

Anhang IIa: Identifizierungen putativ phosphorylierter Proteine aus dem 2D-Gel (*S. aureus*)

Spot	Genort	Akzessionsnummer	Protein-name	Proteinfunktion	Molekulargewicht (Da)	Protein-Identifizierungswahrscheinlichkeit (%)	Abdeckung (%)	Anzahl einzigartiger Peptide	Phosphorylierungsstelle	Phosphopeptid-Sequenz
AcnA	SACOL1385	gi 57650354	AcnA	aconitate hydratase	98971,3	100	74	68	Y310	(R)ATIANmAPEpYGATCGFFPVDES(LK)(Y)
AhpC	SACOL0452	gi 57652639	AhpC	alkyl hydroperoxide reductase subunit C	20976,7	100	79	11		
AhpF-1	SACOL1985	gi 57650675	AhpF	hypothetical protein SACOL1985	38547,3	100	82	25		
AhpF-2	SACOL1985	gi 57650675	AhpF	hypothetical protein SACOL1985	38547,3	100	64	20		
AhpF-3	SACOL1985	gi 57650675	AhpF	hypothetical protein SACOL1985	38547,3	100	21	8		
ClpX-1	SACOL1721	gi 57650546	ClpX	ATP-dependent protease ATP-binding subunit	46299,1	100	40	15		
ClpX-2	SACOL1721	gi 57650546	ClpX	ATP-dependent protease ATP-binding subunit	46299,1	100	45	16		
CysK	SACOL0557	gi 57651389	CysK	cysteine synthase	32976,4	100	73	27		
DapA	SACOL1430	gi 57651895	DapA	dihydrodipicolinate synthase	32584,7	100	39	11		
Dat	SACOL1800	gi 57652048	Dat	D-alanine aminotransferase	31894,4	100	59	13		
DeoB-1	SACOL0124	gi 57651145	DeoB	phosphopentomutase	43797,3	100	93	39	T87	(K)LSEASVGKDTmpTGHWEImGLNImQPFK(V)
DeoB-2	SACOL0124	gi 57651145	DeoB	phosphopentomutase	43797,3	100	74	30	T87	(K)LSEASVGKDTmpTGHWEImGLNImQPFK(V)
DeoB-3	SACOL0124	gi 57651145	DeoB	phosphopentomutase	43797,3	100	93	32	T87	(K)LSEASVGKDTmpTGHWEImGLNImQPFK(V)
DnaN-1	SACOL0002	gi 57651110	DnaN	DNA polymerase III subunit beta	41915,3	100	28	14		
DnaN-2	SACOL0002	gi 57651110	DnaN	DNA polymerase III subunit beta	41915,3	100	45	17		
Efp	SACOL1587	gi 57650473	Efp	elongation factor P	36062,5	100	26	7		
Eno-1	SACOL0842	gi 57650118	Eno	enolase	47118,3	100	38	15		
Eno-2	SACOL0842	gi 57650118	Eno	enolase	47118,3	100	55	23		
Eno-3	SACOL0842	gi 57650118	Eno	enolase	47118,3	100	62	29		
FbaA-1	SACOL2117	gi 57652147	FbaA	fructose-bisphosphate aldolase	30836,3	100	72	26	T234	(K)INVNpTENQIASAK(A)
FbaA-1	SACOL2117	gi 57652147	FbaA	fructose-bisphosphate aldolase	30836,3	100	71	26	S50/T212	(E)NAPVILGvPSE(G) / (E)IGLSTGLPLVLHGGpTGIPTKD(I)
FbaA-2	SACOL2117	gi 57652147	FbaA	fructose-bisphosphate aldolase	30836,3	100	63	20	T234	(K)INVNpTENQIASAK(A)
FdaB-1	SACOL2622	gi 57652341	FdaB	fructose-1,6-bisphosphate aldolase	33055,6	100	78	24		
FdaB-2	SACOL2622	gi 57652341	FdaB	fructose-1,6-bisphosphate aldolase	33055,6	100	90	32		
FemC-1	SACOL1329	gi 57650300	FemC	glutamine synthetase	50842,1	100	76	26	S392	(R)EAVGIQDLPpSTLYTALK(A)
FemC-2	SACOL1329	gi 57650300	FemC	glutamine synthetase	50842,1	100	80	28		
FtsY	SACOL1251	gi 57651804	FtsY	cell division protein FtsY, putative	46591,1	100	65	21		
FtsZ	SACOL1199	gi 57651756	FtsZ	cell division protein	41037,0	100	67	27		
FusA-1	SACOL0593	gi 57651423	FusA	elongation factor G	76613,0	100	72	47	T388	(K)DTGTGDpTLCGEKNDIILEmEFPEPVIHLSVEPK(S)
FusA-2	SACOL0593	gi 57651423	FusA	elongation factor G	76613,0	100	80	50		
