

description	gene	locus tag	control			1.5 h			2.5 h			3.5 h			4.5 h			5.5 h			6.5 h		
			exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc
proteins upregulated in at least two experiments in at least one time-point																							
1-pyrroline-5-carboxylate dehydrogenase	rocA	SAOUHSC_02869				9.42	16.94	18.68	8.13	13.19	6.53	8.49	11.54	8.88	6.86	8.36	6.49	6.20	5.63	6.74	5.36	4.95	3.12
2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-acetyltransferase	dapD	SAOUHSC_01398				19.65	21.23	-1.10	15.40	10.58	2.25	13.00	3.25	1.21	13.39	1.35	8.69	11.54	1.15	4.07	10.56	-1.03	5.91
2-oxoglutarate dehydrogenase E1 component	sucA, odhA	SAOUHSC_01418				5.23	1.67	13.75	3.28	1.92	3.70	3.10	2.23	7.29	2.83	2.60	3.58	2.05	1.71	4.29	1.72	1.47	1.38
30S ribosomal protein S21	rpsU	SAOUHSC_01678	1.74		-1.90	16.79		-2.44	2.60	206.45	1.13	6.54	3.65	3.28	5.33	4.77	5.63	4.26	11.98	5.24	4.78	12.24	6.07
33 kDa chaperonin		SAOUHSC_00487	-1.40		1.17	-1.29	1.41	1.60	-1.38	-1.57	1.81	-1.11		1.41	-1.09	-1.48	1.16	1.04	3.12	3.72	1.27	2.00	2.20
3-ketoacyl-acyl carrier protein reductase, putative	butA	SAOUHSC_00086		1.21		3.42	3.17	9.41	4.61	4.76	5.20	4.46	4.42	6.41	4.42	3.95	4.44	4.40	3.68	4.21	3.70	3.13	2.99
3-oxoacyl-[acyl-carrier-protein] synthase 3	fabH	SAOUHSC_00920	2.55	-1.81	-2.17	2.12	3.24	2.34	2.36	3.52	2.35	2.00	2.88	2.26	1.62	2.47	2.44	1.10	1.85	1.69	1.07	1.71	1.17
50S ribosomal protein L4	rplD	SAOUHSC_02511	-1.03	-1.05	-1.03	35.42	1.24	2.43	1.61	1.05	1.78	1.61	1.08	2.05	1.14	-1.06	1.17	1.33	-1.10	1.15	-1.22	-1.09	-1.23
50S ribosomal protein L9	rplI	SAOUHSC_00017			-2.71	5.51		3.18	6.74		2.54	7.99		3.69	5.64		6.57	6.88		10.98	5.64		6.07
ABC transporter periplasmic binding protein, putative	htsA	SAOUHSC_02430	3.23	-2.47	-1.90	2.08	2.34	2.38	2.12	2.08	2.30	1.58	1.53	1.97	1.68	1.35	1.38	1.84	1.76	1.51	1.66	1.67	1.10
ABC transporter, substrate-binding protein, putative	mntC	SAOUHSC_00634	3.25	-3.14	-1.52	2.57	2.52	1.20	4.63	2.56	1.48	4.10	2.73	1.37	1.62	2.01	1.13	4.68	2.19	1.54	1.54	2.76	1.58
accessory gene regulator protein A	agrA	SAOUHSC_02265		-2.74	-1.77		5.06	8.29		2.02	1.79		1.44	3.32		1.20	1.72		2.63	2.11		2.06	2.08
acetyl-CoA synthetase, putative	acsA	SAOUHSC_01846					3.17	5.88		8.28	10.81		4.02	8.61		4.37	6.29		2.76	6.21		1.42	2.41
Aminomethyltransferase	gcvT	SAOUHSC_01634	1.60	-2.02	-1.85	3.10	2.46	-1.34	3.09	2.53	1.60	2.46	1.86	2.66	2.87	1.98	1.59	2.44	1.51	1.36	1.93	1.50	1.24
