

# Applied Microbiology and Biotechnology

## ***Streptomyces tsukubaensis* as a new model for carbon repression: transcriptomic response to tacrolimus repressing carbon sources**

María Ordóñez-Robles<sup>1,2</sup>, Fernando Santos-Beneit<sup>2,3</sup>, Silvia M. Albillos<sup>2,4</sup>,  
Paloma Liras<sup>1,2</sup>, Juan F. Martín<sup>1,2</sup>, and Antonio Rodríguez-García<sup>1,2</sup>.

1) Área de Microbiología, Facultad de Ciencias Biológicas y Ambientales,  
Universidad de León, 24071 León, Spain

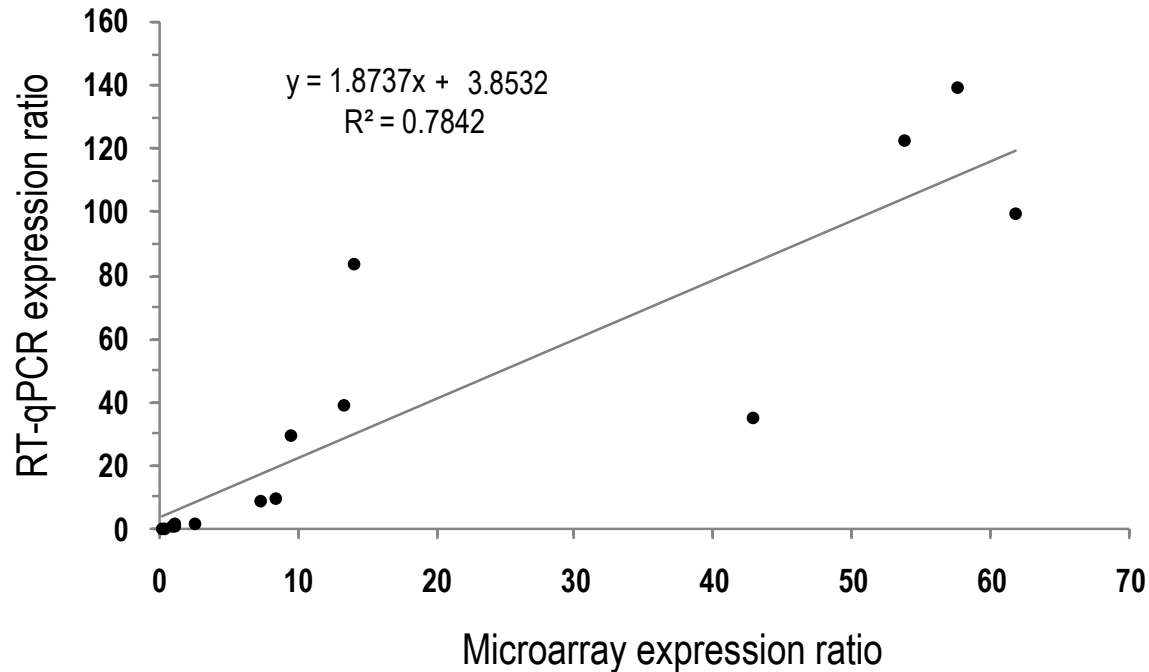
2) Instituto de Biotecnología de León, INBIOTEC, Avda. Real no. 1, 24006  
León, Spain

3) Current address: Centre for Bacterial Cell Biology, Institute for Cell and  
Molecular Biosciences, Medical School, Newcastle University, Newcastle  
upon Tyne, UK

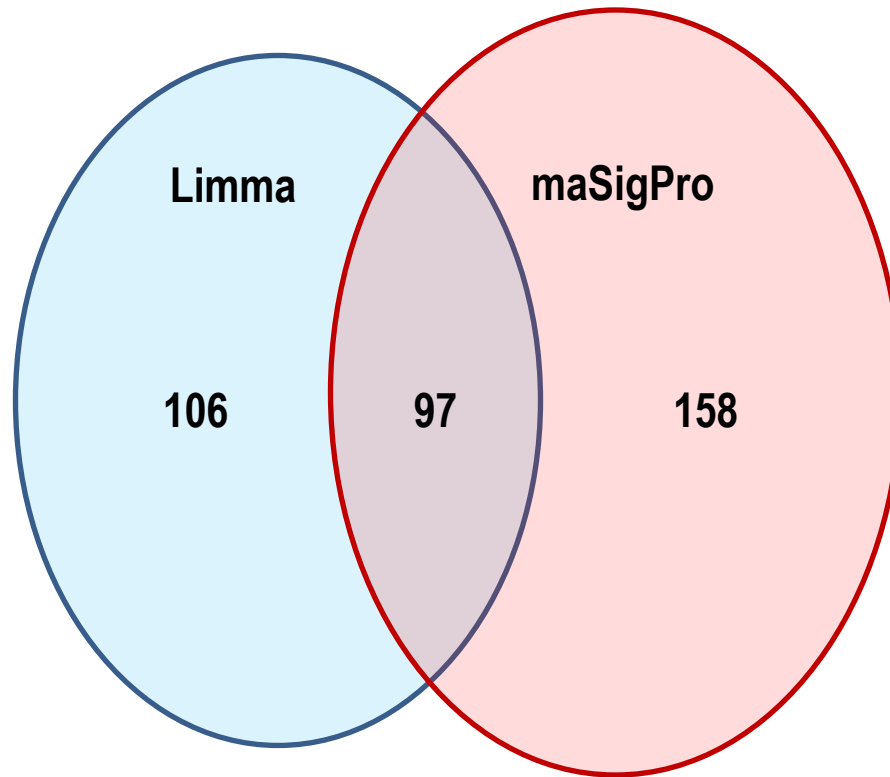
4) Current address: Departamento de Biotecnología y Ciencia de los  
Alimentos, Facultad de Ciencias, Universidad de Burgos, 09001 Burgos,  
Spain

Corresponding author: Antonio Rodríguez-García.

E-mail:[antonio.rodriguez@inbiotec.com](mailto:antonio.rodriguez@inbiotec.com) (Tlf: +34 987 21 03 08).



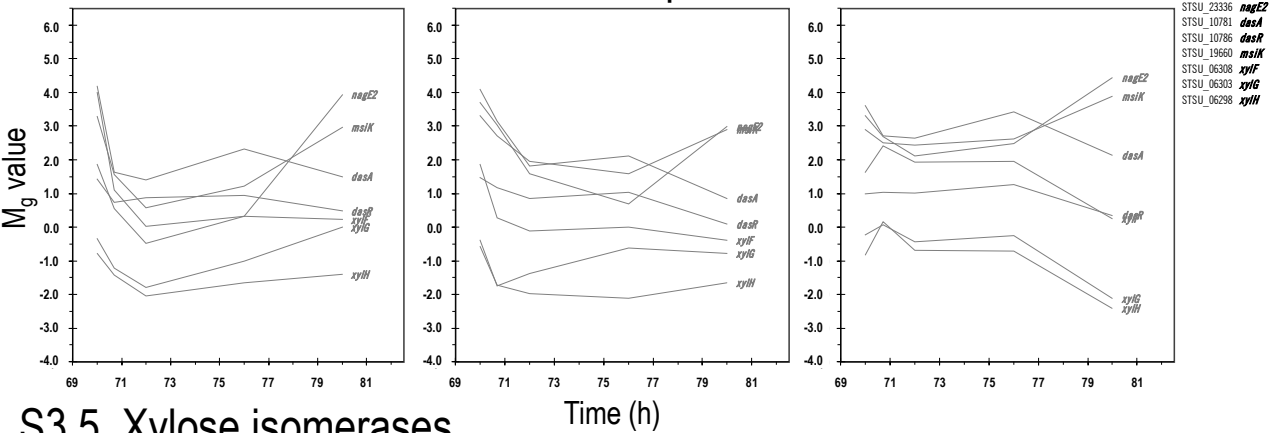
**Fig. S1. Validation of microarray data by RT-qPCR.** The correlation between the  $\log_2$  fold changes in the transcript levels of target genes obtained by microarray and RT-qPCR is represented. Comparisons were performed between 89 h samples from different culture conditions (i. e. glucose vs maltose) but also between time samples from the same experimental conditions (i. e. 89 h and 70 h from glucose cultures).



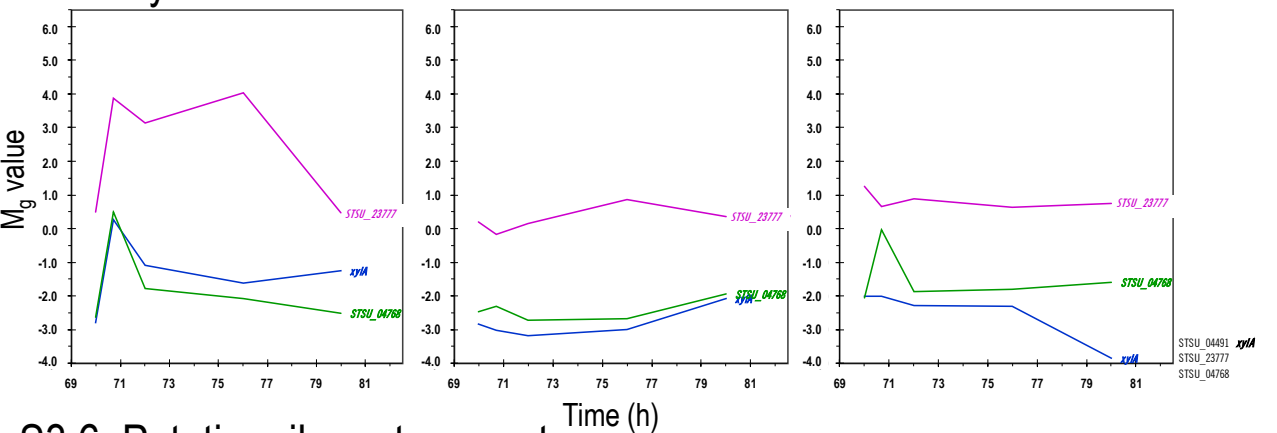
**Fig. S2. Representation of the group of the genes selected for the analysis.** The statistical analysis with limma (blue circle) yielded 203 genes significantly affected after the additions with 2-fold or greater changes at 70.7 h. The statistical analysis using maSigPro (red circle) revealed differences in 255 genes showing  $R^2 \geq 0.9$ . The functional analysis was focused on the set of 361 genes listed in Table S3.



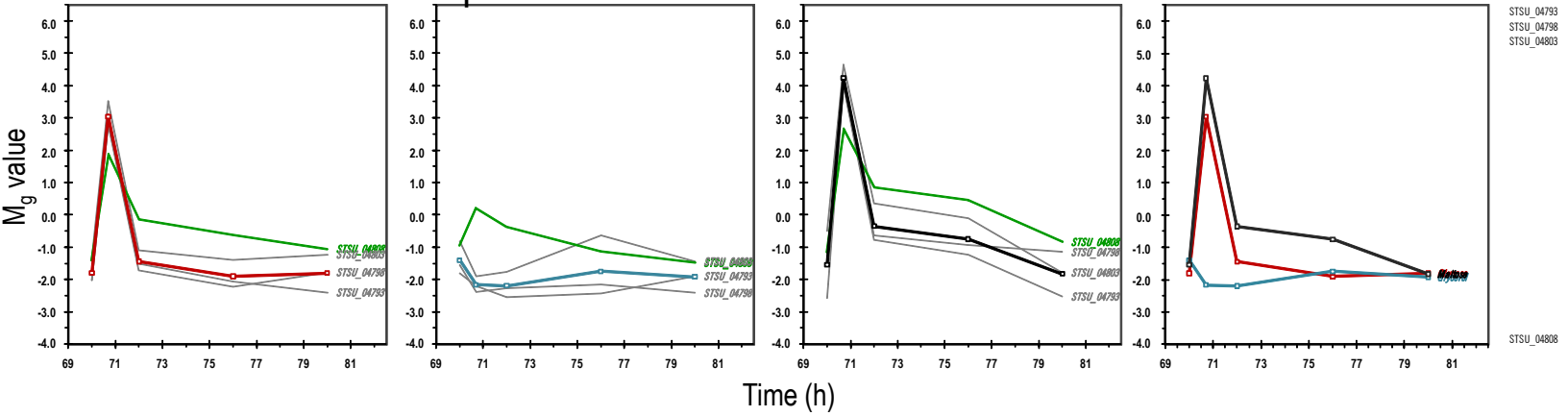
### S3.4. Alternative carbon source transport