GapA1-1	SACOL0838	gi 57650114	GapA1	glycerinaldehyde 3-phosphate dehydrogenase	36280,5	100	91	24	S210	(R)AAENIIPNpSTGA(AK)(A)
GapA1-2	SACOL0838	gi 57650114	GapA1	glycerinaldehyde 3-phosphate dehydrogenase	36280,5	100	56	15		
GapA1-3	SACOL0838	gi 57650114	GapA1	glycerinaldehyde 3-phosphate dehydrogenase	36280,5	100	79	17		
GatB	SACOL1960	gi 57652120	GatB	aspartylglutamy-tRNA amidotransferase subunit B	53658,5	100	79	31		
GatB-1	SACOL1960	gi 57652120	GatB	aspartylglutamy-tRNA amidotransferase subunit B	53658,5	100	55	29		
GatB-2	SACOL1960	gi 57652120	GatB	aspartylglutamy-tRNA amidotransferase subunit B	53658,5	100	89	64	S196	(R)CDANIpSLRPYGQEK(F)
GimM-1	SACOL2151	gi 57652179	GimM	phosphoglucoseamine mutase	49266,0	100	90	38	S102	(R)DmGAELGVMISApSHNPVADNGIK(F)
GimM-2	SACOL2151	gi 57652179	GimM	phosphoglucoseamine mutase	49266,0	100	86	32	S102	(R)DmGAELGVMISApSHNPVADNGIK(F)
GlpD	SACOL1321	gi 57651870	GlpD	aerobic glycerol-3-phosphate dehydrogenase	62389,8	100	34	19		
GluD-1	SACOL0961	gi 57651649	GluD	NAD-specific glutamate dehydrogenase	45761,2	100	74	28	T267/S264	(R)RDSFGpTVTNLFEETISNK(E)/(R)RDpSFGVTVTNLFEETISNK(E)
GluD-2	SACOL0961	gi 57651649	GluD	NAD-specific glutamate dehydrogenase	45761,2	100	54	21	S264	(R)DpSFGVTVTNLFEETISNK(E)
GlyS	SACOL1622	gi 57651958	GlyS	glycyl-tRNA synthetase	53622,4	100	77	41		
Gnd	SACOL1554	gi 57650466	Gnd	6-phosphogluconate dehydrogenase	51805,3	100	64	27	S167	(K)AKDGApSCVTYIGPNAGHYV(K)(M)
Gpm	SACOL2415	gi 57650960	Gpm	phosphoglycerate mutase	26880,8	100	47	7		
GuaB-1	SACOL0460	gi 57652647	GuaB	inosine-5'-monophosphate dehydrogenase	52851,7	100	78	37		
GuaB-2	SACOL0460	gi 57652647	GuaB	inosine-5'-monophosphate dehydrogenase	52851,7	100	51	25		
HchA	SACOL0597	gi 57651427	HchA	chaperone protein HchA	32177,6	100	24	7		
HemL1	SACOL1714	gi 57650539	HemL1	glutamate-1-semialdehyde aminotransferase	46389,6	100	43	15		
HemL2	SACOL1922	gi 57652083	HemL2	glutamate-1-semialdehyde aminotransferase	46757,2	100	63	20		
HisC	SACOL0784	gi 57651560	HisC	histidinol-phosphate aminotransferase	39789,1	100	43	15		
Hom	SACOL1362	gi 57650331	Hom	homoserine dehydrogenase	46874,8	100	17	7		

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IivC-1	SACOL2045	gi 57650728	IivC	ketol-acid reductoisomerase	36955,9	100	54	18		
IivC-2	SACOL2045	gi 57650728	IivC	ketol-acid reductoisomerase	36955,9	100	58	19		
IivE-1	SACOL0600	gi 57651430	IivE	branched-chain amino acid aminotransferase	40087,2	100	72	19		
IivE-2	SACOL0600	gi 57651430	IivE	branched-chain amino acid aminotransferase	40087,2	100	69	22		
IivE-3	SACOL0600	gi 57651430	IivE	branched-chain amino acid aminotransferase	40087,2	100	50	17		
KatA-1	SACOL1368	gi 57650337	KatA	katalase	54944,2	100	53	20		
KatA-2	SACOL1368	gi 57650337	KatA	katalase	54944,2	100	63	35		
LeuA-1	SACOL2046	gi 57650729	LeuA	2-Isopropyl synthase	55674,8	100	42	18		
LeuA-2	SACOL2046	gi 57650729	LeuA	2-Isopropyl synthase	55674,8	100	40	18		
MetE-1	SACOL0428	gi 57652616	MetE	5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	85078,8	100	55	53		
MetE-2	SACOL0428	gi 57652616	MetE	5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	85078,8	100	79	79		