aspartate-semialdehyde dehydrogenase	asd	SAOUHSC_01395				14.19	10.93	10.34	7.53	8.61	10.04	6.34	7.97	6.56	5.36	6.89	7.30	5.76	7.10	7.04	4.85	5.24	4.88
ATP-dependent Clp protease, ATP-binding subunit ClpB	clpB	SAOUHSC_00912	-1.05	-1.01	1.06	1.07	1.40	-1.07	1.10	2.62	1.16	1.61	2.45	1.97	1.78	2.07	2.16	1.83	1.30	2.45	1.42	1.36	1.70
ATP-dependent DNA helicase pcrA	pcrA	SAOUHSC_02123	-1.02	-1.08	-1.21		-2.34	-3.21			-1.59	-1.13		1.53	2.22		1.52	1.54		1.82	1.02	3.28	2.04
Biotin synthase	bioB	SAOUHSC_02714		10.47	-23.17	-94.89	-12.73	-27.39	-6.67	-12.63	-26.30	-3.81	-4.34	-20.79	-1.33	-1.31	-2.04	2.06	1.34	1.19	3.19	2.13	3.56
conserved hypothetical phage protein		SAOUHSC_02218	1.06		1.17		-2.46	1.82	1.09	3.28	1.45	2.41	7.99	1.54	1.37	4.13	1.46	1.61	2.02	1.61	1.69	2.01	1.50
conserved hypothetical protein	espC	SAOUHSC_00819	3.44		-2.47		-75.38	4.27	5.15	1.06	3.57	156.56	2.45	2.93	3.63	5.57	2.33	4.44	2.51	2.23	3.78	2.44	1.73
conserved hypothetical protein	cysK	SAOUHSC_00488	-1.23	1.47	1.63	1.11	2.57	-1.47	1.58	2.71	1.01	1.95	2.33	1.53	2.18	2.35	1.79	2.23	3.18	2.33	2.58	3.51	3.25
conserved hypothetical protein	fadB	SAOUHSC_00196					3.12	3.72		2.40	13.22		3.75	8.44		4.32	6.79		5.46	5.30		4.13	2.81
conserved hypothetical protein	fadD	SAOUHSC_00197					10.34	11.42	4.55	7.01	10.91	11.59	6.26	12.06	5.36	6.55	9.67	7.30	7.32	7.11	8.14	4.92	6.55
conserved hypothetical protein	fhuD2	SAOUHSC_02554	3.11	-2.81	-2.69	3.06	1.32	3.40	2.25	1.78	3.67	1.98	1.33	2.68	1.83	1.13	2.36	1.53	1.41	2.47	2.11	1.50	1.83
conserved hypothetical protein	hit	SAOUHSC_01968	-1.14	1.04			-2.34	4.50	6.39	1.88	3.13	5.43	4.81	1.44	12.92	2.22	1.33	1.34	1.59	1.32	6.84	1.79	1.38
conserved hypothetical protein	hit	SAOUHSC_00371	-1.82		1.73		6.52	2.50		99.01	2.54		3.63	2.49		3.56	2.23		3.19	1.87		2.73	-1.36
conserved hypothetical protein		SAOUHSC_00717	5.54		-2.26	45.48	5.06	1.78	7.32	6.02	1.61	69.33	6.97	2.80	7.46	8.05	2.45	10.03	15.93	3.03	14.41	21.28	4.32
conserved hypothetical protein		SAOUHSC_00833			-2.05	1.12	1.38	1.52	4.84	1.41	1.74	1.48	1.26	1.47	5.89	1.56	2.10		1.27	1.25	4.51	1.46	1.33
conserved hypothetical protein		SAOUHSC_00890	1.51			1.06		1.60		1.40	1.66		2.17	1.99		3.50	2.37		5.24	2.00		8.31	
conserved hypothetical protein		SAOUHSC_01383	1.36		-1.26	3.26	2.03	-1.55	1.48	1.21	1.09	1.04	1.03	-1.22	1.65	1.08	-1.25	1.30	-1.02	1.20	1.33	1.19	1.17