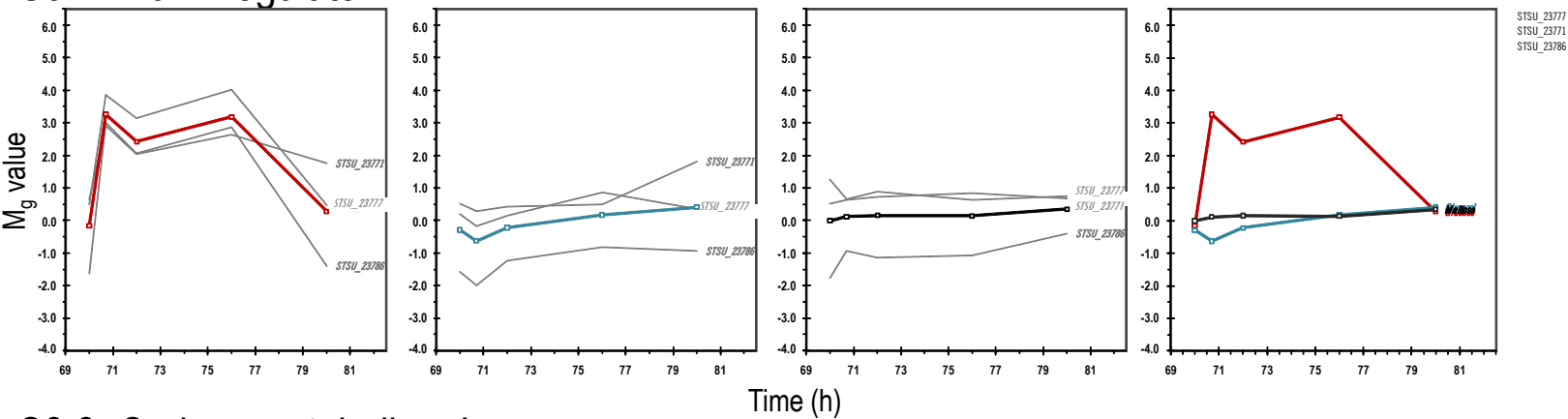
### S3.5. Xylose isomerases



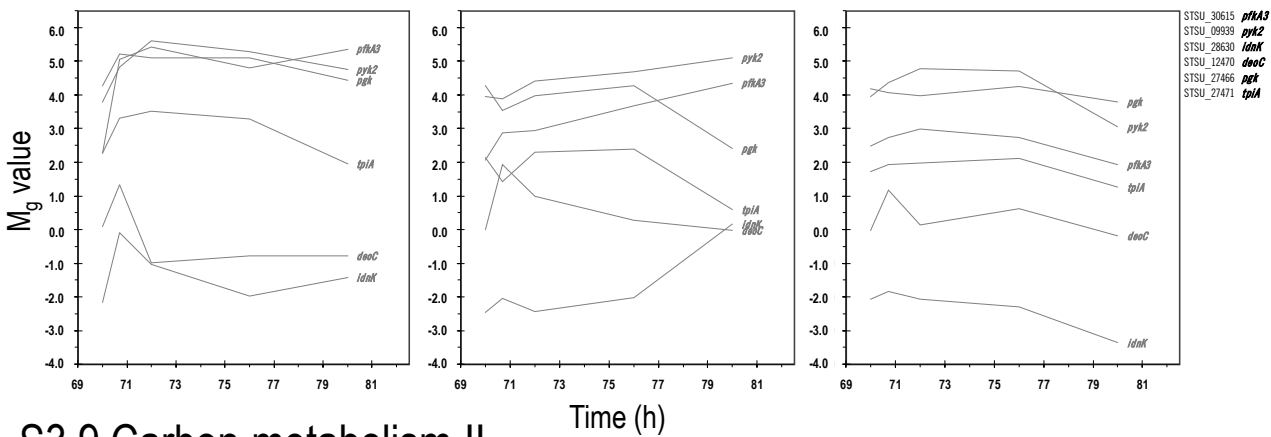
### S3.6. Putative ribose transporter



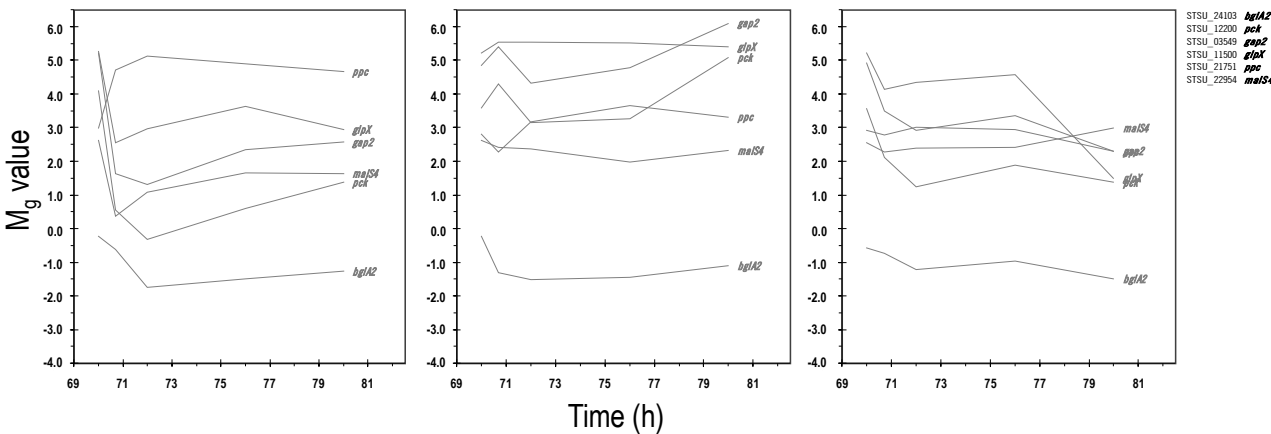
### S3.7. MarR regulator



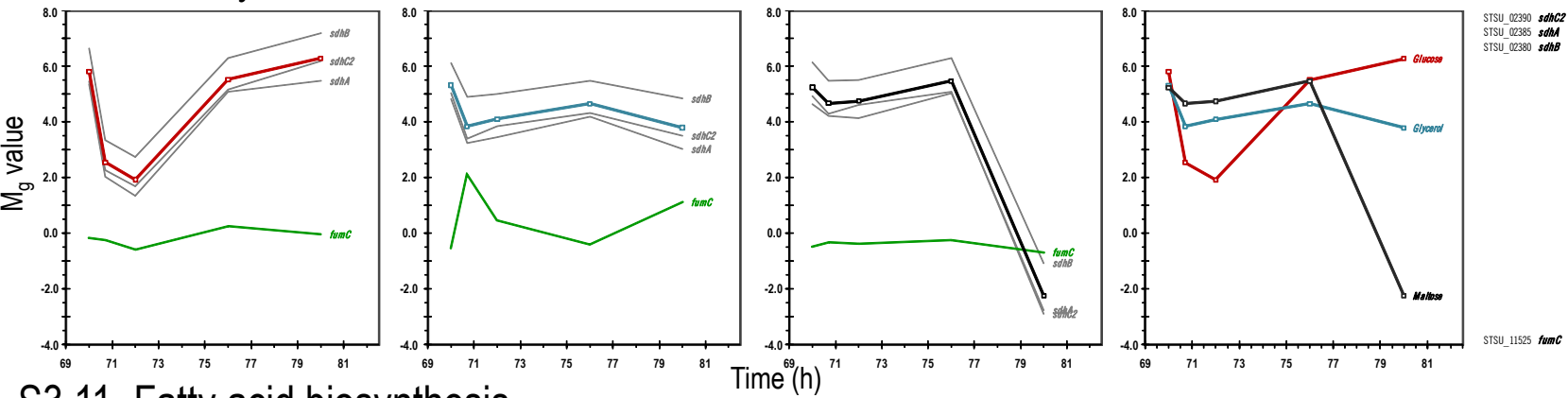
### S3.8. Carbon metabolism I



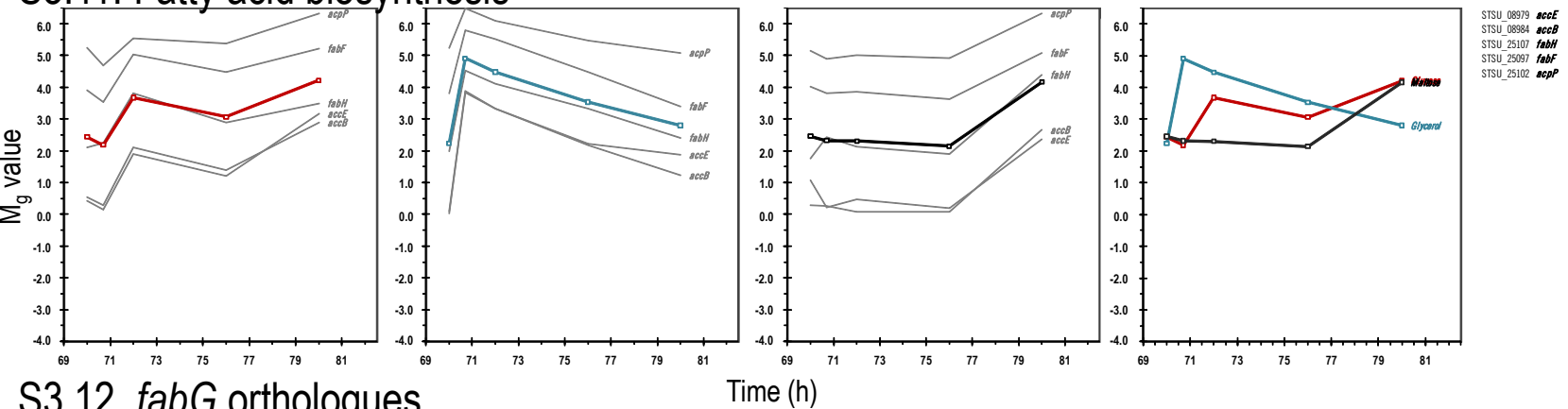
### S3.9. Carbon metabolism II



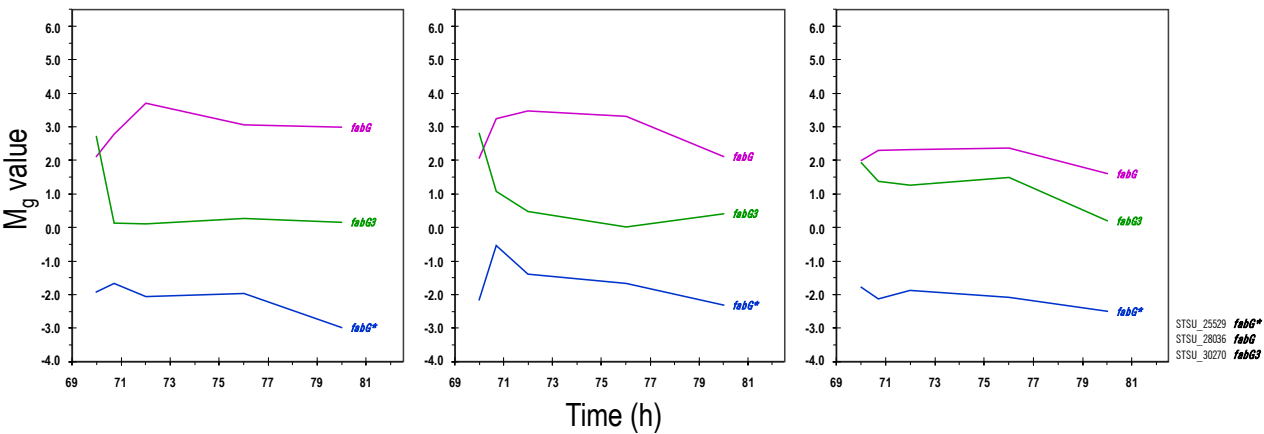
### S3.10. TCA cycle



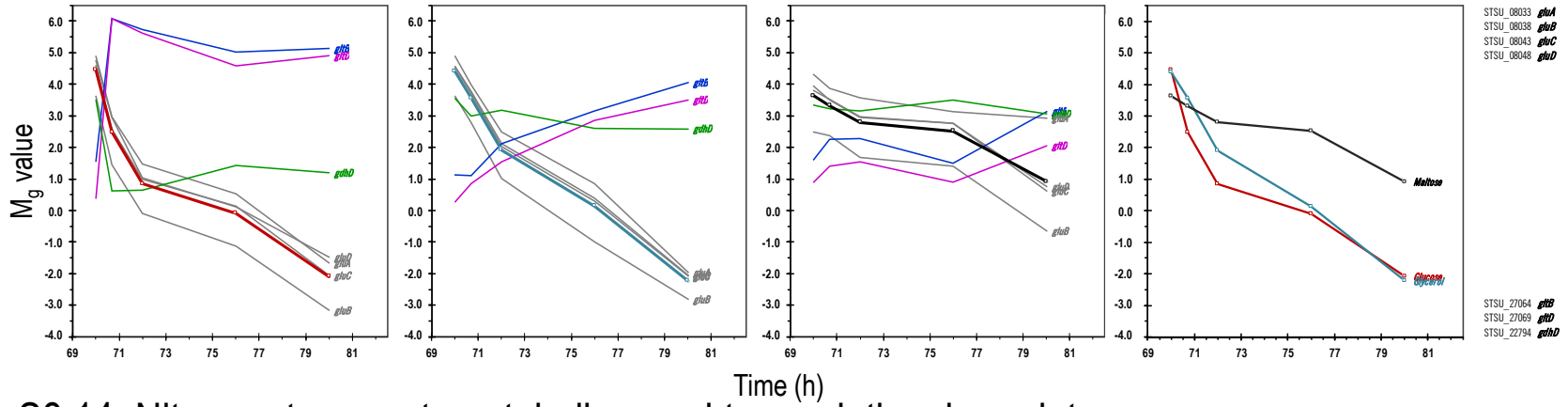
### S3.11. Fatty acid biosynthesis



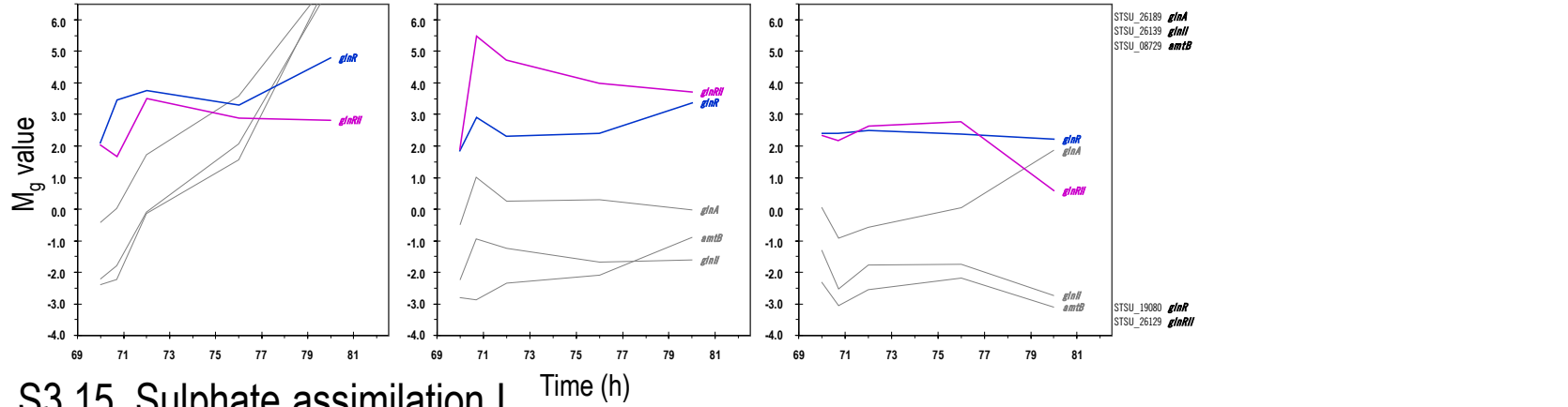
### S3.12. fabG orthologues



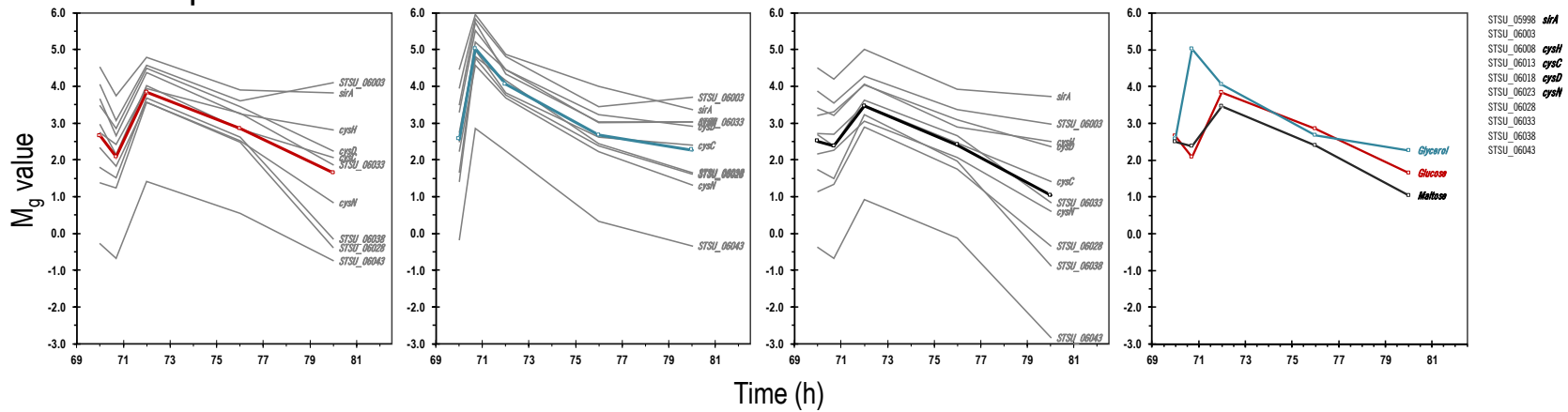
### S3.13. Glutamate metabolism



### S3.14. Nitrogen transport, metabolism and transcriptional regulators

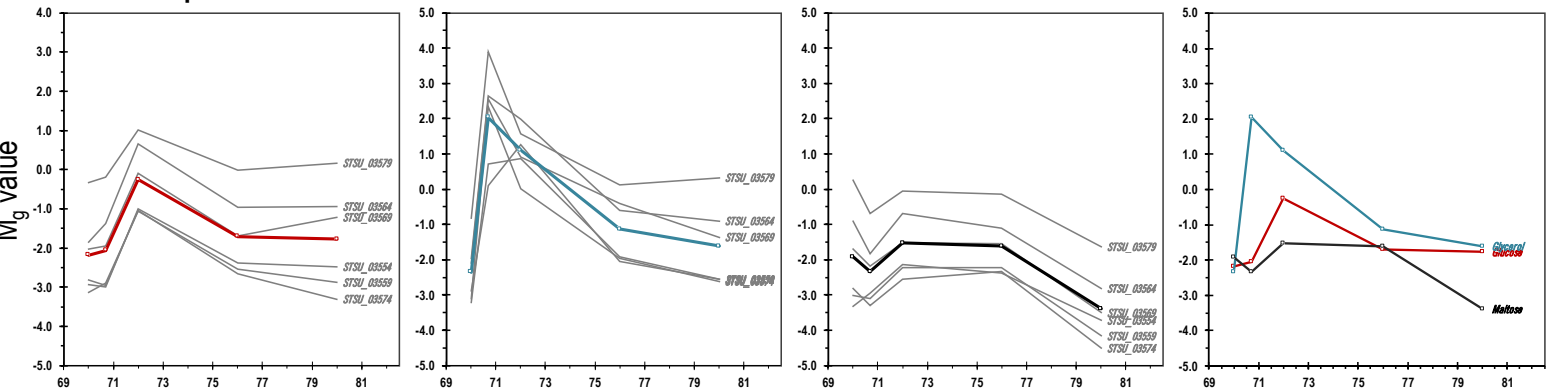


### S3.15. Sulphate assimilation I



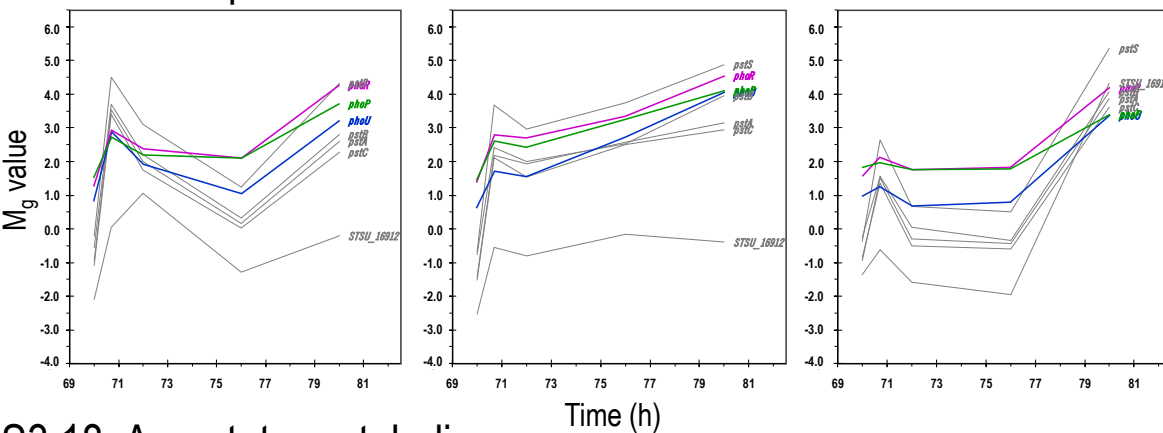


### S3.16. Sulphate assimilation II



STSU\_03554  
STSU\_03559  
STSU\_03564  
STSU\_03569  
STSU\_03574  
STSU\_03579

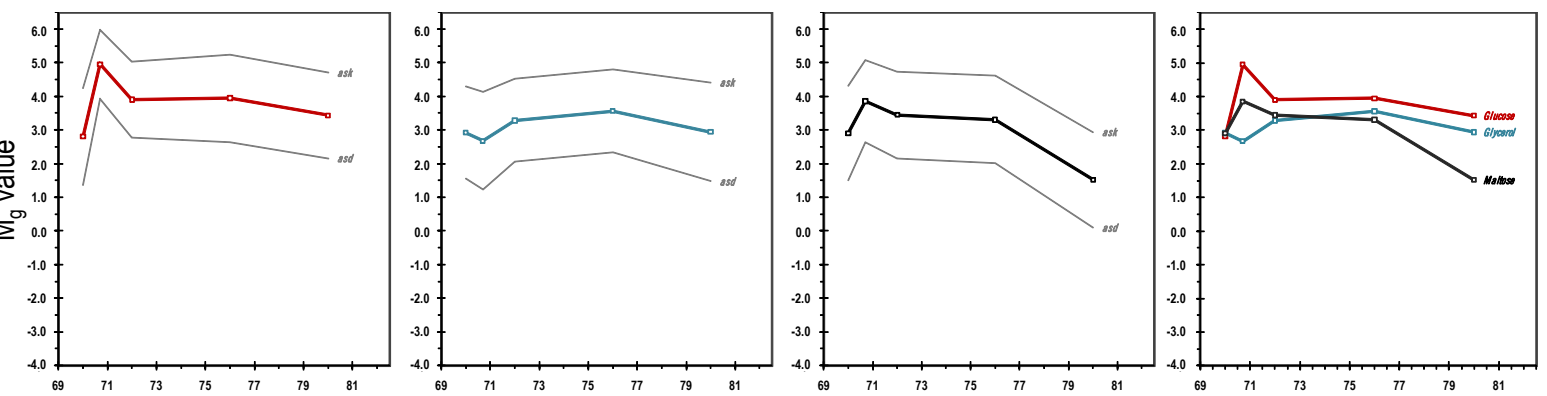
### S3.17. Phosphate assimilation



STSU\_18935 *pstB*  
STSU\_18940 *pstA*  
STSU\_18945 *pstC*  
STSU\_18950 *pstS*  
STSU\_16912

STSU\_19400 *phoU*  
STSU\_19405 *phoR*  
STSU\_19410 *phoP*

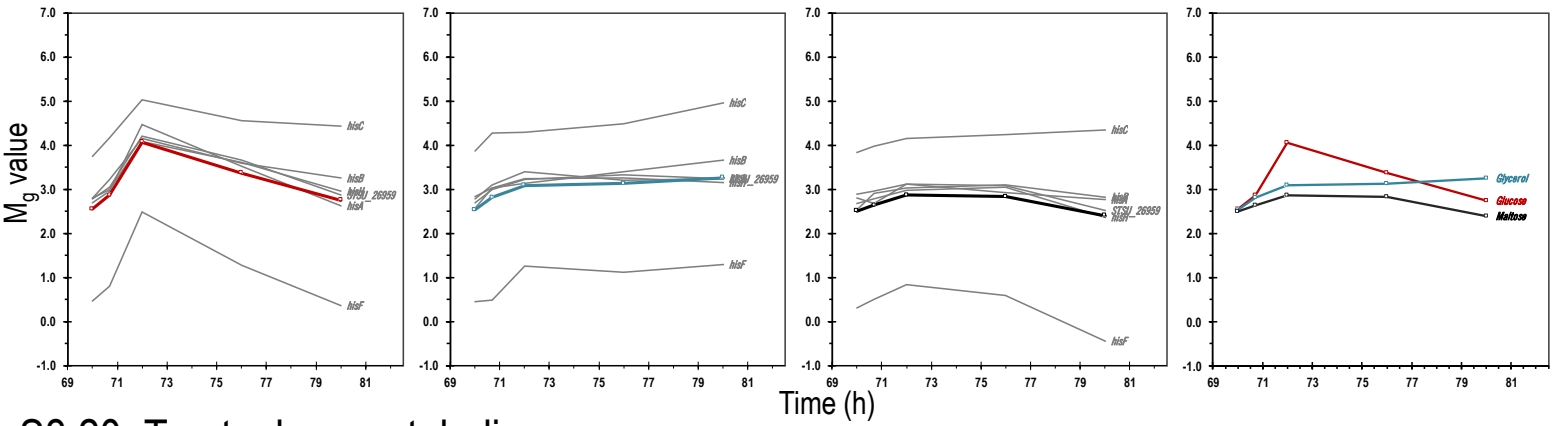
### S3.18. Aspartate metabolism



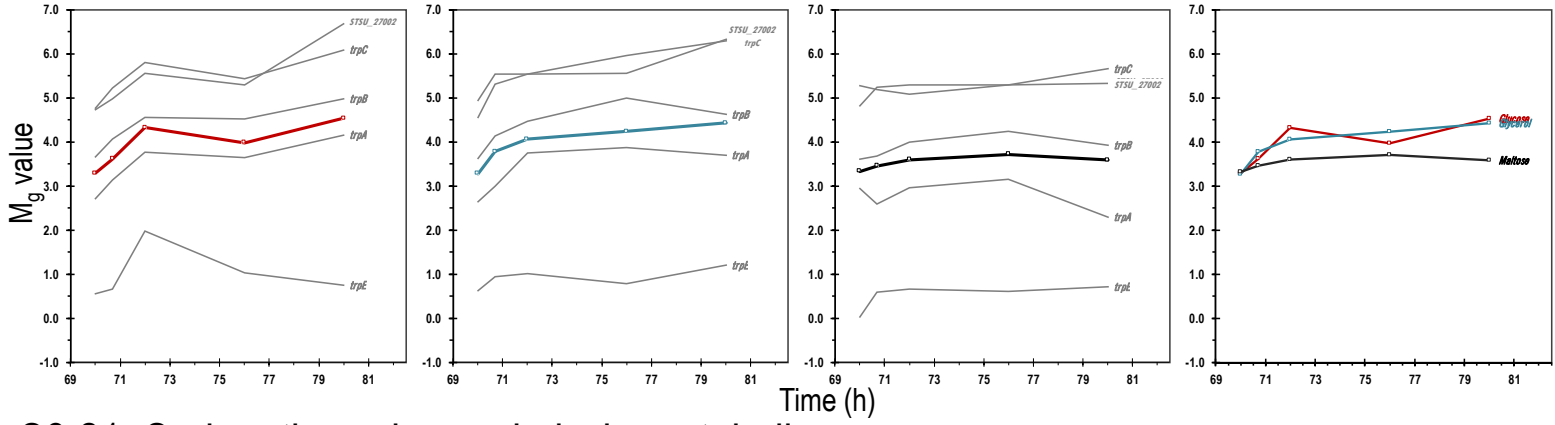
STSU\_15909 *ask*  
STSU\_15904 *asd*

Glucose  
Glycerol  
Maltose

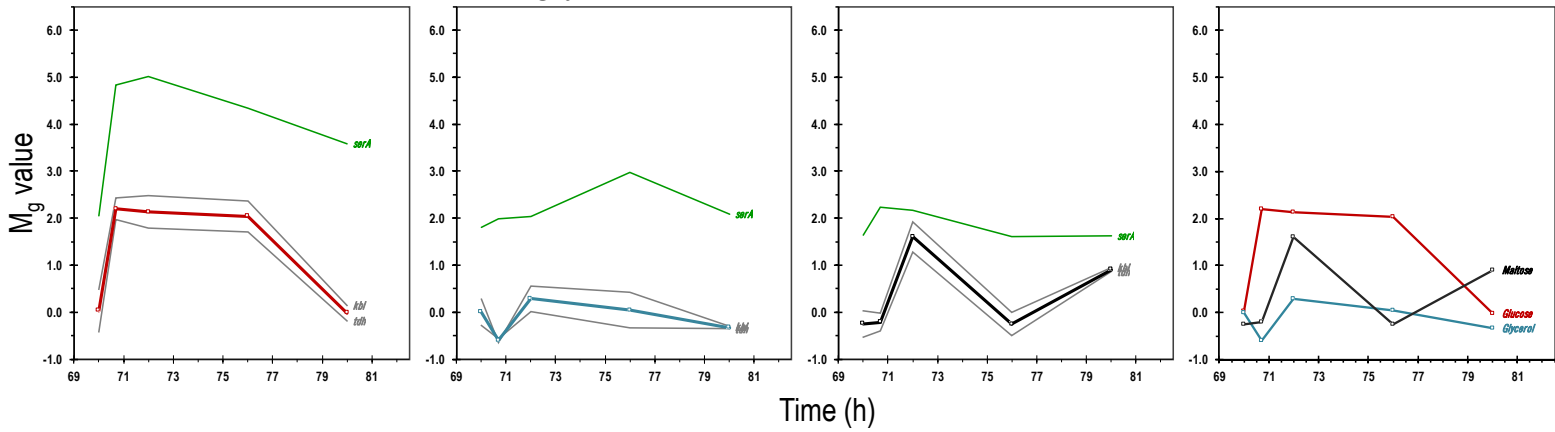
### S3.19. Histidine metabolism



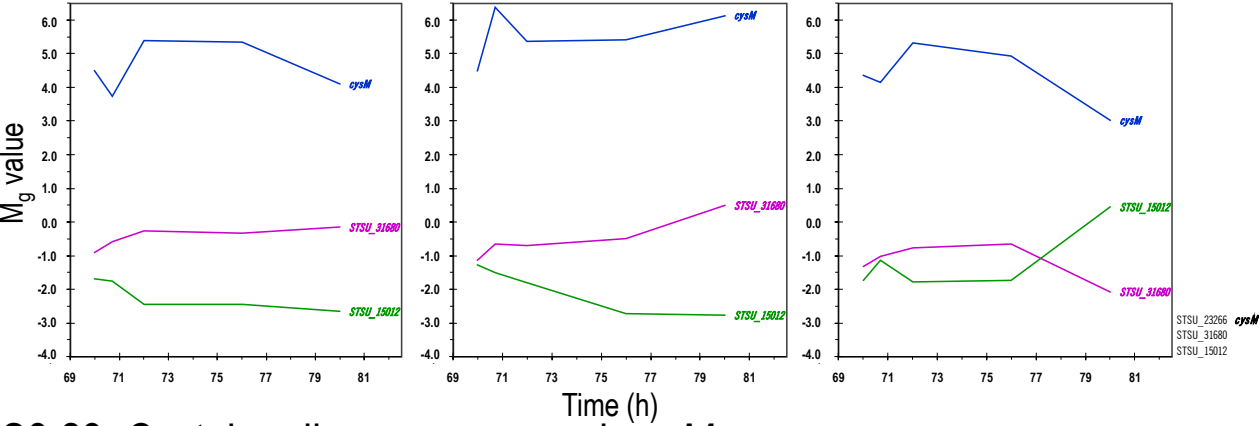
### S3.20. Tryptophan metabolism



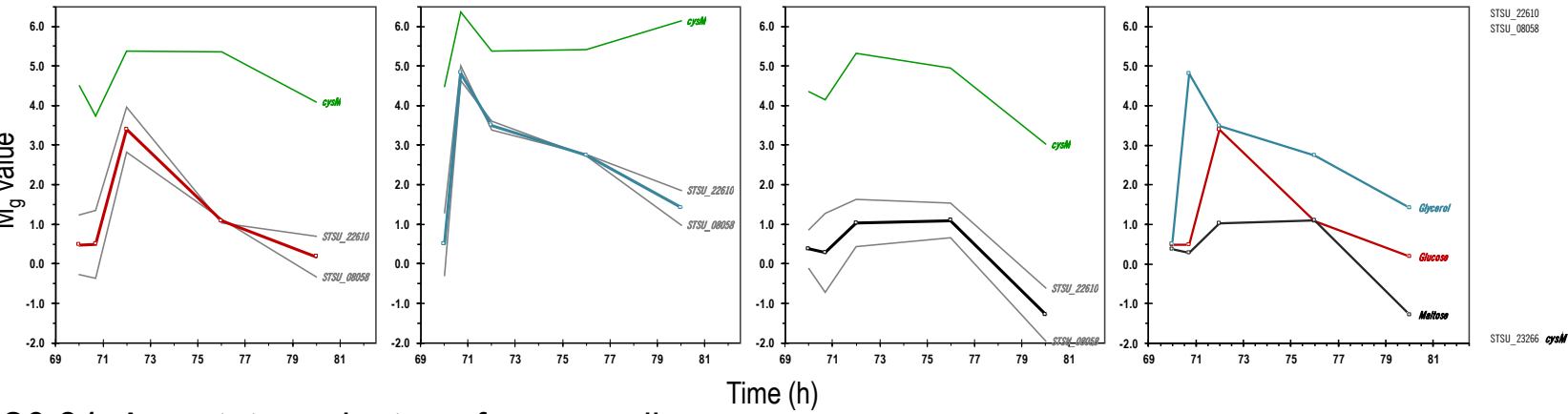
### S3.21. Serine, threonine and glycin metabolism