MetE-3	SACOL0428	gi 57652616	MetE	5-methyltetrahydropteroyltrimethylglutamate--homocysteine methyltransferase	85078,8	100	76	85		
MetK-1	SACOL1837	gi 57650575	MetK	S-adenosylmethionine synthetase	43641,9	100	60	23		
MetK-2	SACOL1837	gi 57650575	MetK	S-adenosylmethionine synthetase	43641,9	100	67	32		
Mqo2-1	SACOL2623	gi 57652342	Mqo2	malate:quinone oxidoreductase	56000,4	100	70	35		
Mqo2-2	SACOL2623	gi 57652342	Mqo2	malate:quinone oxidoreductase	56000,4	100	80	41		
MitD-1	SACOL2149	gi 57652177	MitD	mannitol-1-phosphate 5-dehydrogenase	40952,8	100	40	13		
MitD-2	SACOL2149	gi 57652177	MitD	mannitol-1-phosphate 5-dehydrogenase	40952,8	100	38	10		
PdhC-1	SACOL1104	gi 57651704	PdhC	branched-chain alpha-keto acid dehydrogenase subunit E2	46382,1	100	48	18		
PdhC-2	SACOL1104	gi 57651704	PdhC	branched-chain alpha-keto acid dehydrogenase subunit E2	46382,1	100	50	19		
PdhC-3	SACOL1104	gi 57651704	PdhC	branched-chain alpha-keto acid dehydrogenase subunit E2	46382,1	100	40	15		
PdhD-1	SACOL1105	gi 57651705	PdhD	dihydrolipoamide dehydrogenase	49451,8	100	48	23		
PdhD-2	SACOL1105	gi 57651705	PdhD	dihydrolipoamide dehydrogenase	49451,8	100	58	25		
PepF	SACOL1005	gi 57650193	PepF	oligoendopeptidase	69822,3	100	65	48		
PepV	SACOL1801	gi 57652049	PepV	dipeptidase PepV	52825,4	100	63	39		
Pgi	SACOL0966	gi 57651654	Pgi	glucose-6-phosphate isomerase	49809,6	100	75	37	T143	(K)SGT ^p TTEPAVAFR(L)
Pgk-1	SACOL0839	gi 57650115	Pgk	phosphoglycerate kinase	42603,3	100	62	29		
Pgk-2	SACOL0839	gi 57650115	Pgk	phosphoglycerate kinase	42603,3	100	49	21		
Pgm-1	SACOL0841	gi 57650117	Pgm	phosphoglyceromutase	56425,5	100	19	7		
Pgm-2	SACOL0841	gi 57650117	Pgm	phosphoglyceromutase	56425,5	100	52	20		
Pgm-3	SACOL0841	gi 57650117	Pgm	phosphoglyceromutase	56425,5	100	67	37		
Pnp	SACOL1293	gi 57651844	Pnp	polynucleotide phosphorylase/polyadenylase	77364,4	100	38	21		
PtsH	SACOL1091	gi 57651691	PtsH	phosphocarrier protein HPr	9496,1	100	100	9	S46	(K)VNLK ^p SIMGVMSLGVGK(D)
PtsI	SACOL1092	gi 57651692	PtsI	phosphoenolpyruvate-protein phosphotransferase	63221,0	100	50	33		
Pyk-1	SACOL1745	gi 57650568	Pyk	pyruvate kinase	63102,9	100	81	44	T537	(K)ALGLITEENG ^p TSPSAIVGLEK(G)
Pyk-2	SACOL1745	gi 57650568	Pyk	pyruvate kinase	63102,9	100	74	35	T537	(K)ALGLITEENG ^p TSPSAIVGLEK(G)
Pyk-3	SACOL1745	gi 57650568	Pyk	pyruvate kinase	63102,9	100	68	29	T537	(K)ALGLITEENG ^p TSPSAIVGLEK(G)
Pyk-4	SACOL1745	gi 57650568	Pyk	pyruvate kinase	63102,9	100	32	13	T537	(K)ALGLITEENG ^p TSPSAIVGLEK(G)
Pyk-5	SACOL1745	gi 57650568	Pyk	pyruvate kinase	63102,9	100	81	41	T537	(K)ALGLITEENG ^p TSPSAIVGLEK(G)
RpsA	SACOL1516	gi 57650431	RpsA	30S ribosomal protein S1	43286,8	100	61	27		
RpsB	SACOL1274	gi 57651825	RpsB	30S ribosomal protein S2	29396,4	100	49	18		
RpsB-1	SACOL1274	gi 57651825	RpsB	30S ribosomal protein S2	29396,4	100	36	12		
RpsB-2	SACOL1274	gi 57651825	RpsB	30S ribosomal protein S2	29396,4	100	43	15		
RsbV	SACOL2056	gi 57650738	RsbV	anti-anti-sigma factor RsbV	12204,9	100	100	12	S57	(R)DIYVNLVNSYmD ^p STGLGLFVGTLK(A)