conserved hypothetical protein		SAOUHSC_01433	-1.61	1.55		7.22	6.57		1.46	14.86		-1.59	2.21		1.30	1.42	-2.09	-1.14	1.23	-1.52	-1.26	1.30	-2.15
conserved hypothetical protein		SAOUHSC_01838	1.44		-1.09	-2.38	-3.97	1.20	-1.70	-2.05	1.33	1.13	-1.95	3.57	1.52	-2.13	2.91	1.81	-1.90	4.00	2.95	-1.61	3.68
conserved hypothetical protein		SAOUHSC_01901	1.35		-1.29	1.23	1.81	1.05	2.08	2.06	1.43	2.02	2.22	1.48	2.04	2.54	1.35	1.46	2.46	1.62	1.85	2.75	1.60
conserved hypothetical protein		SAOUHSC_02150	-1.58	1.72		2.47	1.10	-1.04	2.43	1.54	1.76	2.43	1.65	2.02	2.40	1.61	2.84	2.47	1.78	2.24	1.99	1.52	3.21
conserved hypothetical protein		SAOUHSC_02434			-1.73		1.24	3.21		1.33	5.18		-1.16	3.40		3.04	2.47		-1.25	3.23		1.02	1.95
conserved hypothetical protein		SAOUHSC_02724	-1.12	3.55	-2.45	2.13	1.49	-1.37	-2.25	2.33	2.12	1.13	3.16	2.31	-2.19	4.24	6.16	-2.47	3.08	3.58	-2.14	3.48	2.67
conserved hypothetical protein		SAOUHSC_02747				13.12	-1.53	1.92	2.90	2.02	1.22	4.27	1.51	-1.03	2.72	2.39	1.67	1.69	1.92	-1.02	1.64	2.00	1.33
Dihydrodipicolinate synthase	dapA	SAOUHSC_01396				7.83		8.69	8.67		9.69	6.69		9.69	5.59		6.29	6.87		5.69	4.95		4.58
Dihydropolypyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	sucB, odhB	SAOUHSC_01416		2.47			1.74	1.20		1.74	1.90	3.88	1.27	2.45	6.02	1.27	2.64	2.58	1.13	2.67	2.06	-1.59	1.41
DNA-binding response regulator VraR, putative	vraR	SAOUHSC_02098	1.38		1.05	1.74	-1.00	-5.64	1.83	1.58	-1.93	3.86	1.94	2.90	2.59	2.13	-1.36	2.65	2.24	1.69	2.66	2.07	1.47
Foldase protein prsA	prsA	SAOUHSC_01972	1.66	-1.60	-1.25	1.90	3.17	1.56	3.72	4.78	2.63	4.93	5.00	3.54	5.26	5.16	4.97	5.81	5.80	4.58	6.15	5.65	7.24
fumarate hydratase, class II	fumC, citG	SAOUHSC_01983	1.47				-1.33	2.09		2.26	1.86		2.96	2.56		2.52	1.68		2.22	1.82		1.90	-1.01
Glycerol kinase	glpK	SAOUHSC_01276			39.02				3.29	2.23			1.57		1.80	1.16		1.49	1.56		6.63	1.56	
GTP pyrophosphokinase	relA	SAOUHSC_01742	-2.41			4.44		2.01	4.52		-1.14	1.11		1.02	1.32		-1.28	1.38		1.02	2.16		-1.18
GTP-binding protein TypA, putative	typA	SAOUHSC_01058	1.09	-1.42	-1.14	2.02	1.53	2.56	1.13	1.32	1.47	-1.04	1.12	1.19	-1.13	1.12	1.33	-1.27	-1.06	1.15	-1.49	-1.07	-1.19

description	gene	locus tag	control			1.5 h			2.5 h			3.5 h			4.5 h			5.5 h			6.5 h		
			exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc