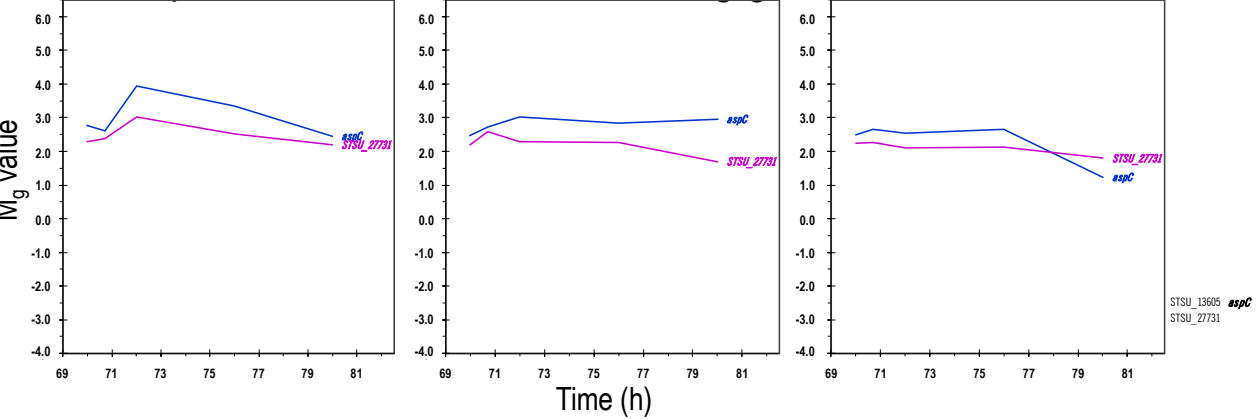
### S3.22. *cysM* paralogs



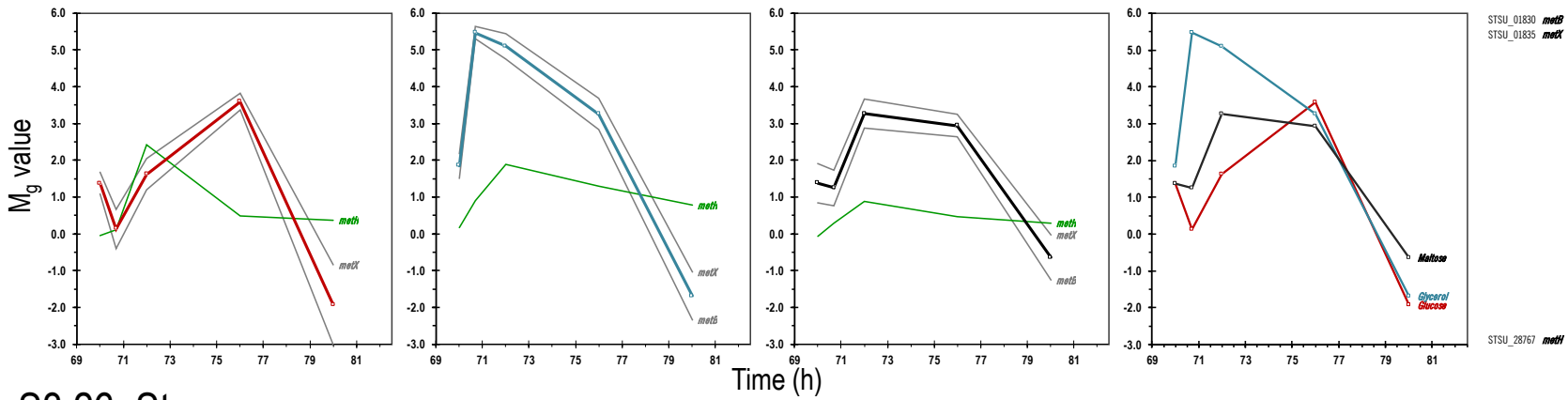
### S3.23. Cysteine dioxygenases and *cysM*



### S3.24. Aspartate aminotransferase coding genes

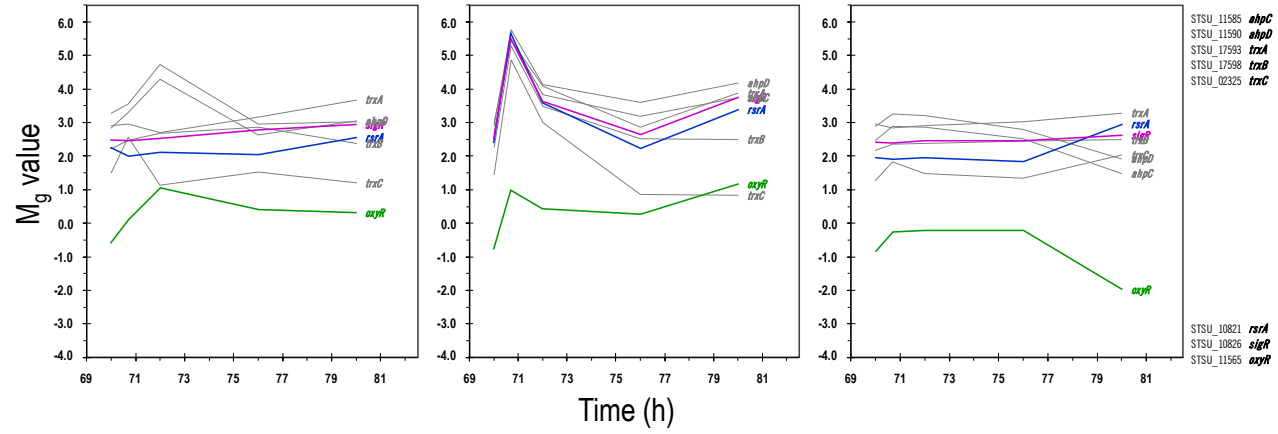


### S3.25. Methionine metabolism

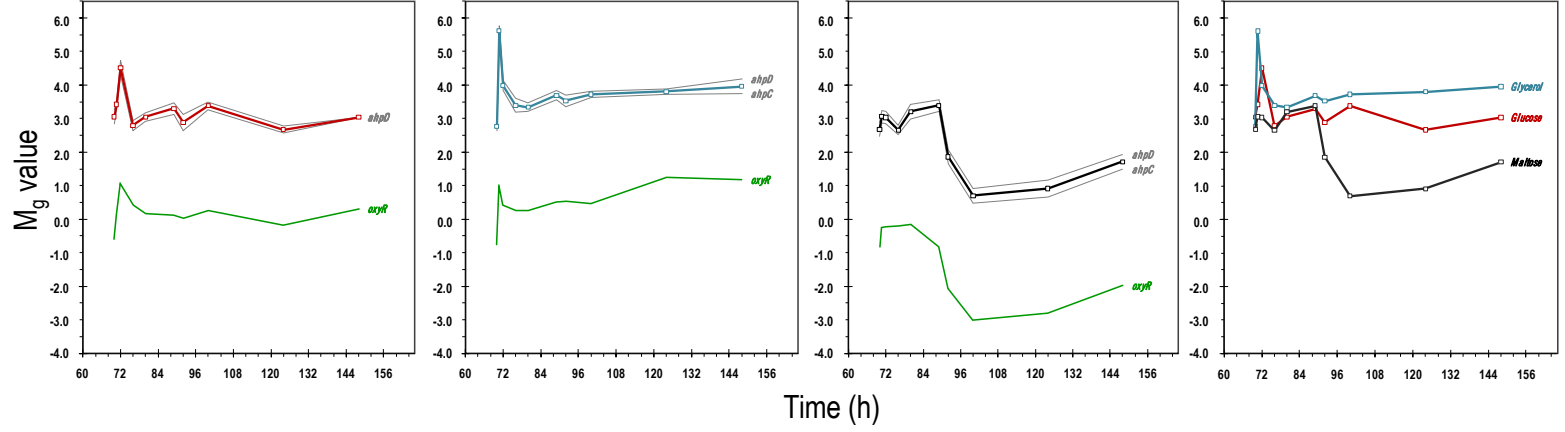


### S3.26. Stress response

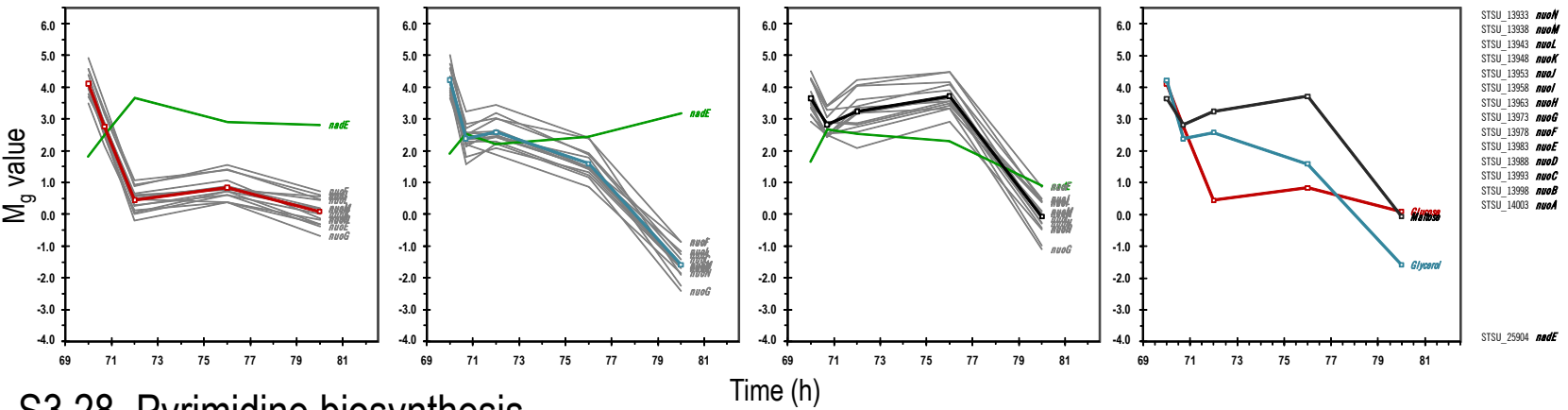
A)



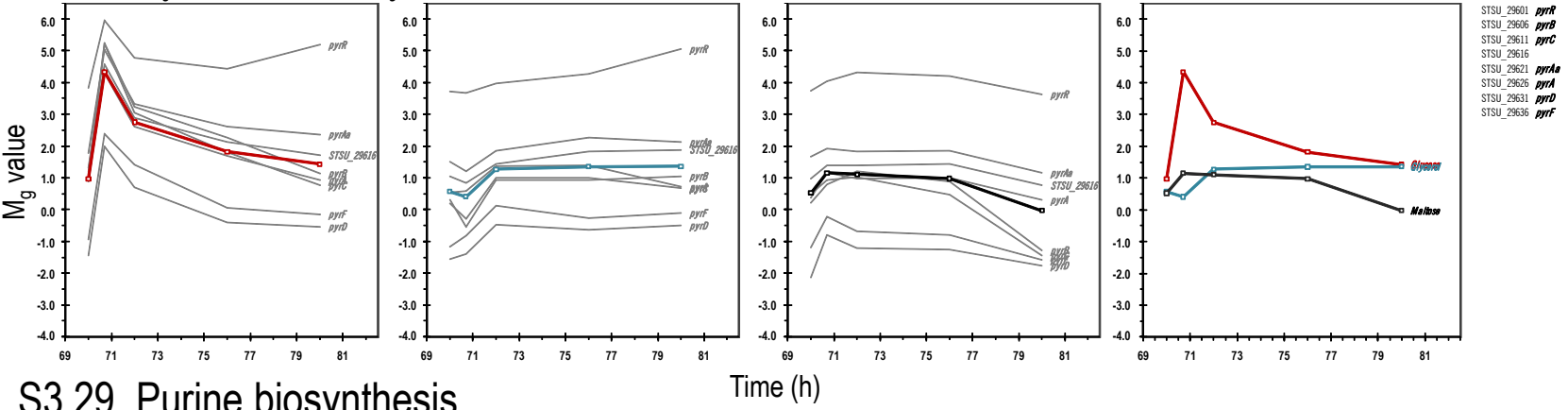
B)



