04	3.51E-12	-42.307	4, 7
88195462	SAOUHSC_01761		hypothetical protein SAOUHSC_01761	18 kDa	x		unb	2.50	#NV	2.18E+06	2.07E+06	7.99E-01	-1.051	
88195515	SAOUHSC_01815		hypothetical protein SAOUHSC_01815	25 kDa		x	zyt	8.87	N	1.27E+06	1.82E+06	1.66E-01	1.724	
88195566	SAOUHSC_01869		hypothetical protein SAOUHSC_01869	16 kDa	x		unb	2.50	Y	6.27E+05	1.57E+05	1.36E-01	-5.733	7, 10
88195613	SAOUHSC_01918		hypothetical protein SAOUHSC_01918	25 kDa	x	x	unb	2.50	N	1.90E+05	2.47E+05	6.83E-01	1.271	
88195660	SAOUHSC_01968	Hit	hypothetical protein SAOUHSC_01968	16 kDa		x	unb	2.50	N	5.39E+05	1.40E+06	5.30E-02	3.021	
88195668	SAOUHSC_01977		hypothetical protein SAOUHSC_01977	13 kDa	x	x	zyt	8.87	#NV	1.52E+07	1.44E+07	8.80E-01	-1.056	
88195723	SAOUHSC_02037		hypothetical protein	15 kDa	x	x	zyt	8.87	N					

Accession- Nummer	Locus- Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
			SAOUHSC_02037											
88195729	SAOUHSC_02044		hypothetical protein SAOUHSC_02044	23 kDa	x	x	zyt	8.87	N	1.91E+07	2.20E+07	3.08E-01	1.242	
88195757	SAOUHSC_02073		hypothetical protein SAOUHSC_02073	21 kDa	x	x	unb	2.50	N	1.05E+07	2.16E+07	1.88E-07	2.101	
88195825	SAOUHSC_02145		hypothetical protein SAOUHSC_02145	7 kDa		x	unb	2.50	Y	2.44E+07	4.09E+07	3.20E-02	1.821	
88195845	SAOUHSC_02167		hypothetical protein SAOUHSC_02167	13 kDa	x	x	unb	3.33	Y	2.99E+07	9.83E+07	4.64E-04	3.448	
88195892	SAOUHSC_02218		hypothetical protein SAOUHSC_02218	11 kDa	x	x	unb	2.50	N	1.04E+06	1.30E+06	2.80E-01	1.266	
88196065	SAOUHSC_02404	FmtB	hypothetical protein SAOUHSC_02404	263 kDa	x	x	zw	10.00	Y	2.59E+05	4.45E+05	4.00E-03	1.727	
88196364	SAOUHSC_02724		hypothetical protein SAOUHSC_02724	26 kDa		x	unb	2.50	N	8.03E+05	1.11E+06	1.82E-01	1.443	
88196290	SAOUHSC_02650		lipoprotein, putative	23 kDa	x	x	unb	4.05	Y	6.77E+06	8.93E+06	9.30E-02	1.451	
88195728	SAOUHSC_02043		phage head protein, putative	37 kDa	x	x	zyt	8.87	N	1.09E+08	1.36E+08	7.50E-02	1.287	
88196598	SAOUHSC_02978		phage infektion protein, putative	109 kDa	x	x	zm	9.99	Y	6.85E+06	1.14E+07	5.52E-05	1.692	
88195722	SAOUHSC_02036		phage structural protein, putative	22 kDa	x	x	unb	2.50	N	8.13E+06	1.22E+07	5.91E-05	1.490	
88195710	SAOUHSC_02022		phage tail fiber protein, putative	44 kDa	x	x	zyt	8.87	N	3.57E+06	5.77E+06	1.58E-04	1.647	
88195727	SAOUHSC_02042		phi Mu50B-like protein	11 kDa	x	x	unb	2.50	N	3.85E+06	7.33E+06	3.27E-05	1.898	
88195715	SAOUHSC_02028		phiETA ORF57-like protein preprotein translocase, SecG subunit	67 kDa	x	x	unb	2.50	N	4.01E+05	6.28E+05	1.11E-01	1.698	
88194561	SAOUHSC_00801	SecG	PV83 orf 23-like protein-related protein	10 kDa	x	x	zm	9.75	N	9.80E+05	1.55E+06	5.55E-01	1.263	
88195747	SAOUHSC_02063		protein	7 kDa		x	zyt	8.87	N					
88195999	SAOUHSC_02333		sceD protein, putative single-strand DNA-binding protein, putative	24 kDa	x	x	ez	9.98	#NV	2.15E+09	6.44E+08	0.00E+00	-3.283	
88195755	SAOUHSC_02071		protein, putative	19 kDa	x	x	unb	2.50	N	2.00E+06	8.45E+06	7.06E-09	4.132	
88195714	SAOUHSC_02027		SLT orf 129-like protein	14 kDa	x	x	unb	2.50	#NV	1.86E+07	2.04E+07	4.46E-01	1.119	

Drei Bioreplikate der Kulturüberstände von der exponentiellen Wachstumsphase von *S. aureus* RN1HG und RN1HG $\Delta sigB$ wurden mittels gelfreier Analyse aufgearbeitet. Proteine mit mindestens 2 Peptiden galten als identifiziert. Anschließend wurden die identifizierten Proteine in funktionelle Gruppen klassifiziert (TigR). Der Fold Change bezieht sich auf die exponentielle Wachstumsphase des Wildtyps.

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

^B Die Lokalisation und die Vorhersage eines Signalpeptides erfolgte über P-Sort. ez = extrazellulär, zw = Zellwand, zm = zytoplasmatische Membran, zyt = Zytoplasma, unb = unbekannt, SP = Signalpeptid, N = kein Signalpeptid, Y = Signalpeptid vorhanden, #NV = Vorhersage nicht möglich.

^C Die Intensitäten, der *p*-Wert und der Fold Change wurde anhand der Elucidator Software ermittelt.

^D Publikation, die den Einfluss von SigB bestätigen: ¹ Kullik et al., 1998; ² Cheung et al., 1999; ³ Nicholas et al., 1999; ⁴ Gertz et al., 2000; ⁵ Ziebandt et al. 2001; ⁶ Horsburgh et al., 2002; ⁷ Bischoff et al., 2004; ⁸ Ziebandt et al. 2004; ⁹ Homerova et al., 2004; ¹⁰ Pané-Farré et al., 2006.

Tab. 62: Identifizierte Proteine der frühen stationären Phase von *S. aureus* RN1HG und RN1HG $\Delta sigB$ in pMEM.

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
Toxine und Hämolyse (7)														
88194865	SAOUHSC_01121	Hla	alpha-hemolysin precursor gamma-hemolysin component	36 kDa	x	x	ez	10.00	Y	2.37E+08	2.00E+09	2.61E-13	7.353	3, 8, 9, 10
88196348	SAOUHSC_02708	HlgA	A	35 kDa	x	x	ez	9.73	#NV	6.90E+06	5.60E+07	3.95E-13	6.897	10
88193943	SAOUHSC_00130	IsdI	hypothetical protein SAOUHSC_00130	13 kDa		x	unb	2.50	N	1.28E+06	2.02E+06	2.25E-01	1.473	
88195915	SAOUHSC_02243		hypothetical protein SAOUHSC_02243	40 kDa	x	x	ez	9.73	Y	1.39E+06	1.01E+07	3.82E-09	6.135	10
88196350	SAOUHSC_02710	HlgB	gamma-hemolysin component B	37 kDa	x	x	ez	9.73	Y	3.00E+07	2.43E+08	1.74E-41	5.682	10
88196349	SAOUHSC_02709	HlgC	gamma-hemolysin component C	36 kDa	x	x	ez	9.73	Y	2.07E+07	2.02E+08	1.77E-42	8.696	10
88195647	SAOUHSC_01954	LukD	leukotoxin, LukD	37 kDa	x	x	ez	9.98	#NV	8.01E+05	2.53E+06	6.21E-08	3.067	8
Virulenz-/Abwehrmechanismen (23)														
88193871	SAOUHSC_00051	Plc	1-phosphatidylinositol phosphodiesterase precursor, putative	37 kDa	x	x	ez	9.97	Y	6.61E+06	2.35E+07	7.10E-04	2.941	10, 11
88196592	SAOUHSC_02971	Aur	aureolysin, putative	55 kDa	x	x	ez	9.97	Y	1.00E+07	1.09E+08	1.64E-22	9.804	10, 11, 5, 10, 12, 13
88194572	SAOUHSC_00812	ClfA	clumping factor	96 kDa	x		zw	10.00	Y	1.89E+07	9.42E+05	2.02E-06	-20.997	
88196585	SAOUHSC_02963	ClfB	clumping factor B, putative cysteine protease precursor, putative	94 kDa	x		zw	10.00	Y	1.15E+07	3.26E+06	1.86E-17	-3.496	
88194744	SAOUHSC_00987	SspB	elastin binding protein	45 kDa	x	x	ez	9.55	Y	2.39E+07	3.74E+07	4.15E-05	1.546	10, 11
88195217	SAOUHSC_01501	EbpS	extracellular matrix and plasma binding protein, putative	53 kDa	x	x	zw	9.06	#NV	1.28E+06	8.84E+05	4.70E-02	-1.640	
88194575	SAOUHSC_00816	Ssp,Empbp	glutamyl endopeptidase precursor, putative	38 kDa	x	x	unb	3.33	Y	8.81E+05	1.25E+06	7.47E-01	1.103	
88194745	SAOUHSC_00988	SspA	hyaluronate lyase	36 kDa	x	x	ez	10.00	Y	1.19E+07	2.90E+07	1.66E-11	2.475	8, 10, 11
88196115	SAOUHSC_02463	HysA	immunoglobulin G-binding protein Sbi, putative	92 kDa		x	ez	10.00	#NV	7.15E+05	8.25E+05	6.35E-01	1.103	
88196346	SAOUHSC_02706	Sbi	lipase	50 kDa	x	x	unb	3.33	#NV	1.41E+07	4.81E+07	7.30E-02	1.761	
88196625	SAOUHSC_03006	Lip	lipase precursor	77 kDa	x	x	ez	9.73	Y	1.69E+09	1.69E+09	7.56E-01	-1.088	11
88194101	SAOUHSC_00300	Geh	protein A	76 kDa	x	x	ez	10.00	Y	4.38E+09	5.98E+09	6.71E-10	1.420	11
88193885	SAOUHSC_00069		sdrD protein, putative	56 kDa	x	x	zw	10.00	Y	1.20E+08	6.61E+07	3.80E-02	-2.975	
88194325	SAOUHSC_00545			146 kDa	x	x	zw	10.00	Y	2.17E+07	6.78E+06	1.00E-03	-3.475	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195636	SAOUHSC_01942	SplA	serine protease SplA	26 kDa		x	ez	9.73	Y	1.13E+05	1.21E+06	1.76E-05	10.870	8, 10, 11
88195635	SAOUHSC_01941	SplB	serine protease SplB	26 kDa	x	x	ez	9.73	Y	3.54E+06	2.92E+07	1.88E-07	7.692	10, 11
88195634	SAOUHSC_01939	SplC	serine protease SplC	26 kDa		x	ez	9.73	Y	2.31E+05	2.17E+06	1.40E-09	9.174	8, 10, 11
88195631	SAOUHSC_01936	SplE	serine protease SplE	26 kDa		x	ez	9.73	Y	3.13E+05	2.00E+06	1.05E-04	5.848	10, 11
88195630	SAOUHSC_01935	SplF	serine protease SplF, putative	26 kDa	x	x	ez	9.73	#NV	2.63E+06	1.29E+07	1.37E-04	4.878	10, 11 8, 10, 11,
88195808	SAOUHSC_02127		staphopain thiol proteinase staphylokinase precursor, putative	44 kDa	x	x	ez	9.73	Y	1.28E+07	1.10E+08	9.89E-05	5.747	13
88195848	SAOUHSC_02171	Sak	putative	19 kDa	x	x	ez	9.98	Y	7.06E+06	2.30E+07	3.27E-12	3.115	10
88194577	SAOUHSC_00818	Nuc	thermonuclease precursor	25 kDa	x	x	ez	10.00	Y	5.15E+06	1.30E+08	2.88E-21	18.519	2, 8, 10, 13
88195480	SAOUHSC_01779	Tig	trigger factor	49 kDa	x	x	zyt	8.87	N	8.21E+06	1.07E+07	4.74E-01	1.267	
Zellwandbiosynthese und -abbau (14)														
88194219	SAOUHSC_00427		autolysin precursor, putative bifunctional autolysin precursor, putative	36 kDa	x	x	ez	9.98	Y	7.75E+07	5.49E+07	1.54E-01	-1.773	11
88194750	SAOUHSC_00994	Atl	precursor, putative	137 kDa	x	x	ez	10.00	#NV	1.02E+09	1.03E+09	6.74E-01	-1.072	13
88195790	SAOUHSC_02108	Ftn	ferritin, putative	20 kDa	x		zyt	9.98	N	1.36E+06	4.93E+05	1.54E-01	-4.543	
88193909	SAOUHSC_00094		hypothetical protein SAOUHSC_00094 immunodominant antigen A, putative	22 kDa	x	x	zw	9.93	Y	1.61E+08	2.18E+08	2.45E-01	1.305	
88196515	SAOUHSC_02887	IsaA	putative	24 kDa	x		ez	10.00	Y	1.74E+09	8.84E+08	1.00E-03	-2.064	11
88195840	SAOUHSC_02161		MHC class II analog protein	66 kDa	x	x	unb	3.33	Y	1.22E+06	7.19E+06	2.16E-04	5.263	
88195184	SAOUHSC_01467	Pbp2	penicillin-binding protein 2	80 kDa	x	x	ez	9.55	N	2.51E+06	2.63E+06	8.78E-01	-1.026	
88195360	SAOUHSC_01652	PbpF,Pbp3	penicillin-binding protein 3 peptidoglycan hydrolase, putative	77 kDa	x	x	zm	9.82	#NV	2.06E+06	2.01E+06	7.86E-01	-1.040	
88194055	SAOUHSC_00248	LytM	putative	34 kDa	x	x	ez	9.98	Y	5.58E+08	1.49E+08	6.32E-05	-3.701	
88194324	SAOUHSC_00544		sdrC protein, putative secretory antigen precursor, putative	108 kDa	x	x	zw	10.00	Y	1.12E+07	8.52E+06	8.94E-01	1.037	
88196215	SAOUHSC_02571	SsaA	secretory antigen SsaA-like protein	29 kDa	x	x	ez	9.04	Y	1.35E+08	1.64E+08	5.62E-01	1.145	10
88194436	SAOUHSC_00671		truncated MHC class II analog protein	28 kDa	x	x	ez	9.73	Y	3.06E+08	1.71E+08	5.00E-03	-1.809	
88196118	SAOUHSC_02466		truncated MHC class II analog protein	15 kDa	x		unb	3.33	Y	1.30E+08	4.50E+05	3.57E-07	-227.869	
88194675	SAOUHSC_00918		truncated MHC class II analog protein	16 kDa	x	x	unb	3.33	Y	1.57E+08	1.98E+08	1.21E-01	1.238	10, 13

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
Zellumhüllung (16)														
88194199	SAOUHSC_00405		hypothetical protein SAOUHSC_00405	29 kDa	x		unb	2.50	N	1.80E+06	1.56E+06	4.10E-01	-1.158	
88194482	SAOUHSC_00717		hypothetical protein SAOUHSC_00717	16 kDa	x	x	unb	3.33	Y	2.27E+07	7.01E+07	1.27E-08	2.639	
88194518	SAOUHSC_00754		hypothetical protein SAOUHSC_00754	34 kDa	x		unb	6.46	Y	9.41E+05	7.60E+05	3.75E-01	-1.241	
88194829	SAOUHSC_01081	IsdA	hypothetical protein SAOUHSC_01081	39 kDa	x	x	zw	10.00	N	4.85E+07	1.71E+08	1.12E-04	2.571	10
88194830	SAOUHSC_01082	IsdC	hypothetical protein SAOUHSC_01082	25 kDa	x	x	unb	3.33	Y	1.11E+07	9.89E+07	4.92E-07	4.386	12
88195062	SAOUHSC_01332		hypothetical protein SAOUHSC_01332	34 kDa	x	x	unb	2.50	#NV	8.32E+06	5.06E+06	8.37E-04	-1.621	
88195443	SAOUHSC_01739	LytH	hypothetical protein SAOUHSC_01739	33 kDa	x		unb	3.33	N	2.06E+06	1.60E+06	1.76E-01	-1.361	
88195542	SAOUHSC_01843		hypothetical protein SAOUHSC_01843	101 kDa	x		zw	10.00	#NV	3.49E+05	5.62E+05	7.81E-01	-1.165	
88195590	SAOUHSC_01895		hypothetical protein SAOUHSC_01895	33 kDa	x	x	ez	9.55	Y	5.06E+06	2.58E+06	5.73E-06	-2.031	
88195802	SAOUHSC_02121		hypothetical protein SAOUHSC_02121	45 kDa	x	x	unb	3.33	Y	7.63E+06	3.46E+06	1.81E-05	-2.266	
88196433	SAOUHSC_02798		hypothetical protein SAOUHSC_02798	179 kDa	x		zw	10.00	N	1.74E+06	6.66E+05	1.90E-02	-2.914	
88196599	SAOUHSC_02979		hypothetical protein SAOUHSC_02979	69 kDa	x	x	ez	9.73	Y	1.69E+08	2.18E+08	1.87E-01	1.230	
88196601	SAOUHSC_02982		hypothetical protein SAOUHSC_02982	71 kDa	x	x	zw	10.00	Y	4.59E+07	3.79E+07	1.56E-01	-1.440	
88193889	SAOUHSC_00074	SirA	periplasmic binding protein, putative rod shape-determining protein	37 kDa	x	x	unb	3.33	Y	7.32E+06	2.51E+07	3.10E-02	1.859	13
88195460	SAOUHSC_01759	Mrec	Mrec	31 kDa	x	x	unb	3.33	Y	7.66E+06	4.70E+06	1.36E-06	-1.637	
88196468	SAOUHSC_02834	SrtA	sortase, putative	24 kDa	x		unb	3.33	Y	4.50E+05	3.62E+05	3.61E-01	-1.333	
Stressantwort (13)														
88194163	SAOUHSC_00365	AhpC BetB,CudA	alkyl hydroperoxide reductase	21 kDa	x	x	zyt	9.98	N	6.91E+07	7.48E+07	9.88E-01	1.005	
88196560	SAOUHSC_02933	,GbsA	betaine aldehyde dehydrogenase	55 kDa	x		zyt	9.98	N	2.92E+05	2.16E+05	4.39E-01	-1.521	
88195057	SAOUHSC_01327	KatA	catalase	55 kDa	x	x	zyt	9.98	N	2.21E+07	1.77E+07	4.42E-01	-1.463	9, 13
88195129	SAOUHSC_01403	CspA	cold shock protein, putative	7 kDa	x	x	zyt	9.98	N	2.57E+07	2.75E+07	7.10E-01	1.049	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt : $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194348	SAOUHSC_00573		hypothetical protein SAOUHSC_00573	29 kDa	x		unb	2.50	N	8.25E+05	8.52E+05	7.05E-01	-1.188	
88194593	SAOUHSC_00835		hypothetical protein SAOUHSC_00835	14 kDa	x	x	zyt	8.87	N	9.27E+05	1.75E+06	2.44E-01	1.795	
88195522	SAOUHSC_01822	Tpx	hypothetical protein SAOUHSC_01822	18 kDa	x	x	unb	2.50	N	3.94E+06	3.14E+06	3.42E-01	-1.913	
88196044	SAOUHSC_02381	Dps	hypothetical protein SAOUHSC_02381	17 kDa	x	x	unb	2.50	N	5.41E+06	4.25E+06	3.27E-01	-1.376	
88196094	SAOUHSC_02441	Asp23	hypothetical protein SAOUHSC_02441	19 kDa	x		unb	2.50	N	2.13E+07	8.46E+05	1.40E-02	-32.705	6, 10, 13
88195361	SAOUHSC_01653	SodA	putative superoxide dismutase, Mn,	23 kDa	x		ez	9.55	N	5.98E+06	2.08E+06	1.11E-01	-4.870	
88193908	SAOUHSC_00093	SodM	superoxide dismutase, putative	23 kDa		x	ez	9.55	N	4.42E+06	1.74E+07	2.00E-03	4.444	10, 13
88194846	SAOUHSC_01100	TrxA,Trx	thioredoxin	11 kDa	x	x	zyt	9.98	N	5.24E+07	3.68E+07	2.32E-01	-1.306	
88194592	SAOUHSC_00834		thioredoxin, putative	12 kDa	x	x	zyt	8.87	N	4.98E+06	3.99E+06	4.45E-01	-1.345	
Regulation (5)														
88194753	SAOUHSC_00997		hypothetical protein SAOUHSC_00997	46 kDa	x	x	unb	3.33	Y	3.18E+06	1.48E+06	6.31E-06	-2.126	
88195657	SAOUHSC_01964	TRAP	hypothetical protein SAOUHSC_01964	20 kDa	x	x	zyt	8.87	#NV	1.76E+07	1.39E+07	7.22E-01	-1.131	
88195154	SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA, putative	18 kDa	x	x	zyt	9.98	N	4.55E+06	3.02E+06	2.52E-01	-1.964	
88194390	SAOUHSC_00620	SarA	staphylococcal accessory regulator T, putative	15 kDa	x		unb	2.50	N	3.29E+05	2.77E+05	2.36E-01	-4.768	1, 4, 6, 7, 10, 13
88196226	SAOUHSC_02583		transcriptional regulator, putative	34 kDa	x		unb	3.33	Y	7.82E+05	4.25E+05	4.00E-03	-1.795	
Transport (16)														
88194087	SAOUHSC_00284		5'-nucleotidase, lipoprotein e(P4) family	33 kDa	x	x	unb	3.33	Y	2.16E+06	6.60E+06	8.98E-05	2.433	10
88194402	SAOUHSC_00634	MntC	ABC transporter, substrate- binding protein, putative	35 kDa	x	x	unb	3.33	Y	7.92E+08	5.99E+08	6.70E-02	-1.396	
88194761	SAOUHSC_01007	Fold	Fold bifunctional protein, putative	31 kDa	x		zyt	8.87	N	1.16E+06	1.24E+06	3.87E-01	-1.917	
88194011	SAOUHSC_00201		hypothetical protein SAOUHSC_00201	53 kDa	x		zw	9.17	N	3.15E+05	1.12E+05	5.70E-02	-3.258	
88194831	SAOUHSC_01084	IsdD	hypothetical protein SAOUHSC_01084	41 kDa	x	x	unb	2.50	Y	6.46E+06	3.41E+07	8.00E-03	2.525	13

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194832	SAOUHSC_01085	IsdE	hypothetical protein SAOUHSC_01085	32 kDa	x	x	zyt	8.87	N	1.11E+06	5.68E+06	1.60E-05	3.165	
88195571	SAOUHSC_01874		hypothetical protein SAOUHSC_01874	11 kDa	x	x	unb	2.50	N	2.62E+06	2.56E+06	8.20E-01	1.104	
88195914	SAOUHSC_02241		hypothetical protein SAOUHSC_02241	39 kDa		x	ez	9.73	Y	2.56E+06	1.26E+07	2.17E-07	4.651	10
88195918	SAOUHSC_02246		hypothetical protein SAOUHSC_02246	35 kDa		x	unb	6.46	Y	3.18E+05	1.42E+06	3.00E-03	3.115	
88196199	SAOUHSC_02554	FhuD2	hypothetical protein SAOUHSC_02554	34 kDa	x	x	unb	3.33	Y	3.67E+06	2.62E+06	1.40E-01	-1.291	
88196339	SAOUHSC_02699		hypothetical protein SAOUHSC_02699	29 kDa	x	x	unb	3.33	Y	2.99E+06	2.05E+06	2.87E-01	-1.508	
88196194	SAOUHSC_02549	ModA	molybdenum ABC transporter, periplasmic molybdate-binding protein	29 kDa	x		unb	3.33	Y	1.42E+06	9.49E+05	1.64E-01	-1.621	
88194828	SAOUHSC_01079	IsdB	neurofilament protein	72 kDa	x	x	zw	10.00	#NV	1.44E+06	8.99E+06	1.90E-02	2.817	
88196403	SAOUHSC_02767	Opp- 1A,Opp1A	peptide ABC transporter, peptide-binding protein, putative phosphocarrier protein hpr,	60 kDa	x	x	zw	9.18	Y	1.43E+06	4.11E+06	6.40E-02	1.767	13
88194781	SAOUHSC_01028	PtsH	putative potassium-transporting ATPase, C subunit	9 kDa	x	x	zyt	10.00	N	2.71E+06	8.43E+05	4.20E-02	-3.991	
88195976	SAOUHSC_02310	KdpC		21 kDa	x	x	unb	3.33	Y	8.68E+06	2.37E+06	4.94E-06	-2.798	
zell. Prozesse (3)														
88194886	SAOUHSC_01144	FtsL	hypothetical protein SAOUHSC_01144	15 kDa	x	x	zyt	8.87	N	1.55E+07	1.27E+07	7.80E-02	-1.190	
88195179	SAOUHSC_01462		hypothetical protein SAOUHSC_01462	13 kDa	x	x	zyt	8.87	N	2.47E+06	1.94E+06	3.53E-01	-1.789	
88195846	SAOUHSC_02169	Chs,Chp	hypothetical protein SAOUHSC_02169	17 kDa	x	x	unb	3.33	Y	1.60E+07	1.56E+08	7.08E-17	6.250	
Energiemetabolismus (30)														
88195316	SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase, decarboxylating	52 kDa	x	x	zyt	8.87	N	3.30E+06	2.46E+06	1.87E-01	-1.658	
88195075	SAOUHSC_01347	CitB,AcnA PdhD,Lpd	aconitate hydratase 1 dihydrolipoamide	99 kDa	x		zyt	9.98	N	5.05E+05	2.00E+05	1.10E-02	-4.097	
88194795	SAOUHSC_01043	A	dehydrogenase D-lactate dehydrogenase, putative	49 kDa	x	x	zyt	9.98	N	1.41E+07	1.28E+07	4.88E-01	-1.374	
88196464	SAOUHSC_02830	Ddh		35 kDa	x		zyt	9.98	N	1.54E+05	1.35E+05	4.08E-01	-2.102	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194559	SAOUHSC_00799	Eno	enolase	47 kDa		x	zyt	9.98	N	2.02E+06	2.14E+06	5.77E-01	1.125	
88196553	SAOUHSC_02926		fructose-bisphosphate aldolase class-I, putative	33 kDa	x	x	unb	2.50	N	8.04E+06	1.27E+07	1.09E-01	1.486	
88195310	SAOUHSC_01599	Zwf	glucose-6-phosphate 1- dehydrogenase	57 kDa	x		zyt	8.87	N	3.82E+05	2.97E+05	4.31E-01	-1.664	
88194657	SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase	50 kDa	x	x	zyt	9.98	N	1.71E+06	1.50E+06	4.79E-01	-1.210	
88194555	SAOUHSC_00795	Gap1,Gap	glyceraldehyde-3-phosphate dehydrogenase, type I	36 kDa	x	x	zyt	9.98	N	4.51E+07	7.66E+07	9.70E-02	1.608	
88194594	SAOUHSC_00836	GevH	glycine cleavage system H protein	14 kDa	x	x	zyt	8.87	N	2.75E+06	1.25E+06	1.15E-01	-1.687	
88194332	SAOUHSC_00553		hypothetical protein SAOUHSC_00553	22 kDa	x	x	zyt	8.87	N	3.85E+06	2.44E+06	2.90E-01	-1.756	6, 10, 13
88194493	SAOUHSC_00728		hypothetical protein SAOUHSC_00728	74 kDa	x	x	zm	9.99	Y	4.14E+08	2.32E+08	6.84E-07	-1.771	
88194654	SAOUHSC_00897	GlpQ	hypothetical protein SAOUHSC_00897	35 kDa	x	x	unb	4.86	#NV	2.15E+07	5.98E+07	1.42E-09	2.488	10, 11
88194760	SAOUHSC_01005		hypothetical protein SAOUHSC_01005	11 kDa	x	x	unb	3.33	#NV	1.09E+07	6.84E+06	6.78E-04	-1.524	
88195558	SAOUHSC_01860		hypothetical protein SAOUHSC_01860	12 kDa	x	x	zyt	8.87	N	9.43E+06	3.50E+06	7.79E-06	-2.319	
88195596	SAOUHSC_01901		hypothetical protein SAOUHSC_01901	26 kDa	x	x	unb	2.50	N	5.24E+06	7.00E+06	5.87E-01	1.250	
88195678	SAOUHSC_01987		hypothetical protein SAOUHSC_01987	22 kDa	x		zyt	8.87	#NV	4.09E+06	2.41E+06	2.01E-01	-2.597	6, 10, 13
88195823	SAOUHSC_02143		hypothetical protein SAOUHSC_02143	39 kDa	x		zyt	8.87	N	6.14E+05	4.34E+05	1.73E-01	-1.608	
88195830	SAOUHSC_02150		hypothetical protein SAOUHSC_02150	22 kDa	x	x	unb	2.50	N	1.55E+06	2.20E+06	9.48E-01	-1.034	
88196029	SAOUHSC_02366	FbaA, Fba	hypothetical protein SAOUHSC_02366	31 kDa	x	x	zyt	8.87	N	1.17E+07	9.97E+06	3.29E-01	-2.083	
88196100	SAOUHSC_02448		hypothetical protein SAOUHSC_02448	33 kDa	x		unb	2.50	Y	5.53E+06	2.56E+06	6.08E-07	-2.167	
88196112	SAOUHSC_02460		hypothetical protein SAOUHSC_02460	32 kDa	x		zyt	8.87	#NV	1.33E+05	1.07E+05	3.38E-01	-2.488	
88196528	SAOUHSC_02900		hypothetical protein SAOUHSC_02900	31 kDa	x		zyt	8.87	N	1.75E+05	1.90E+04	4.40E-02	-10.847	10, 13
88194349	SAOUHSC_00574	Pta	phosphate acetyltransferase	35 kDa	x	x	zyt	8.87	N	4.54E+06	3.39E+06	3.17E-01	-1.644	
88196343	SAOUHSC_02703	GpmA	phosphoglycerate mutase, putative	27 kDa	x	x	unb	2.50	N	1.08E+06	1.38E+06	2.84E-01	1.471	
88194792	SAOUHSC_01040	PdhA	pyruvate dehydrogenase complex, E1 component, alpha subunit, putative	41 kDa	x	x	zyt	8.87	N	1.30E+06	7.16E+05	2.35E-01	-2.716	

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88194793	SAOUHSC_01041	PhdB,PdhB	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	35 kDa	x		zyt	8.87	N	1.86E+06	1.25E+06	3.18E-01	-2.069	
88194758	SAOUHSC_01002	QoxA	putative quinol oxidase AA3, subunit II,	42 kDa	x		zm	10.00	Y	1.60E+06	1.01E+06	4.00E-03	-1.605	
88195066	SAOUHSC_01337	Tkt	transketolase	68 kDa	x	x	unb	2.50	N	2.13E+06	2.74E+06	1.69E-01	1.212	
88194557	SAOUHSC_00797	TpiA,Tpi	triosephosphate isomerase	27 kDa	x	x	unb	2.50	N	2.52E+07	2.18E+07	4.68E-01	-1.446	
Proteinbiosynthese (17)														
88195210	SAOUHSC_01493	RpsA	30S ribosomal protein S1, putative	43 kDa		x	zyt	9.98	N	1.11E+06	1.91E+06	8.00E-03	1.686	
88196150	SAOUHSC_02500	RplE	50S ribosomal protein L5, putative	20 kDa	x	x	zyt	8.87	#NV	1.32E+06	1.08E+06	3.01E-01	-2.142	
88194381	SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	62 kDa	x	x	zyt	9.98	N	6.51E+05	7.86E+05	9.78E-01	1.013	
88195444	SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr) deacylase	17 kDa	x	x	unb	2.50	N	5.51E+05	5.11E+05	5.65E-01	-1.339	
88194290	SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	56 kDa	x	x	zyt	9.65	N	1.15E+06	1.08E+06	7.95E-01	-1.117	
88194261	SAOUHSC_00474	RplY	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	24 kDa	x	x	zyt	8.87	#NV	1.76E+06	3.11E+06	4.17E-01	1.381	
88194299	SAOUHSC_00518	RplK	ribosomal protein L11	15 kDa	x	x	zyt	8.87	N	1.03E+07	1.35E+07	7.88E-01	1.109	
88196144	SAOUHSC_02493	RpmD	ribosomal protein L30	7 kDa	x	x	unb	2.50	N	2.65E+06	3.25E+06	5.59E-01	1.149	
88196024	SAOUHSC_02361	RpmE	ribosomal protein L31	10 kDa	x	x	unb	2.50	N	1.39E+07	1.56E+07	9.83E-01	1.007	
88196147	SAOUHSC_02496	RplF	ribosomal protein L6, putative	20 kDa	x		zyt	8.87	N	1.48E+06	1.47E+06	5.03E-01	-1.433	
88194302	SAOUHSC_00521	RplL	ribosomal protein L7/L12	13 kDa	x		zyt	8.87	N	2.39E+07	2.01E+07	4.22E-01	-1.520	
88193838	SAOUHSC_00017	RplI	ribosomal protein L9	17 kDa	x		zyt	9.65	N	6.57E+05	1.11E+06	3.32E-01	1.477	
88194147	SAOUHSC_00348	RpsF	ribosomal protein S6	12 kDa	x	x	zyt	9.98	#NV	3.36E+06	4.31E+06	7.91E-01	1.110	
88194969	SAOUHSC_01236	Rrf,Frr	ribosome recycling factor	20 kDa	x	x	zyt	9.98	N	9.55E+06	1.28E+07	6.22E-01	1.205	
88194967	SAOUHSC_01234	Tsf	translation elongation factor Ts	32 kDa	x	x	zyt	9.98	#NV	5.48E+07	6.58E+07	7.95E-01	1.098	
88194310	SAOUHSC_00530	Tuf	translation elongation factor Tu	43 kDa	x	x	zyt	9.98	N	1.12E+07	2.65E+07	4.54E-07	2.320	
88194690	SAOUHSC_00933	TrpS	tryptophanyl-tRNA synthetase	37 kDa	x	x	zyt	9.98	N	3.76E+05	4.61E+05	4.77E-01	1.314	
Proteinmetabolismus (12)														
88194939	SAOUHSC_01201	HmrB,Acp P	acyl carrier protein	9 kDa	x	x	zyt	8.87	#NV	3.40E+07	2.80E+07	5.49E-01	-1.129	
88195390	SAOUHSC_01684	GrpE	co-chaperone GrpE	24 kDa	x	x	zyt	8.87	N	7.03E+06	6.65E+06	5.70E-01	-1.299	
88195389	SAOUHSC_01683	DnaK	DNAK protein, putative	66 kDa	x	x	zyt	9.98	N	6.02E+06	1.66E+07	1.61E-05	2.778	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88196491	SAOUHSC_02860	MvaS	HMG-CoA synthase, putative	43 kDa	x	x	zyt	8.87	N	3.83E+06	3.36E+06	4.27E-01	-1.531	
88194313	SAOUHSC_00533		hypothetical protein SAOUHSC_00533	32 kDa	x		unb	2.50	N	3.05E+06	6.82E+05	6.50E-02	-5.022	10, 13
88194972	SAOUHSC_01239		hypothetical protein SAOUHSC_01239	44 kDa	x	x	zm	9.99	N	2.89E+06	1.36E+06	7.00E-04	-2.172	
88195110	SAOUHSC_01383		hypothetical protein SAOUHSC_01383	69 kDa	x		zyt	9.98	N	6.69E+05	6.26E+05	8.51E-01	-1.071	
88195151	SAOUHSC_01427	CtpA	hypothetical protein SAOUHSC_01427	55 kDa	x		unb	2.50	N	6.22E+05	3.98E+05	1.18E-01	-1.620	
88195784	SAOUHSC_02102	Map	methionine aminopeptidase, type I	28 kDa	x		zyt	8.87	N	3.97E+06	3.96E+06	7.03E-01	-1.163	
88194694	SAOUHSC_00937	PepF,PepB	oligoendopeptidase F	70 kDa	x	x	zyt	9.98	N	4.80E+06	5.77E+06	7.86E-01	1.111	
88194790	SAOUHSC_01038	Def	polypeptide deformylase	21 kDa	x	x	zyt	8.87	#NV	3.46E+06	4.26E+06	4.89E-01	1.255	
88195663	SAOUHSC_01972	PrsA	protein export protein PrsA, putative	36 kDa	x	x	unb	3.33	Y	2.43E+07	2.00E+07	1.81E-01	-1.161	
AS-Biosynthese(4)														
88194316	SAOUHSC_00536	IlvE	branched-chain amino acid aminotransferase	40 kDa	x		zyt	8.87	N	7.45E+05	4.52E+05	2.12E-01	-2.741	
88195018	SAOUHSC_01287	GlnA	glutamine synthetase, type I	51 kDa	x	x	zyt	9.98	N	2.96E+06	3.19E+06	6.73E-01	1.106	
88195928	SAOUHSC_02257	SdrH	hypothetical protein SAOUHSC_02257	47 kDa	x	x	zw	9.18	Y	1.44E+07	3.53E+06	1.75E-23	-4.082	
88196017	SAOUHSC_02354	GlyA	serine hydroxymethyltransferase, putative	45 kDa	x	x	zyt	9.98	N	1.73E+06	1.73E+06	7.64E-01	-1.117	
Nukleotidbiosynthese (6)														
88196141	SAOUHSC_02490	Adk	adenylate kinase, putative	24 kDa	x	x	zyt	9.98	N	2.37E+06	2.76E+06	7.39E-01	-1.212	
88194270	SAOUHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	20 kDa	x		zyt	9.98	N	7.19E+05	3.14E+05	1.28E-01	-2.656	
88193914	SAOUHSC_00101	Drm,DeoB	phosphopentomutase	44 kDa	x		zyt	8.87	N	3.29E+05	1.01E+05	1.10E-02	-4.032	
88194766	SAOUHSC_01012	PurQ	phosphoribosylformylglycinami dine synthase I	25 kDa	x		zyt	8.87	N	5.97E+05	4.69E+05	3.66E-01	-1.849	
88194765	SAOUHSC_01011	PurS	phosphoribosylformylglycinami dine synthase, PurS protein	10 kDa	x		zyt	8.87	N	2.26E+06	1.61E+06	3.02E-01	-1.625	
88196043	SAOUHSC_02380	DeoD2	purine nucleoside phosphorylase	26 kDa	x	x	unb	2.50	N	1.28E+07	1.41E+07	8.96E-01	-1.044	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
Transkription und Replikation (4)														
88195207	SAOUHSC_01490	Hup,Hu	DNA-binding protein HU, putative	10 kDa	x	x	unb	2.50	N	2.67E+07	2.95E+07	8.25E-01	-1.112	
88196032	SAOUHSC_02369	RpoE	DNA-directed RNA polymerase, delta subunit, putative	21 kDa	x	x	zyt	8.87	N	1.48E+06	1.97E+06	9.10E-02	1.517	
88196427	SAOUHSC_02791		pyrophosphohydrolase, putative	15 kDa		x	unb	2.50	N	5.91E+05	6.07E+05	7.33E-01	-1.131	
88195419	SAOUHSC_01714	GreA	transcription elongation factor GreA	18 kDa	x	x	zyt	8.87	N	1.17E+07	1.49E+07	5.07E-01	1.277	
Unbekannte Funktion (43)														
88195775	SAOUHSC_02092	PepS,Amp S	aminopeptidase PepS, putative	47 kDa	x		zyt	8.87	N	5.93E+05	4.68E+05	3.22E-01	-1.298	
88195741	SAOUHSC_02057		dUTP pyrophosphatase	19 kDa	x		zyt	8.87	N	1.28E+06	1.49E+06	4.85E-01	1.255	
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025	83 kDa	x	x	zw	10.00	Y	1.27E+06	2.27E+06	1.90E-02	1.761	10
88194032	SAOUHSC_00225		hypothetical protein SAOUHSC_00225	27 kDa	x	x	unb	2.50	N	4.14E+06	5.12E+06	9.03E-01	1.050	
88194062	SAOUHSC_00256		hypothetical protein SAOUHSC_00256	33 kDa	x	x	unb	3.33	Y	5.13E+05	8.29E+05	9.20E-02	1.590	10
88194155	SAOUHSC_00356		hypothetical protein SAOUHSC_00356	21 kDa	x		unb	3.33	Y	4.70E+07	2.16E+06	1.58E-12	-20.631	10, 12, 13
88194160	SAOUHSC_00362		hypothetical protein SAOUHSC_00362	24 kDa	x		unb	3.33	Y	6.27E+05	7.31E+05	1.69E-01	1.212	
88194167	SAOUHSC_00369		hypothetical protein SAOUHSC_00369	36 kDa	x	x	zyt	8.87	#NV	2.42E+06	2.05E+06	4.78E-01	-1.314	
88194169	SAOUHSC_00371		hypothetical protein SAOUHSC_00371	15 kDa	x		zyt	8.87	N	4.41E+06	3.81E+06	7.77E-01	-1.110	6, 10
88194180	SAOUHSC_00383		hypothetical protein SAOUHSC_00383	26 kDa	x	x	unb	6.46	Y	3.27E+06	1.83E+06	3.70E-02	-2.016	
88194194	SAOUHSC_00399		hypothetical protein SAOUHSC_00399	25 kDa	x		ez	9.98	Y	6.74E+05	1.59E+06	5.68E-04	1.953	
88194256	SAOUHSC_00469	SpoVG	hypothetical protein SAOUHSC_00469	11 kDa	x		zyt	8.87	N	3.73E+06	1.56E+06	9.80E-02	-2.848	10
88194387	SAOUHSC_00617		hypothetical protein SAOUHSC_00617	19 kDa	x	x	unb	3.33	Y	5.55E+08	3.77E+08	7.10E-02	-1.497	11
88194469	SAOUHSC_00704		hypothetical protein SAOUHSC_00704	17 kDa	x	x	unb	3.33	Y	1.87E+07	4.67E+06	6.40E-07	-4.087	
88194602	SAOUHSC_00844		hypothetical protein	30 kDa	x	x	zm	9.87	Y	2.41E+06	1.80E+06	3.91E-01	-1.482	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194603	SAOUHSC_00845		SAOUHSC_00844 hypothetical protein SAOUHSC_00845	7 kDa	x		unb	2.50	N	8.41E+06	7.75E+04	5.69E-14	-94.097	6, 10, 12, 13
88194622	SAOUHSC_00865		hypothetical protein SAOUHSC_00865	28 kDa	x		unb	2.50	N	1.12E+06	7.88E+05	3.53E-01	-1.732	
88194877	SAOUHSC_01135		hypothetical protein SAOUHSC_01135	4 kDa	x		unb	2.50	#NV	3.06E+08	6.15E+07	5.50E-02	-8.091	
88194880	SAOUHSC_01138		hypothetical protein SAOUHSC_01138	17 kDa	x	x	unb	2.50	N	7.87E+05	8.39E+05	7.74E-01	-1.171	
88195001	SAOUHSC_01268		hypothetical protein SAOUHSC_01268	11 kDa	x		zyt	8.87	N	1.56E+05	7.33E+04	2.51E-01	-2.118	
88195053	SAOUHSC_01323		hypothetical protein SAOUHSC_01323	30 kDa	x		zyt	8.87	N	1.44E+05	4.56E+04	1.88E-01	-4.200	
88195160	SAOUHSC_01436		hypothetical protein SAOUHSC_01436	16 kDa	x		zyt	8.87	N	6.13E+05	2.90E+05	4.00E-02	-1.741	
88195356	SAOUHSC_01648		hypothetical protein SAOUHSC_01648	17 kDa		x	unb	2.50	#NV	5.73E+05	3.75E+05	5.80E-02	-1.568	
88195462	SAOUHSC_01761		hypothetical protein SAOUHSC_01761	18 kDa	x		unb	2.50	#NV	1.81E+06	1.17E+06	4.00E-03	-1.636	
88195515	SAOUHSC_01815		hypothetical protein SAOUHSC_01815	25 kDa	x		zyt	8.87	N	8.12E+05	2.23E+05	1.30E-01	-3.614	
88195602	SAOUHSC_01907		hypothetical protein SAOUHSC_01907	31 kDa	x		zyt	8.87	N	3.68E+05	2.33E+05	3.27E-01	-1.775	
88195668	SAOUHSC_01977		hypothetical protein SAOUHSC_01977	13 kDa	x	x	zyt	8.87	#NV	3.46E+06	3.67E+06	7.05E-01	-1.232	
88195687	SAOUHSC_01999		hypothetical protein SAOUHSC_01999	17 kDa	x	x	zyt	8.87	N	3.96E+05	5.25E+05	9.87E-01	1.009	
88195729	SAOUHSC_02044		hypothetical protein SAOUHSC_02044	23 kDa	x		zyt	8.87	N	2.22E+06	1.70E+06	9.30E-02	-1.306	
88195845	SAOUHSC_02167		hypothetical protein SAOUHSC_02167	13 kDa	x	x	unb	3.33	Y	1.02E+07	1.60E+07	2.59E-01	1.389	
88195892	SAOUHSC_02218		hypothetical protein SAOUHSC_02218	11 kDa	x		unb	2.50	N	1.33E+06	9.20E+05	6.70E-02	-1.406	
88196330	SAOUHSC_02690		hypothetical protein SAOUHSC_02690	59 kDa	x	x	unb	3.33	Y	1.77E+06	1.88E+06	7.87E-01	-1.096	
88196513	SAOUHSC_02885		hypothetical protein SAOUHSC_02885	69 kDa	x	x	zm	9.99	N	4.46E+06	2.41E+06	4.70E-15	-1.800	
88196593	SAOUHSC_02972	IsaB	hypothetical protein SAOUHSC_02972	19 kDa	x	x	unb	3.33	Y	2.35E+07	1.55E+07	2.90E-02	-1.603	
88196640	SAOUHSC_03022		hypothetical protein SAOUHSC_03022	19 kDa	x		unb	2.50	N	4.44E+05	1.23E+05	1.60E-02	-3.467	10
88196290	SAOUHSC_02650		lipoprotein, putative	23 kDa	x	x	unb	4.05	Y	1.01E+07	8.63E+06	5.96E-01	-1.208	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	<i>p</i> -Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195728	SAOUHSC_02043		phage head protein, putative	37 kDa	x	x	zyt	8.87	N	2.69E+06	2.05E+06	5.00E-01	-1.291	
88196598	SAOUHSC_02978		phage infektion protein, putative preprotein translocase, SecG	109 kDa	x	x	zm	9.99	Y	4.73E+06	3.55E+06	3.00E-03	-1.348	
88194561	SAOUHSC_00801	SecG	subunit	10 kDa	x	x	zm	9.75	N	2.05E+06	1.11E+06	6.50E-02	-2.168	
88195999	SAOUHSC_02333		sceD protein, putative single-strand DNA-binding protein, putative	24 kDa	x	x	ez	9.98	#NV	4.94E+08	6.60E+07	8.44E-05	-7.871	
88195755	SAOUHSC_02071		SLT orf 129-like protein	19 kDa	x		unb	2.50	N	3.23E+06	2.07E+06	1.00E-03	-1.561	
88195714	SAOUHSC_02027		transcription antitermination protein, putative	14 kDa	x		unb	2.50	#NV	2.31E+06	2.28E+06	8.07E-01	-1.054	
88194298	SAOUHSC_00517	NusG	protein, putative	21 kDa	x		zyt	8.87	N	3.93E+05	3.68E+05	4.69E-01	-1.564	

Drei Bioreplikate der Kulturüberstände von der frühen stationären Phase von *S. aureus* RN1HG und RN1HG $\Delta sigB$ wurden mittels gelfreier Analysen aufgearbeitet. Ein Protein wurde als identifiziert angesehen wenn es mit mindestens 2 Peptiden identifiziert wurden. An anschließend erfolgte eine Klassifikation in funktionelle Gruppe (TigR). Der Fold Change bezieht sich auf die frühe stationäre Phase des Wildtyps.

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

^B Die Lokalisation und die Vorhersage eines Signalpeptides erfolgte über P-Sort. ez = extrazellulär, zw = Zellwand, zm = zytoplasmatische Membran, zyt = Zytoplasma, unb = unbekannt, SP = Signalpeptid, N = kein Signalpeptid, Y = Signalpeptid vorhanden, #NV = Vorhersage nicht möglich.

^C Die Intensitäten, der *p*-Wert und der Fold Change wurde anhand der Elucidator Software ermittelt.

^D Publikation, die den Einfluss von SigB besätigen: ¹ Deora et al., 1997; ² Kullik et al., 1998; ³ Cheung et al., 1999; ⁴ Miyazaki et al., 1999; ⁵ Nicholas et al., 1999; ⁶ Gertz et al., 2000; ⁷ Bischoff et al., 2001; ⁸ Ziebandt et al. 2001; ⁹ Horsburgh et al., 2002; ¹⁰ Bischoff et al., 2004; ¹¹ Ziebandt et al. 2004; ¹² Homerova et al., 2004; ¹³ Pané-Farré et al., 2006.

Tab. 63: Identifizierte Proteine der späten stationären Phase von *S. aureus* RN1HG und RN1HG $\Delta sigB$ in pMEM.

Accession- nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
Toxine und Hämolyse (7)														
88194865	SAOUHSC_01121	Hla	alpha-hemolysin precursor gamma-hemolysin component	36 kDa	x	x	ez	10.00	Y	6.25E+07	1.06E+09	0.00E+00	16.393	2, 5, 6, 7
88196348	SAOUHSC_02708	HlgA	A	35 kDa	x	x	ez	9.73	#NV	7.84E+06	1.73E+08	6.55E-20	22.727	7
88193943	SAOUHSC_00130	IsdI	SAOUHSC_00130 hypothetical protein	13 kDa	x	x	unb	2.50	N	1.60E+07	5.94E+06	1.40E-02	-2.107	10
88195915	SAOUHSC_02243		SAOUHSC_02243 hypothetical protein	40 kDa		x	ez	9.73	Y	1.44E+06	6.01E+06	5.04E-05	4.167	7
88196350	SAOUHSC_02710	HlgB	gamma-hemolysin component B	37 kDa	x	x	ez	9.73	Y	2.68E+07	4.12E+08	4.04E-21	15.873	7
88196349	SAOUHSC_02709	HlgC	gamma-hemolysin component C	36 kDa	x	x	ez	9.73	Y	1.97E+07	4.29E+08	0.00E+00	20.833	7
88195647	SAOUHSC_01954	LukD	leukotoxin, LukD	37 kDa	x	x	ez	9.98	#NV	5.94E+05	1.44E+06	1.04E-09	2.445	5
Virulenz-/Abwehrmechanismen (21)														
88193871	SAOUHSC_00051	Plc	1-phosphatidylinositol phosphodiesterase precursor, putative	37 kDa	x	x	ez	9.97	Y	5.05E+06	1.03E+07	6.00E-03	2.012	7, 8
88196592	SAOUHSC_02971	Aur	aureolysin, putative	55 kDa	x	x	ez	9.97	Y	1.34E+07	4.88E+07	1.14E-07	3.584	7, 8
88194572	SAOUHSC_00812	ClfA	clumping factor	96 kDa	x		zw	10.00	Y	1.83E+07	6.70E+05	2.36E-05	-23.875	3, 7, 9, 10
88196585	SAOUHSC_02963	ClfB	clumping factor B, putative cysteine protease precursor, putative	94 kDa	x		zw	10.00	Y	9.54E+06	3.33E+06	6.55E-15	-2.655	
88194744	SAOUHSC_00987	SspB	putative	45 kDa	x	x	ez	9.55	Y	1.48E+07	2.75E+07	1.71E-09	1.908	7, 8
88195217	SAOUHSC_01501	EbpS	elastin binding protein	53 kDa	x	x	zw	9.06	#NV	1.74E+06	1.11E+06	1.76E-04	-1.528	
88194745	SAOUHSC_00988	SspA	glutamyl endopeptidase precursor, putative	36 kDa	x	x	ez	10.00	Y	1.06E+07	1.70E+07	1.20E-02	1.675	5, 7, 8
88196346	SAOUHSC_02706	Sbi	immunoglobulin G-binding protein Sbi, putative	50 kDa	x	x	unb	3.33	#NV	1.41E+07	2.11E+07	3.00E-02	1.490	
88193965	SAOUHSC_00153	IpdC	indolepyruvate decarboxylase, putative	61 kDa	x	x	unb	2.50	N	1.11E+06	5.25E+05	3.97E-01	-1.458	
88196625	SAOUHSC_03006	Lip	lipase	77 kDa	x	x	ez	9.73	Y	2.47E+09	2.12E+09	5.20E-01	-1.072	8
88194101	SAOUHSC_00300	Geh	lipase precursor	76 kDa	x	x	ez	10.00	Y	3.57E+09	7.11E+09	1.95E-10	2.101	8
88193885	SAOUHSC_00069		protein A	56 kDa	x	x	zw	10.00	Y	1.20E+08	3.68E+07	1.10E-02	-3.697	
88194325	SAOUHSC_00545		sdrD protein, putative	146 kDa	x	x	zw	10.00	Y	1.34E+07	4.62E+06	1.30E-02	-3.052	
88195636	SAOUHSC_01942	SplA	serine protease SplA	26 kDa		x	ez	9.73	Y	1.29E+05	6.84E+05	4.52E-05	4.484	5, 7, 8
88195635	SAOUHSC_01941	SplB	serine protease SplB	26 kDa	x	x	ez	9.73	Y	3.66E+06	1.27E+07	2.56E-04	3.546	7, 8

Accession- nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195634	SAOUHSC_01939	SplC	serine protease SplC	26 kDa		x	ez	9.73	Y	2.03E+05	1.35E+06	5.92E-05	6.667	5, 7, 8
88195630	SAOUHSC_01935	SplF	serine protease SplF, putative	26 kDa	x	x	ez	9.73	#NV	2.41E+06	6.40E+06	2.00E-03	2.933	7, 8
88195808	SAOUHSC_02127		staphopain thiol proteinase staphylokinase precursor,	44 kDa	x	x	ez	9.73	Y	1.65E+07	5.56E+07	1.60E-04	3.165	5, 7, 8, 20
88195848	SAOUHSC_02171	Sak	putative	19 kDa		x	ez	9.98	Y	3.54E+06	6.57E+06	2.00E-03	2.481	7
88194577	SAOUHSC_00818	Nuc	thermonuclease precursor	25 kDa	x	x	ez	10.00	Y	7.59E+06	8.28E+07	3.97E-15	11.236	1, 5, 7, 10
88195480	SAOUHSC_01779	Tig	trigger factor	49 kDa	x	x	zyt	8.87	N	6.30E+06	1.19E+07	1.37E-01	2.347	
Zellwandbiosynthese und -abbau (13)														
88194219	SAOUHSC_00427		autolysin precursor, putative bifunctional autolysin	36 kDa	x	x	ez	9.98	Y	4.96E+07	3.06E+07	1.12E-01	-1.681	8
88194750	SAOUHSC_00994	Atl	precursor, putative hypothetical protein	137 kDa	x	x	ez	10.00	#NV	9.81E+08	8.62E+08	2.22E-01	-1.135	10
88193909	SAOUHSC_00094		SAOUHSC_00094 immunodominant antigen A,	22 kDa	x	x	zw	9.93	Y	2.03E+08	1.61E+08	2.60E-01	-1.187	
88196515	SAOUHSC_02887	IsaA	putative	24 kDa	x		ez	10.00	Y	1.11E+09	5.34E+08	2.83E-11	-1.929	8
88195840	SAOUHSC_02161		MHC class II analog protein	66 kDa	x	x	unb	3.33	Y	1.14E+06	1.20E+07	4.00E-03	12.821	
88195184	SAOUHSC_01467	Pbp2	penicillin-binding protein 2	80 kDa	x	x	ez	9.55	N	1.87E+06	2.21E+06	7.90E-02	1.220	
88195360	SAOUHSC_01652	PbpF,Pbp3	penicillin-binding protein 3	77 kDa	x	x	zm	9.82	#NV	2.08E+06	1.44E+06	1.79E-04	-1.421	
88194055	SAOUHSC_00248	LytM	peptidoglycan hydrolase, putative	34 kDa	x	x	ez	9.98	Y	3.86E+08	8.79E+07	2.19E-06	-4.057	
88194324	SAOUHSC_00544		sdrC protein, putative secretory antigen precursor,	108 kDa	x	x	zw	10.00	Y	8.63E+06	6.44E+06	6.11E-01	-1.108	
88196215	SAOUHSC_02571	SsaA	putative secretory antigen SsaA-like	29 kDa	x	x	ez	9.04	Y	6.04E+07	7.04E+07	2.63E-01	1.274	7
88194436	SAOUHSC_00671		protein truncated MHC class II analog	28 kDa	x	x	ez	9.73	Y	1.71E+08	8.48E+07	3.29E-04	-1.890	
88196118	SAOUHSC_02466		protein truncated MHC class II analog	15 kDa	x		unb	3.33	Y	6.33E+07	1.04E+06	5.30E-05	-57.544	
88194675	SAOUHSC_00918		protein	16 kDa	x	x	unb	3.33	Y	1.32E+08	1.29E+08	8.51E-01	-1.028	
Zellumhüllung (15)														
88194199	SAOUHSC_00405		hypothetical protein SAOUHSC_00405	29 kDa	x		unb	2.50	N	2.29E+06	2.56E+06	6.13E-01	1.151	
88194482	SAOUHSC_00717		hypothetical protein SAOUHSC_00717	16 kDa	x	x	unb	3.33	Y	3.75E+07	1.09E+08	5.20E-12	3.077	
88194829	SAOUHSC_01081	IsdA	hypothetical protein SAOUHSC_01081	39 kDa	x	x	zw	10.00	N	8.44E+07	9.15E+07	4.26E-01	1.181	7

Accession- nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	wt	$\Delta sigB$	Lokali- sation ^B	PSort- Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88194830	SAOUHSC_01082	IsdC	hypothetical protein SAOUHSC_01082	25 kDa	x	x	unb	3.33	Y	2.22E+07	4.15E+07	9.00E-03	1.724	10
88195062	SAOUHSC_01332		hypothetical protein SAOUHSC_01332	34 kDa	x	x	unb	2.50	#NV	9.37E+06	7.22E+06	5.50E-02	-1.283	
88195295	SAOUHSC_01584		hypothetical protein SAOUHSC_01584	34 kDa		x	unb	2.50	N	5.16E+05	1.43E+06	4.74E-04	2.833	
88195443	SAOUHSC_01739	LytH	hypothetical protein SAOUHSC_01739	33 kDa	x	x	unb	3.33	N	1.96E+06	9.00E+05	8.55E-14	-2.118	
88195590	SAOUHSC_01895		hypothetical protein SAOUHSC_01895	33 kDa	x	x	ez	9.55	Y	3.54E+06	2.85E+06	1.40E-01	-1.200	
88195802	SAOUHSC_02121		hypothetical protein SAOUHSC_02121	45 kDa	x	x	unb	3.33	Y	7.64E+06	3.15E+06	2.49E-08	-2.309	
88196433	SAOUHSC_02798		hypothetical protein SAOUHSC_02798	179 kDa	x		zw	10.00	N	1.23E+06	3.94E+05	3.00E-03	-3.140	
88196599	SAOUHSC_02979		hypothetical protein SAOUHSC_02979	69 kDa	x	x	ez	9.73	Y	1.40E+08	1.17E+08	8.30E-02	-1.150	
88196601	SAOUHSC_02982		hypothetical protein SAOUHSC_02982	71 kDa	x	x	zw	10.00	Y	4.27E+07	1.93E+07	1.98E-06	-2.049	
88193889	SAOUHSC_00074	SirA	periplasmic binding protein, putative	37 kDa	x	x	unb	3.33	Y	4.52E+07	2.29E+07	2.39E-04	-1.887	
88195460	SAOUHSC_01759	Mrec	rod shape-determining protein Mrec	31 kDa	x		unb	3.33	Y	5.74E+06	3.34E+06	9.11E-07	-1.701	
88196468	SAOUHSC_02834	SrtA	sortase, putative	24 kDa	x		unb	3.33	Y	6.98E+05	3.20E+05	5.49E-05	-2.152	
Stressantwort (14)														
88194163	SAOUHSC_00365	AhpC	alkyl hydroperoxide reductase	21 kDa	x	x	zyt	9.98	N	5.15E+08	1.17E+08	4.23E-06	-3.208	
88195057	SAOUHSC_01327	KatA	catalase	55 kDa	x	x	zyt	9.98	N	4.40E+07	1.93E+07	3.72E-01	-1.427	6, 10
88195129	SAOUHSC_01403	CspA	cold shock protein, putative	7 kDa	x	x	zyt	9.98	N	4.62E+07	2.78E+07	1.10E-02	-1.594	
88194348	SAOUHSC_00573		hypothetical protein SAOUHSC_00573	29 kDa	x	x	unb	2.50	N	2.61E+06	1.12E+06	1.37E-01	-1.819	
88194589	SAOUHSC_00831		hypothetical protein SAOUHSC_00831	15 kDa	x		unb	2.50	N	3.70E+06	1.45E+05	8.50E-17	-19.638	7
88194593	SAOUHSC_00835		hypothetical protein SAOUHSC_00835	14 kDa	x	x	zyt	8.87	N	8.82E+06	1.80E+06	8.16E-06	-4.071	
88195522	SAOUHSC_01822	Tpx	hypothetical protein SAOUHSC_01822	18 kDa	x	x	unb	2.50	N	5.98E+06	4.13E+06	2.63E-01	-1.491	
88196044	SAOUHSC_02381	Dps	hypothetical protein SAOUHSC_02381	17 kDa	x	x	unb	2.50	N	1.32E+07	3.95E+06	3.13E-04	-3.313	
88196094	SAOUHSC_02441	Asp23	hypothetical protein SAOUHSC_02441	19 kDa	x		unb	2.50	N	1.48E+08	1.38E+06	1.02E-11	-61.945	4, 7, 10

Accession-nummer	Locus-Tag ^A	Protein-name ^A	Beschreibung	Molekulargewicht	wt	$\Delta sigB$	Lokalisation ^B	PSort-Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	p-Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195361	SAOUHSC_01653	SodA	superoxide dismutase, Mn, putative	23 kDa	x	x	ez	9.55	N	1.29E+07	2.08E+06	1.23E-06	-4.741	
88193908	SAOUHSC_00093	SodM	superoxide dismutase, putative	23 kDa	x	x	ez	9.55	N	2.27E+07	2.65E+07	2.49E-01	1.305	7, 10
88194846	SAOUHSC_01100	TrxA,Trx	thioredoxin	11 kDa	x	x	zyt	9.98	N	1.52E+08	5.15E+07	6.03E-05	-2.857	
88194546	SAOUHSC_00785	TrxB	thioredoxin reductase	34 kDa	x	x	zyt	9.65	N	3.24E+06	1.26E+06	2.00E-03	-1.931	
88194592	SAOUHSC_00834		thioredoxin, putative	12 kDa	x	x	zyt	8.87	N	1.64E+07	7.62E+06	7.00E-03	-1.863	
Regulation (8)														
88194239	SAOUHSC_00452		hypothetical protein SAOUHSC_00452	12 kDa	x		unb	2.50	N	3.41E+06	1.08E+06	5.75E-04	-2.985	
88194459	SAOUHSC_00694		hypothetical protein SAOUHSC_00694	17 kDa	x		unb	2.50	N	1.47E+06	1.35E+06	9.04E-01	1.041	
88194753	SAOUHSC_00997		hypothetical protein SAOUHSC_00997	46 kDa	x	x	unb	3.33	Y	2.58E+06	1.57E+06	8.00E-03	-1.622	
88194963	SAOUHSC_01228	CodY	hypothetical protein SAOUHSC_01228	29 kDa	x	x	zyt	8.87	N	1.77E+07	8.68E+06	1.47E-01	-1.613	
88195657	SAOUHSC_01964	TRAP	hypothetical protein SAOUHSC_01964	20 kDa	x	x	zyt	8.87	#NV	6.09E+07	1.99E+07	1.17E-07	-2.811	
88195154	SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA, putative	18 kDa	x	x	zyt	9.98	N	6.71E+06	5.22E+06	7.21E-01	-1.119	
88196063	SAOUHSC_02402		PTS system, mannitol-spezific Ila component, putative	16 kDa	x		zyt	9.98	N	1.95E+06	1.88E+05	4.37E-05	-4.666	7, 10
88196226	SAOUHSC_02583		transcriptional regulator, putative	34 kDa	x		unb	3.33	Y	1.22E+06	3.59E+05	8.16E-05	-3.337	
Transport (19)														
88194087	SAOUHSC_00284		5'-nucleotidase, lipoprotein e(P4) family	33 kDa	x	x	unb	3.33	Y	2.66E+06	4.93E+06	1.00E-02	1.802	7
88196085	SAOUHSC_02430	HtsA	ABC transporter periplasmic binding protein, putative	37 kDa	x		unb	3.33	Y	4.76E+06	2.38E+06	4.00E-03	-1.887	
88194402	SAOUHSC_00634	MntC	ABC transporter, substrate-binding protein, putative	35 kDa	x	x	unb	3.33	Y	7.85E+08	3.35E+08	2.69E-24	-2.144	
88194742	SAOUHSC_00985	MenB	enoyl-CoA hydratase/isomerase family protein, putative	30 kDa	x	x	zyt	8.87	N	2.15E+05	5.51E+04	9.75E-01	1.027	
88194761	SAOUHSC_01007	Fold	Fold bifunctional protein, putative	31 kDa	x	x	zyt	8.87	N	3.80E+06	2.88E+06	7.94E-01	-1.108	
88194112	SAOUHSC_00311		hypothetical protein SAOUHSC_00311	10 kDa	x		zyt	8.87	N	9.22E+05	1.62E+05	4.00E-03	-4.295	
88194831	SAOUHSC_01084	IsdD	hypothetical protein SAOUHSC_01084	41 kDa	x	x	unb	2.50	Y	8.13E+06	1.56E+07	1.23E-01	1.661	10

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88194832	SAOUHSC_01085	IsdE	hypothetical protein SAOUHSC_01085	32 kDa	x	x	zyt	8.87	N	3.64E+06	8.00E+06	2.80E-02	1.934	
88195571	SAOUHSC_01874		hypothetical protein SAOUHSC_01874	11 kDa	x	x	unb	2.50	N	6.07E+06	2.87E+06	3.00E-03	-1.882	
88195914	SAOUHSC_02241		hypothetical protein SAOUHSC_02241	39 kDa		x	ez	9.73	Y	1.95E+06	7.09E+06	1.00E-09	3.663	7
88195918	SAOUHSC_02246		hypothetical protein SAOUHSC_02246	35 kDa		x	unb	6.46	Y	1.00E+06	2.89E+06	1.00E-03	3.115	
88196199	SAOUHSC_02554	FhuD2	hypothetical protein SAOUHSC_02554	34 kDa	x	x	unb	3.33	Y	7.65E+06	2.80E+06	1.84E-07	-2.507	
88196339	SAOUHSC_02699		hypothetical protein SAOUHSC_02699	29 kDa	x	x	unb	3.33	Y	5.11E+06	2.74E+06	5.90E-02	-1.705	
88196600	SAOUHSC_02980		hypothetical protein SAOUHSC_02980	21 kDa	x		unb	2.50	N	1.21E+06	3.04E+05	2.00E-03	-2.848	
88196194	SAOUHSC_02549	ModA	molybdenum ABC transporter, periplasmic molybdate-binding protein	29 kDa	x	x	unb	3.33	Y	3.08E+06	1.88E+06	1.45E-01	-1.466	
88194828	SAOUHSC_01079	IsdB	neurofilament protein	72 kDa	x	x	zw	10.00	#NV	2.77E+06	4.50E+06	5.20E-02	1.852	
88196403	SAOUHSC_02767	Opp1A,Opp1A	peptide ABC transporter, peptide-binding protein, putative	60 kDa	x	x	zw	9.18	Y	3.45E+06	2.46E+06	1.06E-01	-1.376	
88194781	SAOUHSC_01028	PtsH	phosphocarrier protein hpr, putative	9 kDa	x	x	zyt	10.00	N	8.47E+06	7.26E+05	5.43E-14	-9.678	
88195976	SAOUHSC_02310	KdpC	potassium-transporting ATPase, C subunit	21 kDa	x	x	unb	3.33	Y	2.54E+06	2.26E+06	5.79E-01	1.105	
zell. Prozesse (4)														
88194886	SAOUHSC_01144	FtsL	hypothetical protein SAOUHSC_01144	15 kDa	x	x	zyt	8.87	N	9.15E+06	8.88E+06	2.39E-01	1.182	
88195179	SAOUHSC_01462		hypothetical protein SAOUHSC_01462	13 kDa	x	x	zyt	8.87	N	7.91E+06	2.88E+06	3.10E-02	-2.185	
88195846	SAOUHSC_02169	Chs,Chp	hypothetical protein SAOUHSC_02169	17 kDa	x	x	unb	3.33	Y	1.85E+07	8.55E+07	7.86E-34	4.444	
88194942	SAOUHSC_01205	FtsY	signal recognition particle-docking protein FtsY	47 kDa	x		zyt	8.87	N	1.01E+06	2.69E+05	3.50E-02	-2.597	
Energiemetabolismus (40)														
88193901	SAOUHSC_00086	ButA	3-ketoacyl-acyl carrier protein reductase, putative	27 kDa	x		zyt	9.65	N	1.04E+06	8.21E+05	7.34E-01	1.229	
88195316	SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase,	52 kDa	x	x	zyt	8.87	N	1.16E+07	5.05E+06	2.28E-01	-1.663	