Helix-turn-helix domain protein		SAOUHSC_01575	1.06			1.08	2.00		-1.30	1.41	1.37	1.68	2.95	2.00	1.42	1.38	2.97	1.58	1.71	1.89	1.87	1.42	1.60
homoserine dehydrogenase, putative	dhoM	SAOUHSC_01320						2.27	22.56		2.72	4.74		6.09	3.17	3.69	2.48		2.73	2.44		7.48	
HTH-type transcriptional regulator sarR	sarR	SAOUHSC_02566			-1.41	2.16	4.11	2.10	2.63	2.59	3.11	3.23	1.86	3.18	2.55	1.77	2.41	2.91	1.90	1.98	2.09	2.14	1.55
hypoxanthine phosphoribosyltransferase	hpt	SAOUHSC_00485		-1.75	1.18	5.65	2.18	-1.01	2.37	1.74	-1.14	1.54	1.06	-1.12	1.50	1.00	-1.14	1.52	1.11	-1.33	-1.07	-1.08	-1.48
isocitrate dehydrogenase, NADP-dependent	icd,citC	SAOUHSC_01801	1.24	-1.60	-1.07	3.50	1.60	1.09	3.74	1.83	1.49	3.59	2.01	1.62	2.38	1.95	1.82	2.40	1.47	2.02	3.03	1.40	1.40
L-lactate dehydrogenase 2	ldh2,ldh	SAOUHSC_02922	1.91	-1.69	-2.23	1.47	-3.22	1.26	1.60	-1.09	1.25	1.73	1.06	1.40	1.78	1.36	1.28	1.81	3.07	2.19	2.48	3.05	2.77
ornithine aminotransferase, putative	rocD	SAOUHSC_00150				3.05	1.27	1.72	2.15	1.95	1.73	1.79	2.02	3.11	2.88	2.15	2.54	4.28	1.88	2.54	2.27	1.44	1.66
ornithine cyclodeaminase, putative		SAOUHSC_00076	6.84	-5.41	-6.77	23.33	7.48	4.60	2.71	5.05	4.74	5.20	4.30	4.82	3.29	1.44	6.72	3.03	6.91	4.67	3.51	6.46	4.24
Peptide methionine sulfoxide reductase msrA 2	msrA2	SAOUHSC_01432			-1.34	6.72	31.98	2.42	5.97	37.92	4.76	11.30	13.88	5.30	8.13	6.28	4.31	8.10	6.15	7.61	7.90	8.59	4.16
Peptide methionine sulfoxide reductase msrB	msrB	SAOUHSC_01431	1.72	-1.76	-1.36	1.53	3.58	1.37	4.62	5.10	2.20	5.52	6.95	2.34	5.71	5.81	2.67	6.39	3.83	3.69	5.93	3.14	3.68
periplasmic binding protein, putative	sirA	SAOUHSC_00074	7.51	-7.48	-6.52	5.95	7.54	4.24	5.60	4.21	4.07	3.50	4.65	3.25	3.52	3.63	2.53	2.84	4.10	2.55	2.69	2.61	2.31
phosphocarrier protein hpr, putative	ptsH	SAOUHSC_01028					4.20	2.58		2.98	1.44		1.16	1.16		2.06	1.54		-1.02	1.10		1.30	1.12
phosphotransferase system enzyme IIA, putative	crr	SAOUHSC_01430	1.26	-1.05	1.06	1.92	1.73	1.32	3.25	3.28	1.86	4.00	3.45	2.42	4.02	2.96	2.83	4.42	3.36	2.81	3.79	3.39	2.77
Probable transglycosylase isaA	isaA	SAOUHSC_02887	1.36		-1.45		1.08		3.95	2.12		5.92	3.89		6.02	3.96		18.07	3.39		5.44	3.53	
proline dipeptidase, putative		SAOUHSC_01626	1.02		-1.02	3.71	3.51	1.27	2.57	-1.06	-1.31	1.22	-1.25	-1.19	1.50	-1.18	-1.34	1.25	1.10	1.18	1.34	1.08	1.74
PTS system glucoside-specific EIICBA component	glcB	SAOUHSC_02848	1.06			2.73	2.54	1.58	1.96	2.48	1.85	1.88	1.84	1.40	1.67	1.72	1.69	1.76	1.93	1.15	1.34	1.65	-1.10