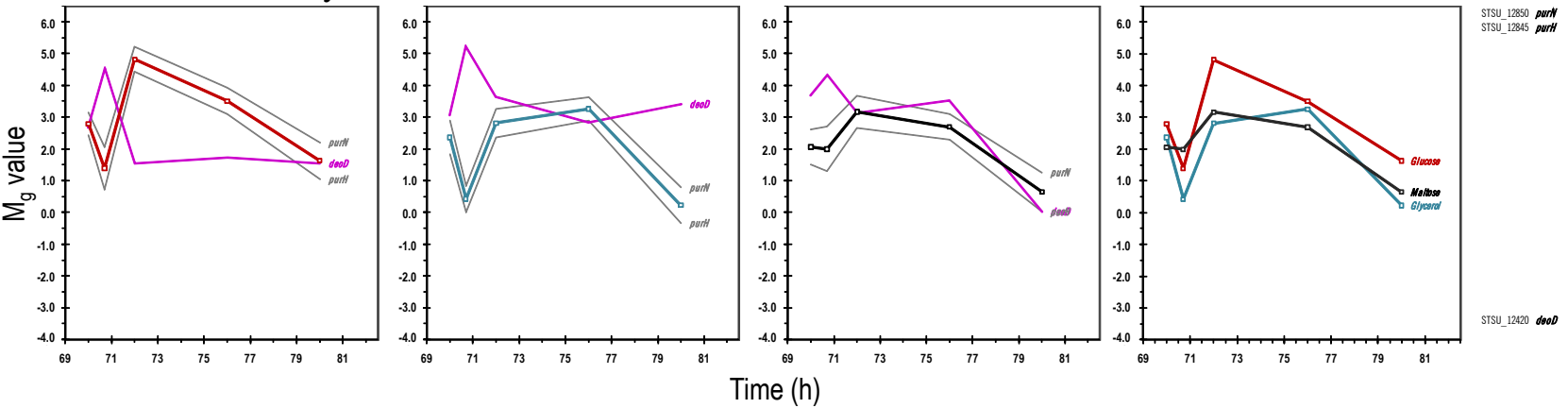
### S3.27. NAD<sup>+</sup> metabolism



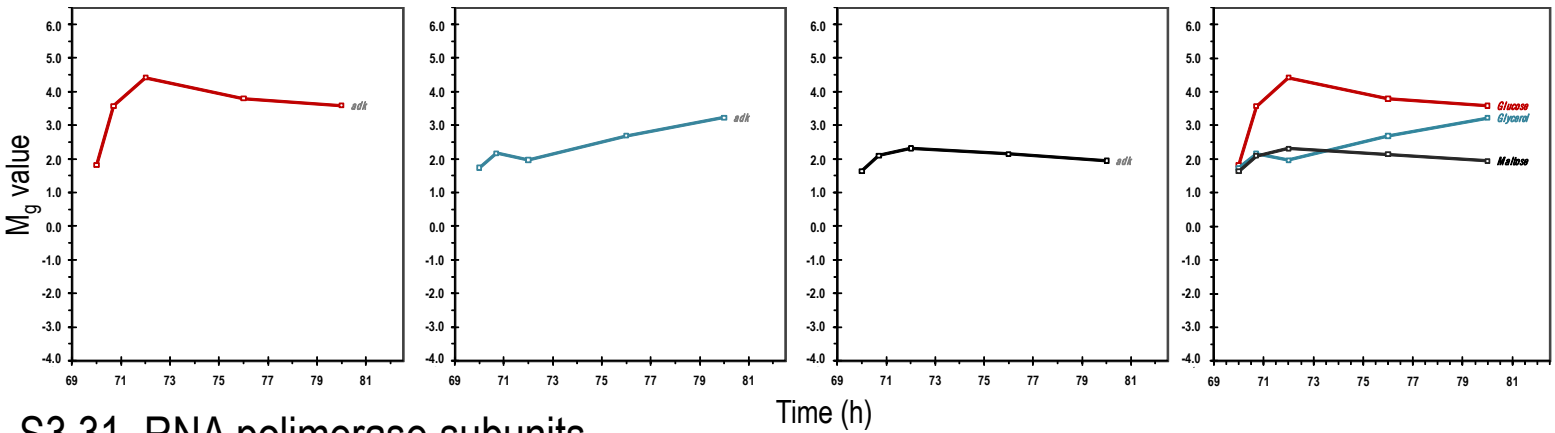
### S3.28. Pyrimidine biosynthesis



### S3.29. Purine biosynthesis

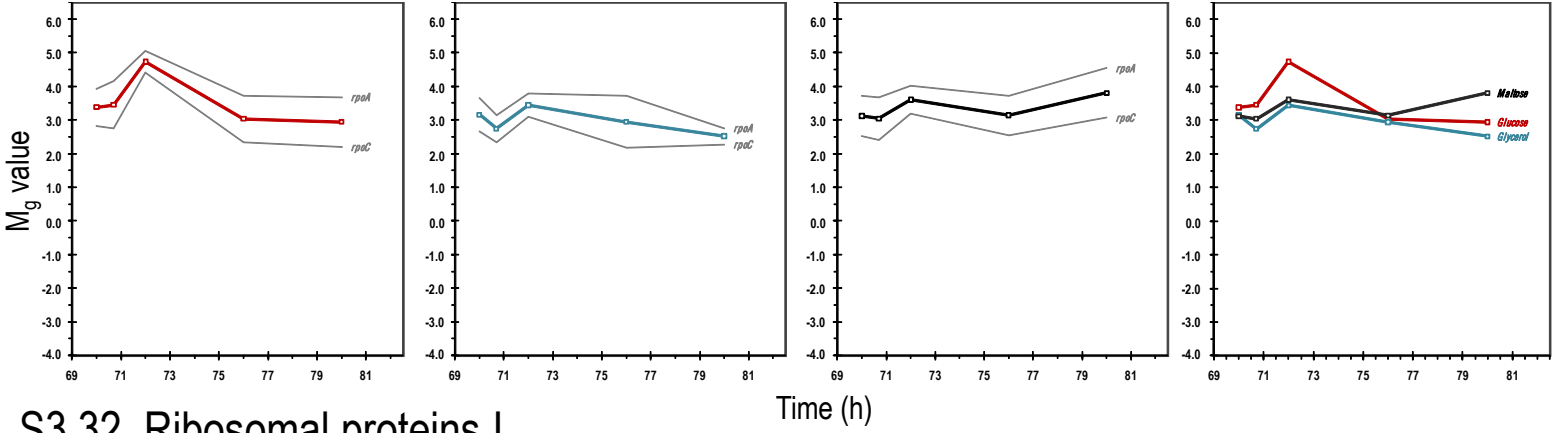


### S3.30. Adenilate kinase coding gene *adk*



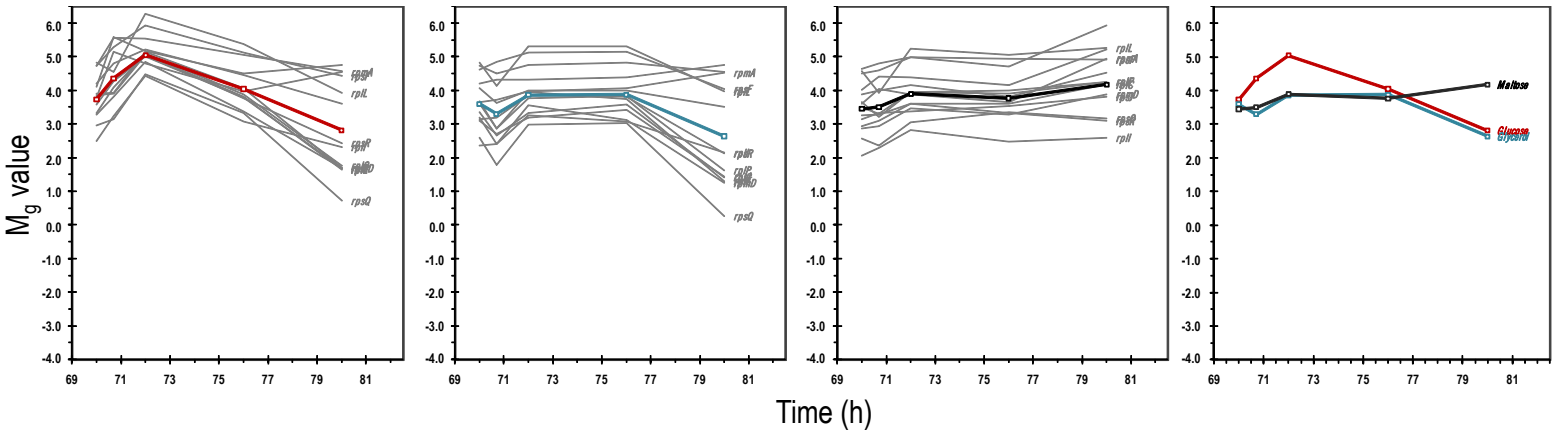
STSU\_13315 *adk*

### S3.31. RNA polymerase subunits



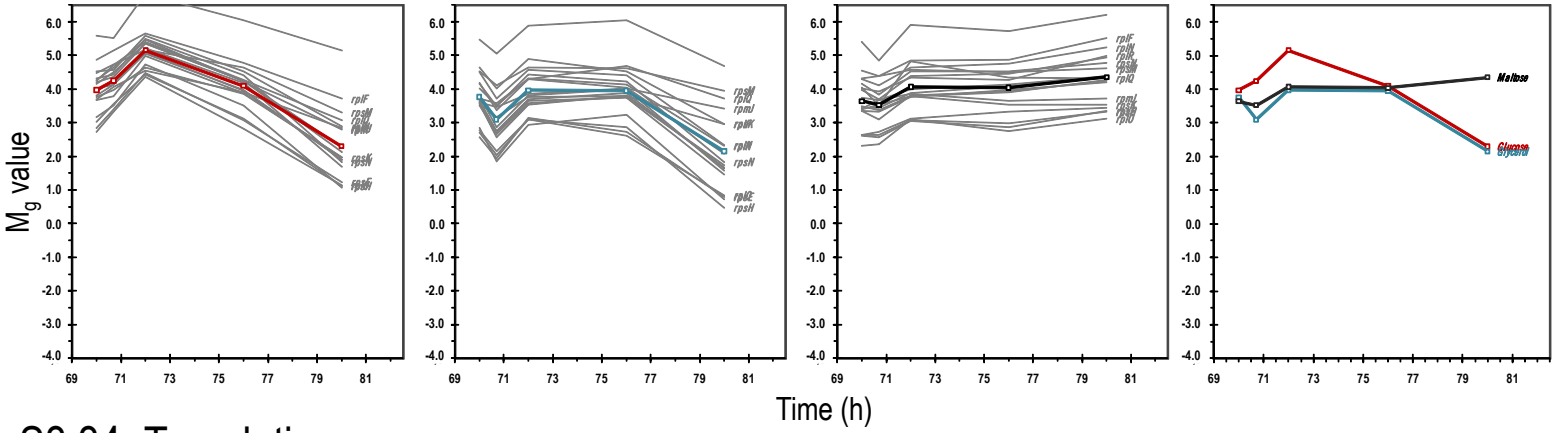
STSU\_13285 *rpoA*  
STSU\_13560 *rpoC*

### S3.32. Ribosomal proteins I



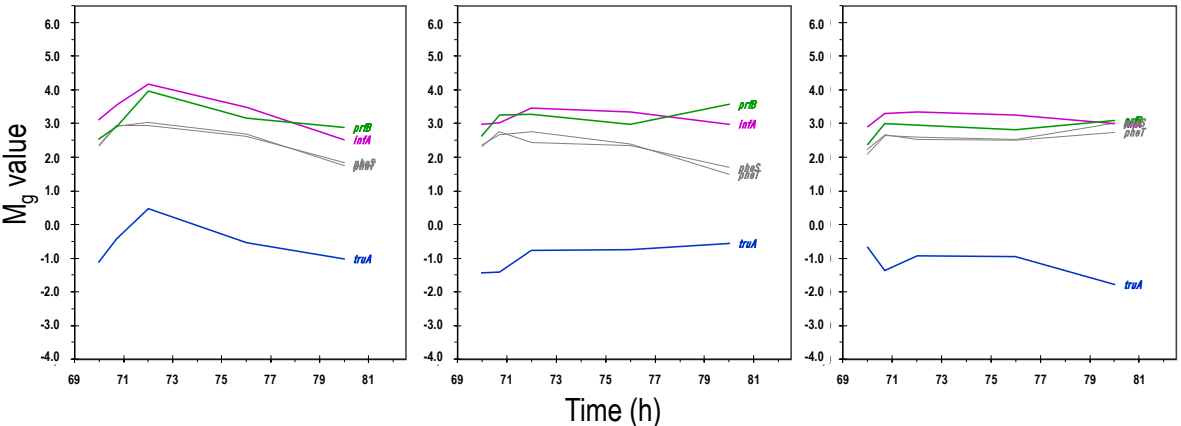
STSU\_13330 *rpmD*  
STSU\_13360 *rplE*  
STSU\_13375 *rpsQ*  
STSU\_13385 *rplP*  
STSU\_13420 *rplC*  
STSU\_13425 *rpsI*  
STSU\_13570 *rplL*  
STSU\_17678 *rpsF*  
STSU\_17688 *rpsR*  
STSU\_17693 *rplU*  
STSU\_24472 *rpmA*  
STSU\_29057 *rpmI*  
STSU\_29062 *rplT*  
STSU\_13640 *rpmG*

### S3.33. Ribosomal proteins II



- STSU\_13280 *rplQ*
- STSU\_13290 *rpsK*
- STSU\_13295 *rpsM*
- STSU\_13300 *rplJ*
- STSU\_13325 *rplO*
- STSU\_13335 *rpsE*
- STSU\_13340 *rpsF*
- STSU\_13345 *rpsH*
- STSU\_13350 *rpsL*
- STSU\_13355 *rpsN*
- STSU\_13365 *rpsP*
- STSU\_13370 *rpsR*
- STSU\_13380 *rpsS*
- STSU\_13390 *rplB*
- STSU\_13400 *rplW*
- STSU\_13410 *rplD*
- STSU\_13415 *rplU*
- STSU\_13575 *rplU*

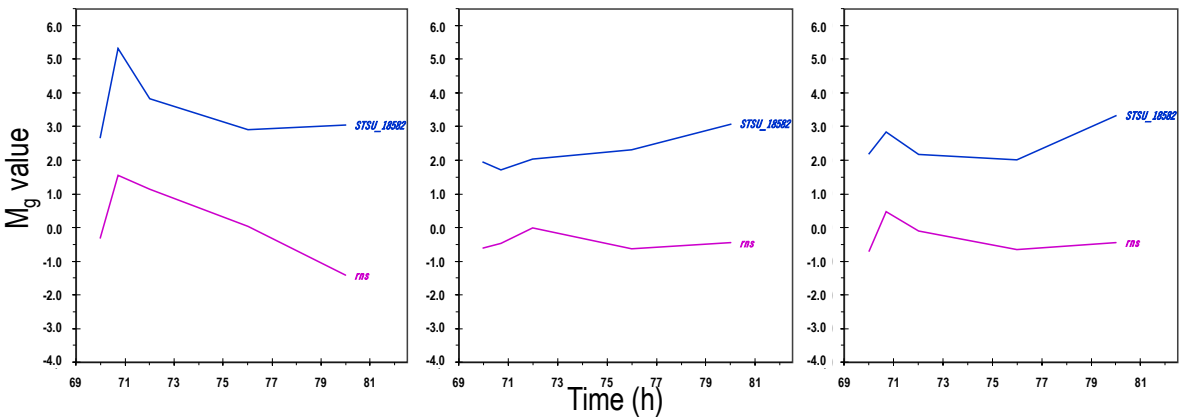
### S3.34. Translation



- STSU\_29077 *prfB*
- STSU\_29082 *infA*

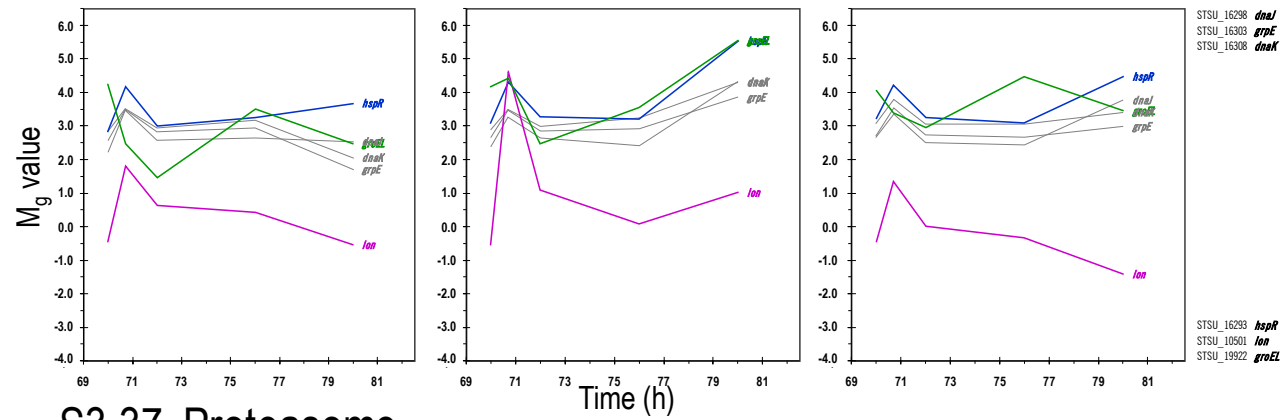
- STSU\_13275 *traA*
- STSU\_13305 *infA*
- STSU\_22864 *prfB*

### S3.35. Ribonuclease E and RNA helicase

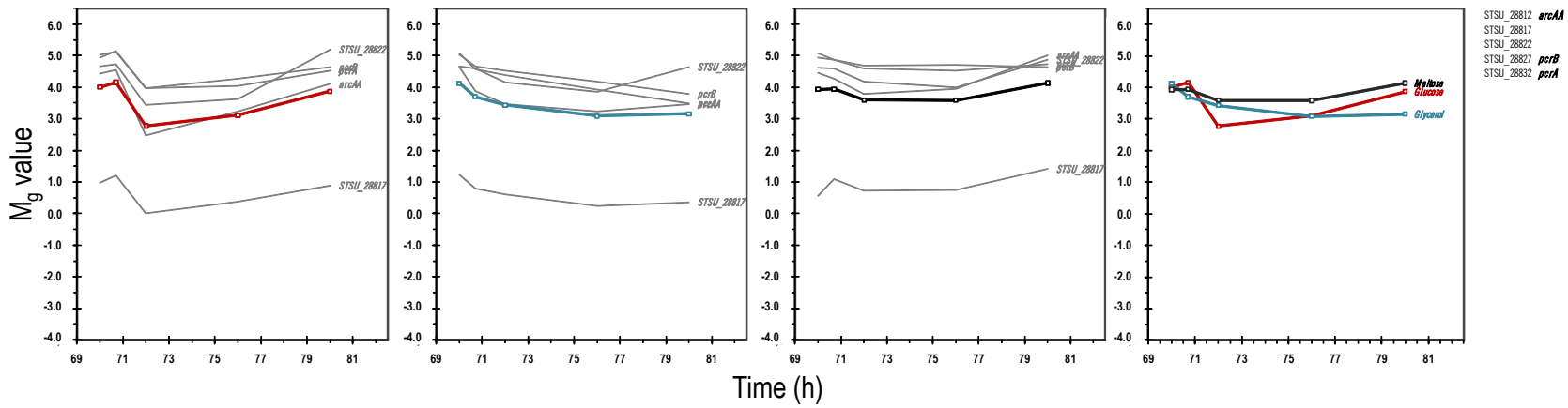


- STSU\_18582
- STSU\_24417 *rns*

### S3.36. Heat shock



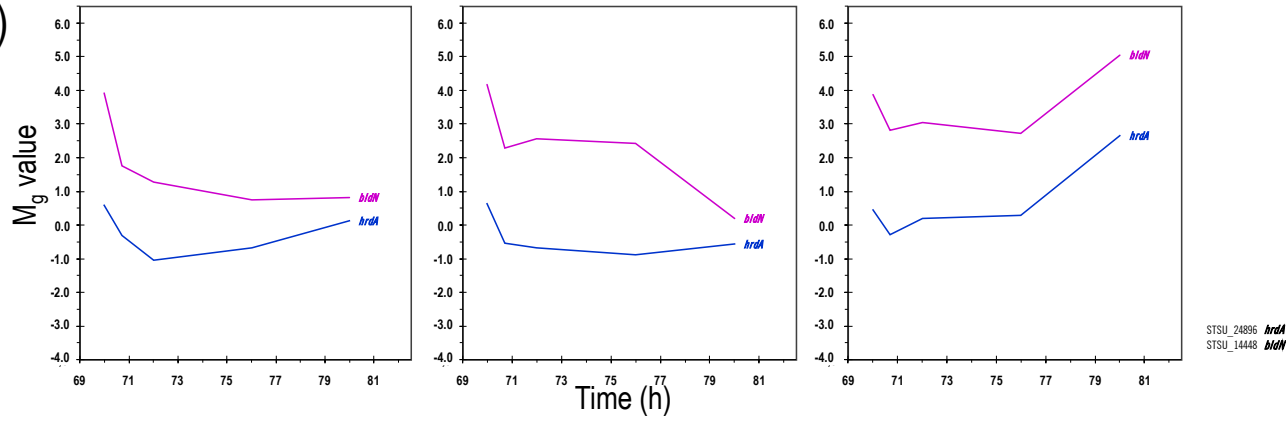
### S3.37. Proteasome



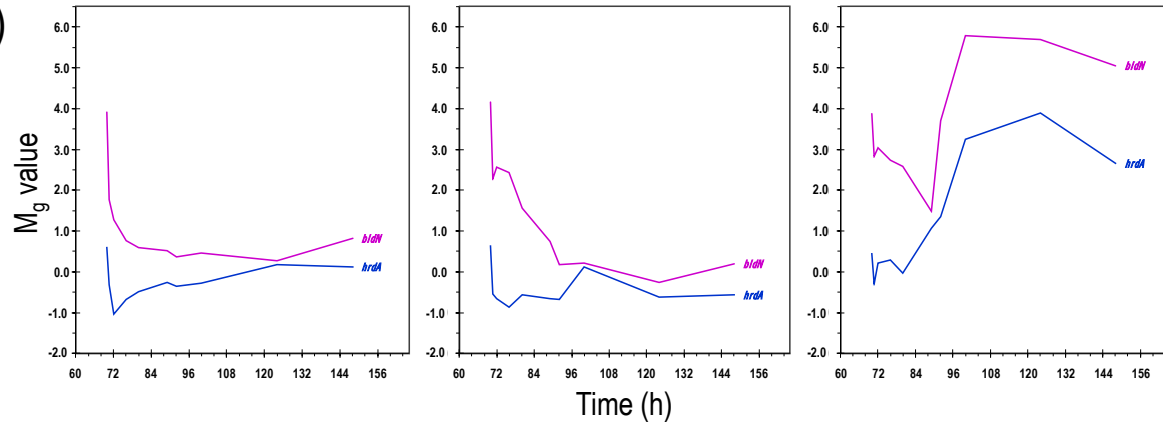


# S3.38. *hrdA* and *bldN*

A)

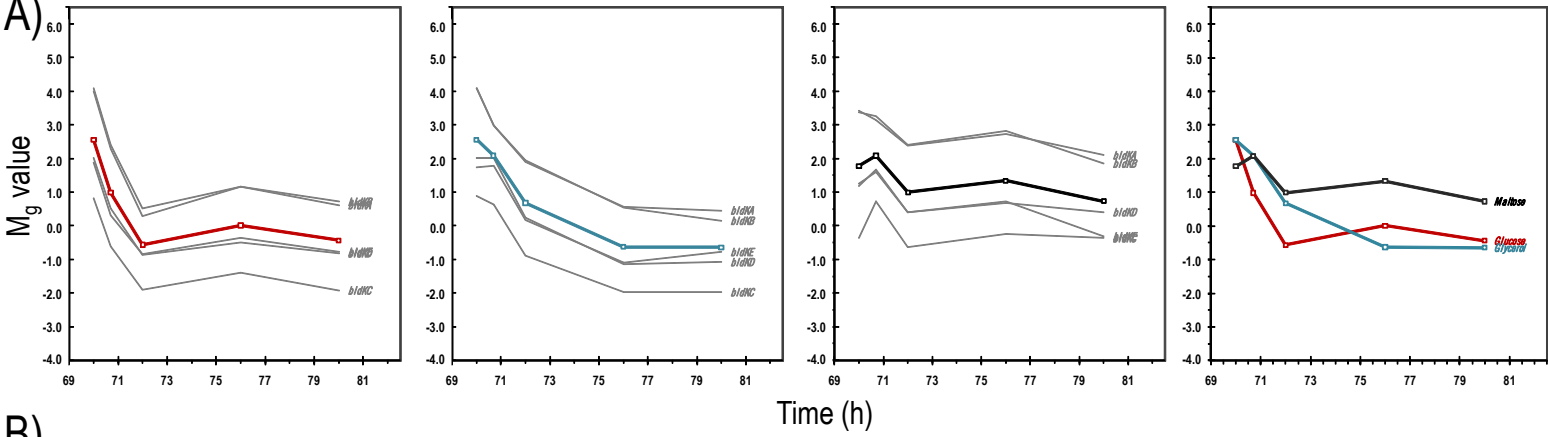


B)

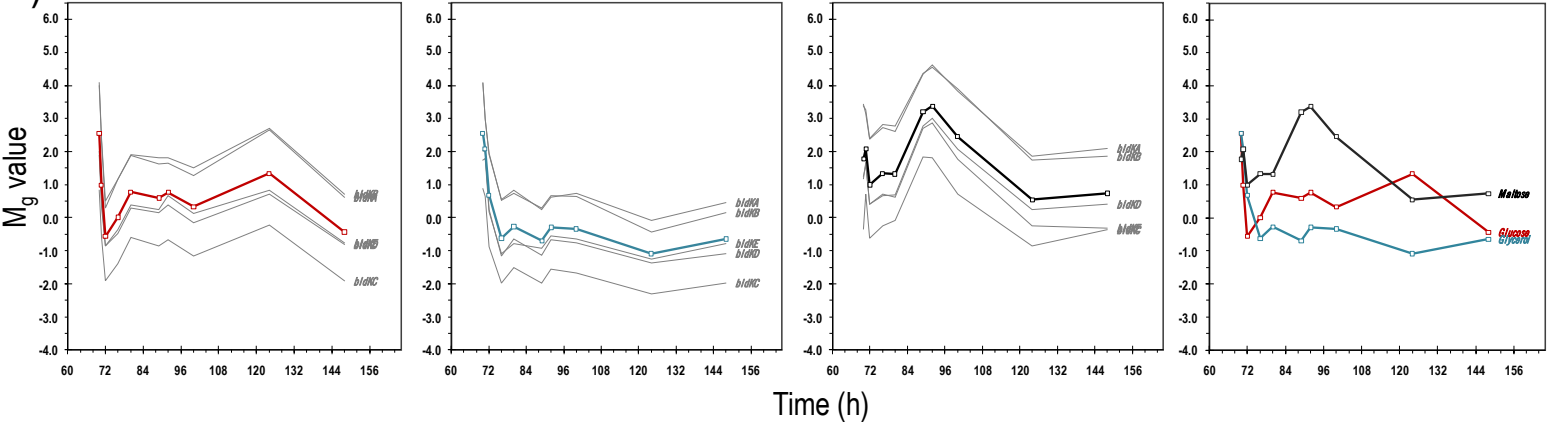


# S3.39. *bldK* transporter

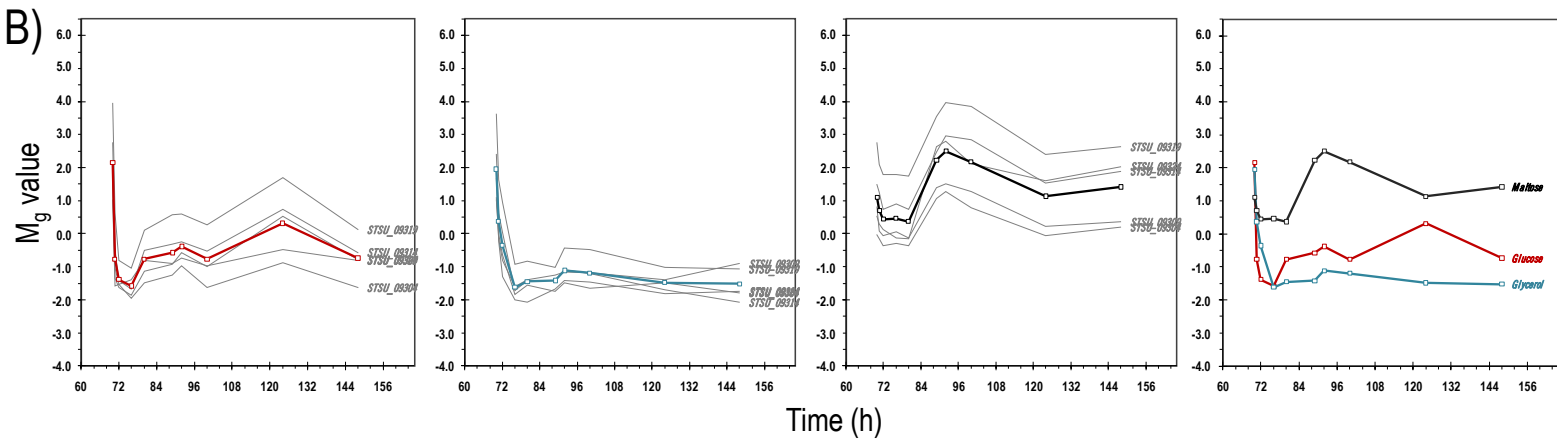
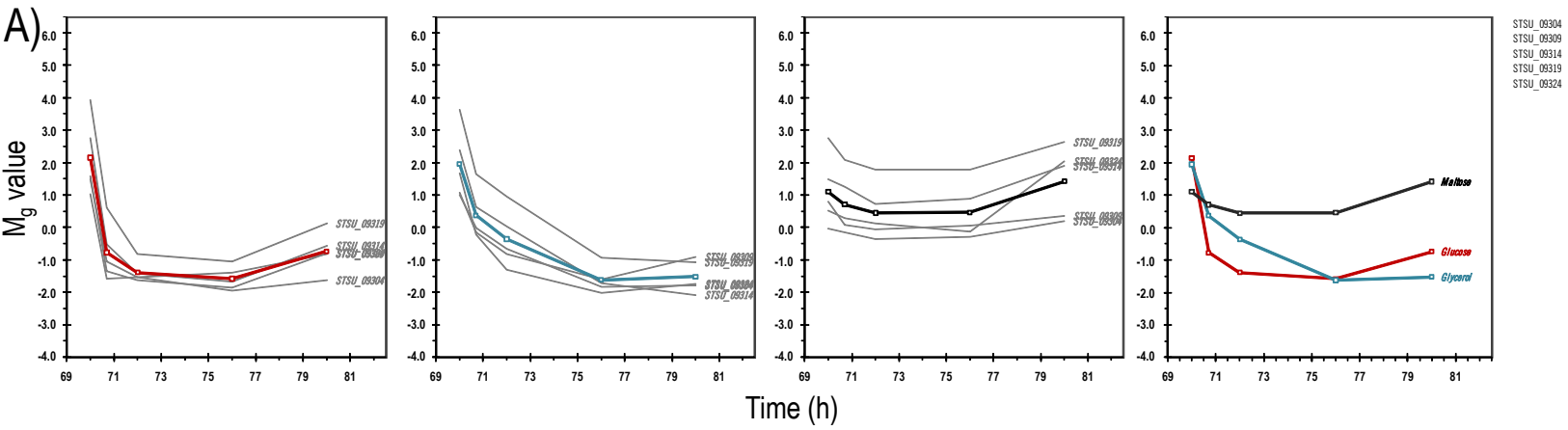
A)