SACOL0427-1	SACOL0427	gi 57652615	SACOL0427	hypothetical protein SACOL0427	28752,7	100	78	21		
SACOL0427-2	SACOL0427	gi 57652615	SACOL0427	hypothetical protein SACOL0427	28752,7	100	55	15		
SACOL0431	SACOL0431	gi 57652619	SACOL0431	trans-sulfuration enzyme family protein	41074,1	100	73	27		
SACOL0534	SACOL0534	gi 57651373	SACOL0534	TatD family deoxyribonuclease	29281,9	100	47	8		
SACOL0564-1	SACOL0564	gi 57651396	SACOL0564	pyridoxin biosynthesis protein	31992,6	100	70	25	T155	(R)TKGEG ^p TGNIVEAVR(H)
SACOL0564-2	SACOL0564	gi 57651396	SACOL0564	pyridoxin biosynthesis protein	31992,6	100	69	22		
SACOL0564-3	SACOL0564	gi 57651396	SACOL0564	pyridoxin biosynthesis protein	31992,6	100	58	18		
SACOL0597	SACOL0597	gi 57651427	SACOL0597	chaperone protein HchA	32177,6	100	39	9		
SACOL0812	SACOL0812	gi 57651587	SACOL0812	degV family protein	32069,5	100	50	9		
SACOL0875	SACOL0875	gi 57650499	SACOL0875	thioredoxin, putative	10303,7	100	95	10	T7	(-)MENFDK ^p TmKFDYEELPTQDVR(D)
SACOL0884-1	SACOL0884	gi 57650157	SACOL0884	ABC transporter, substrate-binding protein	30352,8	100	62	17		

Spot	Genort	Akzessionsnummer	Protein-name	Proteinfunktion	Molekulargewicht (Da)	Protein-Identifizierungswahrscheinlichkeit (%)	Abdeckung (%)	Anzahl einzigartiger Peptide	Phosphorylierungsstelle	Phosphopeptid-Sequenz
SACOL0884-2	SACOL0884	gi 57650157	SACOL0884	ABC transporter, substrate-binding protein	30352,8	100	40	9		
SACOL0884-3	SACOL0884	gi 57650157	SACOL0884	ABC transporter, substrate-binding protein	30352,8	100	73	26		
SACOL0884-4	SACOL0884	gi 57650157	SACOL0884	ABC transporter, substrate-binding protein	30352,8	100	52	12		
SACOL0914	SACOL0914	gi 57651604	SACOL0914	FeS assembly ATPase SufC	28276,7	100	85	22		
SACOL1445	SACOL1445	gi 57651910	SACOL1445	CbbQ/NirQ/NorQ/GpwN family protein	29449,8	100	43	8		
SACOL1483	SACOL1483	gi 57650399	SACOL1483	hypothetical protein SACOL1483	43334,9	100	42	10		
SACOL1561-1	SACOL1561	gi 57650473	SACOL1561	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	36062,5	100	74	25		
SACOL1588	SACOL1588	gi 57651924	SACOL1588	proline dipeptidase	39339,9	100	84	27	T313	(K)LQVNNCVpTVEPGVYIEGLGGR(I)
SACOL1749	SACOL1749	gi 57650572	SACOL1749	NADP-dependent malic enzyme, putative	44234,3	100	42	13		
SACOL1759	SACOL1759	gi 57652008	SACOL1759	universal stress protein	18474,8	100	66	14		
SACOL1958	SACOL1958	gi 57652119	SACOL1958	putative lipid kinase	34888,6	100	48	14		
SACOL2173-1	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	85	17		
SACOL2173-2	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	72	13		
SACOL2173-3	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	63	10		
SACOL2173-4	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	42	12		
SACOL2173-5	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	34	8		
SACOL2173-6	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	47	14		
SACOL2173-7	SACOL2173	gi 57652199	SACOL2173	alkaline shock protein 23	19190,6	100	75	25		
SACOL2501	SACOL2501	gi 57651000	SACOL2501	phosphoglucosyltransferase/phosphomannomutase family protein	68350,6	100	55	32		