PTS system, glucose-specific component	ptsG, glcA	SAOUHSC_00155	1.46	-1.41	-1.42	3.26	1.54	2.27	1.57	1.36	1.75	-1.14	1.09	1.67	1.38	1.52	1.07	1.43	1.41	1.37	1.34	1.22	-1.28
Putative 2-hydroxyacid dehydrogenase SAOUHSC_02577		SAOUHSC_02577	-1.84		1.05	2.17	1.67	2.08	2.50	1.98	3.12	2.42	2.48	3.66	2.20	2.07	2.91	2.36	2.45	2.97	1.92	2.15	1.80
Putative universal stress protein SAOUHSC_01819		SAOUHSC_01819			-1.11	3.74	3.08	3.47	4.02	3.91	4.46	3.66	4.06	4.28	3.83	3.12	4.31	2.79	3.12	4.00	2.82	2.55	2.70
Superoxide dismutase [Mn/Fe] 2	sodM	SAOUHSC_00093	1.38		-1.28	1.45	1.33	1.44	2.85	2.52	1.68	2.74	2.20	1.48	2.00	1.55	1.54	2.11	1.19	1.23	1.95	1.27	-1.06
threonine synthase	thrC	SAOUHSC_01321				4.09	6.05		1.76	-2.40		1.96	1.82		2.36	2.49		2.71	5.73		2.81	6.59	
transcription termination factor Rho	rho	SAOUHSC_02362	1.54	-1.82	-1.57	2.38	2.00	1.81	2.24	2.03	1.64	2.34	1.50	1.36	1.79	1.30	1.27	2.04	1.16	1.30	2.24	-1.17	1.78
transcriptional regulator, putative		SAOUHSC_02583	-1.09		-1.04	2.12	1.44	1.75	3.79	2.25	3.46	3.64	2.58	3.41	4.68	4.27	2.97	2.84	14.36	3.40	3.98	13.21	4.78
Uncharacterized hydrolase SAOUHSC_01399		SAOUHSC_01399				11.39	5.91	10.79	2.57	17.21	8.33	5.75	6.43	6.82	5.60	8.18	7.21	6.08	6.20	6.74	5.28	5.44	6.07
Uncharacterized protein SAOUHSC_00767	yfiA	SAOUHSC_00767	1.46	-1.42	1.05	2.77	2.88	5.05	5.61	5.54	5.48	3.77	5.64	5.80	4.98	5.23	5.28	3.89	5.84	4.58	4.97	4.49	3.25
Uncharacterized protein SAOUHSC_02143		SAOUHSC_02143	-1.37	1.55	1.24	11.66	-1.41	19.55	-1.41	-1.09	22.04	-3.21	1.12	18.14	-1.36	1.39	4.62	-1.08	1.57	2.31	-1.33	1.40	2.16
UPF0051 protein SAOUHSC_00851	sufB	SAOUHSC_00851	1.04	-1.08	1.17	1.00	1.12	-2.04	1.77	1.46	1.31	2.33	1.50	1.43	2.02	1.73	1.71	2.48	1.97	2.15	2.87	2.29	1.54
UPF0457 protein SAOUHSC_02425		SAOUHSC_02425				5.32	10.86	5.79	6.16	29.93	7.86	5.85	11.48	7.82	5.79	8.51	10.75	5.62	4.85	5.83	4.47	4.53	4.16
UPF0477 protein SAOUHSC_00951		SAOUHSC_00951	-1.31		1.21	1.70	1.58	3.69	2.47	1.98	3.67	2.38	2.17	4.12	2.62	2.08	3.54	2.69	1.88	3.60	2.11	1.64	2.58
proteins downregulated in at least two experiments in at least one time-point																							
3-hexulose-6-phosphate synthase		SAOUHSC_00553	-2.34	2.81	2.07	-3.57	1.33	-2.32	-2.84	-1.82	-2.29	-3.34	-2.54	-2.08	-3.50	-2.65	-1.95	-2.91	-2.35	-1.98	-3.69	-2.51	-1.75