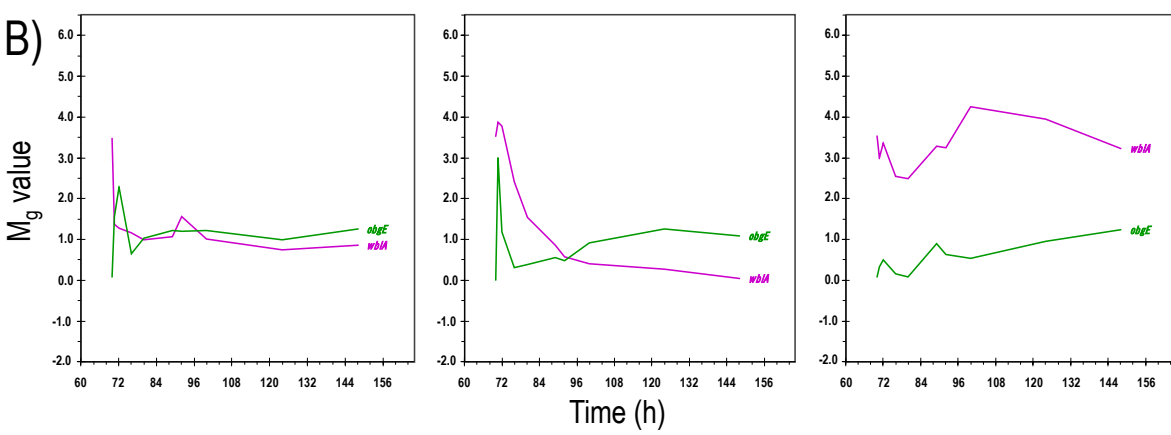
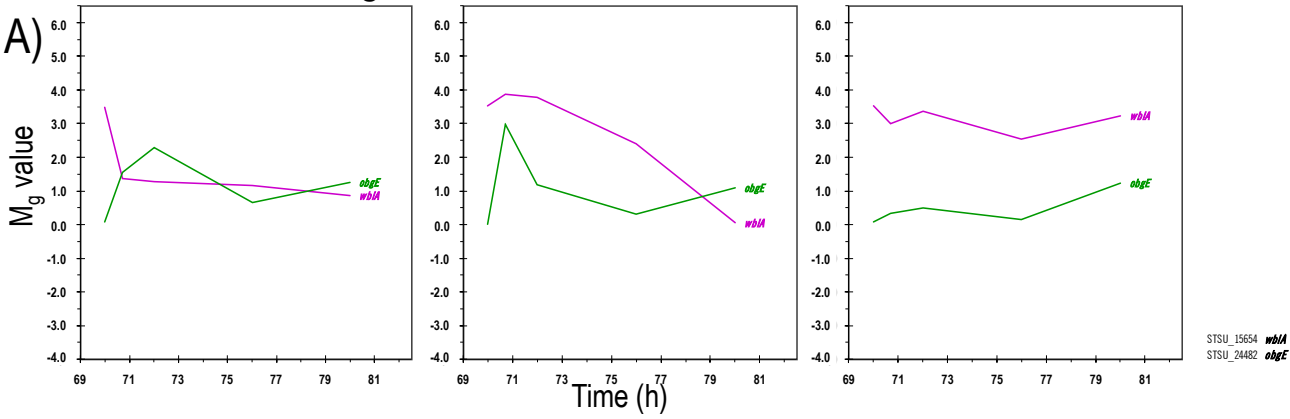
B)



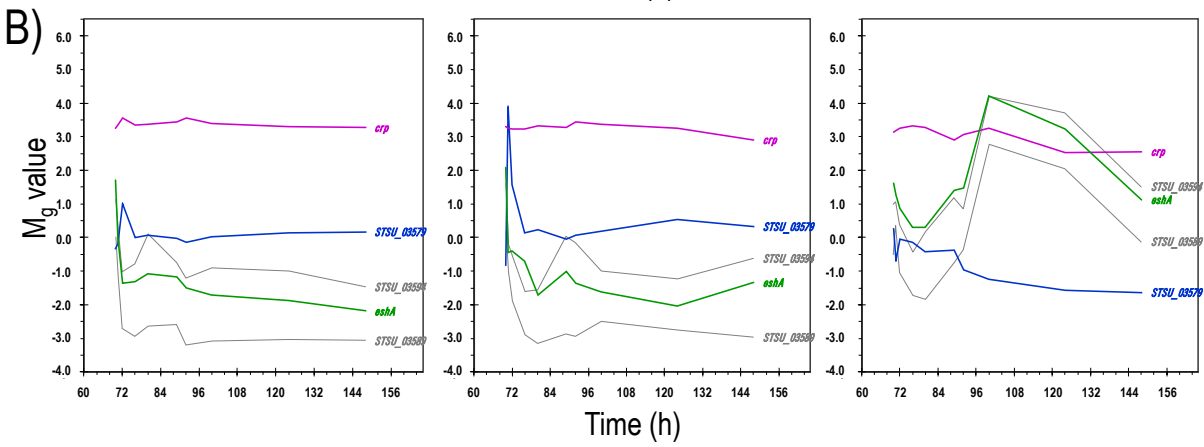
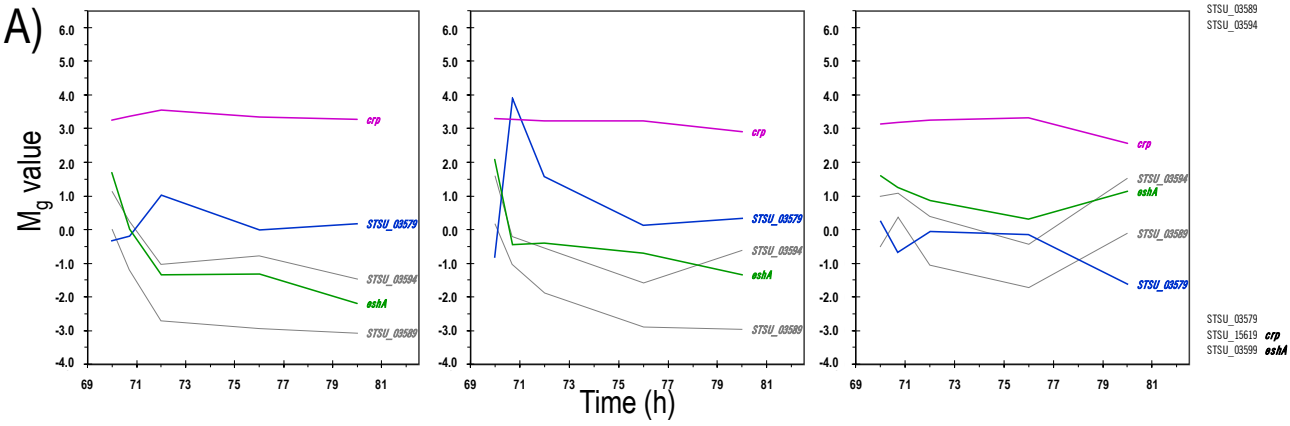
# S3.40. Oligopeptide transporter



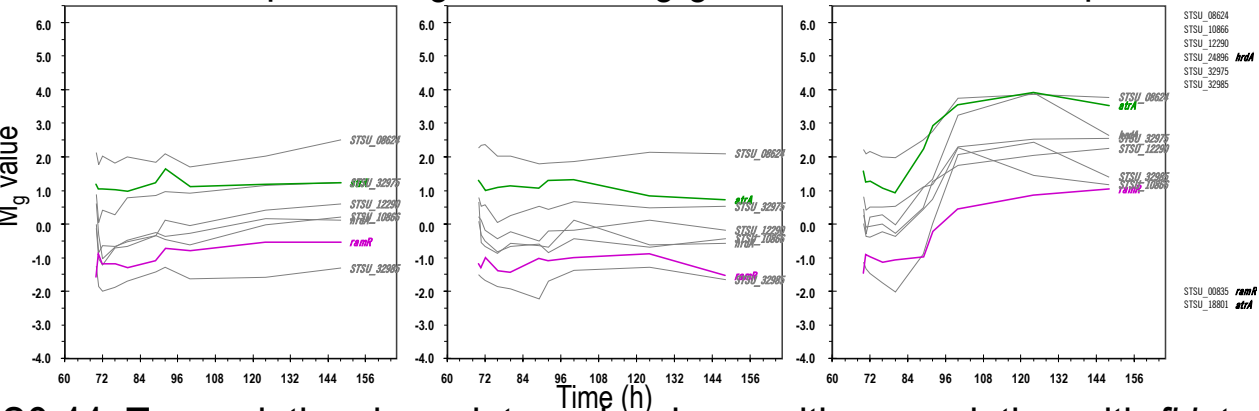
# S3.41. *wblA* and *obgE*



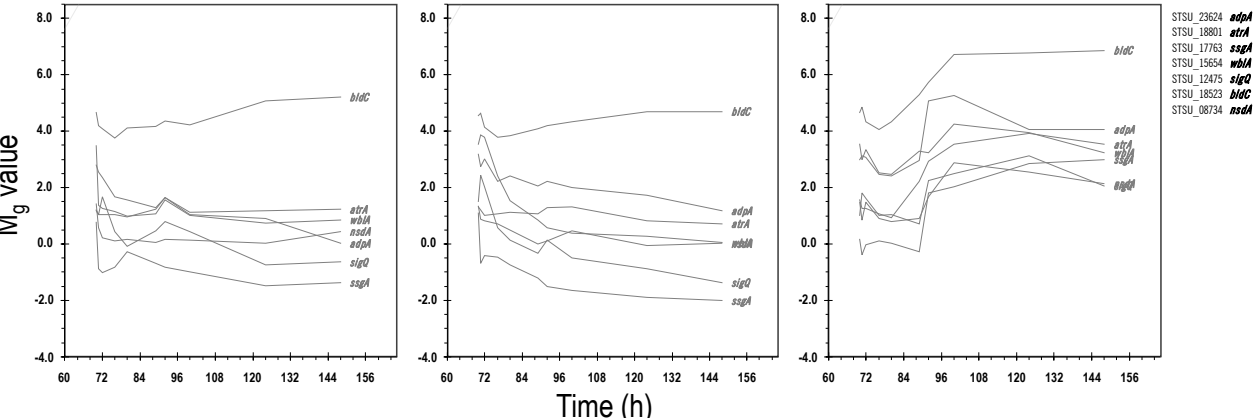
# S3.42. *crp* paralogs



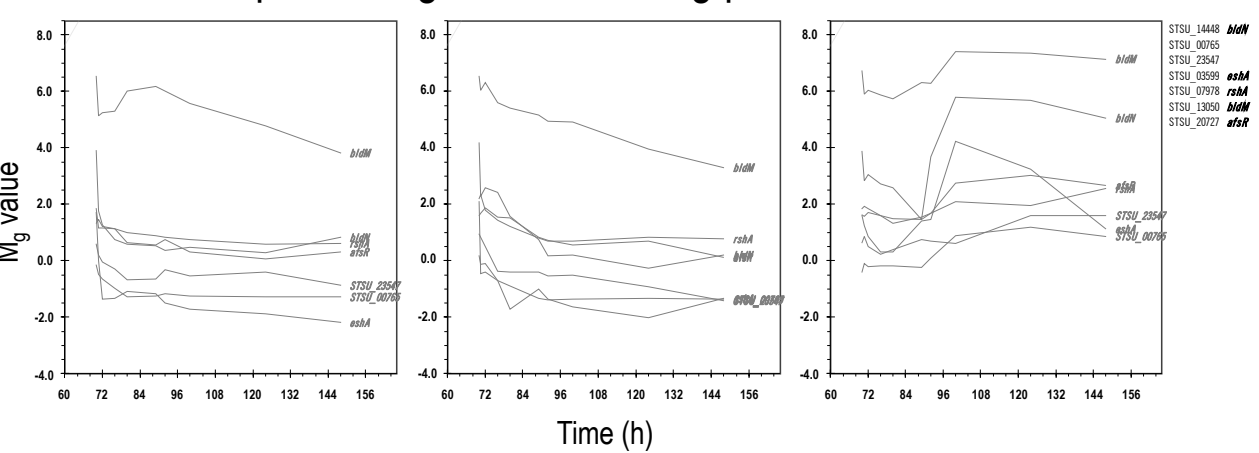
### S3.43. Transcriptional regulator coding genes with a *fbkN*-like profile



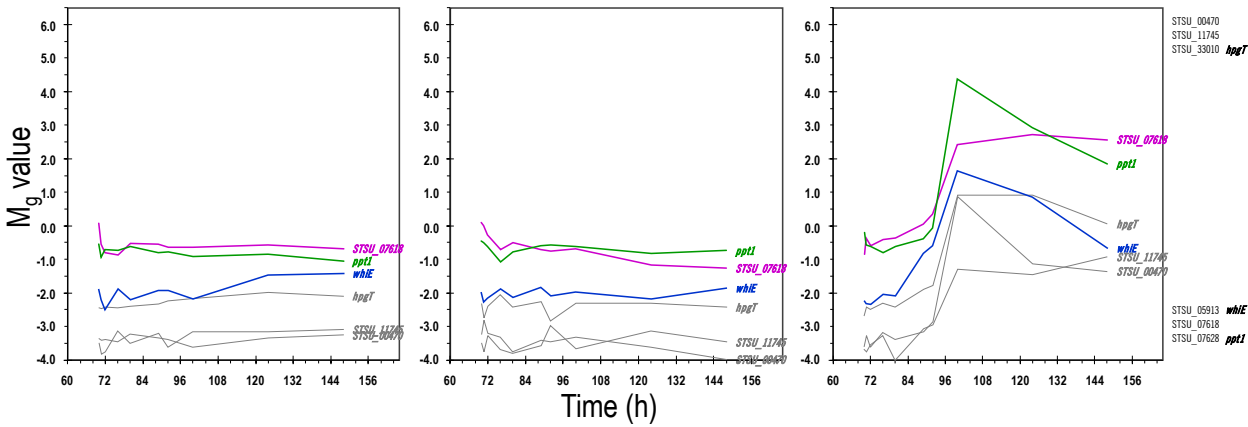
### S3.44. Transcriptional regulators showing positive correlation with *fbk* transcription I



### S3.45 Transcriptional regulators showing positive correlation with *fbk* transcription II



### S3.46. Secondary metabolite biosynthetic genes with a *fbkN*-like profile



**Fig. S3. Transcriptional profiles of selected genes.** The  $\log_2$  transcription values ( $M_g$ ) of selected genes along the cultures are depicted for the three experimental conditions. From left to right, the panels correspond to the glucose, glycerol and maltose (control) conditions. For some figures, we depict a fourth panel on the right indicating the average  $M_g$  transcription values of selected genes under the three experimental conditions to facilitate the comparison of the profiles (in this case, glucose, glycerol and maltose additions are represented as red, blue and black lines). Error bars are omitted to facilitate the visualization of the results. In figures 3.11 and 3.19, transcription of *fabD*, *hisD* and *hisI* is not represented since the microarrays used lacked probes for these genes.

**Table S1. Oligonucleotides used in this work for RT-qPCR validation.** The sequence and target gene are indicated.

<b>Name</b>	<b>Sequence (5'→3')</b>	<b>Target</b>
CMOq40	TCAACGCCGTCAGCGGAATC	<i>pfkA2</i>
CMOq41	TGGATCTCGCCGAGTTCTC	<i>pfkA2</i>
CMOq42	TCTCCTACATGCTCCGCAAAGAG	<i>phoP</i>
CMOq43	ATCAGGTCGAGAAGGACGAGATC	<i>phoP</i>
CMOq44	GCAACCTCGCCCTCGAACTC	<i>glpX</i>
CMOq45	TCCGCGCCGTTCTTGTCTC	<i>glpX</i>
CMOq89	GGTTCCTCGCGACCAATC	<i>pfkA1</i>
CMOq90	GTGTCTGAAGCCGAAGGTGTAG	<i>pfkA1</i>
CMOq91	CCGGTCTGAACGCCGTCATC	<i>pfkA3</i>
CMOq92	CCAGGTCGAGCTTGCGGTAATC	<i>pfkA3</i>
CMOq93	CTCGCCACCACGACCAAATC	<i>crp</i>
CMOq94	CCGTCGCCACGGTGTAG	<i>crp</i>
CMOq95	GGACCGGCCGTTCTGATAG	<i>fkbN</i>
CMOq96	CGGTCAGCACGATGGAGATAC	<i>fkbN</i>
CMOq97	GCTGTTGCGCGAGGAGAAAC	<i>hrdA</i>
CMOq98	AGACCACGAGCCGAGATTC	<i>hrdA</i>
CMOq99	AACACCGGCTTCTGCTCATC	<i>amtB</i>
CMOq100	GGACCATGCCTCCGTAGAAGAAG	<i>amtB</i>
CMOq101	CCACACCGTCGCGGTCTAC	<i>glfD</i>
CMOq102	GCGGTTGATGTGCACCTTCTC	<i>glfD</i>
CMOq103	CCGCAATATGATCGGCCAGTAC	<i>metF</i>
CMOq104	GCGACACCGACGCAGAAG	<i>metF</i>
CMOq105	CGGTGAGCGTGGGCTTCATC	<i>gyrB</i>
CMOq106	GCCGTCGGCGAGGATAGTC	<i>gyrB</i>



**Table S2. Inhibition halo diameters detected by bioassay in the exploratory experiment.** The average values and the standard deviations from triplicate cultures are indicated, except for the cases of lactose and maltose additions, where data from duplicate cultures is given. Note that glucose and glycerol were the unique carbon sources that repressed FK506 production.

Carbon source	Diameter at 112 h (cm)	Diameter at 160 h (cm)
Fructose	1.33±0.06	2.30±0.10
Mannitol	1.30±0.26	2.30±0
Lactose	1.45±0.35	2.45±0.07
Maltose	2.15±0.07	2.35±0.07
Sucrose	1.17±0.06	2.3±0.1
Xylose	1.76±0.15	2.4±0.1
Glucose	0	0
Glycerol	0	0

**Table S3. Genes responding to carbon source additions.** The STSU code, the predicted product according to the NCBI notation, the reciprocal orthologue in *S. coelicolor*, the method of detection and the graph in which the transcriptional profile is depicted are indicated. In column “name”, we indicate the name of the reciprocal orthologue in *S. coelicolor* (black letters) or *S. avermitilis* (grey letters). Columns “Glc·Gol·Mal t70.7h” and “Glc·Gol·Mal t72h” show a summary of the transcriptional response to the additions in the corresponding time sample (A:  $M_c \geq 2$  with  $p_{FDR} \geq 0.05$ ; D:  $M_c \leq -2$  with  $p_{FDR} \geq 0.05$ ; 0: no significant change under our criteria). We also include the  $M_c$  (differences between the  $\log_2$  transcription values respect to  $t_{70h}$ ) and  $p_{FDR}$  values for each statistical contrast. The classification of the genes has been modified from a first classification according to the COG letters assigned to each gene.

Gene	Name	<i>S.coelicolor</i> orthologue	Product	Glc·Gol·Mal t70.7h	Glc·Gol·Mal t72h	$M_c$ Glc t70.7h	$p_{FDR}$ Glc t70.7h	$M_c$ Gol t70.7h	$p_{FDR}$ Gol t70.7h	$M_c$ Mal t70.7h	$p_{FDR}$ Mal t70.7h	Detection method	Graph
<b>CARBOHYDRATE TRANSPORT AND METABOLISM</b>													
STSU_00740		SCO0855	GCN5-like N-acetyltransferase	0	A00	0.74	0.0596	-0.28	0.7523	0.51	0.6764	M	
STSU_02390	<i>sdhC2</i>	SCO0924	cytochrome b subunit	D00	D00	-2.85	0.0018	-1.75	0.0760	-0.82	0.9545	L	S3.10
STSU_03549	<i>gap2</i>	SCO7040	glyceraldehyde-3-phosphate dehydrogenase	D00	D00	-3.36	0.0001	0.41	0.8718	-1.49	0.2993	LM	S3.9
STSU_03729		NA	glycosyltransferase	DD0	DD0	-2.67	0.0023	-1.92	0.0357	0.03	0.9985	L	
STSU_04466		SCO6710	glycosyl hydrolase	A0A	0	1.35	0.0066	0.05	0.9820	3.61	0.0000	L	
STSU_04491	<i>xylA</i>	SCO1169	xylose isomerase	A00	A00	2.81	0.0000	-0.46	0.5746	0.55	0.8461	L	S3.5
STSU_04773		SCO6573	myo-inositol-1-phosphate synthase	A0A	0	3.59	0.0000	-0.01	0.9974	3.79	0.0000	M	
STSU_04793		SCO6569	ABC transporter substrate-binding protein	A0A	0	4.60	0.0000	-0.42	0.7406	5.78	0.0000	M	S3.6
STSU_04798		SCO6568	ABC transporter permease	A0A	0	4.85	0.0000	-0.34	0.8630	6.08	0.0000	M	S3.6
STSU_05993	<i>cysE</i>	SCO6103	GCN5-related N-acetyltransferase	D00	D00	-1.57	0.0003	0.21	0.8789	-0.59	0.6322	M	
STSU_06308	<i>xylF</i>	SCO6009	ABC transporter solute-binding protein	DD0	DD0	-1.24	0.0003	-1.52	0.0000	0.62	0.3026	M	S3.4
STSU_06328		SCO6005	ABC transporter solute-binding protein	0	DD0	-0.83	0.4220	-1.46	0.0651	-0.18	0.9985	M	
STSU_10781	<i>dasA</i>	SCO5232	sugar transporter sugar binding protein	D00	DD0	-2.32	0.0003	-0.81	0.3233	-1.24	0.2111	L	S3.4
STSU_11500	<i>glpX</i>	SCO5047	fructose 1,6-bisphosphatase II	D00	D00	-2.67	0.0003	0.31	0.8951	-1.10	0.5268	LM	S3.9
STSU_12200	<i>pck</i>	SCO4979	phosphoenolpyruvate carboxykinase	D00	D00	-3.19	0.0016	0.56	0.8547	-1.62	0.4557	L	S3.9
STSU_12470	<i>deoC</i>	SCO4914	deoxyribose-phosphate aldolase	AAA	DA0	1.32	0.0003	1.91	0.0000	1.14	0.0089	M	S3.8
STSU_19325	<i>glgA1</i>	SCO4204	D-inositol-3-phosphate glycosyltransferase	0A0	0A0	0.13	0.8890	2.01	0.0000	0.36	0.5897	LM	
STSU_19660	<i>msiK</i>	SCO4240	ABC transporter ATP-binding protein	D00	DD0	-1.60	0.0001	-0.46	0.4056	-0.65	0.4037	M	S3.4
STSU_21456		NA	polysaccharide deacetylase	0A0	0A0	-0.42	0.5906	2.61	0.0000	0.20	0.9985	L	
STSU_21751	<i>ppc</i>	SCO3127	phosphoenolpyruvate carboxylase	A00	A00	1.83	0.0000	-0.63	0.0966	-0.12	0.9985	M	S3.9
STSU_21963		SCO3097	Transglycosylase-like domain protein	A00	A00	2.46	0.0186	0.62	0.8381	1.51	0.5916	LM	
STSU_23336		NA	phosphotransferase system IIC component	D00	DD0	-2.57	0.0000	-0.64	0.4936	-0.98	0.4255	LM	S3.4
STSU_23777		SCO2754	xylose isomerase	A00	A00	3.22	0.0029	-0.83	0.7373	0.02	0.9985	L	S3.5/S3.7
STSU_24103	<i>bglA2</i>	SCO2661	sugar hydrolase	0D0	DDD	-0.28	0.4719	-0.97	0.0002	-0.39	0.5692	M	S3.9
STSU_27466	<i>pgk</i>	SCO1946	phosphoglycerate kinase	AD0	A00	0.99	0.0000	-0.70	0.0000	-0.18	0.8720	M	S3.8
STSU_27726	<i>ectA</i>	SCO1864	L-2,4-diaminobutyric acid acetyltransferase	A0A	0	1.68	0.0028	-0.97	0.1257	2.08	0.0020	LM	
STSU_28235		SCO1777	glycosyl hydrolase	D00	D00	-2.09	0.0018	-0.48	0.7618	-0.77	0.8494	L	
STSU_28630	<i>idnK</i>	SCO1679	gluconate kinase	A00	A00	2.14	0.0000	0.18	0.8933	0.38	0.9395	L	S3.8
STSU_28747	<i>glpD1</i>	SCO1661	glycerol-3-phosphate dehydrogenase	DA0	0A0	-1.06	0.0050	3.91	0.0000	-0.46	0.8108	LM	S3.2
STSU_28752	<i>glpK</i>	SCO1660	glycerol kinase	DA0	DA0	-1.99	0.0000	3.69	0.0000	-0.43	0.8720	LM	S3.2
STSU_28757	<i>glpF</i>	SCO1659	glycerol uptake facilitator protein	0A0	0A0	-1.47	0.0773	4.08	0.0000	-0.16	0.9985	LM	S3.2
STSU_30615	<i>pfkA3</i>	SCO1214	6-phosphofructokinase	A00	A00	2.78	0.0000	0.60	0.2746	0.47	0.8739	LM	S3.8
<b>ENERGY PRODUCTION AND CONVERSION</b>													