SdhA	SACOL1159	gi 57650258	SdhA	succinate dehydrogenase flavoprotein subunit	65505	100	37	16		
SerA	SACOL1773	gi 57652022	SerA	D-3-phosphoglycerate dehydrogenase	57620,9	100	44	17		
SodA2-1	SACOL1610	gi 57651946	SodA2	superoxide dismutase	22711,5	100	38	6		
SodA2-2	SACOL1610	gi 57651946	SodA2	superoxide dismutase	22711,5	100	22	3		
SucC	SACOL1262	gi 57651814	SucC	succinyl-CoA synthetase subunit beta	42057,1	100	33	13	S364	(K)ILKDPsGLAIEPAATMAEGAQK(I)
Tal-1	SACOL1831	gi 57652078	Tal	putative transaldolase	25705,6	100	72	15		
Tal-2	SACOL1831	gi 57652078	Tal	putative transaldolase	25705,6	100	96	41		
Tal-3	SACOL1831	gi 57652078	Tal	putative transaldolase	25705,6	100	85	26		
Tig	SACOL1722	gi 57650547	Tig	trigger factor	48609,3	100	78	49		
Tkt-1	SACOL1377	gi 57650346	Tkt	transketolase	72251,8	100	79	48		
Tkt-2	SACOL1377	gi 57650346	Tkt	transketolase	72251,8	100	69	47		
Tuf-1	SACOL0594	gi 57651424	Tuf	elongation factor Tu	43103,3	100	73	28		
Tuf-1a	SACOL0594	gi 57651424	Tuf	elongation factor Tu	43103,3	100	78	26	S220	(R)DSDKPFmmPVEDVfPpSITGR(G)
Tuf-1b	SACOL0594	gi 57651424	Tuf	elongation factor Tu	43103,3	100	63	20		
Tuf-2a	SACOL0594	gi 57651424	Tuf	elongation factor Tu	43103,3	100	82	30		
Tuf-2b	SACOL0594	gi 57651424	Tuf	elongation factor Tu	43103,3	100	67	21		
Zwf-1	SACOL1549	gi 57650461	Zwf	glucose-6-phosphate 1-dehydrogenase	56967,1	100	48	19		
Zwf-2	SACOL1549	gi 57650461	Zwf	glucose-6-phosphate 1-dehydrogenase	56967,1	100	38	17		

m= Methioninoxidation

p= Phosphorylierung am Serin, Threonin oder Tyrosin

Anhang IIb: Identifizierte phosphorylierte Peptide aus dem gelbasierten Ansatz (*S. aureus*)

Spot	identifiziertes Protein	Genort	modifizierte Peptidsequenz	Start	Stop	MH+ (theoretisch)	m/z Vorläuferion	Ladung z	Peptid- Identifizierungs- Wahrscheinlichkeit (%)	XC (Xcorr Sequest)	dCN	Position	modifizierte Aminosäure
AcnA-1	AcnA	SACOL1385	(R)ATIANmAPEpYGATCGFFPVDDSELK(Y)	301	325	2742,1807	915,0681	3	95,00%	4,13	0,59	310	Y
DeoB-2	DeoB	SACOL0124	(K)LSEASVgKDTmpTGHWEImGLNImQPfK(V)	76	102	3147,3915	787,8557	4	95,00%	3,75	0,48	87	T
DeoB-3	DeoB	SACOL0124	(K)LSEASVgKDTmpTGHWEImGLNImQPfK(V)	76	102	3147,4100	787,8603	4	95,00%	3,89	0,42	87	T
DeoB-1	DeoB	SACOL0124	(K)LSEASVgKDTmpTGHWEImGLNImQPfK(V)	76	102	3147,4060	787,8588	4	95,00%	3,99	0,45	87	T
FbaA-2	FbaA	SACOL2117	(K)INVNpTENQIASAK(A)	230	242	1480,6932	741,3544	2	95,00%	3,51	0,52	234	T
FbaA-1	FbaA	SACOL2117	(K)INVNpTENQIASAK(A)	230	242	1480,6892	741,3524	2	95,00%	3,44	0,52	234	T
FbaA-1	FbaA	SACOL2117	(E)NAPVILGpSE(G)	42	51	1077,5108	539,7627	3	95,00%	1,54	0,54	50	S
FbaA-1	FbaA	SACOL2117	(E)IGLSTGLPLVLHGgpTGIPTKD(I)	198	218	2125,1262	709,3827	3	95,00%	3,49	0,66	212	T
FemC-1	FemC	SACOL1330	(R)EAVGIQDLpSTLYTALK(A)	383	399	1897,9434	949,9795	2	95,00%	3,52	0,53	392	S
FusA-1	FusA	SACOL0593	(K)DTGTGdpTLCGEKNDIILESmEFPEPVIHLSVEPK(S)	382	415	3808,7466	638,7989	6	95,00%	3,03	0,26	388	T
GapA1-1	GapA1	SACOL0838	(R)AAAENIIPpSTGAAK(A)	201	215	1506,7038	754,3597	2	95,00%	2,80	0,50	210	S
GatB-2	GatB	SACOL1960	(R)CDANIpSLRPYGQEK(F)	191	204	1672,7186	558,5807	3	95,00%	1,65	0,30	196	S