ABC transporter, ATP-binding protein, putative		SAOUHSC_00847	-2.71	2.65	1.96	-2.50	-2.70	-1.46	-1.83	-3.51	-1.76	-1.86	-1.72	-1.76	-2.10	-2.37	-1.74	-1.67	-1.48	-1.80	-1.94	-2.06	-2.19
ABC transporter, ATP-binding protein, putative		SAOUHSC_02152		-12.89	2.95	-2.00	-1.26	-2.16	1.21	-1.12	-1.73	1.06	-1.19	-1.22	-1.33	-1.21	1.01	-1.94	-1.27	-1.29	-1.85	-1.44	-1.87
acetyl-CoA synthetase, putative		SAOUHSC_02929		1.97	2.04	-1.51	-3.19	-2.62	2.01	-4.42	-1.26	-1.18	-2.79	-1.45	-1.08	-1.36	-1.25	-1.13	1.20	-1.09	-1.14	-1.23	-1.28
adenosylmethionine-8-amino-7-oxononanoate aminotransferase		SAOUHSC_02715	14.16		6.81	-2.43	-1.18	-3.49	-12.51	-4.01	-18.43	-7.01	-12.43	-13.49	-5.21	-7.08	-8.52	-3.10	-3.84	-4.83	-1.92	-2.20	-1.94
Alkaline shock protein 23	asp23	SAOUHSC_02441	-5.90	6.44	5.51	-2.72	-2.25	-1.65	-2.02	-2.12	-1.58	-2.31	-2.34	-1.58	-2.53	-2.89	-1.81	-2.50	-3.51	-2.12	-2.77	-4.36	-3.47

description	gene	locus tag	control			1.5 h			2.5 h			3.5 h			4.5 h			5.5 h			6.5 h		
			exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc	exp. 1 fc	exp. 2 fc	exp. 3 fc
Alkyl hydroperoxide reductase subunit C	ahpC	SAOUHSC_00365	-1.43	1.28	1.28	-2.11	-1.70	-2.07	-1.54	-1.51	-1.47	-1.62	-1.38	-1.23	-1.42	-1.33	-1.42	-1.30	-1.35	-1.35	-1.40	-1.37	-1.69
Alkyl hydroperoxide reductase subunit F	ahpF	SAOUHSC_00364	-1.28	1.27	1.23	-2.13	-2.02	-1.85	-1.76	-1.48	-1.78	-1.77	-1.66	-1.67	-1.70	-1.63	-1.82	-1.59	-1.62	-1.81	-1.47	-1.49	-1.84
Aminoacyltransferase femB	femB	SAOUHSC_01374	-1.09		1.05	-2.32	-3.29	-1.81	-1.29	-2.24	-1.72	-1.03	-1.70	-1.75	-1.20	-1.43	-1.33	-1.19	-1.21	-1.47	-1.05	-1.12	-1.36
aminotransferase, class V superfamily, putative		SAOUHSC_00849	-1.37	1.41	1.24		-1.50	-2.24		-2.75	-1.43		-2.50	-5.82		-1.91	-1.12		-1.76	-2.01		-2.23	-1.63
anti-sigma B factor, putative	rsbW	SAOUHSC_02299	-2.16		1.24		1.65	-1.16		-2.11	-2.27		-2.67	-3.22		-2.65	-1.54		-2.48	-2.48		-2.61	-1.73
Anti-sigma-B factor antagonist	rsbV	SAOUHSC_02300	-2.40	2.30	2.04	-3.15	-1.83	-2.14	-3.87	-2.31	-1.48	-3.29	-1.88	-4.71	-2.94	-2.22	-2.36	-2.63	-2.34	-1.98	-2.54	-2.27	-5.75
ATP-dependent DNA helicase pcrA	pcrA	SAOUHSC_02123	-1.02	-1.08	-1.21		-2.34	-3.21		-1.59	-1.13		1.53	2.22		1.52	1.54		1.82	1.02		3.28	2.04
Bifunctional purine biosynthesis protein purH	purH	SAOUHSC_01017	-1.58	1.47	1.66	-2.44	-3.71	-3.52	-3.60	-4.13	-3.38	-3.66	-4.37	-3.28	-3.78	-4.32	-3.16	-3.20	-3.75	-2.99	-2.57	-2.90	-2.04