STSU_02380	<b>sdhB</b>	SCO0922	succinate dehydrogenase/fumarate reductase iron-sulfur subunit	D00	D00	-2.94	0.0012	-1.40	0.1878	-0.81	0.9545	L	S3.10
STSU_02385	<b>sdhA</b>	SCO0923	succinate dehydrogenase flavoprotein subunit	D00	D00	-2.90	0.0017	-1.70	0.0921	-0.72	0.9985	L	S3.10
STSU_05768		SCO6170	dehydrogenase	0A0	D00	0.12	0.9973	2.03	0.0374	1.29	0.6478	L	
STSU_09934	<b>ackA</b>	SCO5424	acetate kinase A/propionate kinase 2	A00	AA0	1.14	0.0159	0.47	0.5625	0.59	0.7623	M	
STSU_11525	<b>fumC</b>	SCO5042	fumarate hydratase	0A0	0	0.15	0.9799	2.52	0.0000	0.06	0.9985	L	S3.10
STSU_13938	<b>nuoM</b>	SCO4574	NADH:ubiquinone oxidoreductase subunit M	0D0	DD0	-0.99	0.0657	-1.32	0.0117	-0.98	0.2650	M	S3.27
STSU_13943	<b>nuoL</b>	SCO4573	NADH:ubiquinone oxidoreductase subunit L	DD0	DD0	-1.12	0.0133	-1.31	0.0038	-0.97	0.1562	M	S3.27
STSU_13953	<b>nuoJ</b>	SCO4571	NADH:ubiquinone oxidoreductase subunit J	0D0	DD0	-1.20	0.0850	-1.63	0.0142	-1.19	0.3169	M	S3.27
STSU_13958	<b>nuoI</b>	SCO4570	NADH dehydrogenase subunit I	0D0	DD0	-1.14	0.0926	-1.40	0.0367	-1.23	0.2561	M	S3.27
STSU_13973	<b>nuoG</b>	SCO4568	NADH dehydrogenase subunit G, partial	0D0	DD0	-1.23	0.0859	-2.16	0.0014	-1.23	0.3093	LM	S3.27
STSU_13978	<b>nuoF</b>	SCO4567	NADH dehydrogenase I chain F	DDD	DD0	-1.30	0.0104	-2.30	0.0000	-1.39	0.0435	LM	S3.27
STSU_13983	<b>nuoE</b>	SCO4566	NADH dehydrogenase subunit E	DDD	DD0	-1.44	0.0022	-2.09	0.0000	-1.40	0.0202	LM	S3.27
STSU_13988	<b>nuoD</b>	SCO4565	NADH dehydrogenase subunit D	DDD	DD0	-1.59	0.0004	-1.88	0.0000	-1.40	0.0101	M	S3.27
STSU_13993	<b>nuoC</b>	SCO4564	NADH dehydrogenase subunit C	DDD	DD0	-1.58	0.0002	-1.70	0.0001	-1.37	0.0073	M	S3.27
STSU_13998	<b>nuoB</b>	SCO4563	NADH dehydrogenase subunit B	DD0	DD0	-1.38	0.0013	-1.28	0.0028	-1.13	0.0510	M	S3.27
STSU_22954	<b>malS4</b>	SCO2951	malate oxidoreductase	D00	D00	-2.23	0.0000	-0.19	0.8459	-0.31	0.9332	LM	S3.9
STSU_25904	<b>nadE</b>	SCO2238	NH(3)-dependent NAD(+) synthetase	AAA	A0A	0.71	0.0009	0.74	0.0005	0.89	0.0004	M	S3.27
<b>LIPID TRANSPORT AND METABOLISM</b>													
STSU_05528	<b>macs1</b>	SCO6195	acetyl-CoA synthetase	D00	D00	-2.64	0.0110	-2.16	0.0510	-1.00	0.9315	L	
STSU_06268	<b>fadA8</b>	SCO6027	acetyl-CoA acetyltransferase	DD0	DD0	-2.49	0.0000	-2.06	0.0004	-0.56	0.9285	M	
STSU_08984	<b>accB</b>	SCO5535	carboxyl transferase	0A0	AA0	-0.02	0.9994	3.58	0.0000	-0.04	0.9985	LM	S3.11
STSU_09964	<b>icmA</b>	SCO5415	methylmalonyl-CoA mutase, large subunit	0D0	0D0	-0.99	0.2635	-1.81	0.0137	-0.72	0.9285	M	
STSU_12005		NA	esterase	0A0	0	-0.14	0.9751	2.96	0.0000	-0.45	0.9285	LM	
STSU_12365	<b>echA9</b>	SCO4930	enoyl-CoA hydratase	AD0	0	1.56	0.0007	-1.23	0.0075	1.00	0.1368	M	
STSU_13150		SCO4746	lipase	A00	AA0	0.84	0.0000	0.31	0.1374	0.28	0.5307	M	
STSU_15864		NA	4'-phosphopantetheinyl transferase	D00	D00	-0.85	0.0011	-0.51	0.0644	-0.10	0.9985	M	
STSU_17117	<b>fadE24</b>	SCO3800	acyl-CoA dehydrogenase	0D0	DD0	-0.96	0.0759	-2.81	0.0000	0.36	0.9985	LM	
STSU_18108	<b>fadD9</b>	SCO4006	long-chain-fatty-acid-CoA ligase	DD0	DD0	-2.56	0.0000	-1.31	0.0159	-1.20	0.1306	LM	
STSU_21998	<b>cfa</b>	SCO3091	cyclopropane-fatty-acyl-phospholipid synthase	AA0	0A0	0.83	0.0431	2.53	0.0000	0.11	0.9985	L	
STSU_23711	<b>acdB/acdH2</b>	SCO2774	acyl-CoA dehydrogenase	DD0	DDD	-2.99	0.0000	-2.66	0.0000	-1.44	0.0753	M	
STSU_25107	<b>fabH</b>	SCO2388	3-oxoacyl-(acyl carrier protein) synthase III	0A0	AA0	0.30	0.9684	2.59	0.0046	0.47	0.9985	L	S3.11
STSU_30270	<b>fabG3</b>	SCO1346	3-oxoacyl-ACP reductase	DD0	DD0	-2.35	0.0000	-1.40	0.0045	-1.11	0.1202	LM	S3.12
STSU_30915	<b>pcaI</b>	SCO6703	3-oxoacid CoA-transferase subunit A	DD0	DD0	-3.03	0.0000	-1.61	0.0068	-0.87	0.5692	LM	
<b>AMINO ACID TRANSPORT AND METABOLISM</b>													
STSU_01830		NA	O-acetylhomoserine aminocarboxypropyltransferase	0A0	0A0	-1.54	0.0686	4.17	0.0000	-0.37	0.9985	L	S3.25
STSU_01835		NA	homoserine O-acetyltransferase	0A0	0A0	-1.24	0.1817	3.73	0.0000	-0.19	0.9985	L	S3.25
STSU_03574	<b>ssuC6</b>	SCO7544	taurine ABC transporter permease	0A0	AA0	-0.04	0.9973	5.24	0.0000	-0.37	0.9985	LM	S3.16
STSU_04191		SCO6774	G-D-S-L family lipolytic protein	0A0	0	-0.32	0.7812	2.15	0.0000	-0.15	0.9985	LM	
STSU_04978	<b>dppA2</b>	SCO6486	peptidase M55 D-aminopeptidase	D00	DD0	-0.97	0.0000	-0.25	0.2427	-0.27	0.5220	M	
STSU_08043	<b>gluC</b>	SCO5775	glutamate ABC transporter permease	0	DD0	-1.72	0.0977	-0.59	0.8281	-0.78	0.9985	M	S3.13
STSU_08048	<b>gluD</b>	SCO5774	glutamate ABC transporter permease	0	DD0	-1.48	0.1364	-0.65	0.7643	-0.92	0.9115	M	S3.13
STSU_08058	<b>cdo1</b>	SCO5772	cysteine dioxygenase	0A0	AA0	-0.13	0.9901	4.89	0.0000	-0.47	0.9985	LM	S3.23
STSU_08534		SCO5657	aldehyde dehydrogenase	DD0	DD0	-2.71	0.0000	-0.87	0.0174	-0.66	0.3040	LM	

STSU_09154	<i>serA</i>	SCO5515	D-3-phosphoglycerate dehydrogenase	A00	A00	3.01	0.0000	0.16	0.9219	0.41	0.9455	LM	S3.21
STSU_09304	<i>oppF1</i>	SCO5480	ABC transporter ATP-binding protein	D00	D00	-2.25	0.0221	-0.70	0.7636	-0.82	0.9891	L	S3.40
STSU_09309	<i>oppD1</i>	SCO5479	oligopeptide ABC transporter ATP-binding protein	D00	D00	-2.17	0.0260	-1.29	0.3025	-1.07	0.8739	L	S3.40
STSU_09314	<i>oppB1</i>	SCO5478	oligopeptide transport system integral membrane protein	D00	D00	-2.72	0.0291	-1.61	0.3233	-0.99	0.9985	L	S3.40
STSU_09319	<i>oppA1</i>	SCO5477	oligopeptide-binding lipoprotein	D00	D00	-2.84	0.0236	-1.81	0.2382	-1.36	0.8739	L	S3.40
STSU_09324	<i>oppC1</i>	SCO5476	ABC transporter permease	D00	DD0	-2.61	0.0261	-1.52	0.3233	-1.00	0.9824	L	S3.40
STSU_10219	<i>hemK</i>	SCO5361	N5-glutamine S-adenosyl-L-methionine-dependent methyltransferase	AA0	AA0	1.31	0.0001	2.09	0.0000	0.37	0.8311	L	
STSU_11330	<i>bldKE</i>	SCO5116	peptide ABC transporter	0	D00	-1.32	0.0859	0.15	0.9590	-0.04	0.9985	M	S3.39
STSU_11345	<i>bldKB</i>	SCO5113	BldKB-like transporter extracellular solute-binding protein	0	DD0	-1.45	0.0668	-0.88	0.4292	-0.60	0.9985	M	S3.39
STSU_11350	<i>bldKA</i>	SCO5112	BldKA-like ABC transporter	0	DD0	-1.54	0.0768	-0.86	0.5184	-0.69	0.9941	M	S3.39
STSU_13310	<i>map</i>	SCO4724	methionine aminopeptidase	AA0	AA0	0.72	0.0010	0.65	0.0030	0.06	0.9985	M	
STSU_15904	<i>asd2</i>	SCO3614	aspartate-semialdehyde dehydrogenase	A00	A00	2.45	0.0000	-0.25	0.8810	1.18	0.0952	LM	S3.18
STSU_15909	<i>ask</i>	SCO3615	aspartate kinase	A00	A00	1.70	0.0000	-0.16	0.8650	0.78	0.0531	M	S3.18
STSU_16128	<i>purA</i>	SCO3629	adenylosuccinate synthase	A00	A00	0.51	0.0024	-0.28	0.1422	-0.05	0.9985	M	
STSU_22610	<i>cdo2</i>	SCO3035	cysteine dioxygenase	0A0	AA0	0.23	0.9544	3.88	0.0000	0.15	0.9985	L	S3.23
STSU_22794	<i>gdhD</i>	SCO2999	NAD-glutamate dehydrogenase	D00	D00	-2.83	0.0001	-0.46	0.7852	-0.23	0.9985	L	S3.13
STSU_23266	<i>cysM</i>	SCO2910	cysteine synthase	0A0	AA0	-0.71	0.1583	1.92	0.0000	-0.30	0.9985	M	S3.22/S3.23
STSU_23515	<i>gltKB1</i>	SCO2830	amino acid ABC transporter permease	AD0	0	1.78	0.0007	-2.06	0.0001	1.29	0.0753	LM	
STSU_26949	<i>hisC1</i>	SCO2053	histidinol-phosphate aminotransferase	AA0	AA0	0.36	0.0324	0.46	0.0064	0.16	0.9394	M	S3.19
STSU_26969	<i>hisA</i>	SCO2050	phosphoribosyl isomerase A	0	A00	0.23	0.5520	0.26	0.4891	-0.04	0.9985	M	S3.19
STSU_27064	<i>gltB</i>	SCO2026	Glutamate synthase (ferredoxin)	A00	A00	4.63	0.0000	-0.34	0.7465	0.81	0.3511	LM	S3.13
STSU_27069	<i>gltD</i>	SCO2025	glutamate synthase subunit beta	A00	AA0	5.57	0.0000	0.33	0.7792	0.89	0.2690	LM	S3.13
STSU_27721	<i>ectB</i>	SCO1865	diaminobutyrate--2-oxoglutarate aminotransferase	A0A	D00	1.33	0.0198	-0.83	0.2361	1.70	0.0190	M	
STSU_28767	<i>metH</i>	SCO1657	5-methyltetrahydrofolate:homocysteine S-methyltransferase	0A0	AA0	0.09	0.9866	0.90	0.0126	0.28	0.9985	M	S3.25
STSU_28932	<i>opuAA</i>	SCO1621	glycine betaine/L-proline ABC transporter ATP-binding protein	ADA	A00	3.00	0.0000	-1.26	0.0325	1.56	0.0388	LM	
STSU_28937	<i>opuABC</i>	SCO1620	glycine betaine ABC transporter substrate-binding and permease component	ADA	A00	3.10	0.0000	-1.22	0.0360	1.58	0.0309	LM	
STSU_28987		NA	oligopeptide porter, partial	0A0	AA0	-0.52	0.5244	2.79	0.0000	-0.63	0.8148	LM	
STSU_29022		SCO1611	short chain dehydrogenase	D00	D00	-2.06	0.0053	-1.48	0.0625	-0.59	0.9985	L	
STSU_29177	<i>argG</i>	SCO7036	argininosuccinate synthase	D00	A00	-2.32	0.0005	0.17	0.9408	0.16	0.9985	L	
STSU_29237	<i>metQ1</i>	SCO1557	ABC transporter substrate-binding protein	0A0	AAA	1.47	0.1536	3.89	0.0000	0.71	0.9985	LM	
STSU_30575		SCO1230	tripeptidyl aminopeptidase	D00	DDD	-1.69	0.0040	-1.16	0.0681	-1.09	0.2993	M	
STSU_33105	<i>tdh</i>	SCO6799	L-threonine 3-dehydrogenase	A00	A0A	2.39	0.0000	-0.15	0.9396	0.01	0.9985	LM	S3.21
STSU_33110	<i>kbl</i>	SCO6800	2-amino-3-ketobutyrate coenzyme A ligase	A00	A0A	2.16	0.0001	-0.89	0.1439	-0.28	0.9985	LM	S3.21
<b>NUCLEOTIDE TRANSPORT AND METABOLISM</b>													
STSU_04923		SCO6510	UbiE family methyltransferase	A00	A00	2.52	0.0000	-0.03	0.9906	1.01	0.2155	L	
STSU_06613		SCO5864	dUTPase	AA0	0	0.79	0.0042	1.27	0.0000	0.04	0.9985	M	
STSU_12420	<i>deoD</i>	SCO4917	purine nucleoside phosphorylase	AA0	D00	1.42	0.0021	2.10	0.0000	1.20	0.0532	LM	S3.29
STSU_12845	<i>purH</i>	SCO4814	bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/inosine monophosphate cyclohydrolase	DD0	A00	-1.20	0.0146	-1.90	0.0002	-0.63	0.7325	M	S3.29
STSU_12850	<i>purN</i>	SCO4813	phosphoribosylglycinamide formyltransferase	0D0	A00	-0.82	0.2029	-2.05	0.0003	-0.19	0.9985	L	S3.29
STSU_12965	<i>guaA</i>	SCO4785	GMP synthetase	A00	AA0	0.34	0.0198	0.26	0.1096	0.25	0.3554	M	
STSU_13315	<i>adk</i>	SCO4723	adenylate kinase	A00	A00	1.85	0.0000	0.44	0.3852	0.37	0.9115	M	S3.30

STSU_29606	<i>pyrB</i>	SCO1487	aspartate carbamoyltransferase catalytic subunit	A00	A00	4.68	0.0002	-1.10	0.6231	0.23	0.9985	L	S3.28
STSU_29611	<i>pyrC</i>	SCO1486	dihydroorotase	A00	A00	4.62	0.0000	-0.90	0.6767	0.32	0.9985	L	S3.28
STSU_29621	<i>pyrAa</i>	SCO1484	carbamoyl-phosphate synthase small subunit	A00	A00	3.37	0.0000	-0.44	0.7838	0.27	0.9985	L	S3.28
STSU_29626	<i>pyrA</i>	SCO1483	carbamoyl phosphate synthase large subunit	A00	A00	3.70	0.0000	-0.02	0.9937	0.55	0.9285	LM	S3.28
STSU_29631	<i>pyrD</i>	SCO1482	dihydroorotate dehydrogenase 2	A00	A00	3.69	0.0000	0.32	0.9156	0.92	0.8739	L	S3.28
STSU_29636	<i>pyrF</i>	SCO1481	orotidine 5'-phosphate decarboxylase	A00	AA0	3.47	0.0000	0.27	0.8837	0.87	0.5081	LM	S3.28
STSU_29646	<i>gmk</i>	SCO1479	guanylate kinase	0	A00	-0.16	0.5906	-0.06	0.9209	0.03	0.9985	M	
STSU_30071	<i>mpg3</i>	SCO1388	Nucleotidyl transferase	AD0	A00	2.80	0.0000	-1.29	0.0005	0.76	0.1879	LM	
<b>INORGANIC ION TRANSPORT AND METABOLISM</b>													
STSU_03559		SCO7547	sulfatase	0A0	AA0	0.22	0.9751	3.83	0.0000	0.02	0.9985	L	S3.16
STSU_03564	<i>ssuA2</i>	SCO7546	aliphatic sulfonates family ABC transporter periplasmicligand-binding protein	0A0	AA0	0.19	0.9843	4.22	0.0000	-0.27	0.9985	L	S3.16
STSU_03569	<i>ssuB4</i>	SCO7545	ABC transporter	0A0	AA0	-0.01	0.9995	4.50	0.0000	-0.24	0.9985	L	S3.16
STSU_04291		SCO6751	cation efflux protein	0A0	AA0	-0.75	0.0625	2.52	0.0000	-0.46	0.8266	LM	
STSU_05418	<i>fepD</i>	SCO1787	siderophore ABC transporter, FecCD family protein	0	0	0.55	0.9153	-0.98	0.6952	0.79	0.9985	M	
STSU_05998	<i>sirA</i>	SCO6102	putative nitrite/sulfite reductase	DA0	0	-0.75	0.0172	1.46	0.0000	-0.29	0.9455	M	S3.15
STSU_06008	<i>cysH</i>	SCO6100	phosphoadenosine phosphosulfate reductase	DA0	AA0	-0.86	0.0048	2.22	0.0000	-0.31	0.9227	LM	S3.15
STSU_06013	<i>cysC</i>	SCO6099	adenylyl-sulfate kinase	0A0	AA0	-0.68	0.1031	2.17	0.0000	-0.11	0.9985	LM	S3.15
STSU_06018	<i>cysD</i>	SCO6098	sulfate adenylyltransferase subunit 2	0A0	AA0	-0.47	0.3814	2.21	0.0000	-0.02	0.9985	LM	S3.15
STSU_06023	<i>cysN</i>	SCO6097	sulfate adenylyltransferase subunit 1	0A0	AA0	-0.41	0.7120	2.32	0.0000	0.02	0.9985	L	S3.15
STSU_06028	<i>ssuA3</i>	SCO6096	aliphatic sulfonate ABC transporter substrate-binding protein	0A0	AAA	-0.07	0.9973	3.48	0.0000	0.03	0.9985	LM	S3.15
STSU_06033	<i>ssuB3</i>	SCO6095	ABC transporter-like protein	0A0	AA0	-0.21	0.9734	2.56	0.0001	-0.25	0.9985	L	S3.15
STSU_14108		SCO4498	sodium:dicarboxylate symporter	0A0	DD0	0.41	0.7547	3.15	0.0000	0.09	0.9985	L	
STSU_16497		SCO3698	arsenite efflux transporter	0A0	AA0	0.57	0.4576	2.66	0.0000	0.34	0.9985	L	
STSU_16912		SCO3790	hypothetical protein	A00	A00	2.04	0.0121	1.46	0.1048	1.38	0.3898	L	S3.16
STSU_19400	<i>phoU</i>	SCO4228	phosphate uptake regulator PhoU	AA0	A00	2.08	0.0000	0.90	0.0477	0.44	0.9089	L	S3.16
STSU_33300		SCO7481	tellurium resistance protein	DD0	D00	-0.76	0.0083	-0.62	0.0384	-0.18	0.9985	M	
<b>COENZYME TRANSPORT AND METABOLISM</b>													
STSU_00060		NA	monooxygenase	0A0	0A0	-0.08	0.9774	5.97	0.0000	-0.39	0.6262	LM	
STSU_03479		NA	monooxygenase FAD-binding protein	D00	DD0	-2.01	0.0129	-1.09	0.2948	-1.06	0.7071	LM	
STSU_05133		SCO6423	lipoate-protein ligase A	0A0	0A0	-0.21	0.5240	3.43	0.0000	-0.31	0.5771	LM	
STSU_06043		SCO6093	cobalamin (vitamin B12) biosynthesis CbiX protein	0A0	AA0	-0.41	0.9038	3.13	0.0002	-0.41	0.9985	L	S3.15
STSU_06233		SCO6041	protoporphyrinogen oxidase	0	AA0	0.08	0.9606	0.31	0.3101	0.51	0.1418	M	
STSU_21526		SCO2849	F420-dependent oxidoreductase	0A0	0A0	-0.28	0.6070	3.79	0.0000	-0.15	0.9985	LM	
STSU_22600		SCO3037	F420-0--gamma-glutamyl ligase	0A0	AA0	0.19	0.6979	1.42	0.0000	0.13	0.9985	M	
STSU_22605	<i>cofD</i>	SCO3036	LPPG:FO 2-phospho-L-lactate transferase	0A0	A00	0.37	0.8425	2.13	0.0008	-0.11	0.9985	L	
STSU_23530		NA	LuxAB-like protein (oxygenase)	0A0	D00	-0.16	0.9316	1.73	0.0000	0.18	0.9985	M	
STSU_24253	<i>bioY</i>	SCO2630	biotin synthase	0A0	0	0.14	0.9973	2.17	0.0467	-0.06	0.9985	L	
STSU_26209	<i>lipA</i>	SCO2194	lipoyl synthase	0A0	0	0.56	0.2603	1.70	0.0001	0.00	0.9993	M	
STSU_28450		SCO4419	pyridoxamine 5'-phosphate oxidase-like FMN-binding protein	0A0	0A0	-0.07	0.9950	2.39	0.0000	-0.19	0.9985	LM	
STSU_28707		SCO1669	putative F420-dependent oxidoreductase	DD0	DD0	-1.47	0.0034	-1.82	0.0003	-0.82	0.4304	M	
STSU_30400		SCO1304	CoA-binding domain-containing protein	DA0	DA0	-1.02	0.0258	2.97	0.0000	-0.40	0.9575	LM	
<b>OTHER TRANSPORTERS AND MEMBRANE PROTEINS</b>													
STSU_03989		NA	ABC transporter permease	D00	D00	-2.32	0.0000	-0.32	0.8412	-1.17	0.1478	L	