GlmM-1	GlmM	SACOL2151	(R)DmGAELGVMISApSHNPVADNGIK(F)	90	112	2421,0690	808,0308	3	95,00%	4,88	0,60	103	S
GlmM-2	GlmM	SACOL2151	(R)DmGAELGVMISApSHNPVADNGIK(F)	90	112	2421,0677	808,0303	3	95,00%	4,56	0,59	103	S
GluD-1	GluD	SACOL0961	(R)RDSFGpTVTNLFEETISNK(E)	262	279	2136,9679	713,3304	3	95,00%	5,08	0,57	267	T
GluD-1	GluD	SACOL0961	(R)RDpSFGTVTNLFEETISNK(E)	262	279	2136,9679	1069,4930	2	95,00%	4,99	0,16	264	S
GluD-2	GluD	SACOL0961	(R)RDpSFGTVTNLFEETISNK(E)	262	279	1980,8704	991,4430	2	95,00%	3,81	0,50	264	S
Gnd	Gnd	SACOL1554	(K)AKDGApSCVTYIGPNGAGHYVK(M)	162	182	2186,9967	730,0067	3	95,00%	2,74	0,52	167	S
Pgi	Pgi	SACOL0966	(K)SGTpTTEPAVAFR(L)	140	151	1315,5789	658,7973	2	95,00%	2,26	0,54	143	T
PtsH	PtsH	SACOL1091	(K)VNLKpSIMGVMSLGVGK(D)	42	57	1711,8803	856,9474	2	95,00%	3,25	0,59	46	S
Pyk-1	Pyk	SACOL1745	(K)ALGLITEENgipTSPSAIVGLEK(G)	526	547	2291,1702	1146,5929	2	95,00%	5,59	0,69	537	T
Pyk-2	Pyk	SACOL1745	(K)ALGLITEENgipTSPSAIVGLEK(G)	526	547	2291,1678	764,7314	3	95,00%	6,61	0,69	537	T
Pyk-3	Pyk	SACOL1745	(K)ALGLITEENgipTSPSAIVGLEK(G)	526	547	2292,1560	765,0598	3	95,00%	6,05	0,67	537	T
Pyk-4	Pyk	SACOL1745	(K)ALGLITEENgipTSPSAIVGLEK(G)	526	547	2291,1678	764,7314	3	95,00%	5,78	0,69	537	T
Pyk-5	Pyk	SACOL1745	(K)ALGLITEENgipTSPSAIVGLEK(G)	526	547	2291,1675	1146,5916	2	95,00%	4,86	0,75	537	T
RsbV	RsbV	SACOL2056	(R)DIYVNLNENVSymDpSTGLGLFVGTlk(A)	44	68	2843,3214	948,7816	3	95,00%	3,19	0,44	57	S
SACOL0564-1	SACOL0564	SACOL0564	(R)TKGEPGpTGNIVEAVR(H)	149	163	1606,7728	536,5988	3	95,00%	1,77	0,42	155	T
SACOL0875	SACOL0875	SACOL0875	(-)MENFDKpTmKFDYEEELPTQDVR(D)	1	21	2731,1599	911,3945	3	95,00%	4,14	0,51	7	T
SACOL1588	SACOL1588	SACOL1588	(K)LQVNNCVpTVEPGVYIEGLGGIR(I)	306	327	2409,1983	804,0739	3	95,00%	3,29	0,43	313	T
SucC	SucC	SACOL1262	(K)ILKdpSGLAIEPAATMAEGAQK(I)	360	380	2193,0756	732,0330	3	95,00%	3,29	0,40	364	S
Tuf-1a	Tuf	SACOL0594	(R)DSDKPFmPVEDVfpSITGR(G)	206	224	2281,9577	761,6604	3	95,00%	2,67	0,34	220	S

p= phosphorylierte Aminosäure
m= Methioninoxidation

Anhang IIc: Identifizierte phosphorylierte Peptide aus dem gel-freien Anreicherungsansatz (*S. aureus*)

Protein	Genort	Akzessionsnummer	"Localization Probability"	Anzahl Phosphorylierungen	modifizierte Aminosäure	Position	PEP error probability score ^a	Score (MaxQuant)	modifizierte Peptidsequenz	Phospho (STY)-Wahrscheinlichkeiten	Ladung z	m/z	Massenabweichung [ppm]	Intensität
CloB	SACOL0979	aii57651666	1	1	S	426	0,00722789	141,85	RVMQLEIEEoSALK	RVMQLEIEES(1)ALK	3	542,60432	0,72064	89746
FolD	SACOL1072	aii57651672	0,999865	1	S	190	0,0056461	138,51	NASVTILHoSR	NASVTILHS(1)R	2	589,29001	0,41855	3041300
GlmM	SACOL2151	aii57652179	0,965972	1	S	102	9,927636-07	200,24	DM(o)GAELGVMS(o,034)AS(0,966)HNPVADNGIK	DMGAELGVMS(0,034)AS(0,966)HNPVADNGIK	3	813,3622	-0,60141	1999800
GluD	SACOL0961	aii57651649	0,97135	1	T	267	3,29026E-47	277,37	RDSFGpVTNLFEEISNK	RDS(0,028)FGT(0,971)VT(0,001)NLFEEISNK	3	713,33155	0,044142	28729000
GluD	SACOL0961	aii57651649	0,997212	1	S	264	3,2792E-32	252,91	RDpSFGVTNLFEEISNK	RDS(0,997)FGT(0,003)VTNLFEEISNK	3	713,33155	-0,0035584	126470000