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			decarboxylating											
88194665	SAOUHSC_00908	Cdr	coenzyme A disulfide reductase, putative	49 kDa	x		zyt	9.98	N	2.67E+06	1.03E+06	2.84E-01	-1.635	
88196500	SAOUHSC_02869	RocA	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	57 kDa	x	x	zyt	9.98	#NV	7.54E+06	1.92E+06	8.20E-02	-2.123	
88193913	SAOUHSC_00100	DeoC,DeoC1,Dra	deoxyribose-phosphate aldolase	23 kDa	x	x	zyt	9.98	N			0.00E+00	#DIV/0!	
88194795	SAOUHSC_01043	PdhD,LpdA	dihydrolipoamide dehydrogenase	49 kDa	x	x	zyt	9.98	N	2.20E+07	1.21E+07	4.39E-01	-1.323	
88196464	SAOUHSC_02830	Ddh	D-lactate dehydrogenase, putative	35 kDa	x		zyt	9.98	N	2.31E+05	1.51E+05	9.91E-01	-1.009	
88194559	SAOUHSC_00799	Eno	enolase	47 kDa	x	x	zyt	9.98	N	3.99E+06	3.60E+06	3.07E-01	2.288	
88193954	SAOUHSC_00142	Fdh	formate dehydrogenase, NAD-dependent, putative	38 kDa	x	x	zyt	9.98	N	1.44E+07	1.73E+07	3.28E-01	1.745	
88196553	SAOUHSC_02926		fructose-bisphosphate aldolase class-I, putative	33 kDa	x	x	unb	2.50	N	2.86E+07	2.66E+07	5.51E-01	1.399	
88195310	SAOUHSC_01599	Zwf	glucose-6-phosphate 1-dehydrogenase	57 kDa		x	zyt	8.87	N	4.59E+05	2.04E+05	9.98E-01	1.002	
88194657	SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase	50 kDa	x	x	zyt	9.98	N	4.14E+06	1.67E+06	7.22E-01	-1.207	
88194555	SAOUHSC_00795	Gap1,Gap	glyceraldehyde-3-phosphate dehydrogenase, type I	36 kDa	x	x	zyt	9.98	N	2.25E+08	8.50E+07	7.00E-03	-2.093	
88194594	SAOUHSC_00836	GcvH	glycine cleavage system H protein	14 kDa	x	x	zyt	8.87	N	6.04E+06	2.29E+06	5.30E-02	-2.586	
88194332	SAOUHSC_00553		hypothetical protein SAOUHSC_00553	22 kDa	x	x	zyt	8.87	N	2.17E+07	2.95E+06	1.57E-18	-6.613	4, 7, 10
88194493	SAOUHSC_00728		hypothetical protein SAOUHSC_00728	74 kDa	x	x	zm	9.99	Y	2.06E+08	1.23E+08	1.22E-09	-1.619	
88194654	SAOUHSC_00897	GlpQ	hypothetical protein SAOUHSC_00897	35 kDa	x	x	unb	4.86	#NV	3.04E+07	3.38E+07	1.76E-01	1.186	7, 8
88194760	SAOUHSC_01005		hypothetical protein SAOUHSC_01005	11 kDa	x	x	unb	3.33	#NV	8.33E+06	4.52E+06	1.50E-08	-1.815	
88195558	SAOUHSC_01860		hypothetical protein SAOUHSC_01860	12 kDa	x	x	zyt	8.87	N	2.81E+07	5.71E+06	2.99E-11	-4.504	
88195596	SAOUHSC_01901		hypothetical protein SAOUHSC_01901	26 kDa	x	x	unb	2.50	N	2.19E+07	1.25E+07	1.00E-01	-1.495	
88195678	SAOUHSC_01987		hypothetical protein SAOUHSC_01987	22 kDa	x	x	zyt	8.87	#NV	7.72E+06	3.18E+06	6.00E-03	-2.410	4, 7, 10
88195823	SAOUHSC_02143		hypothetical protein SAOUHSC_02143	39 kDa	x	x	zyt	8.87	N	1.09E+06	7.48E+05	8.96E-01	-1.062	
88195830	SAOUHSC_02150		hypothetical protein SAOUHSC_02150	22 kDa	x	x	unb	2.50	N	3.55E+06	3.55E+06	7.02E-01	1.205	

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88196029	SAOUHSC_02366	FbaA, Fba	hypothetical protein SAOUHSC_02366	31 kDa	x	x	zyt	8.87	N	3.00E+07	1.29E+07	4.10E-02	-1.854	
88196099	SAOUHSC_02447		hypothetical protein SAOUHSC_02447	36 kDa	x		zyt	8.87	N	1.60E+05	4.65E+04	1.45E-01	-2.494	
88196100	SAOUHSC_02448		hypothetical protein SAOUHSC_02448	33 kDa	x	x	unb	2.50	Y	1.05E+07	4.35E+06	4.46E-18	-2.329	
88196112	SAOUHSC_02460		hypothetical protein SAOUHSC_02460	32 kDa		x	zyt	8.87	#NV	4.18E+05	2.81E+05	8.92E-01	1.091	
88196528	SAOUHSC_02900		hypothetical protein SAOUHSC_02900	31 kDa	x		zyt	8.87	N	3.26E+05	3.16E+04	2.20E-02	-10.173	7, 10
88196549	SAOUHSC_02922	Ldh2,Ldh	L-lactate dehydrogenase	34 kDa	x	x	zyt	9.65	N	1.33E+06	1.84E+06	3.70E-02	1.812	
88196554	SAOUHSC_02927	Mqo2	malate:quinone-oxidoreductase	56 kDa		x	unb	4.05	N	1.40E+05	1.63E+05	6.84E-01	1.282	
88194349	SAOUHSC_00574	Pta	phosphate acetyltransferase	35 kDa	x	x	zyt	8.87	N	1.66E+07	4.45E+06	3.67E-04	-2.750	
88195605	SAOUHSC_01910	PckA	phosphoenolpyruvate carboxykinase (ATP)	59 kDa	x	x	unb	2.50	N	3.75E+06	1.25E+06	6.28E-01	-1.338	
88194556	SAOUHSC_00796	Pgk	phosphoglycerate kinase, putative	43 kDa	x	x	zyt	9.91	N	3.07E+05	5.10E+05	5.20E-01	1.812	
88196343	SAOUHSC_02703	GpmA	phosphoglycerate mutase, putative	27 kDa	x	x	unb	2.50	N	6.09E+06	1.90E+06	2.79E-01	-1.676	
88194793	SAOUHSC_01041	PhdB,Pdh B	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	35 kDa		x	zyt	8.87	N	1.56E+06	1.30E+06	6.07E-01	1.357	
88194758	SAOUHSC_01002	QoxA	quinol oxidase AA3, subunit II, putative	42 kDa	x		zm	10.00	Y	2.02E+06	1.42E+06	3.57E-01	-1.248	
88194954	SAOUHSC_01218	SucD	succinyl-CoA synthetase, alpha subunit, putative	32 kDa		x	zyt	8.87	N	6.27E+05	6.28E+05	7.03E-01	1.332	
88194953	SAOUHSC_01216	SucC	succinyl-CoA synthetase, beta subunit, putative	42 kDa		x	zyt	8.87	N	1.75E+05	2.84E+05	3.73E-01	2.336	
88195066	SAOUHSC_01337	Tkt	transketolase	68 kDa	x	x	unb	2.50	N	9.69E+06	3.97E+06	1.25E-01	-1.673	
88194557	SAOUHSC_00797	TpiA,Tpi	triosephosphate isomerase	27 kDa	x	x	unb	2.50	N	5.67E+07	2.27E+07	1.10E-02	-2.036	
Proteinbiosynthese (24)														
88195210	SAOUHSC_01493	RpsA	30S ribosomal protein S1, putative	43 kDa		x	zyt	9.98	N	1.12E+06	2.64E+06	9.40E-02	4.098	
88196150	SAOUHSC_02500	RplE	50S ribosomal protein L5, putative	20 kDa	x	x	zyt	8.87	#NV	2.75E+06	2.32E+06	9.38E-01	1.035	
88194381	SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	62 kDa	x	x	zyt	9.98	N	2.57E+06	1.50E+06	5.64E-01	-1.258	
88195444	SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr)	17 kDa	x	x	unb	2.50	N	2.20E+06	7.44E+05	1.00E-03	-2.451	

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			deacylase											
88194290	SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	56 kDa	x	x	zyt	9.65	N	6.96E+06	2.68E+06	1.06E-01	-1.797	
88195373	SAOUHSC_01666	GlyS	glycyl-tRNA synthetase	54 kDa		x	zyt	10.00	N	3.78E+05	2.09E+05	2.70E-02	-1.749	
88194708	SAOUHSC_00951		hypothetical protein SAOUHSC_00951	19 kDa		x	zyt	8.87	N	1.51E+05	6.60E+04	7.29E-01	-1.305	
88194261	SAOUHSC_00474	RplY	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	24 kDa	x	x	zyt	8.87	#NV	1.95E+06	3.08E+06	3.04E-01	1.613	
88194299	SAOUHSC_00518	RplK	ribosomal protein L11	15 kDa	x	x	zyt	8.87	N	2.80E+07	2.18E+07	3.04E-01	-1.231	
88196135	SAOUHSC_02484	RplQ	ribosomal protein L17	14 kDa	x	x	zyt	8.87	N	1.20E+06	8.25E+05	1.92E-01	-1.383	
88196146	SAOUHSC_02495	RplR	ribosomal protein L18	13 kDa	x		zyt	8.87	N	2.43E+06	2.25E+06	8.32E-01	1.086	
88196144	SAOUHSC_02493	RpmD	ribosomal protein L30	7 kDa	x	x	unb	2.50	N	8.32E+06	4.02E+06	8.58E-09	-1.935	
88196024	SAOUHSC_02361	RpmE	ribosomal protein L31	10 kDa	x	x	unb	2.50	N	3.11E+07	1.72E+07	6.40E-02	-1.431	
88196147	SAOUHSC_02496	RplF	ribosomal protein L6, putative	20 kDa	x	x	zyt	8.87	N	2.85E+06	1.94E+06	6.02E-01	-1.272	
88194302	SAOUHSC_00521	RplL	ribosomal protein L7/L12	13 kDa	x		zyt	8.87	N	9.40E+07	5.39E+07	7.40E-02	-1.547	
88193838	SAOUHSC_00017	RplI	ribosomal protein L9	17 kDa	x	x	zyt	9.65	N	3.54E+06	1.66E+06	2.40E-02	-1.979	
88194147	SAOUHSC_00348	RpsF	ribosomal protein S6	12 kDa	x	x	zyt	9.98	#NV	6.08E+06	6.77E+06	4.92E-01	1.274	
88194969	SAOUHSC_01236	Rrf,Frr	ribosome recycling factor	20 kDa	x	x	zyt	9.98	N	3.39E+07	1.96E+07	5.40E-02	-1.582	
88193832	SAOUHSC_00009	SerS	seryl-tRNA synthetase	49 kDa	x	x	zyt	10.00	N	3.39E+05	1.41E+05	3.66E-01	-1.697	
88194309	SAOUHSC_00529	FusA,Fus	translation elongation factor G	77 kDa		x	zyt	9.98	N	7.53E+05	1.23E+06	1.48E-01	2.179	
88194967	SAOUHSC_01234	Tsf	translation elongation factor Ts	32 kDa	x	x	zyt	9.98	#NV	2.06E+08	9.30E+07	2.00E-03	-1.891	
88194310	SAOUHSC_00530	Tuf	translation elongation factor Tu	43 kDa	x	x	zyt	9.98	N	1.86E+07	2.60E+07	1.55E-01	1.575	
88195487	SAOUHSC_01786	InfC	translation initiation factor IF- 3	20 kDa	x		zyt	9.98	#NV	1.63E+06	1.20E+06	3.61E-01	-1.532	
88194690	SAOUHSC_00933	TrpS	tryptophanyl-tRNA synthetase	37 kDa	x	x	zyt	9.98	N	2.40E+06	7.86E+05	3.40E-02	-2.041	
Proteinmetabolismus (18)														
88194678	SAOUHSC_00921	FabF,Fab	3-oxoacyl- synthase, putative	44 kDa	x		zyt	9.98	N	3.66E+06	2.56E+06	7.04E-01	-1.147	
88194937	SAOUHSC_01199	FabG	3-oxoacyl-(acyl-carrier- protein) reductase, putative	26 kDa	x		zyt	9.98	N	1.49E+05	1.03E+05	5.08E-01	-1.413	
88194939	SAOUHSC_01201	HmrB,Acp P	acyl carrier protein	9 kDa	x	x	zyt	8.87	#NV	9.26E+07	5.07E+07	3.90E-02	-1.635	
88195390	SAOUHSC_01684	GrpE	co-chaperone GrpE	24 kDa	x	x	zyt	8.87	N	1.57E+07	1.07E+07	2.96E-01	-1.315	
88195389	SAOUHSC_01683	DnaK	DNAk protein, putative	66 kDa	x	x	zyt	9.98	N	5.87E+06	1.54E+07	3.00E-02	2.833	
88196491	SAOUHSC_02860	MvaS	HMG-CoA synthase, putative	43 kDa	x	x	zyt	8.87	N	1.09E+07	5.04E+06	4.75E-01	-1.382	

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88194313	SAOUHSC_00533		hypothetical protein SAOUHSC_00533	32 kDa	x		unb	2.50	N	1.18E+07	1.10E+06	6.09E-14	-8.822	7, 10
88194972	SAOUHSC_01239		hypothetical protein SAOUHSC_01239	44 kDa	x		zm	9.99	N	1.92E+06	9.85E+05	2.85E-04	-1.878	
88194988	SAOUHSC_01255		hypothetical protein SAOUHSC_01255	49 kDa	x		zyt	8.87	N	1.11E+06	3.72E+05	3.81E-04	-2.665	
88194989	SAOUHSC_01256		hypothetical protein SAOUHSC_01256	50 kDa	x		unb	2.50	N	1.51E+06	4.67E+05	4.16E-04	-2.694	
88195110	SAOUHSC_01383		hypothetical protein SAOUHSC_01383	69 kDa	x	x	zyt	9.98	N	3.79E+06	9.61E+05	8.95E-05	-3.141	
88195151	SAOUHSC_01427	CtpA	hypothetical protein SAOUHSC_01427	55 kDa	x	x	unb	2.50	N	1.66E+06	1.52E+06	5.88E-01	-1.095	
88195516	SAOUHSC_01816		hypothetical protein SAOUHSC_01816	40 kDa	x		zyt	8.87	N	3.61E+06	8.98E+05	5.74E-04	-2.969	
88195784	SAOUHSC_02102	Map	methionine aminopeptidase, type I	28 kDa	x	x	zyt	8.87	N	2.33E+07	6.17E+06	1.46E-06	-3.283	
88194694	SAOUHSC_00937	PepF,PepB	oligoendopeptidase F	70 kDa	x	x	zyt	9.98	N	3.02E+07	8.50E+06	3.03E-07	-2.895	
88194790	SAOUHSC_01038	Def	polypeptide deformylase	21 kDa	x	x	zyt	8.87	#NV	2.26E+07	7.67E+06	1.42E-04	-2.528	
88195663	SAOUHSC_01972	PrsA	protein export protein PrsA, putative	36 kDa	x	x	unb	3.33	Y	8.07E+07	5.78E+07	9.10E-02	-1.317	
88194660	SAOUHSC_00903	SpsB	Signal peptidase IB, putative	18 kDa	x		unb	4.05	N	2.43E+06	9.07E+05	1.79E-09	-2.588	
AS-Biosynthese (6)														
88194316	SAOUHSC_00536	IlvE	branched-chain amino acid aminotransferase	40 kDa	x	x	zyt	8.87	N	3.39E+06	1.72E+06	5.65E-01	-1.287	
88195018	SAOUHSC_01287	GlnA	glutamine synthetase, type I	51 kDa	x	x	zyt	9.98	N	3.42E+06	2.43E+06	7.52E-01	1.264	
88194273	SAOUHSC_00488	CysK	hypothetical protein SAOUHSC_00488	33 kDa	x	x	zyt	8.87	N	4.13E+06	2.14E+06	5.04E-01	-1.369	
88195550	SAOUHSC_01852		hypothetical protein SAOUHSC_01852	41 kDa		x	zyt	8.87	#NV	1.10E+04	3.84E+04	3.75E-01	3.175	
88195928	SAOUHSC_02257	SdrH	hypothetical protein SAOUHSC_02257	47 kDa	x	x	zw	9.18	Y	9.80E+06	2.79E+06	3.10E-16	-3.348	
88196017	SAOUHSC_02354	GlyA	serine hydroxymethyltransferase, putative	45 kDa	x	x	zyt	9.98	N	5.35E+06	2.42E+06	3.53E-01	-1.487	
Nukleotidbiosynthese (8)														
88196141	SAOUHSC_02490	Adk	adenylate kinase, putative	24 kDa		x	zyt	9.98	N	2.37E+06	3.37E+06	2.25E-01	1.567	
88195544	SAOUHSC_01845	Geh	formate-tetrahydrofolate ligase, putative	60 kDa	x	x	zyt	8.87	#NV	8.60E+05	1.01E+06	3.22E-01	2.457	

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88194270	SAOUHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	20 kDa	x	x	zyt	9.98	N	2.37E+06	5.58E+05	8.38E-07	-3.456	
88193914	SAOUHSC_00101	Drm,DeoB	phosphopentomutase phosphoribosylformylglycina	44 kDa	x	x	zyt	8.87	N	4.41E+05	3.66E+05	6.41E-01	1.406	
88194766	SAOUHSC_01012	PurQ	midine synthase I phosphoribosylformylglycina	25 kDa	x		zyt	8.87	N	8.42E+05	8.09E+05	7.06E-01	1.220	
88194765	SAOUHSC_01011	PurS	midine synthase, PurS protein purine nucleoside	10 kDa	x		zyt	8.87	N	3.87E+06	2.78E+06	4.10E-01	-1.302	
88196043	SAOUHSC_02380	DeoD2	phosphorylase uracil	26 kDa	x	x	unb	2.50	N	4.83E+07	1.75E+07	3.62E-04	-2.497	
88196016	SAOUHSC_02353	Upp	phosphoribosyltransferase	23 kDa	x		zyt	8.87	N			0.00E+00	0.000	
Transkription und Replikation (3)														
88195207	SAOUHSC_01490	Hup,Hu	DNA-binding protein HU, putative	10 kDa	x	x	unb	2.50	N	1.27E+08	5.99E+07	4.00E-02	-1.645	
88194530	SAOUHSC_00767	YfiA	SAOUHSC_00767 transcription elongation factor	22 kDa	x		zyt	8.87	N	1.36E+06	7.01E+05	2.45E-01	-1.568	
88195419	SAOUHSC_01714	GreA	GreA	18 kDa	x	x	zyt	8.87	N	3.84E+07	2.05E+07	3.10E-02	0.589	
Unbekannte Funktion (57)														
88194218	SAOUHSC_00426	PepS,Amp S	ABC transporter, substrate- binding protein, putative	30 kDa	x		unb	3.33	Y	5.85E+06	2.77E+06	1.20E-02	-2.371	
88195775	SAOUHSC_02092		aminopeptidase PepS, putative D-isomer spezific 2- hydroxyacid dehydrogenase,	47 kDa	x	x	zyt	8.87	N	6.47E+05	9.71E+05	1.34E-01	1.745	
88196221	SAOUHSC_02577		NAD binding domain protein	35 kDa	x	x	zyt	9.98	N	2.56E+06	1.03E+06	3.21E-01	-1.614	
88195741	SAOUHSC_02057		dUTP pyrophosphatase	19 kDa	x	x	zyt	8.87	N	3.69E+06	9.51E+05	2.01E-05	-3.380	
88194173	SAOUHSC_00375	GuaA	GMP synthase, putative hypothetical protein	58 kDa	x		zyt	8.87	N	2.69E+05	1.66E+05	8.82E-01	1.106	
88193846	SAOUHSC_00025		SAOUHSC_00025 hypothetical protein	83 kDa		x	zw	10.00	Y	1.16E+06	1.32E+06	3.43E-01	1.153	7
88194032	SAOUHSC_00225		SAOUHSC_00225 hypothetical protein	27 kDa	x	x	unb	2.50	N	1.90E+07	7.27E+06	7.70E-02	-1.757	
88194062	SAOUHSC_00256		SAOUHSC_00256 hypothetical protein	33 kDa		x	unb	3.33	Y	2.20E+05	3.53E+05	1.86E-01	1.522	7
88194155	SAOUHSC_00356		SAOUHSC_00356 hypothetical protein	21 kDa	x		unb	3.33	Y	7.33E+07	3.27E+06	3.09E-22	-15.505	7, 9, 10
88194160	SAOUHSC_00362		SAOUHSC_00362	24 kDa	x		unb	3.33	Y	1.21E+06	1.09E+06	7.80E-01	-1.064	

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88194167	SAOUHSC_00369		hypothetical protein SAOUHSC_00369	36 kDa	x	x	zyt	8.87	#NV	9.05E+06	3.50E+06	1.75E-04	-2.230	
88194169	SAOUHSC_00371		hypothetical protein SAOUHSC_00371	15 kDa	x		zyt	8.87	N	1.68E+07	7.19E+06	4.00E-03	-2.059	4, 7
88194180	SAOUHSC_00383		hypothetical protein SAOUHSC_00383	26 kDa	x		unb	6.46	Y	3.10E+06	1.30E+06	7.12E-06	-2.299	
88194194	SAOUHSC_00399		hypothetical protein SAOUHSC_00399	25 kDa		x	ez	9.98	Y	2.80E+05	8.30E+05	2.67E-05	2.513	
88194256	SAOUHSC_00469	SpoVG	hypothetical protein SAOUHSC_00469	11 kDa	x	x	zyt	8.87	N	2.00E+07	3.53E+06	8.57E-08	-4.478	7
88194387	SAOUHSC_00617		hypothetical protein SAOUHSC_00617	19 kDa	x	x	unb	3.33	Y	6.33E+08	2.78E+08	3.42E-08	-2.061	8
88194469	SAOUHSC_00704		hypothetical protein SAOUHSC_00704	17 kDa	x		unb	3.33	Y	1.69E+07	2.77E+06	9.25E-11	-4.990	
88194602	SAOUHSC_00844		hypothetical protein SAOUHSC_00844	30 kDa	x	x	zm	9.87	Y	6.08E+06	3.06E+06	3.22E-01	-1.517	
88194603	SAOUHSC_00845		hypothetical protein SAOUHSC_00845	7 kDa	x		unb	2.50	N	2.92E+07	1.88E+05	0.00E+00	-114.723	4, 7, 9, 10
88194622	SAOUHSC_00865		hypothetical protein SAOUHSC_00865	28 kDa	x	x	unb	2.50	N	2.45E+06	1.18E+06	2.30E-01	-1.708	
88194663	SAOUHSC_00906		hypothetical protein SAOUHSC_00906	33 kDa		x	zyt	8.87	N	1.25E+06	9.42E+05	9.76E-01	1.015	
88194788	SAOUHSC_01036		hypothetical protein SAOUHSC_01036	9 kDa	x	x	zyt	8.87	N	9.69E+06	3.88E+06	1.29E-04	-1.919	
88194802	SAOUHSC_01050		hypothetical protein SAOUHSC_01050	40 kDa	x		zm	9.99	Y	5.24E+05	1.88E+05	4.90E-02	-2.506	
88194877	SAOUHSC_01135		hypothetical protein SAOUHSC_01135	4 kDa	x	x	unb	2.50	#NV	5.72E+08	8.48E+07	4.00E-03	-6.880	
88194880	SAOUHSC_01138		hypothetical protein SAOUHSC_01138	17 kDa	x		unb	2.50	N	1.77E+06	1.68E+06	7.10E-01	1.209	
88195001	SAOUHSC_01268		hypothetical protein SAOUHSC_01268	11 kDa	x		zyt	8.87	N	5.36E+05	1.90E+05	7.10E-02	-2.052	
88195160	SAOUHSC_01436		hypothetical protein SAOUHSC_01436	16 kDa	x		zyt	8.87	N	5.37E+05	3.42E+05	3.72E-01	-1.367	
88195162	SAOUHSC_01438		hypothetical protein SAOUHSC_01438	9 kDa		x	unb	2.50	N	9.70E+05	8.43E+05	4.50E-01	1.284	
88195424	SAOUHSC_01719		hypothetical protein SAOUHSC_01719	12 kDa	x		zyt	8.87	N	2.42E+06	3.76E+05	5.00E-03	-3.284	
88195426	SAOUHSC_01721		hypothetical protein SAOUHSC_01721	10 kDa	x		unb	2.50	N	3.52E+06	1.26E+06	3.00E-03	-2.343	
88195462	SAOUHSC_01761		hypothetical protein SAOUHSC_01761	18 kDa	x		unb	2.50	#NV	2.21E+06	1.25E+06	9.40E-02	-1.468	

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88195514	SAOUHSC_01814		hypothetical protein SAOUHSC_01814	15 kDa	x	x	unb	2.50	N	7.91E+05	4.51E+05	1.56E-01	-1.828	
88195515	SAOUHSC_01815		hypothetical protein SAOUHSC_01815	25 kDa	x		zyt	8.87	N	3.13E+06	7.02E+05	3.00E-03	-3.002	
88195519	SAOUHSC_01819		hypothetical protein SAOUHSC_01819	18 kDa	x		zyt	8.87	N	3.17E+06	2.25E+06	8.07E-01	-1.126	
88195602	SAOUHSC_01907		hypothetical protein SAOUHSC_01907	31 kDa	x	x	zyt	8.87	N	1.72E+06	4.63E+05	4.30E-04	-2.937	
88195668	SAOUHSC_01977		hypothetical protein SAOUHSC_01977	13 kDa	x	x	zyt	8.87	#NV	1.23E+07	7.11E+06	9.80E-02	-1.545	
88195687	SAOUHSC_01999		hypothetical protein SAOUHSC_01999	17 kDa	x	x	zyt	8.87	N	1.10E+06	7.00E+05	4.86E-01	-1.296	
88195701	SAOUHSC_02013		hypothetical protein SAOUHSC_02013	19 kDa	x		zyt	8.87	N	5.37E+06	2.01E+05	2.20E-06	-18.948	4, 7, 10
88195757	SAOUHSC_02073		hypothetical protein SAOUHSC_02073	21 kDa	x	x	unb	2.50	N	2.75E+06	2.33E+06	9.61E-01	-1.025	
88195845	SAOUHSC_02167		hypothetical protein SAOUHSC_02167	13 kDa	x	x	unb	3.33	Y	6.44E+06	1.22E+07	4.20E-02	1.669	
88195892	SAOUHSC_02218		hypothetical protein SAOUHSC_02218	11 kDa	x	x	unb	2.50	N	4.95E+06	1.73E+06	9.46E-04	-2.626	
88196067	SAOUHSC_02406		hypothetical protein SAOUHSC_02406	35 kDa	x		unb	2.50	Y	1.50E+06	9.88E+05	8.00E-03	-1.502	
88196212	SAOUHSC_02568		hypothetical protein SAOUHSC_02568	13 kDa	x		zyt	8.87	#NV	3.66E+06	4.83E+05	1.88E-05	-5.678	
88196330	SAOUHSC_02690		hypothetical protein SAOUHSC_02690	59 kDa	x	x	unb	3.33	Y	6.77E+06	3.86E+06	1.32E-01	-1.908	
88196364	SAOUHSC_02724		hypothetical protein SAOUHSC_02724	26 kDa	x	x	unb	2.50	N	1.91E+06	9.14E+05	1.04E-01	-1.747	
88196410	SAOUHSC_02774		hypothetical protein SAOUHSC_02774	16 kDa	x		zyt	8.87	N	5.38E+05	6.97E+04	5.99E-04	-7.576	4, 7, 10
88196513	SAOUHSC_02885		hypothetical protein SAOUHSC_02885	69 kDa	x		zm	9.99	N	6.31E+06	2.68E+06	1.33E-08	-2.284	
88196593	SAOUHSC_02972	IsaB	hypothetical protein SAOUHSC_02972	19 kDa	x	x	unb	3.33	Y	3.27E+07	2.12E+07	9.10E-02	-1.607	
88196640	SAOUHSC_03022		hypothetical protein SAOUHSC_03022	19 kDa	x	x	unb	2.50	N	2.66E+06	3.36E+05	1.32E-07	-5.777	7
88196290	SAOUHSC_02650		lipoprotein, putative phage infektion protein,	23 kDa	x	x	unb	4.05	Y	2.05E+07	9.00E+06	9.18E-04	-2.292	
88196598	SAOUHSC_02978		putative	109 kDa	x	x	zm	9.99	Y	4.44E+06	2.58E+06	2.90E-06	-1.587	
88195758	SAOUHSC_02074		phi PVL orf 39-like protein	13 kDa	x		unb	2.50	Y	2.49E+06	3.01E+05	4.86E-05	-5.433	
88194561	SAOUHSC_00801	SecG	preprotein translocase, SecG subunit	10 kDa	x	x	zm	9.75	N	2.27E+06	5.54E+05	1.09E-12	-3.787	

Accession-nummer	Locus-Tag ^A	Protein-name ^A	Beschreibung	Molekulargewicht	wt	$\Delta sigB$	Lokalisation ^B	PSort-Score ^B	SP ^B	Intensität [wt] ^C	Intensität [$\Delta sigB$] ^C	<i>p</i> -Wert [wt: $\Delta sigB$] ^C	F. Ch. wt : $\Delta sigB$ ^C	Referenz ^D
88195999	SAOUHSC_02333		sceD protein, putative single-strand DNA-binding	24 kDa	x	x	ez	9.98	#NV	3.69E+08	3.36E+07	1.94E-05	-12.041	
88195755	SAOUHSC_02071		protein, putative	19 kDa	x	x	unb	2.50	N	1.29E+07	2.86E+06	4.05E-04	-3.824	
88195714	SAOUHSC_02027		SLT orf 129-like protein	14 kDa	x		unb	2.50	#NV	1.44E+06	1.08E+06	1.98E-01	-1.270	
88195966	SAOUHSC_02300	RsbV	STAS domain, putative	12 kDa	x		zyt	8.87	N	9.01E+06	2.06E+05	5.35E-15	-35.456	7

Drei Bioreplikate der Kulturüberstände der späten stationären Phase von *S. aureus* RN1HG und RN1HG $\Delta sigB$ wurden mittels gelfreier Analysen aufgearbeitet. Proteine mit mindestens 2 Peptiden galten als identifiziert und wurden nachfolgend in funktionelle Gruppen klassifiziert (TigR). Der Fold Change bezieht sich auf die späte stationäre Phase des Wildtyps.

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

^B Die Lokalisation und die Vorhersage eines Signalpeptides erfolgte über P-Sort. ez = extrazellulär, zw = Zellwand, zm = zytoplasmatische Membran, zyt = Zytoplasma, unb = unbekannt, SP = Signalpeptid, N = kein Signalpeptid, Y = Signalpeptid vorhanden, #NV = Vorhersage nicht möglich.

^C Die Intensitäten, der *p*-Wert und der Fold Change wurde anhand der Elucidator Software ermittelt.

^D Publikationen, die den Einfluss von SigB bestätigen: ¹ Kullik et al., 1998; ² Cheung et al., 1999; ³ Nicholas et al., 1999; ⁴ Gertz et al., 2000; ⁵ Ziebandt et al. 2001; ⁶ Horsburgh et al., 2002; ⁷ Bischoff et al., 2004; ⁸ Ziebandt et al. 2004; ⁹ Homerova et al., 2004; ¹⁰ Pané-Farré et al., 2006.

Tab. 64: Proteine, die für die in Abb. 25 dargestellten Proteinprofile ausgewählter Virulenzfaktoren denselben bzw. ähnlichen Trend aufzeigen.

Profil	Protein	Trend für ...
Abb. 25 A	α -Hämolysin (Hla)	1-Phosphatidylinositol-Phosphodiesterase (Plc), Glytamyldopeptidase (SspA), Leukotoxin LukD, Neurofilament-Protein (IsdB), Staphopain (StpH), Thermo-nuklease (Nuc), Serin-Proteasen SplA/B/C/F, unbekannte Proteine (SAOUHSC_00897/01081/01082/02241/02243)
Abb. 25 B	γ -Hämolysin (α -Untereinheit) (HlgA)	γ -Hämolysin (β -Untereinheit), γ -Hämolysin (γ -Untereinheit), MHC class II analoges Protein, unbekannte Proteine (SAOUHSC_00717/01085/02246)
Abb. 25 C	Aureolysin (Aur)	Dihydrolipoamide S-Acetyltransferase (PdhC), DNak Protein (DNak), Glutanyl-tRNA amidotransferase, Immunoglobulin G-Bindeprotein Sbi, Staphylokinase (Sak), unbekannte Proteine (SAOUHSC_00258/02169)
Abb. 25 D	Alkaline Shock Protein (Asp23)	Hypoxanthine-Phosphoribosyltransferase, Phospho-Carrierprotein Hpr, phi PVL orf 39-like Protein, Purin-Nukleosid-Phosphorylase, STAS Domain Protein, Translationsinitiationsfaktor IF-1, unbekannte Proteine (SAOUHSC_00311/00469/00533/00553/00831/01256/01383/01806/01860/01907/02013/02774)
Abb. 25 E	Clumping Faktor (Clf)	Elastin-Bindeprotein (EbpS), Fibrinogen-Bindeprotein (Efb), LysM Domain Protein, Peptidoglykanhydrolase (LytM), SAOUHSC_00356/00704/00845/01336/01535, SceD Protein
Abb. 25 F	Immunodominant Antigen A (IsaA)	Ferritin, Glukose-6-Phosphat-1-Dehydrogenase (Zwf), LysM Domain Protein, unbekannte Proteine (SAOUHSC_01239/01739/01895)

Tab. 65: Übersicht über die identifizierten 2D-Spots von *S. aureus* RN1HG und RN1HG $\Delta sigB$ während der Kultur in pMEM für den pH-Bereich 4-7.

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
1	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	28%	2	119	107.68
2	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.06	9.05	45%	35	515	250.32
3	88196625	SAOUHSC_03006	Lip	1	lipase	76629.23	7.05	66%	38	539	239.86
4	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.06	9.05	26%	22	561	354.05
5	88194795	SAOUHSC_01043	PdhD,LpdA	1	dihydrolipoamide dehydrogenase	49450.53	4.95	63%	33	707	413.69
6	88194559	SAOUHSC_00799	Eno	1	Enolase	47087.78	4.55	64%	28	535	299.60
7	88194559	SAOUHSC_00799	Eno	1	Enolase	47087.78	4.55	68%	32	613	326.42
8	88194555	SAOUHSC_00795	Gap1,Gap	1	glyceraldehyde-3-phosphate dehydrogenase, type I	36258.36	4.89	72%	22	459	268.95
9	88194967	SAOUHSC_01234	Tsf	1	translation elongation factor Ts	32473.66	5.05	78%	25	445	203.14
10	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.42	6.16	39%	10	461	386.73
11	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.42	6.16	24%	7	411	366.48
12	88196349	SAOUHSC_02709	HlgC	1	gamma-hemolysin component C	35591.93	9.29	61%	20	457	300.01
12	88194865	SAOUHSC_01121	Hla	2	alpha-hemolysin precursor	35950.97	8.7	52%	18	198	63.08
13	88195728	SAOUHSC_02043		1	phage head protein, putative	36747.75	5.13	82%	30	572	264.25
14	88195999	SAOUHSC_02333		1	sceD protein, putative	24051.50	5.52	36%	10	323	250.36
15	88194557	SAOUHSC_00797	TpiA,Tpi	1	triosephosphate isomerase	27274.76	4.8	95%	21	248	53.94
15	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	20%	3	127	116.39
16	88196043	SAOUHSC_02380	DeoD2	1	purine nucleoside phosphorylase	25891.82	4.85	63%	18	354	184.94
16	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	15%	2	97.10	90.06
17	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	187	171.53
18	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	197	180.86
19	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	191	175.21
20	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	203	187.30
21	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	355	339.23

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
22	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	20%	3	341	329.28
23	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	195	179.35
24	88194163	SAOUHSC_00365	AhpC	1	alkyl hydroperoxide reductase	20963.49	4.88	79%	15	500	361.31
25	88193908	SAOUHSC_00093	SodM	1	superoxide dismutase, putative	23026.35	5.32	84%	13	285	173.39
26	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	28%	2	124	113.08
27	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	111	106.66
28	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	13%	2	211	204.57
29	88196094	SAOUHSC_02441	Asp23	1	hypothetical protein SAOUHSC_02441	19179.68	5.13	88%	16	211	64.20
29	88196220	SAOUHSC_02576		2	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	93.30	88.98
30	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	28%	2	119	107.85
31	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	28%	2	121	110.01
32	88195657	SAOUHSC_01964	TRAP	1	hypothetical protein SAOUHSC_01964	19535.51	6.13	95%	18	561	376.49
33	88196044	SAOUHSC_02381	Dps	1	hypothetical protein SAOUHSC_02381	16681.04	4.57	76%	10	218	132.59
33	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	24%	4	75.40	60.04
34	88194302	SAOUHSC_00521	RplL	1	ribosomal protein L7/L12	12703.75	4.63	83%	9	171	92.40
34	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	20%	3	118	107.90
35	88194877	SAOUHSC_01135		1	hypothetical protein SAOUHSC_01135	4493.39	4.79	90%	2	160	141.19
36	88194878	SAOUHSC_01136		1	hypothetical protein SAOUHSC_01136	4453.37	5.36	40%	1	132	124.27
36	88194163	SAOUHSC_00365	AhpC	2	alkyl hydroperoxide reductase	20963.49	4.88	38%	4	47.10	25.74
37	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.43	6.13	26%	5	151	130.38
37	88196220	SAOUHSC_02576		2	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	117	112.99
38	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.43	6.13	20%	4	373	355.85
39	88195848	SAOUHSC_02171	Sak	1	staphylokinase precursor, putative	18492.72	6.75	68%	13	428	310.49
39	88194436	SAOUHSC_00671		2	secretory antigen SsaA-like protein	28169.43	6.13	20%	4	72	56.77

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
40	88195657	SAOUHSC_01964	TRAP	1	hypothetical protein SAOUHSC_01964	19535.51	6.13	95%	18	541	356.70
41	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	107	101.99
42	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	111	106.21
43	88194325	SAOUHSC_00545		1	sdrD protein, putative	145999.95	4.17	21%	19	86.90	36.50
43	88195999	SAOUHSC_02333		2	sceD protein, putative	24051.50	5.52	22%	5	49.60	26.16
44	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	98.40	93.89
46	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.06	9.59	46%	40	284	51.63
47	88195075	SAOUHSC_01347	CitB,AcnA	1	aconitate hydratase 1	98907.78	4.83	45%	35	303	78.33
48	88195075	SAOUHSC_01347	CitB,AcnA	1	aconitate hydratase 1	98907.78	4.83	55%	42	513	197.76
49	88194309	SAOUHSC_00529	FusA,Fus	1	translation elongation factor G	76563.96	4.8	57%	37	321	22.98
50	88195480	SAOUHSC_01779	Tig	1	trigger factor	48579.31	4.34	47%	20	225	88.11
51	88195389	SAOUHSC_01683	DnaK	1	DNAk protein, putative	66320.98	4.65	48%	25	255	94.38
52	88194782	SAOUHSC_01029	PtsI	1	phosphoEnolpyruvate-protein phosphotransferase	63179.34	4.66	39%	20	226	111.75
53	88194558	SAOUHSC_00798	Pgm,GpmI	1	phosphoglycerate mutase, 2,3-bisphospho- glycerate-independent	56389.09	4.74	43%	24	426	265.34
54	88195925	SAOUHSC_02254	GroL,GroEL	1	chaperonin, 60 kDa, GrpEL, putative	57628.57	4.55	51%	26	312	122.36
55	88194195	SAOUHSC_00400		1	hypothetical protein SAOUHSC_00400	56512.20	4.79	52%	20	164	35.72
56	88195066	SAOUHSC_01337	Tkt	1	transketolase	68317.11	4.97	32%	19	137	39.87
56	88194794	SAOUHSC_01042	PdhC	2	dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase complex E2, putative	46325.62	4.9	26%	12	100	42.09
57	88195066	SAOUHSC_01337	Tkt	1	transketolase	68317.11	4.97	35%	20	252	144.01
58	88195066	SAOUHSC_01337	Tkt	1	transketolase	68317.11	4.97	45%	25	309	147.59
59	88194694	SAOUHSC_00937	PepF,PepB	1	oligoendopeptidase F	69775.73	5.14	41%	32	296	63.40
60	88194694	SAOUHSC_00937	PepF,PepB	1	oligoendopeptidase F	69775.73	5.14	51%	38	409	98.80
61	88194694	SAOUHSC_00937	PepF,PepB	1	oligoendopeptidase F	69775.73	5.14	51%	37	406	110.07

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
62	88194694	SAOUHSC_00937	PepF,PepB	1	oligoendopeptidase F	69775.73	5.14	51%	36	383	102.11
63	88196031	SAOUHSC_02368	PyrG,CtrA	1	CTP synthase	59944.64	5	48%	24	256	97.09
64	88196599	SAOUHSC_02979		1	hypothetical protein SAOUHSC_02979	69211.67	5.96	59%	31	481	242.89
65	88196599	SAOUHSC_02979		1	hypothetical protein SAOUHSC_02979	69211.67	5.96	54%	29	446	233.16
66	88196599	SAOUHSC_02979		1	hypothetical protein SAOUHSC_02979	69211.67	5.96	57%	30	467	236.73
67	88196625	SAOUHSC_03006	Lip	1	lipase	76629.23	7.05	40%	35	399	155.39
68	88196625	SAOUHSC_03006	Lip	1	lipase	76629.23	7.05	58%	37	554	270.64
69	88196625	SAOUHSC_03006	Lip	1	lipase	76629.23	7.05	57%	34	525	277.06
70	88195210	SAOUHSC_01493	RpsA	1	30S ribosomal protein S1, putative	43261.11	4.51	58%	17	345	232.59
71	88195565	SAOUHSC_01868		1	hypothetical protein SAOUHSC_01868 alkyl hydroperoxide reductase, subunit F, putative	52790.73	4.58	53%	23	336	167.45
72	88194162	SAOUHSC_00364	AhpF	1	hypothetical protein SAOUHSC_00369	54686.87	4.68	53%	21	305	165.06
73	88194167	SAOUHSC_00369		1	hypothetical protein SAOUHSC_00369	35590.61	4.74	43%	15	230	109.68
74	88194626	SAOUHSC_00869	DltA	1	D-alanine-activating enzyme	54635.58	4.83	41%	19	265	145.63
75	88194795	SAOUHSC_01043	PdhD,LpdA	1	dihydrolipoamide dehydrogenase	49450.53	4.95	41%	18	155	51.38
76	88194795	SAOUHSC_01043	PdhD,LpdA	1	dihydrolipoamide dehydrogenase	49450.53	4.95	66%	33	680	386.75
77	88194795	SAOUHSC_01043	PdhD,LpdA	1	dihydrolipoamide dehydrogenase delta-1-pyrroline-5-carboxylate dehydrogenase, putative	49450.53	4.95	64%	28	515	291.80
78	88196500	SAOUHSC_02869	RocA	1	dehydrogenase, putative	56831.67	4.98	49%	22	320	178.15
79	88194381	SAOUHSC_00611	ArgS	1	arginyl-tRNA synthetase	62342.45	5.08	49%	19	162	54.01
79	88194173	SAOUHSC_00375	GuaA	3	GMP synthase, putative	58193.66	5.03	19%	10	49.90	16.50
80	88194381	SAOUHSC_00611	ArgS	1	arginyl-tRNA synthetase	62342.45	5.08	57%	28	365	155.69
81	88194381	SAOUHSC_00611	ArgS	1	arginyl-tRNA synthetase	62342.45	5.08	44%	16	135	52.17
82	88193965	SAOUHSC_00153	IpdC	1	indolepyruvate decarboxylase, putative	60500.72	5.14	31%	13	111	54.25
83	88195057	SAOUHSC_01327	KatA	1	catalase	54908.49	5.17	58%	29	427	193.65
84	88195057	SAOUHSC_01327	KatA	1	catalase	54908.49	5.17	66%	31	421	162.79
85	88195057	SAOUHSC_01327	KatA	1	catalase	54908.49	5.17	64%	31	416	158.32
86	88195544	SAOUHSC_01845	Geh	1	formate-tetrahydrofolate ligase, putative	59819.08	5.62	35%	17	144	55.11

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
87	88195544	SAOUHSC_01845	Geh	1	formate-tetrahydrofolate ligase, putative	59819.08	5.62	47%	23	297	148.92
88	88195544	SAOUHSC_01845	Geh	1	formate-tetrahydrofolate ligase, putative	59819.08	5.62	49%	26	415	229.41
89	88194055	SAOUHSC_00248	LytM	2	peptidoglycan hydrolase, putative phosphoEnolpyruvate carboxykinase (ATP)	34295.42	6.16	13%	2	70.10	62.11
90	88195605	SAOUHSC_01910	PckA	1		59340.09	5.74	60%	31	532	287.13
92	88194290	SAOUHSC_00509	GltX	1	glutamyl-tRNA synthetase	56253.39	5.21	60%	32	351	84.51
93	88195018	SAOUHSC_01287	GlnA	1	glutamine synthetase, type I	50808.40	5.08	52%	24	243	80.50
94	88195018	SAOUHSC_01287	GlnA	1	glutamine synthetase, type I	50808.40	5.08	63%	32	433	172.61
95	88194310	SAOUHSC_00530	Tuf	1	translation elongation factor Tu	43076.60	4.74	76%	28	464	217.75
96	88194657	SAOUHSC_00900	Pgi	1	glucose-6-phosphate isomerase 6-phosphogluconate dehydrogenase, decarboxylating	49791.00	4.83	60%	27	496	276.32
97	88195316	SAOUHSC_01605	Gnd	1		51770.07	5.02	41%	18	253	145.21
98	88194678	SAOUHSC_00921	FabF,Fab	1	3-oxoacyl- synthase, putative	43711.82	5.03	62%	19	266	130.06
99	88193840	SAOUHSC_00019	PurA	1	adenylosuccinate synthetase	47549.28	5.1	66%	28	413	184.27
100	88194312	SAOUHSC_00532	Kbl	1	hypothetical protein SAOUHSC_00532 serine hydroxymethyltransferase,	42863.78	5.2	58%	21	264	113.03
101	88196017	SAOUHSC_02354	GlyA	1	putative serine hydroxymethyltransferase,	45144.10	5.75	44%	19	179	58.70
102	88196017	SAOUHSC_02354	GlyA	1	putative serine hydroxymethyltransferase,	45144.10	5.75	56%	25	426	233.35
103	88196017	SAOUHSC_02354	GlyA	1	putative	45144.10	5.75	57%	26	438	230.49
104	88194493	SAOUHSC_00728		1	hypothetical protein SAOUHSC_00728	74353.00	9.04	52%	31	388	163.40
105	88194988	SAOUHSC_01255		1	hypothetical protein SAOUHSC_01255	48587.68	5.74	47%	23	216	54.21
105	88194753	SAOUHSC_00997		2	hypothetical protein SAOUHSC_00997	45657.15	6.02	40%	14	205	125.16
106	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.06	9.05	24%	26	367	202.53
107	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.06	9.05	26%	25	278	130.68
108	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.06	9.05	29%	24	215	80.54
109	88196350	SAOUHSC_02710	HlgB	1	gamma-hemolysin component B	36688.34	9.35	55%	16	345	236.54
110	88196350	SAOUHSC_02710	HlgB	1	gamma-hemolysin component B	36688.34	9.35	61%	20	444	290.46

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
111	88196348	SAOUHSC_02708		1	gamma-hemolysin h-gamma-ii subunit, putative	34934.13	9.59	54%	18	187	51.69
112	88194792	SAOUHSC_01040	PdhA	1	pyruvate dehydrogenase complex, E1 component, alpha subunit, putative	41356.84	4.9	42%	17	169	48.77
113	88195516	SAOUHSC_01816		1	hypothetical protein SAOUHSC_01816 NADP-dependent malic enzyme, putative	39529.07	4.99	41%	16	334	230.42
114	88195510	SAOUHSC_01810		1	putative	44205.82	5.07	44%	18	342	219.56
115	88194556	SAOUHSC_00796	Pgk	1	phosphoglycerate kinase, putative	42575.44	5.17	57%	20	385	243.77
116	88194744	SAOUHSC_00987	SspB	1	cysteine protease precursor, putative	44491.26	5.68	53%	20	307	161.04
116	88196599	SAOUHSC_02979		2	hypothetical protein SAOUHSC_02979	69211.67	5.96	19%	7	54.90	35.13
117	88194744	SAOUHSC_00987	SspB	1	cysteine protease precursor, putative glyceraldehyde-3-phosphate dehydrogenase, type I	44491.26	5.68	56%	25	394	189.49
118	88194555	SAOUHSC_00795	Gap1,Gap	1	dehydrogenase, type I	36258.36	4.89	72%	22	373	185.77
119	88196491	SAOUHSC_02860	MvaS	1	HMG-CoA synthase, putative	43178.47	4.93	48%	22	249	88.59
120	88194967	SAOUHSC_01234	Tsf	1	translation elongation factor Ts	32473.66	5.05	80%	24	332	110.45
121	88194967	SAOUHSC_01234	Tsf	1	translation elongation factor Ts D-isomer spezific 2-hydroxyacid dehydrogenase, NAD binding domain protein	32473.66	5.05	74%	23	234	27.14
122	88196221	SAOUHSC_02577		1	protein	34653.02	5.14	80%	28	378	106.97
123	88195092	SAOUHSC_01365		2	hypothetical protein SAOUHSC_01365 secretory antigen precursor SsaA, putative	37832.05	5.26	60%	15	121	21.73
123	88196220	SAOUHSC_02576		3	putative	17388.15	5.77	9%	1	108	103.32
124	88194761	SAOUHSC_01007	FolD	1	FolD bifunctional protein, putative succinyl-CoA synthetase, alpha subunit, putative	30824.45	5.38	59%	19	432	275.63
125	88194954	SAOUHSC_01218	SucD	1	formate dehydrogenase, NAD- dependent, putative	31522.23	5.47	55%	19	353	195.94
126	88193954	SAOUHSC_00142	Fdh	1	formate dehydrogenase, NAD- dependent, putative	38094.45	5.62	50%	19	302	159.82
126	88194055	SAOUHSC_00248	LytM	2	peptidoglycan hydrolase, putative	34295.42	6.16	20%	4	102	88.51
127	88193954	SAOUHSC_00142	Fdh	1	formate dehydrogenase, NAD- dependent, putative	38094.45	5.62	50%	20	396	237.65
128	88193954	SAOUHSC_00142	Fdh	1	formate dehydrogenase, NAD- dependent, putative	38094.45	5.62	50%	20	338	183.58
128	88194055	SAOUHSC_00248	LytM	2	peptidoglycan hydrolase, putative	34295.42	6.16	20%	4	180	166.70

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
129	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.42	6.16	24%	7	336	302.15
130	88196592	SAOUHSC_02971	Aur	1	aureolysin, putative	54952.19	4.98	44%	19	484	358.36
132	88195390	SAOUHSC_01684	GrpE	1	co-chaperone GrpE pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	23993.88	4.42	45%	11	323	246.46
133	88194793	SAOUHSC_01041	PhdB,PdhB	1	beta subunit, putative	35224.15	4.65	67%	21	421	240.85
134	88194349	SAOUHSC_00574	Pta	1	phosphate acetyltransferase	34930.13	4.72	60%	16	466	342.79
134	88195820	SAOUHSC_02140	PpaC	2	hypothetical protein SAOUHSC_02140 glutamyl endopeptidase precursor, putative	34047.33	4.69	35%	9	73.10	24.60
135	88194745	SAOUHSC_00988	SspA	1	glutamyl endopeptidase precursor, putative	36303.60	4.99	39%	15	303	197.25
136	88194745	SAOUHSC_00988	SspA	1	putative fructose-bisphosphate aldolase class-I, putative	36303.60	4.99	25%	8	160	124.83
138	88196553	SAOUHSC_02926		1	fructose-bisphosphate aldolase class-I, putative	33034.08	4.92	88%	29	527	239.67
139	88196553	SAOUHSC_02926		1	putative	33034.08	4.92	80%	24	414	195.10
140	88194546	SAOUHSC_00785	TrxB	1	thioredoxin reductase	33595.00	5.21	85%	24	397	176.83
142	88195823	SAOUHSC_02143		1	hypothetical protein SAOUHSC_02143 secretory antigen precursor SsaA, putative	38522.92	5.04	93%	30	417	131.07
142	88196220	SAOUHSC_02576		2	putative	17388.15	5.77	9%	1	96.80	92.54
143	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.42	6.16	26%	9	317	268.90
144	88194273	SAOUHSC_00488	CysK	1	hypothetical protein SAOUHSC_00488	32955.13	5.39	74%	21	458	272.50
145	88196601	SAOUHSC_02982		1	hypothetical protein SAOUHSC_02982	70889.02	7.7	26%	15	157	92.71
146	88194965	SAOUHSC_01232	RpsB	1	ribosomal protein S2	27715.46	5.23	62%	17	210	88.66
147	88195999	SAOUHSC_02333		1	sceD protein, putative	24051.50	5.52	30%	6	146	115.18
148	88195728	SAOUHSC_02043		1	phage head protein, putative	36747.75	5.13	66%	23	371	176.40
149	88196029	SAOUHSC_02366	FbaA,Fba	1	hypothetical protein SAOUHSC_02366 secretory antigen precursor SsaA, putative	30816.68	5.01	61%	16	196	66.06
149	88196220	SAOUHSC_02576		2	putative	17388.15	5.77	9%	1	71.40	67.20
150	88195728	SAOUHSC_02043		1	phage head protein, putative	36747.75	5.13	54%	16	292	176.80
151	88196029	SAOUHSC_02366	FbaA,Fba	1	hypothetical protein SAOUHSC_02366	30816.68	5.01	79%	19	259	92.87

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
154	88194663	SAOUHSC_00906		1	hypothetical protein SAOUHSC_00906	33092.86	4.84	51%	11	97.80	29.30
156	88195999	SAOUHSC_02333		1	sceD protein, putative	24051.50	5.52	36%	7	265	226.01
157	88195784	SAOUHSC_02102	Map	1	methionine aminopeptidase, type I	27485.06	5.18	64%	16	343	196.57
158	88196343	SAOUHSC_02703	GpmA	1	phosphoglycerate mutase, putative	26663.49	5.23	63%	19	276	110.02
159	88195729	SAOUHSC_02044		1	hypothetical protein SAOUHSC_02044	23382.76	5.22	58%	13	266	168.32
160	88196343	SAOUHSC_02703	GpmA	1	phosphoglycerate mutase, putative	26663.49	5.23	71%	19	398	228.77
161	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.43	6.13	29%	6	226	197.87
162	88194963	SAOUHSC_01228	CodY	1	hypothetical protein SAOUHSC_01228	28737.36	5.87	94%	31	527	199.15
163	88194194	SAOUHSC_00399		1	hypothetical protein SAOUHSC_00399	25350.10	8.52	71%	15	240	116.95
164	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	118	101.68
165	88194790	SAOUHSC_01038	Def	1	polypeptide deformylase	20546.61	5.68	67%	12	112	19.09
165	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	24%	4	68.5	52.79
166	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	24%	4	64.5	48.55
167	88194557	SAOUHSC_00797	TpiA,Tpi	1	triosephosphate isomerase	27274.76	4.8	67%	19	177	19.26
169	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	13%	2	56.70	49.68
170	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	19%	3	71.30	60.48
172	88194332	SAOUHSC_00553		1	hypothetical protein SAOUHSC_00553 peptidyl-prolyl cis-trans isomerase, cyclophilin- type, putative	22421.67	4.57	90%	16	357	205.82
173	88194648	SAOUHSC_00891		1		21605.47	4.57	55%	14	357	231.73
174	88194163	SAOUHSC_00365	AhpC	1	alkyl hydroperoxide reductase	20963.49	4.88	65%	13	435	326.40
175	88194163	SAOUHSC_00365	AhpC	1	alkyl hydroperoxide reductase	20963.49	4.88	73%	13	300	189.25
176	88194969	SAOUHSC_01236	Rrf,Frr	1	ribosome recycling factor	20340.58	5.04	72%	13	305	191.25
177	88195757	SAOUHSC_02073		1	hypothetical protein SAOUHSC_02073	20634.63	5.04	49%	11	124	44.86
177	88196220	SAOUHSC_02576		2	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	113	108.52
178	88194163	SAOUHSC_00365	AhpC	1	alkyl hydroperoxide reductase	20963.49	4.88	67%	11	179	91.29
178	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.45	6.11	19%	3	54.5	44.04
179	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	19%	3	48.80	38.10

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
180	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	89.20	84.62
181	88193908	SAOUHSC_00093	SodM	1	superoxide dismutase, putative	23026.35	5.32	55%	9	119	54.90
182	88195830	SAOUHSC_02150		1	hypothetical protein SAOUHSC_02150 transcription antitermination protein, putative	21902.02	5.16	76%	19	379	197.31
182	88194298	SAOUHSC_00517	NusG	2		20650.67	5.1	62%	11	119	38.57
183	88195678	SAOUHSC_01987		1	hypothetical protein SAOUHSC_01987	22329.59	5.33	94%	20	321	122.99
185	88195515	SAOUHSC_01815		1	hypothetical protein SAOUHSC_01815	25234.47	5.11	57%	11	160	79.59
186	88195741	SAOUHSC_02057		1	dUTP pyrophosphatase	19427.04	5.27	63%	11	241	127.36
188	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.45	6.11	13%	2	173	165.74
190	88195519	SAOUHSC_01819		1	hypothetical protein SAOUHSC_01819 phosphotransferase system enzyme IIA, putative	18463.50	5.6	87%	15	292	147.21
191	88195154	SAOUHSC_01430	Crr	1		17949.29	4.52	46%	7	182	117.15
192	88195419	SAOUHSC_01714	GreA	1	transcription elongation factor GreA secretory antigen precursor SsaA, putative	17731.90	4.53	74%	10	279	195.31
192	88196220	SAOUHSC_02576		2		17388.15	5.77	9%	1	92.5	88.28
193	88195522	SAOUHSC_01822	Tpx	1	hypothetical protein SAOUHSC_01822 secretory antigen precursor SsaA, putative	17994.10	4.56	64%	10	249	165.94
193	88196220	SAOUHSC_02576		2		17388.15	5.77	9%	1	73.10	68.70
194	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	115	110.37
198	88194169	SAOUHSC_00371		1	hypothetical protein SAOUHSC_00371	15112.58	4.86	94%	12	224	97.28
199	88195155	SAOUHSC_01431	MsrB	1	methionine sulfoxide reductase, putative	16266.87	4.76	48%	6	130	63.75
200	88194880	SAOUHSC_01138		1	hypothetical protein SAOUHSC_01138	16991.49	4.85	40%	7	143	87.46
201	88194310	SAOUHSC_00530	Tuf	1	translation elongation factor Tu secretory antigen precursor SsaA, putative	43076.60	4.74	21%	10	94.60	48.20
203	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	112	107.26
204	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.15	5.77	9%	1	111	106.14
205	88196002	SAOUHSC_02336	FabZ	1	beta-hydroxyacyl-ACP dehydratase, putative	16071.39	5.71	60%	10	115	18.69
206	88195582	SAOUHSC_01886	RibH	1	riboflavin synthase, beta subunit	16385.61	5.7	51%	8	140	63.30

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
207	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.43	6.13	14%	2	71.90	64.23
208	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.97	8.7	31%	9	164	111.60
209	88196593	SAOUHSC_02972	IsaB	1	hypothetical protein SAOUHSC_02972	19358.23	9.67	49%	11	96.90	18.21
210	88195846	SAOUHSC_02169	Chs,Chp	1	hypothetical protein SAOUHSC_02169	17028.92	9.57	46%	8	99.30	40.38
211	88194387	SAOUHSC_00617		1	hypothetical protein SAOUHSC_00617	18582.46	9.17	60%	12	184	82.30
212	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.43	6.13	25%	4	92.5	75.64

Die Proteinspots wurden manuell aus dem Gel gecuttet und nach dem Verdau an der Ettan Spot Handling Workstation am Maldi-TOF/TOF Analyzers 4800 ABI vermessen. Proteine mit einem Proteinscore >47 (p -Value <0.05) und einem Peptidscore >18 wurden als signifikant angesehen. Das Label entspricht der Position der Spotnummer auf dem 2D-Gel.

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

Tab. 66: Übersicht über die identifizierten 2D-Spots von *S. aureus* RN1HG und RN1HG $\Delta sigB$ während der Kultur in pMEM für den pH-Bereich 6-11.