Biotin synthase	bioB	SAOUHSC_02714																					
Chaperone protein hchA	hchA	SAOUHSC_00533	-5.21	6.80	5.21	-94.89	-12.73	-27.39	-6.67	-12.63	-26.30	-3.81	-4.34	-20.79	-1.33	-1.31	-2.04	2.06	1.34	1.19	3.19	2.13	3.56
conserved hypothetical protein		SAOUHSC_02381	-1.78			-1.89	-2.53	-3.71	-1.87	-1.77	-2.96	-1.25	-1.50	-2.48	1.00	-1.11	-1.99	1.15	-1.04	-1.55	1.10	-1.11	-1.84
conserved hypothetical protein		SAOUHSC_00848	-2.67	1.83	1.91		-2.03	-2.28		-1.80	-1.74		-1.88	-1.93		-2.09	-1.89		-1.89	-1.36		-1.68	-1.96
conserved hypothetical protein		SAOUHSC_00356	-11.20	11.51	7.44	-18.17	-3.90		-9.90	-4.38		-11.87	-5.21		-13.35	-10.04		-11.33	-14.90		-13.38	-13.83	
conserved hypothetical protein		SAOUHSC_01854	-2.34	2.63	1.95	-2.56	-1.46	-3.28	-2.28	-2.23	-2.28	-2.16	-2.77	-1.90	-2.70	-2.64	-2.31	-2.49	-2.41	-2.03	-2.35	-2.57	-2.35
conserved hypothetical protein		SAOUHSC_02443	-10.36		7.13	-4.34	-3.02		-3.06	-2.91		-4.49	-3.30		-5.29	-4.66		-4.58	-5.37		-6.26	-7.03	
conserved hypothetical protein		SAOUHSC_01729	-8.53		7.06	-2.52	-2.25	-2.34	-2.53	-2.55	-1.95	-2.91	-3.37	-1.79	-4.34	-3.70	-2.26	-3.07	-4.00	-2.45	-3.39	-4.66	-3.18
conserved hypothetical protein		SAOUHSC_01838	1.44		-1.09	-2.38	-3.97	1.20	-1.70	-2.05	1.33	1.13	-1.95	3.57	1.52	-2.13	2.91	1.81	-1.90	4.00	2.95	-1.61	3.68
Glutamate-1-semialdehyde 2,1-aminomutase 1	hemL1	SAOUHSC_01771	-1.14	1.39	-1.08	1.07	-3.01	-2.01	-1.24	-1.81	-1.24	1.10	-2.88	-1.11	-1.10	-2.93	-1.66	-1.22	-1.99	1.11	-1.09	-2.12	1.04
glutamine synthetase, type I		SAOUHSC_01287	-4.60	4.71	3.89	-4.03	-2.61	-4.04	-1.73	-2.75	-2.63	-1.72	-2.00	-1.69	-1.47	-1.97	-1.60	-1.28	-1.79	-1.40	-1.37	-1.69	-1.58
Glycyl-tRNA synthetase	glyQS	SAOUHSC_01666	-1.86	2.33	2.43	-1.23	-2.53	-4.86	-2.37	-2.18	-4.54	-1.89	-2.09	-3.96	-1.83	-2.00	-2.41	-1.57	-1.53	-2.41	-1.30	-1.27	-1.45
Phenylalanyl-tRNA synthetase alpha chain	pheS	SAOUHSC_01092	1.28		1.18	-1.40	1.06	-1.55	-1.84	-1.40	-1.49	-1.67	-1.82	-1.73	-1.64	-1.86	-2.05	-1.44	-2.24	-2.13	-1.83	-2.40	-2.40
phenylalanyl-tRNA synthetase, beta subunit		SAOUHSC_01093	1.10	-1.08	-1.14	-1.84	-1.51	-1.87	-1.84	-2.05	-1.58	-2.18	-1.71	-1.77	-2.28	-1.95	-2.01	-2.51	-1.46	-1.96	-2.66	-1.41	-1.95
phosphoribosylamine-glycine ligase		SAOUHSC_01018	-1.41	1.41	1.73	-3.95	-1.53	-2.62	-2.29	-2.62	-1.58	-2.61	-3.81	-2.61	-2.78	-4.20	-2.76	-2.50	-3.83	-2.88	-2.11	-2.54	-1.81