GlvA	SACOL2105	aii57652135	0,999917	1	Y	51	0,00784825	127,64	YIAEGYpQR	YIAEGYpQR	2	574,74887	-1,7953	79144
HemC	SACOL1717	aii57650542	1	2	S	136	0,00392995	137,52	GAQLsSKpYVPLNLEIK	GAQLS(1)K(1)Y(1)PNLEIK	2	867,41686	-0,43203	200930
HemC	SACOL1717	aii57650542	1	2	Y	138	0,00392995	137,52	GAQLLoSKpYVPLNLEIK	GAQLS(1)K(1)Y(1)PNLEIK	2	867,41686	-0,43203	200930
HemF	SACOL1889	aii57650622	1	1	S	92	0,00110448	183,1	pSGIGpVIHNPik	S(1)GIGpVIHNPik	2	656,340509	0,65643	1058300
IsdB	SACOL1138	aii57651738	0,989558	2	Y	440	0,000610574	142,14	TIDpYDGQpYHVRIVDK	T(0,01)IDY(0,99)DGQY(1)HVRIVDK	2	991,42318	-3,1525	1058200
IsdB	SACOL1138	aii57651738	0,989558	2	Y	444	0,000610574	142,14	TIDpYDGQpYHVRIVDK	T(0,01)IDY(0,99)DGQY(1)HVRIVDK	2	991,42318	-3,1525	1058200
MetE	SACOL0428	aii57652616	1	1	S	363	0,009578	157,77	LFNQNDpSVKYDK	LFNQND(1)VKYDK	2	775,85058	3,3909	903960
MetE	SACOL0428	aii57652616	0,826166	1	T	393	0,069596	117,9	NLDYDFESVVRoTSR	NLDYDFESV(0,162)VVRT(0,826)S(0,012)R	2	841,36769	3,8409	128330
MetE	SACOL0428	aii57652616	0,991361	1	S	394	0,00141149	157,28	NLDYDFESVVRtoSR	NLDYDFESV(0,008)S(0,991)R	2	841,3664	2,4695	643230
Pfm	SACOL0841	aii57650117	1	1	S	62	2,14E-09	201,44	YPTTQIEASGLDVGLPPEGOM(o)GNpSeVGHM(o)INIGAGR	YPTTQIEASGLDVGLPPEGOMGNS(1)EVGHM(0)INIGAGR	4	900,15725	2,0903	30873000
Pvk	SACOL1745	aii57650568	1	1	S	198	0,00248258	137,32	RpSDVLEIR	RPS(1)DVLEIR	2	582,79264	0,68289	875530
SACOL0178	SACOL0178	aii57651194	0,893418	1	Y	187	0,010695	133,06	DGM(o)LaApYIAFTGINAAK	DGMLA(Y,0,893)LAIF(0,107)GINAAK	3	622,3012	-1,2576	9351300
SACOL0413	SACOL0413	aii57652602	0,785412	2	Y	169	0,0040008	137,12	DNELLNGIYSSpYpYSLLK	DNELLNGIY(0,001)S(0,001)S(0,028)S(0,184)Y(0,785)Y(0,972)S(0,028)LLK	2	1176,52917	2,6836	2333400
SACOL0413	SACOL0413	aii57652602	0,971608	2	Y	171	0,0040008	137,12	DNELLNGIYSSpYpYSLLK	DNELLNGIY(0,001)S(0,001)S(0,028)S(0,184)Y(0,785)Y(0,972)S(0,028)LLK	2	1176,52917	2,6836	2333400
SACOL0427	SACOL0427	aii57652615	1	1	Y	52	0,0111959	131,18	DHGFpYVQR	DHGFY(1)VQR	2	551,22987	1,1182	31097
SACOL0552	SACOL0552	aii57651384	1	1	S	105	0,12945	85,17	KLpSNFLK	KL(1)NFK	2	465,24667	0,58491	637710
SACOL0617	SACOL0617	aii57651446	1	1	S	52	9,42534E-05	183,95	HMAIDNISoINVK	HMAIDNIS(1)NVK	2	604,76003	-0,051348	1140800
SACOL0875	SACOL0875	aii57650149	1	1	S	88	0,00371101	164,19	IAHLHoSANAK	IAHLS(1)ANAK	2	571,28059	2,3656	6665900
SACOL0912	SACOL0912	aii57651602	0,999926	1	T	22	3,396E-24	243,86	_GNVKETVGNpTNDNK_	GNVKETVGNVT(1)DNK	2	777,8634	2,377	16726000
SACOL1680	SACOL1680	aii57650507	0,999926	1	T	22	3,396E-24	243,86	_GNVKETVGNpTNDNK_	GNVKETVGNVT(1)DNK	2	777,8634	2,377	16726000
SACOL0912	SACOL0912	aii57651602	1	1	S	37	4,85493E-17	231,26	NLENEGKEDKAsoGK	NLENEGKEDKAS(1)GK	2	799,85789	1,8057	193280
SACOL0912	SACOL0912	aii57651602	1	1	S	5	0,016085	128,79	ADepSKFEQAK_	ADES(1)KFEQAK	2	616,76432	1,7393	54620000
SACOL0912	SACOL0912	aii57651602	1	1	T	17	9,216E-51	279,93	_GNVKEpT_VGNVTNDNK_	GNVKET(1)VGNVTDNK	2	777,86273	1,4214	30319000
SACOL1680	SACOL1680	aii57650507	1	1	T	17	9,216E-51	279,93	_GNVKEpT_VGNVTNDNK_	GNVKET(1)VGNVTDNK	2	777,86273	1,4214	30319000