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
1	88194829	SAOUHSC_01081	IsdA	1	hypothetical protein SAOUHSC_01081	38721.9414	9.64	35%	12	359	289.38
2	88195630	SAOUHSC_01935	SplF	1	serine protease SplF, putative	25639.2305	9.16	63%	15	549	420.78
3	88196150	SAOUHSC_02500	RplE	1	50S ribosomal protein L5, putative	20253.7305	9.32	91%	21	308	117.89
4	88194577	SAOUHSC_00818	Nuc	1	thermonuclease precursor	25104	9.27	58%	16	318	197.57
5	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.4492	6.11	20%	3	213	201.19
6	88196593	SAOUHSC_02972	IsaB	1	hypothetical protein SAOUHSC_02972	19358.2305	9.67	54%	15	376	245.27
7	88194387	SAOUHSC_00617		1	hypothetical protein SAOUHSC_00617	18582.4609	9.17	75%	15	485	352.25
7	88196515	SAOUHSC_02887	IsaA	2	immunodominant antigen A, putative	24188.4492	6.11	20%	3	53	42.68
8	88196215	SAOUHSC_02571	SsaA	1	secretory antigen precursor, putative	29309.2207	8.96	42%	9	515	458.98
9	88195848	SAOUHSC_02171	Sak	1	staphylokinase precursor, putative	18492.7207	6.75	59%	12	368	263.83
10	88195657	SAOUHSC_01964	TRAP	1	hypothetical protein SAOUHSC_01964	19535.5098	6.13	95%	18	515	330.94
11	88195657	SAOUHSC_01964	TRAP	1	hypothetical protein SAOUHSC_01964	19535.5098	6.13	95%	18	513	328.61
12	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.4297	6.13	20%	4	330	312.37
13	88194830	SAOUHSC_01082	IsdC	1	hypothetical protein SAOUHSC_01082	24839.6602	8.93	39%	11	348	270.90
14	88195846	SAOUHSC_02169	Chs,Chp	1	hypothetical protein SAOUHSC_02169	17028.9199	9.57	46%	8	222	162.67
15	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	53%	41	672	323.70
17	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	60%	40	597	257.89
18	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	60%	43	672	258.08
19	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	46%	35	517	247.20
20	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	52%	37	653	358.53
21	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	53%	33	513	264.93
22	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	42%	24	394	197.63
23	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	29%	16	386	241.53
24	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	50%	30	512	269.01
25	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	62%	42	628	251.12
26	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	66%	40	599	266.32
27	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	64%	42	604	254.09
28	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	56%	35	587	296.00
29	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	45%	33	567	262.00
30	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	31%	24	533	298.46
31	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	48%	35	546	281.57

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
32	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	38%	33	464	220.70
33	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	48%	37	472	183.67
34	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative glyceraldehyde-3-phosphate	137300.063	9.59	31%	34	526	341.72
35	88194555	SAOUHSC_00795	Gap1,Gap	1	dehydrogenase, type I	36258.3594	4.89	65%	18	228	93.39
36	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.4219	6.16	23%	6	452	403.98
37	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	50%	38	594	288.20
38	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	32%	36	471	282.84
39	88194493	SAOUHSC_00728		1	hypothetical protein SAOUHSC_00728	74353	9.04	53%	35	519	241.84
40	88194493	SAOUHSC_00728		1	hypothetical protein SAOUHSC_00728	74353	9.04	55%	34	553	287.59
41	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	44%	36	691	404.34
42	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	36%	33	426	183.86
43	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	27%	23	301	149.23
44	88194493	SAOUHSC_00728		1	hypothetical protein SAOUHSC_00728	74353	9.04	55%	34	568	302.25
45	88194493	SAOUHSC_00728		1	hypothetical protein SAOUHSC_00728	74353	9.04	47%	31	460	235.91
46	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	51%	40	557	223.06
47	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	34%	32	451	224.83
48	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	40%	31	407	191.52
49	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	25%	30	332	200.08
50	88196350	SAOUHSC_02710	HlgB	1	gamma-hemolysin component B	36688.3398	9.35	53%	21	565	393.90
51	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	21%	18	214	155.95
52	88194219	SAOUHSC_00427		1	autolysin precursor, putative	35813.7383	9.67	43%	12	407	333.34
53	88195663	SAOUHSC_01972	PrsA	1	protein export protein PrsA, putative	35615.7383	9.01	29%	11	230	184.31
53	88196349	SAOUHSC_02709	HlgC	2	gamma-hemolysin component C	35591.9297	9.29	53%	15	122	21.40
54	88196349	SAOUHSC_02709	HlgC	1	gamma-hemolysin component C	35591.9297	9.29	79%	27	684	434.01
55	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	70%	25	657	422.68
56	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	71%	25	541	310.20
57	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	70%	23	486	287.13
58	88194654	SAOUHSC_00897	GlpQ	1	hypothetical protein SAOUHSC_00897 gamma-hemolysin h-gamma-ii subunit, putative	35288.8711	8.67	72%	27	484	229.32
59	88196348	SAOUHSC_02708		1	putative	34934.1289	9.59	70%	22	441	254.26
60	88194829	SAOUHSC_01081	IsdA	1	hypothetical protein SAOUHSC_01081	38721.9414	9.64	49%	16	402	292.61
61	88194300	SAOUHSC_00519	RplA	1	ribosomal protein L1	24692.8906	9	47%	12	133	42.99

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
62	88195635	SAOUHSC_01941	SplB	1	serine protease SplB	26080.5195	9.21	48%	14	483	379.09
63	88194829	SAOUHSC_01081	IsdA	1	hypothetical protein SAOUHSC_01081	38721.9414	9.64	40%	15	295	197.31
63	88194219	SAOUHSC_00427		2	autolysin precursor, putative	35813.7383	9.67	36%	8	59.20	21.67
64	88194180	SAOUHSC_00383		1	hypothetical protein SAOUHSC_00383	25631.3105	8.46	69%	18	259	101.95
65	88193909	SAOUHSC_00094		1	hypothetical protein SAOUHSC_00094	21833.5996	9	80%	11	245	153.29
66	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.4492	6.11	24%	4	293	276.98
67	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	37%	36	587	311.27
68	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	40%	40	282	56.10
69	88196350	SAOUHSC_02710	HlgB	1	gamma-hemolysin component B	36688.3398	9.35	55%	16	309	200.54
70	88196350	SAOUHSC_02710	HlgB	1	gamma-hemolysin component B	36688.3398	9.35	61%	19	429	287.67
71	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	30%	30	378	176.72
72	88195460	SAOUHSC_01759	Mrec	1	rod shape-determining protein Mrec	30991.2402	9.04	66%	21	343	164.20
73	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	27%	8	125	84.13
74	88195636	SAOUHSC_01942	SplA	1	serine protease SplA	25533.0703	8.98	48%	11	145	60.34
75	88196156	SAOUHSC_02506	RpsC	1	ribosomal protein S3	24085.0508	9.76	70%	18	235	85.97
76	88195630	SAOUHSC_01935	SplF	1	serine protease SplF, putative	25639.2305	9.16	54%	10	234	165.18
77	88195631	SAOUHSC_01936	SplE	1	serine protease SplE	25663.4102	9.32	41%	11	166	94.58
78	88194187	SAOUHSC_00392		1	hypothetical protein SAOUHSC_00392	26151.7402	8.92	71%	21	270	79.35
79	88196592	SAOUHSC_02971	Aur	1	aureolysin, putative	54952.1914	4.98	14%	6	71.20	42.16
80	88196147	SAOUHSC_02496	RplF	1	ribosomal protein L6, putative	19774.4102	9.54	84%	19	278	84.87
81	88194163	SAOUHSC_00365	AhpC	1	alkyl hydroperoxide reductase	20963.4902	4.88	43%	6	86.60	48.74
82	88195808	SAOUHSC_02127		1	staphopain thiol proteinase	44234.5898	9.61	33%	19	279	148.66
83	88195808	SAOUHSC_02127		1	staphopain thiol proteinase	44234.5898	9.61	32%	17	223	110.33
84	88196468	SAOUHSC_02834	SrtA	1	sortase, putative	23526.2305	8.85	35%	9	156	94.72
85	88195808	SAOUHSC_02127		1	staphopain thiol proteinase	44234.5898	9.61	33%	12	275	205.25
86	88194153	SAOUHSC_00354		1	hypothetical protein SAOUHSC_00354	23151.2598	9.52	48%	11	174	86.81
87	88195014	SAOUHSC_01282	BsaA	1	hypothetical protein SAOUHSC_01282	18106.1309	6.31	46%	8	138	65.33
89	88195808	SAOUHSC_02127		1	staphopain thiol proteinase	44234.5898	9.61	29%	9	265	224.79
91	88196130	SAOUHSC_02478	RplM	1	ribosomal protein L13	16323.3701	9.3	90%	17	275	98.27
93	88193838	SAOUHSC_00017	RplI	1	ribosomal protein L9	16629.0195	9.46	67%	10	203	122.97
94	88196157	SAOUHSC_02507	RplV	1	ribosomal protein L22	12827	9.92	78%	11	172	82.63
95	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	27%	31	378	244.38

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
96	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	20%	24	320	238.69
97	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	22%	20	337	269.62
98	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	22%	25	296	205.14
99	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	26%	30	346	218.29
100	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.4492	6.11	15%	2	48.5	39.56
102	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	41%	13	207	127.67
104	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	24%	8	150	114.93
105	88194436	SAOUHSC_00671		1	secretory antigen SsaA-like protein	28169.4297	6.13	26%	5	67	45.60
106	88195848	SAOUHSC_02171	Sak	1	staphylokinase precursor, putative	18492.7207	6.75	55%	10	138	57.54
107	88193909	SAOUHSC_00094		1	hypothetical protein SAOUHSC_00094	21833.5996	9	75%	9	200	109.00
109	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.4492	6.11	15%	2	50.30	41.27
111	88196220	SAOUHSC_02576		1	secretory antigen precursor SsaA, putative	17388.1504	5.77	9%	1	106	101.42
114	88194830	SAOUHSC_01082	IsdC	1	hypothetical protein SAOUHSC_01082	24839.6602	8.93	35%	9	369	299.69
115	88196515	SAOUHSC_02887	IsaA	1	immunodominant antigen A, putative	24188.4492	6.11	24%	4	78.5	62.65
116	88194963	SAOUHSC_01228	CodY	1	hypothetical protein SAOUHSC_01228	28737.3594	5.87	89%	28	426	140.87
117	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	11%	11	116	79.80
118	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	52%	17	383	260.79
119	88193871	SAOUHSC_00051	plc	1	1-phosphatidylinositol phosphodiesterase precursor, putative	37063.3711	8.24	49%	18	225	97.51
120	88194865	SAOUHSC_01121	Hla	1	alpha-hemolysin precursor	35950.9688	8.7	68%	23	464	267.80
121	88194402	SAOUHSC_00634	MntC	1	ABC transporter, substrate-binding protein, putative	35049.1289	8.67	42%	13	182	90.84
122	88194654	SAOUHSC_00897	GlpQ	1	hypothetical protein SAOUHSC_00897	35288.8711	8.67	66%	25	408	185.65
123	88196215	SAOUHSC_02571	SsaA	1	secretory antigen precursor, putative	29309.2207	8.96	62%	12	540	448.98
124	88196215	SAOUHSC_02571	SsaA	1	secretory antigen precursor, putative	29309.2207	8.96	62%	10	198	131.04
124	88194602	SAOUHSC_00844		2	hypothetical protein SAOUHSC_00844	30332.1602	8.96	42%	12	102	26.30
126	88194832	SAOUHSC_01085	IsdE	1	hypothetical protein SAOUHSC_01085	32036.7891	9.26	70%	17	158	35.83
126	88194829	SAOUHSC_01081	IsdA	2	hypothetical protein SAOUHSC_01081	38721.9414	9.64	28%	9	64.20	21.67
127	88194829	SAOUHSC_01081	IsdA	1	hypothetical protein SAOUHSC_01081	38721.9414	9.64	31%	12	132	64.27
128	88196100	SAOUHSC_02448		1	hypothetical protein SAOUHSC_02448	33165.3281	9.57	34%	12	182	110.11
128	88194219	SAOUHSC_00427		2	autolysin precursor, putative	35813.7383	9.67	29%	8	75.5	39.58
129	88196162	SAOUHSC_02512	RplC	1	ribosomal protein L3, putative	23703.4902	9.8	50%	11	122	40.54
130	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	24%	24	220	133.17

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
131	88195062	SAOUHSC_01332		1	hypothetical protein SAOUHSC_01332	33569.6719	9.3	77%	27	453	202.25
133	88195663	SAOUHSC_01972	PrsA	1	protein export protein PrsA, putative	35615.7383	9.01	30%	9	75.5	40.99
134	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	20%	22	342	261.74
135	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	22%	17	124	49.68
136	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	24%	25	323	220.06
137	88195914	SAOUHSC_02241		1	hypothetical protein SAOUHSC_02241	38662.1602	8.72	45%	18	290	164.83
138	88195647	SAOUHSC_01954	LukD	1	leukotoxin, LukD	36866.3398	9.21	54%	16	304	196.88
139	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	22%	25	306	209.70
140	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	26%	30	360	224.76
141	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	25%	27	308	197.15
142	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	23%	23	165	86.61
142	88194829	SAOUHSC_01081	IsdA	2	hypothetical protein SAOUHSC_01081	38721.9414	9.64	34%	13	122	46.92
143	88194690	SAOUHSC_00933	TrpS	1	tryptophanyl-tRNA synthetase	36886.0781	7.66	33%	14	130	32.20
144	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	32%	28	347	175.84
145	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	31%	28	315	149.25
146	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	20%	20	210	118.01
147	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	22%	20	192	73.93
148	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	27%	24	253	116.37
149	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	14%	14	93.60	30.82
149	88194402	SAOUHSC_00634	MntC	2	ABC transporter, substrate-binding protein, putative	35049.1289	8.67	26%	7	54.90	27.59
150	88196226	SAOUHSC_02583		1	transcriptional regulator, putative	33783.4883	7.86	56%	17	169	45.61
151	88196599	SAOUHSC_02979		1	hypothetical protein SAOUHSC_02979	69211.6719	5.96	22%	12	143	100.05
151	88194101	SAOUHSC_00300	Geh	2	lipase precursor	76341.0625	9.05	11%	10	73.80	45.03
152	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	10%	8	75.30	57.07
153	88194402	SAOUHSC_00634	MntC	1	ABC transporter, substrate-binding protein, putative	35049.1289	8.67	28%	6	97.5	71.52
156	88195057	SAOUHSC_01327	katA	1	catalase	54908.4883	5.17	50%	19	133	15.71
157	88194795	SAOUHSC_01043	PdhD,LpdA	1	dihydrolipoamide dehydrogenase	49450.5313	4.95	45%	18	166	54.47
158	88194657	SAOUHSC_00900	Pgi	1	glucose-6-phosphate isomerase	49791	4.83	45%	15	97.5	15.10
159	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.4219	6.16	16%	3	222	206.20
160	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.4219	6.16	21%	4	196	181.43
161	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.4219	6.16	26%	9	299	251.12

Label	Accession-Nummer	Locus-Tag ^A	Protein-name ^A	Rang	Beschreibung	Molekulargewicht	pH	Sequenz-Abdeckung	Peptid-Anzahl	Protein-Score	Total-Ion-Score
162	88194055	SAOUHSC_00248	LytM	1	peptidoglycan hydrolase, putative	34295.4219	6.16	26%	8	266	227.25
164	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	51%	39	424	118.52
165	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	43%	45	346	64.78
166	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	43%	32	356	133.96
167	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	35%	35	357	170.84
168	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	28%	29	340	211.01
169	88194750	SAOUHSC_00994	Atl	1	bifunctional autolysin precursor, putative	137300.063	9.59	25%	27	300	193.32
170	88194829	SAOUHSC_01081	IsdA	1	hypothetical protein SAOUHSC_01081	38721.9414	9.64	43%	17	201	87.86
170	88196349	SAOUHSC_02709	HlgC	2	gamma-hemolysin component C	35591.9297	9.29	35%	10	64.5	15.07
171	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	40%	25	243	97.16
172	88196330	SAOUHSC_02690		1	hypothetical protein SAOUHSC_02690	59149.8398	6.55	21%	10	69.30	24.41
173	88196330	SAOUHSC_02690		1	hypothetical protein SAOUHSC_02690	59149.8398	6.55	22%	9	76.10	40.14
174	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	42%	30	269	74.61
175	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	32%	25	276	91.48
176	88196625	SAOUHSC_03006	Lip	1	lipase	76629.2266	7.05	40%	25	181	38.87
177	88194828	SAOUHSC_01079	IsdB	1	neurofilament protein	72147.8984	9.02	26%	16	201	138.91
178	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	50%	35	397	135.11
179	88196346	SAOUHSC_02706	Sbi	1	immunoglobulin G-binding protein Sbi, putative	50039.9219	9.38	49%	26	229	33.30
179	88194101	SAOUHSC_00300	Geh	2	lipase precursor	76341.0625	9.05	21%	15	82.80	25.57
179	88194750	SAOUHSC_00994	Atl	4	bifunctional autolysin precursor, putative	137300.063	9.59	15%	12	48.90	26.53
180	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	42%	33	394	157.07
181	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	43%	35	416	155.66
182	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	37%	30	418	208.63
183	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	33%	28	233	56.27
184	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	34%	27	340	169.87
185	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	25%	27	388	210.98
185	88196625	SAOUHSC_03006	Lip	2	lipase	76629.2266	7.05	11%	8	47.10	30.26
186	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	33%	32	443	218.64
187	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	43%	31	334	121.21
188	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	29%	23	231	106.30
190	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	34%	29	336	151.10

Label	Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Rang	Beschreibung	Molekular- gewicht	pH	Sequenz- Abdeckung	Peptid- Anzahl	Protein- Score	Total- Ion- Score
191	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	51%	37	399	119.24
192	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	47%	36	376	109.40
192	88196625	SAOUHSC_03006	Lip	2	lipase	76629.2266	7.05	12%	10	58.20	32.17
193	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	37%	31	358	147.37
194	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	33%	28	375	195.22
195	88194101	SAOUHSC_00300	Geh	1	lipase precursor	76341.0625	9.05	42%	32	364	136.07

Die Proteinspots wurden manuell aus dem Gel gecuttet, an der Ettan Spot Handling Workstation verdaut und am Maldi-TOF/TOF Analyzers 4800 ABI vermessen. Signifikante Proteine wiesen einen Proteinscore >47 (p -Value <0.05) und einem Peptidscore >18 auf. Das Label entspricht der Position der Spotnummer auf dem 2D-Gel.

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

Tab. 67: Vergleich der identifizierten Proteine zwischen der gelfreien und der gelbasierten Methode.

Accession- Nummer	Locus-Tag ^A	Protein -name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
Toxins und Hämolsine										
88194865	SAOUHSC_01121	Hla	alpha-hemolysin precursor	36 kDa	ez	10.00	Y	x	x	x
88196348	SAOUHSC_02708	HlgA	gamma-hemolysin component A	35 kDa	ez	9.73	#NV	x	x	x
88196350	SAOUHSC_02710	HlgB	gamma-hemolysin component B	37 kDa	ez	9.73	Y	x	x	x
88196349	SAOUHSC_02709	HlgC	gamma-hemolysin component C	36 kDa	ez	9.73	Y	x	x	x
88193943	SAOUHSC_00130	IsdI	hypothetical protein SAOUHSC_00130	13 kDa	unb	2.50	N	x		
88195915	SAOUHSC_02243		hypothetical protein SAOUHSC_02243	40 kDa	ez	9.73	Y	x		
88195647	SAOUHSC_01954	LukD	leukotoxin, LukD	37 kDa	ez	9.98	#NV	x		x
Virulenz-/Abwehrmechanismen										
88193871	SAOUHSC_00051	Plc	1-phosphatidylinositol phosphodiesterase precursor, putative	37 kDa	ez	9.97	Y	x		x
88196592	SAOUHSC_02971	Aur	aureolysin, putative	55 kDa	ez	9.97	Y	x	x	x
88194572	SAOUHSC_00812	ClfA	clumping factor	96 kDa	zw	10.00	Y	x		
88196585	SAOUHSC_02963	ClfB	clumping factor B, putative	94 kDa	zw	10.00	Y	x		
88194744	SAOUHSC_00987	SspB	cysteine protease precursor, putative	45 kDa	ez	9.55	Y	x	x	
88195217	SAOUHSC_01501	EbpS	elastin binding protein extracellular matrix and plasma binding protein, putative	53 kDa	zw	9.06	#NV	x		
88194575	SAOUHSC_00816	Ssp,Empbp	protein, putative	38 kDa	unb	3.33	Y	x		
88194860	SAOUHSC_01114	Efb	fibrinogen-binding protein	19 kDa	ez	9.98	Y	x		
88194745	SAOUHSC_00988	SspA	glutamyl endopeptidase precursor, putative	36 kDa	ez	10.00	Y	x	x	
88196115	SAOUHSC_02463	HysA	hyaluronate lyase	92 kDa	ez	10.00	#NV	x		
88194063	SAOUHSC_00257		hypothetical protein SAOUHSC_00257	11 kDa	unb	2.50	N	x		
88196346	SAOUHSC_02706	Sbi	immunoglobulin G-binding protein Sbi, putative	50 kDa	unb	3.33	#NV	x		x
88193965	SAOUHSC_00153	IpdC	indolepyruvate decarboxylase, putative	61 kDa	unb	2.50	N	x	x	
88196625	SAOUHSC_03006	Lip	lipase	77 kDa	ez	9.73	Y	x	x	x
88194101	SAOUHSC_00300	Geh	lipase precursor	76 kDa	ez	10.00	Y	x	x	x

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88196512	SAOUHSC_02883		LysM domain protein	28 kDa	ez	9.04	Y	x		
88193885	SAOUHSC_00069		protein A	56 kDa	zw	10.00	Y	x		
88194325	SAOUHSC_00545		sdrD protein, putative	146 kDa	zw	10.00	Y	x	x	
88195636	SAOUHSC_01942	SplA	serine protease SplA	26 kDa	ez	9.73	Y	x		x
88195635	SAOUHSC_01941	SplB	serine protease SplB	26 kDa	ez	9.73	Y	x		x
88195634	SAOUHSC_01939	SplC	serine protease SplC	26 kDa	ez	9.73	Y	x		
88195631	SAOUHSC_01936	SplE	serine protease SplE	26 kDa	ez	9.73	Y	x		x
88195630	SAOUHSC_01935	SplF	serine protease SplF, putative	26 kDa	ez	9.73	#NV	x		x
88195808	SAOUHSC_02127		staphopain thiol proteinase	44 kDa	ez	9.73	Y	x		x
88195848	SAOUHSC_02171	Sak	staphylokinase precursor, putative	19 kDa	ez	9.98	Y	x	x	x
88194577	SAOUHSC_00818	Nuc	thermonuclease precursor	25 kDa	ez	10.00	Y	x		x
88195480	SAOUHSC_01779	Tig	trigger factor	49 kDa	zyt	8.87	N	x	x	
Zellwandbiosynthese und -abbau										
88194219	SAOUHSC_00427		autolysin precursor, putative	36 kDa	ez	9.98	Y	x		x
88194750	SAOUHSC_00994	Atl	bifunctional autolysin precursor, putative	137 kDa	ez	10.00	#NV	x	x	x
88195790	SAOUHSC_02108	Ftn	ferritin, putative	20 kDa	zyt	9.98	N	x		
88193909	SAOUHSC_00094		hypothetical protein SAOUHSC_00094	22 kDa	zw	9.93	Y	x		x
88196515	SAOUHSC_02887	IsaA	immunodominant antigen A, putative	24 kDa	ez	10.00	Y	x	x	x
88195840	SAOUHSC_02161		MHC class II analog protein	66 kDa	unb	3.33	Y	x		
88194887	SAOUHSC_01145	PbpA	penicillin-binding protein 1	83 kDa	zm	9.82	Y	x		
88195184	SAOUHSC_01467	Pbp2	penicillin-binding protein 2	80 kDa	ez	9.55	N	x		
88195360	SAOUHSC_01652	PbpF,Pbp3	penicillin-binding protein 3	77 kDa	zm	9.82	#NV	x		
88194055	SAOUHSC_00248	LytM	peptidoglycan hydrolase, putative	34 kDa	ez	9.98	Y	x	x	x
88194324	SAOUHSC_00544		sdrC protein, putative	108 kDa	zw	10.00	Y	x		
88196215	SAOUHSC_02571	SsaA	secretory antigen precursor, putative	29 kDa	ez	9.04	Y	x		x
88194436	SAOUHSC_00671		secretory antigen SsaA-like protein	28 kDa	ez	9.73	Y	x	x	x

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88196118	SAOUHSC_02466		truncated MHC class II analog protein	15 kDa	unb	3.33	Y	x		
88194675	SAOUHSC_00918		truncated MHC class II analog protein	16 kDa	unb	3.33	Y	x		
Zellumhüllung										
88194626	SAOUHSC_00869	DltA	D-alanine-activating enzyme	55 kDa	zyt	9.98	N	x	x	
88194628	SAOUHSC_00871	DltC	D-alanyl carrier protein	9 kDa	zyt	8.87	N	x		
88194199	SAOUHSC_00405		hypothetical protein SAOUHSC_00405	29 kDa	unb	2.50	N	x		
88194482	SAOUHSC_00717		hypothetical protein SAOUHSC_00717	16 kDa	unb	3.33	Y	x		
88194518	SAOUHSC_00754		hypothetical protein SAOUHSC_00754	34 kDa	unb	6.46	Y	x		
88194829	SAOUHSC_01081	IsdA	hypothetical protein SAOUHSC_01081	39 kDa	zw	10.00	N	x		x
88194830	SAOUHSC_01082	IsdC	hypothetical protein SAOUHSC_01082	25 kDa	unb	3.33	Y	x		x
88195062	SAOUHSC_01332		hypothetical protein SAOUHSC_01332	34 kDa	unb	2.50	#NV	x		x
88195295	SAOUHSC_01584		hypothetical protein SAOUHSC_01584	34 kDa	unb	2.50	N	x		
88195443	SAOUHSC_01739	LytH	hypothetical protein SAOUHSC_01739	33 kDa	unb	3.33	N	x		
88195542	SAOUHSC_01843		hypothetical protein SAOUHSC_01843	101 kDa	zw	10.00	#NV	x		
88195590	SAOUHSC_01895		hypothetical protein SAOUHSC_01895	33 kDa	ez	9.55	Y	x		
88195802	SAOUHSC_02121		hypothetical protein SAOUHSC_02121	45 kDa	unb	3.33	Y	x		
88196419	SAOUHSC_02783		hypothetical protein SAOUHSC_02783	31 kDa	unb	2.50	#NV	x		
88196425	SAOUHSC_02789		hypothetical protein SAOUHSC_02789	28 kDa	zyt	8.87	N	x		
88196433	SAOUHSC_02798		hypothetical protein SAOUHSC_02798	179 kDa	zw	10.00	N	x		
88196599	SAOUHSC_02979		hypothetical protein SAOUHSC_02979	69 kDa	ez	9.73	Y	x	x	x
88196601	SAOUHSC_02982		hypothetical protein SAOUHSC_02982	71 kDa	zw	10.00	Y	x	x	
88193889	SAOUHSC_00074	SirA	periplasmic binding protein, putative	37 kDa	unb	3.33	Y	x		
88195460	SAOUHSC_01759	Mrec	rod shape-determining protein Mrec	31 kDa	unb	3.33	Y	x		x
88196220	SAOUHSC_02576		secretory antigen precursor SsaA, putative	17 kDa	unb	3.33	Y		x	x
88196468	SAOUHSC_02834	SrtA	sortase, putative	24 kDa	unb	3.33	Y	x		x

Accession- Nummer	Locus-Tag ^A	Protein -name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
Stressantwort										
88194163	SAOUHSC_00365	AhpC	alkyl hydroperoxide reductase	21 kDa	zyt	9.98	N	x	x	x
88194162	SAOUHSC_00364	AhpF	alkyl hydroperoxide reductase, subunit F, putative	55 kDa	zyt	9.98	N	x	x	
88196560	SAOUHSC_02933	bsA	betaine aldehyde dehydrogenase	55 kDa	zyt	9.98	N	x		
88195057	SAOUHSC_01327	KatA	catalase	55 kDa	zyt	9.98	N	x	x	x
88195926	SAOUHSC_02255	GroES	chaperonin, 10 kDa, GroES, putative	10 kDa	zyt	10.00	N	x		
88195925	SAOUHSC_02254	GroL,GroEL	chaperonin, 60 kDa, GrpEL, putative	58 kDa	zyt	9.98	N	x	x	
88195129	SAOUHSC_01403	CspA	cold shock protein, putative	7 kDa	zyt	9.98	N	x		
88194348	SAOUHSC_00573		hypothetical protein SAOUHSC_00573	29 kDa	unb	2.50	N	x		
88194589	SAOUHSC_00831		hypothetical protein SAOUHSC_00831	15 kDa	unb	2.50	N	x		
88194593	SAOUHSC_00835		hypothetical protein SAOUHSC_00835	14 kDa	zyt	8.87	N	x		
88195014	SAOUHSC_01282	BsaA	hypothetical protein SAOUHSC_01282	18 kDa	unb	2.50	N			x
88195522	SAOUHSC_01822	Tpx	hypothetical protein SAOUHSC_01822	18 kDa	unb	2.50	N	x	x	
88196044	SAOUHSC_02381	Dps	hypothetical protein SAOUHSC_02381	17 kDa	unb	2.50	N	x	x	
88196094	SAOUHSC_02441	Asp23	hypothetical protein SAOUHSC_02441	19 kDa	unb	2.50	N	x	x	
88195155	SAOUHSC_01431	MsrB	methionine sulfoxide reductase, putative	16 kDa	zyt	8.87	N		x	
88195361	SAOUHSC_01653	SodA	superoxide dismutase, Mn, putative	23 kDa	ez	9.55	N	x		
88193908	SAOUHSC_00093	SodM	superoxide dismutase, putative	23 kDa	ez	9.55	N	x	x	
88194846	SAOUHSC_01100	TrxA,Trx	thioredoxin	11 kDa	zyt	9.98	N	x		
88194546	SAOUHSC_00785	TrxB	thioredoxin reductase	34 kDa	zyt	9.65	N	x	x	
88194592	SAOUHSC_00834		thioredoxin, putative	12 kDa	zyt	8.87	N	x		
Regulation										
88194239	SAOUHSC_00452		hypothetical protein SAOUHSC_00452	12 kDa	unb	2.50	N	x		
88194459	SAOUHSC_00694		hypothetical protein SAOUHSC_00694	17 kDa	unb	2.50	N	x		
88194753	SAOUHSC_00997		hypothetical protein SAOUHSC_00997	46 kDa	unb	3.33	Y	x	x	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88194963	SAOUHSC_01228	CodY	hypothetical protein SAOUHSC_01228	29 kDa	zyt	8.87	N	x	x	x
88195657	SAOUHSC_01964	TRAP	hypothetical protein SAOUHSC_01964	20 kDa	zyt	8.87	#NV	x	x	x
88195154	SAOUHSC_01430	Crr	phosphotransferase system enzyme IIA, putative	18 kDa	zyt	9.98	N	x	x	
88196063	SAOUHSC_02402		PTS system, mannitol-spezifisch IIA component, putative	16 kDa	zyt	9.98	N	x		
88194390	SAOUHSC_00620	SarA	staphylococcal accessory regulator T, putative	15 kDa	unb	2.50	N	x		
88196226	SAOUHSC_02583		transcriptional regulator, putative	34 kDa	unb	3.33	Y	x		x
Transport										
88194087	SAOUHSC_00284		5'-nucleotidase, lipoprotein e(P4) family ABC transporter periplasmic binding protein, putative	33 kDa	unb	3.33	Y	x		
88196085	SAOUHSC_02430	HtsA	ABC transporter, substrate-binding protein, putative	37 kDa	unb	3.33	Y	x		
88194402	SAOUHSC_00634	MntC	enoyl-CoA hydratase/isomerase family protein, putative	35 kDa	unb	3.33	Y	x		x
88194742	SAOUHSC_00985	MenB	protein, putative	30 kDa	zyt	8.87	N	x		
88194761	SAOUHSC_01007	FolD	FolD bifunctional protein, putative	31 kDa	zyt	8.87	N	x	x	
88194011	SAOUHSC_00201		hypothetical protein SAOUHSC_00201	53 kDa	zw	9.17	N	x		
88194112	SAOUHSC_00311		hypothetical protein SAOUHSC_00311	10 kDa	zyt	8.87	N	x		
88194831	SAOUHSC_01084	IsdD	hypothetical protein SAOUHSC_01084	41 kDa	unb	2.50	Y	x		
88194832	SAOUHSC_01085	IsdE	hypothetical protein SAOUHSC_01085	32 kDa	zyt	8.87	N	x		x
88195556	SAOUHSC_01858		hypothetical protein SAOUHSC_01858	22 kDa	zyt	9.98	N	x		
88195571	SAOUHSC_01874		hypothetical protein SAOUHSC_01874	11 kDa	unb	2.50	N	x		
88195914	SAOUHSC_02241		hypothetical protein SAOUHSC_02241	39 kDa	ez	9.73	Y	x		x
88195918	SAOUHSC_02246		hypothetical protein SAOUHSC_02246	35 kDa	unb	6.46	Y	x		
88196199	SAOUHSC_02554	FhuD2	hypothetical protein SAOUHSC_02554	34 kDa	unb	3.33	Y	x		
88196339	SAOUHSC_02699		hypothetical protein SAOUHSC_02699	29 kDa	unb	3.33	Y	x		
88196600	SAOUHSC_02980		hypothetical protein SAOUHSC_02980	21 kDa	unb	2.50	N	x		
88196194	SAOUHSC_02549	ModA	molybdenum ABC transporter, periplasmic	29 kDa	unb	3.33	Y	x		

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
			molybdate-binding protein							
88194828	SAOUHSC_01079	IsdB	neurofilament protein	72 kDa	zw	10.00	#NV	x		x
88194684	SAOUHSC_00927	OppA	oligopeptide ABC transporter, substrate- binding protein, putative	62 kDa	zw	9.18	Y	x		
88196403	SAOUHSC_02767	Opp- 1A,Opp1A	peptide ABC transporter, peptide-binding protein, putative	60 kDa	zw	9.18	Y	x		
88194781	SAOUHSC_01028	PtsH	phosphocarrier protein hpr, putative	9 kDa	zyt	10.00	N	x		
88195976	SAOUHSC_02310	KdpC	potassium-transporting ATPase, C subunit	21 kDa	unb	3.33	Y	x		
88195582	SAOUHSC_01886	RibH	riboflavin synthase, beta subunit	16 kDa	zyt	8.87	N		x	
zell. Prozesse										
88194892	SAOUHSC_01150	FtsZ	cell division protein FtsZ	41 kDa	zyt	8.87	N	x		
88194891	SAOUHSC_01149	FtsA	cell division protein, putative	53 kDa	zyt	8.87	N	x		
88194886	SAOUHSC_01144	FtsL	hypothetical protein SAOUHSC_01144	15 kDa	zyt	8.87	N	x		
88194898	SAOUHSC_01158		hypothetical protein SAOUHSC_01158	24 kDa	zyt	8.87	N	x		
88195179	SAOUHSC_01462		hypothetical protein SAOUHSC_01462	13 kDa	zyt	8.87	N	x		
88195846	SAOUHSC_02169	Chs,Chp	hypothetical protein SAOUHSC_02169 signal recognition particle-docking protein	17 kDa	unb	3.33	Y	x	x	x
88194942	SAOUHSC_01205	FtsY	FtsY	47 kDa	zyt	8.87	N	x		
Energiemetabolismus										
88193901	SAOUHSC_00086	ButA	3-ketoacyl-acyl carrier protein reductase, putative	27 kDa	zyt	9.65	N	x		
88195316	SAOUHSC_01605	Gnd	6-phosphogluconate dehydrogenase, decarboxylating	52 kDa	zyt	8.87	N	x	x	
88195075	SAOUHSC_01347	CitB,AcnA	aconitate hydratase 1	99 kDa	zyt	9.98	N	x	x	
88196007	SAOUHSC_02341	AtpD	ATP synthase F1, beta subunit	51 kDa	zyt	8.87	N	x		
88194665	SAOUHSC_00908	Cdr	coenzyme A disulfide reductase, putative	49 kDa	zyt	9.98	N	x		
88196500	SAOUHSC_02869	RocA	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	57 kDa	zyt	9.98	#NV	x	x	
88193913	SAOUHSC_00100	DeoC,DeoC1, Dra	deoxyribose-phosphate aldolase	23 kDa	zyt	9.98	N	x		

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88194795	SAOUHSC_01043	PdhD,LpdA	dihydrolipoamide dehydrogenase dihydrolipoamide S-acetyltransferase component of pyruvate dehydrogenase	49 kDa	zyt	9.98	N	x	x	x
88194794	SAOUHSC_01042	PdhC	complex E2, putative	46 kDa	zyt	9.98	N	x	x	
88196464	SAOUHSC_02830	Ddh	D-lactate dehydrogenase, putative	35 kDa	zyt	9.98	N	x		
88194559	SAOUHSC_00799	Eno	enolase	47 kDa	zyt	9.98	N	x	x	
88193954	SAOUHSC_00142	Fdh	formate dehydrogenase, NAD-dependent, putative	38 kDa	zyt	9.98	N	x	x	
88196553	SAOUHSC_02926		fructose-bisphosphate aldolase class-I, putative	33 kDa	unb	2.50	N	x	x	
88195310	SAOUHSC_01599	Zwf	glucose-6-phosphate 1-dehydrogenase	57 kDa	zyt	8.87	N	x		
88194657	SAOUHSC_00900	Pgi	glucose-6-phosphate isomerase glyceraldehyde-3-phosphate	50 kDa	zyt	9.98	N	x	x	x
88194555	SAOUHSC_00795	Gap1,Gap	dehydrogenase, type I	36 kDa	zyt	9.98	N	x	x	x
88194594	SAOUHSC_00836	GcvH	glycine cleavage system H protein	14 kDa	zyt	8.87	N	x		
88194312	SAOUHSC_00532	Kbl	hypothetical protein SAOUHSC_00532	43 kDa	zyt	8.87	N	x	x	
88194332	SAOUHSC_00553		hypothetical protein SAOUHSC_00553	22 kDa	zyt	8.87	N	x	x	
88194493	SAOUHSC_00728		hypothetical protein SAOUHSC_00728	74 kDa	zm	9.99	Y	x	x	x
88194654	SAOUHSC_00897	GlpQ	hypothetical protein SAOUHSC_00897	35 kDa	unb	4.86	#NV	x		x
88194760	SAOUHSC_01005		hypothetical protein SAOUHSC_01005	11 kDa	unb	3.33	#NV	x		
88195141	SAOUHSC_01415		hypothetical protein SAOUHSC_01415	30 kDa	zyt	8.87	N	x		
88195558	SAOUHSC_01860		hypothetical protein SAOUHSC_01860	12 kDa	zyt	8.87	N	x		
88195596	SAOUHSC_01901		hypothetical protein SAOUHSC_01901	26 kDa	unb	2.50	N	x		
88195678	SAOUHSC_01987		hypothetical protein SAOUHSC_01987	22 kDa	zyt	8.87	#NV	x	x	
88195820	SAOUHSC_02140	PpaC	hypothetical protein SAOUHSC_02140	34 kDa	zyt	8.87	N	x	x	
88195823	SAOUHSC_02143		hypothetical protein SAOUHSC_02143	39 kDa	zyt	8.87	N	x	x	
88195830	SAOUHSC_02150		hypothetical protein SAOUHSC_02150	22 kDa	unb	2.50	N	x	x	
88196029	SAOUHSC_02366	FbaA, Fba	hypothetical protein SAOUHSC_02366	31 kDa	zyt	8.87	N	x	x	
88196098	SAOUHSC_02445		hypothetical protein SAOUHSC_02445	37 kDa	zyt	8.87	N	x		

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88196099	SAOUHSC_02447		hypothetical protein SAOUHSC_02447	36 kDa	zyt	8.87	N	x		
88196100	SAOUHSC_02448		hypothetical protein SAOUHSC_02448	33 kDa	unb	2.50	Y	x		x
88196112	SAOUHSC_02460		hypothetical protein SAOUHSC_02460	32 kDa	zyt	8.87	#NV	x		
88196528	SAOUHSC_02900		hypothetical protein SAOUHSC_02900	31 kDa	zyt	8.87	N	x		
88196549	SAOUHSC_02922	Ldh2,Ldh	L-lactate dehydrogenase	34 kDa	zyt	9.65	N	x		
88196554	SAOUHSC_02927	Mqo2	malate:quinone-oxidoreductase	56 kDa	unb	4.05	N	x		
88195510	SAOUHSC_01810		NADP-dependent malic enzyme, putative peptidyl-prolyl cis-trans isomerase, cyclophilin-type, putative	44 kDa	zm	7.63	N	x	x	
88194648	SAOUHSC_00891			22 kDa	zyt	9.98	N		x	
88194349	SAOUHSC_00574	Pta	phosphate acetyltransferase phosphoenolpyruvate carboxykinase (ATP)	35 kDa	zyt	8.87	N	x	x	
88195605	SAOUHSC_01910	PckA	phosphoenolpyruvate-protein phosphotransferase	59 kDa	unb	2.50	N	x	x	
88194782	SAOUHSC_01029	PtsI	phosphoglycerate kinase, putative phosphoglycerate mutase, 2,3- bisphosphoglycerate-independent	63 kDa	zyt	10.00	N	x	x	
88194556	SAOUHSC_00796	Pgk	phosphoglycerate kinase, putative phosphoglycerate mutase, 2,3- bisphosphoglycerate-independent	43 kDa	zyt	9.91	N	x	x	
88194558	SAOUHSC_00798	Pgm,GpmI	phosphoglycerate kinase, putative phosphoglycerate mutase, 2,3- bisphosphoglycerate-independent	56 kDa	zyt	9.98	N		x	
88196343	SAOUHSC_02703	GpmA	phosphoglycerate mutase, putative pyruvate dehydrogenase complex, E1 component, alpha subunit, putative pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	27 kDa	unb	2.50	N	x	x	
88194792	SAOUHSC_01040	PdhA	pyruvate dehydrogenase complex, E1 component, alpha subunit, putative pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	41 kDa	zyt	8.87	N	x	x	
88194793	SAOUHSC_01041	PhdB,PdhB	pyruvate dehydrogenase complex, E1 component, pyruvate dehydrogenase beta subunit, putative	35 kDa	zyt	8.87	N	x	x	
88195506	SAOUHSC_01806	PykA,Pyk	pyruvate kinase	63 kDa	zyt	8.87	N	x		
88194758	SAOUHSC_01002	QoxA	quinol oxidase AA3, subunit II, putative succinyl-CoA synthetase, alpha subunit, putative	42 kDa	zm	10.00	Y	x		
88194954	SAOUHSC_01218	SucD	succinyl-CoA synthetase, alpha subunit, putative	32 kDa	zyt	8.87	N	x	x	
88194953	SAOUHSC_01216	SucC	succinyl-CoA synthetase, beta subunit, putative	42 kDa	zyt	8.87	N	x		
88195066	SAOUHSC_01337	Tkt	transketolase	68 kDa	unb	2.50	N	x	x	
88194557	SAOUHSC_00797	TpiA,Tpi	triosephosphate isomerase	27 kDa	unb	2.50	N	x	x	

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
Proteinbiosynthese										
88195210	SAOUHSC_01493	RpsA	30S ribosomal protein S1, putative	43 kDa	zyt	9.98	N	x	x	
88196150	SAOUHSC_02500	RplE	50S ribosomal protein L5, putative	20 kDa	zyt	8.87	#NV	x		x
88194381	SAOUHSC_00611	ArgS	arginyl-tRNA synthetase	62 kDa	zyt	9.98	N	x	x	
88195444	SAOUHSC_01741	Dtd	D-tyrosyl-tRNA(Tyr) deacylase	17 kDa	unb	2.50	N	x		
88194290	SAOUHSC_00509	GltX	glutamyl-tRNA synthetase	56 kDa	zyt	9.65	N	x	x	
88195799	SAOUHSC_02117	GatA	glutamyl-tRNA(Gln) amidotransferase, A subunit	53 kDa	zyt	8.87	N	x		
88195798	SAOUHSC_02116	GatB	glutamyl-tRNA(Gln) amidotransferase, B subunit	54 kDa	zyt	8.87	#NV	x		
88195800	SAOUHSC_02118		glutamyl-tRNA(Gln) amidotransferase, C subunit	11 kDa	zyt	8.87	N	x		
88195373	SAOUHSC_01666	GlyS	glycyl-tRNA synthetase	54 kDa	zyt	10.00	N	x		
88194708	SAOUHSC_00951		hypothetical protein SAOUHSC_00951	19 kDa	zyt	8.87	N	x		
88196138	SAOUHSC_02487	RpsM	hypothetical protein SAOUHSC_02487	14 kDa	zyt	8.87	N	x		
88196161	SAOUHSC_02511	RplD	hypothetical protein SAOUHSC_02511	22 kDa	unb	2.50	N	x		
88196022	SAOUHSC_02359	PrfA	peptide chain release factor 1 ribosomal 5S rRNA E-loop binding	40 kDa	zyt	9.98	N	x		
88194261	SAOUHSC_00474	RplY	protein Ctc/L25/TL5	24 kDa	zyt	8.87	#NV	x		
88194300	SAOUHSC_00519	RplA	ribosomal protein L1	25 kDa	zyt	8.87	N	x		x
88194301	SAOUHSC_00520	RplJ	ribosomal protein L10	18 kDa	zyt	8.87	N	x		
88194299	SAOUHSC_00518	RplK	ribosomal protein L11	15 kDa	zyt	8.87	N	x		
88196130	SAOUHSC_02478	RplM	ribosomal protein L13	16 kDa	unb	2.50	N	x		x
88196143	SAOUHSC_02492	RplO	ribosomal protein L15	16 kDa	unb	2.50	N	x		
88196135	SAOUHSC_02484	RplQ	ribosomal protein L17	14 kDa	zyt	8.87	N	x		
88196146	SAOUHSC_02495	RplR	ribosomal protein L18	13 kDa	zyt	8.87	N	x		
88195458	SAOUHSC_01757	RplU	ribosomal protein L21	11 kDa	unb	2.50	N	x		
88196157	SAOUHSC_02507	RplV	ribosomal protein L22	13 kDa	zyt	8.87	Y	x		x

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88196154	SAOUHSC_02504	RpmC	ribosomal protein L29	8 kDa	zyt	8.87	N	x		
88196162	SAOUHSC_02512	RplC	ribosomal protein L3, putative	24 kDa	zyt	8.87	N			x
88196144	SAOUHSC_02493	RpmD	ribosomal protein L30	7 kDa	unb	2.50	N	x		
88196024	SAOUHSC_02361	RpmE	ribosomal protein L31	10 kDa	unb	2.50	N	x		
88196147	SAOUHSC_02496	RplF	ribosomal protein L6, putative	20 kDa	zyt	8.87	N	x		x
88194302	SAOUHSC_00521	RplL	ribosomal protein L7/L12	13 kDa	zyt	8.87	N	x	x	
88193838	SAOUHSC_00017	RplI	ribosomal protein L9	17 kDa	zyt	9.65	N	x		x
88194965	SAOUHSC_01232	RpsB	ribosomal protein S2	28 kDa	zyt	8.87	#NV	x	x	
88196156	SAOUHSC_02506	RpsC	ribosomal protein S3	24 kDa	zyt	8.87	N			x
88196145	SAOUHSC_02494	RpsE	ribosomal protein S5	18 kDa	zyt	8.87	#NV	x		
88194147	SAOUHSC_00348	RpsF	ribosomal protein S6	12 kDa	zyt	9.98	#NV	x		
88194308	SAOUHSC_00528	RpsG	ribosomal protein S7	18 kDa	zyt	8.87	N	x		
88196148	SAOUHSC_02498	RpsH	ribosomal protein S8, putative	15 kDa	zyt	8.87	N	x		
88196129	SAOUHSC_02477	RpsI	ribosomal protein S9, putative	15 kDa	unb	2.50	#NV	x		
88194969	SAOUHSC_01236	Rrf,Frr	ribosome recycling factor	20 kDa	zyt	9.98	N	x	x	
88193832	SAOUHSC_00009	SerS	seryl-tRNA synthetase	49 kDa	zyt	10.00	N	x		
88194309	SAOUHSC_00529	FusA,Fus	translation elongation factor G	77 kDa	zyt	9.98	N	x	x	
88194967	SAOUHSC_01234	Tsf	translation elongation factor Ts	32 kDa	zyt	9.98	#NV	x	x	
88194310	SAOUHSC_00530	Tuf	translation elongation factor Tu	43 kDa	zyt	9.98	N	x	x	
88195487	SAOUHSC_01786	InfC	translation initiation factor IF-3	20 kDa	zyt	9.98	#NV	x		
88194690	SAOUHSC_00933	TrpS	tryptophanyl-tRNA synthetase	37 kDa	zyt	9.98	N	x		x
Proteinmetabolismus										
88194678	SAOUHSC_00921	FabF,Fab	3-oxoacyl- synthase, putative	44 kDa	zyt	9.98	N	x	x	
88194937	SAOUHSC_01199	FabG	3-oxoacyl-(acyl-carrier-protein) reductase, putative	26 kDa	zyt	9.98	N	x		
88194939	SAOUHSC_01201	HmrB,AcpP	acyl carrier protein	9 kDa	zyt	8.87	#NV	x		

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88196002	SAOUHSC_02336	FabZ	beta-hydroxyacyl-ACP dehydratase, putative	16 kDa	zyt	8.87	N		x	
88195390	SAOUHSC_01684	GrpE	co-chaperone GrpE	24 kDa	zyt	8.87	N	x	x	
88195389	SAOUHSC_01683	DnaK	DNAk protein, putative	66 kDa	zyt	9.98	N	x	x	
88196491	SAOUHSC_02860	MvaS	HMG-CoA synthase, putative	43 kDa	zyt	8.87	N	x	x	
88194271	SAOUHSC_00486	FtsH	hypothetical protein SAOUHSC_00486	78 kDa	zm	10.00	Y	x		
88194313	SAOUHSC_00533		hypothetical protein SAOUHSC_00533	32 kDa	unb	2.50	N	x		
88194677	SAOUHSC_00920	FabH	hypothetical protein SAOUHSC_00920	34 kDa	unb	2.50	#NV	x		
88194972	SAOUHSC_01239		hypothetical protein SAOUHSC_01239	44 kDa	zm	9.99	N	x		
88194988	SAOUHSC_01255		hypothetical protein SAOUHSC_01255	49 kDa	zyt	8.87	N	x	x	
88194989	SAOUHSC_01256		hypothetical protein SAOUHSC_01256	50 kDa	unb	2.50	N	x		
88195092	SAOUHSC_01365		hypothetical protein SAOUHSC_01365	38 kDa	zyt	8.87	N		x	
88195110	SAOUHSC_01383		hypothetical protein SAOUHSC_01383	69 kDa	zyt	9.98	N	x		
88195151	SAOUHSC_01427	CtpA	hypothetical protein SAOUHSC_01427	55 kDa	unb	2.50	N	x		
88195516	SAOUHSC_01816		hypothetical protein SAOUHSC_01816	40 kDa	zyt	8.87	N	x	x	
88195565	SAOUHSC_01868		hypothetical protein SAOUHSC_01868	53 kDa	zyt	8.87	N	x	x	
88194936	SAOUHSC_01198	FabD	malonyl CoA-acyl carrier protein transacylase	34 kDa	zyt	8.87	N	x		
88195784	SAOUHSC_02102	Map	methionine aminopeptidase, type I	28 kDa	zyt	8.87	N	x	x	
88194694	SAOUHSC_00937	PepF,PepB	oligoendopeptidase F	70 kDa	zyt	9.98	N	x	x	
88194521	SAOUHSC_00757	PepT	peptidase T, putative	46 kDa	zyt	9.98	N	x		
88194790	SAOUHSC_01038	Def	polypeptide deformylase	21 kDa	zyt	8.87	#NV	x	x	
88195663	SAOUHSC_01972	PrsA	protein export protein PrsA, putative	36 kDa	unb	3.33	Y	x		x
88194660	SAOUHSC_00903	SpsB	Signal peptidase IB, putative	18 kDa	unb	4.05	N	x		
AS-Biosynthese										
88194316	SAOUHSC_00536	IlvE	branched-chain amino acid aminotransferase	40 kDa	zyt	8.87	N	x		

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88195018	SAOUHSC_01287	GlnA	glutamine synthetase, type I	51 kDa	zyt	9.98	N	x	x	
88194273	SAOUHSC_00488	CysK	hypothetical protein SAOUHSC_00488	33 kDa	zyt	8.87	N	x	x	
88195550	SAOUHSC_01852		hypothetical protein SAOUHSC_01852	41 kDa	zyt	8.87	#NV	x		
88195928	SAOUHSC_02257	SdrH	hypothetical protein SAOUHSC_02257	47 kDa	zw	9.18	Y	x		
88196017	SAOUHSC_02354	GlyA	serine hydroxymethyltransferase, putative	45 kDa	zyt	9.98	N	x	x	
Nukleotidbiosynthese										
88196141	SAOUHSC_02490	Adk	adenylate kinase, putative	24 kDa	zyt	9.98	N	x		
88195807	SAOUHSC_02126	PurB	adenylosuccinate lyase	50 kDa	zyt	8.87	N	x		
88193840	SAOUHSC_00019	PurA	adenylosuccinate synthetase	48 kDa	zyt	8.87	N	x	x	
88196031	SAOUHSC_02368	PyrG,CtrA	CTP synthase	60 kDa	zyt	8.87	N	x	x	
88194907	SAOUHSC_01168	PyrC	dihydroorotase	46 kDa	zyt	8.87	N	x		
88195544	SAOUHSC_01845	Geh	formate-tetrahydrofolate ligase, putative	60 kDa	zyt	8.87	#NV	x	x	
88194270	SAOUHSC_00485	Hpt	hypoxanthine phosphoribosyltransferase	20 kDa	zyt	9.98	N	x		
88193914	SAOUHSC_00101	Drm,DeoB	phosphopentomutase	44 kDa	zyt	8.87	N	x		
88194766	SAOUHSC_01012	PurQ	phosphoribosylformylglycinamidine synthase I	25 kDa	zyt	8.87	N	x		
88194765	SAOUHSC_01011	PurS	phosphoribosylformylglycinamidine synthase, PurS protein	10 kDa	zyt	8.87	N	x		
88196043	SAOUHSC_02380	DeoD2	purine nucleoside phosphorylase	26 kDa	unb	2.50	N	x	x	
88194508	SAOUHSC_00743	Rir2,NrdF	ribonucleotide-disphosphate reductase beta chain, putative	38 kDa	zyt	8.87	N	x		
88196016	SAOUHSC_02353	Upp	uracil phosphoribosyltransferase	23 kDa	zyt	8.87	N	x		
Transkription and Replikation										
88195207	SAOUHSC_01490	Hup,Hu	DNA-binding protein HU, putative	10 kDa	unb	2.50	N	x		
88196136	SAOUHSC_02485	RpoA	DNA-directed RNA polymerase alpha chain, putative	35 kDa	zyt	9.98	N	x		
88196032	SAOUHSC_02369	RpoE	DNA-directed RNA polymerase, delta subunit, putative	21 kDa	zyt	8.87	N	x		
88193826	SAOUHSC_00003		hypothetical protein SAOUHSC_00003	9 kDa	zyt	8.87	N	x		

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88194530	SAOUHSC_00767	YfiA	hypothetical protein SAOUHSC_00767	22 kDa	zyt	8.87	N	x		
88194916	SAOUHSC_01177	RpoZ	hypothetical protein SAOUHSC_01177	8 kDa	unb	2.50	N	x		
88196427	SAOUHSC_02791		pyrophosphohydrolase, putative	15 kDa	unb	2.50	N	x		
88195419	SAOUHSC_01714	GreA	transcription elongation factor GreA	18 kDa	zyt	8.87	N	x	x	
88194976	SAOUHSC_01243	NusA	transcription termination-antitermination factor, putative	44 kDa	zyt	8.87	N	x		
unbekannte Funktion										
88194218	SAOUHSC_00426		ABC transporter, substrate-binding protein, putative	30 kDa	unb	3.33	Y	x		
88194136	SAOUHSC_00336	Thl	acetyl-CoA acetyltransferase, putative	42 kDa	zyt	9.98	#NV	x		
88195775	SAOUHSC_02092	PepS,AmpS	aminopeptidase PepS, putative	47 kDa	zyt	8.87	N	x		
88195764	SAOUHSC_02080		bacteriophage L54a, antirepressor, putative	30 kDa	zyt	8.87	N	x		
88194148	SAOUHSC_00349	Ssb	bacteriophage L54a, single-stranded DNA binding protein	19 kDa	unb	2.50	N	x		
88196221	SAOUHSC_02577		D-isomer spezific 2-hydroxyacid dehydrogenase, NAD binding domain protein	35 kDa	zyt	9.98	N	x	x	
88195741	SAOUHSC_02057		dUTP pyrophosphatase	19 kDa	zyt	8.87	N	x	x	
88194173	SAOUHSC_00375	GuaA	GMP synthase, putative	58 kDa	zyt	8.87	N	x	x	
88193846	SAOUHSC_00025		hypothetical protein SAOUHSC_00025	83 kDa	zw	10.00	Y	x		
88194032	SAOUHSC_00225		hypothetical protein SAOUHSC_00225	27 kDa	unb	2.50	N	x		
88194059	SAOUHSC_00253		hypothetical protein SAOUHSC_00253	58 kDa	unb	3.33	Y	x		
88194062	SAOUHSC_00256		hypothetical protein SAOUHSC_00256	33 kDa	unb	3.33	Y	x		
88194064	SAOUHSC_00258		hypothetical protein SAOUHSC_00258	115 kDa	zm	9.35	Y	x		
88194145	SAOUHSC_00346	YchF	hypothetical protein SAOUHSC_00346	41 kDa	zyt	8.87	#NV	x		
88194153	SAOUHSC_00354		hypothetical protein SAOUHSC_00354	23 kDa	unb	2.50	#NV			x
88194155	SAOUHSC_00356		hypothetical protein SAOUHSC_00356	21 kDa	unb	3.33	Y	x		
88194160	SAOUHSC_00362		hypothetical protein SAOUHSC_00362	24 kDa	unb	3.33	Y	x		
88194167	SAOUHSC_00369		hypothetical protein SAOUHSC_00369	36 kDa	zyt	8.87	#NV	x	x	

Accession- Nummer	Locus-Tag ^A	Protein -name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88194169	SAOUHSC_00371		hypothetical protein SAOUHSC_00371	15 kDa	zyt	8.87	N	x	x	
88194180	SAOUHSC_00383		hypothetical protein SAOUHSC_00383	26 kDa	unb	6.46	Y	x		x
88194187	SAOUHSC_00392		hypothetical protein SAOUHSC_00392	26 kDa	ez	9.98	Y	x		x
88194194	SAOUHSC_00399		hypothetical protein SAOUHSC_00399	25 kDa	ez	9.98	Y	x	x	
88194195	SAOUHSC_00400		hypothetical protein SAOUHSC_00400	57 kDa	unb	3.33	Y	x	x	
88194196	SAOUHSC_00401		hypothetical protein SAOUHSC_00401	11 kDa	unb	3.33	Y	x		
88194202	SAOUHSC_00408		hypothetical protein SAOUHSC_00408	12 kDa	zyt	8.87	N	x		
88194256	SAOUHSC_00469	SpoVG	hypothetical protein SAOUHSC_00469	11 kDa	zyt	8.87	N	x		
88194387	SAOUHSC_00617		hypothetical protein SAOUHSC_00617	19 kDa	unb	3.33	Y	x	x	x
88194451	SAOUHSC_00686		hypothetical protein SAOUHSC_00686	11 kDa	zyt	8.87	N	x		
88194469	SAOUHSC_00704		hypothetical protein SAOUHSC_00704	17 kDa	unb	3.33	Y	x		
88194602	SAOUHSC_00844		hypothetical protein SAOUHSC_00844	30 kDa	zm	9.87	Y	x		x
88194603	SAOUHSC_00845		hypothetical protein SAOUHSC_00845	7 kDa	unb	2.50	N	x		
88194622	SAOUHSC_00865		hypothetical protein SAOUHSC_00865	28 kDa	unb	2.50	N	x		
88194663	SAOUHSC_00906		hypothetical protein SAOUHSC_00906	33 kDa	zyt	8.87	N	x	x	
88194788	SAOUHSC_01036		hypothetical protein SAOUHSC_01036	9 kDa	zyt	8.87	N	x		
88194802	SAOUHSC_01050		hypothetical protein SAOUHSC_01050	40 kDa	zm	9.99	Y	x		
88194858	SAOUHSC_01112		hypothetical protein SAOUHSC_01112	15 kDa	unb	3.33	#NV	x		
88194877	SAOUHSC_01135		hypothetical protein SAOUHSC_01135	4 kDa	unb	2.50	#NV	x	x	
88194878	SAOUHSC_01136		hypothetical protein SAOUHSC_01136	4 kDa	unb	2.50	N		x	
88194880	SAOUHSC_01138		hypothetical protein SAOUHSC_01138	17 kDa	unb	2.50	N	x	x	
88194895	SAOUHSC_01154		hypothetical protein SAOUHSC_01154	21 kDa	unb	2.50	N	x		
88195001	SAOUHSC_01268		hypothetical protein SAOUHSC_01268	11 kDa	zyt	8.87	N	x		
88195053	SAOUHSC_01323		hypothetical protein SAOUHSC_01323	30 kDa	zyt	8.87	N	x		
88195140	SAOUHSC_01414		hypothetical protein SAOUHSC_01414	13 kDa	unb	2.50	N	x		
88195160	SAOUHSC_01436		hypothetical protein SAOUHSC_01436	16 kDa	zyt	8.87	N	x		

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88195162	SAOUHSC_01438		hypothetical protein SAOUHSC_01438	9 kDa	unb	2.50	N	x		
88195321	SAOUHSC_01610		hypothetical protein SAOUHSC_01610	16 kDa	zyt	8.87	N	x		
88195356	SAOUHSC_01648		hypothetical protein SAOUHSC_01648	17 kDa	unb	2.50	#NV	x		
88195424	SAOUHSC_01719		hypothetical protein SAOUHSC_01719	12 kDa	zyt	8.87	N	x		
88195426	SAOUHSC_01721		hypothetical protein SAOUHSC_01721	10 kDa	unb	2.50	N	x		
88195435	SAOUHSC_01730	CsbD	hypothetical protein SAOUHSC_01730	7 kDa	unb	2.50	#NV	x		
88195462	SAOUHSC_01761		hypothetical protein SAOUHSC_01761	18 kDa	unb	2.50	#NV	x		
88195514	SAOUHSC_01814		hypothetical protein SAOUHSC_01814	15 kDa	unb	2.50	N	x		
88195515	SAOUHSC_01815		hypothetical protein SAOUHSC_01815	25 kDa	zyt	8.87	N	x	x	
88195519	SAOUHSC_01819		hypothetical protein SAOUHSC_01819	18 kDa	zyt	8.87	N	x	x	
88195566	SAOUHSC_01869		hypothetical protein SAOUHSC_01869	16 kDa	unb	2.50	Y	x		
88195602	SAOUHSC_01907		hypothetical protein SAOUHSC_01907	31 kDa	zyt	8.87	N	x		
88195613	SAOUHSC_01918		hypothetical protein SAOUHSC_01918	25 kDa	unb	2.50	N	x		
88195660	SAOUHSC_01968	Hit	hypothetical protein SAOUHSC_01968	16 kDa	unb	2.50	N	x		
88195668	SAOUHSC_01977		hypothetical protein SAOUHSC_01977	13 kDa	zyt	8.87	#NV	x		
88195687	SAOUHSC_01999		hypothetical protein SAOUHSC_01999	17 kDa	zyt	8.87	N	x		
88195701	SAOUHSC_02013		hypothetical protein SAOUHSC_02013	19 kDa	zyt	8.87	N	x		
88195723	SAOUHSC_02037		hypothetical protein SAOUHSC_02037	15 kDa	zyt	8.87	N	x		
88195729	SAOUHSC_02044		hypothetical protein SAOUHSC_02044	23 kDa	zyt	8.87	N	x	x	
88195757	SAOUHSC_02073		hypothetical protein SAOUHSC_02073	21 kDa	unb	2.50	N	x	x	
88195825	SAOUHSC_02145		hypothetical protein SAOUHSC_02145	7 kDa	unb	2.50	Y	x		
88195845	SAOUHSC_02167		hypothetical protein SAOUHSC_02167	13 kDa	unb	3.33	Y	x		
88195892	SAOUHSC_02218		hypothetical protein SAOUHSC_02218	11 kDa	unb	2.50	N	x		
88196065	SAOUHSC_02404	FmtB	hypothetical protein SAOUHSC_02404	263 kDa	zw	10.00	Y	x		
88196067	SAOUHSC_02406		hypothetical protein SAOUHSC_02406	35 kDa	unb	2.50	Y	x		
88196212	SAOUHSC_02568		hypothetical protein SAOUHSC_02568	13 kDa	zyt	8.87	#NV	x		

Accession- Nummer	Locus-Tag ^A	Protein- name ^A	Beschreibung	Molekular- gewicht	Lokalisation ^B	PSort- Score ^B	SP ^B	Gelfrei	2D-Page pH4-7	2D-Page pH6-11
88196330	SAOUHSC_02690		hypothetical protein SAOUHSC_02690	59 kDa	unb	3.33	Y	x		x
88196364	SAOUHSC_02724		hypothetical protein SAOUHSC_02724	26 kDa	unb	2.50	N	x		
88196410	SAOUHSC_02774		hypothetical protein SAOUHSC_02774	16 kDa	zyt	8.87	N	x		
88196513	SAOUHSC_02885		hypothetical protein SAOUHSC_02885	69 kDa	zm	9.99	N	x		
88196593	SAOUHSC_02972	IsaB	hypothetical protein SAOUHSC_02972	19 kDa	unb	3.33	Y	x	x	x
88196640	SAOUHSC_03022		hypothetical protein SAOUHSC_03022	19 kDa	unb	2.50	N	x		
88196290	SAOUHSC_02650		lipoprotein, putative	23 kDa	unb	4.05	Y	x		
88195728	SAOUHSC_02043		phage head protein, putative	37 kDa	zyt	8.87	N	x	x	
88196598	SAOUHSC_02978		phage infeztion protein, putative	109 kDa	zm	9.99	Y	x		
88195722	SAOUHSC_02036		phage structural protein, putative	22 kDa	unb	2.50	N	x		
88195710	SAOUHSC_02022		phage tail fiber protein, putative	44 kDa	zyt	8.87	N	x		
88195727	SAOUHSC_02042		phi Mu50B-like protein	11 kDa	unb	2.50	N	x		
88195758	SAOUHSC_02074		phi PVL orf 39-like protein	13 kDa	unb	2.50	Y	x		
88195715	SAOUHSC_02028		phiETA ORF57-like protein	67 kDa	unb	2.50	N	x		
88194561	SAOUHSC_00801	SecG	preprotein translocase, SecG subunit	10 kDa	zm	9.75	N	x		
88195747	SAOUHSC_02063		PV83 orf 23-like protein-related protein	7 kDa	zyt	8.87	N	x		
88195999	SAOUHSC_02333		sceD protein, putative single-strand DNA-binding protein, putative	24 kDa	ez	9.98	#NV	x	x	
88195755	SAOUHSC_02071		SLT orf 129-like protein	19 kDa	unb	2.50	N	x		
88195714	SAOUHSC_02027		STAS domain, putative	14 kDa	unb	2.50	#NV	x		
88195966	SAOUHSC_02300	RsbV	transcription antitermination protein, putative	12 kDa	zyt	8.87	N	x		
88194298	SAOUHSC_00517	NusG	putative	21 kDa	zyt	8.87	N	x	x	

Auflistung aller identifizierten Proteine für *S. aureus* RN1HG und RN1HG $\Delta sigB$ in pMEM im Vergleich zwischen der gelfreien und der gelbasierten Methode.

^A Locus und Proteinname beziehen sich auf *S. aureus* 8325.

^B Die Lokalisation und die Vorhersage eines Signalpeptides erfolgte über P-Sort. ez = extrazellulär, zw = Zellwand, zm = zytoplasmatische Membran, zyt = Zytoplasma, unb = unbekannt, SP = Signalpeptid, N = kein Signalpeptid, Y = Signalpeptid vorhanden, #NV = Vorhersage nicht möglich.

Tab. 68: Liste der identifizierten Proteine der S9-Zellen mit und ohne Infektion mit *S. aureus* RN1HG pMV158.