Phosphoribosylaminoimidazole-succinocarboxamide synthase	purC	SAOUHSC_01010	-1.48		1.63	-2.69	-3.08	-3.10	-2.30	-3.30	-2.91	-2.71	-3.21	-2.57	-2.18	-3.34	-2.56	-1.95	-3.78	-2.79	-2.12	-3.56	-2.08
Phosphoribosylformylglycinamide cyclo-ligase	purM	SAOUHSC_01015			1.64		-8.99	-2.89		-3.88	-2.51		-3.61	-2.15		-3.84	-3.03		-2.44	-2.40		-2.31	-1.64
Phosphoribosylformylglycinamide synthase 1	purQ	SAOUHSC_01012	-1.04		1.56	5.56	-4.69	-3.15	-2.55	-2.12	-2.87	-1.62	-1.81	-2.61	-2.62	-2.41	-2.41	-2.27	-2.09	-2.23	-1.54	-1.33	-1.39
Phosphoribosylformylglycinamide synthase 2	purL	SAOUHSC_01013	-1.34	1.78	1.56	-3.80	-3.33	-2.68	-2.69	-3.22	-2.74	-2.99	-3.11	-3.48	-2.37	-3.21	-2.87	-2.36	-2.42	-3.17	-1.81	-2.06	-3.31
phosphoribosylformylglycinamide synthase, PurS protein		SAOUHSC_01011	-1.26	2.15	1.70		-3.74	-1.60		-4.47	-2.86		-4.99	-2.42		-3.66	-3.16		-2.36	-2.37		-2.20	-1.82
Putative aldehyde dehydrogenase SAOUHSC_02363		SAOUHSC_02363	-6.30		4.48		-1.98	-1.16		-2.60	-1.84		-2.37	-1.66		-2.97	-2.63		-3.30	-2.44		-2.82	-1.87
Putative septation protein spoVG	spoVG	SAOUHSC_00469	-3.17	3.27	3.76	-1.29	1.11	-1.06	-1.68	-1.44	-1.14	-1.59	-2.00	-1.38	-2.58	-2.52	-1.98	-2.32	-1.90	-1.85	-2.50	-2.19	-2.61
ribonucleotide-diphosphate reductase beta chain, putative		SAOUHSC_00743	1.09	-1.52	1.24	-2.50	-2.03	-1.97	-2.24	-2.22	-2.33	-2.50	-2.34	-2.20	-2.08	-1.80	-2.20	-1.79	-1.62	-1.71	-1.57	-1.40	-1.12
thioredoxin reductase		SAOUHSC_00785	-1.38	1.01	1.19	1.03	-3.07	-2.79	-1.37	-1.97	-2.66	1.04	-1.80	-3.45	-1.15	-1.56	-3.01	-1.09	-1.78	-1.39	-1.03	-1.93	-1.49
Threonyl-tRNA synthetase	thrS	SAOUHSC_01788	1.04	-1.03	-1.25	-2.52	-2.14	1.42	-1.73	-1.48	1.73	-1.59	-1.30	-1.24	-1.71	-1.21	-1.17	-1.62	-1.27	1.75	-1.31	-1.21	1.21
Transcriptional regulator sarA	sarA	SAOUHSC_00620	-6.56	8.21	5.30	-2.29	-2.17	-1.30	-1.63	-1.28	-1.35	-1.30	-1.37	-1.05	-1.56	-1.59	-1.03	-1.52	-1.80	1.03	-1.68	-1.73	-1.26
Uncharacterized protein SAOUHSC_01413		SAOUHSC_01413			-1.10	-7.12	-5.57		-1.79	-2.74		-1.80	-2.61		-1.26	-2.73		-1.59	-1.49		-1.35	-1.58	
UPF0337 protein SAOUHSC_00845		SAOUHSC_00845	-5.87		5.67	-1.51	-1.39	-1.12	-1.58	-1.43	-1.10	-1.98	-1.77	-1.25	-2.28	-2.19	-1.70	-2.24	-2.70	-1.66	-2.44	-3.02	-2.30
UPF0478 protein SAOUHSC_01855		SAOUHSC_01855	-3.15	4.06	2.95	-2.50	-2.33	-1.45	-2.50	-2.15	-1.23	-2.97	-2.61	-1.62	-3.20	-3.30	-1.97	-3.19	-3.46	-2.17	-3.21	-3.54	-2.55