STSU_04908		SCO6524	integral membrane protein	0A0	AA0	0.17	0.8721	1.46	0.0000	0.45	0.6122	M	
STSU_05408		NA	ABC transporter	0	0	-0.20	0.9958	-0.71	0.8022	0.49	0.9985	M	
STSU_06038	<b>ssuC3</b>	SCO6094	ABC transporter permease	0A0	AA0	-0.22	0.9563	3.08	0.0000	-0.24	0.9985	LM	S3.15
STSU_08564	<b>thiQ</b>	SCO5648	ABC transporter-like protein	A00	0	1.19	0.0024	0.19	0.8841	-0.08	0.9985	M	
STSU_09734		NA	MFS transporter	0A0	A00	-0.02	0.9973	3.03	0.0000	0.05	0.9985	L	
STSU_12520		SCO4896	major facilitator superfamily MFS_1	AA0	AA0	3.47	0.0000	2.68	0.0002	1.71	0.0854	M	
STSU_12555		SCO4887	ABC transporter permease	A00	D00	1.21	0.0252	0.83	0.1876	0.66	0.7858	M	
STSU_17878		SCO3958	ABC transporter ATP-binding protein	A0A	0	2.15	0.0000	-0.38	0.4275	0.90	0.0407	LM	
STSU_20067	<b>cmiR1</b>	SCO7526	major facilitator superfamily MFS_1	0A0	AA0	0.28	0.5728	6.24	0.0000	0.33	0.8827	LM	
STSU_20202	<b>pbuG1</b>	SCO4334	permease	0D0	A00	-0.99	0.3722	-2.20	0.0085	-0.84	0.9205	L	
STSU_20232		SCO4337	integral membrane efflux protein	A00	AA0	2.21	0.0000	0.52	0.4345	0.84	0.2902	L	
STSU_21222		SCO3206	EmrB/QacA subfamily drug resistance transporter	0A0	0A0	0.67	0.4738	5.43	0.0000	0.18	0.9985	LM	
STSU_21546		SCO3166	transmembrane transport protein	A00	A00	2.20	0.0120	0.82	0.6107	0.66	0.9985	L	
STSU_23751		SCO2763	ABC transporter-like protein	0A0	0	-0.34	0.8810	2.01	0.0017	0.32	0.9985	L	
STSU_27229	<b>livK3</b>	SCO2008	ABC transporter substrate-binding protein	D00	DD0	-1.80	0.0242	-1.09	0.2827	-0.68	0.9847	M	
STSU_27681		NA	transport associated protein, partial	DD0	D00	-1.52	0.0000	-0.70	0.0177	-0.13	0.9985	M	
STSU_28056		SCO1812	integral membrane transporter	AA0	A00	3.23	0.0001	2.37	0.0028	-0.39	0.9985	M	
STSU_28967		NA	extracellular solute-binding protein	0A0	AA0	-0.45	0.8778	3.30	0.0001	-0.74	0.9545	L	
STSU_28972		SCO6113	ABC transporter permease	0A0	AA0	-0.55	0.5035	2.94	0.0000	-0.72	0.6894	LM	
STSU_28977		NA	binding-protein-dependent transport system inner membrane prot	0A0	AA0	-0.56	0.4994	2.99	0.0000	-0.58	0.8800	LM	
STSU_28982		NA	ABC transporter ATP-binding protein	0A0	AA0	-0.49	0.5703	3.23	0.0000	-0.66	0.7531	LM	
STSU_28992		NA	ABC transporter related protein, partial	0A0	AA0	0.25	0.9410	2.49	0.0001	0.11	0.9985	LM	
STSU_29232		SCO1558	ABC transporter	AA0	AA0	2.07	0.0050	4.21	0.0000	0.91	0.7985	M	
<b>POSTTRANSLATIONAL MODIFICATION, PROTEIN TURNOVER, CHAPERONES</b>													
STSU_10501	<b>lon</b>	SCO5285	ATP-dependent protease La	AAA	AA0	2.30	0.0000	5.09	0.0000	1.83	0.0018	M	S3.36
STSU_12315	<b>msrA</b>	SCO4956	Peptide methionine sulfoxide reductase msrA	0A0	0A0	-0.09	0.9755	3.36	0.0000	-0.13	0.9985	LM	
STSU_14652	<b>clpC2</b>	SCO3373	ATPase AAA-2 domain-containing protein	A00	D00	0.45	0.0126	0.24	0.3118	0.11	0.9985	M	
STSU_17978	<b>pepD3</b>	SCO3977	serine protease	DD0	DD0	-1.44	0.0000	-1.13	0.0003	-0.80	0.0548	M	
STSU_19922	<b>groEL</b>	SCO4296	chaperonin GroEL	D00	DDD	-1.69	0.0000	0.28	0.6954	-0.77	0.1086	M	S3.36
STSU_24323	<b>clpP2</b>	SCO2618	ATP-dependent Clp protease proteolytic subunit	0A0	DD0	-0.42	0.1112	0.72	0.0033	-0.37	0.5542	M	
STSU_24417	<b>rns</b>	SCO2599	ribonuclease E	A00	A00	2.09	0.0000	0.05	0.9786	1.02	0.1202	L	S3.35
STSU_28832	<b>pcrA</b>	SCO1643	proteasome subunit alpha	0	DD0	0.17	0.7006	-0.41	0.0964	-0.11	0.9985	M	S3.37
STSU_33245		NA	M6 family metalloprotease domain-containing protein	0	0	-0.21	0.9841	0.56	0.7663	-0.64	0.9985	M	
<b>REPLICATION, RECOMBINATION AND REPAIR</b>													
STSU_18582		SCO4096	ATP-dependent RNA helicase	A00	A00	3.04	0.0000	-0.57	0.3087	0.56	0.7316	LM	S3.35
STSU_26629	<b>nfo</b>	SCO2111	apurinic endonuclease Apn1	0A0	AA0	0.70	0.0539	0.90	0.0111	0.57	0.4449	M	
<b>TRANSCRIPTION</b>													
STSU_02445	<b>sig56</b>	SCO0942	RNA polymerase sigma factor SigL	D00	D00	-3.13	0.0065	-0.55	0.8846	-1.14	0.9285	L	
STSU_03579		NA	CRP family transcriptional regulator	0A0	AA0	0.11	0.9973	4.19	0.0000	-0.38	0.9985	L	S3.16/S3.42
STSU_03599	<b>eshA</b>	SCO7699	Crp/Fnr family transcriptional regulator	0D0	DD0	-1.80	0.0747	-2.26	0.0217	-0.56	0.9985	L	S3.42
STSU_03714		SCO2426	regulatory protein	DD0	DD0	-2.02	0.0014	-1.55	0.0152	-0.25	0.9985	LM	
STSU_03999		NA	AsnC family transcriptional regulator	D00	D00	-0.99	0.0029	0.57	0.1312	0.18	0.9985	M	
STSU_05108	<b>alkA1</b>	SCO6461	AraC family transcriptional regulator	DA0	DA0	-0.69	0.0019	0.80	0.0004	-0.32	0.6087	M	

STSU_06388		NA	putative LacI family transcriptional regulator	A00	A00	1.57	0.0000	0.33	0.5354	0.23	0.9985	M	
STSU_10009	<i>rapA1</i>	SCO5403	two-component system response regulator	AA0	AA0	0.45	0.0287	0.70	0.0005	0.24	0.8266	M	
STSU_10821	<i>rsrA</i>	SCO5217	anti-sigma factor	0A0	0A0	-0.20	0.8346	3.46	0.0000	-0.30	0.9664	LM	S3.26
STSU_10826	<i>sigR</i>	SCO5216	RNA polymerase sigma factor RpoE	0A0	0A0	-0.03	0.9973	3.03	0.0000	-0.09	0.9985	LM	S3.26
STSU_11625		SCO2481	Transcriptional regulator	0A0	0A0	0.22	0.5712	2.96	0.0000	-0.05	0.9985	LM	
STSU_12236f		SCO4969	regulatory protein	A00	A00	3.99	0.0000	-0.71	0.3884	1.07	0.3089	M	
STSU_13560	<i>rpoC</i>	SCO4655	DNA-directed RNA polymerase subunit beta'	0	A00	0.09	0.9799	-0.33	0.5138	-0.26	0.9985	M	S3.31
STSU_14253		NA	AraC family transcriptional regulator	0A0	0	-0.13	0.9477	2.84	0.0000	0.09	0.9985	LM	
STSU_14448	<i>bldN</i>	SCO3323	ECF subfamily RNA polymerase sigma-24 subunit	DD0	D00	-2.22	0.0055	-1.70	0.0459	-1.16	0.6030	L	S3.38
STSU_14997		NA	RNA polymerase ECF-subfamily sigma factor	DD0	DDD	-1.02	0.0055	-1.14	0.0022	-0.75	0.2058	M	
STSU_15654	<i>wblA</i>	SCO3579	regulatory protein	D00	D00	-2.14	0.0000	0.36	0.6055	-0.52	0.6626	LM	S3.41
STSU_15899	<i>sig40</i>	SCO3613	RNA polymerase, sigma-24 subunit, ECF subfamily protein	0	D00	-1.06	0.0685	0.54	0.5763	-0.21	0.9985	M	
STSU_16293	<i>hspR</i>	SCO3668	transcriptional regulator, MerR family protein	AAA	0	1.13	0.0001	1.26	0.0000	1.17	0.0002	M	S3.36
STSU_17474	<i>sig58</i>	SCO0803	sigma factor	AD0	A00	3.36	0.0000	-0.90	0.0468	1.01	0.1016	LM	
STSU_19270		SCO4198	helix-turn-helix domain-containing protein	A00	AA0	1.80	0.0000	0.47	0.2951	0.73	0.1796	M	
STSU_21217		SCO3207	regulatory protein TetR	0A0	0A0	0.26	0.8111	3.55	0.0000	-0.02	0.9985	LM	
STSU_21726		SCO3134	two-component system response regulator	0	D00	0.33	0.6645	-0.50	0.3728	0.04	0.9985	M	
STSU_23771		SCO2757	LysR family transcriptional regulator	A00	A00	2.37	0.0000	-0.26	0.8587	0.07	0.9985	L	S3.7
STSU_23786		SCO5228	MarR family transcriptional regulator	A00	A00	4.67	0.0000	-0.30	0.8635	0.73	0.7481	LM	S3.7
STSU_24036		NA	IclR family transcriptional regulator	A0A	A0A	1.94	0.0000	-0.68	0.1127	1.54	0.0008	M	
STSU_24896	<i>hrdA</i>	SCO2465	RNA polymerase sigma factor	DD0	DD0	-0.87	0.0302	-1.12	0.0055	-0.86	0.1556	M	S3.38/S3.43
STSU_25664		SCO2279	bifunctional DNA primase/polymerase	AAA	AA0	0.63	0.0001	2.94	0.0000	0.44	0.0397	LM	
STSU_26129	<i>glnRll</i>	SCO2213	regulatory protein	0A0	0A0	-0.41	0.9247	3.40	0.0003	0.10	0.9985	L	S3.14
STSU_27551		SCO1926	transcriptional regulator, ArsR family protein	0A0	0	0.06	0.9973	2.34	0.0014	0.45	0.9985	L	
STSU_28051		SCO1813	GntR family transcriptional regulator	AA0	AA0	2.37	0.0000	1.46	0.0012	0.07	0.9985	L	
STSU_28230		SCO1778	regulatory protein, partial	D00	D00	-1.23	0.0000	-0.46	0.1156	-0.59	0.1200	M	
STSU_28742		NA	GntR family transcriptional regulator	0A0	0A0	0.23	0.6932	2.30	0.0000	0.12	0.9985	LM	S3.2
STSU_28762	<i>gylR</i>	SCO1658	glycerol operon regulatory protein	0A0	AA0	0.58	0.0662	3.40	0.0000	0.28	0.9545	LM	S3.2
STSU_29601	<i>pyrR</i>	SCO1488	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	A00	0	2.19	0.0003	-0.08	0.9769	0.28	0.9985	L	S3.28
STSU_30495		SCO1262	GntR family transcriptional regulator	D00	DD0	-1.47	0.0000	-0.22	0.7408	-0.66	0.1118	M	
STSU_30860	<i>sigK</i>	SCO6520	RNA polymerase sigma factor	ADA	0	2.17	0.0001	-1.28	0.0232	1.72	0.0122	L	
STSU_32415		NA	LuxR family transcriptional regulator, partial	DA0	DA0	-1.36	0.0001	1.15	0.0004	-0.39	0.8021	M	
STSU_33340		SCO0407	MerR family transcriptional regulator	0	AA0	0.29	0.4609	0.24	0.6244	0.01	0.9985	M	
<b>TRANSLATION, RIBOSOMAL STRUCTURE AND BIOGENESIS</b>													
STSU_01255		NA	peptidase C60 sortase A and B	D00	D00	-2.35	0.0038	-1.03	0.3502	-0.70	0.9782	LM	
STSU_03919		SCO0780	alcohol dehydrogenase zinc-binding domain-containing protein	0A0	0A0	-0.21	0.9450	2.54	0.0000	-0.54	0.9285	L	
STSU_06128		SCO0723	nucleoside triphosphate hydrolase domain-containing protei	0A0	AA0	0.34	0.3215	1.54	0.0000	0.36	0.6784	M	
STSU_13375	<i>rpsQ</i>	SCO4711	30S ribosomal protein S17	0	A00	0.45	0.5520	-0.91	0.0726	-0.34	0.9985	M	S3.32
STSU_13385	<i>rplP</i>	SCO4709	50S ribosomal protein L16	0	A00	0.27	0.7928	-0.79	0.0730	-0.34	0.9891	M	S3.32
STSU_13570	<i>rplL</i>	SCO4653	50S ribosomal protein L7/L12	0	A00	-0.18	0.8865	-0.61	0.1017	-0.81	0.0925	M	S3.32
STSU_13640	<i>rpmG3</i>	SCO4635	50S ribosomal protein L33	AA0	A00	1.07	0.0000	0.79	0.0002	0.36	0.3536	M	S3.32
STSU_17693	<i>rplI</i>	SCO3909	50S ribosomal protein L9	A00	AA0	0.93	0.0029	0.10	0.9254	-0.01	0.9985	M	S3.32

STSU_19450		SCO4236	TrmH family RNA methyltransferase	AA0	AA0	0.60	0.0013	0.59	0.0014	0.13	0.9985	M	
STSU_22864	<i>prfB</i>	SCO2972	peptide chain release factor 2	AAA	AAA	0.39	0.0049	0.75	0.0000	0.49	0.0033	M	S3.34
STSU_24472	<i>rplU</i>	SCO2597	50S ribosomal protein L21	A00	A00	1.47	0.0000	0.21	0.5195	0.29	0.5801	M	S3.32
STSU_28141		SCO1795	HNH endonuclease	A00	0	1.32	0.0007	-0.33	0.6752	0.38	0.9275	M	
STSU_29062	<i>rplT</i>	SCO1598	50S ribosomal protein L20	A00	A00	0.76	0.0006	-0.41	0.0823	-0.05	0.9985	M	S3.32
STSU_29641		SCO1480	integration host factor	D00	D00	-1.57	0.0001	-0.76	0.0781	-0.62	0.4853	M	
STSU_31540		SCO1101	peptidase M48 Ste24p	DA0	0	-1.07	0.0033	1.58	0.0000	0.19	0.9985	M	
STSU_32615		SCO1355	subtilisin-like serine protease	0A0	0A0	-0.27	0.8491	2.72	0.0000	0.18	0.9985	L	
<b>CELL CYCLE CONTROL AND CELL WALL</b>													
STSU_24482	<i>obg</i>	SCO2595	GTPase CgtA	AA0	AA0	1.50	0.0024	2.93	0.0000	0.28	0.9985	LM	S3.41
STSU_06353	<i>murA2</i>	SCO5998	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	A00	0	2.56	0.0000	-0.90	0.1346	1.17	0.1368	L	
<b>GENERAL FUNCTIONS</b>													
STSU_04366		SCO0501	x-prolyl-dipeptidyl aminopeptidase	DD0	DD0	-2.13	0.0005	-1.78	0.0030	-0.62	0.9089	LM	
STSU_04788		SCO6570	oxidoreductase	A0A	0	5.59	0.0000	-0.52	0.7705	6.78	0.0000	M	
STSU_09929	<i>pta</i>	SCO5425	phosphate acetyltransferase	A00	AA0	1.18	0.0102	0.60	0.3257	0.79	0.3760	M	
STSU_28650	<i>blaB4</i>	SCO0740	hydrolase	D00	D00	-2.15	0.0016	-0.60	0.6462	-0.30	0.9985	L	
STSU_29711		SCO1455	hydrolase	0A0	0	0.80	0.0949	2.23	0.0000	-0.09	0.9985	L	
STSU_04456		SCO6712	multicopper oxidase type 2	A0A	A00	3.10	0.0000	-0.31	0.6902	3.29	0.0000	M	
STSU_04783		SCO6571	Xylose isomerase domain-containing protein TIM barrel	A0A	0	4.22	0.0000	-0.15	0.9679	4.97	0.0000	M	
STSU_08063		SCO5771	Rhodanese domain-containing protein	0A0	AA0	0.45	0.4466	3.02	0.0000	-0.65	0.4713	LM	
STSU_12465		SCO4913	aldehyde dehydrogenase	AAA	D00	1.20	0.0059	1.94	0.0000	1.28	0.0262	M	
STSU_12565		SCO4884	lipoprotein	0	DD0	-0.33	0.8157	-0.09	0.9679	0.04	0.9985	M	
STSU_12740		SCO4846	ribonuclease BN	A0A	A00	2.13	0.0001	-0.55	0.5214	1.52	0.0309	L	
STSU_13240		SCO7440	alpha/beta hydrolase fold protein	0A0	AA0	0.61	0.6277	7.05	0.0000	-0.23	0.9985	LM	
STSU_17142		SCO0142	redoxin domain-containing protein	0A0	0A0	0.08	0.9973	2.43	0.0001	0.15	0.9985	L	
STSU_17903		SCO3963	Dyp-type peroxidase	0D0	A00	0.08	0.9901	-1.00	0.0060	-0.28	0.9985	M	
STSU_19085		SCO4160	hydrolase	AA0	AA0	0.47	0.0235	0.53	0.0111	0.43	0.1879	M	
STSU_21938		SCO3101	lipoprotein	D00	D00	-1.67	0.0004	-0.52	0.4496	-0.88	0.2614	M	
STSU_25352		SCO2346	HAD-superfamily hydrolase	A0A	A0A	1.91	0.0000	0.00	0.9989	1.21	0.0122	M	
STSU_30695		SCO1142	oxidoreductase	0A0	0A0	0.42	0.3483	2.88	0.0000	-0.14	0.9985	LM	
STSU_33260		SCO5324	oxidoreductase	D00	DD0	-1.38	0.0008	-0.68	0.1450	-0.84	0.1879	M	
<b>SECONDARY METABOLISM</b>													
STSU_15167		NA	beta-lactamase	0A0	0A0	-0.33	0.7071	1.59	0.0003	-0.19	0.9985	M	
STSU_05633		NA	cytochrome P450	0D0	DDD	0.56	0.2971	-1.20	0.0049	0.02	0.9985	M	
STSU_30920		NA	muconolactone Delta-isomerase	D00	D00	-2.38	0.0344	-0.90	0.7060	-0.54	0.9985	L	
STSU_30925		SCO3842	catechol 1,2-dioxygenase	DD0	D00	-2.30	0.0012	-1.53	0.0377	-0.99	0.6278	L	
<b>STRESS RESPONSE</b>													
STSU_02325	<i>trxC</i>	SCO0885	thioredoxin	AA0	0A0	1.16	0.0028	3.46	0.0000	0.42	0.8749	LM	S3.26
STSU_11585	<i>ahpC</i>	SCO5032	alkyl hydroperoxide reductase	0A0	A00	0.65	0.5652	2.81	0.0001	0.23	0.9985	L	S3.26
STSU_11590	<i>ahpD</i>	SCO5031	alkyl hydroperoxide reductase AhpD	0A0	AA0	0.53	0.5247	2.75	0.0000	0.23	0.9985	L	S3.26
STSU_17593	<i>trxA</i>	SCO3889	thioredoxin	0A0	0A0	0.01	0.9973	2.50	0.0000	-0.11	0.9985	LM	S3.26
STSU_17598	<i>trxB</i>	SCO3890	thioredoxin reductase	0A0	0A0	0.25	0.5968	3.06	0.0000	0.12	0.9985	LM	S3.26
STSU_27691	<i>frnE</i>	SCO1869	protein dithiol-disulfide isomerase	0A0	0A0	0.46	0.3428	4.80	0.0000	0.13	0.9985	LM	