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
MTND_HUMAN	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	21 kDa							2	2				
CH10_HUMAN	10 kDa heat shock protein, mitochondrial	11 kDa	4	4	4	4	6	6	4	4	4	4	4	4
U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein component	109 kDa	8	9	8	9	10	11	7	8	7	8	8	9
1433B_HUMAN	14-3-3 protein beta/alpha	28 kDa	12	17	11	16	11	14	12	16	13	17	13	15
1433E_HUMAN	14-3-3 protein epsilon	29 kDa	14	17	14	17	13	16	13	16	14	17	13	16
1433F_HUMAN	14-3-3 protein eta	28 kDa	5	6	7	7	6	6	5	5	5	5	6	6
1433G_HUMAN	14-3-3 protein gamma	28 kDa	8	10	8	10	8	10	8	11	7	10	8	10
1433S_HUMAN	14-3-3 protein sigma	28 kDa	8	9	7	8	7	8	8	11	8	9	5	6
1433T_HUMAN	14-3-3 protein theta	28 kDa	13	16	12	14	10	12	10	13	10	13	9	10
1433Z_HUMAN	14-3-3 protein zeta/delta	28 kDa	14	17	17	20	14	17	16	20	17	21	15	18
CN37_HUMAN	2',3'-cyclic-nucleotide 3'-phosphodiesterase	48 kDa	3	3	2	2		1	2	2	3	3	3	3
PRS4_HUMAN	26S protease regulatory subunit 4	49 kDa	2	2	2	2	2	2	2	2	2	2	2	2
PRS6A_HUMAN	26S protease regulatory subunit 6A	49 kDa	7	7	7	7	8	9	8	8	6	6	8	8
PRS6B_HUMAN	26S protease regulatory subunit 6B	47 kDa	2	2	2	2	2	2		1	3	3	2	2
PRS7_HUMAN	26S protease regulatory subunit 7	49 kDa	5	5	5	5	6	6	5	5	4	4	5	5
PRS8_HUMAN	26S protease regulatory subunit 8	46 kDa	3	3	2	2	4	4	4	4		1	2	2
PRS10_HUMAN	26S protease regulatory subunit S10B	44 kDa	4	4	4	4	2	2	2	2	4	4	4	4
PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1	106 kDa	4	4	3	3	3	3	3	3	2	2		1
PSD11_HUMAN	26S proteasome non-ATPase regulatory subunit 11	47 kDa	4	4	5	5	4	4	4	4	5	5	4	4
PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12	53 kDa	3	3	3	3	3	3	3	3	4	4	4	4
PSD13_HUMAN	26S proteasome non-ATPase regulatory subunit 13	43 kDa		1		1		1					3	3
PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14	35 kDa	4	5	4	5	4	5	4	5	4	5	4	5
PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2	100 kDa	7	7	6	6	6	6	6	6	6	6	7	7
PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3	61 kDa	4	4	4	4	3	3	4	4	4	4	3	3

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
PSMD4_HUMAN	26S proteasome non-ATPase regulatory subunit 4	41 kDa	2	2	2	2	2	2	2	2	2	2		1
PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5	56 kDa	2	2	3	3	3	3	3	3	3	3	2	2
PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6	46 kDa	3	3	2	2	3	3	3	3	2	2	2	2
PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 9	25 kDa	3	3	2	2		1		1		1		1
HAP28_HUMAN	28 kDa heat 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor	21 kDa	2	2	3	3		1	3	3	3	3		1
ODO1_HUMAN	116 kDa	116 kDa	3	3	3	3	3	3			3	3	3	3
D3D2_HUMAN	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	33 kDa	2	2		1	2	2		1		1	2	2
RM12_HUMAN	39S ribosomal protein L12, mitochondrial precursor	21 kDa		1	2	2	3	3		1		1	2	2
RM41_HUMAN	39S ribosomal protein L41, mitochondrial precursor	15 kDa										1	2	2
HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	27 kDa	5	6	3	4	5	5	5	6	3	4	4	5
3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35 kDa	3	3	3	3	4	4	2	2	3	3	5	5
THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial	42 kDa	3	3	3	3	3	3	4	4	2	2	3	3
RS10_HUMAN	40S ribosomal protein S10	19 kDa	2	2	2	2		1	2	2		1		1
RS11_HUMAN	40S ribosomal protein S11	18 kDa	2	2		1			2	2		1	3	3
RS12_HUMAN	40S ribosomal protein S12	15 kDa	2	2	3	3	3	3	3	3	2	2	3	3
RS14_HUMAN	40S ribosomal protein S14	16 kDa	2	2	2	2	2	2	2	2	2	2	2	2
RS15_HUMAN	40S ribosomal protein S15	17 kDa		1		1		1	2	2		1		1
RS15A_HUMAN	40S ribosomal protein S15a	15 kDa		1		1	2	2	2	2		1		1
RS16_HUMAN	40S ribosomal protein S16	16 kDa	2	2		1		1						
RS17_HUMAN	40S ribosomal protein S17	16 kDa		2	2	3		2						
RS18_HUMAN	40S ribosomal protein S18	18 kDa	2	2	3	3		1	3	3	2	2	3	3
RS19_HUMAN	40S ribosomal protein S19	16 kDa		1	2	2		1						
RS2_HUMAN	40S ribosomal protein S2	31 kDa	5	5	5	5	4	4	4	4	4	4	5	6
RS21_HUMAN	40S ribosomal protein S21	9 kDa	3	3	3	3	3	3	3	3	3	3	3	3
RS23_HUMAN	40S ribosomal protein S23	16 kDa	2	2	2	2								

Accessionnummer	Proteinbeschreibung	Molekular- gewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
RS27_HUMAN	40S ribosomal protein S27	9 kDa							3	3		1		1
RS28_HUMAN	40S ribosomal protein S28	8 kDa	3	3		1		1	2	2		1	2	2
RS3_HUMAN	40S ribosomal protein S3	27 kDa	7	7	7	7	6	6	7	7	6	6	5	5
RS3A_HUMAN	40S ribosomal protein S3a	30 kDa	2	2		1		1	2	2				1
RS4X_HUMAN	40S ribosomal protein S4, X isoform	30 kDa	5	5	5	5	4	4	5	5	4	4	5	5
RS5_HUMAN	40S ribosomal protein S5	23 kDa	4	5	3	4	3	4	4	5	3	4	3	3
RS6_HUMAN	40S ribosomal protein S6	29 kDa								1			2	2
RS7_HUMAN	40S ribosomal protein S7	22 kDa	4	4	3	3	4	4	4	4	5	5	5	5
RS8_HUMAN	40S ribosomal protein S8	24 kDa	7	7	6	6	5	5	6	6	5	5	5	5
RSSA_HUMAN	40S ribosomal protein SA	33 kDa	7	7	5	5	6	6	5	5	6	6	7	7
4F2_HUMAN	4F2 cell-surface antigen heavy chain	58 kDa		1	2	2	2	2	2	2	3	3	2	2
AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase	54 kDa		1	2	2	3	3	2	2		1	2	2
OASL_HUMAN	59 kDa 2'-5'-oligoadenylate synthetase-like protein	59 kDa			2	2					4	4	3	3
CH60_HUMAN	60 kDa heat shock protein, mitochondrial precursor	61 kDa	21	26	21	25	22	29	22	25	22	25	26	30
RO60_HUMAN	60 kDa SS-A/Ro ribonucleoprotein	61 kDa	2	2	2	2		1		1		1		1
RLA0_HUMAN	60S acidic ribosomal protein P0	34 kDa	6	7	6	7	4	5	4	5	6	7	4	5
RLA1_HUMAN	60S acidic ribosomal protein P1	12 kDa	2	3	2	3	2	3	2	3	2	3	2	3
RLA2_HUMAN	60S acidic ribosomal protein P2	12 kDa	6	7	5	6	5	6	5	6	5	6	5	6
RL10_HUMAN	60S ribosomal protein L10	25 kDa	3	3	3	3		1	2	2	2	2	3	3
RL11_HUMAN	60S ribosomal protein L11	20 kDa	3	3	3	3	2	2	2	2	2	2		1
RL12_HUMAN	60S ribosomal protein L12	18 kDa	5	5	3	3	5	5	5	5	4	4	4	4
RL13_HUMAN	60S ribosomal protein L13	24 kDa		1	2	2		1	2	2	2	2	2	2
RL15_HUMAN	60S ribosomal protein L15	24 kDa		1		1	2	2	2	2		1		1
RL18_HUMAN	60S ribosomal protein L18	22 kDa	2	2	2	2		1	2	2	2	2		1
RL18A_HUMAN	60S ribosomal protein L18a	21 kDa							2	2		1		1

Accessionnummer	Proteinbeschreibung	Molekular- gewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
RL19_HUMAN	60S ribosomal protein L19	23 kDa								1	2	2		
RL22_HUMAN	60S ribosomal protein L22	15 kDa	3	3	2	2	2	2	2	2	2	2	2	2
RL23_HUMAN	60S ribosomal protein L23	15 kDa		1		1	2	2	2	2	2	2		1
RL23A_HUMAN	60S ribosomal protein L23a	18 kDa	2	2	2	2	2	2	2	2	3	3	2	2
RL27A_HUMAN	60S ribosomal protein L27a	17 kDa	3	3	2	2	2	2	2	2	2	2	2	2
RL3_HUMAN	60S ribosomal protein L3	46 kDa	3	3	4	4	2	2	5	6	5	5	3	3
RL30_HUMAN	60S ribosomal protein L30	13 kDa	2	2	2	2	2	2	2	2	2	2	2	2
RL32_HUMAN	60S ribosomal protein L32	16 kDa	2	2	2	2		1	2	2	2	2	2	2
RL36_HUMAN	60S ribosomal protein L36	12 kDa	2	2	2	2	2	2	2	2	2	2	2	2
RL4_HUMAN	60S ribosomal protein L4	48 kDa	6	6	6	6	5	6	6	6	6	6	6	6
RL5_HUMAN	60S ribosomal protein L5	34 kDa	4	4	2	2		1	3	3	2	2		1
RL6_HUMAN	60S ribosomal protein L6	33 kDa	2	2		1				1		1	2	2
RL7_HUMAN	60S ribosomal protein L7	29 kDa	4	4	3	3	3	3	3	3	3	3	3	3
RL7A_HUMAN	60S ribosomal protein L7a	30 kDa	2	2	2	2			2	2		1		
RL9_HUMAN	60S ribosomal protein L9	22 kDa	2	2	2	2	2	2	2	2	2	2	2	2
K6PP_HUMAN	6-phosphofruktokinase type C	86 kDa	11	11	12	12	10	10	11	11	10	10	11	11
K6PL_HUMAN	6-phosphofruktokinase, liver type	85 kDa	3	3	4	4	3	3	3	3	4	4	2	2
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating	53 kDa	5	5	5	5	3	3	7	7	5	5	2	2
6PGL_HUMAN	6-phosphogluconolactonase	28 kDa	2	2	2	2	2	2		1	2	2		1
GRP78_HUMAN	78 kDa glucose-regulated protein precursor	72 kDa	21	24	20	22	25	28	20	22	21	24	29	34
THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic	41 kDa	8	9	8	11	8	9	8	9	8	11	8	9
THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial precursor	45 kDa	4	4	3	3	4	4	5	5	3	3	3	3
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A	29 kDa	2	2		1			2	2		1		1
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B	29 kDa	2	2	2	2	2	2	2	2	2	2	2	2
AN32E_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member E	31 kDa	2	2	2	2	2	2	2	2	2	2	2	2

Accessionnummer	Proteinbeschreibung	Molekular- gewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
ACON_HUMAN	Aconitate hydratase, mitochondrial precursor	85 kDa	3	3	3	3	5	5	3	3	2	2	6	6
ACTB_HUMAN	Actin, cytoplasmic 1	42 kDa												
ACTG_HUMAN	Actin, cytoplasmic 2	42 kDa	25	35	23	32	25	35						
ACL6A_HUMAN	Actin-like protein 6A	47 kDa		1	3	3	2	2		1		1	3	3
ARP2_HUMAN	Actin-related protein 2	45 kDa	7	7	6	6	7	7	7	7	6	6	7	7
ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B	41 kDa	2	2	2	2		1	2	2	2	2		1
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3	21 kDa	3	3	4	4	3	3	3	3	4	5	3	3
ARP3_HUMAN	Actin-related protein 3	47 kDa	9	9	9	9	9	10	9	9	9	9	9	9
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15	14 kDa	3	3		1		1	3	3	3	3		1
ACPH_HUMAN	Acylamino-acid-releasing enzyme Acyl-CoA dehydrogenase family member 9, mitochondrial precursor	81 kDa	2	2	2	2	2	2	2	2	2	2	2	2
ACAD9_HUMAN		69 kDa	2	2	2	2		1		1		1		1
ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9	46 kDa	3	3		1	3	3	2	2	2	2	3	3
APT_HUMAN	Adenine phosphoribosyltransferase	20 kDa	3	3	2	2		1	2	2		1		1
ADK_HUMAN	Adenosine kinase	41 kDa		1	2	2		1						
SAHH_HUMAN	Adenosylhomocysteinase	48 kDa	9	9	11	12	9	10	11	12	10	11	10	10
KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial	26 kDa	2	2	2	2		1	2	2	2	2	3	3
CAP1_HUMAN	Adenylyl cyclase-associated protein 1	52 kDa	10	12	9	11	8	10	10	12	9	11	9	11
CAP2_HUMAN	Adenylyl cyclase-associated protein 2	53 kDa					2	2		1			2	2
APMAP_HUMAN	Adipocyte plasma membrane-associated protein	46 kDa		1		1	2	2			2	2	4	4
ADT2_HUMAN	ADP/ATP translocase 2	33 kDa	5	5	3	3	3	3	6	6	4	4	5	5
ARF1_HUMAN	ADP-ribosylation factor 1	21 kDa												
ARF4_HUMAN	ADP-ribosylation factor 4	21 kDa	3	3	3	3		1	3	3	2	2		1
ARF5_HUMAN	ADP-ribosylation factor 5	21 kDa	3	3	3	3	3	3	3	3	3	3		
ARFG1_HUMAN	ADP-ribosylation factor GTPase-activating protein 1	45 kDa		1	2	2		1		1		1		1
NUDT5_HUMAN	ADP-sugar pyrophosphatase	24 kDa	2	2	2	2								

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2	40 kDa	2	2	2	2		1	2	2	2	2		1
AGRIN_HUMAN	Aggrin precursor	215 kDa	2	2	2	2	2	2			3	3		1
AIP_HUMAN	AH receptor-interacting protein	38 kDa								1	2	2		
AKA12_HUMAN	A-kinase anchor protein 12	191 kDa	7	7	5	5	4	4	6	6	6	6	5	5
AKAP2_HUMAN	A-kinase anchor protein 2	96 kDa					2	2				1	2	2
SYAC_HUMAN	Alanyl-tRNA synthetase, cytoplasmic	107 kDa	10	10	8	8	8	8	10	10	8	8	8	8
AL1B1_HUMAN	Aldehyde dehydrogenase X, mitochondrial precursor	57 kDa			2	2	2	2		1		1	2	2
ADAS_HUMAN	Alkyldihydroxyacetonephosphate synthase, peroxisomal precursor	73 kDa		1	3	3	2	2		1	2	2	2	2
FETUA_HUMAN	Alpha-2-HS-glycoprotein precursor	39 kDa	2	2	2	2			2	2	2	2		
ACTN1_HUMAN	Alpha-actinin-1	103 kDa	19	20	18	21	19	20	16	18	16	18	19	22
ACTN4_HUMAN	Alpha-actinin-4	105 kDa	37	39	36	39	35	37	37	38	35	36	35	39
ADDA_HUMAN	Alpha-adducin	81 kDa				1	2	2				1		1
AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	55 kDa	8	8	7	7	9	9	6	7	5	5	6	6
ACTZ_HUMAN	Alpha-centractin	43 kDa	5	5	4	4	3	3	4	4	4	4	3	3
ENOA_HUMAN	Alpha-enolase	47 kDa	23	35	23	34	24	37	24	37	24	37	23	33
AINX_HUMAN	Alpha-internexin	55 kDa	2	2		1	3	3		1			3	3
SNAA_HUMAN	Alpha-soluble NSF attachment protein	33 kDa	2	2	2	2	3	3	2	2	2	2	3	3
AMPB_HUMAN	Aminopeptidase B	73 kDa	2	2				1	2	2	2	2		
ANXA1_HUMAN	Annexin A1	39 kDa	20	23	17	21	17	20	18	20	18	21	14	16
ANX11_HUMAN	Annexin A11	54 kDa	3	3	3	3	3	3	4	4	3	3	3	3
ANXA2_HUMAN	Annexin A2	39 kDa	25	36	27	36	26	33	24	32	25	34	27	36
ANXA3_HUMAN	Annexin A3	36 kDa	7	7	8	8	7	7	6	6	6	6	7	7
ANXA4_HUMAN	Annexin A4	36 kDa	5	5	3	3	3	3	4	4	4	4	4	4
ANXA5_HUMAN	Annexin A5	36 kDa	12	12	13	14	9	11	13	15	13	14	11	11
ANXA6_HUMAN	Annexin A6	76 kDa	7	7	8	8	6	6	9	9	8	8	8	8

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
AP2A1_HUMAN	AP-2 complex subunit alpha-1	108 kDa	2	2	2	2	5	5	5	5	3	3	3	3
AP2A2_HUMAN	AP-2 complex subunit alpha-2	104 kDa		1	2	2								
AP2B1_HUMAN	AP-2 complex subunit beta-1	105 kDa	5	5	5	5	4	4	4	4	3	4	5	5
AP2M1_HUMAN	AP-2 complex subunit mu-1	50 kDa	2	2	2	2				1	2	2		1
AP3S1_HUMAN	AP-3 complex subunit sigma-1	22 kDa								1	2	2		
APOL2_HUMAN	Apolipoprotein-L2	37 kDa	3	3	3	3	4	4	3	3	3	3	6	6
API5_HUMAN	Apoptosis inhibitor 5	58 kDa	2	2	2	2	2	2	3	3	2	2	2	2
BAX_HUMAN	Apoptosis regulator BAX	21 kDa		1	2	2	2	2		1	2	2		1
AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial precursor	67 kDa	5	5	6	6	6	6	5	5	5	5	6	6
ACINU_HUMAN	Apoptotic chromatin condensation inducer in the nucleus	152 kDa	2	2	2	2		1	3	3	2	2	2	2
SYRC_HUMAN	Arginyl-tRNA synthetase, cytoplasmic	75 kDa	7	7	7	7	6	6	9	9	7	7	7	7
ARSA1_HUMAN	Arsenical pump-driving ATPase	39 kDa	2	2		1		1	2	3		1	2	2
ARS2_HUMAN	Arsenite-resistance protein 2	101 kDa	3	3	3	3	2	2	3	3	3	3	2	2
SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic	63 kDa	4	4	4	4	3	3	5	5	4	4	4	4
AATC_HUMAN	Aspartate aminotransferase, cytoplasmic	46 kDa							2	2		1		1
AATM_HUMAN	Aspartate aminotransferase, mitochondrial precursor	47 kDa	5	5	5	5	5	5	3	3	4	4	6	6
SYDC_HUMAN	Aspartyl-tRNA synthetase, cytoplasmic	57 kDa	4	4	5	5	3	3	3	3	4	4	5	5
PEA15_HUMAN	Astrocytic phosphoprotein PEA-15	15 kDa	3	4	2	3	3	3	2	3	2	3	2	3
ATX10_HUMAN	Ataxin-10	53 kDa	3	3	3	3	2	2	4	4	3	3	2	2
ATLA3_HUMAN	Atlastin-3	61 kDa								1	2	2		
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial precursor	60 kDa	15	16	14	15	14	16	13	14	13	14	15	17
AT5F1_HUMAN	ATP synthase subunit b, mitochondrial precursor	29 kDa	2	2		1	2	2		1		1	3	3
ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor	57 kDa	17	19	17	20	20	26	19	21	14	16	21	27
ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	18 kDa	3	3	4	4	6	6	3	3	3	3	6	6
ATPK_HUMAN	ATP synthase subunit f, mitochondrial	11 kDa	2	2	2	2	2	2	2	2	2	2		1

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
ATPO_HUMAN	ATP synthase subunit O, mitochondrial precursor	23 kDa	4	4	5	5	5	5	4	4	5	5	7	7
ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial precursor	13 kDa	3	3		1	3	3				1	3	4
ATD3A_HUMAN	ATPase family AAA domain-containing protein 3A	71 kDa		1	2	2		1		1	2	2	5	5
ABCE1_HUMAN	ATP-binding cassette sub-family E member 1	67 kDa							2	2		1		
ACLY_HUMAN	ATP-citrate synthase	121 kDa	13	14	14	14	8	8	13	13	12	12	11	11
KU70_HUMAN	ATP-dependent DNA helicase 2 subunit 1	70 kDa	9	10	10	11	5	6	9	10	8	9	9	10
KU86_HUMAN	ATP-dependent DNA helicase 2 subunit 2	83 kDa	16	19	12	14	11	12	13	15	12	15	13	15
RECQ1_HUMAN	ATP-dependent DNA helicase Q1	73 kDa	6	6	6	6	4	4	6	6	6	6	5	5
DHX9_HUMAN	ATP-dependent RNA helicase A	141 kDa	13	13	10	10	10	10	10	10	10	10	11	11
DDX1_HUMAN	ATP-dependent RNA helicase DDX1	82 kDa	3	4	2	3	3	4	3	4	3	4	3	4
DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X	73 kDa	9	9	9	9	7	7	7	7	7	7	6	6
E41L2_HUMAN	Band 4.1-like protein 2	113 kDa	5	5	4	4	4	4	4	4	5	5		1
BAF_HUMAN	Barrier-to-autointegration factor	10 kDa								1		1	2	2
BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1	48 kDa	4	4	3	4	2	2	3	3	4	4	2	2
BASI_HUMAN	Basigin precursor	42 kDa	4	4	4	4	4	4	4	4	4	4	5	6
BAP31_HUMAN	B-cell receptor-associated protein 31	28 kDa	2	2	2	2	2	2	2	2	2	2	2	2
B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin form pI 5.3]	14 kDa	3	4	3	4	3	4	3	4	3	4	3	4
SNTB2_HUMAN	Beta-2-syntrophin	58 kDa											1	2
HEXA_HUMAN	Beta-hexosaminidase alpha chain precursor	61 kDa		1	2	2		1		1				1
HEXB_HUMAN	Beta-hexosaminidase beta chain precursor	63 kDa	2	2	2	2	4	4	2	2	2	2	6	6
BID_HUMAN	BH3-interacting domain death agonist	22 kDa	2	2	2	2	2	2	2	2	2	2		
SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase	171 kDa	6	6	6	6	2	2	6	6	6	6	7	7
PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase	65 kDa	6	6	6	6	5	5	6	6	6	6	5	5
BIEA_HUMAN	Biliverdin reductase A precursor	33 kDa		1		1	2	2		1		1		1
BASP_HUMAN	Brain acid soluble protein 1	23 kDa	4	4	6	6	5	5	5	5	5	6	8	8

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	102 kDa	7	7	8	8	7	7	7	7	8	8	6	6
CAD13_HUMAN	Cadherin-13 precursor	78 kDa	3	3	3	3		1	3	3	3	3		1
CMC2_HUMAN	Calcium-binding mitochondrial carrier protein Aralar2	74 kDa								1			2	2
SCMC1_HUMAN	Calcium-binding mitochondrial carrier protein SCaMC-1	53 kDa											4	4
CYBP_HUMAN	Calcyclin-binding protein	26 kDa	2	2	2	2		1	2	2	2	2	3	3
CALD1_HUMAN	Caldesmon	93 kDa	3	3	4	4	4	4	4	4	4	4	4	4
CALX_HUMAN	Calnexin precursor	68 kDa	7	9	7	8	7	8	9	10	8	9	8	10
CAN2_HUMAN	Calpain-2 catalytic subunit precursor	80 kDa	7	7	6	6	5	5	5	5	6	6	6	6
ICAL_HUMAN	Calpastatin	77 kDa	4	4	4	5	5	5	4	4	3	3	5	5
CNN2_HUMAN	Calponin-2	34 kDa	6	6	6	6	4	4	6	7	4	5	4	4
CNN3_HUMAN	Calponin-3	36 kDa	6	6	6	6	5	5	6	6	5	5	4	4
CALR_HUMAN	Calreticulin precursor	48 kDa	13	15	15	20	19	20	14	18	15	18	17	22
CALU_HUMAN	Calumenin precursor	37 kDa	5	5	3	3	6	7	6	6	5	5	8	8
CAPR1_HUMAN	Caprin-1	73 kDa	3	3	4	4	3	3	4	4	3	3	3	3
CBR1_HUMAN	Carbonyl reductase [NADPH] 1	30 kDa	5	5	5	5	4	4	5	5	6	6	5	5
CSK2B_HUMAN	Casein kinase II subunit beta	25 kDa		1	2	2		1						
CTNA1_HUMAN	Catenin alpha-1	100 kDa	5	5	4	4	3	3	5	5	5	5	4	4
CTNB1_HUMAN	Catenin beta-1	85 kDa	2	2	3	3	3	3	2	2	2	2	3	3
CATB_HUMAN	Cathepsin B precursor	38 kDa											2	2
CATD_HUMAN	Cathepsin D precursor	45 kDa	8	8	6	6	7	8	6	6	6	6	7	8
CATZ_HUMAN	Cathepsin Z precursor	34 kDa		1	2	2	3	3	2	2	2	2	3	3
CAV1_HUMAN	Caveolin-1	20 kDa	2	2	2	2	2	2	2	2	2	2		1
CD109_HUMAN	CD109 antigen precursor	162 kDa	3	3	5	5			3	3		1		
CD166_HUMAN	CD166 antigen precursor	65 kDa	2	2		1	4	5	3	3	3	3	3	3
CD2B2_HUMAN	CD2 antigen cytoplasmic tail-binding protein 2	38 kDa	2	2	2	2	2	2	2	2	2	2	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
CD44_HUMAN	CD44 antigen precursor	82 kDa	3	3	2	2	4	4	3	3	3	3	2	2
CD9_HUMAN	CD9 antigen	25 kDa	2	2	3	3		1	3	3	2	2	3	3
CDC2_HUMAN	Cell division control protein 2 homolog	34 kDa	4	4	5	5	2	2	4	4	4	4	4	4
MUC18_HUMAN	Cell surface glycoprotein MUC18 precursor	72 kDa	5	5	5	5	3	3	5	5	5	5	2	2
CNBP_HUMAN	Cellular nucleic acid-binding protein	19 kDa	2	2		1								
P53_HUMAN	Cellular tumor antigen p53	44 kDa	2	2	2	2	2	2	2	2	2	2	2	2
CETN2_HUMAN	Centrin-2	20 kDa	2	2	2	2		1	2	2	2	2		1
CHM4B_HUMAN	Charged multivesicular body protein 4b	25 kDa	3	3	4	4	3	3	4	4	3	3	3	3
CHMP5_HUMAN	Charged multivesicular body protein 5	25 kDa	2	2	2	2	2	2	3	3	2	2	2	2
CLIC1_HUMAN	Chloride intracellular channel protein 1	27 kDa	9	10	8	10	7	8	8	10	7	8	6	7
CLIC4_HUMAN	Chloride intracellular channel protein 4	29 kDa	9	10	7	8	8	8	8	9	7	7	6	6
CBX1_HUMAN	Chromobox protein homolog 1	21 kDa		1		1		1		1			3	3
CBX3_HUMAN	Chromobox protein homolog 3	21 kDa	6	6	5	5	5	5	5	5	6	6	7	8
CBX5_HUMAN	Chromobox protein homolog 5	22 kDa		1		1	2	2						
CISY_HUMAN	Citrate synthase, mitochondrial precursor	52 kDa	3	3	3	3	3	3	4	4	3	3	3	3
JIP4_HUMAN	C-jun-amino-terminal kinase-interacting protein 4	146 kDa		1		1	2	2						
CLH1_HUMAN	Clathrin heavy chain 1	192 kDa	34	38	27	31	24	27	29	34	25	29	29	35
EPN4_HUMAN	Clathrin interactor 1	68 kDa					2	2		1		1		1
CPSF5_HUMAN	Cleavage and polyadenylation specificity factor subunit 5	26 kDa	2	2	2	2	2	2	3	3	3	3	2	2
CPSF6_HUMAN	Cleavage and polyadenylation specificity factor subunit 6	59 kDa	2	3		2		2	2	3		2		2
CPSF7_HUMAN	Cleavage and polyadenylation specificity factor subunit 7	52 kDa	3	3	3	3	4	4	3	4	3	4	4	5
COTL1_HUMAN	Coactosin-like protein	16 kDa							2	3		2		1
COPA_HUMAN	Coatomer subunit alpha	138 kDa	7	7	3	3			3	3	3	3		
COPB_HUMAN	Coatomer subunit beta	107 kDa							2	2		1		1
COPB2_HUMAN	Coatomer subunit beta'	102 kDa								1		1	3	3

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
COPD_HUMAN	Coatomer subunit delta	57 kDa	2	2	2	2		1		1		1		1
COPE_HUMAN	Coatomer subunit epsilon	34 kDa	3	3	4	5	2	3	4	5	4	4	3	4
COPG_HUMAN	Coatomer subunit gamma	98 kDa		1	4	4	2	2	2	2				
COPG2_HUMAN	Coatomer subunit gamma-2	98 kDa	2	2						1		1	2	2
COPZ1_HUMAN	Coatomer subunit zeta-1	20 kDa		1		1		1	2	2		1	2	2
COF1_HUMAN	Cofilin-1	19 kDa	10	12	9	12	9	11	11	13	10	12	9	11
CCD47_HUMAN	Coiled-coil domain-containing protein 47 precursor	56 kDa	2	3	2	2	2	4	2	3	2	3	2	2
CHCH2_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial precursor	16 kDa							2	2	2	2	2	2
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	31 kDa	3	3	2	2	2	2	3	3	2	2	3	3
CND1_HUMAN	Condensin complex subunit 1	157 kDa	3	3	5	5		1	3	3	2	2		
CTGF_HUMAN	Connective tissue growth factor precursor	38 kDa		1		1	2	2						
CSN3_HUMAN	COP9 signalosome complex subunit 3	48 kDa		1	2	2	2	2	2	2	2	2	2	2
CSN4_HUMAN	COP9 signalosome complex subunit 4	46 kDa	2	2	2	2	2	2	2	2	2	2	2	2
CSN6_HUMAN	COP9 signalosome complex subunit 6	36 kDa	2	2		1				1				1
CPNE1_HUMAN	Copine-1	59 kDa	4	6	4	6	3	5	4	5	5	6	3	4
CPNE3_HUMAN	Copine-3	60 kDa	2	2		1	2	2		1				1
H2AY_HUMAN	Core histone macro-H2A.1	40 kDa		1	2	2		1	2	2		1	2	2
COR1B_HUMAN	Coronin-1B	54 kDa	3	3	2	2	2	2	2	2	3	3	2	2
COR1C_HUMAN	Coronin-1C	53 kDa	8	8	8	8	5	5	8	8	7	7	7	7
PYRG1_HUMAN	CTP synthase 1	67 kDa		1	2	2		1						
CUL4B_HUMAN	Cullin-4B	102 kDa	2	2		1			2	2		1		
CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1	136 kDa	9	9	8	8	3	3	8	8	9	9	5	5
CD2A1_HUMAN	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	17 kDa		1		1		1	2	2	2	2	2	2
CSR1_HUMAN	Cysteine and glycine-rich protein 1	21 kDa	4	4	4	4	4	4	4	4	4	4	3	3
CRIP2_HUMAN	Cysteine-rich protein 2	22 kDa	3	3	3	3	2	2	2	2	2	2	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial precursor	53 kDa	2	2	2	2	3	3	2	2	2	2	3	3
QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial precursor	48 kDa	3	3	3	3	3	3	3	3	2	2	4	4
CYC_HUMAN	Cytochrome c	12 kDa		1	2	2		1	2	3	2	2	2	2
COX2_HUMAN	Cytochrome c oxidase subunit 2	26 kDa							2	2		1	2	2
COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	20 kDa	2	2		1	2	2	3	3	2	2	3	3
COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial precursor	17 kDa	3	4	3	3	3	3	2	3	2	2	4	5
COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial precursor	14 kDa	2	2		1	2	2		1	2	2	2	2
CX6B1_HUMAN	Cytochrome c oxidase subunit VIb isoform 1	10 kDa	2	2	2	2	2	2	2	2	2	2	3	3
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	532 kDa	26	27	28	28	15	15	29	29	31	31	13	13
DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2	71 kDa	3	3	3	3	3	3	3	3	3	3	3	3
DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate chain 2	54 kDa	3	3		1	2	2	3	3	3	3		1
CYFP1_HUMAN	Cytoplasmic FMR1-interacting protein 1	145 kDa	2	2		1		1						
CKAP4_HUMAN	Cytoskeleton-associated protein 4	66 kDa	7	7	6	6	7	7	7	7	6	6	10	10
AMPL_HUMAN	Cytosol aminopeptidase	56 kDa	6	6	7	7	5	5	4	4	5	5	4	4
BACH_HUMAN	Cytosolic acyl coenzyme A thioester hydrolase	42 kDa	4	4	2	2	4	4	3	3	2	2	2	2
CNDP2_HUMAN	Cytosolic non-specific dipeptidase	53 kDa		1		1	3	3	2	2		1		1
5NTC_HUMAN	Cytosolic purine 5'-nucleotidase	65 kDa	2	2		1		1						
SERA_HUMAN	D-3-phosphoglycerate dehydrogenase	57 kDa	7	8	8	9	7	8	7	8	7	8	6	7
DAZP1_HUMAN	DAZ-associated protein 1	43 kDa	3	3	3	3	2	2	2	2	2	2	2	2
DCNL1_HUMAN	DCN1-like protein 1	30 kDa		1	2	2		1	2	2		1	2	2
ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	36 kDa	4	4	3	3	5	5	3	3	4	4	6	6
P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthetase	87 kDa	2	2	2	2	2	2	3	3	2	2	4	4
DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor	27 kDa	4	4	4	4	4	4	3	4	5	5	4	4
DCD_HUMAN	Dermeidin precursor	11 kDa	2	2										
DEST_HUMAN	Destrin	19 kDa	2	2		1								

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
DRG1_HUMAN	Developmentally-regulated GTP-binding protein 1	41 kDa			2	2		1						
DYR_HUMAN	Dihydrofolate reductase	21 kDa	2	2	2	2	2	2	2	2	2	2	2	2
DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial precursor	54 kDa	3	3	3	3	4	4	3	3	3	3	5	5
ODP2_HUMAN	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial precursor	66 kDa										1	2	2
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2	62 kDa	6	6	6	6	6	6	7	7	7	7	6	6
DPP3_HUMAN	Dipeptidyl-peptidase 3	83 kDa	2	2	2	2	2	2		1	2	2		1
DDB1_HUMAN	DNA damage-binding protein 1	127 kDa								1		1	2	2
MSH2_HUMAN	DNA mismatch repair protein Msh2	105 kDa		1		1	3	3						
MSH6_HUMAN	DNA mismatch repair protein MSH6	153 kDa	3	3	3	3		1	3	3		1		
MCM2_HUMAN	DNA replication licensing factor MCM2	102 kDa	8	8	9	9	7	7	9	9	8	8	9	9
MCM3_HUMAN	DNA replication licensing factor MCM3	91 kDa	5	6	6	6	3	3	4	4	5	5	5	5
MCM4_HUMAN	DNA replication licensing factor MCM4	97 kDa	3	3	5	5	4	5	4	4	3	3	3	3
MCM5_HUMAN	DNA replication licensing factor MCM5	82 kDa	6	6	4	4		1	3	3	4	4		1
MCM6_HUMAN	DNA replication licensing factor MCM6	93 kDa	4	4	4	4	3	3	3	3	2	2	4	4
MCM7_HUMAN	DNA replication licensing factor MCM7	81 kDa	7	7	6	6	4	4	5	5	4	4	5	5
APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase	36 kDa	4	4	6	6	3	3	6	6	6	6	3	3
DBPA_HUMAN	DNA-binding protein A	40 kDa	2	2	2	2		1	2	2		1		1
PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit	469 kDa	12	12	11	11			10	10	14	14		
DNJA1_HUMAN	DnaJ homolog subfamily A member 1	45 kDa	5	6	6	7	5	6	6	7	6	7	5	6
DNJA2_HUMAN	DnaJ homolog subfamily A member 2	46 kDa	2	2	3	3	2	2	3	3	2	2		1
DNJB1_HUMAN	DnaJ homolog subfamily B member 1	38 kDa	3	3	5	5	2	2	3	3	3	3	2	2
DJB11_HUMAN	DnaJ homolog subfamily B member 11 precursor	41 kDa	2	2		1	2	2		1		1	3	3
DNJC7_HUMAN	DnaJ homolog subfamily C member 7	56 kDa											1	2
DNJC8_HUMAN	DnaJ homolog subfamily C member 8	30 kDa	2	2	3	3			2	2	2	2		1
DNJC9_HUMAN	DnaJ homolog subfamily C member 9	30 kDa	3	3	3	3	2	2	3	3	3	3	3	3

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	49 kDa		1	3	3	4	4	3	3	3	3	4	4
RIB2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor	69 kDa	2	2		1	3	3	2	2	2	2	4	4
RIB1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	69 kDa	7	7	7	7	5	5	6	6	7	7	6	6
STAU1_HUMAN	Double-stranded RNA-binding protein Staufen homolog 1	63 kDa	5	5	4	4	3	3	3	3	4	4	3	3
DSRAD_HUMAN	Double-stranded RNA-specific adenosine deaminase	136 kDa	2	2		1				1			2	2
DREB_HUMAN	Drebrin	71 kDa	3	3	3	3	3	3	3	3	3	3	3	3
DBNL_HUMAN	Drebrin-like protein	48 kDa	4	4	4	4	3	3	4	4	3	3	3	3
MP2K2_HUMAN	Dual specificity mitogen-activated protein kinase kinase 2	44 kDa							2	3		1		1
DCTN1_HUMAN	Dynactin subunit 1	142 kDa			2	2				1	3	3		
DCTN2_HUMAN	Dynactin subunit 2	44 kDa	3	3	5	5	5	5	5	5	4	5	4	4
DNM1L_HUMAN	Dynamamin-1-like protein	82 kDa	4	4	3	3	4	4	4	4	4	5	2	2
DYN2_HUMAN	Dynamamin-2	98 kDa	2	2	3	3	2	2	2	2		1	2	2
DYL1_HUMAN	Dynein light chain 1, cytoplasmic	10 kDa	2	3		2	2	3						
DYL2_HUMAN	Dynein light chain 2, cytoplasmic EGF-like repeat and discoidin I-like domain-containing protein 3 precursor	10 kDa							2	3	2	2	2	2
EDIL3_HUMAN		54 kDa			2	2								
EHD1_HUMAN	EH domain-containing protein 1	61 kDa	6	6	8	8	6	6	8	8	7	7	7	7
EHD2_HUMAN	EH domain-containing protein 2	61 kDa	3	3	3	3	2	2	2	2	2	2	2	2
EHD4_HUMAN	EH domain-containing protein 4	61 kDa							2	2				
ELAV1_HUMAN	ELAV-like protein 1	36 kDa	4	4	2	2	3	3	4	4	3	3	5	5
ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial precursor	35 kDa	5	5	4	4	4	4	3	3	5	5	4	4
ETFB_HUMAN	Electron transfer flavoprotein subunit beta	28 kDa	2	2		1	3	3		1			2	2
EF1A1_HUMAN	Elongation factor 1-alpha 1	50 kDa	19	26	18	27	14	18	19	29	17	24	15	17
EF1B_HUMAN	Elongation factor 1-beta	25 kDa							2	2		1	2	2
EF1D_HUMAN	Elongation factor 1-delta	31 kDa	5	5	5	5	5	5	5	5	5	5	5	5

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
EF1G_HUMAN	Elongation factor 1-gamma	50 kDa	11	11	10	10	9	9	11	11	11	11	9	9
EF2_HUMAN	Elongation factor 2	95 kDa	32	38	27	33	19	23	31	37	30	36	20	25
EFTU_HUMAN	Elongation factor Tu, mitochondrial precursor	50 kDa	7	7	7	8	9	9	6	6	6	6	11	12
EMD_HUMAN	Emerin	29 kDa	2	2		1			2	2		1		
SH3G1_HUMAN	Endophilin-A2	41 kDa	4	4	3	3	4	4	3	3	4	4	2	2
ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1	107 kDa		1		1	2	2	2	2		1	4	4
ERP29_HUMAN	Endoplasmic reticulum protein ERp29 precursor	29 kDa	6	7	6	7	7	8	7	8	6	7	7	8
ENPL_HUMAN	Endoplasmic precursor	92 kDa	27	30	26	28	27	29	24	27	25	28	31	35
ERH_HUMAN	Enhancer of rudimentary homolog	12 kDa	2	2	2	2	3	3	2	2	2	2	3	3
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial precursor	31 kDa	3	4	5	6	5	6	3	4	4	5	5	6
EPHA2_HUMAN	Ephrin type-A receptor 2 precursor	108 kDa		1	3	3	2	2	3	3	3	3	5	5
ES8L2_HUMAN	Epidermal growth factor receptor kinase substrate 8-like protein 2	81 kDa	2	2	2	2		1	2	2		2		1
EGFR_HUMAN	Epidermal growth factor receptor precursor	134 kDa								1	2	2		1
EP15R_HUMAN	Epidermal growth factor receptor substrate 15-like 1	94 kDa		1		1	2	2						
NPC2_HUMAN	Epididymal secretory protein E1 precursor	17 kDa		1		1	2	2		1		1	2	2
EPIPL_HUMAN	Epiplakin	553 kDa	4	4	3	3	4	4	7	8	6	6	7	8
ERLN1_HUMAN	Erlin-1	39 kDa								1	2	2	4	4
ERO1A_HUMAN	ERO1-like protein alpha precursor	54 kDa	2	2	3	3	4	4	2	2	3	3	4	4
STOM_HUMAN	Erythrocyte band 7 integral membrane protein	32 kDa	2	2	2	2	2	3	2	2	2	2	2	2
ETHE1_HUMAN	ETHE1 protein, mitochondrial precursor	28 kDa	2	2	2	2		1		1		1	2	2
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I	46 kDa	14	14	14	14	11	12	17	20	13	16	11	13
IF4A2_HUMAN	Eukaryotic initiation factor 4A-II	46 kDa		1	2	2		1	2	2		1		1
IF4A3_HUMAN	Eukaryotic initiation factor 4A-III	47 kDa	3	3	2	2	3	4	2	2	2	2	4	4
IF1AX_HUMAN	Eukaryotic translation initiation factor 1A, X-chromosomal	16 kDa												
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1	36 kDa	4	4	4	4	4	4	4	4	4	4	4	4

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2	38 kDa	2	2	4	4	3	3	3	3	2	2		1
IF2G_HUMAN	Eukaryotic translation initiation factor 2 subunit 3	51 kDa	2	2	3	3	3	3	3	3	2	2	4	4
EIF2A_HUMAN	Eukaryotic translation initiation factor 2A	65 kDa		1	2	2	2	2		1	2	2		1
EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A	167 kDa	7	7	7	7	5	5	7	7	7	7	6	6
EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B	92 kDa	3	3	4	4	3	3	3	3	3	3	3	3
EIF3C_HUMAN	Eukaryotic translation initiation factor 3 subunit C	105 kDa							2	2		1		
EIF3D_HUMAN	Eukaryotic translation initiation factor 3 subunit D	64 kDa		1	3	3		1						
EIF3E_HUMAN	Eukaryotic translation initiation factor 3 subunit E	52 kDa	2	2	2	2	3	3		1	3	3	3	3
IF3EI_HUMAN	Eukaryotic translation initiation factor 3 subunit E-interacting protein	67 kDa	4	4	5	5	3	3	7	7	4	4	4	4
EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F	38 kDa		2	2	2	2	2						
EIF3G_HUMAN	Eukaryotic translation initiation factor 3 subunit G	36 kDa		1				1		1	2	2		1
EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I	37 kDa	2	2		1	2	2		1		1		1
EIF3K_HUMAN	Eukaryotic translation initiation factor 3 subunit K	25 kDa			2	2								
EIF3M_HUMAN	Eukaryotic translation initiation factor 3 subunit M	43 kDa		1	2	2		1		1		1	2	2
IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	176 kDa	5	5	5	5	6	6	6	6	6	6	5	5
IF4E_HUMAN	Eukaryotic translation initiation factor 4E	25 kDa								1	2	2		
IF4H_HUMAN	Eukaryotic translation initiation factor 4H	27 kDa	3	3	3	3	3	3	3	3	3	3	4	4
IF5_HUMAN	Eukaryotic translation initiation factor 5	49 kDa									2	2		
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1	17 kDa	4	5	3	3	2	2	4	4	3	3	2	2
IF6_HUMAN	Eukaryotic translation initiation factor 6	27 kDa	5	6	4	5	5	6	6	7	5	6	5	6
XPO1_HUMAN	Exportin-1	123 kDa	5	7	5	5	4	5	4	5	5	6	5	5
XPO2_HUMAN	Exportin-2	110 kDa	18	22	15	18	11	14	17	20	15	18	12	15
ESYT1_HUMAN	Extended-synaptotagmin-1	123 kDa	5	5	5	5	3	3	5	5	5	5	7	7
EZRI_HUMAN	Ezrin	69 kDa	11	12	11	13	9	10	10	12	11	12	9	11
NHERF_HUMAN	Ezrin-radixin-moesin-binding phosphoprotein 50	39 kDa	2	2	2	2	2	2	2	2	2	2	3	3

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
SP16H_HUMAN	FACT complex subunit SPT16	120 kDa	6	6	7	7	3	3	5	5	6	6	4	4
SSRP1_HUMAN	FACT complex subunit SSRP1	81 kDa		1	2	2		1		1		1		1
CAZA1_HUMAN	F-actin-capping protein subunit alpha-1	33 kDa	5	5	5	5	6	6	5	5	4	4	5	5
CAPZB_HUMAN	F-actin-capping protein subunit beta	31 kDa	8	8	5	6	5	5	6	7	7	8	7	8
FUBP1_HUMAN	Far upstream element-binding protein 1	68 kDa	7	7	4	4	5	5	4	4	3	3	6	6
FUBP2_HUMAN	Far upstream element-binding protein 2	73 kDa	10	10	10	10	10	10	8	8	10	10	13	13
FUBP3_HUMAN	Far upstream element-binding protein 3	62 kDa	2	2	2	2	2	2		1		1	3	3
FPPS_HUMAN	Farnesyl pyrophosphate synthetase	41 kDa	4	4	3	3	2	2	4	4	4	5	3	3
FSCN1_HUMAN	Fascin	55 kDa	5	5	4	4	4	4	5	5	5	5	5	5
FAS_HUMAN	Fatty acid synthase	273 kDa	35	35	34	37	24	24	39	41	36	37	29	30
FERM2_HUMAN	Fermitin family homolog 2	78 kDa	2	2	4	4	2	2	2	2	3	3	3	3
FINC_HUMAN	Fibronectin precursor	263 kDa	15	16	12	12	2	2	20	21	19	19	3	3
FLNA_HUMAN	Filamin-A	281 kDa	79	87	75	82	66	74	73	79	70	77	71	76
FLNB_HUMAN	Filamin-B	278 kDa	50	53	47	50	46	48	47	51	49	53	52	55
FLNC_HUMAN	Filamin-C	291 kDa	12	12	12	12	7	7	15	15	9	9	9	9
FKBP3_HUMAN	FK506-binding protein 3	25 kDa		1		1		1	2	2		1		1
FKBP4_HUMAN	FK506-binding protein 4	52 kDa	8	9	9	9	8	9	7	8	7	8	9	9
FKBP8_HUMAN	FK506-binding protein 8	38 kDa	2	2		1		1	2	2	2	2	3	3
FEN1_HUMAN	Flap endonuclease 1	43 kDa	4	4	5	5	3	3	5	5	3	3	2	2
BLVRB_HUMAN	Flavin reductase	22 kDa								1	2	2		1
FHL2_HUMAN	Four and a half LIM domains protein 2	32 kDa	3	3	3	3	3	3	3	3	4	4	3	3
FXR1_HUMAN	Fragile X mental retardation syndrome-related protein 1	70 kDa	2	3	2	3	3	4	2	3	2	3	3	4
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	39 kDa	15	18	15	18	15	16	17	20	14	16	14	17
ALDOC_HUMAN	Fructose-bisphosphate aldolase C	39 kDa		2	2	3		2	2	3	2	3		2
FUMH_HUMAN	Fumarate hydratase, mitochondrial precursor	55 kDa	3	3	2	2		1	2	2	2	2	4	4

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
GSPT1_HUMAN	G1 to S phase transition protein 1 homolog	56 kDa	2	2	2	2			2	2	2	2		1
LEG1_HUMAN	Galectin-1	15 kDa	7	8	7	8	7	8	7	8	8	9	8	8
LG3BP_HUMAN	Galectin-3-binding protein precursor	65 kDa	3	3	3	3	4	4		1	3	3	7	7
ENOG_HUMAN	Gamma-enolase	47 kDa	6	7	6	9	7	7	5	5	6	7	5	5
OFUT1_HUMAN	GDP-fucose protein O-fucosyltransferase 1 precursor	44 kDa		1	2	2	3	3	2	2	2	2	4	4
FCL_HUMAN	GDP-L-fucose synthetase	36 kDa		1	2	2								
GELS_HUMAN	Gelsolin precursor	86 kDa	6	6	5	5	4	4	6	6	4	4	4	4
TF3C4_HUMAN	General transcription factor 3C polypeptide 4	92 kDa	2	3		2								
GTF2I_HUMAN	General transcription factor II-I	112 kDa	2	2	5	5	2	2	3	3	2	2		1
GNPI_HUMAN	Glucosamine-6-phosphate isomerase	33 kDa	4	4	3	3	4	4	3	3	3	3	3	3
GFPT1_HUMAN	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	79 kDa	3	3	2	2			3	3	2	2		
G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	59 kDa	9	9	9	9	8	8	9	9	8	8	7	7
G6PI_HUMAN	Glucose-6-phosphate isomerase	63 kDa	10	11	11	13	11	12	13	14	12	13	10	11
GLU2B_HUMAN	Glucosidase 2 subunit beta precursor	59 kDa	9	10	7	8	7	8	7	7	7	8	8	9
DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial precursor	61 kDa	5	5	5	5	5	5	5	5	4	4	8	8
GLSK_HUMAN	Glutaminase kidney isoform, mitochondrial precursor	73 kDa		1		1	3	3		1		1	2	2
SYQ_HUMAN	Glutamyl-tRNA synthetase	88 kDa	2	2	2	2	3	3	3	3	2	2	2	2
GLRX5_HUMAN	Glutaredoxin-related protein 5	17 kDa		1	2	2		1		1		1	2	2
GSHR_HUMAN	Glutathione reductase, mitochondrial precursor	56 kDa		1	2	2		1						
GSTK1_HUMAN	Glutathione S-transferase kappa 1	25 kDa	2	2	2	2	2	2	2	2	2	2	2	2
GSTP1_HUMAN	Glutathione S-transferase P	23 kDa	7	10	7	10	7	9	7	10	7	10	7	8
GSHB_HUMAN	Glutathione synthetase	52 kDa								1		1	2	2
GSTO1_HUMAN	Glutathione transferase omega-1	28 kDa	2	2		1		1	2	2	2	2	2	2
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	36 kDa	21	27	16	21	19	25	17	24	15	21	18	21
GPDM_HUMAN	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor	81 kDa		1			2	2				1		1

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
GCSH_HUMAN	Glycine cleavage system H protein, mitochondrial precursor	19 kDa	2	2	2	2	2	2	2	2	2	2	2	2
PYGL_HUMAN	Glycogen phosphorylase, liver form	97 kDa	3	3	3	3		1	3	3	2	2		1
GT251_HUMAN	Glycosyltransferase 25 family member 1 precursor	72 kDa	2	2	2	2	2	2	2	2	2	2	2	2
NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase 1	57 kDa	2	2	2	2		1	2	2	2	2		1
SYG_HUMAN	Glycyl-tRNA synthetase	83 kDa	5	5	5	5	3	4	6	6	5	5	6	7
GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase	36 kDa	2	2		1	2	2	2	2	2	2	2	2
GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing]	77 kDa	5	5	6	6	3	3	6	6	5	5	4	4
GRN_HUMAN	Granulins precursor	64 kDa		1				4	5			1	4	5
GRB2_HUMAN	Growth factor receptor-bound protein 2	25 kDa			2	2		1						
RAN_HUMAN	GTP-binding nuclear protein Ran	24 kDa	6	6	5	5	6	6	5	5	5	5	7	7
SAR1A_HUMAN	GTP-binding protein SAR1a	22 kDa			2	2				1	2	2		1
GNAI2_HUMAN	Guanine nucleotide-binding protein G(i), alpha-2 subunit	40 kDa	5	5	6	6		1	5	5	5	5	4	4
GBG12_HUMAN	Guanine nucleotide-binding protein G(l)/G(s)/G(o) subunit gamma-12 precursor	8 kDa	2	2	2	2	2	2		1	2	2	2	2
GBB1_HUMAN	Guanine nucleotide-binding protein G(l)/G(s)/G(t) subunit beta-1	37 kDa	5	5	6	6	8	9	7	7	6	6	8	9
GBB2_HUMAN	Guanine nucleotide-binding protein G(l)/G(s)/G(t) subunit beta-2	37 kDa	3	3	3	3	3	3	3	3	3	3	5	5
GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	111 kDa	5	5	3	3	4	4	3	3	3	3	2	2
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1	35 kDa	9	9	9	9	8	8	8	9	8	8	11	11
GBP3_HUMAN	Guanylate-binding protein 3	64 kDa								1	2	2		1
HSP71_HUMAN	Heat shock 70 kDa protein 1	70 kDa	25	27	24	28	23	24	22	23	23	24	23	25
HSP74_HUMAN	Heat shock 70 kDa protein 4	94 kDa	15	16	15	16	16	16	20	22	16	18	18	18
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	71 kDa	31	38	32	38	30	34	30	35	30	35	31	37
HSBP1_HUMAN	Heat shock factor-binding protein 1	9 kDa	3	4	2	3	2	3	2	3	2	2		2
HS105_HUMAN	Heat shock protein 105 kDa	97 kDa	8	9	10	10	9	9	8	8	8	9	7	7
TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondrial precursor	80 kDa	4	4	6	6	6	6	4	4	4	4	6	6

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
HSPB1_HUMAN	Heat shock protein beta-1	23 kDa	8	9	7	8	6	6	7	8	7	8	6	6
HS90A_HUMAN	Heat shock protein HSP 90-alpha	85 kDa	23	27	22	25	21	23	20	25	19	22	17	19
HS90B_HUMAN	Heat shock protein HSP 90-beta	83 kDa	39	46	32	38	31	35	34	40	32	38	34	41
HN1_HUMAN	Hematological and neurological expressed 1 protein	16 kDa	2	2	2	2	2	2	2	2	2	2	2	2
HN1L_HUMAN	Hematological and neurological expressed 1-like protein	20 kDa	2	2	2	2	3	3	3	3	2	2	3	3
HEBP2_HUMAN	Heme-binding protein 2	23 kDa											2	2
HDGF_HUMAN	Hepatoma-derived growth factor	27 kDa	4	4	5	5	4	4	3	3	5	5	5	5
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B	36 kDa	2	2	2	2	4	4	4	4	3	3	3	3
ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0	31 kDa		1	2	2	2	2		1	2	2	3	3
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1	39 kDa	8	8	7	7	8	8	7	7	7	7	9	9
ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3	40 kDa	5	5	4	4	4	4	4	4	5	5	6	6
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	38 kDa	8	8	8	8	8	8	7	7	8	8	8	9
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like	46 kDa	4	4	3	3	3	4	4	4	3	3	4	5
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	46 kDa	3	3	3	3	3	3	3	3	3	3	3	4
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G	42 kDa	2	2	2	2	4	4	2	2	2	2	3	3
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	49 kDa	7	9	9	10	7	9	7	9	6	8	7	9
HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	49 kDa	2	3	2	2	2	3	2	3	2	3	2	3
HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3	37 kDa	3	4	3	4	3	4	3	4	3	4	4	5
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	51 kDa	14	16	15	17	14	17	14	17	14	17	13	16
HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	60 kDa	13	14	8	9	11	12	10	11	8	9	11	12
HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M	78 kDa	11	12	11	12	13	14	12	13	10	11	14	15
HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q	70 kDa	8	9	8	9	7	8	8	9	6	7	8	9
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R	71 kDa	3	3	3	3	4	4	3	3	3	3	3	3
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	91 kDa	12	13	11	12	9	10	11	12	13	14	11	12
HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1	96 kDa	2	2	3	3		1	3	3	3	3	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	85 kDa	5	5	5	6	8	8	4	4	6	6	7	7
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1	37 kDa	13	15	11	13	13	16	11	13	10	12	11	14
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	34 kDa	7	7	7	7	6	7	6	6	4	4	5	5
HXK1_HUMAN	Hexokinase-1	102 kDa	2	2	2	2			2	2		1		1
HMGB1_HUMAN	High mobility group protein B1	25 kDa	3	4		1			2	2	2	2		
HMGB2_HUMAN	High mobility group protein B2	24 kDa	3	3		1			2	2		1		
HINT1_HUMAN	Histidine triad nucleotide-binding protein 1	14 kDa	3	3	3	3	2	2	3	3	3	3	2	2
HINT2_HUMAN	Histidine triad nucleotide-binding protein 2	17 kDa										1	2	2
SYHC_HUMAN	Histidyl-tRNA synthetase, cytoplasmic	57 kDa	3	3	4	4	4	4	6	6	5	5	4	4
HAT1_HUMAN	Histone acetyltransferase type B catalytic subunit	50 kDa	4	4	5	5	4	4	3	3	4	4	5	5
HDAC2_HUMAN	Histone deacetylase 2	55 kDa	2	2	2	2	2	2	2	2	2	2	3	3
H13_HUMAN	Histone H1.3	22 kDa							1			1	2	2
H2A1D_HUMAN	Histone H2A type 1-D	14 kDa												
H2A2A_HUMAN	Histone H2A type 2-A	14 kDa												
H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I	14 kDa												
H2B1D_HUMAN	Histone H2B type 1-D	14 kDa							2	3	2	3	3	4
H33_HUMAN	Histone H3.3	15 kDa	4	5	4	5	3	3	4	5	4	5	4	5
H4_HUMAN	Histone H4	11 kDa	9	10	9	9	8	8	10	10	10	10	10	10
RBBP4_HUMAN	Histone-binding protein RBBP4	48 kDa	5	5	3	3	4	4	3	3	2	2	3	3
RBBP7_HUMAN	Histone-binding protein RBBP7	48 kDa	2	2					1	2	2	3	3	3
1A02_HUMAN	HLA class I histocompatibility antigen, A-2 alpha chain precursor	41 kDa	9	9	9	9	10	11	10	10	11	11	10	10
1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain precursor	40 kDa	3	3	3	3	4	4	4	4	3	3	4	4
HCFC1_HUMAN	Host cell factor	209 kDa	2	2	3	3	2	2	2	2	3	3	3	3
F10A1_HUMAN	Hsc70-interacting protein	41 kDa	2	2	3	3	2	2	4	4	2	2	3	3
CDC37_HUMAN	Hsp90 co-chaperone Cdc37	44 kDa	4	4	5	5	6	6	6	6	6	6	4	4

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor	34 kDa		1		1	2	2		1		1	3	3
HMCS1_HUMAN	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	57 kDa	2	2	3	3		1	5	5	3	3		1
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase	25 kDa	8	9	8	9	8	8	8	9	8	9	8	8
HYOU1_HUMAN	Hypoxia up-regulated protein 1 precursor	111 kDa	6	7	3	4	6	7	6	7	6	7	9	11
TIM50_HUMAN	Import inner membrane translocase subunit TIM50, mitochondrial precursor	40 kDa											2	2
IMA1_HUMAN	Importin subunit alpha-1	60 kDa								1		1	2	2
IMA2_HUMAN	Importin subunit alpha-2	58 kDa	8	9	9	10	7	7	9	10	9	10	7	7
IMA4_HUMAN	Importin subunit alpha-4	58 kDa							2	3		2		2
IMA7_HUMAN	Importin subunit alpha-7	60 kDa	3	3	2	2	3	3	3	4	3	3	2	2
IMB1_HUMAN	Importin subunit beta-1	97 kDa	9	10	10	13	10	10	10	12	10	11	10	11
IMB3_HUMAN	Importin subunit beta-3	124 kDa	7	7	4	4	4	4	5	5	3	3	2	2
IPO7_HUMAN	Importin-7	120 kDa	2	2	3	3	2	2	4	4	3	3	2	2
IPO9_HUMAN	Importin-9	116 kDa	2	2	2	2	2	2						
IPYR_HUMAN	Inorganic pyrophosphatase	33 kDa	7	7	7	7	5	5	7	7	6	6	6	6
IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase 2	56 kDa	7	7	4	4	3	3	7	7	5	5	6	6
IF2B1_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 1	63 kDa			2	2								
IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2	62 kDa	3	3	3	3	3	3	4	4	4	4	3	3
ITA3_HUMAN	Integrin alpha-3 precursor	119 kDa		1	4	4	6	6		1		1	3	3
ITA6_HUMAN	Integrin alpha-6 precursor	127 kDa	4	4	3	3	3	3	3	3	4	4	3	3
ITB1_HUMAN	Integrin beta-1 precursor	88 kDa	5	5	7	7	8	8	7	7	6	6	7	8
ILK_HUMAN	Integrin-linked protein kinase	51 kDa		1	2	2		1						
ICAM1_HUMAN	Intercellular adhesion molecule 1 precursor	58 kDa		1	2	2	2	2	2	2	2	2	2	2
UCRP_HUMAN	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein	18 kDa	3	3	2	2	3	3	2	2	3	3	4	4
MX1_HUMAN	Interferon-induced GTP-binding protein Mx1	76 kDa	3	3	2	2	3	3	5	5	7	7	6	6
IFIT1_HUMAN	Interferon-induced protein with tetratricopeptide repeats 1	55 kDa	5	5	7	7	3	3	4	4	7	8	6	6

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
IFIT2_HUMAN	Interferon-induced protein with tetratricopeptide repeats 2	55 kDa	3	3	2	2	3	3	3	3	6	6	9	9
IFIT3_HUMAN	Interferon-induced protein with tetratricopeptide repeats 3	56 kDa	8	8	7	7	6	6	6	6	9	9	9	9
E2AK2_HUMAN	Interferon-induced, double-stranded RNA-activated protein kinase	62 kDa			2	2			1	2	2	2	2	2
ILF2_HUMAN	Interleukin enhancer-binding factor 2	43 kDa	4	4	3	4	5	6	3	3	3	3	4	4
ILF3_HUMAN	Interleukin enhancer-binding factor 3	95 kDa	10	10	9	9	8	8	8	8	8	8	7	7
IREB1_HUMAN	Iron-responsive element-binding protein 1	98 kDa							2	2	2	2		
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic	47 kDa	2	2	2	2	3	3	3	3	3	3	4	4
IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial precursor	51 kDa	2	2	2	2	5	5	4	4		1	5	5
SYIC_HUMAN	Isoleucyl-tRNA synthetase, cytoplasmic	145 kDa	3	3	2	2	2	2	2	2	2	2	2	2
K1C10_HUMAN	Keratin, type I cytoskeletal 10	60 kDa	16	17	4	4	13	16	18	22	6	6	14	15
K1C14_HUMAN	Keratin, type I cytoskeletal 14	52 kDa	2	2				1						
K1C16_HUMAN	Keratin, type I cytoskeletal 16	51 kDa	2	2										
K1C17_HUMAN	Keratin, type I cytoskeletal 17	48 kDa	7	7	6	6	9	9	7	7	8	8	11	11
K1C18_HUMAN	Keratin, type I cytoskeletal 18	48 kDa	20	24	17	21	20	23	19	25	19	24	22	26
K1C9_HUMAN	Keratin, type I cytoskeletal 9	62 kDa	14	15	6	6	12	14	9	9		1	10	10
K2C1_HUMAN	Keratin, type II cytoskeletal 1	66 kDa	20	22	6	6	19	21	13	13	5	5	11	11
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	66 kDa	6	6	2	2	7	7	11	11	2	2	5	5
K2C6C_HUMAN	Keratin, type II cytoskeletal 6C	60 kDa	6	6		1		1						
K2C8_HUMAN	Keratin, type II cytoskeletal 8	54 kDa	35	42	31	34	39	44	31	37	32	36	36	41
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1	48 kDa	3	4	2	2			1	3	3	3		1
KTN1_HUMAN	Kinectin	156 kDa	2	2	2	2				1	2	2	2	2
KINH_HUMAN	Kinesin-1 heavy chain	110 kDa	5	5	6	6	7	7	7	7	8	8	6	6
LGUL_HUMAN	Lactoylglutathione lyase	21 kDa	3	4	3	4	2	3	3	4	3	4	3	4
LMNA_HUMAN	Lamin-A/C	74 kDa	31	32	33	35	35	37	33	34	30	31	36	38
LAP2A_HUMAN	Lamina-associated polypeptide 2 isoform alpha	75 kDa	6	6	5	5	4	4	6	6	2	2	3	3

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
LMNB1_HUMAN	Lamin-B1	66 kDa	18	19	15	15	19	22	16	17	14	15	20	23
LMNB2_HUMAN	Lamin-B2	68 kDa	5	5	4	4	10	10	3	3	5	5	9	10
LAMA5_HUMAN	Laminin subunit alpha-5 precursor	400 kDa	3	3	3	3	2	2		1	2	2	2	2
LAMB1_HUMAN	Laminin subunit beta-1 precursor	198 kDa	2	3	2	3	2	2		1		1	2	2
LAMC1_HUMAN	Laminin subunit gamma-1 precursor	178 kDa		1	3	3		1		1		1	2	2
LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial precursor	158 kDa	9	9	9	10	9	9	10	10	11	11	12	13
LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1	89 kDa	5	5	3	3		1	6	6	4	4	3	3
SYLC_HUMAN	Leucyl-tRNA synthetase, cytoplasmic	134 kDa	3	3	4	4		1	5	5	3	3	3	3
LKHA4_HUMAN	Leukotriene A-4 hydrolase	69 kDa		1	2	2		1	3	3	3	3		1
LASP1_HUMAN	LIM and SH3 domain protein 1	30 kDa	7	7	7	7	5	5	8	8	7	7	6	6
LIMA1_HUMAN	LIM domain and actin-binding protein 1	85 kDa	2	2		1		1		1		1		1
LMO7_HUMAN	LIM domain only protein 7	193 kDa											2	2
LDHA_HUMAN	L-lactate dehydrogenase A chain	37 kDa	16	20	14	18	13	17	15	19	15	19	13	17
LDHB_HUMAN	L-lactate dehydrogenase B chain	37 kDa	9	10	10	11	10	11	9	10	11	12	8	9
LONM_HUMAN	Lon protease homolog, mitochondrial precursor	106 kDa	4	4	2	2	5	5	3	3	2	2	6	6
ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3	80 kDa		1		1			2	2	2	2		1
ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	79 kDa	2	2	2	2	2	2	3	3	2	2	2	2
LA_HUMAN	Lupus La protein	47 kDa		1	3	3		1		1		1		1
LU_HUMAN	Lutheran blood group glycoprotein precursor	67 kDa	3	3	3	3	2	2	3	3	2	2	2	2
PPGB_HUMAN	Lysosomal protective protein precursor	54 kDa	3	3	3	3	2	2	3	3	4	4	3	3
SYK_HUMAN	Lysyl-tRNA synthetase	68 kDa	3	3	3	3	3	3	3	3	3	3	3	3
CAPG_HUMAN	Macrophage-capping protein	39 kDa	4	4	4	4	4	4	4	4	4	4	4	4
MVP_HUMAN	Major vault protein	99 kDa	9	9	8	8	8	8	6	6	8	8	8	8
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic	36 kDa	7	7	7	7	6	6	7	7	6	6	6	6
MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor	36 kDa	13	13	12	12	14	15	13	14	13	13	14	14

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
M6PBP_HUMAN	Mannose-6-phosphate receptor-binding protein 1	47 kDa	10	10	10	11	9	9	8	9	10	10	7	7
MRP_HUMAN	MARCKS-related protein	20 kDa	2	2	2	2	2	2	2	2	2	2	2	2
MATR3_HUMAN	Matrin-3	95 kDa	12	14	11	12	9	11	11	12	10	12	10	11
PGRC1_HUMAN	Membrane-associated progesterone receptor component 1	22 kDa	3	3	3	3	3	3	4	4	2	3	5	5
MAT2B_HUMAN	Methionine adenosyltransferase 2 subunit beta	38 kDa	3	3	2	2	3	3	2	2	2	2	3	3
SYMC_HUMAN	Methionyl-tRNA synthetase, cytoplasmic	101 kDa	2	2	5	5		1	3	3	4	4	2	2
MCCB_HUMAN	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial precursor	61 kDa					2	2				1	2	2
MAP1B_HUMAN	Microtubule-associated protein 1B	271 kDa	3	3	6	6	3	3	7	7	5	5	2	2
MAP4_HUMAN	Microtubule-associated protein 4	121 kDa	12	13	13	14	11	12	13	14	11	12	14	15
MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1	30 kDa	7	8	5	7	4	5	4	6	6	7	4	6
TIM13_HUMAN	Mitochondrial import inner membrane translocase subunit Tim13	11 kDa					2	2						1
TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog	16 kDa	2	2	2	2	2	2	2	2	2	2	2	2
IMMT_HUMAN	Mitochondrial inner membrane protein	84 kDa	6	6	6	6	8	8	6	6	6	6	10	10
TOM70_HUMAN	Mitochondrial precursor proteins import receptor	67 kDa		1		1	2	2		1	2	2	2	2
BUB3_HUMAN	Mitotic checkpoint protein BUB3	37 kDa	4	4	5	5	6	6	4	4	3	3	4	4
MOES_HUMAN	Moesin	68 kDa	18	19	17	19	14	16	16	18	16	19	13	14
RAE1L_HUMAN	mRNA export factor	41 kDa		1		1	2	2		1		1	3	3
PUR6_HUMAN	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	47 kDa	7	7	8	9	4	4	7	7	7	7	5	5
MCA2_HUMAN	Multisynthetase complex auxiliary component p38	35 kDa	2	2		1		1	2	2	2	2		1
MYL6_HUMAN	Myosin light polypeptide 6	17 kDa	10	11	9	11	8	10	8	10	8	10	11	13
MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric	20 kDa	9	10	7	8	7	8	8	9	8	9	7	8
MYH10_HUMAN	Myosin-10	229 kDa	7	7	9	9	8	8	8	8	7	7	9	9
MYH9_HUMAN	Myosin-9	227 kDa	88	107	80	97	76	89	87	105	89	107	87	103
MYO1B_HUMAN	Myosin-Ib	132 kDa			2	2				1		1		
MYO1C_HUMAN	Myosin-Ic	118 kDa	5	5	4	4	4	4	5	5	6	6	5	5

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
MTPN_HUMAN	Myotrophin	13 kDa		1		1	2	2		1		1		1
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate	32 kDa	6	7	4	4	5	6	4	5	4	4	5	6
GNS_HUMAN	N-acetylglucosamine-6-sulfatase precursor	62 kDa	4	4	3	3	5	5	4	4	4	4	5	5
NQO1_HUMAN	NAD(P)H dehydrogenase [quinone] 1	31 kDa	2	2	2	2		1	2	2	2	2		1
MAOM_HUMAN	NAD-dependent malic enzyme, mitochondrial precursor	65 kDa		1		1	2	2						1
NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	13 kDa		1		1	3	3	2	2		1	3	3
NDUBA_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	21 kDa		1			2	2						
NDUV1_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial precursor	51 kDa											2	2
NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	30 kDa	2	2	2	2	4	4	2	2		1	5	5
NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor	24 kDa	2	2	2	2	2	2		1	2	2	2	2
NB5R3_HUMAN	NADH-cytochrome b5 reductase 3	34 kDa	2	2	3	3	2	2	3	3		1	2	2
NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	79 kDa	3	3	4	4	4	4	2	2	2	2	5	5
LTB4D_HUMAN	NADP-dependent leukotriene B4 12-hydroxydehydrogenase	36 kDa	4	4	3	4	4	4	4	5	5	6		1
NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha	23 kDa	4	4	4	4	4	4	4	4	4	4	4	4
NCKP1_HUMAN	Nck-associated protein 1	129 kDa								1	2	2		
UBC12_HUMAN	NEDD8-conjugating enzyme Ubc12	21 kDa	2	2	2	2				1	2	2		
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK	629 kDa	65	65	61	61	53	53	60	61	61	61	52	52
GANAB_HUMAN	Neutral alpha-glucosidase AB precursor	107 kDa	13	14	15	16	17	18	14	15	15	16	15	17
AAAT_HUMAN	Neutral amino acid transporter B(0)	57 kDa								1	2	2		1
NH2L1_HUMAN	NHP2-like protein 1	14 kDa	2	2	2	2	2	2	2	2	2	2	2	2
NIBL1_HUMAN	Niban-like protein 1	83 kDa	3	3	6	6	2	2	3	3		1		1
NNMT_HUMAN	Nicotinamide N-methyltransferase	30 kDa	5	6	5	6	5	5	5	6	5	6	5	5
NAMPT_HUMAN	Nicotinamide phosphoribosyltransferase	56 kDa	3	3		1		1	5	5	3	3		
PNCB_HUMAN	Nicotinate phosphoribosyltransferase	58 kDa									2	2		