SACOL0912	SACOL0912	aii57651602	1	1	T	52	0,012319	123,6257	EKAoTDFIDK	EKAT(1)DFIDK	2	573,75802	0,87614	8608900
SACOL1522	SACOL1522	aii57650436	1	1	T	64	0,00257365	147,79	DLAoTINHnk	DLAT(1)INHnk	2	496,71283	-1,4162	27763
SACOL1522	SACOL1522	aii57650436	1	1	S	128	4,03193E-08	168,91	pSHPPEIEDNDKHDTK	S(1)HPEIEDNDKHDTK	3	652,28983	0,19556	1671800
SACOL1522	SACOL1522	aii57650436	1	1	S	2	0,00412821	143,06	oSNNFkDpFEK	S(1)NNFKDpFEK	2	662,26502	-1,8861	23531000
SACOL1672	SACOL1672	aii57650499	0,961679	1	Y	12	0,000400726	144,24	TMKFDoYEELPTQDVR	T(0,008)MKFDY(0,962)EELPTQDVR	3	651,28947	1,6194	1110900
SACOL1679	SACOL1679	aii57650506	0,999997	1	S	35	0,0014405	163,89	INeYTGSoINNEEKK	INEYTG(1)NNEEKK	2	803,3447	1,882	404100
SACOL1679	SACOL1679	aii57650506	1	1	S	17	1,58378E-57	285,83	FKNpSDNEQVK	FKNS(1)DNEQVK	2	644,78191	-0,2037	3009000
SACOL1680	SACOL1680	aii57650507	1	1	T	52	0,00018422	163,13	NKItDAIDK	NKIT(1)DAIDK	2	549,26525	-0,46773	4672400
SACOL1788	SACOL1788	aii57652036	0,997405	1	S	371	7,4287E-210	401,82	KNDVpSETETVNDINK	KNDV(0,997)ET(0,003)ETVNDINK	2	893,40341	5,2696	277890
SACOL1789	SACOL1789	aii57652037	0,750517	1	T	105	1,74E-13	220,25	VTNSIoTHNISQNEQK	VT(0,002)NS(0,02)IT(0,751)HNIS(0,227)QNEQK	2	890,4005	1,7014	218260
SACOL1789	SACOL1789	aii57652037	0,969965	1	S	103	5,86568E-39	269,51	VTNSoTHNISQNEQK	VT(0,022)NS(0,97)IT(0,008)HNISQNEQK	2	890,39822	-1,1171	688910
SACOL1895	SACOL1895	aii57650628	1	1	S	43	1,41336E-58	290,69	NNTIDRTAPTGS(1)K	NNTIDRTAPTGS(1)K	2	727,83484	-0,69296	2863600
SACOL1895	SACOL1895	aii57650628	0,999996	1	T	34	1,9341E-11	219,62	NNoTIDRTAPTGSK	NNT(1)IDRTAPTGSK	2	727,83553	0,2386	1311000
SACOL2173	SACOL2173	aii57652199	0,99909	1	S	45	8,99083E-60	292,31	NKLTpSoSDEVVEK	NKLT(0,001)FS(0,999)DEVVEK	2	744,853163	0,57121	72427
SACOL2255	SACOL2255	aii57650847	1	1	Y	11	0,0123295	132,06	MILKFDHIIHoYIDQLDR	MILKFDHIIH(1)IDQLDR	3	750,70923	-0,40002	59494000
SACOL2450	SACOL2450	aii57652260	1	1	S	228	0,0087674	154,76	NQSNHRPQSoINM	NQSNHRPQS(1)INM	2	753,3187	-0,83729	13929000
SACOL2501	SACOL2501	aii57651000	0,981856	1	S	193	4,64725E-08	179,19	NLNTTAGIM(o)IoTApSHNPk	NLNTTAGIMIT(0,018)AS(0,982)HNPk	2	939,9393	-3,5798	91061
SarA	SACOL0872	aii57650082	0,999997	1	S	106	7,5557E-04	153,89	KIESoLLSR	KIES(1)LLSR	2	513,27256	-1,1291	5733300
SarA	SACOL0872	aii57650082	0,999998	1	S	109	1,7651E-02	125,9	KIESLLoSR	KIESL(1)SR	2	513,2737	0,95166	1230700
SodA2/ SodA1	SACOL1610	aii57651946	0,999975	1	T	34	0,00195138	149,88	_HHNpTYVTk_	HHNT(1)YVTk	2	540,23626	-1,4045	203800
SodA2/ SodA1	SACOL1610	aii57652481	0,999975	1	T	34	0,00195138	149,88	_HHNpTYVTk_	HHNT(1)YVTk	2	540,23626	-1,4045	203800
SufD	SACOL0915	aii57651605	0,999891	1	S	24	0,00382824	176,17	AHNEPpSwMTELr	AHNEPS(1)WMTELr	2	775,82773	1,6014	1066600
TpiA	SACOL0840	aii57650116	1	1	S	215	0,00141247	157,34	IQYGGoSVKPNNIk	IQYGGS(1)VKPNNIk	2	749,37785	1,5695	127170

In roten Buchstaben geschriebene Proteinnamen weisen auf eine uneindeutige Identifizierung hin.

p = phosphorylierte Aminosäure
(ox) = Methioninoxidation