STSU_27711	<b>ectD</b>	SCO1867	ectoine hydroxylase	A0A	0	1.45	0.0028	0.10	0.9607	1.59	0.0077	M
STSU_27716	<b>ectC</b>	SCO1866	L-ectoine synthase	A00	0	1.53	0.0483	-0.29	0.9116	1.95	0.0565	M
<b>HYPOTHETICAL PROTEINS</b>												
STSU_01680		SCO0882	hypothetical protein	0A0	0A0	0.15	0.9009	3.58	0.0000	-0.04	0.9985	LM
STSU_01735		NA	hypothetical protein	0	DD0	-0.53	0.3699	-0.46	0.5138	-0.65	0.5721	M
STSU_03494		NA	hypothetical protein	D00	DD0	-2.04	0.0109	-1.07	0.3060	-1.00	0.7771	L
STSU_03554		NA	hypothetical protein	0A0	AA0	0.04	0.9973	3.16	0.0000	0.11	0.9985	L S3.16
STSU_03734		NA	hypothetical protein	D00	D00	-2.23	0.0136	-1.69	0.0864	0.11	0.9985	L
STSU_03739		NA	hypothetical protein	DD0	DD0	-2.28	0.0008	-1.95	0.0040	0.03	0.9985	LM
STSU_04461		SCO6711	hypothetical protein	A0A	0	1.75	0.0034	-0.10	0.9670	4.41	0.0000	L
STSU_04556		NA	hypothetical protein STSU_4556	AAA	AA0	2.15	0.0000	0.86	0.0178	0.97	0.0435	LM
STSU_04778		SCO6572	hypothetical protein	A0A	0	3.16	0.0000	-0.11	0.9689	3.35	0.0001	M
STSU_04928		SCO6493	hypothetical protein	A00	A00	1.17	0.0012	0.44	0.3848	0.24	0.9985	M
STSU_05093		NA	hypothetical protein	0A0	0A0	-0.36	0.9190	2.82	0.0004	-0.14	0.9985	L
STSU_06003		SCO6101	hypothetical protein	DA0	AA0	-0.89	0.0083	1.88	0.0000	-0.41	0.8185	M S3.15
STSU_06123		NA	hypothetical protein	D00	DD0	-0.80	0.0001	-0.15	0.7248	-0.20	0.9010	M
STSU_06618		SCO5865	hypothetical protein STSU_6618	AA0	D00	0.73	0.0000	0.89	0.0000	0.01	0.9985	M
STSU_07233		SCO6841	hypothetical protein	0A0	0A0	0.27	0.6070	2.36	0.0000	0.03	0.9985	L
STSU_07503		NA	hypothetical protein	A00	0	3.05	0.0000	0.12	0.9493	-0.21	0.9985	LM
STSU_07508		NA	hypothetical protein	D00	D00	-0.95	0.0015	-0.42	0.2579	-0.29	0.9285	M
STSU_07743		NA	hypothetical protein	A00	A0A	0.83	0.0020	0.02	0.9884	0.56	0.1879	M
STSU_08699		SCO5590	hypothetical protein	D00	D00	-1.03	0.0004	-0.35	0.3882	-0.13	0.9985	M
STSU_08774		NA	hypothetical protein	D00	0	-0.80	0.0153	0.23	0.7668	0.34	0.9115	M
STSU_08979	<b>accE</b>	SCO5536	hypothetical protein	0A0	0A0	-0.36	0.9389	3.34	0.0002	-0.29	0.9985	L S3.11
STSU_09294		SCO5482	hypothetical protein	DD0	DD0	-1.96	0.0000	-1.67	0.0000	-0.63	0.3725	M
STSU_09739		NA	hypothetical protein	0A0	0	0.36	0.8068	2.73	0.0000	-0.82	0.5605	L
STSU_09744		SCO1044	hypothetical protein	0A0	0	-0.15	0.9715	3.49	0.0000	-0.67	0.5581	LM
STSU_10284		NA	hypothetical protein STSU_1284	D00	D00	-2.12	0.0046	-0.18	0.9465	-0.22	0.9985	L
STSU_10289		NA	hypothetical protein	D00	D00	-2.15	0.0018	-0.27	0.9108	-0.11	0.9985	L
STSU_10294		NA	hypothetical protein	D00	D00	-2.07	0.0042	-0.29	0.9102	-0.01	0.9985	L
STSU_10836		SCO5214	hypothetical protein	AA0	0A0	1.48	0.0000	2.50	0.0000	0.33	0.9275	LM
STSU_10980		SCO5191	hypothetical protein	0A0	A00	0.20	0.9799	2.58	0.0002	0.57	0.9985	L
STSU_11130		SCO5163	hypothetical protein STSU_1113	AA0	AA0	3.06	0.0000	4.15	0.0000	0.67	0.8266	M
STSU_12010		NA	hypothetical protein	0A0	0	0.03	0.9973	2.89	0.0000	-0.04	0.9985	LM
STSU_12390		SCO4924	hypothetical protein STSU_1239	A00	0	2.01	0.0061	-0.42	0.8474	-0.30	0.9985	L
STSU_12685		NA	hypothetical protein	D00	DD0	-1.31	0.0001	-0.22	0.7701	-0.69	0.1527	M
STSU_13245		SCO0239	hypothetical protein	0A0	0	0.44	0.8390	3.20	0.0000	-0.52	0.9985	L
STSU_13883		NA	hypothetical protein	DA0	DA0	-0.63	0.0243	1.93	0.0000	-0.05	0.9985	M
STSU_15037		NA	hypothetical protein	0A0	0A0	0.13	0.9747	4.88	0.0000	0.34	0.9985	LM
STSU_15719		NA	hypothetical protein	0	D00	-0.73	0.1144	-0.68	0.1700	0.09	0.9985	M
STSU_15739		NA	hypothetical protein	0A0	0A0	0.30	0.7732	2.61	0.0000	0.07	0.9985	L
STSU_15839		NA	hypothetical protein	A0A	A0A	2.07	0.0000	-0.73	0.1887	1.98	0.0004	L
STSU_15884		SCO3611	hypothetical protein STSU_15884	0A0	AAA	0.47	0.0767	0.76	0.0030	0.61	0.0899	M

STSU_16687	NA	hypothetical protein	DDD	DDD	-2.11	0.0000	-1.23	0.0000	-0.83	0.0147	LM
STSU_16692	SCO3286	hypothetical protein	DD0	DD0	-1.90	0.0003	-1.65	0.0011	-0.79	0.4853	M
STSU_17007	NA	hypothetical protein	D00	D00	-1.06	0.0013	-0.36	0.4789	-0.50	0.5438	M
STSU_17469	NA	hypothetical protein	A00	0	2.22	0.0053	-1.58	0.0651	1.14	0.6159	L
STSU_17519	SCO3875	hypothetical protein STSU_17519	0	AA0	0.12	0.7928	0.23	0.3233	0.13	0.9985	M
STSU_17778	SCO3940	hypothetical protein	D00	D00	-1.50	0.0003	-0.72	0.1103	-0.39	0.9307	M
STSU_17948	<i>prpB7</i> SCO3971	hypothetical protein	D00	D00	-2.29	0.0001	0.10	0.9662	-0.68	0.8311	LM
STSU_19275	SCO4199	hypothetical protein STSU_19275	A00	AA0	1.50	0.0001	0.20	0.8547	0.50	0.6626	M
STSU_20102	NA	hypothetical protein	0	DDD	-0.03	0.9973	-0.78	0.0785	-0.61	0.5558	M
STSU_20117	NA	hypothetical protein	A00	0	1.95	0.0003	-0.42	0.7094	0.29	0.9985	M
STSU_20717	NA	hypothetical protein	D00	D00	-2.21	0.0008	-0.58	0.6473	-0.67	0.9089	L
STSU_21077	SCO4440	hypothetical protein	D00	DD0	-2.24	0.0055	-1.34	0.1472	-0.78	0.9285	L
STSU_21137	NA	hypothetical protein	0D0	0	-0.21	0.9901	-2.15	0.0131	-0.54	0.9985	L
STSU_21324	SCO3187	hypothetical protein STSU_21324	0A0	0	-0.19	0.9841	2.97	0.0001	-0.18	0.9985	L
STSU_21461	NA	hypothetical protein	0A0	0	0.52	0.6350	2.68	0.0000	0.82	0.6626	L
STSU_21641	SCO3152	hypothetical protein	D00	D00	-1.28	0.0042	0.45	0.5548	-0.22	0.9985	M
STSU_22595	SCO3038	hypothetical protein STSU_22595	0AA	AAA	0.01	0.9973	0.92	0.0003	0.68	0.0409	M
STSU_22754	SCO3009	hypothetical protein	0	DD0	0.11	0.8911	-0.39	0.0792	0.16	0.9985	M
STSU_22884	SCO2970	hypothetical protein	0A0	0A0	-0.04	0.9973	3.18	0.0000	0.20	0.9985	LM
STSU_23261	SCO2911	hypothetical protein	0A0	0A0	-0.65	0.2976	1.96	0.0001	-0.36	0.9985	M
STSU_23356	SCO2903	hypothetical protein	0	DD0	-0.02	0.9973	-0.20	0.8874	-0.38	0.9677	M
STSU_24233	SCO2634	hypothetical protein	0A0	0A0	-0.23	0.9057	2.44	0.0000	-0.23	0.9985	L
STSU_24397	NA	hypothetical protein STSU_24397, partial	DD0	DDD	-1.67	0.0000	-1.21	0.0000	-0.40	0.4937	M
STSU_25067	NA	hypothetical protein	D00	DD0	-1.70	0.0125	-1.07	0.1852	-0.98	0.6122	M
STSU_26019	NA	hypothetical protein	0D0	DDD	-1.45	0.0724	-2.25	0.0035	-1.35	0.3511	LM
STSU_26204	SCO2195	hypothetical protein	0A0	AA0	1.25	0.0947	2.22	0.0015	0.12	0.9985	L
STSU_26494	SCO2137	hypothetical protein	AA0	AA0	1.03	0.0004	0.78	0.0070	0.60	0.1807	M
STSU_26564	SCO2124	hypothetical protein	DA0	0	-0.52	0.0252	1.50	0.0000	-0.34	0.5581	M
STSU_27286	SCO1997	hypothetical protein	0A0	0A0	-0.09	0.9522	3.19	0.0000	-0.02	0.9985	LM
STSU_27296	SCO1995	hypothetical protein	AA0	D00	0.74	0.0401	1.81	0.0000	0.46	0.7289	M
STSU_27556	<i>sufB</i> SCO1925	hypothetical protein	0A0	0	0.13	0.9973	2.02	0.0107	0.35	0.9985	L
STSU_27581	SCO1920	hypothetical protein	0A0	AA0	0.27	0.8514	2.63	0.0000	0.24	0.9985	LM
STSU_27586	SCO1919	hypothetical protein	0A0	AA0	0.40	0.5231	2.40	0.0000	0.30	0.9985	L
STSU_27911	SCO1839	hypothetical protein	D00	D00	-1.77	0.0004	-0.58	0.4128	-0.33	0.9985	M
STSU_28962	NA	hypothetical protein	0A0	AA0	-0.62	0.6783	3.08	0.0001	-0.53	0.9985	L
STSU_29302	SCO1548	hypothetical protein STSU_2932	D0D	D0D	-0.92	0.0007	-0.25	0.5895	-0.72	0.0448	M
STSU_29357	SCO1540	hypothetical protein	AA0	0A0	0.42	0.0478	1.04	0.0000	0.35	0.3882	M
STSU_29364	NA	hypothetical protein STSU_29364	A00	0	2.06	0.0038	-0.21	0.9402	-0.57	0.9985	L
STSU_29616	SCO1485	hypothetical protein	A00	A00	3.46	0.0000	-0.26	0.8630	0.29	0.9985	LM S3.28
STSU_29866	SCO1431	hypothetical protein STSU_29866	D00	D00	-1.86	0.0036	-0.12	0.9656	-0.16	0.9985	M
STSU_29911	<i>rbpA</i> SCO1421	hypothetical protein	0A0	DA0	0.16	0.8285	1.66	0.0000	0.10	0.9985	M
STSU_29996	SCO1403	hypothetical protein STSU_29996	0A0	DA0	0.48	0.0658	1.50	0.0000	0.37	0.5692	M
STSU_30480	NA	hypothetical protein	D00	D00	-2.20	0.0075	0.18	0.9568	-0.26	0.9985	L

STSU_30567	NA	hypothetical protein	D00	DD0	-1.40	0.0033	0.07	0.9738	0.23	0.9985	M
STSU_31720	SCO1021	hypothetical protein	D00	D00	-2.25	0.0008	-0.46	0.7706	-0.73	0.8739	L
STSU_33195	SCO0694	hypothetical protein	0	D00	0.01	0.9994	0.33	0.6764	0.11	0.9985	M

**Table S4. Genes showing an *fkbN*-like transcriptional profile along the cultures.** Those genes with a Pearson correlation coefficient equal or higher than 0.9 respect to the transcriptional profile of *fkbN* are indicated. The STSU code, the predicted product according to the NCBI notation, the reciprocal orthologue in *S. coelicolor* and the graph in which the transcriptional profile is depicted are indicated. In column “name”, we indicate the name assigned to the reciprocal orthologue in *S. coelicolor* (black letters) or in *S. avermitilis* (grey letters). The classification of the genes has been modified from a first classification according to the COG letters assigned to each gene.

Gene	Name	<i>S.coelicolor</i> orthologue	Product	Graph
<b>GENERAL REACTIONS</b>				
STSU_01420		SCO0392	putative methyltransferase	
STSU_33005		NA	4-hydroxyphenylpyruvate dioxygenase	
STSU_01415		SCO0393	transferase	
STSU_01440		SCO0387	putative bi-domain oxidoreductase	
STSU_01455		SCO0384	lipopolysaccharide biosynthesis protein	
STSU_04833		NA	methylenetetrahydromethanopterin reductase	
STSU_05828	<i>poxB</i>	SCO6155	pyruvate dehydrogenase	
STSU_06934	<i>lipW</i>	SCO7131	esterase	
STSU_16403		NA	NAD-dependent epimerase/dehydratase	
STSU_16408		NA	glutamine--scyllo-inositol aminotransferase	
STSU_22355		NA	L-lysine 6-monooxygenase	
STSU_28595	<i>fadE17</i>	SCO1690	acyl-CoA dehydrogenase domain-containing protein	
STSU_30945		NA	benzoate 1,2-dioxygenase subunit beta	
<b>COFACTOR AND VITAMIN METABOLISM</b>				
STSU_01375		SCO0401	glutamate-1-semialdehyde 2,1-aminomutase	
STSU_29836		NA	type 11 methyltransferase	
<b>ENERGY METABOLISM</b>				
STSU_11375	<i>sdhA2</i>	SCO5107	succinate dehydrogenase flavoprotein subunit	
STSU_11380	<i>shdB2</i>	SCO5106	fumarate reductase iron-sulfur subunit	
<b>MEMBRANE PROTEINS</b>				
STSU_01430		SCO0390	putative integral membrane protein	
STSU_28126		SCO1797	membrane protein	
STSU_28892	<i>tatC</i>	SCO1632	integral membrane protein	
<b>OTHER FUNCTIONS</b>				
STSU_01435		SCO0388	heparinase II/III family protein	
STSU_05873		SCO7453	secreted protein	
STSU_07608	<i>aveR</i>	SCO4263	ATPase-like protein	
STSU_14872		NA	tRNA(Ile)-lysine synthase, partial	
STSU_27766		NA	radical SAM domain containing protein	
STSU_11535	<i>katA2</i>	SCO7590	catalase	
STSU_32970		NA	signal transduction histidine kinase-like protein	
<b>SECONDARY METABOLISM</b>				
STSU_00470		NA	penicillin g amidase	S3.46
STSU_05913	<i>whiE</i>	SCO5319	Cupin 2 barrel domain-containing protein	S3.46

STSU_07618	<i>scoT</i>	SCO6287	thioesterase	S3.46
STSU_07628	<i>ppt1*</i>	SCO6673	4'-phosphopantetheinyl transferase	S3.46
STSU_11745	<i>actI/ORF2</i>	SCO5088	beta-ketoacyl synthase	S3.46
STSU_33010		SCO3227	FMN-dependent alpha-hydroxy acid dehydrogenase	S3.46
<b>TRANSCRIPTION</b>				
STSU_00835	<i>ramR</i>	SCO6685	transcriptional regulator	S3.43
STSU_08624		SCO5622	TetR family transcriptional regulator	S3.43
STSU_10866		SCO5209	TetR family transcriptional regulator	S3.43
STSU_12290	<i>sig59</i>	SCO4960	sigma factor	S3.43
STSU_18801	<i>atrA</i>	SCO4118	TetR family transcriptional regulator	S3.43
STSU_24896	<i>hrdA</i>	SCO2465	RNA polymerase sigma factor	S3.43
STSU_32975		NA	two-component regulator CutR	S3.43
STSU_32985		NA	StrR-like regulatory protein	S3.43
STSU_32995		NA	StrR-like regulatory protein	
<b>TRANSPORT</b>				
STSU_11190	<i>tatB</i>	SCO5150	sec-independent translocase	
STSU_21561		SCO3161	cobalt ABC transporter, ATPase subunit	
<b>HYPOTHETICAL PROTEINS</b>				
STSU_00005		NA	hypothetical protein	
STSU_00475		NA	hypothetical protein	
STSU_00480		NA	hypothetical protein	
STSU_01385		SCO0399	hypothetical protein	
STSU_01400		SCO0396	hypothetical protein	
STSU_01410		SCO0394	hypothetical protein	
STSU_01460		SCO0383	hypothetical protein	
STSU_01735		NA	hypothetical protein	
STSU_03794		NA	hypothetical protein	
STSU_03864		NA	hypothetical protein	
STSU_05368		NA	hypothetical protein	
STSU_05668		NA	hypothetical protein	
STSU_05703		SCO3289	hypothetical protein	
STSU_07623		SCO6831	hypothetical protein	
STSU_07888		SCO5814	hypothetical protein	
STSU_09604		NA	hypothetical protein	
STSU_10084		SCO5389	hypothetical protein	
STSU_11365		SCO5109	hypothetical protein	
STSU_11370		SCO5108	hypothetical protein	
STSU_13445		SCO4675	hypothetical protein	
STSU_14175		NA	hypothetical protein	
STSU_14473	<i>bdtA</i>	SCO3328	hypothetical protein	
STSU_14927		SCO4371	hypothetical protein	
STSU_15092		NA	hypothetical protein	
STSU_17267		NA	hypothetical protein	
STSU_20392		SCO4402	hypothetical protein	
STSU_22335		NA	hypothetical protein	

STSU_22380	NA	hypothetical protein
STSU_23311	NA	hypothetical protein
STSU_24083	SCO2665	hypothetical protein
STSU_24522	SCO2584	hypothetical protein
STSU_25969	SCO3108	hypothetical protein
STSU_28712	SCO1668	hypothetical protein
STSU_30585	NA	hypothetical protein
STSU_32315	NA	hypothetical protein
STSU_32930	NA	hypothetical protein

\* STSU\_07628 has been named *ppf1* by Ordóñez-Robles and coworkers (2016).

**Table S5. Genes coding for secondary metabolism regulators and showing a *fkfN*-like transcriptional profile.** From the set of genes listed by van Wezel and McDowell (2011), we selected those encoding secondary metabolism regulators in *S. coelicolor* that have a reciprocal orthologue in *S. tsukubaensis*. Positive correlation between the transcriptional pattern of *fkfN* is indicated as (+).

Gene	SCO	STSU	<i>fkfN</i> profile correlation
<i>bldH (adpA)</i>	SCO2792	STSU_23624	+
<i>scbA(afsA)</i>	SCO6266	STSU_00255	
<i>arfA</i>	SCO3841	STSU_17382	
<i>actII-orf4</i>	SCO5085	STSU_00225	
<i>dasR</i>	SCO5231	STSU_10786	
<i>atrA</i>	SCO4118	STSU_18801	+
<i>rok7b7</i>	SCO6008	STSU_06313	
<i>absA2</i>	SCO3226	STSU_09809	
<i>cpkO(kasO)</i>	SCO6280	STSU_02170	
<i>scbR</i>	SCO6265	STSU_00240	
<i>ndgR</i>	SCO5552	STSU_08914	
<i>relA</i>	SCO1513	STSU_29481	
<i>rshA</i>	SCO5794	STSU_07978	+
<i>rplK</i>	SCO4648	STSU_13590	
<i>rpoB</i>	SCO4654	STSU_13565	
<i>afsR</i>	SCO4426	STSU_20727	+
<i>afsK</i>	SCO4423	STSU_20667	
<i>phoP</i>	SCO4230	STSU_19410	
<i>dmdR1/adm</i>	SCO4394	STSU_20342	
<i>sigQ</i>	SCO4908	STSU_12475	+
<i>afsQ1</i>	SCO4907	STSU_12480	
<i>rpoZ</i>	SCO1478	STSU_29651	
<i>cutR</i>	SCO5862	STSU_06603	
<i>bldB</i>	SCO5723	STSU_08304	
<i>bldC</i>	SCO4091	STSU_18523	+
<i>bldD</i>	SCO1489	STSU_29596	
<i>bldG</i>	SCO3549	STSU_15482	
<i>bldM</i>	SCO4768	STSU_13050	+
<i>bldN</i>	SCO3323	STSU_14448	+
<i>absB</i>	SCO5572	STSU_08794	
<i>absC</i>	SCO5405	STSU_09999	
<i>absR2</i>	SCO6993	STSU_27656	
<i>cdgA</i>	SCO2817	STSU_23547	+
<i>eshA</i>	SCO7699	STSU_03599	+
<i>nsdA</i>	SCO5582	STSU_08734	+
<i>nsdB</i>	SCO7252	STSU_00765	+
<i>rapA1</i>	SCO5403	STSU_10009	

<i>rrdA</i>	SCO1104	STSU_31530	
<i>ssgA</i>	SCO3926	STSU_17763	+
<i>wblA</i>	SCO3579	STSU_15654	+
	SCO1712	STSU_28535	