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
NOMO2_HUMAN	Nodal modulator 2 precursor	139 kDa												
NONO_HUMAN	Non-POU domain-containing octamer-binding protein	54 kDa	10	11	7	8	13	15	10	11	7	8	12	15
NLTP_HUMAN	Non-specific lipid-transfer protein	59 kDa	2	2	3	3	2	2		1		1	2	2
SP100_HUMAN	Nuclear autoantigen Sp-100	100 kDa		1		1	2	2			2	2	2	2
NASP_HUMAN	Nuclear autoantigenic sperm protein	85 kDa	4	5	6	7	6	7	4	5	4	5	5	6
NCBP1_HUMAN	Nuclear cap-binding protein subunit 1	92 kDa	2	2	3	3	2	2	2	2	2	2	2	2
NUDC_HUMAN	Nuclear migration protein nudC	38 kDa	2	2	2	2	3	3	2	2	2	2		1
NUMA1_HUMAN	Nuclear mitotic apparatus protein 1	238 kDa	9	9	12	12	8	8	6	6	6	6	11	11
NU155_HUMAN	Nuclear pore complex protein Nup155	155 kDa	2	3	2	2	5	5	4	4	4	4	8	9
NUP93_HUMAN	Nuclear pore complex protein Nup93	93 kDa	3	3	3	3	3	3	3	3	3	3	5	5
HCC1_HUMAN	Nuclear protein Hcc-1	24 kDa		1		1	2	2		1		1	2	2
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1	36 kDa	6	6	6	6	5	5	7	7	7	7	6	6
NUCL_HUMAN	Nucleolin	77 kDa	10	12	13	16	11	13	13	16	12	14	13	15
TIA1_HUMAN	Nucleolysin TIA-1 isoform p40	43 kDa	2	2	2	2		1	2	2		1	2	2
NPM_HUMAN	Nucleophosmin	33 kDa	6	9	5	7	6	8	6	8	5	7	6	8
NUP53_HUMAN	Nucleoporin NUP53	35 kDa									2	2	2	2
TPR_HUMAN	Nucleoprotein TPR	266 kDa	6	6	6	6	9	10	4	4	4	4	9	9
NDKA_HUMAN	Nucleoside diphosphate kinase A	17 kDa	6	6	4	4	4	4	6	7	6	7	4	4
NDKB_HUMAN	Nucleoside diphosphate kinase B	17 kDa	2	3	2	3	2	3	2	3	2	3		2
NP1L1_HUMAN	Nucleosome assembly protein 1-like 1	45 kDa	4	4	4	5	4	4	4	4	4	4	4	4
NP1L4_HUMAN	Nucleosome assembly protein 1-like 4	43 kDa	4	4	6	6	5	6	6	6	7	7	4	4
NUDC2_HUMAN	NudC domain-containing protein 2	18 kDa	2	2		1		1	2	2				
OLA1_HUMAN	Obg-like ATPase 1	45 kDa	3	3	2	2	3	3	3	3	3	3	3	3
OGFR_HUMAN	Opioid growth factor receptor	73 kDa		1	2	2		1		1		1	2	2
OAT_HUMAN	Ornithine aminotransferase, mitochondrial precursor	49 kDa	4	4	5	5	6	6	3	3	4	4	6	6

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
OSTF1_HUMAN	Osteoclast-stimulating factor 1	24 kDa								1	2	2		1
PSPC1_HUMAN	Paraspeckle component 1	59 kDa			2	2								
PAXI_HUMAN	Paxillin	65 kDa	2	2	2	2	2	2	2	2	2	2	2	2
PSIP1_HUMAN	PC4 and SFRS1-interacting protein	60 kDa	3	3	3	3	2	2	3	4	3	3	3	3
PDL1_HUMAN	PDZ and LIM domain protein 1	36 kDa	7	7	6	6	7	7	7	7	7	7	6	6
PDLI5_HUMAN	PDZ and LIM domain protein 5	64 kDa	3	3				1	3	3	2	2		1
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A	18 kDa	10	11	11	12	10	11	10	11	9	10	9	10
PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor	23 kDa	10	10	9	9	9	9	10	10	10	10	10	10
PIN1_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	18 kDa		1		1		1		1		1	2	2
PIN4_HUMAN	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	14 kDa	2	2	2	2		1		1		1		1
PRDX1_HUMAN	Peroxiredoxin-1	22 kDa	10	11	10	11	8	8	9	10	9	10	8	9
PRDX2_HUMAN	Peroxiredoxin-2	22 kDa	3	3	3	3	2	2	4	4		1	3	3
PRDX4_HUMAN	Peroxiredoxin-4	31 kDa	2	2	2	2	3	3	2	2	2	2	3	3
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial precursor	22 kDa	7	8	6	6	5	6	7	8	6	6	6	7
PRDX6_HUMAN	Peroxiredoxin-6	25 kDa	8	8	8	9	7	7	7	7	6	6	6	6
DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2	80 kDa	5	5	4	4	9	9	4	4	5	5	8	8
PHF5A_HUMAN	PHD finger-like domain-containing protein 5A	12 kDa	2	2	2	2	2	2	2	2	2	2	2	2
MPCP_HUMAN	Phosphate carrier protein, mitochondrial precursor	40 kDa	4	4	4	4	2	2	2	2	3	3	3	4
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1	21 kDa	4	4	3	3	4	4	4	4	4	4	3	3
PICAL_HUMAN	Phosphatidylinositol-binding clathrin assembly protein	71 kDa		1	2	2			2	2		1	2	2
PGM1_HUMAN	Phosphoglucomutase-1	61 kDa	2	2	4	4	2	2		1	2	2		1
PGK1_HUMAN	Phosphoglycerate kinase 1	45 kDa	18	22	20	26	15	19	18	22	18	22	16	19
PGAM1_HUMAN	Phosphoglycerate mutase 1	29 kDa	9	11	11	13	9	11	10	12	10	12	9	11
PUR4_HUMAN	Phosphoribosylformylglycinamide synthase	145 kDa	4	4		1	2	2	3	3	3	3	2	2
SERC_HUMAN	Phosphoserine aminotransferase	40 kDa										1	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein	45 kDa	3	3	3	3		1	2	2	2	2		
PLST_HUMAN	Plastin-3	70 kDa	10	10	9	10	11	11	12	12	11	11	11	11
LIS1_HUMAN	Platelet-activating factor acetylhydrolase IB subunit alpha	47 kDa	4	4		1	3	3	2	2	2	2		1
PLEC1_HUMAN	Plectin-1	532 kDa	60	62	65	67	64	68	58	60	54	55	73	75
PODXL_HUMAN	Podocalyxin-like protein 1 precursor	56 kDa	2	2	2	2		1	2	2	2	2	2	2
PARP1_HUMAN	Poly [ADP-ribose] polymerase 1	113 kDa	7	7	7	7	2	2	6	6	7	7		
PCBP1_HUMAN	Poly(rC)-binding protein 1	37 kDa	8	9	6	7	6	6	6	6	7	7	6	6
PCBP2_HUMAN	Poly(rC)-binding protein 2	39 kDa	5	5	5	5	4	4	4	4	5	5	5	5
PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60	60 kDa	3	3	3	3	3	4	4	4	2	2	3	3
PABP1_HUMAN	Polyadenylate-binding protein 1	71 kDa	9	9	10	10	5	5	12	12	8	8	7	7
PTRF_HUMAN	Polymerase I and transcript release factor	43 kDa	3	5	3	5	3	5	5	7	2	4	2	3
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1	57 kDa	10	12	7	9	7	8	9	11	7	9	11	14
PFD2_HUMAN	Prefoldin subunit 2	17 kDa	2	2	2	2	2	2	3	3	2	2	2	2
PFD3_HUMAN	Prefoldin subunit 3	23 kDa	2	2	2	2		1	2	2	2	2		1
PFD5_HUMAN	Prefoldin subunit 5	17 kDa			2	3			2	3		1		1
PRP19_HUMAN	Pre-mRNA-processing factor 19	55 kDa	2	2		1	4	4	3	3	3	3	5	5
PRP6_HUMAN	Pre-mRNA-processing factor 6	107 kDa	2	2	2	2	2	2	2	2	2	2		1
PCYOX_HUMAN	Preylcysteine oxidase 1 precursor	57 kDa				1	2	2		1		1	2	2
PAWR_HUMAN	PRKC apoptosis WT1 regulator protein	37 kDa	2	2	2	2	2	2	2	2	2	2	2	2
SAP_HUMAN	Proactivator polypeptide precursor [Contains: Saposin-A	58 kDa	4	5	4	5	4	5	4	5	4	5	4	5
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17	72 kDa	8	8	7	7	6	6	7	7	7	7	8	8
DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46	117 kDa	3	3		1		1	2	2	2	2		1
DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5	69 kDa	13	13	12	12	11	11	14	14	13	13	14	15
HERC5_HUMAN	Probable E3 ubiquitin-protein ligase HERC5	117 kDa								1	3	3		1
SCPDH_HUMAN	Probable saccharopine dehydrogenase	47 kDa			2	2		1						

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
PML_HUMAN	Probable transcription factor PML	98 kDa					2	2				1	2	2
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor	84 kDa	3	3	5	5	5	5	3	3	4	4	6	6
PLOD2_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 precursor	85 kDa	6	6	7	8	8	8	5	5	6	6	9	9
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor	85 kDa	2	2	3	3	4	4	2	2	2	2	4	4
PROF1_HUMAN	Profilin-1	15 kDa	10	11	9	10	9	10	8	9	8	9	9	9
PROF2_HUMAN	Profilin-2	15 kDa								1		1	2	2
PDC61_HUMAN	Programmed cell death 6-interacting protein	96 kDa	7	7	5	5	4	4	6	6	6	6	5	5
PDCD5_HUMAN	Programmed cell death protein 5	14 kDa	2	2		1	2	2	3	3	2	2	2	2
PHB_HUMAN	Prohibitin	30 kDa	5	5	4	5	6	7	5	6	4	4	5	6
PHB2_HUMAN	Prohibitin-2	33 kDa	5	5	5	5	5	5	4	4	4	4	6	7
PCNA_HUMAN	Proliferating cell nuclear antigen	29 kDa	7	8	6	8	6	8	5	6	5	6	6	7
PA2G4_HUMAN	Proliferation-associated protein 2G4	44 kDa	8	8	8	8	7	7	5	5	6	6	6	6
P3H1_HUMAN	Prolyl 3-hydroxylase 1 precursor	83 kDa	2	2	3	3	4	4	2	2	3	3	4	4
P4HA1_HUMAN	Prolyl 4-hydroxylase subunit alpha-1 precursor	61 kDa	2	2		1	6	7	2	2		1	6	6
P4HA2_HUMAN	Prolyl 4-hydroxylase subunit alpha-2 precursor	61 kDa	4	4	2	2	6	6	4	4	4	4	8	8
PPCE_HUMAN	Prolyl endopeptidase	81 kDa	2	2	3	3	2	2	3	3	3	3	2	2
TEBP_HUMAN	Prostaglandin E synthase 3	19 kDa	4	4	4	4	2	2	4	4	4	4	2	2
PSME1_HUMAN	Proteasome activator complex subunit 1	29 kDa	8	8	8	8	6	6	7	7	7	7	10	10
PSME2_HUMAN	Proteasome activator complex subunit 2	27 kDa	5	8	4	7	3	6	5	8	4	7	4	7
PSME3_HUMAN	Proteasome activator complex subunit 3	30 kDa	2	2	3	3		1	2	3		1	2	2
PSA1_HUMAN	Proteasome subunit alpha type-1	30 kDa		1	2	2	2	2		1		1	2	2
PSA2_HUMAN	Proteasome subunit alpha type-2	26 kDa		1					2	2		1		1
PSA4_HUMAN	Proteasome subunit alpha type-4	29 kDa	4	5	4	5	4	5	3	3	3	4	3	4
PSA5_HUMAN	Proteasome subunit alpha type-5	26 kDa	3	3	4	4	3	3		1	3	3	6	6
PSA6_HUMAN	Proteasome subunit alpha type-6	27 kDa	6	6	4	4	6	6	6	6	6	6	5	5

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	
PSA7_HUMAN	Proteasome subunit alpha type-7	28 kDa	5	5	5	5	5	5	5	5	5	5	5	4	4
PSB1_HUMAN	Proteasome subunit beta type-1 precursor	26 kDa	4	5	3	3	3	3	3	3	3	3	3	3	3
PSB2_HUMAN	Proteasome subunit beta type-2	23 kDa	2	2	2	2	2	2	2	2	2	2	2	2	2
PSB4_HUMAN	Proteasome subunit beta type-4 precursor	29 kDa	4	4	4	4	5	5	3	3	3	3	3	3	3
PSB5_HUMAN	Proteasome subunit beta type-5 precursor	23 kDa	4	4	3	3	4	4	3	3	2	2	5	5	
PSB6_HUMAN	Proteasome subunit beta type-6 precursor	25 kDa		1		1		1	2	2		1	2	2	
PSB7_HUMAN	Proteasome subunit beta type-7 precursor	30 kDa			2	2	2	2		1	2	2	2	2	
PSB8_HUMAN	Proteasome subunit beta type-8 precursor	30 kDa		1			2	2				1	2	2	
ANM1_HUMAN	Protein arginine N-methyltransferase 1	42 kDa	5	5	3	3	3	4	4	4	4	5	7	7	
ANM5_HUMAN	Protein arginine N-methyltransferase 5	73 kDa							2	2		1			
ARMET_HUMAN	Protein ARMET precursor	20 kDa		1		1	3	3							
C10_HUMAN	Protein C10	13 kDa	2	2	2	2		1	4	4	2	2	2	2	
CN166_HUMAN	Protein C14orf166	28 kDa	2	2	3	3	2	2		1	2	2	2	2	
CNPY2_HUMAN	Protein canopy homolog 2 precursor	21 kDa	2	2		1	3	4	2	2	2	2	3	4	
CNPY3_HUMAN	Protein canopy homolog 3 precursor	31 kDa		1			2	2							
CDV3_HUMAN	Protein CDV3 homolog	27 kDa	2	2		2	3	3	2	2	3	3	3	3	
CUTA_HUMAN	Protein CutA precursor	19 kDa	2	2	2	2			2	2	2	2		1	
CYR61_HUMAN	Protein CYR61 precursor	42 kDa			2	2									
DEK_HUMAN	Protein DEK	43 kDa		1	2	2			4	4	3	3			
DIAP1_HUMAN	Protein diaphanous homolog 1	139 kDa	3	3	4	4		1	4	4	3	3	5	5	
PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor	57 kDa	18	19	19	20	21	23	17	19	18	19	21	23	
PDIA4_HUMAN	Protein disulfide-isomerase A4 precursor	73 kDa	21	21	19	19	18	18	17	17	17	17	21	21	
PDIA6_HUMAN	Protein disulfide-isomerase A6 precursor	48 kDa	12	13	11	13	13	16	12	14	10	11	14	16	
PDIA1_HUMAN	Protein disulfide-isomerase precursor	57 kDa	18	21	18	22	21	25	16	19	17	20	20	25	
PARK7_HUMAN	Protein DJ-1	20 kDa	7	9	6	7	8	9	6	7	7	9	5	5	

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
DPY30_HUMAN	Protein dpy-30 homolog	11 kDa		2	2	3		2	2	3		2		2
ENAH_HUMAN	Protein enabled homolog	67 kDa											3	3
F136A_HUMAN	Protein FAM136A	16 kDa					2	2				1		1
FA50A_HUMAN	Protein FAM50A	40 kDa							2	2		1		1
FA98B_HUMAN	Protein FAM98B	37 kDa	2	2	2	2		1		1		1		1
FATSO_HUMAN	Protein fatso	58 kDa									2	2		
K1967_HUMAN	Protein KIAA1967	103 kDa	3	3	2	2	6	6	3	3		1	6	6
NIPS1_HUMAN	Protein NipSnap1	33 kDa			2	2	3	3		1			2	2
NPS3A_HUMAN	Protein NipSnap3A	28 kDa		1		1	3	3		1		1	2	2
MYPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A	115 kDa	2	2		1		1		1	2	2		
PPIR7_HUMAN	Protein phosphatase 1 regulatory subunit 7	42 kDa		1	2	2		2						
PPM1G_HUMAN	Protein phosphatase 1G	59 kDa	2	2		1		1	2	2	2	2	2	2
PPME1_HUMAN	Protein phosphatase methylesterase 1	42 kDa	3	3	3	3		1	2	2	3	3		
RCC2_HUMAN	Protein RCC2	56 kDa								1	4	4		
S10AA_HUMAN	Protein S100-A10	11 kDa	4	4	4	4	4	4	4	4	4	4	4	4
S10AB_HUMAN	Protein S100-A11	12 kDa	6	8	7	8	5	6	7	9	7	9	5	5
SEC13_HUMAN	Protein SEC13 homolog	36 kDa		1	2	2		1						
SET_HUMAN	Protein SET	33 kDa	4	5	4	4	3	3	4	5	4	4	4	4
TFG_HUMAN	Protein TFG	43 kDa		1	2	2		1	2	2		1	2	2
SC23A_HUMAN	Protein transport protein Sec23A	86 kDa	4	4	5	5	3	3	5	5	5	5	4	4
SC31A_HUMAN	Protein transport protein Sec31A	133 kDa								1	2	2	2	2
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	25 kDa	3	3	2	2	2	2	3	3	3	3	2	2
PTMA_HUMAN	Prothymosin alpha [Contains: Thymosin alpha-1]	12 kDa	5	5	4	4	5	5	3	3	3	3	3	3
PSA_HUMAN	Puromycin-sensitive aminopeptidase	103 kDa	14	14	13	13	11	11	13	13	13	13	12	12
DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	91 kDa	3	3	6	6	5	5	5	5	5	5	5	5

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
RBM3_HUMAN	Putative RNA-binding protein 3	17 kDa	5	6	5	6	4	4	5	6	5	5	4	4
PDXK_HUMAN	Pyridoxal kinase	35 kDa	3	3	3	3	2	2	2	2	3	3		1
ODPA_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	43 kDa		1	3	3	4	4	2	2		1	4	4
ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	39 kDa	5	5	4	4	5	5	4	4	5	5	5	5
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2	58 kDa	31	42	30	39	27	34	30	40	31	41	30	38
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha	51 kDa	11	14	12	14	11	12	11	14	12	14	10	10
GDIB_HUMAN	Rab GDP dissociation inhibitor beta	51 kDa	7	8	5	6	6	7	6	7	6	7	5	6
RADI_HUMAN	Radixin	69 kDa		1	2	2	2	2	2	2		1	2	2
RAGP1_HUMAN	Ran GTPase-activating protein 1	64 kDa	3	3	4	4	4	4	3	3	4	4	3	3
RGPD4_HUMAN	RANBP2-like and GRIP domain-containing protein 4	198 kDa					2	2						
RANG_HUMAN	Ran-specific GTPase-activating protein	23 kDa	5	6	4	4	3	3	4	4	4	4	4	4
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1	52 kDa	6	6	6	7	3	4	6	7	4	4	6	6
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	189 kDa	23	24	22	24	15	16	23	24	24	25	17	18
RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 precursor	21 kDa	2	2	2	2		1	2	2	3	3	2	2
RB11A_HUMAN	Ras-related protein Rab-11A	24 kDa							2	2		1		1
RAB14_HUMAN	Ras-related protein Rab-14	24 kDa	6	6	5	5	4	4	2	2	2	2	2	2
RAB18_HUMAN	Ras-related protein Rab-18	23 kDa		1	2	2	2	2					2	2
RAB1B_HUMAN	Ras-related protein Rab-1B	22 kDa	3	3	2	2	2	2	8	8	7	7	8	9
RAB32_HUMAN	Ras-related protein Rab-32	25 kDa							2	2		1		1
RAB5C_HUMAN	Ras-related protein Rab-5C	23 kDa	2	2		1		1		1	3	3		1
RAB7A_HUMAN	Ras-related protein Rab-7a	23 kDa	3	3	3	3	2	2	2	2	2	2	2	2
RAP1B_HUMAN	Ras-related protein Rap-1b precursor	21 kDa	3	3	3	3	3	3	3	3	3	3	3	3
RRAS2_HUMAN	Ras-related protein R-Ras2 precursor	23 kDa	2	2	2	2	2	2	2	2	2	2	2	2
RCC1_HUMAN	Regulator of chromosome condensation	45 kDa		1				3	3				2	2
RFC4_HUMAN	Replication factor C subunit 4	40 kDa		1		1	2	2	2	2		1	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
RFA3_HUMAN	Replication protein A 14 kDa subunit	14 kDa							2	2				1
RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit	68 kDa	3	3	4	4	4	4	2	2	4	4	7	7
RCN1_HUMAN	Reticulocalbin-1 precursor	39 kDa	4	4	3	3	4	4	4	4	3	3	5	6
RCN2_HUMAN	Reticulocalbin-2 precursor	37 kDa		1	2	2	2	2				1	3	3
RTN4_HUMAN	Reticulon-4	130 kDa	2	2		1				1	2	2		
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1	23 kDa	2	2	3	3	2	2	2	2	2	2	3	3
RHG01_HUMAN	Rho GTPase-activating protein 1	50 kDa		1	2	2	2	2	2	2	2	2	2	2
RINI_HUMAN	Ribonuclease inhibitor	50 kDa	7	7	6	6	7	7	7	8	8	8	7	7
RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit	90 kDa	3	3	6	6		1	5	5	3	3	3	3
RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2	45 kDa	2	2	2	2	3	3	3	3	3	3	2	2
PRPS1_HUMAN	Ribose-phosphate pyrophosphokinase 1	35 kDa	3	3	3	3	2	2	3	3	3	3	2	2
RRBP1_HUMAN	Ribosome-binding protein 1	152 kDa	6	6	4	4	7	8	7	7	5	5	10	10
RBM12_HUMAN	RNA-binding protein 12	97 kDa		1	2	2		1		1	2	2	2	2
RBM14_HUMAN	RNA-binding protein 14	69 kDa		1	3	3	3	3	2	2	3	3	3	3
RBM39_HUMAN	RNA-binding protein 39	59 kDa	4	4	3	3	4	4	4	4	3	3		1
RBM8A_HUMAN	RNA-binding protein 8A	20 kDa	2	2		1		1	2	2		1		1
EWS_HUMAN	RNA-binding protein EWS	68 kDa		1		1		1		1		1	2	2
FUS_HUMAN	RNA-binding protein FUS	53 kDa	4	5	4	5	5	6	4	5	4	5	4	5
RALY_HUMAN	RNA-binding protein Raly	32 kDa	6	6	5	5	4	4	6	6	3	3	5	5
RUVB1_HUMAN	RuvB-like 1	50 kDa	6	6	7	7	6	6	6	6	7	7	7	7
RUVB2_HUMAN	RuvB-like 2	51 kDa	8	8	6	6	7	7	5	5	6	6	9	9
METK2_HUMAN	S-adenosylmethionine synthetase isoform type-2	44 kDa	2	2	2	2	2	2	2	2	2	2	2	2
SAMH1_HUMAN	SAM domain and HD domain-containing protein 1	72 kDa	6	6	6	6	7	7	6	6	7	7	6	6
SLN11_HUMAN	Schlafen family member 11	103 kDa							2	2		1		1
SCRN1_HUMAN	Secernin-1	46 kDa		1		1	2	2	2	2		1		1

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
SEPT2_HUMAN	Septin-2	41 kDa	6	7	5	5	6	6	5	5	5	6	5	5
SEPT7_HUMAN	Septin-7	51 kDa	5	5	8	8	4	4	5	5	5	5	5	5
SEPT9_HUMAN	Septin-9	65 kDa	6	7	6	6	4	4	6	6	6	6	5	5
SQSTM_HUMAN	Sequestosome-1	48 kDa	2	2		1		1	2	2		1	3	3
GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic	53 kDa	5	5	3	3	4	4	4	4	5	5	5	5
GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial precursor	56 kDa	4	5	6	7	4	5	6	7	3	4	7	8
PAK2_HUMAN	Serine/threonine-protein kinase PAK 2	58 kDa	2	2		1	2	2		1	2	2	3	3
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	65 kDa	14	15	11	11	11	12	13	14	11	12	13	13
PP2AA_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	36 kDa	7	7	4	4	6	6	5	5	7	7	7	7
PP2BA_HUMAN	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	59 kDa	2	2				1						
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	38 kDa	6	7	6	7	4	6	3	3	4	5	6	7
PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	37 kDa	2	2	2	2	2	2	2	2	2	2	2	2
STRAP_HUMAN	Serine-threonine kinase receptor-associated protein	38 kDa	2	2		1	2	2	2	2	2	2	2	2
SPB6_HUMAN	Serpin B6	43 kDa	3	3	2	2	5	5	2	2	3	3	2	2
SERPH_HUMAN	Serpin H1 precursor	46 kDa	12	13	8	9	10	12	10	11	10	11	14	15
ESTD_HUMAN	S-formylglutathione hydrolase	31 kDa	2	2	3	4	2	2	2	2	2	2		1
SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein	13 kDa	2	2		1	2	2	2	2		1	2	2
SIAS_HUMAN	Sialic acid synthase	40 kDa	4	4	4	4	3	3	4	4	4	4	3	3
SFXN1_HUMAN	Sideroflexin-1	36 kDa	3	3	3	3	3	3	3	3	2	2	3	3
SRP14_HUMAN	Signal recognition particle 14 kDa protein	15 kDa	2	2	2	2	2	2	2	2	2	2	2	2
STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta	87 kDa	4	4	5	6	4	4	5	5	6	6	5	5
STAT3_HUMAN	Signal transducer and activator of transcription 3	88 kDa	3	3	3	3		1	3	3	4	4		1
SSB_HUMAN	Single-stranded DNA-binding protein, mitochondrial precursor	17 kDa	3	3	3	3	3	3	3	3	3	3	4	4
SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein A	34 kDa	2	2	3	3	2	2		1	2	2	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
RUXE_HUMAN	Small nuclear ribonucleoprotein E	11 kDa	2	2		1	3	3	2	2	2	2	2	2
RUXF_HUMAN	Small nuclear ribonucleoprotein F	10 kDa	2	2	2	2	2	2	2	2	2	2	2	2
SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1	13 kDa	2	3		2		2						
SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2	14 kDa	2	2	2	2	2	2	2	2	2	2	2	2
SUMO2_HUMAN	Small ubiquitin-related modifier 2 precursor	11 kDa	2	2	2	2	2	2	2	2	2	2		1
MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase	31 kDa	2	2	3	3	2	2	2	2	2	2	3	3
SMU1_HUMAN	Smu-1 suppressor of mec-8 and unc-52 protein homolog	58 kDa				1	2	2					2	2
AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 precursor	113 kDa	10	10	10	10	7	7	9	9	9	9	8	8
AT1B3_HUMAN	Sodium/potassium-transporting ATPase subunit beta-3	32 kDa		1		1	2	2						
SORCN_HUMAN	Sorcin	22 kDa	2	2	2	3	2	2	2	2	2	2	2	2
SNX1_HUMAN	Sorting nexin-1	59 kDa		1	2	2	2	2	3	3	2	2	2	2
SNX3_HUMAN	Sorting nexin-3	19 kDa		1		1	2	2		1	3	3	3	3
SNX6_HUMAN	Sorting nexin-6	47 kDa		1	2	2	2	2	2	2	2	2	2	2
SPTA2_HUMAN	Spectrin alpha chain, brain	285 kDa	22	22	26	26	27	27	24	26	21	22	30	31
SPTB2_HUMAN	Spectrin beta chain, brain 1	275 kDa	22	22	19	20	26	28	22	23	20	21	29	30
SKP1_HUMAN	S-phase kinase-associated protein 1	19 kDa	3	4		1	4	4	3	4	3	4	4	4
UAP56_HUMAN	Spliceosome RNA helicase BAT1	49 kDa	4	4	3	3	5	5	4	4	7	7	6	6
SF01_HUMAN	Splicing factor 1	68 kDa		1	3	3	2	2		1	2	2	2	2
SF3A1_HUMAN	Splicing factor 3 subunit 1	89 kDa	3	4	4	5	5	6	4	5	2	3	6	7
SF3A3_HUMAN	Splicing factor 3A subunit 3	59 kDa								1	2	2		1
SF3B2_HUMAN	Splicing factor 3B subunit 2	98 kDa							2	2		1		1
SF3B3_HUMAN	Splicing factor 3B subunit 3	136 kDa	10	10	11	11	10	10	7	7	8	8	12	12
U2AF1_HUMAN	Splicing factor U2AF 35 kDa subunit	28 kDa	2	2	2	2	2	2	2	2		1		1
U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit	54 kDa	4	6	4	6	2	3	4	5	3	4	2	2
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1	28 kDa	5	5	7	7	7	7	6	6	7	7	5	5

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
SFRS2_HUMAN	Splicing factor, arginine/serine-rich 2	25 kDa	2	2	2	2	2	2	2	2	2	2	2	2
SFRS3_HUMAN	Splicing factor, arginine/serine-rich 3	19 kDa	4	4	3	3	3	3	3	3	3	3	2	2
SFRS6_HUMAN	Splicing factor, arginine/serine-rich 6	40 kDa		1		1	2	2	2	2	2	2		1
SFRS7_HUMAN	Splicing factor, arginine/serine-rich 7	27 kDa		1	2	2		1	2	2	2	2		1
SFRS9_HUMAN	Splicing factor, arginine/serine-rich 9	26 kDa	2	2	2	2	5	5	2	2	2	2	3	3
SFPQ_HUMAN	Splicing factor, proline	76 kDa	10	11	9	10	9	10	10	11	10	11	12	13
SRC8_HUMAN	Src substrate cortactin	62 kDa	7	7	7	7	5	5	6	6	7	7	6	6
SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1	102 kDa	9	12	10	12	5	5	12	14	10	12	6	7
STMN1_HUMAN	Stathmin	17 kDa	6	6	5	5	7	7	6	6	5	5	4	4
STML2_HUMAN	Stomatin-like protein 2	39 kDa	7	9	7	9	8	11	7	9	7	9	10	13
GRP75_HUMAN	Stress-70 protein, mitochondrial precursor	74 kDa	10	10	11	11	12	12	10	10	11	11	12	12
STIP1_HUMAN	Stress-induced-phosphoprotein 1	63 kDa	11	11	13	13	12	12	11	11	10	10	12	12
SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A	143 kDa	2	2	2	2	2	2	3	3	2	2	3	3
SMC2_HUMAN	Structural maintenance of chromosomes protein 2	136 kDa	7	7	6	6	3	3	5	5	6	7	3	3
SMC3_HUMAN	Structural maintenance of chromosomes protein 3	142 kDa	6	6	5	5	4	4	4	4	3	3	5	5
SMC4_HUMAN	Structural maintenance of chromosomes protein 4	147 kDa	6	6	4	4	4	4	5	5	5	5	4	4
DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	73 kDa	4	5	3	3	6	6	3	4	3	4	6	7
DHSB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor	32 kDa				1	3	3	2	2	2	2	2	2
SCOT_HUMAN	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor	56 kDa	2	2	2	3	3	3	2	2		1	2	2
SAE1_HUMAN	SUMO-activating enzyme subunit 1	38 kDa							3	3		1		1
SAE2_HUMAN	SUMO-activating enzyme subunit 2	71 kDa		1	2	2		1	2	2	3	3	3	3
UBC9_HUMAN	SUMO-conjugating enzyme UBC9	18 kDa	2	2		1		1	2	2	2	2	2	2
SK2L2_HUMAN	Superkiller viralicidic activity 2-like 2	118 kDa		1	2	2				1		1	2	2
SODC_HUMAN	Superoxide dismutase [Cu-Zn]	16 kDa	3	3	3	3	4	4	3	3	4	4	3	3
SMN_HUMAN	Survival motor neuron protein	32 kDa	2	2	2	2			2	2		1		

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
SMRC1_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1	123 kDa	2	2	2	2		1	2	2		1	2	2
SMRC2_HUMAN	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2	133 kDa		1	2	2	3	3					3	3
VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog	42 kDa	3	3	3	3	2	2	3	3	3	3	3	3
TLN1_HUMAN	Talin-1	270 kDa	49	56	47	56	31	34	47	55	46	53	41	44
TADBP_HUMAN	TAR DNA-binding protein 43	45 kDa	4	4	4	4	5	5	5	5	4	4	5	5
RBP56_HUMAN	TATA-binding protein-associated factor 2N	62 kDa		1			2	2						
TCPA_HUMAN	T-complex protein 1 subunit alpha	60 kDa	14	14	14	15	13	13	14	14	16	17	14	15
TCPB_HUMAN	T-complex protein 1 subunit beta	57 kDa	11	12	11	14	9	10	12	13	13	14	12	13
TCPD_HUMAN	T-complex protein 1 subunit delta	58 kDa	10	11	12	13	10	10	12	12	10	10	12	12
TCPE_HUMAN	T-complex protein 1 subunit epsilon	60 kDa	16	18	11	12	12	13	15	16	13	14	16	17
TCPH_HUMAN	T-complex protein 1 subunit eta	59 kDa	13	14	13	14	12	13	13	14	13	14	11	12
TCPG_HUMAN	T-complex protein 1 subunit gamma	61 kDa	14	17	14	16	13	15	13	16	15	18	12	14
TCPQ_HUMAN	T-complex protein 1 subunit theta	60 kDa	16	16	19	20	14	14	15	15	15	15	13	13
TCPZ_HUMAN	T-complex protein 1 subunit zeta	58 kDa	11	12	9	10	5	6	11	12	10	11	7	8
TENA_HUMAN	Tenascin precursor	241 kDa	2	2	2	2			5	5	5	5		
TES_HUMAN	Testin	48 kDa		1	2	2				1	2	2		
TTC1_HUMAN	Tetratricopeptide repeat protein 1	34 kDa	2	2		1	2	2		1	2	2		
THOP1_HUMAN	Thimet oligopeptidase	79 kDa	2	2	4	5	2	2	3	3	2	2	2	2
THIO_HUMAN	Thioredoxin	12 kDa	5	5	5	5	3	3	7	7	4	4	2	2
TXND1_HUMAN	Thioredoxin domain-containing protein 1 precursor	32 kDa			2	2			2	2	2	2	2	2
TXND4_HUMAN	Thioredoxin domain-containing protein 4 precursor	47 kDa	4	4		1	2	2	4	4	2	2	3	3
TXND5_HUMAN	Thioredoxin domain-containing protein 5 precursor	48 kDa	4	4	3	3	6	7	3	3	2	2	6	6
TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic	71 kDa	2	2	2	2	2	2	4	4	3	3	2	2
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	28 kDa	2	2	2	2	2	2	3	3	2	2	4	5
THOC4_HUMAN	THO complex subunit 4	27 kDa		1		1		2		1	2	2	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic	83 kDa	11	11	10	10	9	9	10	10	11	11	7	7
TSP1_HUMAN	Thrombospondin-1 precursor	129 kDa	11	11	9	9	5	5	11	11	12	12	7	7
KITH_HUMAN	Thymidine kinase, cytosolic	25 kDa	2	2	2	2		1	3	3	2	2		1
TYSY_HUMAN	Thymidylate synthase	36 kDa		1	3	3		1	2	2	2	2		1
TYB10_HUMAN	Thymosin beta-10	5 kDa	2	2	2	2	2	2	2	2	2	2	2	2
TYB4_HUMAN	Thymosin beta-4	5 kDa	3	3	3	3	3	3	3	3	3	3	3	3
ZO1_HUMAN	Tight junction protein ZO-1	195 kDa		1	3	3								
ZO2_HUMAN	Tight junction protein ZO-2	134 kDa	4	4	4	4	4	4	3	3	4	4	2	2
TOR1A_HUMAN	Torsin-1A precursor	38 kDa								1		1	2	2
TOIP1_HUMAN	Torsin-1A-interacting protein 1	66 kDa	3	3	4	4	5	5	2	2	4	4	5	5
TALDO_HUMAN	Transaldolase	38 kDa	7	8	6	7	6	6	7	8	7	8	4	5
TCAL4_HUMAN	Transcription elongation factor A protein-like 4	25 kDa								1			2	2
ELOC_HUMAN	Transcription elongation factor B polypeptide 1	12 kDa	2	2	2	2	2	2	2	2	2	2	2	2
ELOB_HUMAN	Transcription elongation factor B polypeptide 2	13 kDa			2	2				1		1	2	2
TIF1B_HUMAN	Transcription intermediary factor 1-beta	89 kDa	9	9	9	9	11	11	8	8	9	9	11	11
TFR1_HUMAN	Transferrin receptor protein 1	85 kDa	9	9	10	10	8	8	7	7	9	9	8	8
RHOA_HUMAN	Transforming protein RhoA precursor	22 kDa	4	5	4	5	3	3	4	5	3	4	3	4
TAGL_HUMAN	Transgelin	23 kDa	4	4	4	4	3	3	5	5	4	4	3	3
TAGL2_HUMAN	Transgelin-2	22 kDa	11	12	11	13	10	11	11	12	10	11	9	10
TERA_HUMAN	Transitional endoplasmic reticulum ATPase	89 kDa	19	22	21	23	21	24	19	21	19	21	20	23
TKT_HUMAN	Transketolase	68 kDa	13	17	12	17	12	15	13	17	12	16	13	17
TCTP_HUMAN	Translationally-controlled tumor protein	20 kDa	2	2	2	2	2	2	2	2	2	2	2	2
SSRD_HUMAN	Translocon-associated protein subunit delta precursor	19 kDa	2	2		1		1						
TMEDA_HUMAN	Transmembrane emp24 domain-containing protein 10 precursor	25 kDa			2	2	2	2					2	2
TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 precursor	25 kDa	2	2	2	2	2	2	2	2	2	2	2	2

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
TNPO1_HUMAN	Transportin-1	101 kDa	7	7	7	8	6	6	7	8	6	6	3	3
ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial precursor	83 kDa	7	7	7	7	8	8	8	8	8	8	15	15
ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial precursor	51 kDa		1	2	2	2	2		1		1	3	3
PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase	108 kDa	3	3	3	3	3	3	3	3	3	3	3	3
TPIS_HUMAN	Triosephosphate isomerase	27 kDa	17	20	15	18	14	17	14	17	14	17	14	15
TPP1_HUMAN	Tripeptidyl-peptidase 1 precursor	61 kDa		1		1	3	3		1		1	2	2
TR112_HUMAN	TRM112-like protein	14 kDa		1				1		1	2	2	2	2
NSUN2_HUMAN	tRNA	86 kDa	5	5	2	2		1	3	3	3	3	2	2
TMOD3_HUMAN	Tropomodulin-3	40 kDa	2	2	3	3	3	3	3	3	2	2	3	3
TPM1_HUMAN	Tropomyosin alpha-1 chain	33 kDa							5	5	5	5	4	4
TPM3_HUMAN	Tropomyosin alpha-3 chain	33 kDa		1			4	4						
TPM4_HUMAN	Tropomyosin alpha-4 chain	29 kDa	12	12	10	10	16	17	14	14	14	14	15	15
TPM2_HUMAN	Tropomyosin beta chain	33 kDa	3	3	3	3	3	3	5	5	3	3	6	6
SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic	53 kDa	7	8	7	9	5	6	7	9	8	10	7	9
TBA1A_HUMAN	Tubulin alpha-1A chain	50 kDa	2	2	2	2	2	2	2	2	2	2	2	2
TBA1B_HUMAN	Tubulin alpha-1B chain	50 kDa	23	35	19	30	22	31	20	31	23	33	18	27
TBA4A_HUMAN	Tubulin alpha-4A chain	50 kDa		1		1	2	2						
TBB5_HUMAN	Tubulin beta chain	50 kDa	31	51	31	49	29	44	31	48	31	47	31	47
TBB2A_HUMAN	Tubulin beta-2A chain	50 kDa												
TBB2C_HUMAN	Tubulin beta-2C chain	50 kDa	4	5	4	5	4	5	4	5	4	5	4	5
TBB3_HUMAN	Tubulin beta-3 chain	50 kDa	5	5	5	5	3	3	4	4	4	4	4	4
TBB6_HUMAN	Tubulin beta-6 chain	50 kDa	6	7	6	7	6	6	6	7	6	7	6	6
TBCB_HUMAN	Tubulin folding cofactor B	27 kDa	2	2	2	2	3	3	3	3	2	2		1
TBCA_HUMAN	Tubulin-specific chaperone A	13 kDa	3	3	3	3		1	2	2	2	2	3	3
TPD54_HUMAN	Tumor protein D54	22 kDa	4	4	3	3	3	3	5	5	5	5	4	4

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			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	
TACD2_HUMAN	Tumor-associated calcium signal transducer 2 precursor	36 kDa		1				2	2		1		1	2	2
PTN1_HUMAN	Tyrosine-protein phosphatase non-receptor type 1	50 kDa	2	2	2	2		1	2	2	2	2	3	3	
RU17_HUMAN	U1 small nuclear ribonucleoprotein 70 kDa	52 kDa		1		1		1		1		1	2	2	
SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A	31 kDa							2	2		1		1	
RU1C_HUMAN	U1 small nuclear ribonucleoprotein C	17 kDa		1		1	2	2		1		1	2	2	
RU2A_HUMAN	U2 small nuclear ribonucleoprotein A'	28 kDa		1		1	2	2				1		1	
PRP4_HUMAN	U4/U6 small nuclear ribonucleoprotein Prp4	58 kDa		1		1	2	2	3	3	2	2	2	2	
SNUT1_HUMAN	U4/U6.U5 tri-snRNP-associated protein 1	90 kDa								1	2	2			
U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase	245 kDa	7	7	10	10	12	12	12	12	7	7	11	12	
UBQL1_HUMAN	Ubiquilin-1	63 kDa	3	4	3	4	2	3	3	4	4	5	2	3	
UBIQ_HUMAN	Ubiquitin	9 kDa	3	3	2	2	2	2	2	2	2	2	3	3	
UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14	56 kDa	2	2	2	2	2	2	2	2	2	2	3	3	
UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5	96 kDa	6	6	7	7	5	5	5	5	5	5	6	6	
UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7	128 kDa	2	2		1	3	3	2	2	2	2	3	3	
UCHL3_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L3	26 kDa	2	2	2	2	2	2	2	2	2	2	2	2	
UFD1_HUMAN	Ubiquitin fusion degradation protein 1 homolog	35 kDa		1	3	3	2	2							
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1	31 kDa	2	2	3	3	2	2	2	2		1		1	
UBP2L_HUMAN	Ubiquitin-associated protein 2-like	115 kDa	3	3	3	3	3	3	3	3	3	3	3	3	
UBE2C_HUMAN	Ubiquitin-conjugating enzyme E2 C	20 kDa	2	2	2	2		1	2	2		1			
UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N	17 kDa	2	2	2	2	2	2		1	2	2	2	2	
UB2V1_HUMAN	Ubiquitin-conjugating enzyme E2 variant 1	26 kDa	2	2	2	2	2	2	2	2	2	2			
UBE2Z_HUMAN	Ubiquitin-conjugating enzyme E2 Z	38 kDa								1	2	2		1	
UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1	118 kDa	25	27	22	25	18	22	23	26	21	24	18	20	
UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 precursor	175 kDa	4	4		1	5	5	5	5	4	4	9	9	
KCY_HUMAN	UMP-CMP kinase	22 kDa	3	3		2	2	3		1	2	2	2	3	

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
CL005_HUMAN	Uncharacterized protein C12orf5	30 kDa	2	2		1	2	2	2	2	2	2		
CS010_HUMAN	Uncharacterized protein C19orf10 precursor	19 kDa	2	2	2	2	2	2	2	2	2	2	2	2
CT077_HUMAN	Uncharacterized protein C20orf77	37 kDa		1	2	2		1	2	2		1		1
CV028_HUMAN	UPF0027 protein C22orf28	55 kDa	3	3	3	3	2	2	3	3	4	4	3	3
CP080_HUMAN	UPF0468 protein C16orf80	23 kDa		1	2	2				1		1		
UTRO_HUMAN	Utrophin	394 kDa	6	6	7	7	4	4	4	4	3	3	10	10
RD23B_HUMAN	UV excision repair protein RAD23 homolog B	43 kDa	3	4	3	4		2	3	4	3	4		2
VATA_HUMAN	Vacuolar ATP synthase catalytic subunit A	68 kDa		1	2	2	2	2	2	2	2	2	2	2
VATB2_HUMAN	Vacuolar ATP synthase subunit B, brain isoform	57 kDa							2	2		1	2	2
VP26A_HUMAN	Vacuolar protein sorting-associated protein 26A	38 kDa	2	2		1	2	2	2	2	2	2		1
VPS35_HUMAN	Vacuolar protein sorting-associated protein 35	92 kDa	4	4	4	4	5	5	4	4	5	5	5	5
ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	70 kDa	2	2	2	2	8	8	4	4	4	4	9	9
VAMP3_HUMAN	Vesicle-associated membrane protein 3	11 kDa	2	2	2	2	2	2	2	2	2	2	2	2
VAPB_HUMAN	Vesicle-associated membrane protein-associated protein B/C	27 kDa	2	2	2	2			2	2		1	4	4
NSF_HUMAN	Vesicle-fusing ATPase	83 kDa	2	2		1	2	2	2	2		1	3	3
SC22B_HUMAN	Vesicle-trafficking protein SEC22b	25 kDa	2	2		1		1		1		1		1
VIGLN_HUMAN	Vigilin	141 kDa	5	5	6	6	4	4	4	4	3	3	4	4
VIME_HUMAN	Vimentin	54 kDa	42	52	39	48	43	54	41	48	42	49	44	58
VINC_HUMAN	Vinculin	124 kDa	18	19	19	19	17	17	19	20	17	18	16	17
VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	31 kDa	7	7	6	6	7	7	7	7	7	8	7	7
VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2	32 kDa	2	2	2	2		1	2	2	2	2		1
WDR1_HUMAN	WD repeat-containing protein 1	66 kDa	6	6	6	6	5	5	7	8	6	6	5	5
WDR5_HUMAN	WD repeat-containing protein 5	37 kDa				1	2	2					3	3
WDR61_HUMAN	WD repeat-containing protein 61	34 kDa		1		1	2	2		1	2	2	2	2
XTP3A_HUMAN	XTP3-transactivated gene A protein	19 kDa	2	2	2	2	2	2	2	2	2	2	2	2

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Co t _{2 h 30}		S9-inf t _{2 h 30}		S9-int t _{2 h 30}		Co t _{6 h 30}		S9-inf t _{6 h 30}		S9-int t _{6 h 30}	
			unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec	unique pep	unique spec
YLPM1_HUMAN	YLP motif-containing protein 1	220 kDa											2	2
ZCC2_HUMAN	Zinc finger CCCH type antiviral protein 1	101 kDa	4	4	5	5	2	2	3	3	4	4	3	3
ZYX_HUMAN	Zyxin	61 kDa	5	5	6	6	5	5	6	6	6	6	6	6

Die Tabelle enthält alle identifizierbaren Proteine für die Probenzeitpunkte t_{2 h 30} und t_{6 h 30}. Für jeden Probenansatz wurden jeweils 4 unabhängige biologische Replikate gelfrei verdaut und massenspektrometrisch analysiert. Ein Protein galt als signifikant, wenn es mit mindestens 2 Peptiden identifiziert wurde. Zusätzlich zur Anzahl der unique Peptide (unique pep) wurde die Anzahl der unique Spektren (unique spec) dokumentiert.

Co = Kontrolle S9-Zellen, S9-inf= *S.aureus*-infizierte S9-Zellen, S9-int = *S. aureus*-internalisierte S9-Zellen.

Tab. 69: Liste der quantifizierbaren Proteine für S9-Zellen nach einer *S. aureus*-Behandlung zum Zeitpunkt t_2 h30.

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
CH10_HUMAN	10 kDa heat shock protein, mitochondrial	11 kDa	41.58	47.40	78.41	1.14	3.01E-02	1.89	1.08E-01
U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein component	109 kDa	44.26	52.21	61.79	1.18	3.78E-01	1.40	4.08E-01
1433B_HUMAN	14-3-3 protein beta/alpha	28 kDa	137.13	141.20	125.16	1.03	7.67E-01	-1.10	5.56E-03
1433E_HUMAN	14-3-3 protein epsilon	29 kDa	152.31	153.23	142.82	1.01	9.94E-01	-1.07	3.17E-02
1433F_HUMAN	14-3-3 protein eta	28 kDa	55.87	53.41	43.09	-1.05	4.87E-01	-1.30	2.58E-03
1433G_HUMAN	14-3-3 protein gamma	28 kDa	95.16	93.10	87.76	-1.02	4.80E-01	-1.08	5.82E-02
1433S_HUMAN	14-3-3 protein sigma	28 kDa	70.16	60.63	37.90	-1.16	2.75E-01	-1.85	3.30E-03
1433T_HUMAN	14-3-3 protein theta	28 kDa	110.34	109.93	92.95	-1.00	8.51E-01	-1.19	6.36E-03
1433Z_HUMAN	14-3-3 protein zeta/delta	28 kDa	144.28	152.02	133.47	1.05	5.11E-01	-1.08	5.06E-02
CN37_HUMAN	2',3'-cyclic-nucleotide 3'-phosphodiesterase	48 kDa	8.54	6.51	3.62	-1.31	3.94E-01	-2.36	2.45E-02
PRS4_HUMAN	26S protease regulatory subunit 4	49 kDa	13.90	13.73	15.04	-1.01	8.79E-01	1.08	5.65E-01
PRS6A_HUMAN	26S protease regulatory subunit 6A	49 kDa	28.18	31.77	39.97	1.13	5.85E-01	1.42	5.10E-01
PRS7_HUMAN	26S protease regulatory subunit 7	49 kDa	21.04	20.94	26.47	-1.00	9.63E-01	1.26	5.99E-01
PRS8_HUMAN	26S protease regulatory subunit 8	46 kDa	4.97	2.91	14.00	-1.71	1.76E-01	2.82	7.62E-03
PSD11_HUMAN	26S proteasome non-ATPase regulatory subunit 11	47 kDa	21.04	18.54	23.35	-1.13	3.44E-01	1.11	5.69E-01
PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14	35 kDa	18.36	14.93	21.28	-1.23	3.40E-01	1.16	9.37E-01
PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2	100 kDa	15.68	14.93	15.04	-1.05	7.78E-01	-1.04	5.02E-01
PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3	61 kDa	19.25	19.74	9.85	1.03	8.60E-01	-1.95	1.39E-02
PSMD4_HUMAN	26S proteasome non-ATPase regulatory subunit 4	41 kDa	5.86	8.92	10.89	1.52	3.01E-01	1.86	1.90E-01
PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5	56 kDa	6.75	10.12	5.69	1.50	3.97E-01	-1.19	4.82E-01
PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6	46 kDa	6.75	5.31	8.81	-1.27	4.98E-01	1.31	8.76E-01
PSD7_HUMAN	26S proteasome non-ATPase regulatory subunit 7	37 kDa	4.07	1.70	0.50	-2.39	3.30E-01	-8.14	5.73E-02
HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprotein	21 kDa	11.22	18.54	3.62	1.65	9.48E-02	-3.10	1.84E-02
ODO1_HUMAN	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor	116 kDa	4.97	5.31	6.73	1.07	9.79E-01	1.36	8.65E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
D3D2_HUMAN	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	33 kDa	7.64	6.51	11.93	-1.17	2.49E-01	1.56	1.86E-01
RM12_HUMAN	39S ribosomal protein L12, mitochondrial precursor	21 kDa	5.86	8.92	18.16	1.52	1.55E-01	3.10	6.45E-03
HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	27 kDa	18.36	16.13	22.31	-1.14	6.80E-01	1.22	7.42E-01
3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35 kDa	9.43	10.12	21.28	1.07	7.24E-01	2.26	4.09E-02
THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial	42 kDa	11.22	13.73	16.08	1.22	4.68E-01	1.43	3.74E-01
RS10_HUMAN	40S ribosomal protein S10	19 kDa	17.47	17.34	14.00	-1.01	9.33E-01	-1.25	1.01E-01
RS12_HUMAN	40S ribosomal protein S12	15 kDa	13.90	16.13	21.28	1.16	2.86E-01	1.53	2.86E-01
RS14_HUMAN	40S ribosomal protein S14	16 kDa	12.11	11.32	14.00	-1.07	7.97E-01	1.16	9.31E-01
RS15_HUMAN	40S ribosomal protein S15	17 kDa	9.43	7.72	5.69	-1.22	3.09E-01	-1.66	4.11E-02
RS15A_HUMAN	40S ribosomal protein S15a	15 kDa	5.86	6.51	11.93	1.11	7.21E-01	2.04	2.73E-01
RS17_HUMAN	40S ribosomal protein S17	16 kDa	18.36	19.74	16.08	1.08	6.24E-01	-1.14	3.86E-02
RS18_HUMAN	40S ribosomal protein S18	18 kDa	10.32	7.72	6.73	-1.34	3.40E-01	-1.53	9.74E-02
RS2_HUMAN	40S ribosomal protein S2	31 kDa	14.79	12.53	12.97	-1.18	8.36E-01	-1.14	5.88E-01
RS21_HUMAN	40S ribosomal protein S21	9 kDa	13.00	14.93	19.20	1.15	5.91E-01	1.48	3.60E-01
RS26_HUMAN	40S ribosomal protein S26	13 kDa	13.90	12.53	12.97	-1.11	1.95E-01	-1.07	1.19E-01
RS27_HUMAN	40S ribosomal protein S27	9 kDa	7.64	6.51	5.69	-1.17	5.15E-01	-1.34	1.77E-01
RS3_HUMAN	40S ribosomal protein S3	27 kDa	45.15	49.81	46.21	1.10	6.27E-01	1.02	4.47E-01
RS4X_HUMAN	40S ribosomal protein S4, X isoform	30 kDa	25.50	32.97	25.43	1.29	2.41E-01	-1.00	4.79E-01
RS5_HUMAN	40S ribosomal protein S5	23 kDa	28.18	32.97	24.39	1.17	3.07E-01	-1.16	4.14E-02
RS7_HUMAN	40S ribosomal protein S7	22 kDa	29.97	24.55	27.51	-1.22	2.20E-01	-1.09	6.83E-02
RS8_HUMAN	40S ribosomal protein S8	24 kDa	38.01	38.98	26.47	1.03	9.00E-01	-1.44	8.05E-03
RSSA_HUMAN	40S ribosomal protein SA	33 kDa	47.83	52.21	53.48	1.09	5.06E-01	1.12	8.18E-01
4F2_HUMAN	4F2 cell-surface antigen heavy chain	58 kDa	4.07	8.92	7.77	2.19	1.47E-02	1.91	4.66E-01
AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase	54 kDa	5.86	6.51	7.77	1.11	7.59E-01	1.33	6.30E-01
CH60_HUMAN	60 kDa heat shock protein, mitochondrial precursor	61 kDa	188.93	204.94	295.52	1.08	2.30E-01	1.56	2.35E-02
RLA0_HUMAN	60S acidic ribosomal protein P0	34 kDa	39.79	32.97	27.51	-1.21	2.65E-01	-1.45	1.99E-02

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
RLA1_HUMAN	60S acidic ribosomal protein P1	12 kDa	30.86	31.77	34.78	1.03	7.53E-01	1.13	7.65E-01
RLA2_HUMAN	60S acidic ribosomal protein P2	12 kDa	54.97	51.01	57.63	-1.08	4.09E-01	1.05	2.57E-01
RL10_HUMAN	60S ribosomal protein L10	25 kDa	9.43	10.12	5.69	1.07	7.40E-01	-1.66	1.84E-02
RL11_HUMAN	60S ribosomal protein L11	20 kDa	12.11	13.73	11.93	1.13	5.96E-01	-1.02	7.49E-01
RL12_HUMAN	60S ribosomal protein L12	18 kDa	31.76	23.35	30.63	-1.36	1.85E-02	-1.04	4.81E-01
RL13_HUMAN	60S ribosomal protein L13	24 kDa	9.43	11.32	6.73	1.20	5.78E-01	-1.40	1.56E-01
RL15_HUMAN	60S ribosomal protein L15	24 kDa	11.22	10.12	9.85	-1.11	7.23E-01	-1.14	1.94E-01
RL18_HUMAN	60S ribosomal protein L18	22 kDa	8.54	8.92	3.62	1.04	7.84E-01	-2.36	5.56E-03
RL22_HUMAN	60S ribosomal protein L22	15 kDa	24.61	22.15	19.20	-1.11	2.83E-01	-1.28	3.22E-02
RL23_HUMAN	60S ribosomal protein L23	15 kDa	7.64	6.51	5.69	-1.17	5.54E-01	-1.34	2.64E-01
RL23A_HUMAN	60S ribosomal protein L23a	18 kDa	10.32	11.32	7.77	1.10	6.82E-01	-1.33	1.38E-02
RL27A_HUMAN	60S ribosomal protein L27a	17 kDa	13.90	12.53	10.89	-1.11	5.24E-01	-1.28	7.69E-02
RL3_HUMAN	60S ribosomal protein L3	46 kDa	10.32	14.93	8.81	1.45	4.39E-01	-1.17	4.27E-01
RL30_HUMAN	60S ribosomal protein L30	13 kDa	13.90	13.73	12.97	-1.01	9.47E-01	-1.07	2.92E-01
RL32_HUMAN	60S ribosomal protein L32	16 kDa	7.64	6.51	1.54	-1.17	6.34E-01	-4.97	7.09E-03
RL4_HUMAN	60S ribosomal protein L4	48 kDa	31.76	31.77	31.66	1.00	9.91E-01	-1.00	3.16E-01
RL5_HUMAN	60S ribosomal protein L5	34 kDa	9.43	6.51	3.62	-1.45	3.50E-01	-2.61	1.63E-02
RL6_HUMAN	60S ribosomal protein L6	33 kDa	10.32	10.12	0.50	-1.02	8.41E-01	-20.65	1.75E-05
RL7_HUMAN	60S ribosomal protein L7	29 kDa	18.36	18.54	14.00	1.01	9.54E-01	-1.31	5.21E-02
RL9_HUMAN	60S ribosomal protein L9	22 kDa	13.90	12.53	11.93	-1.11	4.40E-01	-1.17	1.12E-01
K6PP_HUMAN	6-phosphofruktokinase type C	86 kDa	51.40	53.41	31.66	1.04	9.40E-01	-1.62	1.57E-02
K6PL_HUMAN	6-phosphofruktokinase, liver type	85 kDa	16.57	19.74	11.93	1.19	4.40E-01	-1.39	1.24E-01
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating	53 kDa	13.00	14.93	6.73	1.15	7.48E-01	-1.93	1.66E-01
GRP78_HUMAN	78 kDa glucose-regulated protein precursor	72 kDa	225.54	225.38	297.60	-1.00	7.37E-01	1.32	2.08E-01
THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic	41 kDa	52.30	47.40	29.59	-1.10	3.79E-01	-1.77	2.31E-04
THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial precursor	45 kDa	12.11	10.12	17.12	-1.20	4.37E-01	1.41	4.24E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B	29 kDa	13.00	11.32	9.85	-1.15	5.94E-01	-1.32	1.40E-01
AN32E_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member E	31 kDa	10.32	10.12	7.77	-1.02	8.51E-01	-1.33	3.26E-01
ACON_HUMAN	Aconitate hydratase, mitochondrial precursor	85 kDa	4.07	7.72	12.97	1.89	1.59E-01	3.18	3.16E-02
ACTS_HUMAN	Actin, alpha skeletal muscle	42 kDa	362.17	345.64	303.83	-1.05	6.57E-01	-1.19	1.86E-02
ACTG_HUMAN	Actin, cytoplasmic 2	42 kDa	1835.65	1699.73	1548.31	-1.08	2.02E-02	-1.19	3.13E-05
ACL6A_HUMAN	Actin-like protein 6A	47 kDa	6.75	10.12	6.73	1.50	5.65E-02	-1.00	4.88E-01
ARP2_HUMAN	Actin-related protein 2	45 kDa	31.76	42.59	38.94	1.34	1.41E-01	1.23	6.67E-01
ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B	41 kDa	7.64	8.92	8.81	1.17	5.39E-01	1.15	8.52E-01
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3	21 kDa	10.32	14.93	12.97	1.45	8.28E-02	1.26	6.40E-01
ARP3_HUMAN	Actin-related protein 3	47 kDa	50.51	53.41	56.60	1.06	6.66E-01	1.12	6.15E-01
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15	14 kDa	12.11	7.72	5.69	-1.57	2.56E-01	-2.13	2.85E-02
ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9	46 kDa	4.07	2.91	11.93	-1.40	7.65E-01	2.93	1.16E-01
APT_HUMAN	Adenine phosphoribosyltransferase	20 kDa	10.32	8.92	9.85	-1.16	5.87E-01	-1.05	4.77E-01
ADK_HUMAN	Adenosine kinase	41 kDa	13.90	13.73	6.73	-1.01	7.88E-01	-2.06	3.66E-03
SAHH_HUMAN	Adenosylhomocysteinase	48 kDa	58.55	67.84	63.87	1.16	4.00E-01	1.09	6.54E-01
KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial	26 kDa	3.18	5.31	4.66	1.67	5.64E-01	1.46	6.04E-01
CAP1_HUMAN	Adenylyl cyclase-associated protein 1	52 kDa	79.98	79.87	81.53	-1.00	9.21E-01	1.02	1.33E-01
ADT2_HUMAN	ADP/ATP translocase 2	33 kDa	27.29	25.75	21.28	-1.06	7.49E-01	-1.28	1.21E-01
ARF1_HUMAN	ADP-ribosylation factor 1	21 kDa	25.50	37.78	18.16	1.48	3.08E-01	-1.40	2.11E-01
ARF4_HUMAN	ADP-ribosylation factor 4	21 kDa	12.11	14.93	2.58	1.23	7.32E-01	-4.70	8.73E-03
ARF5_HUMAN	ADP-ribosylation factor 5	21 kDa	10.32	10.12	9.85	-1.02	8.94E-01	-1.05	5.67E-01
ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2	40 kDa	4.97	4.11	3.62	-1.21	4.63E-01	-1.37	1.51E-01
AKA12_HUMAN	A-kinase anchor protein 12	191 kDa	19.25	11.32	12.97	-1.70	2.98E-01	-1.48	1.33E-01
SYAC_HUMAN	Alanyl-tRNA synthetase, cytoplasmic	107 kDa	36.22	40.18	41.01	1.11	5.88E-01	1.13	8.95E-01
FETUA_HUMAN	Alpha-2-HS-glycoprotein precursor	39 kDa	11.22	14.93	0.50	1.33	4.77E-01	-22.43	1.18E-02
ACTN1_HUMAN	Alpha-actinin-1	103 kDa	267.51	265.06	285.13	-1.01	4.98E-01	1.07	4.99E-02

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ACTN4_HUMAN	Alpha-actinin-4	105 kDa	319.31	333.61	342.27	1.04	4.38E-01	1.07	5.65E-02
AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	55 kDa	32.65	36.58	36.86	1.12	3.98E-01	1.13	8.16E-01
ACTZ_HUMAN	Alpha-centractin	43 kDa	25.50	22.15	18.16	-1.15	2.14E-01	-1.40	4.58E-02
ENOA_HUMAN	Alpha-enolase	47 kDa	1057.83	1055.15	901.14	-1.00	7.91E-01	-1.17	8.91E-03
AINX_HUMAN	Alpha-internexin	55 kDa	6.75	1.70	11.93	-3.97	4.37E-01	1.77	5.99E-01
ANXA1_HUMAN	Annexin A1	39 kDa	188.93	190.51	183.33	1.01	9.85E-01	-1.03	3.16E-01
ANXA2_HUMAN	Annexin A2	39 kDa	554.17	507.98	455.49	-1.09	7.34E-02	-1.22	2.93E-04
ANXA3_HUMAN	Annexin A3	36 kDa	29.97	32.97	31.66	1.10	1.56E-01	1.06	6.95E-01
ANXA4_HUMAN	Annexin A4	36 kDa	14.79	14.93	12.97	1.01	9.72E-01	-1.14	3.22E-01
ANXA5_HUMAN	Annexin A5	36 kDa	69.26	91.90	75.29	1.33	2.96E-02	1.09	4.78E-01
ANXA6_HUMAN	Annexin A6	76 kDa	23.72	32.97	22.31	1.39	2.44E-02	-1.06	2.94E-01
AP2A1_HUMAN	AP-2 complex subunit alpha-1	108 kDa	8.54	6.51	8.81	-1.31	5.15E-01	1.03	5.84E-01
AP2B1_HUMAN	AP-2 complex subunit beta-1	105 kDa	13.00	14.93	10.89	1.15	8.67E-01	-1.19	2.93E-01
APOL2_HUMAN	Apolipoprotein-L2	37 kDa	6.75	6.51	14.00	-1.04	8.14E-01	2.07	1.12E-01
API5_HUMAN	Apoptosis inhibitor 5	58 kDa	12.11	14.93	6.73	1.23	2.95E-01	-1.80	4.71E-02
AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial precursor	67 kDa	21.04	23.35	32.70	1.11	5.52E-01	1.55	1.97E-01
SYRC_HUMAN	Arginyl-tRNA synthetase, cytoplasmic	75 kDa	28.18	23.35	19.20	-1.21	4.25E-01	-1.47	5.08E-02
SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic	63 kDa	14.79	18.54	9.85	1.25	2.57E-02	-1.50	2.59E-03
AATM_HUMAN	Aspartate aminotransferase, mitochondrial precursor	47 kDa	17.47	20.94	26.47	1.20	3.89E-01	1.52	2.09E-01
SYDC_HUMAN	Aspartyl-tRNA synthetase, cytoplasmic	57 kDa	13.00	14.93	12.97	1.15	5.42E-01	-1.00	4.10E-01
PEA15_HUMAN	Astrocytic phosphoprotein PEA-15	15 kDa	21.93	18.54	21.28	-1.18	1.19E-01	-1.03	3.37E-02
ATX10_HUMAN	Ataxin-10	53 kDa	16.57	12.53	12.97	-1.32	1.35E-01	-1.28	1.58E-01
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial precursor	60 kDa	103.20	105.12	180.21	1.02	8.95E-01	1.75	3.52E-03
AT5F1_HUMAN	ATP synthase subunit b, mitochondrial precursor	29 kDa	9.43	2.91	9.85	-3.25	7.47E-02	1.04	6.98E-01
ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor	57 kDa	136.24	142.40	207.22	1.05	3.92E-01	1.52	5.24E-02
ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	18 kDa	23.72	19.74	34.78	-1.20	7.36E-02	1.47	7.01E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ATPK_HUMAN	ATP synthase subunit f, mitochondrial	11 kDa	7.64	11.32	7.77	1.48	3.20E-02	1.02	5.39E-01
ATPO_HUMAN	ATP synthase subunit O, mitochondrial precursor	23 kDa	4.97	8.92	18.16	1.80	2.70E-01	3.66	3.75E-02
ACLY_HUMAN	ATP-citrate synthase	121 kDa	57.65	65.44	48.28	1.14	2.88E-01	-1.19	1.29E-02
KU70_HUMAN	ATP-dependent DNA helicase 2 subunit 1	70 kDa	63.90	64.24	55.56	1.01	9.22E-01	-1.15	4.94E-02
KU86_HUMAN	ATP-dependent DNA helicase 2 subunit 2	83 kDa	78.19	81.07	70.10	1.04	7.69E-01	-1.12	6.27E-02
RECQ1_HUMAN	ATP-dependent DNA helicase Q1	73 kDa	31.76	28.16	22.31	-1.13	3.87E-01	-1.42	2.22E-02
DHX9_HUMAN	ATP-dependent RNA helicase A	141 kDa	49.62	43.79	46.21	-1.13	1.80E-01	-1.07	1.59E-01
DDX1_HUMAN	ATP-dependent RNA helicase DDX1	82 kDa	14.79	13.73	11.93	-1.08	6.03E-01	-1.24	1.50E-01
DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X	73 kDa	53.19	53.41	39.97	1.00	9.05E-01	-1.33	3.69E-03
E41L2_HUMAN	Band 4.1-like protein 2	113 kDa	7.64	8.92	4.66	1.17	7.28E-01	-1.64	3.42E-01
BAF_HUMAN	Barrier-to-autointegration factor	10 kDa	7.64	7.72	9.85	1.01	9.88E-01	1.29	6.08E-01
BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1	48 kDa	13.00	11.32	4.66	-1.15	7.35E-01	-2.79	8.57E-02
BASI_HUMAN	Basigin precursor	42 kDa	24.61	30.56	36.86	1.24	2.96E-01	1.50	1.51E-01
B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin form pI 5.3]	14 kDa	34.43	31.77	33.74	-1.08	5.57E-01	-1.02	2.42E-01
HEXB_HUMAN	Beta-hexosaminidase beta chain precursor	63 kDa	14.79	13.73	20.24	-1.08	8.75E-01	1.37	6.50E-01
SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase	171 kDa	13.00	16.13	8.81	1.24	5.10E-01	-1.48	8.54E-02
PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase	65 kDa	35.33	31.77	27.51	-1.11	9.05E-03	-1.28	1.18E-02
BASP_HUMAN	Brain acid soluble protein 1	23 kDa	24.61	24.55	30.63	-1.00	8.53E-01	1.24	5.79E-01
C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	102 kDa	36.22	40.18	35.82	1.11	4.40E-01	-1.01	1.14E-01
CAD13_HUMAN	Cadherin-13 precursor	78 kDa	15.68	14.93	5.69	-1.05	6.61E-01	-2.75	6.64E-04
CALD1_HUMAN	Caldesmon	93 kDa	18.36	22.15	16.08	1.21	2.75E-02	-1.14	1.11E-04
CALX_HUMAN	Calnexin precursor	68 kDa	54.97	55.82	43.09	1.02	9.46E-01	-1.28	8.42E-02
CAN2_HUMAN	Calpain-2 catalytic subunit precursor	80 kDa	31.76	30.56	22.31	-1.04	7.46E-01	-1.42	1.27E-01
ICAL_HUMAN	Calpastatin	77 kDa	16.57	19.74	18.16	1.19	6.53E-01	1.10	7.88E-01
CNN2_HUMAN	Calponin-2	34 kDa	42.47	40.18	42.05	-1.06	5.26E-01	-1.01	1.38E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
CNN3_HUMAN	Calponin-3	36 kDa	30.86	32.97	28.55	1.07	7.02E-01	-1.08	4.95E-02
CALR_HUMAN	Calreticulin precursor	48 kDa	205.89	216.96	241.50	1.05	4.86E-01	1.17	7.59E-01
CALU_HUMAN	Calumenin precursor	37 kDa	23.72	18.54	26.47	-1.28	3.74E-01	1.12	9.12E-01
CAPR1_HUMAN	Caprin-1	73 kDa	11.22	17.34	23.35	1.55	1.41E-01	2.08	7.46E-02
CBR1_HUMAN	Carbonyl reductase [NADPH] 1	30 kDa	25.50	26.96	27.51	1.06	7.61E-01	1.08	8.07E-01
CSK2B_HUMAN	Casein kinase II subunit beta	25 kDa	5.86	7.72	7.77	1.32	4.59E-01	1.33	5.93E-01
CTNA1_HUMAN	Catenin alpha-1	100 kDa	16.57	17.34	14.00	1.05	6.92E-01	-1.18	9.56E-03
CTNB1_HUMAN	Catenin beta-1	85 kDa	10.32	10.12	12.97	-1.02	8.48E-01	1.26	4.07E-01
CATD_HUMAN	Cathepsin D precursor	45 kDa	34.43	40.18	57.63	1.17	2.91E-01	1.67	6.66E-02
CATZ_HUMAN	Cathepsin Z precursor	34 kDa	7.64	8.92	11.93	1.17	5.28E-02	1.56	1.08E-01
CAV1_HUMAN	Caveolin-1	20 kDa	8.54	8.92	5.69	1.04	9.75E-01	-1.50	7.95E-02
CD166_HUMAN	CD166 antigen precursor	65 kDa	4.07	4.11	18.16	1.01	9.23E-01	4.46	2.59E-03
CD2B2_HUMAN	CD2 antigen cytoplasmic tail-binding protein 2	38 kDa	8.54	6.51	7.77	-1.31	1.55E-01	-1.10	6.75E-01
CD44_HUMAN	CD44 antigen precursor	82 kDa	9.43	8.92	12.97	-1.06	7.61E-01	1.37	6.92E-01
CD9_HUMAN	CD9 antigen	25 kDa	13.90	16.13	5.69	1.16	5.72E-01	-2.44	4.93E-02
CDC2_HUMAN	Cell division control protein 2 homolog	34 kDa	9.43	7.72	5.69	-1.22	5.55E-01	-1.66	1.23E-01
MUC18_HUMAN	Cell surface glycoprotein MUC18 precursor	72 kDa	11.22	12.53	4.66	1.12	7.70E-01	-2.41	4.87E-02
P53_HUMAN	Cellular tumor antigen p53	44 kDa	11.22	10.12	12.97	-1.11	5.60E-01	1.16	9.21E-01
CETN2_HUMAN	Centrin-2	20 kDa	4.97	7.72	6.73	1.55	1.73E-01	1.36	4.53E-01
CHM4B_HUMAN	Charged multivesicular body protein 4b	25 kDa	13.00	13.73	19.20	1.06	9.57E-01	1.48	1.04E-01
CHMP5_HUMAN	Charged multivesicular body protein 5	25 kDa	11.22	16.13	12.97	1.44	4.36E-02	1.16	8.27E-01
CLIC1_HUMAN	Chloride intracellular channel protein 1	27 kDa	62.12	66.64	62.83	1.07	6.00E-01	1.01	4.31E-01
CLIC4_HUMAN	Chloride intracellular channel protein 4	29 kDa	45.15	46.20	36.86	1.02	9.10E-01	-1.22	8.72E-03
CBX1_HUMAN	Chromobox protein homolog 1	21 kDa	13.90	11.32	20.24	-1.23	4.09E-01	1.46	7.25E-01
CBX3_HUMAN	Chromobox protein homolog 3	21 kDa	35.33	31.77	42.05	-1.11	4.49E-01	1.19	8.93E-01
CISY_HUMAN	Citrate synthase, mitochondrial precursor	52 kDa	20.15	17.34	19.20	-1.16	3.89E-01	-1.05	1.44E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
CLH1_HUMAN	Clathrin heavy chain 1	192 kDa	180.00	186.90	167.75	1.04	7.53E-01	-1.07	6.80E-02
CPSF6_HUMAN	Cleavage and polyadenylation specificity factor subunit 6	59 kDa	7.64	5.31	6.73	-1.44	3.66E-01	-1.14	4.32E-01
CPSF7_HUMAN	Cleavage and polyadenylation specificity factor subunit 7	52 kDa	7.64	6.51	10.89	-1.17	6.96E-01	1.42	8.55E-02
COPA_HUMAN	Coatomer subunit alpha	138 kDa	11.22	6.51	0.50	-1.72	8.50E-02	-22.43	4.89E-04
COPD_HUMAN	Coatomer subunit delta	57 kDa	6.75	5.31	4.66	-1.27	5.93E-01	-1.45	1.97E-01
COPE_HUMAN	Coatomer subunit epsilon	34 kDa	11.22	14.93	11.93	1.33	1.49E-01	1.06	6.11E-01
COF1_HUMAN	Cofilin-1	19 kDa	163.03	137.59	119.96	-1.18	2.40E-01	-1.36	4.18E-03
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	31 kDa	20.15	18.54	28.55	-1.09	4.86E-01	1.42	1.67E-01
CSN4_HUMAN	COP9 signalosome complex subunit 4	46 kDa	7.64	6.51	5.69	-1.17	6.63E-01	-1.34	3.76E-01
CPNE1_HUMAN	Copine-1	59 kDa	36.22	40.18	29.59	1.11	3.98E-01	-1.22	1.43E-01
COR1B_HUMAN	Coronin-1B	54 kDa	13.00	10.12	8.81	-1.28	3.46E-01	-1.48	8.78E-02
COR1C_HUMAN	Coronin-1C	53 kDa	35.33	34.17	23.35	-1.03	6.90E-01	-1.51	3.20E-02
CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1	136 kDa	24.61	23.35	8.81	-1.05	7.26E-01	-2.79	7.40E-03
CD2A1_HUMAN	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	17 kDa	10.32	10.12	10.89	-1.02	8.47E-01	1.05	5.37E-01
CSR1_HUMAN	Cysteine and glycine-rich protein 1	21 kDa	26.40	25.75	23.35	-1.02	9.47E-01	-1.13	2.07E-01
CRIP2_HUMAN	Cysteine-rich protein 2	22 kDa	13.90	12.53	8.81	-1.11	5.32E-01	-1.58	1.16E-01
QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial precursor	53 kDa	4.97	6.51	12.97	1.31	2.95E-01	2.61	2.70E-02
QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial precursor	48 kDa	14.79	19.74	27.51	1.33	3.11E-01	1.86	5.05E-02
COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	20 kDa	7.64	6.51	9.85	-1.17	2.49E-01	1.29	7.52E-01
COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial precursor	17 kDa	29.08	22.15	23.35	-1.31	4.34E-02	-1.25	1.16E-02
COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial precursor	14 kDa	7.64	7.72	12.97	1.01	8.79E-01	1.70	1.77E-01
CX6B1_HUMAN	Cytochrome c oxidase subunit VIb isoform 1	10 kDa	8.54	4.11	12.97	-2.08	1.97E-01	1.52	3.75E-01
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	532 kDa	71.94	90.69	22.31	1.26	1.86E-01	-3.22	9.57E-04
DC112_HUMAN	Cytoplasmic dynein 1 intermediate chain 2	71 kDa	8.54	6.51	12.97	-1.31	6.43E-01	1.52	1.61E-01
CKAP4_HUMAN	Cytoskeleton-associated protein 4	66 kDa	24.61	23.35	26.47	-1.05	6.21E-01	1.08	6.64E-01
AMPL_HUMAN	Cytosol aminopeptidase	56 kDa	15.68	24.55	20.24	1.57	9.64E-02	1.29	5.83E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
BACH_HUMAN	Cytosolic acyl coenzyme A thioester hydrolase	42 kDa	15.68	11.32	14.00	-1.38	4.07E-01	-1.12	3.70E-01
SERA_HUMAN	D-3-phosphoglycerate dehydrogenase	57 kDa	43.36	49.81	36.86	1.15	4.27E-01	-1.18	2.73E-02
DAZP1_HUMAN	DAZ-associated protein 1	43 kDa	14.79	14.93	18.16	1.01	9.60E-01	1.23	6.96E-01
ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	36 kDa	13.90	13.73	21.28	-1.01	9.41E-01	1.53	2.10E-01
P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthetase	87 kDa	17.47	17.34	14.00	-1.01	8.93E-01	-1.25	1.88E-01
DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor	27 kDa	16.57	18.54	20.24	1.12	6.51E-01	1.22	8.30E-01
DYR_HUMAN	Dihydrofolate reductase	21 kDa	13.90	12.53	8.81	-1.11	4.20E-01	-1.58	1.18E-02
DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial precursor	54 kDa	10.32	13.73	23.35	1.33	3.52E-01	2.26	1.04E-01
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2	62 kDa	34.43	35.37	31.66	1.03	9.19E-01	-1.09	2.25E-01
MCM2_HUMAN	DNA replication licensing factor MCM2	102 kDa	24.61	24.55	27.51	-1.00	8.52E-01	1.12	6.85E-01
MCM3_HUMAN	DNA replication licensing factor MCM3	91 kDa	13.90	20.94	12.97	1.51	3.19E-02	-1.07	3.95E-01
MCM4_HUMAN	DNA replication licensing factor MCM4	97 kDa	11.22	10.12	18.16	-1.11	6.74E-01	1.62	6.68E-02
MCM5_HUMAN	DNA replication licensing factor MCM5	82 kDa	13.90	14.93	2.58	1.07	7.40E-01	-5.39	1.96E-03
MCM6_HUMAN	DNA replication licensing factor MCM6	93 kDa	5.86	5.31	5.69	-1.10	6.21E-01	-1.03	5.37E-01
MCM7_HUMAN	DNA replication licensing factor MCM7	81 kDa	27.29	20.94	16.08	-1.30	2.25E-01	-1.70	2.38E-02
APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase	36 kDa	21.93	29.36	19.20	1.34	1.12E-02	-1.14	2.85E-02
PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit	469 kDa	24.61	20.94	0.50	-1.18	6.62E-01	-49.22	1.51E-02
DNJA1_HUMAN	DnaJ homolog subfamily A member 1	45 kDa	22.83	22.15	21.28	-1.03	8.05E-01	-1.07	1.85E-01
DNJA2_HUMAN	DnaJ homolog subfamily A member 2	46 kDa	4.07	5.31	4.66	1.30	7.70E-01	1.14	9.32E-01
DNJB1_HUMAN	DnaJ homolog subfamily B member 1	38 kDa	18.36	22.15	12.97	1.21	3.50E-01	-1.42	8.11E-02
DNJC9_HUMAN	DnaJ homolog subfamily C member 9	30 kDa	8.54	12.53	11.93	1.47	2.44E-02	1.40	1.42E-01
OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	49 kDa	1.39	6.51	12.97	4.68	1.79E-02	9.31	8.29E-02
RIB2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor	69 kDa	2.29	2.91	19.20	1.27	7.80E-01	8.40	3.43E-03
RIB1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	69 kDa	24.61	25.75	18.16	1.05	8.12E-01	-1.36	3.49E-02
STAU1_HUMAN	Double-stranded RNA-binding protein Staufen homolog 1	63 kDa	13.90	16.13	11.93	1.16	4.37E-01	-1.17	1.69E-01
DREB_HUMAN	Drebrin	71 kDa	14.79	14.93	20.24	1.01	9.97E-01	1.37	5.41E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
DBNL_HUMAN	Drebrin-like protein	48 kDa	17.47	16.13	15.04	-1.08	6.92E-01	-1.16	1.88E-01
DCTN2_HUMAN	Dynactin subunit 2	44 kDa	8.54	12.53	15.04	1.47	2.48E-01	1.76	3.64E-01
DNM1L_HUMAN	Dynamamin-1-like protein	82 kDa	14.79	13.73	14.00	-1.08	7.70E-01	-1.06	5.14E-01
DYL1_HUMAN	Dynein light chain 1, cytoplasmic	10 kDa	18.36	17.34	22.31	-1.06	7.74E-01	1.22	5.83E-01
DLRB1_HUMAN	Dynein light chain roadblock-type 1	11 kDa	9.43	7.72	9.85	-1.22	6.42E-01	1.04	6.84E-01
EHD1_HUMAN	EH domain-containing protein 1	61 kDa	29.97	29.36	24.39	-1.02	8.28E-01	-1.23	2.67E-02
EHD2_HUMAN	EH domain-containing protein 2	61 kDa	11.22	8.92	6.73	-1.26	3.38E-01	-1.67	9.41E-02
ELAV1_HUMAN	ELAV-like protein 1	36 kDa	13.90	13.73	22.31	-1.01	9.55E-01	1.61	9.20E-02
ETFAL_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial precursor	35 kDa	13.00	16.13	20.24	1.24	2.21E-02	1.56	2.81E-02
ETFB_HUMAN	Electron transfer flavoprotein subunit beta	28 kDa	2.29	1.70	5.69	-1.34	7.77E-01	2.49	2.31E-01
EF1A1_HUMAN	Elongation factor 1-alpha 1	50 kDa	365.74	343.23	230.07	-1.07	1.35E-01	-1.59	1.04E-05
EF1B_HUMAN	Elongation factor 1-beta	25 kDa	10.32	10.12	10.89	-1.02	8.84E-01	1.05	7.47E-01
EF1D_HUMAN	Elongation factor 1-delta	31 kDa	42.47	49.81	55.56	1.17	3.66E-02	1.31	9.63E-02
EF1G_HUMAN	Elongation factor 1-gamma	50 kDa	88.02	82.27	87.76	-1.07	4.38E-01	-1.00	1.90E-01
EF2_HUMAN	Elongation factor 2	95 kDa	389.86	366.08	286.17	-1.06	2.61E-01	-1.36	2.09E-04
EFTU_HUMAN	Elongation factor Tu, mitochondrial precursor	50 kDa	36.22	42.59	55.56	1.18	1.12E-01	1.53	1.59E-01
SH3G1_HUMAN	Endophilin-A2	41 kDa	11.22	10.12	12.97	-1.11	3.05E-01	1.16	9.73E-01
ERP29_HUMAN	Endoplasmic reticulum protein ERp29 precursor	29 kDa	52.30	58.22	63.87	1.11	4.17E-01	1.22	6.50E-01
ENPL_HUMAN	Endoplasmin precursor	92 kDa	185.35	201.33	257.08	1.09	3.34E-01	1.39	1.43E-01
ERH_HUMAN	Enhancer of rudimentary homolog	12 kDa	13.90	17.34	22.31	1.25	2.74E-01	1.61	2.78E-02
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial precursor	31 kDa	20.15	17.34	32.70	-1.16	4.10E-01	1.62	3.57E-02
NPC2_HUMAN	Epididymal secretory protein E1 precursor	17 kDa	7.64	8.92	11.93	1.17	3.62E-01	1.56	8.59E-02
EPIPL_HUMAN	Epiplakin	553 kDa	21.04	17.34	19.20	-1.21	1.57E-01	-1.10	2.50E-01
ERO1A_HUMAN	ERO1-like protein alpha precursor	54 kDa	2.29	7.72	14.00	3.38	3.62E-02	6.13	6.89E-03
STOM_HUMAN	Erythrocyte band 7 integral membrane protein	32 kDa	13.90	14.93	9.85	1.07	7.40E-01	-1.41	1.45E-01
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I	46 kDa	89.80	93.10	97.11	1.04	7.31E-01	1.08	5.73E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
IF4A2_HUMAN	Eukaryotic initiation factor 4A-II	46 kDa	44.26	59.43	47.25	1.34	4.12E-01	1.07	7.73E-01
IF4A3_HUMAN	Eukaryotic initiation factor 4A-III	47 kDa	22.83	18.54	25.43	-1.23	1.07E-01	1.11	9.31E-01
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1	36 kDa	25.50	23.35	26.47	-1.09	6.30E-01	1.04	3.08E-01
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2	38 kDa	4.07	10.12	4.66	2.49	1.06E-01	1.14	9.29E-01
IF2G_HUMAN	Eukaryotic translation initiation factor 2 subunit 3	51 kDa	17.47	19.74	18.16	1.13	3.15E-01	1.04	3.93E-01
EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A	167 kDa	27.29	25.75	17.12	-1.06	7.43E-01	-1.59	9.24E-03
EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B	92 kDa	12.11	16.13	9.85	1.33	1.80E-01	-1.23	2.61E-01
IF3EI_HUMAN	Eukaryotic translation initiation factor 3 subunit E-interacting protein	67 kDa	10.32	10.12	6.73	-1.02	9.49E-01	-1.53	2.91E-01
IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	176 kDa	17.47	17.34	12.97	-1.01	9.80E-01	-1.35	1.22E-01
IF4H_HUMAN	Eukaryotic translation initiation factor 4H	27 kDa	21.04	16.13	9.85	-1.30	2.19E-01	-2.14	1.70E-02
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1	17 kDa	26.40	23.35	17.12	-1.13	6.12E-01	-1.54	6.21E-02
IF6_HUMAN	Eukaryotic translation initiation factor 6	27 kDa	34.43	35.37	34.78	1.03	7.38E-01	1.01	2.89E-01
XPO1_HUMAN	Exportin-1	123 kDa	21.04	17.34	19.20	-1.21	3.78E-01	-1.10	3.48E-01
XPO2_HUMAN	Exportin-2	110 kDa	116.59	121.96	75.29	1.05	3.50E-01	-1.55	2.44E-03
ESYT1_HUMAN	Extended-synaptotagmin-1	123 kDa	15.68	18.54	9.85	1.18	6.63E-01	-1.59	1.09E-02
EZRI_HUMAN	Ezrin	69 kDa	116.59	108.73	98.15	-1.07	4.22E-01	-1.19	3.84E-04
SP16H_HUMAN	FACT complex subunit SPT16	120 kDa	15.68	16.13	7.77	1.03	9.45E-01	-2.02	7.01E-03
CAZA1_HUMAN	F-actin-capping protein subunit alpha-1	33 kDa	23.72	25.75	31.66	1.09	4.71E-01	1.33	3.52E-01
CAPZB_HUMAN	F-actin-capping protein subunit beta	31 kDa	29.08	26.96	31.66	-1.08	7.84E-01	1.09	7.16E-01
FUBP1_HUMAN	Far upstream element-binding protein 1	68 kDa	20.15	17.34	26.47	-1.16	5.80E-01	1.31	3.90E-01
FUBP2_HUMAN	Far upstream element-binding protein 2	73 kDa	40.69	38.98	53.48	-1.04	7.10E-01	1.31	3.07E-01
FPPS_HUMAN	Farnesyl pyrophosphate synthetase	41 kDa	10.32	7.72	7.77	-1.34	4.56E-01	-1.33	2.44E-01
FSCN1_HUMAN	Fascin	55 kDa	18.36	24.55	20.24	1.34	1.64E-01	1.10	6.81E-01
FAS_HUMAN	Fatty acid synthase	273 kDa	141.60	142.40	87.76	1.01	9.22E-01	-1.61	1.86E-02
FERM2_HUMAN	Fermitin family homolog 2	78 kDa	10.32	12.53	4.66	1.21	6.62E-01	-2.22	6.80E-03
FINC_HUMAN	Fibronectin precursor	263 kDa	58.55	55.82	4.66	-1.05	8.62E-01	-12.58	2.07E-03

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
FLNA_HUMAN	Filamin-A	281 kDa	567.57	582.54	518.86	1.03	6.91E-01	-1.09	1.85E-02
FLNB_HUMAN	Filamin-B	278 kDa	352.35	336.02	284.09	-1.05	2.55E-01	-1.24	2.44E-02
FLNC_HUMAN	Filamin-C	291 kDa	104.98	100.31	78.41	-1.05	7.11E-01	-1.34	5.73E-02
FKBP3_HUMAN	FK506-binding protein 3	25 kDa	10.32	11.32	7.77	1.10	4.86E-01	-1.33	1.38E-02
FKBP4_HUMAN	FK506-binding protein 4	52 kDa	37.11	45.00	48.28	1.21	3.59E-01	1.30	4.93E-01
FEN1_HUMAN	Flap endonuclease 1	43 kDa	12.11	14.93	5.69	1.23	3.94E-01	-2.13	4.40E-02
FHL2_HUMAN	Four and a half LIM domains protein 2	32 kDa	12.11	14.93	14.00	1.23	2.00E-01	1.16	8.46E-01
FXR1_HUMAN	Fragile X mental retardation syndrome-related protein 1	70 kDa	6.75	7.72	10.89	1.14	7.35E-01	1.61	7.88E-02
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	39 kDa	155.89	164.05	127.23	1.05	5.45E-01	-1.23	4.91E-04
ALDOC_HUMAN	Fructose-bisphosphate aldolase C	39 kDa	42.47	46.20	38.94	1.09	5.88E-01	-1.09	4.16E-02
FUMH_HUMAN	Fumarate hydratase, mitochondrial precursor	55 kDa	11.22	8.92	9.85	-1.26	3.34E-01	-1.14	3.69E-01
LEG1_HUMAN	Galectin-1	15 kDa	179.10	162.85	173.98	-1.10	3.65E-01	-1.03	8.06E-02
LG3BP_HUMAN	Galectin-3-binding protein precursor	65 kDa	5.86	4.11	11.93	-1.43	4.54E-01	2.04	2.28E-01
ENOG_HUMAN	Gamma-enolase	47 kDa	205.00	222.98	143.85	1.09	8.37E-01	-1.43	9.42E-04
OFUT1_HUMAN	GDP-fucose protein O-fucosyltransferase 1 precursor	44 kDa	8.54	8.92	15.04	1.04	8.12E-01	1.76	1.56E-01
GELS_HUMAN	Gelsolin precursor	86 kDa	19.25	24.55	21.28	1.28	3.41E-01	1.11	9.02E-01
GTF2I_HUMAN	General transcription factor II-I	112 kDa	4.07	10.12	4.66	2.49	1.30E-01	1.14	8.86E-01
GNPI_HUMAN	Glucosamine-6-phosphate isomerase	33 kDa	12.11	12.53	11.93	1.03	8.79E-01	-1.02	4.57E-01
G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	59 kDa	42.47	40.18	32.70	-1.06	7.66E-01	-1.30	4.02E-02
G6PI_HUMAN	Glucose-6-phosphate isomerase	63 kDa	96.05	99.11	79.45	1.03	9.12E-01	-1.21	9.02E-03
GLU2B_HUMAN	Glucosidase 2 subunit beta precursor	59 kDa	38.90	42.59	52.44	1.09	4.27E-01	1.35	1.54E-01
DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial precursor	61 kDa	8.54	12.53	22.31	1.47	5.30E-01	2.61	2.54E-02
SYQ_HUMAN	Glutaminyl-tRNA synthetase	88 kDa	9.43	10.12	10.89	1.07	8.96E-01	1.15	9.92E-01
GSTK1_HUMAN	Glutathione S-transferase kappa 1	25 kDa	13.90	14.93	16.08	1.07	4.66E-01	1.16	9.74E-01
GSTP1_HUMAN	Glutathione S-transferase P	23 kDa	90.69	87.08	75.29	-1.04	3.80E-01	-1.20	5.37E-03
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	36 kDa	628.29	542.86	437.83	-1.16	3.93E-03	-1.43	7.50E-05

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
GCSH_HUMAN	Glycine cleavage system H protein, mitochondrial precursor	19 kDa	6.75	6.51	14.00	-1.04	8.19E-01	2.07	8.26E-03
PYGL_HUMAN	Glycogen phosphorylase, liver form	97 kDa	10.32	11.32	4.66	1.10	8.22E-01	-2.22	4.01E-02
GT251_HUMAN	Glycosyltransferase 25 family member 1 precursor	72 kDa	13.00	10.12	21.28	-1.28	3.46E-01	1.64	5.20E-02
SYG_HUMAN	Glycyl-tRNA synthetase	83 kDa	15.68	19.74	12.97	1.26	4.88E-01	-1.21	6.11E-02
GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase	36 kDa	9.43	7.72	6.73	-1.22	2.49E-01	-1.40	3.02E-02
GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing]	77 kDa	20.15	16.13	15.04	-1.25	1.69E-01	-1.34	1.38E-01
GRN_HUMAN	Granulins precursor	64 kDa	1.39	0.50	14.00	-2.79	4.37E-01	10.05	6.96E-02
RAN_HUMAN	GTP-binding nuclear protein Ran	24 kDa	39.79	41.39	48.28	1.04	8.33E-01	1.21	7.28E-01
GNAI2_HUMAN	Guanine nucleotide-binding protein G(i), alpha-2 subunit	40 kDa	27.29	32.97	15.04	1.21	4.92E-01	-1.81	3.67E-02
GBG12_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 precursor	8 kDa	10.32	6.51	5.69	-1.59	3.18E-01	-1.81	1.68E-01
GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	37 kDa	29.08	32.97	36.86	1.13	2.52E-02	1.27	7.77E-01
GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	37 kDa	28.18	34.17	38.94	1.21	2.36E-01	1.38	5.17E-01
GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	111 kDa	14.79	19.74	16.08	1.33	2.99E-01	1.09	7.32E-01
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1	35 kDa	49.62	58.22	50.36	1.17	1.21E-01	1.02	1.04E-01
HSP71_HUMAN	Heat shock 70 kDa protein 1	70 kDa	254.12	253.04	268.51	-1.00	8.44E-01	1.06	5.12E-01
HSP74_HUMAN	Heat shock 70 kDa protein 4	94 kDa	89.80	91.90	78.41	1.02	7.52E-01	-1.15	1.22E-02
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	71 kDa	553.28	544.06	546.91	-1.02	7.45E-01	-1.01	7.54E-02
HSBP1_HUMAN	Heat shock factor-binding protein 1	9 kDa	7.64	11.32	8.81	1.48	1.93E-01	1.15	9.51E-01
HS105_HUMAN	Heat shock protein 105 kDa	97 kDa	40.69	46.20	36.86	1.14	4.61E-01	-1.10	1.93E-01
TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondrial precursor	80 kDa	45.15	48.60	61.79	1.08	5.20E-01	1.37	2.42E-02
HSPB1_HUMAN	Heat shock protein beta-1	23 kDa	73.73	66.64	63.87	-1.11	8.81E-02	-1.15	1.04E-01
HS90A_HUMAN	Heat shock protein HSP 90-alpha	85 kDa	505.06	465.89	470.04	-1.08	3.41E-01	-1.07	5.10E-02
HS90B_HUMAN	Heat shock protein HSP 90-beta	83 kDa	459.51	446.65	444.07	-1.03	7.14E-01	-1.03	1.06E-01
HN1_HUMAN	Hematological and neurological expressed 1 protein	16 kDa	14.79	13.73	15.04	-1.08	4.77E-01	1.02	8.05E-01
HN1L_HUMAN	Hematological and neurological expressed 1-like protein	20 kDa	12.11	14.93	17.12	1.23	6.01E-02	1.41	3.01E-01
HDGF_HUMAN	Hepatoma-derived growth factor	27 kDa	13.00	16.13	19.20	1.24	5.03E-01	1.48	2.81E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B	36 kDa	34.43	42.59	65.94	1.24	4.41E-01	1.92	7.03E-02
ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0	31 kDa	8.54	13.73	15.04	1.61	1.79E-01	1.76	1.50E-01
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1	39 kDa	109.45	99.11	126.19	-1.10	2.87E-01	1.15	9.08E-01
ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3	40 kDa	27.29	30.56	47.25	1.12	2.90E-01	1.73	4.48E-03
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	38 kDa	54.08	60.63	80.49	1.12	6.49E-01	1.49	2.14E-01
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like	46 kDa	21.04	22.15	39.97	1.05	9.06E-01	1.90	4.75E-02
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	46 kDa	57.65	57.02	76.33	-1.01	5.76E-01	1.32	4.86E-02
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G	42 kDa	13.90	14.93	24.39	1.07	7.51E-01	1.76	4.11E-02
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	49 kDa	80.87	88.29	108.54	1.09	7.36E-03	1.34	6.82E-02
HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	49 kDa	58.55	58.22	76.33	-1.01	9.25E-01	1.30	1.62E-01
HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3	37 kDa	26.40	29.36	37.90	1.11	2.30E-01	1.44	2.16E-02
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	51 kDa	112.13	109.93	115.81	-1.02	6.72E-01	1.03	6.94E-02
HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	60 kDa	41.58	28.16	48.28	-1.48	1.07E-01	1.16	9.18E-01
HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M	78 kDa	97.84	96.71	126.19	-1.01	8.03E-01	1.29	3.04E-01
HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q	70 kDa	35.33	41.39	36.86	1.17	3.29E-01	1.04	4.41E-01
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R	71 kDa	12.11	20.94	24.39	1.73	3.44E-02	2.01	6.33E-02
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	91 kDa	89.80	87.08	92.95	-1.03	6.86E-01	1.04	3.96E-01
HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1	96 kDa	8.54	7.72	3.62	-1.11	7.38E-01	-2.36	5.05E-03
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	85 kDa	21.04	19.74	24.39	-1.07	5.20E-01	1.16	8.95E-01
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1	37 kDa	130.88	146.01	186.45	1.12	2.97E-01	1.42	6.70E-02
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	34 kDa	65.69	66.64	77.37	1.01	8.60E-01	1.18	9.94E-01
HMGB1_HUMAN	High mobility group protein B1	25 kDa	9.43	2.91	0.50	-3.25	1.81E-01	-18.86	4.35E-02
HINT1_HUMAN	Histidine triad nucleotide-binding protein 1	14 kDa	21.93	19.74	16.08	-1.11	1.52E-01	-1.36	1.15E-02
SYHC_HUMAN	Histidyl-tRNA synthetase, cytoplasmic	57 kDa	8.54	7.72	10.89	-1.11	8.55E-01	1.28	7.71E-01
HAT1_HUMAN	Histone acetyltransferase type B catalytic subunit	50 kDa	17.47	18.54	15.04	1.06	6.99E-01	-1.16	2.03E-01
HDAC2_HUMAN	Histone deacetylase 2	55 kDa	11.22	8.92	10.89	-1.26	1.92E-01	-1.03	2.82E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
H2A2A_HUMAN	Histone H2A type 2-A	14 kDa	200.54	180.89	196.83	-1.11	3.27E-01	-1.02	1.50E-03
H2B1C_HUMAN	Histone H2B type 1-C/E/F/G/I	14 kDa	173.75	190.51	217.61	1.10	4.79E-01	1.25	2.21E-01
H33_HUMAN	Histone H3.3	15 kDa	25.50	22.15	10.89	-1.15	5.54E-01	-2.34	1.61E-02
H4_HUMAN	Histone H4	11 kDa	188.03	189.30	185.41	1.01	9.35E-01	-1.01	5.93E-02
RBBP4_HUMAN	Histone-binding protein RBBP4	48 kDa	17.47	17.34	23.35	-1.01	9.96E-01	1.34	6.26E-01
RBBP7_HUMAN	Histone-binding protein RBBP7	48 kDa	9.43	7.72	6.73	-1.22	8.01E-01	-1.40	6.77E-01
1A02_HUMAN	HLA class I histocompatibility antigen, A-2 alpha chain precursor	41 kDa	111.23	117.15	133.47	1.05	5.75E-01	1.20	9.10E-01
1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain precursor	40 kDa	38.90	20.94	19.20	-1.86	3.70E-01	-2.03	2.68E-01
HCFC1_HUMAN	Host cell factor	209 kDa	6.75	11.32	5.69	1.68	5.95E-02	-1.19	4.09E-01
F10A1_HUMAN	Hsc70-interacting protein	41 kDa	4.97	6.51	10.89	1.31	7.66E-01	2.19	2.12E-01
CDC37_HUMAN	Hsp90 co-chaperone Cdc37	44 kDa	11.22	18.54	18.16	1.65	1.95E-01	1.62	3.45E-01
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase	25 kDa	65.69	66.64	63.87	1.01	9.58E-01	-1.03	3.71E-02
HYOU1_HUMAN	Hypoxia up-regulated protein 1 precursor	111 kDa	18.36	14.93	25.43	-1.23	6.30E-01	1.39	7.72E-01
IMA2_HUMAN	Importin subunit alpha-2	58 kDa	26.40	30.56	17.12	1.16	7.14E-01	-1.54	8.30E-02
IMA7_HUMAN	Importin subunit alpha-7	60 kDa	9.43	7.72	10.89	-1.22	2.65E-01	1.15	8.50E-01
IMB1_HUMAN	Importin subunit beta-1	97 kDa	61.23	72.65	54.52	1.19	9.90E-02	-1.12	4.25E-02
IMB3_HUMAN	Importin subunit beta-3	124 kDa	14.79	10.12	10.89	-1.46	2.44E-01	-1.36	1.96E-01
IPYR_HUMAN	Inorganic pyrophosphatase	33 kDa	13.00	23.35	17.12	1.80	1.02E-01	1.32	7.59E-01
IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase 2	56 kDa	21.04	13.73	15.04	-1.53	2.59E-02	-1.40	4.54E-03
IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2	62 kDa	4.07	6.51	9.85	1.60	5.10E-01	2.42	7.59E-02
ITA3_HUMAN	Integrin alpha-3 precursor	119 kDa	1.39	5.31	17.12	3.81	1.61E-01	12.29	1.35E-02
ITA6_HUMAN	Integrin alpha-6 precursor	127 kDa	8.54	7.72	4.66	-1.11	6.88E-01	-1.83	1.57E-01
ITB1_HUMAN	Integrin beta-1 precursor	88 kDa	20.15	26.96	39.97	1.34	4.67E-02	1.98	2.39E-02
UCRP_HUMAN	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein	18 kDa	4.07	8.92	9.85	2.19	3.94E-01	2.42	3.05E-01
IFIT1_HUMAN	Interferon-induced protein with tetratricopeptide repeats 1	55 kDa	16.57	18.54	7.77	1.12	8.64E-01	-2.13	2.56E-02
IFIT2_HUMAN	Interferon-induced protein with tetratricopeptide repeats 2	55 kDa	5.86	8.92	6.73	1.52	1.73E-01	1.15	8.25E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
IFIT3_HUMAN	Interferon-induced protein with tetratricopeptide repeats 3	56 kDa	30.86	36.58	34.78	1.19	5.74E-01	1.13	7.72E-01
ILF2_HUMAN	Interleukin enhancer-binding factor 2	43 kDa	20.15	19.74	26.47	-1.02	8.32E-01	1.31	5.39E-01
ILF3_HUMAN	Interleukin enhancer-binding factor 3	95 kDa	39.79	40.18	38.94	1.01	9.15E-01	-1.02	4.51E-01
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic	47 kDa	13.90	12.53	11.93	-1.11	2.51E-01	-1.17	1.17E-02
IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial precursor	51 kDa	4.07	5.31	12.97	1.30	7.13E-01	3.18	9.73E-02
SYIC_HUMAN	Isoleucyl-tRNA synthetase, cytoplasmic	145 kDa	7.64	7.72	6.73	1.01	9.89E-01	-1.14	4.32E-01
K1C10_HUMAN	Keratin, type I cytoskeletal 10	60 kDa	59.44	13.73	80.49	-4.33	2.38E-01	1.35	8.60E-01
K1C14_HUMAN	Keratin, type I cytoskeletal 14	52 kDa	24.61	14.93	30.63	-1.65	3.88E-01	1.24	8.05E-01
K1C16_HUMAN	Keratin, type I cytoskeletal 16	51 kDa	10.32	0.50	0.50	-20.65	4.37E-01	-20.65	3.56E-01
K1C17_HUMAN	Keratin, type I cytoskeletal 17	48 kDa	21.93	20.94	36.86	-1.05	9.34E-01	1.68	2.31E-01
K1C18_HUMAN	Keratin, type I cytoskeletal 18	48 kDa	249.65	238.61	285.13	-1.05	5.48E-01	1.14	9.66E-01
K1C9_HUMAN	Keratin, type I cytoskeletal 9	62 kDa	39.79	20.94	74.25	-1.90	6.74E-01	1.87	6.14E-01
K2C1_HUMAN	Keratin, type II cytoskeletal 1	66 kDa	423.79	278.29	692.34	-1.52	4.21E-01	1.63	4.28E-01
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	66 kDa	34.43	22.15	47.25	-1.55	2.41E-01	1.37	7.19E-01
K2C6C_HUMAN	Keratin, type II cytoskeletal 6C	60 kDa	20.15	19.74	21.28	-1.02	9.44E-01	1.06	9.51E-01
K2C8_HUMAN	Keratin, type II cytoskeletal 8	54 kDa	674.73	583.75	1079.81	-1.16	5.09E-01	1.60	1.09E-01
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1	48 kDa	11.22	2.91	2.58	-3.86	1.03E-02	-4.35	4.27E-03
KINH_HUMAN	Kinesin-1 heavy chain	110 kDa	10.32	13.73	20.24	1.33	3.08E-01	1.96	3.18E-03
LGUL_HUMAN	Lactoylglutathione lyase	21 kDa	30.86	31.77	30.63	1.03	7.70E-01	-1.01	6.87E-02
LMNA_HUMAN	Lamin-A/C	74 kDa	223.75	232.60	351.61	1.04	4.20E-01	1.57	7.17E-03
LAP2A_HUMAN	Lamina-associated polypeptide 2 isoform alpha	75 kDa	13.90	10.12	8.81	-1.37	4.38E-01	-1.58	1.79E-01
LMNB1_HUMAN	Lamin-B1	66 kDa	95.16	100.31	146.97	1.05	6.70E-01	1.54	1.62E-02
LMNB2_HUMAN	Lamin-B2	68 kDa	21.04	17.34	35.82	-1.21	6.11E-01	1.70	1.96E-01
LAMA5_HUMAN	Laminin subunit alpha-5 precursor	400 kDa	7.64	7.72	5.69	1.01	9.89E-01	-1.34	3.51E-01
LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial precursor	158 kDa	25.50	31.77	33.74	1.25	6.17E-02	1.32	6.08E-01
LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1	89 kDa	8.54	4.11	4.66	-2.08	1.11E-01	-1.83	3.71E-02

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
SYLC_HUMAN	Leucyl-tRNA synthetase, cytoplasmic	134 kDa	9.43	12.53	4.66	1.33	4.50E-01	-2.03	6.76E-02
LASP1_HUMAN	LIM and SH3 domain protein 1	30 kDa	44.26	38.98	34.78	-1.14	8.17E-02	-1.27	7.34E-02
LDHA_HUMAN	L-lactate dehydrogenase A chain	37 kDa	327.34	363.68	303.83	1.11	2.67E-02	-1.08	7.19E-04
LDHB_HUMAN	L-lactate dehydrogenase B chain	37 kDa	119.27	119.55	91.91	1.00	8.39E-01	-1.30	2.34E-04
LONM_HUMAN	Lon protease homolog, mitochondrial precursor	106 kDa	12.11	10.12	22.31	-1.20	4.05E-01	1.84	1.90E-01
ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3	80 kDa	6.75	4.11	0.50	-1.64	5.63E-01	-13.50	1.37E-01
ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	79 kDa	13.00	11.32	7.77	-1.15	4.87E-01	-1.67	2.52E-02
LA_HUMAN	Lupus La protein	47 kDa	8.54	10.12	7.77	1.19	4.22E-01	-1.10	1.44E-01
LU_HUMAN	Lutheran blood group glycoprotein precursor	67 kDa	11.22	12.53	6.73	1.12	7.06E-01	-1.67	7.48E-02
PPGB_HUMAN	Lysosomal protective protein precursor	54 kDa	9.43	10.12	6.73	1.07	8.51E-01	-1.40	2.10E-01
SYK_HUMAN	Lysyl-tRNA synthetase	68 kDa	13.90	14.93	11.93	1.07	7.00E-01	-1.17	1.21E-01
MIF_HUMAN	Macrophage migration inhibitory factor	12 kDa	9.43	10.12	14.00	1.07	7.24E-01	1.49	2.44E-01
CAPG_HUMAN	Macrophage-capping protein	39 kDa	22.83	24.55	24.39	1.08	6.86E-01	1.07	7.34E-01
MVP_HUMAN	Major vault protein	99 kDa	27.29	32.97	24.39	1.21	1.01E-01	-1.12	2.00E-01
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic	36 kDa	39.79	41.39	45.17	1.04	7.97E-01	1.14	8.24E-01
MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor	36 kDa	140.70	137.59	194.76	-1.02	6.74E-01	1.38	8.71E-02
M6PBP_HUMAN	Mannose-6-phosphate receptor-binding protein 1	47 kDa	42.47	51.01	38.94	1.20	6.41E-01	-1.09	2.31E-01
MRP_HUMAN	MARCKS-related protein	20 kDa	15.68	13.73	14.00	-1.14	3.72E-01	-1.12	1.84E-02
MATR3_HUMAN	Matrin-3	95 kDa	54.08	59.43	58.67	1.10	6.20E-01	1.08	4.72E-01
PGRC1_HUMAN	Membrane-associated progesterone receptor component 1	22 kDa	11.22	10.12	11.93	-1.11	6.28E-01	1.06	6.85E-01
MAT2B_HUMAN	Methionine adenosyltransferase 2 subunit beta	38 kDa	10.32	8.92	3.62	-1.16	5.50E-01	-2.85	5.56E-02
SYMC_HUMAN	Methionyl-tRNA synthetase, cytoplasmic	101 kDa	2.29	11.32	1.54	4.95	2.11E-01	-1.49	6.54E-01
MAP1B_HUMAN	Microtubule-associated protein 1B	271 kDa	5.86	11.32	5.69	1.93	1.87E-01	-1.03	6.32E-01
MAP4_HUMAN	Microtubule-associated protein 4	121 kDa	54.08	59.43	50.36	1.10	6.30E-01	-1.07	1.48E-01
MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1	30 kDa	20.15	20.94	20.24	1.04	9.74E-01	1.00	4.61E-01
TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog	16 kDa	4.07	6.51	16.08	1.60	5.16E-01	3.95	6.91E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
IMMT_HUMAN	Mitochondrial inner membrane protein	84 kDa	21.93	20.94	38.94	-1.05	8.10E-01	1.78	5.02E-02
BUB3_HUMAN	Mitotic checkpoint protein BUB3	37 kDa	17.47	18.54	28.55	1.06	7.27E-01	1.63	7.17E-02
MOES_HUMAN	Moesin	68 kDa	123.74	119.55	98.15	-1.03	5.88E-01	-1.26	2.44E-04
PUR6_HUMAN	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase]	47 kDa	27.29	35.37	19.20	1.30	5.52E-01	-1.42	8.52E-02
MYL6_HUMAN	Myosin light polypeptide 6	17 kDa	104.98	106.33	123.08	1.01	8.54E-01	1.17	7.84E-01
MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric	20 kDa	46.94	43.79	52.44	-1.07	3.30E-01	1.12	7.12E-01
MYH10_HUMAN	Myosin-10	229 kDa	68.37	61.83	46.21	-1.11	3.55E-01	-1.48	3.36E-02
MYH9_HUMAN	Myosin-9	227 kDa	792.61	700.39	635.21	-1.13	2.95E-02	-1.25	1.35E-04
MYO1C_HUMAN	Myosin-Ic	118 kDa	23.72	18.54	14.00	-1.28	1.42E-01	-1.69	2.79E-02
MTPN_HUMAN	Myotrophin	13 kDa	11.22	13.73	12.97	1.22	6.15E-02	1.16	8.37E-01
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate	32 kDa	21.93	13.73	27.51	-1.60	2.07E-01	1.25	8.82E-01
GNS_HUMAN	N-acetylglucosamine-6-sulfatase precursor	62 kDa	10.32	13.73	23.35	1.33	2.58E-01	2.26	1.07E-01
MAOM_HUMAN	NAD-dependent malic enzyme, mitochondrial precursor	65 kDa	1.39	2.91	6.73	2.09	3.92E-01	4.83	7.85E-02
NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	13 kDa	4.07	7.72	6.73	1.89	6.25E-04	1.65	6.80E-01
NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	30 kDa	3.18	5.31	10.89	1.67	3.58E-01	3.42	1.08E-01
NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor	24 kDa	4.97	6.51	10.89	1.31	5.40E-01	2.19	9.58E-02
NB5R3_HUMAN	NADH-cytochrome b5 reductase 3	34 kDa	9.43	12.53	6.73	1.33	2.62E-01	-1.40	1.39E-01
NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	79 kDa	6.75	7.72	15.04	1.14	7.55E-01	2.23	1.29E-01
LTB4D_HUMAN	NADP-dependent leukotriene B4 12-hydroxydehydrogenase	36 kDa	8.54	12.53	6.73	1.47	1.53E-01	-1.27	8.27E-02
NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha	23 kDa	47.83	45.00	45.17	-1.06	7.97E-02	-1.06	1.25E-02
AHNB_HUMAN	Neuroblast differentiation-associated protein AHNK	629 kDa	261.26	286.71	205.14	1.10	3.28E-01	-1.27	4.59E-02
GANAB_HUMAN	Neutral alpha-glucosidase AB precursor	107 kDa	68.37	60.63	77.37	-1.13	3.60E-01	1.13	7.57E-01
NH2L1_HUMAN	NHP2-like protein 1	14 kDa	13.90	11.32	20.24	-1.23	3.33E-01	1.46	1.39E-01
NIBL1_HUMAN	Niban-like protein 1	83 kDa	8.54	14.93	5.69	1.75	3.29E-01	-1.50	2.03E-01
NNMT_HUMAN	Nicotinamide N-methyltransferase	30 kDa	38.90	38.98	31.66	1.00	8.50E-01	-1.23	9.26E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
NONO_HUMAN	Non-POU domain-containing octamer-binding protein	54 kDa	44.26	51.01	74.25	1.15	1.47E-01	1.68	2.78E-02
NASP_HUMAN	Nuclear autoantigenic sperm protein	85 kDa	22.83	22.15	23.35	-1.03	7.24E-01	1.02	3.80E-01
NUMA1_HUMAN	Nuclear mitotic apparatus protein 1	238 kDa	15.68	19.74	21.28	1.26	6.07E-01	1.36	7.92E-01
NU155_HUMAN	Nuclear pore complex protein Nup155	155 kDa	4.97	2.91	10.89	-1.71	4.07E-01	2.19	2.94E-01
NUP93_HUMAN	Nuclear pore complex protein Nup93	93 kDa	9.43	10.12	12.97	1.07	8.49E-01	1.37	2.68E-01
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1	36 kDa	41.58	34.17	27.51	-1.22	5.45E-04	-1.51	1.58E-03
NUCL_HUMAN	Nucleolin	77 kDa	51.40	79.87	77.37	1.55	7.12E-02	1.51	1.49E-01
NPM_HUMAN	Nucleophosmin	33 kDa	86.23	89.49	102.30	1.04	7.00E-01	1.19	7.38E-01
TPR_HUMAN	Nucleoprotein TPR	266 kDa	9.43	7.72	23.35	-1.22	5.89E-01	2.48	8.74E-02
NDKA_HUMAN	Nucleoside diphosphate kinase A	17 kDa	30.86	32.97	22.31	1.07	8.96E-01	-1.38	3.94E-02
NDKB_HUMAN	Nucleoside diphosphate kinase B	17 kDa	73.73	72.65	61.79	-1.01	8.71E-01	-1.19	4.01E-02
NP1L1_HUMAN	Nucleosome assembly protein 1-like 1	45 kDa	31.76	26.96	26.47	-1.18	6.54E-02	-1.20	3.54E-04
NP1L4_HUMAN	Nucleosome assembly protein 1-like 4	43 kDa	15.68	18.54	20.24	1.18	8.06E-01	1.29	7.28E-01
OLA1_HUMAN	Obg-like ATPase 1	45 kDa	9.43	7.72	14.00	-1.22	6.73E-01	1.49	3.96E-01
OAT_HUMAN	Ornithine aminotransferase, mitochondrial precursor	49 kDa	11.22	13.73	26.47	1.22	5.36E-01	2.36	9.80E-02
PAXI_HUMAN	Paxillin	65 kDa	11.22	10.12	12.97	-1.11	5.51E-01	1.16	9.77E-01
PSIP1_HUMAN	PC4 and SFRS1-interacting protein	60 kDa	9.43	12.53	6.73	1.33	6.01E-01	-1.40	4.06E-01
PDL1_HUMAN	PDZ and LIM domain protein 1	36 kDa	46.94	40.18	46.21	-1.17	4.23E-01	-1.02	2.54E-01
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A	18 kDa	166.60	168.86	175.02	1.01	8.54E-01	1.05	6.80E-01
PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor	23 kDa	62.12	63.03	60.75	1.01	9.07E-01	-1.02	2.03E-01
PRDX1_HUMAN	Peroxiredoxin-1	22 kDa	84.44	82.27	75.29	-1.03	7.62E-01	-1.12	4.64E-02
PRDX2_HUMAN	Peroxiredoxin-2	22 kDa	13.00	17.34	12.97	1.33	2.61E-01	-1.00	5.92E-01
PRDX4_HUMAN	Peroxiredoxin-4	31 kDa	19.25	20.94	16.08	1.09	6.31E-01	-1.20	2.43E-01
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial precursor	22 kDa	33.54	30.56	31.66	-1.10	4.23E-01	-1.06	1.16E-01
PRDX6_HUMAN	Peroxiredoxin-6	25 kDa	45.15	40.18	38.94	-1.12	6.71E-02	-1.16	1.86E-02
DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2	80 kDa	13.90	13.73	28.55	-1.01	9.73E-01	2.05	1.57E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
MPCP_HUMAN	Phosphate carrier protein, mitochondrial precursor	40 kDa	17.47	20.94	16.08	1.20	5.41E-01	-1.09	1.17E-01
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1	21 kDa	38.90	34.17	32.70	-1.14	2.32E-01	-1.19	1.04E-01
PGM1_HUMAN	Phosphoglucomutase-1	61 kDa	7.64	6.51	7.77	-1.17	5.61E-01	1.02	6.59E-01
PGK1_HUMAN	Phosphoglycerate kinase 1	45 kDa	267.51	250.63	188.52	-1.07	1.43E-01	-1.42	2.36E-04
PGAM1_HUMAN	Phosphoglycerate mutase 1	29 kDa	67.48	77.46	59.71	1.15	1.42E-01	-1.13	1.22E-02
PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein	45 kDa	11.22	11.32	3.62	1.01	9.28E-01	-3.10	1.45E-01
PLST_HUMAN	Plastin-3	70 kDa	46.94	51.01	42.05	1.09	5.13E-01	-1.12	8.09E-02
PLEC1_HUMAN	Plectin-1	532 kDa	163.92	202.53	278.90	1.24	9.31E-02	1.70	5.00E-02
PARP1_HUMAN	Poly [ADP-ribose] polymerase 1	113 kDa	25.50	19.74	2.58	-1.29	4.93E-01	-9.89	5.99E-03
PCBP1_HUMAN	Poly(rC)-binding protein 1	37 kDa	57.65	61.83	64.91	1.07	4.02E-01	1.13	9.71E-01
PCBP2_HUMAN	Poly(rC)-binding protein 2	39 kDa	56.76	59.43	72.18	1.05	6.79E-01	1.27	4.06E-01
PUF60_HUMAN	Poly(U)-binding-splicing factor PUF60	60 kDa	4.97	5.31	7.77	1.07	9.78E-01	1.57	5.24E-01
PABP1_HUMAN	Polyadenylate-binding protein 1	71 kDa	47.83	45.00	45.17	-1.06	2.91E-01	-1.06	5.97E-02
PTRF_HUMAN	Polymerase I and transcript release factor	43 kDa	25.50	25.75	29.59	1.01	9.83E-01	1.16	8.75E-01
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1	57 kDa	54.97	42.59	38.94	-1.29	1.63E-01	-1.41	1.41E-02
PFD2_HUMAN	Prefoldin subunit 2	17 kDa	10.32	10.12	14.00	-1.02	9.33E-01	1.36	3.94E-01
PRP19_HUMAN	Pre-mRNA-processing factor 19	55 kDa	9.43	6.51	18.16	-1.45	1.41E-01	1.93	2.37E-01
PAWR_HUMAN	PRKC apoptosis WT1 regulator protein	37 kDa	7.64	7.72	10.89	1.01	9.42E-01	1.42	4.08E-01
SAP_HUMAN	Proactivator polypeptide precursor [Contains: Saposin-A	58 kDa	43.36	41.39	61.79	-1.05	6.81E-01	1.42	7.98E-02
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17	72 kDa	74.62	69.05	76.33	-1.08	3.63E-01	1.02	9.50E-02
DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5	69 kDa	76.41	78.67	74.25	1.03	7.46E-01	-1.03	7.35E-02
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor	84 kDa	6.75	13.73	24.39	2.03	5.50E-02	3.61	3.70E-02
PLOD2_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 precursor	85 kDa	30.86	32.97	39.97	1.07	6.49E-01	1.30	3.47E-01
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor	85 kDa	5.86	10.12	17.12	1.73	1.66E-01	2.92	1.93E-02
PROF1_HUMAN	Profilin-1	15 kDa	186.25	188.10	164.63	1.01	9.22E-01	-1.13	1.72E-03
PDC6L_HUMAN	Programmed cell death 6-interacting protein	96 kDa	21.93	25.75	16.08	1.17	4.99E-01	-1.36	2.13E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
PHB_HUMAN	Prohibitin	30 kDa	18.36	16.13	28.55	-1.14	5.07E-01	1.55	3.95E-01
PHB2_HUMAN	Prohibitin-2	33 kDa	29.08	36.58	38.94	1.26	2.21E-01	1.34	3.77E-01
PCNA_HUMAN	Proliferating cell nuclear antigen	29 kDa	46.04	55.82	52.44	1.21	2.58E-01	1.14	9.67E-01
PA2G4_HUMAN	Proliferation-associated protein 2G4	44 kDa	26.40	30.56	29.59	1.16	2.99E-01	1.12	7.12E-01
P3H1_HUMAN	Prolyl 3-hydroxylase 1 precursor	83 kDa	13.00	14.93	21.28	1.15	6.52E-01	1.64	1.37E-02
P4HA1_HUMAN	Prolyl 4-hydroxylase subunit alpha-1 precursor	61 kDa	4.07	1.70	19.20	-2.39	2.54E-01	4.71	1.15E-03
P4HA2_HUMAN	Prolyl 4-hydroxylase subunit alpha-2 precursor	61 kDa	10.32	11.32	23.35	1.10	6.80E-01	2.26	2.17E-02
TEBP_HUMAN	Prostaglandin E synthase 3	19 kDa	20.15	20.94	15.04	1.04	8.80E-01	-1.34	1.61E-01
PSME1_HUMAN	Proteasome activator complex subunit 1	29 kDa	45.15	47.40	37.90	1.05	8.04E-01	-1.19	2.77E-02
PSME2_HUMAN	Proteasome activator complex subunit 2	27 kDa	56.76	45.00	48.28	-1.26	2.56E-01	-1.18	1.08E-01
PSA4_HUMAN	Proteasome subunit alpha type-4	29 kDa	26.40	26.96	24.39	1.02	9.73E-01	-1.08	2.98E-01
PSA5_HUMAN	Proteasome subunit alpha type-5	26 kDa	9.43	11.32	9.85	1.20	4.55E-01	1.04	7.16E-01
PSA6_HUMAN	Proteasome subunit alpha type-6	27 kDa	13.90	24.55	22.31	1.77	1.55E-01	1.61	3.72E-01
PSA7_HUMAN	Proteasome subunit alpha type-7	28 kDa	29.08	19.74	24.39	-1.47	6.65E-02	-1.19	7.81E-02
PSB1_HUMAN	Proteasome subunit beta type-1 precursor	26 kDa	12.11	14.93	10.89	1.23	4.41E-01	-1.11	4.45E-01
PSB2_HUMAN	Proteasome subunit beta type-2	23 kDa	10.32	11.32	12.97	1.10	8.82E-01	1.26	8.70E-01
PSB4_HUMAN	Proteasome subunit beta type-4 precursor	29 kDa	30.86	32.97	30.63	1.07	1.77E-01	-1.01	1.85E-01
PSB5_HUMAN	Proteasome subunit beta type-5 precursor	23 kDa	12.11	12.53	14.00	1.03	8.07E-01	1.16	9.43E-01
PSB6_HUMAN	Proteasome subunit beta type-6 precursor	25 kDa	6.75	7.72	6.73	1.14	4.16E-01	-1.00	4.88E-01
ANM1_HUMAN	Protein arginine N-methyltransferase 1	42 kDa	14.79	8.92	10.89	-1.66	5.07E-02	-1.36	1.63E-01
C10_HUMAN	Protein C10	13 kDa	7.64	8.92	6.73	1.17	5.30E-01	-1.14	5.66E-01
CNPY2_HUMAN	Protein canopy homolog 2 precursor	21 kDa	3.18	5.31	11.93	1.67	5.78E-01	3.75	9.77E-02
CDV3_HUMAN	Protein CDV3 homolog	27 kDa	5.86	5.31	8.81	-1.10	8.09E-01	1.50	1.79E-01
DIAP1_HUMAN	Protein diaphanous homolog 1	139 kDa	8.54	7.72	5.69	-1.11	7.92E-01	-1.50	9.95E-02
PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor	57 kDa	154.99	165.25	250.85	1.07	5.06E-01	1.62	7.21E-02
PDIA4_HUMAN	Protein disulfide-isomerase A4 precursor	73 kDa	89.80	103.92	115.81	1.16	1.29E-01	1.29	2.31E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
PDIA6_HUMAN	Protein disulfide-isomerase A6 precursor	48 kDa	85.34	87.08	124.12	1.02	9.22E-01	1.45	1.30E-01
PDIA1_HUMAN	Protein disulfide-isomerase precursor	57 kDa	142.49	156.83	182.29	1.10	8.85E-02	1.28	1.29E-01
PARK7_HUMAN	Protein DJ-1	20 kDa	38.90	40.18	35.82	1.03	8.22E-01	-1.09	3.31E-02
DPY30_HUMAN	Protein dpy-30 homolog	11 kDa	7.64	7.72	7.77	1.01	8.80E-01	1.02	9.78E-02
K1967_HUMAN	Protein KIAA1967	103 kDa	5.86	7.72	9.85	1.32	3.78E-01	1.68	4.48E-01
PP1R7_HUMAN	Protein phosphatase 1 regulatory subunit 7	42 kDa	7.64	8.92	5.69	1.17	6.43E-01	-1.34	1.30E-01
PPME1_HUMAN	Protein phosphatase methylesterase 1	42 kDa	10.32	5.31	3.62	-1.94	1.97E-01	-2.85	6.79E-02
S10AA_HUMAN	Protein S100-A10	11 kDa	19.25	19.74	21.28	1.03	9.68E-01	1.11	9.25E-01
S10AB_HUMAN	Protein S100-A11	12 kDa	66.58	66.64	62.83	1.00	9.63E-01	-1.06	2.37E-03
SET_HUMAN	Protein SET	33 kDa	77.30	59.43	41.01	-1.30	3.18E-02	-1.88	9.49E-06
SC23A_HUMAN	Protein transport protein Sec23A	86 kDa	11.22	16.13	7.77	1.44	4.10E-01	-1.44	1.77E-01
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	25 kDa	16.57	12.53	7.77	-1.32	1.18E-01	-2.13	6.30E-03
PTMA_HUMAN	Prothymosin alpha [Contains: Thymosin alpha-1]	12 kDa	24.61	30.56	26.47	1.24	2.18E-01	1.08	6.28E-01
PSA_HUMAN	Puromycin-sensitive aminopeptidase	103 kDa	64.80	73.86	53.48	1.14	9.43E-02	-1.21	5.88E-03
DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	91 kDa	16.57	18.54	19.20	1.12	4.22E-01	1.16	8.36E-01
RBM3_HUMAN	Putative RNA-binding protein 3	17 kDa	28.18	19.74	23.35	-1.43	1.19E-01	-1.21	5.60E-02
PDXK_HUMAN	Pyridoxal kinase	35 kDa	8.54	10.12	6.73	1.19	5.30E-01	-1.27	7.75E-02
ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	39 kDa	10.32	7.72	18.16	-1.34	3.43E-01	1.76	2.79E-01
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2	58 kDa	763.14	730.46	621.70	-1.04	2.23E-01	-1.23	1.73E-04
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha	51 kDa	82.66	83.48	68.02	1.01	9.07E-01	-1.22	1.42E-03
GDIB_HUMAN	Rab GDP dissociation inhibitor beta	51 kDa	86.23	75.06	53.48	-1.15	2.98E-01	-1.61	5.84E-04
RADI_HUMAN	Radixin	69 kDa	31.76	40.18	33.74	1.27	5.76E-01	1.06	7.30E-01
RAGP1_HUMAN	Ran GTPase-activating protein 1	64 kDa	10.32	13.73	14.00	1.33	7.69E-02	1.36	6.61E-01
RANG_HUMAN	Ran-specific GTPase-activating protein	23 kDa	19.25	23.35	19.20	1.21	3.62E-01	-1.00	7.01E-01
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1	52 kDa	19.25	22.15	17.12	1.15	6.20E-01	-1.12	1.07E-01
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	189 kDa	97.84	109.93	77.37	1.12	4.02E-01	-1.26	4.45E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 precursor	21 kDa	10.32	8.92	7.77	-1.16	5.85E-01	-1.33	1.67E-01
RB11A_HUMAN	Ras-related protein Rab-11A	24 kDa	7.64	8.92	6.73	1.17	3.75E-01	-1.14	3.51E-01
RAB14_HUMAN	Ras-related protein Rab-14	24 kDa	24.61	31.77	33.74	1.29	6.32E-01	1.37	5.76E-01
RAB1B_HUMAN	Ras-related protein Rab-1B	22 kDa	41.58	42.59	46.21	1.02	9.38E-01	1.11	8.31E-01
RAP1B_HUMAN	Ras-related protein Rap-1b precursor	21 kDa	17.47	16.13	11.93	-1.08	7.15E-01	-1.46	1.42E-01
RRAS2_HUMAN	Ras-related protein R-Ras2 precursor	23 kDa	7.64	8.92	6.73	1.17	7.55E-01	-1.14	3.62E-01
RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit	68 kDa	14.79	14.93	12.97	1.01	9.68E-01	-1.14	2.05E-01
RCN1_HUMAN	Reticulocalbin-1 precursor	39 kDa	21.93	18.54	26.47	-1.18	1.93E-01	1.21	3.61E-01
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1	23 kDa	17.47	17.34	17.12	-1.01	9.23E-01	-1.02	5.71E-01
RHG01_HUMAN	Rho GTPase-activating protein 1	50 kDa	8.54	10.12	5.69	1.19	5.14E-01	-1.50	8.54E-02
RINI_HUMAN	Ribonuclease inhibitor	50 kDa	28.18	31.77	24.39	1.13	2.56E-01	-1.16	4.76E-02
RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit	90 kDa	12.11	16.13	6.73	1.33	2.85E-01	-1.80	9.78E-03
RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2	45 kDa	7.64	6.51	5.69	-1.17	5.37E-01	-1.34	2.87E-01
PRPS1_HUMAN	Ribose-phosphate pyrophosphokinase 1	35 kDa	15.68	12.53	11.93	-1.25	2.72E-01	-1.31	8.62E-02
RRBP1_HUMAN	Ribosome-binding protein 1	152 kDa	8.54	6.51	23.35	-1.31	4.79E-01	2.74	8.49E-02
RBM14_HUMAN	RNA-binding protein 14	69 kDa	4.97	6.51	11.93	1.31	3.89E-01	2.40	2.31E-02
RBM39_HUMAN	RNA-binding protein 39	59 kDa	12.11	10.12	7.77	-1.20	4.62E-01	-1.56	1.28E-01
RBM8A_HUMAN	RNA-binding protein 8A	20 kDa	8.54	7.72	9.85	-1.11	4.61E-01	1.15	8.98E-01
FUS_HUMAN	RNA-binding protein FUS	53 kDa	25.50	26.96	32.70	1.06	7.11E-01	1.28	6.30E-01
RALY_HUMAN	RNA-binding protein Raly	32 kDa	22.83	17.34	21.28	-1.32	3.40E-01	-1.07	3.78E-01
RUVB1_HUMAN	RuvB-like 1	50 kDa	27.29	28.16	26.47	1.03	9.27E-01	-1.03	1.92E-01
RUVB2_HUMAN	RuvB-like 2	51 kDa	25.50	25.75	45.17	1.01	9.47E-01	1.77	3.97E-02
METK2_HUMAN	S-adenosylmethionine synthetase isoform type-2	44 kDa	15.68	16.13	19.20	1.03	8.15E-01	1.22	5.32E-01
SAMH1_HUMAN	SAM domain and HD domain-containing protein 1	72 kDa	32.65	35.37	31.66	1.08	3.21E-01	-1.03	1.41E-01
SEPT2_HUMAN	Septin-2	41 kDa	35.33	31.77	37.90	-1.11	2.75E-01	1.07	7.57E-01
SEPT7_HUMAN	Septin-7	51 kDa	19.25	24.55	11.93	1.28	4.57E-01	-1.61	7.14E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
SEPT9_HUMAN	Septin-9	65 kDa	29.08	29.36	19.20	1.01	9.47E-01	-1.51	5.69E-03
GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic	53 kDa	14.79	12.53	19.20	-1.18	5.74E-01	1.30	3.66E-01
GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial precursor	56 kDa	20.15	23.35	35.82	1.16	4.33E-01	1.78	3.52E-02
PAK2_HUMAN	Serine/threonine-protein kinase PAK 2	58 kDa	8.54	6.51	5.69	-1.31	1.69E-01	-1.50	1.69E-02
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	65 kDa	60.33	60.63	51.40	1.00	9.15E-01	-1.17	1.29E-01
PP2AA_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	36 kDa	31.76	26.96	30.63	-1.18	1.69E-01	-1.04	1.48E-01
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	38 kDa	35.33	37.78	37.90	1.07	6.57E-01	1.07	4.83E-01
PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	37 kDa	31.76	29.36	35.82	-1.08	5.51E-01	1.13	7.89E-01
SPB6_HUMAN	Serpin B6	43 kDa	5.86	5.31	6.73	-1.10	8.62E-01	1.15	9.66E-01
SERPH_HUMAN	Serpin H1 precursor	46 kDa	67.48	67.84	84.64	1.01	9.07E-01	1.25	4.51E-01
ESTD_HUMAN	S-formylglutathione hydrolase	31 kDa	14.79	17.34	9.85	1.17	3.44E-01	-1.50	1.06E-02
SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3	10 kDa	10.32	10.12	9.85	-1.02	9.78E-01	-1.05	2.63E-01
SIAS_HUMAN	Sialic acid synthase	40 kDa	13.90	16.13	17.12	1.16	5.76E-01	1.23	8.49E-01
SFXN1_HUMAN	Sideroflexin-1	36 kDa	7.64	5.31	7.77	-1.44	2.67E-01	1.02	5.16E-01
SRP14_HUMAN	Signal recognition particle 14 kDa protein	15 kDa	8.54	10.12	5.69	1.19	4.22E-01	-1.50	3.54E-02
SRP09_HUMAN	Signal recognition particle 9 kDa protein	10 kDa	8.54	10.12	9.85	1.19	3.80E-01	1.15	8.96E-01
STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta	87 kDa	22.83	28.16	18.16	1.23	3.11E-04	-1.26	1.51E-02
STAT3_HUMAN	Signal transducer and activator of transcription 3	88 kDa	8.54	5.31	1.54	-1.61	2.79E-01	-5.55	8.31E-03
SSB_HUMAN	Single-stranded DNA-binding protein, mitochondrial precursor	17 kDa	29.97	31.77	35.82	1.06	7.90E-01	1.20	7.73E-01
RUXE_HUMAN	Small nuclear ribonucleoprotein E	11 kDa	6.75	4.11	12.97	-1.64	5.13E-01	1.92	2.43E-01
RUXF_HUMAN	Small nuclear ribonucleoprotein F	10 kDa	13.00	11.32	14.00	-1.15	4.26E-01	1.08	7.53E-01
SMD1_HUMAN	Small nuclear ribonucleoprotein Sm D1	13 kDa	10.32	7.72	7.77	-1.34	3.70E-01	-1.33	2.37E-01
SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2	14 kDa	18.36	17.34	18.16	-1.06	7.94E-01	-1.01	4.51E-02
SUMO2_HUMAN	Small ubiquitin-related modifier 2 precursor	11 kDa	13.00	16.13	10.89	1.24	1.50E-01	-1.19	1.58E-01
MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase	31 kDa	13.90	17.34	7.77	1.25	5.66E-02	-1.79	3.10E-04
AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 precursor	113 kDa	46.04	49.81	24.39	1.08	4.92E-01	-1.89	1.00E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
SORCN_HUMAN	Sorcin	22 kDa	6.75	8.92	6.73	1.32	2.79E-01	-1.00	4.50E-01
SPTA2_HUMAN	Spectrin alpha chain, brain	285 kDa	79.09	82.27	112.69	1.04	8.87E-01	1.42	4.11E-01
SPTB2_HUMAN	Spectrin beta chain, brain 1	275 kDa	88.02	82.27	126.19	-1.07	4.08E-01	1.43	1.31E-01
SKP1_HUMAN	S-phase kinase-associated protein 1	19 kDa	4.07	4.11	10.89	1.01	9.79E-01	2.67	2.66E-01
UAP56_HUMAN	Spliceosome RNA helicase BAT1	49 kDa	22.83	24.55	33.74	1.08	8.74E-01	1.48	7.41E-02
SF01_HUMAN	Splicing factor 1	68 kDa	11.22	10.12	9.85	-1.11	5.80E-01	-1.14	2.09E-01
SF3A1_HUMAN	Splicing factor 3 subunit 1	89 kDa	8.54	8.92	20.24	1.04	9.75E-01	2.37	8.96E-02
SF3B3_HUMAN	Splicing factor 3B subunit 3	136 kDa	30.86	29.36	45.17	-1.05	7.46E-01	1.46	2.85E-01
U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit	54 kDa	13.90	13.73	7.77	-1.01	8.49E-01	-1.79	1.11E-01
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1	28 kDa	18.36	23.35	27.51	1.27	2.22E-01	1.50	8.60E-02
SFRS2_HUMAN	Splicing factor, arginine/serine-rich 2	25 kDa	12.11	14.93	14.00	1.23	4.65E-01	1.16	9.78E-01
SFRS3_HUMAN	Splicing factor, arginine/serine-rich 3	19 kDa	11.22	10.12	7.77	-1.11	5.39E-01	-1.44	1.03E-01
SFRS9_HUMAN	Splicing factor, arginine/serine-rich 9	26 kDa	7.64	10.12	16.08	1.32	5.09E-02	2.10	9.18E-02
SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich	76 kDa	57.65	58.22	65.94	1.01	9.46E-01	1.14	7.71E-01
SRC8_HUMAN	Src substrate cortactin	62 kDa	26.40	26.96	28.55	1.02	8.92E-01	1.08	4.65E-01
SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1	102 kDa	29.08	28.16	14.00	-1.03	7.57E-01	-2.08	8.32E-03
STMN1_HUMAN	Stathmin	17 kDa	74.62	52.21	54.52	-1.43	8.08E-03	-1.37	1.04E-02
STML2_HUMAN	Stomatin-like protein 2	39 kDa	31.76	32.97	37.90	1.04	9.43E-01	1.19	9.45E-01
GRP75_HUMAN	Stress-70 protein, mitochondrial precursor	74 kDa	97.84	107.53	125.16	1.10	1.44E-01	1.28	2.19E-01
STIP1_HUMAN	Stress-induced-phosphoprotein 1	63 kDa	48.72	71.45	61.79	1.47	5.46E-03	1.27	1.89E-01
SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A	143 kDa	9.43	10.12	6.73	1.07	8.66E-01	-1.40	9.08E-02
SMC2_HUMAN	Structural maintenance of chromosomes protein 2	136 kDa	14.79	12.53	8.81	-1.18	5.93E-01	-1.68	1.42E-01
SMC3_HUMAN	Structural maintenance of chromosomes protein 3	142 kDa	10.32	7.72	10.89	-1.34	3.68E-01	1.05	7.62E-01
SMC4_HUMAN	Structural maintenance of chromosomes protein 4	147 kDa	15.68	17.34	16.08	1.11	7.68E-01	1.03	5.65E-01
DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	73 kDa	27.29	23.35	31.66	-1.17	2.35E-01	1.16	9.40E-01
SCOT_HUMAN	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor	56 kDa	3.18	5.31	10.89	1.67	3.90E-01	3.42	1.41E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
UBC9_HUMAN	SUMO-conjugating enzyme UBC9	18 kDa	10.32	4.11	4.66	-2.51	8.93E-02	-2.22	4.76E-02
SODC_HUMAN	Superoxide dismutase [Cu-Zn]	16 kDa	29.08	22.15	20.24	-1.31	1.82E-01	-1.44	2.34E-02
VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog	42 kDa	13.90	14.93	12.97	1.07	6.85E-01	-1.07	2.27E-01
TLN1_HUMAN	Talin-1	270 kDa	246.97	256.65	161.51	1.04	7.66E-01	-1.53	1.82E-03
TADBP_HUMAN	TAR DNA-binding protein 43	45 kDa	21.04	22.15	31.66	1.05	7.19E-01	1.50	1.21E-02
RBP56_HUMAN	TATA-binding protein-associated factor 2N	62 kDa	6.75	4.11	15.04	-1.64	4.36E-01	2.23	2.72E-01
TCPA_HUMAN	T-complex protein 1 subunit alpha	60 kDa	76.41	70.25	73.22	-1.09	4.06E-01	-1.04	2.43E-01
TCPB_HUMAN	T-complex protein 1 subunit beta	57 kDa	63.90	75.06	70.10	1.17	2.05E-01	1.10	5.93E-01
TCPD_HUMAN	T-complex protein 1 subunit delta	58 kDa	55.87	73.86	60.75	1.32	5.03E-02	1.09	4.96E-01
TCPE_HUMAN	T-complex protein 1 subunit epsilon	60 kDa	89.80	79.87	71.14	-1.12	2.66E-02	-1.26	6.82E-03
TCPH_HUMAN	T-complex protein 1 subunit eta	59 kDa	71.94	76.26	68.02	1.06	5.84E-01	-1.06	7.11E-02
TCPG_HUMAN	T-complex protein 1 subunit gamma	61 kDa	104.98	96.71	98.15	-1.09	2.18E-01	-1.07	1.13E-02
TCPQ_HUMAN	T-complex protein 1 subunit theta	60 kDa	65.69	77.46	69.06	1.18	1.98E-01	1.05	2.48E-01
TCPZ_HUMAN	T-complex protein 1 subunit zeta	58 kDa	47.83	51.01	41.01	1.07	6.35E-01	-1.17	5.99E-02
THIO_HUMAN	Thioredoxin	12 kDa	49.62	43.79	46.21	-1.13	3.42E-01	-1.07	1.95E-02
TXND4_HUMAN	Thioredoxin domain-containing protein 4 precursor	47 kDa	6.75	2.91	7.77	-2.32	2.73E-01	1.15	8.96E-01
TXND5_HUMAN	Thioredoxin domain-containing protein 5 precursor	48 kDa	13.00	11.32	16.08	-1.15	4.96E-01	1.24	6.39E-01
TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic	71 kDa	8.54	7.72	6.73	-1.11	5.50E-01	-1.27	2.25E-01
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	28 kDa	8.54	8.92	8.81	1.04	8.12E-01	1.03	4.94E-01
THOC4_HUMAN	THO complex subunit 4	27 kDa	2.29	2.91	5.69	1.27	7.62E-01	2.49	2.64E-01
SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic	83 kDa	40.69	51.01	35.82	1.25	5.06E-02	-1.14	1.54E-01
TSP1_HUMAN	Thrombospondin-1 precursor	129 kDa	38.90	37.78	17.12	-1.03	8.19E-01	-2.27	1.26E-03
KITH_HUMAN	Thymidine kinase, cytosolic	25 kDa	11.22	13.73	6.73	1.22	2.88E-01	-1.67	4.44E-02
TYB10_HUMAN	Thymosin beta-10	5 kDa	18.36	16.13	18.16	-1.14	4.30E-01	-1.01	5.43E-01
TYB4_HUMAN	Thymosin beta-4	5 kDa	38.01	29.36	38.94	-1.29	4.71E-02	1.02	6.61E-01
ZO2_HUMAN	Tight junction protein ZO-2	134 kDa	12.11	10.12	10.89	-1.20	3.98E-01	-1.11	3.78E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
TOIP1_HUMAN	Torsin-1A-interacting protein 1	66 kDa	4.07	7.72	11.93	1.89	2.01E-01	2.93	6.68E-02
TALDO_HUMAN	Transaldolase	38 kDa	27.29	28.16	25.43	1.03	9.05E-01	-1.07	4.40E-01
ELOC_HUMAN	Transcription elongation factor B polypeptide 1	12 kDa	10.32	13.73	12.97	1.33	7.12E-02	1.26	5.21E-01
TIF1B_HUMAN	Transcription intermediary factor 1-beta	89 kDa	45.15	49.81	70.10	1.10	3.97E-01	1.55	1.00E-02
TFR1_HUMAN	Transferrin receptor protein 1	85 kDa	50.51	58.22	51.40	1.15	1.61E-01	1.02	3.04E-01
RHOA_HUMAN	Transforming protein RhoA precursor	22 kDa	20.15	16.13	10.89	-1.25	3.71E-01	-1.85	3.49E-02
TAGL_HUMAN	Transgelin	23 kDa	17.47	18.54	15.04	1.06	7.88E-01	-1.16	1.62E-01
TAGL2_HUMAN	Transgelin-2	22 kDa	91.59	95.50	101.26	1.04	6.26E-01	1.11	6.57E-01
TERA_HUMAN	Transitional endoplasmic reticulum ATPase	89 kDa	185.35	185.70	185.41	1.00	9.38E-01	1.00	3.56E-02
TKT_HUMAN	Transketolase	68 kDa	132.67	137.59	127.23	1.04	7.69E-01	-1.04	5.38E-02
TCTP_HUMAN	Translationally-controlled tumor protein	20 kDa	17.47	13.73	12.97	-1.27	1.63E-01	-1.35	4.37E-02
TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 precursor	25 kDa	8.54	12.53	8.81	1.47	3.59E-01	1.03	7.29E-01
TNPO1_HUMAN	Transportin-1	101 kDa	14.79	13.73	12.97	-1.08	6.03E-01	-1.14	2.98E-01
ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial precursor	83 kDa	29.97	30.56	31.66	1.02	9.57E-01	1.06	5.48E-01
PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase	108 kDa	21.04	23.35	18.16	1.11	3.05E-01	-1.16	1.29E-01
TPIS_HUMAN	Triosephosphate isomerase	27 kDa	209.47	207.34	216.57	-1.01	8.19E-01	1.03	3.94E-01
NSUN2_HUMAN	tRNA	86 kDa	8.54	6.51	1.54	-1.31	4.75E-01	-5.55	1.79E-02
TMOD3_HUMAN	Tropomodulin-3	40 kDa	13.90	13.73	16.08	-1.01	8.86E-01	1.16	8.71E-01
TPM3_HUMAN	Tropomyosin alpha-3 chain	33 kDa	39.79	38.98	57.63	-1.02	9.01E-01	1.45	1.78E-01
TPM4_HUMAN	Tropomyosin alpha-4 chain	29 kDa	80.87	79.87	106.46	-1.01	8.55E-01	1.32	3.07E-01
TPM2_HUMAN	Tropomyosin beta chain	33 kDa	61.23	63.03	79.45	1.03	7.83E-01	1.30	4.03E-01
SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic	53 kDa	27.29	32.97	20.24	1.21	3.88E-01	-1.35	1.24E-02
TBA1A_HUMAN	Tubulin alpha-1A chain	50 kDa	498.80	492.35	423.29	-1.01	7.69E-01	-1.18	2.90E-03
TBA1B_HUMAN	Tubulin alpha-1B chain	50 kDa	619.36	621.03	527.17	1.00	8.98E-01	-1.17	6.71E-04
TBB5_HUMAN	Tubulin beta chain	50 kDa	921.20	912.05	787.91	-1.01	8.45E-01	-1.17	2.43E-06

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
TBB2A_HUMAN	Tubulin beta-2A chain	50 kDa	631.86	636.66	540.68	1.01	9.31E-01	-1.17	1.86E-06
TBB2C_HUMAN	Tubulin beta-2C chain	50 kDa	789.93	780.97	654.94	-1.01	8.43E-01	-1.21	2.69E-06
TBB3_HUMAN	Tubulin beta-3 chain	50 kDa	505.06	491.15	320.45	-1.03	7.66E-01	-1.58	2.75E-02
TBB6_HUMAN	Tubulin beta-6 chain	50 kDa	230.90	256.65	212.42	1.11	1.26E-01	-1.09	2.81E-03
TBCB_HUMAN	Tubulin folding cofactor B	27 kDa	8.54	10.12	8.81	1.19	7.43E-01	1.03	4.74E-01
TBCA_HUMAN	Tubulin-specific chaperone A	13 kDa	13.90	10.12	8.81	-1.37	1.15E-01	-1.58	9.77E-03
TPD54_HUMAN	Tumor protein D54	22 kDa	28.18	23.35	30.63	-1.21	4.31E-01	1.09	8.61E-01
RU1C_HUMAN	U1 small nuclear ribonucleoprotein C	17 kDa	7.64	7.72	7.77	1.01	8.79E-01	1.02	5.16E-01
U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase	245 kDa	24.61	28.16	37.90	1.14	6.07E-01	1.54	4.68E-01
UBQL1_HUMAN	Ubiquilin-1	63 kDa	13.90	16.13	8.81	1.16	6.25E-01	-1.58	2.81E-02
UBIQ_HUMAN	Ubiquitin	9 kDa	23.72	24.55	24.39	1.04	6.85E-01	1.03	2.73E-01
UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5	96 kDa	23.72	28.16	17.12	1.19	3.80E-01	-1.39	6.38E-02
UFD1_HUMAN	Ubiquitin fusion degradation protein 1 homolog	35 kDa	4.07	10.12	4.66	2.49	1.39E-01	1.14	8.70E-01
UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N	17 kDa	7.64	10.12	11.93	1.32	5.95E-01	1.56	3.22E-01
UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1	118 kDa	151.42	154.43	127.23	1.02	8.78E-01	-1.19	3.89E-03
UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 precursor	175 kDa	6.75	4.11	11.93	-1.64	2.49E-01	1.77	4.21E-01
CS010_HUMAN	Uncharacterized protein C19orf10 precursor	19 kDa	7.64	7.72	14.00	1.01	8.90E-01	1.83	8.65E-02
CV028_HUMAN	UPF0027 protein C22orf28	55 kDa	4.97	10.12	12.97	2.04	2.15E-01	2.61	1.32E-01
UTRO_HUMAN	Utrophin	394 kDa	8.54	13.73	5.69	1.61	1.38E-01	-1.50	2.44E-01
RD23B_HUMAN	UV excision repair protein RAD23 homolog B	43 kDa	13.90	13.73	8.81	-1.01	9.07E-01	-1.58	1.91E-01
VPS35_HUMAN	Vacuolar protein sorting-associated protein 35	92 kDa	21.93	16.13	21.28	-1.36	9.85E-02	-1.03	1.78E-01
ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	70 kDa	10.32	12.53	21.28	1.21	3.17E-01	2.06	2.36E-01
VAMP3_HUMAN	Vesicle-associated membrane protein 3	11 kDa	7.64	4.11	3.62	-1.86	1.61E-01	-2.11	7.17E-02
VIGLN_HUMAN	Vigilin	141 kDa	13.00	14.93	12.97	1.15	7.64E-01	-1.00	6.59E-01
VIME_HUMAN	Vimentin	54 kDa	672.05	720.84	1056.96	1.07	4.00E-02	1.57	7.23E-03
VINC_HUMAN	Vinculin	124 kDa	88.02	96.71	79.45	1.10	5.03E-01	-1.11	1.05E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	31 kDa	36.22	34.17	61.79	-1.06	7.38E-01	1.71	9.97E-02
WDR1_HUMAN	WD repeat-containing protein 1	66 kDa	22.83	31.77	20.24	1.39	8.58E-02	-1.13	1.68E-01
ZCC2_HUMAN	Zinc finger CCCH type antiviral protein 1	101 kDa	11.22	8.92	5.69	-1.26	1.79E-01	-1.97	1.75E-02
ZYX_HUMAN	Zyxin	61 kDa	21.93	22.15	19.20	1.01	9.66E-01	-1.14	1.97E-01

Aufgelistet sind alle quantifizierbaren Proteine. Die Anzahl der assigned Spektren wurde zunächst innerhalb der Bioreplikate für jeden Probensatz normalisiert und zu 0.5 addiert. Als in der Proteinmenge signifikant veränderte Proteine wurden Proteine mit einem p -Wert ≤ 0.5 (≥ 1.5 -fach bzw. ≤ -1.5 -fach) angesehen. Der Fold Change bezieht sich jeweils auf die zeitgleiche Kontrolle.

Co = zeitgleiche Kontrolle der S9-Zellen, S9-inf = *S. aureus*-infizierte S9-Zellen, S9-int = *S. aureus* internalisierte S9-Zellen.

Tab. 70: Liste der quantifizierbaren Proteine für S9-Zellen nach einer *S. aureus*-Behandlung zum Zeitpunkt $t_{6\text{ h}30}$.

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
CH10_HUMAN	10 kDa heat shock protein, mitochondrial	11 kDa	55.29	59.33	77.78	1.07	8.71E-01	1.41	1.61E-03
U5S1_HUMAN	116 kDa U5 small nuclear ribonucleoprotein component	109 kDa	47.73	53.35	66.88	1.12	6.17E-01	1.40	1.85E-02
1433B_HUMAN	14-3-3 protein beta/alpha	28 kDa	144.09	147.08	125.34	1.02	5.04E-01	-1.15	3.30E-03
1433E_HUMAN	14-3-3 protein epsilon	29 kDa	160.15	160.05	157.05	-1.00	3.15E-01	-1.02	9.88E-02
1433F_HUMAN	14-3-3 protein eta	28 kDa	58.12	53.35	36.17	-1.09	2.57E-01	-1.61	1.72E-03
1433G_HUMAN	14-3-3 protein gamma	28 kDa	105.36	100.22	80.76	-1.05	1.87E-01	-1.30	3.56E-04
1433S_HUMAN	14-3-3 protein sigma	28 kDa	76.07	62.32	39.14	-1.22	1.32E-01	-1.94	1.17E-03
1433T_HUMAN	14-3-3 protein theta	28 kDa	123.30	123.15	82.74	-1.00	3.95E-01	-1.49	1.58E-04
1433Z_HUMAN	14-3-3 protein zeta/delta	28 kDa	158.26	171.02	142.19	1.08	5.60E-01	-1.11	1.13E-02
CN37_HUMAN	2',3'-cyclic-nucleotide 3'-phosphodiesterase	48 kDa	5.22	7.48	6.44	1.43	5.33E-01	1.23	4.90E-01
PRS4_HUMAN	26S protease regulatory subunit 4	49 kDa	16.56	15.46	14.37	-1.07	4.44E-01	-1.15	2.77E-01
PRS6A_HUMAN	26S protease regulatory subunit 6A	49 kDa	28.84	28.42	38.15	-1.01	5.22E-01	1.32	2.30E-03
PRS7_HUMAN	26S protease regulatory subunit 7	49 kDa	23.17	20.44	27.25	-1.13	5.09E-01	1.18	4.76E-01
PRS8_HUMAN	26S protease regulatory subunit 8	46 kDa	9.00	1.50	7.44	-6.01	1.96E-02	-1.21	5.40E-01
PRS10_HUMAN	26S protease regulatory subunit S10B	44 kDa	4.28	5.49	11.40	1.28	6.76E-01	2.66	2.59E-02
PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1	106 kDa	8.06	5.49	4.46	-1.47	3.48E-01	-1.81	1.87E-01
PSD11_HUMAN	26S proteasome non-ATPase regulatory subunit 11	47 kDa	22.23	19.45	25.27	-1.14	7.13E-02	1.14	4.13E-01
PSD12_HUMAN	26S proteasome non-ATPase regulatory subunit 12	53 kDa	8.06	10.47	11.40	1.30	4.76E-01	1.41	2.82E-01
PSDE_HUMAN	26S proteasome non-ATPase regulatory subunit 14	35 kDa	19.39	17.45	25.27	-1.11	1.81E-01	1.30	1.39E-01
PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2	100 kDa	16.56	15.46	20.32	-1.07	7.93E-01	1.23	6.30E-01
PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3	61 kDa	15.61	23.43	8.43	1.50	1.37E-02	-1.85	3.49E-03
PSMD4_HUMAN	26S proteasome non-ATPase regulatory subunit 4	41 kDa	9.00	7.48	7.44	-1.20	3.88E-01	-1.21	2.06E-01
PSMD5_HUMAN	26S proteasome non-ATPase regulatory subunit 5	56 kDa	4.28	5.49	4.46	1.28	7.53E-01	1.04	9.99E-01
PSMD6_HUMAN	26S proteasome non-ATPase regulatory subunit 6	46 kDa	6.17	5.49	9.42	-1.12	6.75E-01	1.53	8.83E-02

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
HAP28_HUMAN	28 kDa heat- and acid-stable phosphoprotein	21 kDa	13.73	16.45	4.46	1.20	2.44E-01	-3.08	5.47E-03
ODO1_HUMAN	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor	116 kDa	0.50	5.49	9.42	10.97	4.06E-02	18.83	3.77E-02
D3D2_HUMAN	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	33 kDa	7.11	7.48	12.39	1.05	9.97E-01	1.74	3.82E-02
RM12_HUMAN	39S ribosomal protein L12, mitochondrial precursor	21 kDa	8.06	10.47	17.34	1.30	1.33E-01	2.15	2.10E-04
HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	27 kDa	22.23	18.45	24.28	-1.20	4.22E-02	1.09	6.52E-01
3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35 kDa	9.95	8.48	19.33	-1.17	3.12E-01	1.94	3.92E-03
THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial	42 kDa	12.78	8.48	19.33	-1.51	8.60E-02	1.51	2.98E-02
RS10_HUMAN	40S ribosomal protein S10	19 kDa	20.34	21.44	13.38	1.05	9.84E-01	-1.52	5.16E-02
RS12_HUMAN	40S ribosomal protein S12	15 kDa	14.67	18.45	13.38	1.26	3.45E-01	-1.10	5.28E-01
RS14_HUMAN	40S ribosomal protein S14	16 kDa	13.73	11.47	12.39	-1.20	1.84E-01	-1.11	2.90E-01
RS15_HUMAN	40S ribosomal protein S15	17 kDa	10.89	10.47	8.43	-1.04	6.82E-01	-1.29	1.73E-01
RS15A_HUMAN	40S ribosomal protein S15a	15 kDa	8.06	7.48	5.45	-1.08	6.12E-01	-1.48	2.73E-01
RS18_HUMAN	40S ribosomal protein S18	18 kDa	10.89	10.47	5.45	-1.04	6.77E-01	-2.00	2.31E-02
RS2_HUMAN	40S ribosomal protein S2	31 kDa	19.39	10.47	16.35	-1.85	4.31E-02	-1.19	5.26E-01
RS21_HUMAN	40S ribosomal protein S21	9 kDa	13.73	16.45	19.33	1.20	8.81E-02	1.41	1.15E-02
RS27_HUMAN	40S ribosomal protein S27	9 kDa	10.89	9.47	6.44	-1.15	6.40E-01	-1.69	2.22E-01
RS3_HUMAN	40S ribosomal protein S3	27 kDa	52.46	54.35	33.20	1.04	9.41E-01	-1.58	2.81E-02
RS4X_HUMAN	40S ribosomal protein S4, X isoform	30 kDa	26.95	29.42	23.29	1.09	8.92E-01	-1.16	4.62E-01
RS5_HUMAN	40S ribosomal protein S5	23 kDa	33.56	37.40	16.35	1.11	6.58E-01	-2.05	6.81E-03
RS7_HUMAN	40S ribosomal protein S7	22 kDa	29.78	36.40	38.15	1.22	3.74E-01	1.28	3.11E-02
RS8_HUMAN	40S ribosomal protein S8	24 kDa	37.34	39.39	32.21	1.05	1.00E+00	-1.16	5.09E-02
RSSA_HUMAN	40S ribosomal protein SA	33 kDa	52.46	58.34	54.00	1.11	5.26E-01	1.03	8.26E-01
4F2_HUMAN	4F2 cell-surface antigen heavy chain	58 kDa	9.95	13.46	12.39	1.35	8.17E-02	1.25	5.24E-01
OASL_HUMAN	59 kDa 2'-5'-oligoadenylate synthetase-like protein	59 kDa	0.50	9.47	8.43	18.95	1.46E-04	16.85	3.01E-02
CH60_HUMAN	60 kDa heat shock protein, mitochondrial precursor	61 kDa	207.38	232.84	314.59	1.12	3.20E-01	1.52	3.35E-04
RLA0_HUMAN	60S acidic ribosomal protein P0	34 kDa	32.62	40.39	28.24	1.24	8.96E-02	-1.15	1.02E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
RLA1_HUMAN	60S acidic ribosomal protein P1	12 kDa	35.45	35.40	30.22	-1.00	4.29E-01	-1.17	2.58E-02
RLA2_HUMAN	60S acidic ribosomal protein P2	12 kDa	58.12	57.34	47.07	-1.01	5.72E-01	-1.23	6.13E-02
RL10_HUMAN	60S ribosomal protein L10	25 kDa	10.89	8.48	7.44	-1.28	1.68E-01	-1.46	1.19E-01
RL11_HUMAN	60S ribosomal protein L11	20 kDa	9.95	11.47	12.39	1.15	7.76E-01	1.25	5.20E-01
RL12_HUMAN	60S ribosomal protein L12	18 kDa	29.78	32.41	30.22	1.09	7.03E-01	1.01	6.15E-01
RL13_HUMAN	60S ribosomal protein L13	24 kDa	10.89	12.47	8.43	1.14	7.32E-01	-1.29	1.81E-01
RL15_HUMAN	60S ribosomal protein L15	24 kDa	11.84	12.47	11.40	1.05	9.96E-01	-1.04	6.33E-01
RL18_HUMAN	60S ribosomal protein L18	22 kDa	9.95	7.48	4.46	-1.33	3.14E-01	-2.23	2.79E-02
RL22_HUMAN	60S ribosomal protein L22	15 kDa	22.23	23.43	6.44	1.05	9.91E-01	-3.45	3.12E-05
RL23_HUMAN	60S ribosomal protein L23	15 kDa	9.00	7.48	6.44	-1.20	2.20E-01	-1.40	9.55E-02
RL23A_HUMAN	60S ribosomal protein L23a	18 kDa	12.78	10.47	8.43	-1.22	3.23E-01	-1.52	1.59E-01
RL27A_HUMAN	60S ribosomal protein L27a	17 kDa	13.73	14.46	13.38	1.05	9.81E-01	-1.03	6.71E-01
RL3_HUMAN	60S ribosomal protein L3	46 kDa	21.28	14.46	12.39	-1.47	5.27E-02	-1.72	3.02E-02
RL30_HUMAN	60S ribosomal protein L30	13 kDa	16.56	13.46	17.34	-1.23	1.24E-01	1.05	9.85E-01
RL36_HUMAN	60S ribosomal protein L36	12 kDa	5.22	8.48	6.44	1.62	1.77E-01	1.23	5.55E-01
RL4_HUMAN	60S ribosomal protein L4	48 kDa	32.62	36.40	36.17	1.12	7.29E-01	1.11	5.46E-01
RL5_HUMAN	60S ribosomal protein L5	34 kDa	10.89	6.48	3.47	-1.68	2.18E-01	-3.14	4.13E-02
RL6_HUMAN	60S ribosomal protein L6	33 kDa	10.89	8.48	10.41	-1.28	4.23E-01	-1.05	7.77E-01
RL7_HUMAN	60S ribosomal protein L7	29 kDa	18.45	18.45	11.40	1.00	8.04E-01	-1.62	2.30E-01
RL9_HUMAN	60S ribosomal protein L9	22 kDa	18.45	12.47	11.40	-1.48	9.98E-03	-1.62	1.21E-02
K6PP_HUMAN	6-phosphofruktokinase type C	86 kDa	59.07	54.35	51.03	-1.09	1.52E-01	-1.16	1.07E-01
K6PL_HUMAN	6-phosphofruktokinase, liver type	85 kDa	20.34	22.44	17.34	1.10	7.10E-01	-1.17	9.72E-02
6PGD_HUMAN	6-phosphogluconate dehydrogenase, decarboxylating	53 kDa	20.34	14.46	2.48	-1.41	4.68E-02	-8.20	1.98E-04
GRP78_HUMAN	78 kDa glucose-regulated protein precursor	72 kDa	234.77	255.77	347.28	1.09	5.95E-01	1.48	1.54E-03
THIC_HUMAN	Acetyl-CoA acetyltransferase, cytosolic	41 kDa	56.23	60.33	39.14	1.07	8.54E-01	-1.44	6.79E-03
THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial precursor	45 kDa	14.67	12.47	17.34	-1.18	2.46E-01	1.18	4.38E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
AN32A_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A	29 kDa	9.95	12.47	6.44	1.25	5.90E-01	-1.54	4.65E-01
AN32B_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B	29 kDa	14.67	16.45	11.40	1.12	6.15E-01	-1.29	1.10E-01
AN32E_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member E	31 kDa	10.89	11.47	9.42	1.05	9.73E-01	-1.16	4.78E-01
ACON_HUMAN	Aconitate hydratase, mitochondrial precursor	85 kDa	7.11	6.48	15.36	-1.10	5.22E-01	2.16	1.12E-01
ACTC_HUMAN	Actin, alpha cardiac muscle 1	42 kDa	385.92	364.47	323.50	-1.06	1.69E-01	-1.19	1.16E-02
ACTB_HUMAN	Actin, cytoplasmic 1	42 kDa	1943.64	1862.21	1743.34	-1.04	1.43E-03	-1.11	3.09E-04
ACL6A_HUMAN	Actin-like protein 6A	47 kDa	6.17	7.48	11.40	1.21	5.74E-01	1.85	7.90E-02
ARP2_HUMAN	Actin-related protein 2	45 kDa	36.40	36.40	37.16	1.00	7.89E-01	1.02	8.97E-01
ARC1B_HUMAN	Actin-related protein 2/3 complex subunit 1B	41 kDa	7.11	7.48	6.44	1.05	9.54E-01	-1.10	5.44E-01
ARPC3_HUMAN	Actin-related protein 2/3 complex subunit 3	21 kDa	12.78	12.47	16.35	-1.03	8.00E-01	1.28	2.99E-01
ARP3_HUMAN	Actin-related protein 3	47 kDa	62.85	67.31	60.94	1.07	8.44E-01	-1.03	3.47E-01
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15	14 kDa	14.67	14.46	6.44	-1.01	8.46E-01	-2.28	2.75E-02
ACOT9_HUMAN	Acyl-coenzyme A thioesterase 9	46 kDa	4.28	4.49	21.31	1.05	9.58E-01	4.98	1.10E-04
APT_HUMAN	Adenine phosphoribosyltransferase	20 kDa	8.06	7.48	6.44	-1.08	6.16E-01	-1.25	3.68E-01
ADK_HUMAN	Adenosine kinase	41 kDa	14.67	11.47	6.44	-1.28	1.19E-01	-2.28	7.88E-03
SAHH_HUMAN	Adenosylhomocysteinase	48 kDa	62.85	71.30	61.93	1.13	3.85E-01	-1.01	4.46E-01
KAD1_HUMAN	Adenylate kinase isoenzyme 1	22 kDa	12.78	13.46	11.40	1.05	9.76E-01	-1.12	2.32E-01
KAD2_HUMAN	Adenylate kinase isoenzyme 2, mitochondrial	26 kDa	2.39	3.49	10.41	1.46	6.79E-01	4.36	2.97E-03
CAP1_HUMAN	Adenylyl cyclase-associated protein 1	52 kDa	91.19	90.24	80.76	-1.01	3.24E-01	-1.13	5.38E-03
ADT2_HUMAN	ADP/ATP translocase 2	33 kDa	32.62	33.41	24.28	1.02	8.81E-01	-1.34	1.05E-01
ARF1_HUMAN	ADP-ribosylation factor 1	21 kDa	30.73	34.40	16.35	1.12	7.63E-01	-1.88	1.11E-01
ARF4_HUMAN	ADP-ribosylation factor 4	21 kDa	10.89	15.46	5.45	1.42	1.91E-01	-2.00	1.25E-01
ARF5_HUMAN	ADP-ribosylation factor 5	21 kDa	10.89	14.46	2.48	1.33	4.26E-01	-4.39	3.90E-02
AKA12_HUMAN	A-kinase anchor protein 12	191 kDa	16.56	20.44	17.34	1.23	4.45E-01	1.05	9.83E-01
SYAC_HUMAN	Alanyl-tRNA synthetase, cytoplasmic	107 kDa	43.95	46.37	43.10	1.05	9.98E-01	-1.02	5.68E-01
FETUA_HUMAN	Alpha-2-HS-glycoprotein precursor	39 kDa	11.84	18.45	0.50	1.56	1.69E-01	-23.67	7.63E-03

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ACTN1_HUMAN	Alpha-actinin-1	103 kDa	294.29	301.64	309.63	1.03	4.15E-01	1.05	9.49E-01
ACTN4_HUMAN	Alpha-actinin-4	105 kDa	355.69	358.48	340.35	1.01	1.28E-02	-1.05	3.38E-02
AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	55 kDa	26.95	30.41	34.19	1.13	6.25E-01	1.27	1.92E-01
ACTZ_HUMAN	Alpha-centractin	43 kDa	24.12	21.44	17.34	-1.12	3.01E-01	-1.39	1.32E-01
ENOA_HUMAN	Alpha-enolase	47 kDa	1144.47	1027.58	777.30	-1.11	1.26E-02	-1.47	1.92E-05
AINX_HUMAN	Alpha-internexin	55 kDa	7.11	0.50	21.31	-14.23	9.16E-02	3.00	1.17E-01
SNAA_HUMAN	Alpha-soluble NSF attachment protein	33 kDa	6.17	5.49	5.45	-1.12	7.46E-01	-1.13	7.56E-01
ANXA1_HUMAN	Annexin A1	39 kDa	204.54	208.91	165.97	1.02	2.46E-01	-1.23	4.41E-04
ANX11_HUMAN	Annexin A11	54 kDa	8.06	8.48	5.45	1.05	9.88E-01	-1.48	1.46E-01
ANXA2_HUMAN	Annexin A2	39 kDa	569.18	585.84	463.21	1.03	2.30E-01	-1.23	1.47E-03
ANXA3_HUMAN	Annexin A3	36 kDa	26.95	32.41	27.25	1.20	4.74E-01	1.01	8.67E-01
ANXA4_HUMAN	Annexin A4	36 kDa	14.67	16.45	11.40	1.12	7.50E-01	-1.29	1.68E-01
ANXA5_HUMAN	Annexin A5	36 kDa	77.02	89.25	70.85	1.16	4.08E-01	-1.09	2.15E-01
ANXA6_HUMAN	Annexin A6	76 kDa	30.73	30.41	31.22	-1.01	4.73E-01	1.02	7.52E-01
AP2A1_HUMAN	AP-2 complex subunit alpha-1	108 kDa	10.89	11.47	11.40	1.05	9.96E-01	1.05	9.87E-01
AP2B1_HUMAN	AP-2 complex subunit beta-1	105 kDa	17.50	17.45	16.35	-1.00	7.76E-01	-1.07	6.67E-01
APOL2_HUMAN	Apolipoprotein-L2	37 kDa	5.22	5.49	23.29	1.05	9.81E-01	4.46	1.70E-03
API5_HUMAN	Apoptosis inhibitor 5	58 kDa	17.50	12.47	6.44	-1.40	7.48E-02	-2.72	7.67E-03
AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial precursor	67 kDa	24.12	26.43	33.20	1.10	7.85E-01	1.38	3.15E-02
SYRC_HUMAN	Arginyl-tRNA synthetase, cytoplasmic	75 kDa	30.73	27.42	19.33	-1.12	1.38E-01	-1.59	5.76E-03
SYNC_HUMAN	Asparaginyl-tRNA synthetase, cytoplasmic	63 kDa	15.61	20.44	14.37	1.31	3.17E-01	-1.09	3.53E-01
AATM_HUMAN	Aspartate aminotransferase, mitochondrial precursor	47 kDa	20.34	27.42	33.20	1.35	3.82E-02	1.63	2.21E-04
SYDC_HUMAN	Aspartyl-tRNA synthetase, cytoplasmic	57 kDa	9.95	13.46	16.35	1.35	1.14E-01	1.64	3.07E-02
PEA15_HUMAN	Astrocytic phosphoprotein PEA-15	15 kDa	20.34	21.44	14.37	1.05	9.84E-01	-1.42	3.85E-02
ATX10_HUMAN	Ataxin-10	53 kDa	15.61	16.45	8.43	1.05	9.80E-01	-1.85	8.81E-03
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial precursor	60 kDa	112.91	116.17	203.62	1.03	7.06E-01	1.80	7.55E-05

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
AT5F1_HUMAN	ATP synthase subunit b, mitochondrial precursor	29 kDa	8.06	3.49	10.41	-2.31	9.10E-02	1.29	3.08E-01
ATPB_HUMAN	ATP synthase subunit beta, mitochondrial precursor	57 kDa	143.14	149.08	222.44	1.04	7.79E-01	1.55	4.69E-03
ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	18 kDa	24.12	24.43	31.22	1.01	4.31E-01	1.29	7.45E-02
ATPK_HUMAN	ATP synthase subunit f, mitochondrial	11 kDa	9.95	12.47	7.44	1.25	5.29E-01	-1.34	9.11E-02
ATPO_HUMAN	ATP synthase subunit O, mitochondrial precursor	23 kDa	9.00	10.47	24.28	1.16	8.14E-01	2.70	2.21E-02
ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial precursor	13 kDa	0.50	1.50	11.40	2.99	3.56E-01	22.80	5.12E-03
ACLY_HUMAN	ATP-citrate synthase	121 kDa	73.24	67.31	56.98	-1.09	4.88E-02	-1.29	7.33E-03
KU70_HUMAN	ATP-dependent DNA helicase 2 subunit 1	70 kDa	65.68	67.31	66.88	1.02	8.25E-01	1.02	8.35E-01
KU86_HUMAN	ATP-dependent DNA helicase 2 subunit 2	83 kDa	72.29	80.27	80.76	1.11	7.01E-01	1.12	6.84E-01
RECQ1_HUMAN	ATP-dependent DNA helicase Q1	73 kDa	30.73	32.41	24.28	1.05	9.96E-01	-1.27	1.40E-01
DHX9_HUMAN	ATP-dependent RNA helicase A	141 kDa	45.84	49.36	57.97	1.08	8.69E-01	1.26	1.70E-02
DDX1_HUMAN	ATP-dependent RNA helicase DDX1	82 kDa	20.34	12.47	16.35	-1.63	8.81E-02	-1.24	2.63E-01
DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X	73 kDa	42.06	49.36	44.10	1.17	4.03E-01	1.05	9.82E-01
E41L2_HUMAN	Band 4.1-like protein 2	113 kDa	9.00	9.47	1.49	1.05	9.62E-01	-6.04	1.96E-02
BAF_HUMAN	Barrier-to-autointegration factor	10 kDa	9.00	7.48	8.43	-1.20	2.07E-01	-1.07	6.29E-01
BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1	48 kDa	11.84	11.47	5.45	-1.03	6.15E-01	-2.17	6.57E-03
BASI_HUMAN	Basigin precursor	42 kDa	31.67	34.40	46.08	1.09	7.61E-01	1.45	7.39E-03
B2MG_HUMAN	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin form pI 5.3]	14 kDa	34.51	38.39	38.15	1.11	2.25E-01	1.11	2.39E-01
HEXB_HUMAN	Beta-hexosaminidase beta chain precursor	63 kDa	10.89	13.46	24.28	1.24	6.98E-01	2.23	1.19E-01
SYEP_HUMAN	Bifunctional aminoacyl-tRNA synthetase	171 kDa	15.61	19.45	10.41	1.25	5.11E-01	-1.50	9.52E-02
PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase	65 kDa	41.12	36.40	28.24	-1.13	2.34E-02	-1.46	7.37E-04
BASP_HUMAN	Brain acid soluble protein 1	23 kDa	28.84	30.41	38.15	1.05	9.64E-01	1.32	7.73E-02
C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	102 kDa	44.90	49.36	31.22	1.10	4.47E-01	-1.44	3.90E-04
CAD13_HUMAN	Cadherin-13 precursor	78 kDa	14.67	19.45	8.43	1.33	1.90E-01	-1.74	3.45E-04
CALD1_HUMAN	Caldesmon	93 kDa	24.12	22.44	19.33	-1.07	4.77E-01	-1.25	2.05E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
CALX_HUMAN	Calnexin precursor	68 kDa	68.51	68.31	48.06	-1.00	6.68E-01	-1.43	1.06E-01
CAN2_HUMAN	Calpain-2 catalytic subunit precursor	80 kDa	40.18	31.41	27.25	-1.28	9.26E-03	-1.47	6.53E-03
ICAL_HUMAN	Calpastatin	77 kDa	16.56	15.46	20.32	-1.07	6.01E-01	1.23	5.73E-01
CNN2_HUMAN	Calponin-2	34 kDa	46.79	40.39	32.21	-1.16	4.00E-02	-1.45	7.37E-03
CNN3_HUMAN	Calponin-3	36 kDa	37.34	28.42	24.28	-1.31	2.10E-02	-1.54	1.53E-02
CALR_HUMAN	Calreticulin precursor	48 kDa	222.49	221.87	263.07	-1.00	2.08E-01	1.18	3.49E-02
CALU_HUMAN	Calumenin precursor	37 kDa	27.89	30.41	38.15	1.09	8.34E-01	1.37	1.27E-01
CAPR1_HUMAN	Caprin-1	73 kDa	15.61	18.45	19.33	1.18	5.00E-01	1.24	2.21E-01
CBR1_HUMAN	Carbonyl reductase [NADPH] 1	30 kDa	30.73	32.41	23.29	1.05	9.88E-01	-1.32	3.27E-02
CTNA1_HUMAN	Catenin alpha-1	100 kDa	17.50	20.44	16.35	1.17	3.37E-01	-1.07	6.80E-01
CTNB1_HUMAN	Catenin beta-1	85 kDa	9.95	7.48	13.38	-1.33	2.29E-01	1.35	2.30E-01
CATD_HUMAN	Cathepsin D precursor	45 kDa	43.95	47.37	59.95	1.08	8.65E-01	1.36	1.39E-02
CATZ_HUMAN	Cathepsin Z precursor	34 kDa	9.00	8.48	11.40	-1.06	6.04E-01	1.27	4.05E-01
CAV1_HUMAN	Caveolin-1	20 kDa	8.06	8.48	7.44	1.05	9.57E-01	-1.08	7.65E-01
CD166_HUMAN	CD166 antigen precursor	65 kDa	4.28	5.49	18.33	1.28	6.74E-01	4.29	1.49E-03
CD2B2_HUMAN	CD2 antigen cytoplasmic tail-binding protein 2	38 kDa	5.22	6.48	7.44	1.24	5.57E-01	1.42	2.23E-01
CD44_HUMAN	CD44 antigen precursor	82 kDa	10.89	12.47	9.42	1.14	7.30E-01	-1.16	3.98E-01
CD9_HUMAN	CD9 antigen	25 kDa	14.67	14.46	8.43	-1.01	7.69E-01	-1.74	1.45E-01
CDC2_HUMAN	Cell division control protein 2 homolog	34 kDa	7.11	6.48	7.44	-1.10	8.24E-01	1.05	9.96E-01
MUC18_HUMAN	Cell surface glycoprotein MUC18 precursor	72 kDa	9.95	10.47	7.44	1.05	9.88E-01	-1.34	2.39E-01
P53_HUMAN	Cellular tumor antigen p53	44 kDa	9.00	10.47	16.35	1.16	5.66E-01	1.82	7.19E-04
CETN2_HUMAN	Centrin-2	20 kDa	7.11	6.48	8.43	-1.10	5.33E-01	1.18	4.33E-01
CHM4B_HUMAN	Charged multivesicular body protein 4b	25 kDa	17.50	15.46	17.34	-1.13	3.86E-01	-1.01	7.49E-01
CHMP5_HUMAN	Charged multivesicular body protein 5	25 kDa	11.84	12.47	8.43	1.05	9.70E-01	-1.40	2.76E-01
CLIC1_HUMAN	Chloride intracellular channel protein 1	27 kDa	67.57	66.31	54.99	-1.02	4.06E-01	-1.23	2.32E-02
CLIC4_HUMAN	Chloride intracellular channel protein 4	29 kDa	48.68	45.37	34.19	-1.07	1.82E-01	-1.42	4.66E-03

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
CBX1_HUMAN	Chromobox protein homolog 1	21 kDa	6.17	9.47	30.22	1.54	6.27E-01	4.90	1.86E-02
CBX3_HUMAN	Chromobox protein homolog 3	21 kDa	36.40	38.39	59.95	1.05	9.85E-01	1.65	1.33E-02
CISY_HUMAN	Citrate synthase, mitochondrial precursor	52 kDa	17.50	19.45	22.30	1.11	8.35E-01	1.27	4.04E-01
CLH1_HUMAN	Clathrin heavy chain 1	192 kDa	177.15	190.96	231.36	1.08	7.93E-01	1.31	1.23E-04
CPSF5_HUMAN	Cleavage and polyadenylation specificity factor subunit 5	26 kDa	8.06	5.49	7.44	-1.47	1.75E-01	-1.08	6.02E-01
CPSF6_HUMAN	Cleavage and polyadenylation specificity factor subunit 6	59 kDa	9.95	8.48	7.44	-1.17	3.57E-01	-1.34	2.33E-01
CPSF7_HUMAN	Cleavage and polyadenylation specificity factor subunit 7	52 kDa	9.00	12.47	22.30	1.38	2.89E-01	2.48	6.12E-03
COTL1_HUMAN	Coactosin-like protein	16 kDa	13.73	8.48	2.48	-1.62	1.30E-01	-5.53	1.89E-03
COPB2_HUMAN	Coatomer subunit beta'	102 kDa	8.06	7.48	10.41	-1.08	7.11E-01	1.29	4.69E-01
COPB_HUMAN	Coatomer subunit beta	107 kDa	12.78	11.47	12.39	-1.11	2.27E-01	-1.03	3.97E-01
COPD_HUMAN	Coatomer subunit delta	57 kDa	6.17	4.49	5.45	-1.37	1.49E-01	-1.13	5.27E-01
COPE_HUMAN	Coatomer subunit epsilon	34 kDa	15.61	12.47	18.33	-1.25	1.46E-01	1.17	3.80E-01
COF1_HUMAN	Cofilin-1	19 kDa	175.26	153.07	112.46	-1.14	1.28E-02	-1.56	8.08E-05
CCD47_HUMAN	Coiled-coil domain-containing protein 47 precursor	56 kDa	9.00	9.47	8.43	1.05	9.74E-01	-1.07	2.67E-01
CHCH2_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial precursor	16 kDa	7.11	6.48	12.39	-1.10	5.45E-01	1.74	9.21E-02
C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	31 kDa	23.17	25.43	32.21	1.10	8.11E-01	1.39	1.46E-01
CND1_HUMAN	Condensin complex subunit 1	157 kDa	9.00	2.49	0.50	-3.61	1.87E-02	-18.00	2.89E-03
CSN4_HUMAN	COP9 signalosome complex subunit 4	46 kDa	5.22	8.48	8.43	1.62	3.76E-01	1.61	2.99E-01
CPNE1_HUMAN	Copine-1	59 kDa	34.51	40.39	33.20	1.17	4.88E-01	-1.04	3.07E-01
COR1B_HUMAN	Coronin-1B	54 kDa	15.61	15.46	15.36	-1.01	3.74E-01	-1.02	4.07E-01
COR1C_HUMAN	Coronin-1C	53 kDa	37.34	38.39	33.20	1.03	8.69E-01	-1.12	4.24E-01
CAND1_HUMAN	Cullin-associated NEDD8-dissociated protein 1	136 kDa	26.01	25.43	11.40	-1.02	5.90E-01	-2.28	9.30E-03
CD2A1_HUMAN	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3	17 kDa	10.89	14.46	9.42	1.33	8.71E-02	-1.16	3.92E-01
CSRP1_HUMAN	Cysteine and glycine-rich protein 1	21 kDa	32.62	30.41	19.33	-1.07	3.44E-01	-1.69	7.60E-03
CRIP2_HUMAN	Cysteine-rich protein 2	22 kDa	9.00	8.48	8.43	-1.06	6.10E-01	-1.07	6.21E-01
QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial precursor	53 kDa	4.28	7.48	13.38	1.75	2.58E-01	3.13	2.48E-03

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial precursor	48 kDa	16.56	17.45	24.28	1.05	9.74E-01	1.47	1.14E-02
CYC_HUMAN	Cytochrome c	12 kDa	6.17	4.49	9.42	-1.37	7.31E-01	1.53	5.26E-01
COX2_HUMAN	Cytochrome c oxidase subunit 2	26 kDa	11.84	11.47	9.42	-1.03	6.28E-01	-1.26	4.64E-01
COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	20 kDa	9.95	9.47	13.38	-1.05	6.75E-01	1.35	3.46E-01
COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial precursor	17 kDa	26.01	26.43	33.20	1.02	5.08E-01	1.28	2.18E-02
COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial precursor	14 kDa	8.06	8.48	18.33	1.05	9.95E-01	2.28	2.90E-03
CX6B1_HUMAN	Cytochrome c oxidase subunit VIb isoform 1	10 kDa	4.28	5.49	11.40	1.28	7.08E-01	2.66	9.10E-02
DYHC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	532 kDa	80.80	81.27	28.24	1.01	8.42E-01	-2.86	4.24E-04
DC1I2_HUMAN	Cytoplasmic dynein 1 intermediate chain 2	71 kDa	8.06	7.48	11.40	-1.08	7.79E-01	1.41	2.83E-01
DC1L2_HUMAN	Cytoplasmic dynein 1 light intermediate chain 2	54 kDa	9.00	6.48	3.47	-1.39	7.55E-02	-2.59	3.35E-03
CKAP4_HUMAN	Cytoskeleton-associated protein 4	66 kDa	26.95	24.43	45.09	-1.10	1.98E-01	1.67	9.03E-03
AMPL_HUMAN	Cytosol aminopeptidase	56 kDa	16.56	20.44	14.37	1.23	5.43E-01	-1.15	5.61E-01
BACH_HUMAN	Cytosolic acyl coenzyme A thioester hydrolase	42 kDa	11.84	12.47	9.42	1.05	9.75E-01	-1.26	2.87E-01
SERA_HUMAN	D-3-phosphoglycerate dehydrogenase	57 kDa	39.23	45.37	37.16	1.16	3.41E-01	-1.06	5.50E-01
DAZP1_HUMAN	DAZ-associated protein 1	43 kDa	16.56	15.46	17.34	-1.07	2.43E-01	1.05	9.70E-01
ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	36 kDa	11.84	16.45	21.31	1.39	7.70E-02	1.80	2.59E-02
P5CS_HUMAN	Delta-1-pyrroline-5-carboxylate synthetase	87 kDa	21.28	22.44	24.28	1.05	9.90E-01	1.14	6.82E-01
DUT_HUMAN	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial precursor	27 kDa	21.28	19.45	24.28	-1.09	1.34E-01	1.14	5.12E-01
DYR_HUMAN	Dihydrofolate reductase	21 kDa	14.67	12.47	9.42	-1.18	2.83E-01	-1.56	5.94E-03
DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial precursor	54 kDa	12.78	14.46	25.27	1.13	6.38E-01	1.98	1.30E-02
DPYL2_HUMAN	Dihydropyrimidinase-related protein 2	62 kDa	37.34	40.39	28.24	1.08	8.46E-01	-1.32	5.83E-02
MCM2_HUMAN	DNA replication licensing factor MCM2	102 kDa	21.28	23.43	28.24	1.10	7.54E-01	1.33	8.42E-02
MCM3_HUMAN	DNA replication licensing factor MCM3	91 kDa	17.50	21.44	16.35	1.22	1.94E-01	-1.07	3.26E-01
MCM4_HUMAN	DNA replication licensing factor MCM4	97 kDa	13.73	12.47	13.38	-1.10	6.10E-01	-1.03	7.22E-01
MCM5_HUMAN	DNA replication licensing factor MCM5	82 kDa	9.00	10.47	4.46	1.16	7.51E-01	-2.02	3.60E-02
MCM6_HUMAN	DNA replication licensing factor MCM6	93 kDa	4.28	3.49	9.42	-1.23	6.82E-01	2.20	2.06E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
MCM7_HUMAN	DNA replication licensing factor MCM7	81 kDa	18.45	22.44	22.30	1.22	3.42E-01	1.21	1.56E-01
APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase	36 kDa	30.73	29.42	21.31	-1.04	4.68E-01	-1.44	3.68E-03
PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit	469 kDa	26.95	32.41	0.50	1.20	6.74E-01	-53.90	4.49E-04
DNJA1_HUMAN	DnaJ homolog subfamily A member 1	45 kDa	31.67	30.41	30.22	-1.04	2.89E-01	-1.05	2.94E-01
DNJA2_HUMAN	DnaJ homolog subfamily A member 2	46 kDa	6.17	7.48	4.46	1.21	5.11E-01	-1.38	1.23E-01
DNJB1_HUMAN	DnaJ homolog subfamily B member 1	38 kDa	19.39	19.45	12.39	1.00	6.95E-01	-1.57	6.33E-03
DJB11_HUMAN	DnaJ homolog subfamily B member 11 precursor	41 kDa	3.33	3.49	11.40	1.05	9.87E-01	3.42	1.09E-02
DNJC9_HUMAN	DnaJ homolog subfamily C member 9	30 kDa	9.95	14.46	14.37	1.45	1.44E-01	1.44	2.17E-01
OST48_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	49 kDa	4.28	5.49	14.37	1.28	6.73E-01	3.36	1.21E-01
RIB2_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor	69 kDa	5.22	10.47	24.28	2.00	1.69E-01	4.65	3.61E-03
RIB1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	69 kDa	26.01	36.40	34.19	1.40	1.62E-01	1.31	2.82E-01
STAU1_HUMAN	Double-stranded RNA-binding protein Staufen homolog 1	63 kDa	9.95	13.46	8.43	1.35	2.14E-01	-1.18	3.52E-01
DREB_HUMAN	Drebrin	71 kDa	17.50	16.45	26.26	-1.06	4.82E-01	1.50	1.83E-02
DBNL_HUMAN	Drebrin-like protein	48 kDa	18.45	14.46	11.40	-1.28	1.65E-02	-1.62	1.07E-03
DCTN2_HUMAN	Dynactin subunit 2	44 kDa	10.89	15.46	17.34	1.42	3.03E-01	1.59	1.08E-01
DNM1L_HUMAN	Dynamamin-1-like protein	82 kDa	12.78	14.46	11.40	1.13	6.47E-01	-1.12	3.73E-01
DYL1_HUMAN	Dynein light chain 1, cytoplasmic	10 kDa	18.45	21.44	21.31	1.16	3.75E-01	1.15	2.01E-01
DLRB1_HUMAN	Dynein light chain roadblock-type 1	11 kDa	9.00	10.47	5.45	1.16	7.15E-01	-1.65	1.23E-01
EHD1_HUMAN	EH domain-containing protein 1	61 kDa	28.84	35.40	22.30	1.23	3.26E-01	-1.29	1.75E-01
EHD2_HUMAN	EH domain-containing protein 2	61 kDa	10.89	10.47	8.43	-1.04	6.68E-01	-1.29	2.81E-01
ELAV1_HUMAN	ELAV-like protein 1	36 kDa	11.84	10.47	27.25	-1.13	5.34E-01	2.30	2.52E-03
ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial precursor	35 kDa	10.89	18.45	23.29	1.69	3.33E-03	2.14	1.39E-03
EF1A1_HUMAN	Elongation factor 1-alpha 1	50 kDa	406.70	416.32	270.00	1.02	4.74E-01	-1.51	5.40E-04
EF1B_HUMAN	Elongation factor 1-beta	25 kDa	13.73	11.47	15.36	-1.20	1.81E-01	1.12	7.31E-01
EF1D_HUMAN	Elongation factor 1-delta	31 kDa	57.18	58.34	58.96	1.02	5.78E-01	1.03	8.40E-01
EF1G_HUMAN	Elongation factor 1-gamma	50 kDa	103.47	105.20	95.62	1.02	5.20E-01	-1.08	2.73E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
EF2_HUMAN	Elongation factor 2	95 kDa	439.76	410.34	294.77	-1.07	2.78E-02	-1.49	3.93E-05
EFTU_HUMAN	Elongation factor Tu, mitochondrial precursor	50 kDa	47.73	53.35	67.88	1.12	4.25E-01	1.42	6.93E-03
SH3G1_HUMAN	Endophilin-A2	41 kDa	12.78	13.46	9.42	1.05	9.63E-01	-1.36	9.08E-02
ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1	107 kDa	2.39	2.49	13.38	1.04	9.52E-01	5.60	6.07E-03
ERP29_HUMAN	Endoplasmic reticulum protein ERp29 precursor	29 kDa	54.35	59.33	71.84	1.09	7.97E-01	1.32	4.79E-02
ENPL_HUMAN	Endoplasmin precursor	92 kDa	205.49	227.85	261.08	1.11	1.47E-01	1.27	1.47E-03
ERH_HUMAN	Enhancer of rudimentary homolog	12 kDa	15.61	15.46	24.28	-1.01	6.11E-01	1.55	3.79E-02
ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial precursor	31 kDa	20.34	22.44	38.15	1.10	7.48E-01	1.88	1.91E-03
EPHA2_HUMAN	Ephrin type-A receptor 2 precursor	108 kDa	8.06	8.48	9.42	1.05	9.96E-01	1.17	6.28E-01
EPIPL_HUMAN	Epiplakin	553 kDa	39.23	33.41	46.08	-1.17	1.73E-01	1.17	3.66E-01
ERLN1_HUMAN	Erlin-1	39 kDa	4.28	4.49	11.40	1.05	9.86E-01	2.66	3.25E-04
ERO1A_HUMAN	ERO1-like protein alpha precursor	54 kDa	2.39	3.49	16.35	1.46	6.21E-01	6.84	1.25E-03
STOM_HUMAN	Erythrocyte band 7 integral membrane protein	32 kDa	11.84	10.47	9.42	-1.13	6.22E-01	-1.26	3.96E-01
ETHE1_HUMAN	ETHE1 protein, mitochondrial precursor	28 kDa	3.33	4.49	9.42	1.35	3.96E-01	2.82	6.24E-03
IF4A1_HUMAN	Eukaryotic initiation factor 4A-I	46 kDa	105.36	103.21	96.61	-1.02	3.90E-01	-1.09	1.23E-01
IF4A3_HUMAN	Eukaryotic initiation factor 4A-III	47 kDa	19.39	17.45	25.27	-1.11	4.04E-01	1.30	1.75E-02
IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1	36 kDa	29.78	32.41	22.30	1.09	8.07E-01	-1.34	5.02E-02
IF2B_HUMAN	Eukaryotic translation initiation factor 2 subunit 2	38 kDa	8.06	7.48	2.48	-1.08	7.57E-01	-3.25	5.72E-02
IF2G_HUMAN	Eukaryotic translation initiation factor 2 subunit 3	51 kDa	17.50	19.45	18.33	1.11	5.10E-01	1.05	9.94E-01
EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A	167 kDa	27.89	27.42	19.33	-1.02	6.24E-01	-1.44	6.45E-02
EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B	92 kDa	13.73	14.46	9.42	1.05	9.92E-01	-1.46	2.11E-02
IF3EI_HUMAN	Eukaryotic translation initiation factor 3 subunit E-interacting protein	67 kDa	19.39	8.48	8.43	-2.29	2.09E-02	-2.30	2.12E-02
EIF3I_HUMAN	Eukaryotic translation initiation factor 3 subunit I	37 kDa	6.17	8.48	3.47	1.37	1.64E-01	-1.78	1.02E-01
IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	176 kDa	23.17	16.45	18.33	-1.41	1.43E-02	-1.26	1.65E-01
IF4E_HUMAN	Eukaryotic translation initiation factor 4E	25 kDa	5.22	8.48	0.50	1.62	3.13E-01	-10.45	8.34E-02
IF4H_HUMAN	Eukaryotic translation initiation factor 4H	27 kDa	21.28	16.45	18.33	-1.29	7.09E-02	-1.16	2.33E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
IF5A1_HUMAN	Eukaryotic translation initiation factor 5A-1	17 kDa	30.73	26.43	15.36	-1.16	7.72E-02	-2.00	3.27E-03
IF6_HUMAN	Eukaryotic translation initiation factor 6	27 kDa	36.40	31.41	33.20	-1.16	2.57E-01	-1.10	3.73E-01
XPO1_HUMAN	Exportin-1	123 kDa	15.61	19.45	18.33	1.25	6.34E-01	1.17	7.04E-01
XPO2_HUMAN	Exportin-2	110 kDa	118.58	123.15	73.82	1.04	8.17E-01	-1.61	4.84E-04
ESYT1_HUMAN	Extended-synaptotagmin-1	123 kDa	19.39	18.45	23.29	-1.05	3.63E-01	1.20	3.75E-01
EZRI_HUMAN	Ezrin	69 kDa	114.80	114.18	98.59	-1.01	4.73E-01	-1.16	3.84E-02
SP16H_HUMAN	FACT complex subunit SPT16	120 kDa	14.67	20.44	5.45	1.39	3.90E-01	-2.69	3.38E-02
CAZA1_HUMAN	F-actin-capping protein subunit alpha-1	33 kDa	27.89	29.42	24.28	1.05	9.91E-01	-1.15	2.58E-01
CAPZB_HUMAN	F-actin-capping protein subunit beta	31 kDa	26.01	42.38	29.23	1.63	3.59E-03	1.12	7.16E-01
FUBP1_HUMAN	Far upstream element-binding protein 1	68 kDa	17.50	11.47	24.28	-1.53	1.56E-01	1.39	3.50E-01
FUBP2_HUMAN	Far upstream element-binding protein 2	73 kDa	41.12	40.39	71.84	-1.02	4.76E-01	1.75	8.16E-03
FUBP3_HUMAN	Far upstream element-binding protein 3	62 kDa	4.28	3.49	11.40	-1.23	6.35E-01	2.66	1.28E-02
FPPS_HUMAN	Farnesyl pyrophosphate synthetase	41 kDa	14.67	13.46	8.43	-1.09	5.02E-01	-1.74	8.40E-02
FSCN1_HUMAN	Fascin	55 kDa	24.12	19.45	21.31	-1.24	5.93E-02	-1.13	1.82E-01
FAS_HUMAN	Fatty acid synthase	273 kDa	168.65	176.00	104.54	1.04	9.12E-01	-1.61	2.59E-03
FERM2_HUMAN	Fermitin family homolog 2	78 kDa	12.78	13.46	9.42	1.05	9.80E-01	-1.36	1.85E-01
FINC_HUMAN	Fibronectin precursor	263 kDa	86.46	92.24	8.43	1.07	8.91E-01	-10.26	9.05E-05
FLNA_HUMAN	Filamin-A	281 kDa	657.98	648.66	546.44	-1.01	6.14E-02	-1.20	7.70E-03
FLNB_HUMAN	Filamin-B	278 kDa	383.08	395.38	334.40	1.03	4.41E-01	-1.15	3.65E-02
FLNC_HUMAN	Filamin-C	291 kDa	117.64	116.17	85.71	-1.01	5.31E-01	-1.37	2.60E-02
FKBP3_HUMAN	FK506-binding protein 3	25 kDa	10.89	11.47	9.42	1.05	9.91E-01	-1.16	2.23E-01
FKBP4_HUMAN	FK506-binding protein 4	52 kDa	38.29	44.38	51.03	1.16	3.64E-01	1.33	3.51E-02
FEN1_HUMAN	Flap endonuclease 1	43 kDa	17.50	12.47	5.45	-1.40	3.82E-01	-3.21	7.46E-02
FHL2_HUMAN	Four and a half LIM domains protein 2	32 kDa	17.50	20.44	19.33	1.17	4.53E-01	1.10	6.59E-01
FXR1_HUMAN	Fragile X mental retardation syndrome-related protein 1	70 kDa	7.11	6.48	12.39	-1.10	7.15E-01	1.74	1.03E-01
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	39 kDa	170.54	167.03	121.38	-1.02	1.62E-01	-1.40	5.96E-04

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ALDOC_HUMAN	Fructose-bisphosphate aldolase C	39 kDa	51.51	49.36	39.14	-1.04	2.74E-01	-1.32	7.80E-04
FUMH_HUMAN	Fumarate hydratase, mitochondrial precursor	55 kDa	9.95	11.47	15.36	1.15	5.82E-01	1.54	2.24E-02
LEG1_HUMAN	Galectin-1	15 kDa	194.15	198.94	172.90	1.02	6.71E-01	-1.12	2.61E-02
LG3BP_HUMAN	Galectin-3-binding protein precursor	65 kDa	1.44	6.48	18.33	4.49	1.81E-02	12.69	2.85E-03
ENOG_HUMAN	Gamma-enolase	47 kDa	253.67	201.93	140.20	-1.26	4.15E-04	-1.81	4.90E-05
OFUT1_HUMAN	GDP-fucose protein O-fucosyltransferase 1 precursor	44 kDa	9.95	9.47	18.33	-1.05	5.33E-01	1.84	6.90E-02
GELS_HUMAN	Gelsolin precursor	86 kDa	19.39	22.44	21.31	1.16	4.20E-01	1.10	6.66E-01
GNPI_HUMAN	Glucosamine-6-phosphate isomerase	33 kDa	14.67	13.46	11.40	-1.09	3.88E-01	-1.29	1.97E-01
G6PD_HUMAN	Glucose-6-phosphate 1-dehydrogenase	59 kDa	43.01	45.37	38.15	1.05	9.79E-01	-1.13	3.18E-01
G6PI_HUMAN	Glucose-6-phosphate isomerase	63 kDa	112.91	112.18	84.72	-1.01	4.05E-01	-1.33	3.06E-03
GLU2B_HUMAN	Glucosidase 2 subunit beta precursor	59 kDa	38.29	48.36	69.86	1.26	7.87E-02	1.82	3.03E-03
DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial precursor	61 kDa	9.95	9.47	26.26	-1.05	7.38E-01	2.64	2.74E-02
SYQ_HUMAN	Glutaminyl-tRNA synthetase	88 kDa	8.06	11.47	8.43	1.42	1.30E-01	1.05	9.69E-01
GLRX3_HUMAN	Glutaredoxin-3	37 kDa	9.95	8.48	6.44	-1.17	1.60E-01	-1.54	6.11E-02
GLRX5_HUMAN	Glutaredoxin-related protein 5	17 kDa	6.17	5.49	10.41	-1.12	5.45E-01	1.69	5.38E-02
GSTK1_HUMAN	Glutathione S-transferase kappa 1	25 kDa	13.73	15.46	16.35	1.13	5.04E-01	1.19	9.86E-02
GSTP1_HUMAN	Glutathione S-transferase P	23 kDa	94.96	98.22	71.84	1.03	8.12E-01	-1.32	2.99E-03
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	36 kDa	611.69	513.04	385.93	-1.19	8.62E-03	-1.58	6.85E-05
GCSH_HUMAN	Glycine cleavage system H protein, mitochondrial precursor	19 kDa	8.06	7.48	13.38	-1.08	3.38E-01	1.66	3.61E-02
PYGL_HUMAN	Glycogen phosphorylase, liver form	97 kDa	10.89	10.47	7.44	-1.04	6.71E-01	-1.46	2.93E-02
GT251_HUMAN	Glycosyltransferase 25 family member 1 precursor	72 kDa	13.73	14.46	18.33	1.05	9.92E-01	1.34	2.58E-01
SYG_HUMAN	Glycyl-tRNA synthetase	83 kDa	19.39	19.45	19.33	1.00	6.93E-01	-1.00	5.82E-01
GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase	36 kDa	9.95	10.47	8.43	1.05	9.87E-01	-1.18	4.58E-01
GUAA_HUMAN	GMP synthase [glutamine-hydrolyzing]	77 kDa	26.95	21.44	20.32	-1.26	6.93E-02	-1.33	1.42E-02
GRN_HUMAN	Granulins precursor	64 kDa	0.50	1.50	20.32	2.99	3.56E-01	40.63	3.13E-03
RAN_HUMAN	GTP-binding nuclear protein Ran	24 kDa	44.90	48.36	44.10	1.08	8.62E-01	-1.02	6.66E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
GNAI2_HUMAN	Guanine nucleotide-binding protein G(i), alpha-2 subunit	40 kDa	21.28	19.45	13.38	-1.09	5.03E-01	-1.59	1.79E-01
GBG12_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-12 precursor	8 kDa	6.17	6.48	11.40	1.05	9.83E-01	1.85	1.62E-02
GBB1_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	37 kDa	29.78	26.43	43.10	-1.13	2.78E-01	1.45	1.38E-01
GBB2_HUMAN	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	37 kDa	26.01	26.43	43.10	1.02	7.87E-01	1.66	3.45E-02
GNAS1_HUMAN	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	111 kDa	11.84	18.45	14.37	1.56	2.14E-01	1.21	5.68E-01
GBLP_HUMAN	Guanine nucleotide-binding protein subunit beta-2-like 1	35 kDa	54.35	59.33	51.03	1.09	7.13E-01	-1.06	8.33E-02
HSP71_HUMAN	Heat shock 70 kDa protein 1	70 kDa	260.28	272.73	265.05	1.05	8.86E-01	1.02	5.67E-01
HSP74_HUMAN	Heat shock 70 kDa protein 4	94 kDa	99.69	96.23	92.65	-1.04	2.73E-01	-1.08	1.64E-01
HSP7C_HUMAN	Heat shock cognate 71 kDa protein	71 kDa	555.95	579.85	576.16	1.04	7.10E-01	1.04	7.25E-01
HSBP1_HUMAN	Heat shock factor-binding protein 1	9 kDa	6.17	8.48	5.45	1.37	1.13E-01	-1.13	5.42E-01
HS105_HUMAN	Heat shock protein 105 kDa	97 kDa	42.06	50.36	40.13	1.20	2.42E-01	-1.05	4.28E-01
TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondrial precursor	80 kDa	47.73	49.36	61.93	1.03	7.76E-01	1.30	3.52E-02
HSPB1_HUMAN	Heat shock protein beta-1	23 kDa	78.91	83.26	72.83	1.06	9.79E-01	-1.08	5.13E-02
HS90A_HUMAN	Heat shock protein HSP 90-alpha	85 kDa	494.55	479.14	424.57	-1.03	2.89E-04	-1.16	1.37E-04
HS90B_HUMAN	Heat shock protein HSP 90-beta	83 kDa	469.99	484.13	438.44	1.03	3.96E-01	-1.07	1.01E-02
HN1_HUMAN	Hematological and neurological expressed 1 protein	16 kDa	16.56	14.46	15.36	-1.15	2.54E-01	-1.08	4.83E-01
HN1L_HUMAN	Hematological and neurological expressed 1-like protein	20 kDa	14.67	14.46	11.40	-1.01	7.58E-01	-1.29	3.58E-01
HBA_HUMAN	Hemoglobin subunit alpha	15 kDa	9.95	13.46	0.50	1.35	5.32E-01	-19.89	2.90E-02
HDGF_HUMAN	Hepatoma-derived growth factor	27 kDa	14.67	14.46	14.37	-1.01	7.24E-01	-1.02	5.36E-01
ROAA_HUMAN	Heterogeneous nuclear ribonucleoprotein A/B	36 kDa	46.79	43.38	66.88	-1.08	3.64E-01	1.43	2.79E-02
ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0	31 kDa	9.95	13.46	18.33	1.35	7.94E-02	1.84	1.07E-02
ROA1_HUMAN	Heterogeneous nuclear ribonucleoprotein A1	39 kDa	106.30	105.20	140.20	-1.01	4.06E-01	1.32	1.61E-02
ROA3_HUMAN	Heterogeneous nuclear ribonucleoprotein A3	40 kDa	30.73	34.40	60.94	1.12	5.54E-01	1.98	8.55E-05
HNRPD_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	38 kDa	64.74	63.32	93.64	-1.02	4.27E-01	1.45	2.30E-03
HNRDL_HUMAN	Heterogeneous nuclear ribonucleoprotein D-like	46 kDa	33.56	26.43	53.01	-1.27	1.07E-01	1.58	6.40E-03
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	46 kDa	63.79	66.31	82.74	1.04	7.73E-01	1.30	8.62E-03

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
HNRPG_HUMAN	Heterogeneous nuclear ribonucleoprotein G	42 kDa	17.50	20.44	19.33	1.17	2.09E-01	1.10	7.05E-01
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	49 kDa	90.24	97.23	122.37	1.08	5.66E-01	1.36	2.04E-04
HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	49 kDa	68.51	75.29	90.66	1.10	5.18E-01	1.32	5.44E-03
HNRH3_HUMAN	Heterogeneous nuclear ribonucleoprotein H3	37 kDa	28.84	32.41	36.17	1.12	4.39E-01	1.25	1.31E-01
HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	51 kDa	124.25	126.14	144.17	1.02	3.15E-01	1.16	6.82E-02
HNRPL_HUMAN	Heterogeneous nuclear ribonucleoprotein L	60 kDa	36.40	31.41	57.97	-1.16	3.22E-01	1.59	2.37E-02
HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M	78 kDa	104.41	110.19	119.40	1.06	9.96E-01	1.14	6.56E-02
HNRPQ_HUMAN	Heterogeneous nuclear ribonucleoprotein Q	70 kDa	39.23	49.36	34.19	1.26	1.69E-01	-1.15	3.28E-01
HNRPR_HUMAN	Heterogeneous nuclear ribonucleoprotein R	71 kDa	14.67	16.45	26.26	1.12	7.84E-01	1.79	2.74E-03
HNRPU_HUMAN	Heterogeneous nuclear ribonucleoprotein U	91 kDa	94.96	105.20	106.52	1.11	5.72E-01	1.12	5.15E-01
HNRL1_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 1	96 kDa	9.00	8.48	7.44	-1.06	7.51E-01	-1.21	5.64E-01
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein U-like protein 2	85 kDa	16.56	22.44	27.25	1.36	2.94E-01	1.65	1.77E-02
ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1	37 kDa	145.03	142.10	212.53	-1.02	2.63E-01	1.47	2.34E-04
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2	34 kDa	63.79	59.33	64.90	-1.08	1.68E-01	1.02	7.92E-01
HINT1_HUMAN	Histidine triad nucleotide-binding protein 1	14 kDa	23.17	19.45	14.37	-1.19	1.49E-01	-1.61	8.62E-03
HINT2_HUMAN	Histidine triad nucleotide-binding protein 2	17 kDa	0.50	4.49	11.40	8.98	2.73E-12	22.80	3.18E-05
HAT1_HUMAN	Histone acetyltransferase type B catalytic subunit	50 kDa	14.67	15.46	14.37	1.05	9.87E-01	-1.02	8.27E-01
HDAC2_HUMAN	Histone deacetylase 2	55 kDa	13.73	12.47	15.36	-1.10	5.76E-01	1.12	8.24E-01
H2A2A_HUMAN	Histone H2A type 2-A	14 kDa	204.54	206.91	180.83	1.01	5.30E-01	-1.13	4.31E-02
H2B1D_HUMAN	Histone H2B type 1-D	14 kDa	206.43	220.87	237.30	1.07	8.57E-01	1.15	1.85E-01
H33_HUMAN	Histone H3.3	15 kDa	26.95	25.43	20.32	-1.06	5.05E-01	-1.33	2.00E-02
H4_HUMAN	Histone H4	11 kDa	180.93	191.96	194.70	1.06	9.43E-01	1.08	5.75E-01
RBBP4_HUMAN	Histone-binding protein RBBP4	48 kDa	18.45	23.43	21.31	1.27	4.17E-01	1.15	6.42E-01
1A02_HUMAN	HLA class I histocompatibility antigen, A-2 alpha chain precursor	41 kDa	113.86	131.13	153.09	1.15	4.89E-01	1.34	7.29E-02
1B55_HUMAN	HLA class I histocompatibility antigen, B-55 alpha chain precursor	40 kDa	14.67	46.37	16.35	3.16	2.09E-01	1.11	9.81E-01
HCFC1_HUMAN	Host cell factor	209 kDa	10.89	14.46	7.44	1.33	2.17E-01	-1.46	1.09E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
F10A1_HUMAN	Hsc70-interacting protein	41 kDa	8.06	6.48	9.42	-1.24	3.35E-01	1.17	5.70E-01
CDC37_HUMAN	Hsp90 co-chaperone Cdc37	44 kDa	19.39	20.44	12.39	1.05	9.97E-01	-1.57	2.61E-03
HCDH_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial precursor	34 kDa	1.44	3.49	9.42	2.42	1.86E-01	6.52	9.31E-03
HMCS1_HUMAN	Hydroxymethylglutaryl-CoA synthase, cytoplasmic	57 kDa	9.95	7.48	1.49	-1.33	5.86E-01	-6.67	1.09E-01
HPRT_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase	25 kDa	77.96	81.27	73.82	1.04	8.51E-01	-1.06	2.68E-01
HYOU1_HUMAN	Hypoxia up-regulated protein 1 precursor	111 kDa	18.45	21.44	36.17	1.16	4.82E-01	1.96	1.48E-02
IMA2_HUMAN	Importin subunit alpha-2	58 kDa	35.45	35.40	21.31	-1.00	7.44E-01	-1.66	1.87E-02
IMA4_HUMAN	Importin subunit alpha-4	58 kDa	8.06	8.48	5.45	1.05	9.98E-01	-1.48	1.69E-01
IMA7_HUMAN	Importin subunit alpha-7	60 kDa	11.84	10.47	9.42	-1.13	5.52E-01	-1.26	3.55E-01
IMB1_HUMAN	Importin subunit beta-1	97 kDa	67.57	74.29	69.86	1.10	6.38E-01	1.03	7.73E-01
IMB3_HUMAN	Importin subunit beta-3	124 kDa	7.11	4.49	4.46	-1.58	5.61E-01	-1.59	5.44E-01
IPO7_HUMAN	Importin-7	120 kDa	9.95	8.48	4.46	-1.17	6.40E-01	-2.23	4.93E-02
IPYR_HUMAN	Inorganic pyrophosphatase	33 kDa	21.28	25.43	21.31	1.19	5.97E-01	1.00	8.11E-01
IMDH2_HUMAN	Inosine-5'-monophosphate dehydrogenase 2	56 kDa	21.28	21.44	23.29	1.01	5.63E-01	1.09	8.07E-01
IF2B2_HUMAN	Insulin-like growth factor 2 mRNA-binding protein 2	62 kDa	9.00	6.48	4.46	-1.39	3.84E-01	-2.02	9.47E-02
ITA6_HUMAN	Integrin alpha-6 precursor	127 kDa	5.22	5.49	9.42	1.05	9.82E-01	1.80	1.82E-01
ITB1_HUMAN	Integrin beta-1 precursor	88 kDa	21.28	21.44	35.18	1.01	8.20E-01	1.65	6.57E-02
UCRP_HUMAN	Interferon-induced 17 kDa protein precursor [Contains: Ubiquitin cross-reactive protein	18 kDa	9.00	15.46	15.36	1.72	1.14E-01	1.71	1.51E-01
MX1_HUMAN	Interferon-induced GTP-binding protein Mx1	76 kDa	11.84	21.44	23.29	1.81	2.43E-01	1.97	1.62E-01
IFIT1_HUMAN	Interferon-induced protein with tetratricopeptide repeats 1	55 kDa	16.56	45.37	22.30	2.74	1.86E-03	1.35	3.36E-01
IFIT2_HUMAN	Interferon-induced protein with tetratricopeptide repeats 2	55 kDa	8.06	45.37	50.04	5.63	3.41E-04	6.21	1.53E-05
IFIT3_HUMAN	Interferon-induced protein with tetratricopeptide repeats 3	56 kDa	26.95	68.31	70.85	2.53	8.43E-04	2.63	5.02E-04
E2AK2_HUMAN	Interferon-induced, double-stranded RNA-activated protein kinase	62 kDa	9.95	8.48	9.42	-1.17	5.56E-01	-1.06	6.85E-01
ILF2_HUMAN	Interleukin enhancer-binding factor 2	43 kDa	22.23	22.44	27.25	1.01	8.05E-01	1.23	2.85E-01
ILF3_HUMAN	Interleukin enhancer-binding factor 3	95 kDa	38.29	43.38	35.18	1.13	4.06E-01	-1.09	5.09E-01
IDHC_HUMAN	Isocitrate dehydrogenase [NADP] cytoplasmic	47 kDa	12.78	15.46	11.40	1.21	4.15E-01	-1.12	5.42E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial precursor	51 kDa	5.22	4.49	23.29	-1.16	3.67E-01	4.46	5.15E-04
SYIC_HUMAN	Isoleucyl-tRNA synthetase, cytoplasmic	145 kDa	6.17	8.48	4.46	1.37	3.73E-01	-1.38	3.68E-01
K1C10_HUMAN	Keratin, type I cytoskeletal 10	60 kDa	130.86	15.46	64.90	-8.47	5.64E-02	-2.02	2.31E-01
K1C17_HUMAN	Keratin, type I cytoskeletal 17	48 kDa	29.78	38.39	61.93	1.29	3.24E-01	2.08	1.12E-03
K1C18_HUMAN	Keratin, type I cytoskeletal 18	48 kDa	270.67	264.75	327.47	-1.02	1.84E-02	1.21	9.54E-03
K1C9_HUMAN	Keratin, type I cytoskeletal 9	62 kDa	41.12	1.50	54.00	-27.47	5.67E-02	1.31	6.69E-01
K2C1_HUMAN	Keratin, type II cytoskeletal 1	66 kDa	432.20	162.04	760.45	-2.67	1.31E-02	1.76	2.06E-03
K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	66 kDa	60.01	7.48	49.05	-8.02	4.30E-02	-1.22	5.42E-01
K2C6A_HUMAN	Keratin, type II cytoskeletal 6A	60 kDa	11.84	11.47	30.22	-1.03	9.49E-01	2.55	1.96E-01
K2C8_HUMAN	Keratin, type II cytoskeletal 8	54 kDa	715.60	569.88	1185.51	-1.26	7.49E-03	1.66	3.65E-05
KHDR1_HUMAN	KH domain-containing, RNA-binding, signal transduction-associated protein 1	48 kDa	8.06	7.48	5.45	-1.08	7.50E-01	-1.48	2.63E-01
KINH_HUMAN	Kinesin-1 heavy chain	110 kDa	14.67	20.44	14.37	1.39	1.72E-01	-1.02	8.21E-01
LGUL_HUMAN	Lactoylglutathione lyase	21 kDa	32.62	35.40	20.32	1.09	7.70E-01	-1.61	5.36E-03
LMNA_HUMAN	Lamin-A/C	74 kDa	248.00	255.77	384.94	1.03	6.40E-01	1.55	1.02E-03
LAP2A_HUMAN	Lamina-associated polypeptide 2 isoform alpha	75 kDa	11.84	8.48	5.45	-1.40	2.43E-01	-2.17	4.31E-02
LMNB1_HUMAN	Lamin-B1	66 kDa	98.74	103.21	162.99	1.05	8.47E-01	1.65	4.70E-05
LMNB2_HUMAN	Lamin-B2	68 kDa	15.61	17.45	35.18	1.12	8.86E-01	2.25	3.16E-02
LAMA5_HUMAN	Laminin subunit alpha-5 precursor	400 kDa	4.28	6.48	5.45	1.52	1.30E-01	1.27	7.12E-01
LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial precursor	158 kDa	26.01	36.40	55.99	1.40	9.52E-02	2.15	1.84E-02
LRRF1_HUMAN	Leucine-rich repeat flightless-interacting protein 1	89 kDa	9.95	4.49	8.43	-2.22	1.01E-01	-1.18	1.12E-01
SYLC_HUMAN	Leucyl-tRNA synthetase, cytoplasmic	134 kDa	12.78	11.47	7.44	-1.11	3.95E-01	-1.72	1.06E-01
LASP1_HUMAN	LIM and SH3 domain protein 1	30 kDa	44.90	44.38	27.25	-1.01	6.31E-01	-1.65	1.71E-02
LIMA1_HUMAN	LIM domain and actin-binding protein 1	85 kDa	6.17	6.48	8.43	1.05	9.73E-01	1.37	1.08E-01
LDHA_HUMAN	L-lactate dehydrogenase A chain	37 kDa	351.91	366.46	290.81	1.04	8.59E-01	-1.21	1.68E-02
LDHB_HUMAN	L-lactate dehydrogenase B chain	37 kDa	122.36	124.15	93.64	1.01	4.43E-01	-1.31	2.20E-04
LONM_HUMAN	Lon protease homolog, mitochondrial precursor	106 kDa	11.84	15.46	35.18	1.31	3.10E-02	2.97	1.85E-05

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ACSL3_HUMAN	Long-chain-fatty-acid--CoA ligase 3	80 kDa	7.11	7.48	3.47	1.05	9.79E-01	-2.05	4.51E-01
ACSL4_HUMAN	Long-chain-fatty-acid--CoA ligase 4	79 kDa	13.73	13.46	10.41	-1.02	5.41E-01	-1.32	3.52E-02
LA_HUMAN	Lupus La protein	47 kDa	8.06	9.47	8.43	1.18	3.57E-01	1.05	9.59E-01
LU_HUMAN	Lutheran blood group glycoprotein precursor	67 kDa	10.89	8.48	6.44	-1.28	1.67E-01	-1.69	1.74E-02
PPGB_HUMAN	Lysosomal protective protein precursor	54 kDa	7.11	11.47	10.41	1.61	1.63E-01	1.46	3.60E-01
SYK_HUMAN	Lysyl-tRNA synthetase	68 kDa	19.39	17.45	15.36	-1.11	1.81E-01	-1.26	1.03E-01
CAPG_HUMAN	Macrophage-capping protein	39 kDa	21.28	22.44	23.29	1.05	1.00E+00	1.09	6.38E-01
MVP_HUMAN	Major vault protein	99 kDa	19.39	30.41	16.35	1.57	1.49E-02	-1.19	4.27E-01
MDHC_HUMAN	Malate dehydrogenase, cytoplasmic	36 kDa	51.51	47.37	37.16	-1.09	1.91E-01	-1.39	9.16E-04
MDHM_HUMAN	Malate dehydrogenase, mitochondrial precursor	36 kDa	160.15	156.06	231.36	-1.03	1.25E-01	1.44	1.15E-04
M6PBP_HUMAN	Mannose-6-phosphate receptor-binding protein 1	47 kDa	40.18	43.38	40.13	1.08	7.93E-01	-1.00	6.91E-01
MRP_HUMAN	MARCKS-related protein	20 kDa	14.67	16.45	13.38	1.12	5.27E-01	-1.10	3.56E-01
MATR3_HUMAN	Matrin-3	95 kDa	63.79	60.33	61.93	-1.06	5.28E-01	-1.03	6.05E-01
PGRC1_HUMAN	Membrane-associated progesterone receptor component 1	22 kDa	14.67	10.47	21.31	-1.40	1.64E-01	1.45	9.55E-02
MAT2B_HUMAN	Methionine adenosyltransferase 2 subunit beta	38 kDa	13.73	10.47	8.43	-1.31	4.25E-02	-1.63	8.91E-02
SYMC_HUMAN	Methionyl-tRNA synthetase, cytoplasmic	101 kDa	6.17	8.48	2.48	1.37	6.22E-01	-2.49	3.13E-01
MAP1B_HUMAN	Microtubule-associated protein 1B	271 kDa	9.95	13.46	2.48	1.35	5.74E-01	-4.01	1.82E-01
MAP4_HUMAN	Microtubule-associated protein 4	121 kDa	63.79	62.32	49.05	-1.02	2.57E-01	-1.30	1.16E-01
MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1	30 kDa	24.12	24.43	22.30	1.01	7.81E-01	-1.08	3.81E-01
TOM22_HUMAN	Mitochondrial import receptor subunit TOM22 homolog	16 kDa	9.95	7.48	16.35	-1.33	2.28E-01	1.64	6.71E-02
IMMT_HUMAN	Mitochondrial inner membrane protein	84 kDa	22.23	25.43	40.13	1.14	4.92E-01	1.81	3.74E-04
BUB3_HUMAN	Mitotic checkpoint protein BUB3	37 kDa	19.39	14.46	19.33	-1.34	1.38E-01	-1.00	7.64E-01
MOES_HUMAN	Moesin	68 kDa	128.97	139.11	100.57	1.08	6.70E-01	-1.28	7.04E-04
PUR6_HUMAN	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole-succinocarboxamide synthase	47 kDa	38.29	29.42	24.28	-1.30	8.50E-02	-1.58	9.17E-03
MYL6_HUMAN	Myosin light polypeptide 6	17 kDa	116.69	119.16	124.35	1.02	5.49E-01	1.07	8.65E-01

Accessionnummer	Proteinbeschreibung	Molekular- gewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
MLRM_HUMAN	Myosin regulatory light chain 2, nonsarcomeric	20 kDa	60.96	56.34	61.93	-1.08	4.29E-02	1.02	7.34E-01
MYH10_HUMAN	Myosin-10	229 kDa	84.57	85.26	80.76	1.01	5.87E-01	-1.05	4.68E-01
MYH9_HUMAN	Myosin-9	227 kDa	857.30	843.11	733.70	-1.02	1.85E-02	-1.17	1.15E-02
MYO1C_HUMAN	Myosin-Ic	118 kDa	24.12	26.43	24.28	1.10	7.47E-01	1.01	8.15E-01
MTPN_HUMAN	Myotrophin	13 kDa	12.78	13.46	10.41	1.05	9.78E-01	-1.23	1.05E-01
MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate	32 kDa	20.34	21.44	23.29	1.05	9.79E-01	1.15	5.87E-01
GNS_HUMAN	N-acetylglucosamine-6-sulfatase precursor	62 kDa	11.84	18.45	24.28	1.56	2.73E-02	2.05	2.02E-03
NQO1_HUMAN	NAD(P)H dehydrogenase [quinone] 1	31 kDa	9.95	7.48	3.47	-1.33	2.17E-01	-2.86	3.23E-03
NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	13 kDa	4.28	6.48	13.38	1.52	3.83E-01	3.13	4.23E-03
NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	30 kDa	3.33	5.49	17.34	1.65	3.48E-01	5.20	3.38E-03
NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial precursor	24 kDa	3.33	5.49	9.42	1.65	3.86E-01	2.82	3.26E-02
NB5R3_HUMAN	NADH-cytochrome b5 reductase 3	34 kDa	11.84	10.47	7.44	-1.13	6.32E-01	-1.59	3.38E-01
NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	79 kDa	5.22	5.49	21.31	1.05	9.72E-01	4.08	9.09E-04
LTB4D_HUMAN	NADP-dependent leukotriene B4 12-hydroxydehydrogenase	36 kDa	8.06	15.46	1.49	1.92	1.19E-01	-5.40	3.41E-02
NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha	23 kDa	53.40	52.35	41.12	-1.02	1.53E-01	-1.30	2.10E-02
AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK	629 kDa	283.89	258.77	206.59	-1.10	4.81E-02	-1.37	5.95E-03
GANAB_HUMAN	Neutral alpha-glucosidase AB precursor	107 kDa	78.91	73.29	99.58	-1.08	3.74E-01	1.26	2.85E-01
NH2L1_HUMAN	NHP2-like protein 1	14 kDa	11.84	13.46	18.33	1.14	7.51E-01	1.55	3.76E-02
NIBL1_HUMAN	Niban-like protein 1	83 kDa	9.00	7.48	9.42	-1.20	3.89E-01	1.05	9.78E-01
NNMT_HUMAN	Nicotinamide N-methyltransferase	30 kDa	36.40	37.40	25.27	1.03	8.89E-01	-1.44	3.24E-02
NONO_HUMAN	Non-POU domain-containing octamer-binding protein	54 kDa	53.40	52.35	93.64	-1.02	3.23E-01	1.75	1.58E-04
NASP_HUMAN	Nuclear autoantigenic sperm protein	85 kDa	24.12	28.42	32.21	1.18	2.27E-01	1.34	7.56E-02
NUDC_HUMAN	Nuclear migration protein nudC	38 kDa	9.95	10.47	7.44	1.05	9.78E-01	-1.34	3.05E-01
NUMA1_HUMAN	Nuclear mitotic apparatus protein 1	238 kDa	12.78	12.47	29.23	-1.03	8.81E-01	2.29	1.88E-01
NU155_HUMAN	Nuclear pore complex protein Nup155	155 kDa	8.06	5.49	22.30	-1.47	4.64E-01	2.77	2.04E-02
NUP93_HUMAN	Nuclear pore complex protein Nup93	93 kDa	10.89	11.47	14.37	1.05	9.87E-01	1.32	9.62E-02

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
HCC1_HUMAN	Nuclear protein Hcc-1	24 kDa	4.28	7.48	9.42	1.75	1.77E-01	2.20	4.22E-02
YBOX1_HUMAN	Nuclease-sensitive element-binding protein 1	36 kDa	40.18	45.37	26.26	1.13	2.30E-01	-1.53	4.48E-05
NUCL_HUMAN	Nucleolin	77 kDa	88.35	96.23	71.84	1.09	8.96E-01	-1.23	4.05E-01
NPM_HUMAN	Nucleophosmin	33 kDa	94.96	102.21	93.64	1.08	7.72E-01	-1.01	4.04E-01
TPR_HUMAN	Nucleoprotein TPR	266 kDa	6.17	7.48	30.22	1.21	5.06E-01	4.90	5.93E-04
NDKA_HUMAN	Nucleoside diphosphate kinase A	17 kDa	43.01	45.37	19.33	1.05	9.77E-01	-2.23	3.55E-03
NDKB_HUMAN	Nucleoside diphosphate kinase B	17 kDa	88.35	82.27	58.96	-1.07	1.93E-01	-1.50	5.91E-04
NPIL1_HUMAN	Nucleosome assembly protein 1-like 1	45 kDa	36.40	34.40	28.24	-1.06	2.79E-01	-1.29	9.55E-03
NPIL4_HUMAN	Nucleosome assembly protein 1-like 4	43 kDa	21.28	20.44	13.38	-1.04	2.07E-01	-1.59	3.19E-02
OLA1_HUMAN	Obg-like ATPase 1	45 kDa	15.61	15.46	12.39	-1.01	6.28E-01	-1.26	1.41E-01
OAT_HUMAN	Ornithine aminotransferase, mitochondrial precursor	49 kDa	10.89	12.47	31.22	1.14	6.14E-01	2.87	1.45E-04
OSTF1_HUMAN	Osteoclast-stimulating factor 1	24 kDa	11.84	12.47	10.41	1.05	9.93E-01	-1.14	1.51E-01
PAXI_HUMAN	Paxillin	65 kDa	12.78	10.47	13.38	-1.22	2.21E-01	1.05	9.97E-01
PSIP1_HUMAN	PC4 and SFRS1-interacting protein	60 kDa	13.73	11.47	8.43	-1.20	4.59E-01	-1.63	1.44E-01
PDLI1_HUMAN	PDZ and LIM domain protein 1	36 kDa	51.51	54.35	38.15	1.06	9.61E-01	-1.35	4.32E-02
PDLI5_HUMAN	PDZ and LIM domain protein 5	64 kDa	7.11	8.48	3.47	1.19	6.54E-01	-2.05	3.45E-02
PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A	18 kDa	194.15	187.97	152.09	-1.03	1.45E-02	-1.28	2.85E-04
PPIB_HUMAN	Peptidyl-prolyl cis-trans isomerase B precursor	23 kDa	65.68	65.32	77.78	-1.01	2.03E-01	1.18	1.30E-02
PRDX1_HUMAN	Peroxiredoxin-1	22 kDa	77.02	72.30	70.85	-1.07	3.61E-02	-1.09	4.97E-02
PRDX2_HUMAN	Peroxiredoxin-2	22 kDa	14.67	10.47	17.34	-1.40	3.47E-01	1.18	7.08E-01
PRDX4_HUMAN	Peroxiredoxin-4	31 kDa	19.39	21.44	28.24	1.11	7.84E-01	1.46	3.24E-02
PRDX5_HUMAN	Peroxiredoxin-5, mitochondrial precursor	22 kDa	36.40	30.41	33.20	-1.20	2.58E-01	-1.10	4.46E-01
PRDX6_HUMAN	Peroxiredoxin-6	25 kDa	51.51	42.38	37.16	-1.22	9.59E-02	-1.39	3.79E-02
DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2	80 kDa	11.84	18.45	33.20	1.56	1.13E-01	2.80	1.01E-03
PHF5A_HUMAN	PHD finger-like domain-containing protein 5A	12 kDa	7.11	6.48	12.39	-1.10	5.32E-01	1.74	3.44E-02
MPCP_HUMAN	Phosphate carrier protein, mitochondrial precursor	40 kDa	15.61	21.44	19.33	1.37	1.25E-01	1.24	5.32E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1	21 kDa	38.29	40.39	26.26	1.05	9.74E-01	-1.46	2.43E-03
PGM1_HUMAN	Phosphoglucomutase-1	61 kDa	7.11	10.47	5.45	1.47	8.90E-02	-1.30	2.18E-01
PGK1_HUMAN	Phosphoglycerate kinase 1	45 kDa	275.39	269.73	200.64	-1.02	7.81E-02	-1.37	3.12E-04
PGAM1_HUMAN	Phosphoglycerate mutase 1	29 kDa	89.30	87.25	64.90	-1.02	4.89E-01	-1.38	2.78E-02
PUR4_HUMAN	Phosphoribosylformylglycinamide synthase	145 kDa	10.89	9.47	4.46	-1.15	4.83E-01	-2.44	1.10E-02
PAIRB_HUMAN	Plasminogen activator inhibitor 1 RNA-binding protein	45 kDa	6.17	4.49	0.50	-1.37	5.38E-01	-12.34	5.31E-02
PLST_HUMAN	Plastin-3	70 kDa	54.35	59.33	51.03	1.09	6.12E-01	-1.06	1.11E-01
LIS1_HUMAN	Platelet-activating factor acetylhydrolase IB subunit alpha	47 kDa	8.06	5.49	3.47	-1.47	2.94E-02	-2.32	2.48E-03
PLEC1_HUMAN	Plectin-1	532 kDa	211.16	213.89	353.23	1.01	4.67E-01	1.67	1.77E-04
PARP1_HUMAN	Poly [ADP-ribose] polymerase 1	113 kDa	18.45	22.44	0.50	1.22	6.98E-01	-36.90	1.35E-02
PCBP1_HUMAN	Poly(rC)-binding protein 1	37 kDa	54.35	62.32	57.97	1.15	1.88E-01	1.07	8.54E-01
PCBP2_HUMAN	Poly(rC)-binding protein 2	39 kDa	62.85	67.31	60.94	1.07	8.26E-01	-1.03	3.02E-01
PABP1_HUMAN	Polyadenylate-binding protein 1	71 kDa	57.18	53.35	37.16	-1.07	6.90E-02	-1.54	5.01E-04
PTRF_HUMAN	Polymerase I and transcript release factor	43 kDa	30.73	28.42	26.26	-1.08	1.28E-01	-1.17	1.17E-01
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1	57 kDa	49.62	33.41	54.99	-1.49	7.96E-02	1.11	7.21E-01
PFD2_HUMAN	Prefoldin subunit 2	17 kDa	11.84	12.47	13.38	1.05	9.93E-01	1.13	4.05E-01
PFD3_HUMAN	Prefoldin subunit 3	23 kDa	8.06	7.48	4.46	-1.08	7.31E-01	-1.81	2.14E-01
PRP19_HUMAN	Pre-mRNA-processing factor 19	55 kDa	9.00	11.47	14.37	1.27	5.85E-01	1.60	2.47E-01
PCYOX_HUMAN	Prenylcysteine oxidase 1 precursor	57 kDa	2.39	2.49	8.43	1.04	9.80E-01	3.53	2.41E-03
PAWR_HUMAN	PRKC apoptosis WT1 regulator protein	37 kDa	10.89	11.47	11.40	1.05	9.80E-01	1.05	9.81E-01
SAP_HUMAN	Proactivator polypeptide precursor [Contains: Saposin-A	58 kDa	43.95	47.37	61.93	1.08	7.44E-01	1.41	2.50E-03
DDX17_HUMAN	Probable ATP-dependent RNA helicase DDX17	72 kDa	79.85	86.26	92.65	1.08	3.02E-01	1.16	1.37E-02
DDX46_HUMAN	Probable ATP-dependent RNA helicase DDX46	117 kDa	6.17	9.47	2.48	1.54	1.08E-01	-2.49	5.48E-02
DDX5_HUMAN	Probable ATP-dependent RNA helicase DDX5	69 kDa	92.13	91.24	97.60	-1.01	3.49E-01	1.06	9.27E-01
PLOD1_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor	84 kDa	7.11	9.47	22.30	1.33	2.13E-01	3.14	7.31E-04
PLOD2_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 precursor	85 kDa	28.84	33.41	51.03	1.16	5.34E-01	1.77	5.42E-03

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
PLOD3_HUMAN	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor	85 kDa	6.17	7.48	19.33	1.21	5.11E-01	3.13	3.36E-03
PROF1_HUMAN	Profilin-1	15 kDa	190.37	186.97	149.12	-1.02	1.11E-01	-1.28	5.24E-05
PROF2_HUMAN	Profilin-2	15 kDa	9.95	11.47	11.40	1.15	6.59E-01	1.15	6.56E-01
PDC61_HUMAN	Programmed cell death 6-interacting protein	96 kDa	20.34	26.43	25.27	1.30	2.11E-01	1.24	2.56E-01
PHB_HUMAN	Prohibitin	30 kDa	19.39	18.45	36.17	-1.05	6.38E-01	1.87	3.62E-03
PHB2_HUMAN	Prohibitin-2	33 kDa	25.06	35.40	46.08	1.41	6.36E-02	1.84	2.54E-02
PCNA_HUMAN	Proliferating cell nuclear antigen	29 kDa	48.68	48.36	50.04	-1.01	3.35E-01	1.03	6.62E-01
PA2G4_HUMAN	Proliferation-associated protein 2G4	44 kDa	25.06	25.43	28.24	1.01	5.67E-01	1.13	6.45E-01
P3H1_HUMAN	Prolyl 3-hydroxylase 1 precursor	83 kDa	13.73	14.46	28.24	1.05	9.99E-01	2.06	2.55E-04
P4HA1_HUMAN	Prolyl 4-hydroxylase subunit alpha-1 precursor	61 kDa	3.33	1.50	15.36	-2.23	2.17E-01	4.61	1.28E-03
P4HA2_HUMAN	Prolyl 4-hydroxylase subunit alpha-2 precursor	61 kDa	9.95	14.46	27.25	1.45	3.43E-01	2.74	1.00E-03
PPCE_HUMAN	Prolyl endopeptidase	81 kDa	8.06	5.49	4.46	-1.47	1.78E-01	-1.81	1.36E-01
TEBP_HUMAN	Prostaglandin E synthase 3	19 kDa	22.23	17.45	7.44	-1.27	1.27E-01	-2.99	1.38E-03
PSME1_HUMAN	Proteasome activator complex subunit 1	29 kDa	57.18	57.34	58.96	1.00	4.77E-01	1.03	8.31E-01
PSME2_HUMAN	Proteasome activator complex subunit 2	27 kDa	66.63	72.30	58.96	1.09	7.17E-01	-1.13	4.56E-02
PSA1_HUMAN	Proteasome subunit alpha type-1	30 kDa	6.17	8.48	6.44	1.37	1.64E-01	1.04	9.79E-01
PSA4_HUMAN	Proteasome subunit alpha type-4	29 kDa	21.28	24.43	23.29	1.15	5.29E-01	1.09	4.79E-01
PSA5_HUMAN	Proteasome subunit alpha type-5	26 kDa	8.06	12.47	15.36	1.55	5.72E-02	1.91	9.78E-03
PSA6_HUMAN	Proteasome subunit alpha type-6	27 kDa	17.50	27.42	21.31	1.57	7.19E-02	1.22	4.84E-01
PSA7_HUMAN	Proteasome subunit alpha type-7	28 kDa	32.62	30.41	25.27	-1.07	2.49E-01	-1.29	1.04E-02
PSB1_HUMAN	Proteasome subunit beta type-1 precursor	26 kDa	12.78	10.47	15.36	-1.22	2.12E-01	1.20	3.57E-01
PSB2_HUMAN	Proteasome subunit beta type-2	23 kDa	14.67	12.47	13.38	-1.18	4.17E-01	-1.10	5.51E-01
PSB4_HUMAN	Proteasome subunit beta type-4 precursor	29 kDa	31.67	32.41	33.20	1.02	4.64E-01	1.05	9.72E-01
PSB5_HUMAN	Proteasome subunit beta type-5 precursor	23 kDa	14.67	10.47	15.36	-1.40	1.26E-01	1.05	9.77E-01
PSB6_HUMAN	Proteasome subunit beta type-6 precursor	25 kDa	9.00	8.48	9.42	-1.06	3.86E-01	1.05	9.77E-01
ANM1_HUMAN	Protein arginine N-methyltransferase 1	42 kDa	17.50	17.45	23.29	-1.00	8.29E-01	1.33	1.47E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
C10_HUMAN	Protein C10	13 kDa	11.84	11.47	7.44	-1.03	6.13E-01	-1.59	1.00E-01
CNPY2_HUMAN	Protein canopy homolog 2 precursor	21 kDa	3.33	4.49	12.39	1.35	6.23E-01	3.72	2.41E-02
CDV3_HUMAN	Protein CDV3 homolog	27 kDa	6.17	8.48	6.44	1.37	1.60E-01	1.04	9.69E-01
DEK_HUMAN	Protein DEK	43 kDa	9.00	9.47	0.50	1.05	9.95E-01	-18.00	9.33E-02
DIAP1_HUMAN	Protein diaphanous homolog 1	139 kDa	9.95	9.47	8.43	-1.05	7.37E-01	-1.18	5.88E-01
PDIA3_HUMAN	Protein disulfide-isomerase A3 precursor	57 kDa	178.09	171.02	266.04	-1.04	5.73E-02	1.49	5.32E-03
PDIA4_HUMAN	Protein disulfide-isomerase A4 precursor	73 kDa	94.02	103.21	144.17	1.10	6.52E-01	1.53	2.01E-03
PDIA6_HUMAN	Protein disulfide-isomerase A6 precursor	48 kDa	87.41	99.22	137.23	1.14	3.81E-01	1.57	1.73E-03
PDIA1_HUMAN	Protein disulfide-isomerase precursor	57 kDa	158.26	151.07	207.58	-1.05	8.45E-03	1.31	1.36E-03
PARK7_HUMAN	Protein DJ-1	20 kDa	35.45	47.37	33.20	1.34	4.91E-02	-1.07	2.85E-01
DPY30_HUMAN	Protein dpy-30 homolog	11 kDa	8.06	7.48	8.43	-1.08	3.38E-01	1.05	9.59E-01
K1967_HUMAN	Protein KIAA1967	103 kDa	5.22	5.49	15.36	1.05	9.66E-01	2.94	7.41E-02
NPS3A_HUMAN	Protein NipSnap3A	28 kDa	1.44	1.50	10.41	1.04	9.70E-01	7.20	9.17E-04
PPME1_HUMAN	Protein phosphatase methylesterase 1	42 kDa	9.00	10.47	0.50	1.16	8.49E-01	-18.00	1.29E-02
S10AA_HUMAN	Protein S100-A10	11 kDa	19.39	22.44	28.24	1.16	7.76E-01	1.46	2.01E-01
S10AB_HUMAN	Protein S100-A11	12 kDa	68.51	73.29	58.96	1.07	8.39E-01	-1.16	1.25E-02
SET_HUMAN	Protein SET	33 kDa	73.24	70.30	42.11	-1.04	2.60E-01	-1.74	3.50E-04
SC23A_HUMAN	Protein transport protein Sec23A	86 kDa	9.00	12.47	12.39	1.38	4.41E-01	1.38	3.87E-01
PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	25 kDa	15.61	18.45	8.43	1.18	4.74E-01	-1.85	2.92E-02
PTMA_HUMAN	Prothymosin alpha [Contains: Thymosin alpha-1]	12 kDa	26.01	34.40	14.37	1.32	1.31E-01	-1.81	6.11E-03
PSA_HUMAN	Puromycin-sensitive aminopeptidase	103 kDa	71.35	74.29	52.02	1.04	8.46E-01	-1.37	7.55E-03
DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	91 kDa	20.34	23.43	26.26	1.15	6.19E-01	1.29	3.13E-01
RBM3_HUMAN	Putative RNA-binding protein 3	17 kDa	29.78	27.42	27.25	-1.09	4.56E-01	-1.09	3.68E-01
PDXK_HUMAN	Pyridoxal kinase	35 kDa	11.84	8.48	6.44	-1.40	1.12E-01	-1.84	1.73E-02
ODPA_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial precursor	43 kDa	3.33	1.50	13.38	-2.23	1.95E-01	4.01	1.10E-02

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	39 kDa	10.89	12.47	29.23	1.14	8.04E-01	2.68	1.93E-04
KPYM_HUMAN	Pyruvate kinase isozymes M1/M2	58 kDa	803.45	799.23	620.75	-1.01	6.06E-02	-1.29	1.02E-05
GDIA_HUMAN	Rab GDP dissociation inhibitor alpha	51 kDa	87.41	90.24	54.99	1.03	8.16E-01	-1.59	4.13E-04
GDIB_HUMAN	Rab GDP dissociation inhibitor beta	51 kDa	86.46	90.24	47.07	1.04	9.09E-01	-1.84	2.13E-04
RADI_HUMAN	Radixin	69 kDa	42.06	33.41	37.16	-1.26	3.74E-01	-1.13	4.29E-02
RAGP1_HUMAN	Ran GTPase-activating protein 1	64 kDa	9.95	13.46	15.36	1.35	3.75E-01	1.54	1.11E-02
RANG_HUMAN	Ran-specific GTPase-activating protein	23 kDa	19.39	21.44	19.33	1.11	8.84E-01	-1.00	8.06E-01
G3BP1_HUMAN	Ras GTPase-activating protein-binding protein 1	52 kDa	22.23	15.46	19.33	-1.44	1.17E-01	-1.15	5.50E-01
IQGA1_HUMAN	Ras GTPase-activating-like protein IQGAP1	189 kDa	115.75	127.14	76.79	1.10	6.77E-01	-1.51	1.35E-02
RAC1_HUMAN	Ras-related C3 botulinum toxin substrate 1 precursor	21 kDa	12.78	12.47	7.44	-1.03	6.08E-01	-1.72	2.84E-02
RB11A_HUMAN	Ras-related protein Rab-11A	24 kDa	8.06	8.48	8.43	1.05	9.59E-01	1.05	9.59E-01
RAB14_HUMAN	Ras-related protein Rab-14	24 kDa	19.39	11.47	11.40	-1.69	3.55E-01	-1.70	3.63E-01
RAB1B_HUMAN	Ras-related protein Rab-1B	22 kDa	36.40	42.38	39.14	1.16	6.21E-01	1.08	9.17E-01
RAB5C_HUMAN	Ras-related protein Rab-5C	23 kDa	4.28	9.47	1.49	2.21	9.24E-02	-2.87	2.47E-02
RAP1B_HUMAN	Ras-related protein Rap-1b precursor	21 kDa	16.56	21.44	17.34	1.29	2.70E-01	1.05	9.63E-01
RRAS2_HUMAN	Ras-related protein R-Ras2 precursor	23 kDa	7.11	9.47	7.44	1.33	1.94E-01	1.05	9.93E-01
RFA1_HUMAN	Replication protein A 70 kDa DNA-binding subunit	68 kDa	15.61	15.46	16.35	-1.01	8.25E-01	1.05	9.83E-01
RCN1_HUMAN	Reticulocalbin-1 precursor	39 kDa	20.34	22.44	31.22	1.10	8.36E-01	1.53	2.28E-02
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1	23 kDa	15.61	19.45	21.31	1.25	2.34E-01	1.36	6.41E-02
RHG01_HUMAN	Rho GTPase-activating protein 1	50 kDa	9.00	10.47	8.43	1.16	4.81E-01	-1.07	6.26E-01
RINI_HUMAN	Ribonuclease inhibitor	50 kDa	33.56	33.41	21.31	-1.00	6.79E-01	-1.58	1.15E-02
RIR1_HUMAN	Ribonucleoside-diphosphate reductase large subunit	90 kDa	14.67	9.47	8.43	-1.55	5.58E-02	-1.74	4.92E-02
RIR2_HUMAN	Ribonucleoside-diphosphate reductase subunit M2	45 kDa	13.73	9.47	7.44	-1.45	2.14E-01	-1.85	7.09E-02
PRPS1_HUMAN	Ribose-phosphate pyrophosphokinase 1	35 kDa	14.67	16.45	11.40	1.12	7.47E-01	-1.29	2.98E-01
RRBP1_HUMAN	Ribosome-binding protein 1	152 kDa	10.89	8.48	25.27	-1.28	4.05E-01	2.32	7.46E-02
RBM14_HUMAN	RNA-binding protein 14	69 kDa	6.17	7.48	16.35	1.21	7.45E-01	2.65	9.47E-03

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
RBM39_HUMAN	RNA-binding protein 39	59 kDa	15.61	9.47	8.43	-1.65	3.97E-02	-1.85	1.80E-02
RBM8A_HUMAN	RNA-binding protein 8A	20 kDa	9.00	8.48	9.42	-1.06	2.66E-01	1.05	9.59E-01
FUS_HUMAN	RNA-binding protein FUS	53 kDa	33.56	33.41	37.16	-1.00	6.99E-01	1.11	6.34E-01
RALY_HUMAN	RNA-binding protein Raly	32 kDa	21.28	20.44	21.31	-1.04	6.10E-01	1.00	7.73E-01
RUVB1_HUMAN	RuvB-like 1	50 kDa	25.06	29.42	25.27	1.17	3.80E-01	1.01	7.18E-01
RUVB2_HUMAN	RuvB-like 2	51 kDa	23.17	28.42	39.14	1.23	3.14E-01	1.69	2.18E-04
METK2_HUMAN	S-adenosylmethionine synthetase isoform type-2	44 kDa	18.45	18.45	19.33	1.00	5.14E-01	1.05	1.00E+00
SAMH1_HUMAN	SAM domain and HD domain-containing protein 1	72 kDa	27.89	34.40	30.22	1.23	1.88E-01	1.08	7.62E-01
SEPT2_HUMAN	Septin-2	41 kDa	33.56	33.41	34.19	-1.00	6.67E-01	1.02	8.33E-01
SEPT7_HUMAN	Septin-7	51 kDa	19.39	21.44	25.27	1.11	8.26E-01	1.30	3.06E-01
SEPT9_HUMAN	Septin-9	65 kDa	28.84	29.42	23.29	1.02	8.32E-01	-1.24	2.61E-01
GLYC_HUMAN	Serine hydroxymethyltransferase, cytosolic	53 kDa	14.67	14.46	11.40	-1.01	5.40E-01	-1.29	1.22E-01
GLYM_HUMAN	Serine hydroxymethyltransferase, mitochondrial precursor	56 kDa	22.23	18.45	40.13	-1.20	9.97E-02	1.81	1.16E-02
PAK2_HUMAN	Serine/threonine-protein kinase PAK 2	58 kDa	5.22	7.48	4.46	1.43	4.68E-01	-1.17	7.55E-01
2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	65 kDa	69.46	60.33	53.01	-1.15	1.46E-01	-1.31	5.85E-03
PP2AA_HUMAN	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	36 kDa	34.51	40.39	30.22	1.17	1.71E-01	-1.14	9.19E-02
PP1A_HUMAN	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	38 kDa	33.56	33.41	36.17	-1.00	6.07E-01	1.08	8.25E-01
PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	37 kDa	28.84	29.42	34.19	1.02	7.70E-01	1.19	3.45E-01
STRAP_HUMAN	Serine-threonine kinase receptor-associated protein	38 kDa	5.22	7.48	9.42	1.43	4.92E-01	1.80	3.00E-02
SPB6_HUMAN	Serpin B6	43 kDa	9.95	8.48	6.44	-1.17	4.60E-01	-1.54	6.04E-02
SERPH_HUMAN	Serpin H1 precursor	46 kDa	70.40	79.28	109.49	1.13	4.99E-01	1.56	1.25E-03
ESTD_HUMAN	S-formylglutathione hydrolase	31 kDa	11.84	14.46	1.49	1.22	2.96E-01	-7.94	7.18E-04
SIAS_HUMAN	Sialic acid synthase	40 kDa	21.28	16.45	15.36	-1.29	7.32E-02	-1.39	7.17E-03
SFXN1_HUMAN	Sideroflexin-1	36 kDa	4.28	3.49	9.42	-1.23	7.99E-01	2.20	1.65E-01
SRP14_HUMAN	Signal recognition particle 14 kDa protein	15 kDa	9.00	9.47	9.42	1.05	9.85E-01	1.05	9.90E-01
SRP09_HUMAN	Signal recognition particle 9 kDa protein	10 kDa	9.00	10.47	11.40	1.16	5.66E-01	1.27	2.38E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
STAT1_HUMAN	Signal transducer and activator of transcription 1-alpha/beta	87 kDa	27.89	28.42	23.29	1.02	7.82E-01	-1.20	1.68E-01
SSB_HUMAN	Single-stranded DNA-binding protein, mitochondrial precursor	17 kDa	29.78	30.41	37.16	1.02	6.94E-01	1.25	5.55E-02
SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein A	34 kDa	2.39	3.49	5.45	1.46	6.60E-01	2.28	9.01E-02
RUXE_HUMAN	Small nuclear ribonucleoprotein E	11 kDa	7.11	7.48	10.41	1.05	9.81E-01	1.46	4.01E-01
RUXF_HUMAN	Small nuclear ribonucleoprotein F	10 kDa	11.84	17.45	21.31	1.47	5.40E-02	1.80	2.49E-02
SMD2_HUMAN	Small nuclear ribonucleoprotein Sm D2	14 kDa	20.34	19.45	16.35	-1.05	3.78E-01	-1.24	8.82E-02
SUMO2_HUMAN	Small ubiquitin-related modifier 2 precursor	11 kDa	13.73	13.46	9.42	-1.02	7.69E-01	-1.46	1.07E-01
MTAP_HUMAN	S-methyl-5'-thioadenosine phosphorylase	31 kDa	12.78	11.47	12.39	-1.11	5.88E-01	-1.03	6.93E-01
AT1A1_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-1 precursor	113 kDa	48.68	53.35	24.28	1.10	8.13E-01	-2.00	3.03E-02
SORCN_HUMAN	Sorcin	22 kDa	8.06	6.48	5.45	-1.24	1.42E-01	-1.48	3.00E-02
SNX1_HUMAN	Sorting nexin-1	59 kDa	8.06	8.48	7.44	1.05	9.69E-01	-1.08	6.77E-01
SNX3_HUMAN	Sorting nexin-3	19 kDa	6.17	8.48	5.45	1.37	3.76E-01	-1.13	5.36E-01
SPTA2_HUMAN	Spectrin alpha chain, brain	285 kDa	82.68	90.24	136.24	1.09	7.86E-01	1.65	2.04E-02
SPTB2_HUMAN	Spectrin beta chain, brain 1	275 kDa	103.47	99.22	147.14	-1.04	1.35E-01	1.42	6.49E-03
SKP1_HUMAN	S-phase kinase-associated protein 1	19 kDa	8.06	8.48	5.45	1.05	9.93E-01	-1.48	2.62E-02
UAP56_HUMAN	Spliceosome RNA helicase BAT1	49 kDa	24.12	27.42	43.10	1.14	5.33E-01	1.79	6.48E-04
SF01_HUMAN	Splicing factor 1	68 kDa	9.95	10.47	11.40	1.05	9.90E-01	1.15	7.62E-01
SF3A1_HUMAN	Splicing factor 3 subunit 1	89 kDa	9.00	7.48	23.29	-1.20	4.79E-01	2.59	2.72E-02
SF3B3_HUMAN	Splicing factor 3B subunit 3	136 kDa	31.67	34.40	64.90	1.09	7.63E-01	2.05	1.24E-04
U2AF2_HUMAN	Splicing factor U2AF 65 kDa subunit	54 kDa	11.84	11.47	8.43	-1.03	7.76E-01	-1.40	1.40E-01
SFRS1_HUMAN	Splicing factor, arginine/serine-rich 1	28 kDa	24.12	27.42	24.28	1.14	6.96E-01	1.01	8.64E-01
SFRS2_HUMAN	Splicing factor, arginine/serine-rich 2	25 kDa	16.56	17.45	12.39	1.05	9.96E-01	-1.34	8.98E-02
SFRS3_HUMAN	Splicing factor, arginine/serine-rich 3	19 kDa	12.78	11.47	12.39	-1.11	5.54E-01	-1.03	7.70E-01
SFRS9_HUMAN	Splicing factor, arginine/serine-rich 9	26 kDa	5.22	10.47	16.35	2.00	1.30E-01	3.13	1.09E-02
SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich	76 kDa	60.01	59.33	77.78	-1.01	3.70E-01	1.30	5.57E-03
SRC8_HUMAN	Src substrate cortactin	62 kDa	26.01	24.43	29.23	-1.06	2.04E-01	1.12	3.59E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
SND1_HUMAN	Staphylococcal nuclease domain-containing protein 1	102 kDa	37.34	37.40	13.38	1.00	7.29E-01	-2.79	2.47E-03
STMN1_HUMAN	Stathmin	17 kDa	47.73	48.36	35.18	1.01	8.09E-01	-1.36	3.88E-02
STML2_HUMAN	Stomatin-like protein 2	39 kDa	34.51	35.40	67.88	1.03	8.26E-01	1.97	3.85E-02
GRP75_HUMAN	Stress-70 protein, mitochondrial precursor	74 kDa	101.58	111.19	132.28	1.09	6.05E-01	1.30	5.21E-03
STIP1_HUMAN	Stress-induced-phosphoprotein 1	63 kDa	60.01	52.35	57.97	-1.15	1.31E-01	-1.04	4.85E-01
SMC1A_HUMAN	Structural maintenance of chromosomes protein 1A	143 kDa	12.78	13.46	8.43	1.05	9.71E-01	-1.52	1.37E-01
SMC2_HUMAN	Structural maintenance of chromosomes protein 2	136 kDa	9.00	15.46	8.43	1.72	1.20E-01	-1.07	8.17E-01
SMC3_HUMAN	Structural maintenance of chromosomes protein 3	142 kDa	7.11	4.49	14.37	-1.58	2.84E-01	2.02	8.10E-02
SMC4_HUMAN	Structural maintenance of chromosomes protein 4	147 kDa	14.67	15.46	20.32	1.05	9.91E-01	1.38	2.54E-01
DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	73 kDa	31.67	30.41	48.06	-1.04	4.51E-01	1.52	1.67E-02
DHSB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial precursor	32 kDa	6.17	8.48	13.38	1.37	5.51E-01	2.17	3.79E-02
SAE1_HUMAN	SUMO-activating enzyme subunit 1	38 kDa	8.06	8.48	3.47	1.05	9.93E-01	-2.32	9.69E-02
UBC9_HUMAN	SUMO-conjugating enzyme UBC9	18 kDa	9.00	9.47	4.46	1.05	9.86E-01	-2.02	8.93E-02
SODC_HUMAN	Superoxide dismutase [Cu-Zn]	16 kDa	29.78	29.42	18.33	-1.01	2.55E-01	-1.62	1.33E-03
VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog	42 kDa	12.78	16.45	10.41	1.29	1.32E-01	-1.23	7.21E-02
TLN1_HUMAN	Talin-1	270 kDa	256.50	252.78	193.71	-1.01	3.97E-01	-1.32	2.85E-02
TADBP_HUMAN	TAR DNA-binding protein 43	45 kDa	24.12	20.44	30.22	-1.18	3.63E-01	1.25	3.57E-01
TCPA_HUMAN	T-complex protein 1 subunit alpha	60 kDa	77.96	80.27	69.86	1.03	7.79E-01	-1.12	1.94E-01
TCPB_HUMAN	T-complex protein 1 subunit beta	57 kDa	70.40	79.28	76.79	1.13	1.22E-01	1.09	5.33E-01
TCPD_HUMAN	T-complex protein 1 subunit delta	58 kDa	69.46	74.29	68.87	1.07	7.47E-01	-1.01	5.39E-01
TCPE_HUMAN	T-complex protein 1 subunit epsilon	60 kDa	94.96	101.21	87.69	1.07	8.27E-01	-1.08	1.88E-01
TCPH_HUMAN	T-complex protein 1 subunit eta	59 kDa	77.96	87.25	61.93	1.12	3.57E-01	-1.26	3.15E-02
TCPG_HUMAN	T-complex protein 1 subunit gamma	61 kDa	119.53	120.16	101.56	1.01	5.43E-01	-1.18	8.92E-03
TCPQ_HUMAN	T-complex protein 1 subunit theta	60 kDa	70.40	74.29	64.90	1.06	9.78E-01	-1.08	2.11E-01
TCPZ_HUMAN	T-complex protein 1 subunit zeta	58 kDa	63.79	59.33	47.07	-1.08	4.34E-01	-1.36	7.58E-02
TENA_HUMAN	Tenascin precursor	241 kDa	5.22	9.47	0.50	1.81	4.70E-01	-10.45	3.56E-01

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			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
THIO_HUMAN	Thioredoxin	12 kDa	52.46	54.35	35.18	1.04	8.47E-01	-1.49	9.75E-03
TXND4_HUMAN	Thioredoxin domain-containing protein 4 precursor	47 kDa	6.17	5.49	11.40	-1.12	6.91E-01	1.85	9.49E-02
TXND5_HUMAN	Thioredoxin domain-containing protein 5 precursor	48 kDa	11.84	13.46	26.26	1.14	6.25E-01	2.22	3.34E-03
TRXR1_HUMAN	Thioredoxin reductase 1, cytoplasmic	71 kDa	16.56	10.47	7.44	-1.58	5.85E-02	-2.23	2.57E-02
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	28 kDa	8.06	9.47	15.36	1.18	7.04E-01	1.91	1.10E-01
SYTC_HUMAN	Threonyl-tRNA synthetase, cytoplasmic	83 kDa	54.35	55.34	30.22	1.02	6.56E-01	-1.80	1.41E-04
TSP1_HUMAN	Thrombospondin-1 precursor	129 kDa	46.79	60.33	17.34	1.29	1.48E-01	-2.70	2.61E-04
KITH_HUMAN	Thymidine kinase, cytosolic	25 kDa	17.50	17.45	9.42	-1.00	7.31E-01	-1.86	1.14E-02
TYB10_HUMAN	Thymosin beta-10	5 kDa	20.34	21.44	20.32	1.05	9.58E-01	-1.00	7.47E-01
TYB4_HUMAN	Thymosin beta-4	5 kDa	41.12	39.39	32.21	-1.04	5.50E-01	-1.28	5.74E-02
ZO2_HUMAN	Tight junction protein ZO-2	134 kDa	11.84	10.47	8.43	-1.13	6.36E-01	-1.40	2.62E-01
TOIP1_HUMAN	Torsin-1A-interacting protein 1	66 kDa	2.39	10.47	15.36	4.38	2.43E-03	6.43	1.12E-04
TALDO_HUMAN	Transaldolase	38 kDa	27.89	31.41	20.32	1.13	6.23E-01	-1.37	7.61E-02
ELOC_HUMAN	Transcription elongation factor B polypeptide 1	12 kDa	13.73	11.47	14.37	-1.20	3.12E-01	1.05	9.87E-01
TIF1B_HUMAN	Transcription intermediary factor 1-beta	89 kDa	51.51	53.35	82.74	1.04	8.06E-01	1.61	3.98E-03
TFR1_HUMAN	Transferrin receptor protein 1	85 kDa	51.51	67.31	65.89	1.31	4.06E-02	1.28	5.33E-02
RHOA_HUMAN	Transforming protein RhoA precursor	22 kDa	20.34	18.45	11.40	-1.10	4.89E-01	-1.78	1.73E-02
TAGL_HUMAN	Transgelin	23 kDa	25.06	28.42	15.36	1.13	5.78E-01	-1.63	1.45E-02
TAGL2_HUMAN	Transgelin-2	22 kDa	108.19	106.20	84.72	-1.02	3.36E-01	-1.28	6.03E-03
TERA_HUMAN	Transitional endoplasmic reticulum ATPase	89 kDa	186.60	201.93	213.52	1.08	5.33E-01	1.14	4.33E-02
TKT_HUMAN	Transketolase	68 kDa	145.98	151.07	141.20	1.03	7.13E-01	-1.03	1.24E-01
TCTP_HUMAN	Translationally-controlled tumor protein	20 kDa	21.28	20.44	21.31	-1.04	4.57E-01	1.00	7.09E-01
TMED9_HUMAN	Transmembrane emp24 domain-containing protein 9 precursor	25 kDa	9.95	10.47	15.36	1.05	9.97E-01	1.54	1.23E-02
TNPO1_HUMAN	Transportin-1	101 kDa	22.23	15.46	10.41	-1.44	6.92E-02	-2.14	1.75E-02
ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial precursor	83 kDa	35.45	34.40	50.04	-1.03	5.40E-01	1.41	3.28E-01
PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--	108 kDa	22.23	24.43	19.33	1.10	6.11E-01	-1.15	2.28E-02

Accessionnummer	Proteinbeschreibung	Molekular- gewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
	glycine ligase								
TPIS_HUMAN	Triosephosphate isomerase	27 kDa	212.10	225.86	198.66	1.06	8.32E-01	-1.07	1.13E-02
TMOD3_HUMAN	Tropomodulin-3	40 kDa	13.73	16.45	21.31	1.20	5.24E-01	1.55	4.12E-02
TPM1_HUMAN	Tropomyosin alpha-1 chain	33 kDa	63.79	68.31	67.88	1.07	8.02E-01	1.06	8.42E-01
TPM4_HUMAN	Tropomyosin alpha-4 chain	29 kDa	105.36	97.23	107.51	-1.08	6.33E-02	1.02	7.21E-01
TPM2_HUMAN	Tropomyosin beta chain	33 kDa	74.18	70.30	74.81	-1.06	1.27E-02	1.01	2.86E-01
SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic	53 kDa	30.73	54.35	48.06	1.77	3.14E-02	1.56	1.37E-03
TBA1B_HUMAN	Tubulin alpha-1B chain	50 kDa	611.69	620.74	543.47	1.01	3.65E-01	-1.13	2.98E-03
TBA1C_HUMAN	Tubulin alpha-1C chain	50 kDa	473.77	487.12	423.58	1.03	5.26E-01	-1.12	1.05E-02
TBB5_HUMAN	Tubulin beta chain	50 kDa	947.98	963.76	837.74	1.02	3.73E-02	-1.13	7.22E-05
TBB2A_HUMAN	Tubulin beta-2A chain	50 kDa	669.31	676.58	585.08	1.01	8.78E-02	-1.14	3.95E-04
TBB2C_HUMAN	Tubulin beta-2C chain	50 kDa	811.95	816.18	705.96	1.01	3.59E-02	-1.15	8.28E-05
TBB3_HUMAN	Tubulin beta-3 chain	50 kDa	512.50	504.07	444.38	-1.02	4.82E-02	-1.15	2.17E-03
TBB6_HUMAN	Tubulin beta-6 chain	50 kDa	267.84	273.72	224.42	1.02	3.86E-01	-1.19	2.89E-05
TBCB_HUMAN	Tubulin folding cofactor B	27 kDa	12.78	9.47	6.44	-1.35	2.08E-02	-1.98	2.05E-03
TBCA_HUMAN	Tubulin-specific chaperone A	13 kDa	14.67	10.47	15.36	-1.40	4.51E-02	1.05	9.92E-01
TPD54_HUMAN	Tumor protein D54	22 kDa	31.67	30.41	21.31	-1.04	2.03E-01	-1.49	2.82E-03
RU1C_HUMAN	U1 small nuclear ribonucleoprotein C	17 kDa	8.06	8.48	10.41	1.05	9.55E-01	1.29	3.62E-01
U520_HUMAN	U5 small nuclear ribonucleoprotein 200 kDa helicase	245 kDa	27.89	25.43	36.17	-1.10	3.96E-01	1.30	4.25E-01
UBQL1_HUMAN	Ubiquilin-1	63 kDa	12.78	16.45	11.40	1.29	2.55E-01	-1.12	5.99E-01
UBIQ_HUMAN	Ubiquitin	9 kDa	23.17	24.43	24.28	1.05	9.95E-01	1.05	9.90E-01
UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14	56 kDa	8.06	5.49	4.46	-1.47	1.72E-01	-1.81	1.30E-01
UBP5_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5	96 kDa	26.01	28.42	21.31	1.09	7.02E-01	-1.22	1.82E-01
UBP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7	128 kDa	6.17	5.49	12.39	-1.12	7.53E-01	2.01	1.66E-01
UCHL3_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L3	26 kDa	7.11	8.48	5.45	1.19	3.35E-01	-1.30	2.08E-01
UBP2L_HUMAN	Ubiquitin-associated protein 2-like	115 kDa	8.06	9.47	6.44	1.18	7.27E-01	-1.25	4.70E-01

Accessionnummer	Proteinbeschreibung	Molekulargewicht	Assigned spectra			Co vs S9-int		Co vs S9-inf	
			Co	S9-inf	S9-int	F.CH.	p-Wert	F.CH.	p-Wert
UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1	118 kDa	151.64	155.06	128.31	1.02	4.91E-01	-1.18	6.87E-03
UGGG1_HUMAN	UDP-glucose:glycoprotein glucosyltransferase 1 precursor	175 kDa	8.06	8.48	23.29	1.05	9.96E-01	2.89	1.30E-03
CS010_HUMAN	Uncharacterized protein C19orf10 precursor	19 kDa	6.17	7.48	15.36	1.21	5.66E-01	2.49	1.11E-03
CV028_HUMAN	UPF0027 protein C22orf28	55 kDa	8.06	11.47	9.42	1.42	3.02E-01	1.17	6.66E-01
UTRO_HUMAN	Utrophin	394 kDa	7.11	6.48	16.35	-1.10	7.20E-01	2.30	8.77E-02
RD23B_HUMAN	UV excision repair protein RAD23 homolog B	43 kDa	17.50	15.46	6.44	-1.13	1.16E-01	-2.72	2.50E-03
VPS35_HUMAN	Vacuolar protein sorting-associated protein 35	92 kDa	21.28	21.44	22.30	1.01	6.71E-01	1.05	9.99E-01
ACADV_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	70 kDa	12.78	14.46	31.22	1.13	7.54E-01	2.44	3.06E-02
VAMP3_HUMAN	Vesicle-associated membrane protein 3	11 kDa	5.22	8.48	5.45	1.62	2.61E-01	1.04	9.78E-01
NSF_HUMAN	Vesicle-fusing ATPase	83 kDa	4.28	3.49	9.42	-1.23	5.90E-01	2.20	4.64E-02
VIGLN_HUMAN	Vigilin	141 kDa	14.67	12.47	9.42	-1.18	5.49E-01	-1.56	2.51E-01
VIME_HUMAN	Vimentin	54 kDa	692.93	707.49	1215.24	1.02	4.26E-01	1.75	1.34E-04
VINC_HUMAN	Vinculin	124 kDa	101.58	95.23	86.70	-1.07	3.04E-01	-1.17	1.53E-01
VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	31 kDa	41.12	53.35	79.77	1.30	1.20E-01	1.94	3.11E-05
VDAC2_HUMAN	Voltage-dependent anion-selective channel protein 2	32 kDa	7.11	9.47	5.45	1.33	5.72E-01	-1.30	3.89E-01
WDR1_HUMAN	WD repeat-containing protein 1	66 kDa	33.56	26.43	27.25	-1.27	7.12E-02	-1.23	1.36E-01
ZCC2_HUMAN	Zinc finger CCCH type antiviral protein 1	101 kDa	8.06	13.46	9.42	1.67	7.75E-02	1.17	6.67E-01
ZYX_HUMAN	Zyxin	61 kDa	28.84	30.41	31.22	1.05	9.78E-01	1.08	7.18E-01

Für alle quantifizierbaren Proteine wurde die Anzahl der assigned Spektren innerhalb der Bioreplikate für jeden Probensatz normalisiert und zu 0.5 addiert. In der Abundanz veränderte Proteine wurden bei einem p -Wert ≤ 0.5 (≥ 1.5 -fach bzw. ≤ -1.5 -fach) als signifikant angesehen. Der Fold Change bezieht sich jeweils auf die zeitgleiche Kontrolle.

Co = zeitgleiche Kontrolle der S9-Zellen, S9-inf = *S. aureus*-infizierte S9-Zellen, S9-int = *S. aureus* internalisierte S9-Zellen.