

Table S1 (Malmström et al)

Protein description	Acc	Gene	u	pep	seq	cov	TH	1%	5%	10%	20%
<b>Reduced</b>											
3-oxoacyl-[acyl-carrier-protein] synthase 2	SPy1748	fabF	22		83%		3.4E+08	2.9E+08	1.2E+08	1.7E+07	5.9E+05
3-oxoacyl-[acyl-carrier-protein] reductase	SPy1749	fabG	11		45%		7.5E+07	5.4E+07	3.8E+07	4.6E+06	6.0E+05
Malonyl-CoA-[acyl-carrier-protein] transacylase	SPy1750	fabD	17		57%		6.3E+07	6.7E+07	4.0E+07	0.0E+00	1.9E+06
Enoyl-[acyl-carrier-protein] reductase	SPy1751	fabK	8		40%		3.1E+07	2.5E+07	1.9E+07	5.4E+05	1.7E+06
GTP-binding protein Era	SPy0476		3		19%		5.5E+06	1.4E+06	1.7E+06	1.2E+06	3.1E+05
Glycine betaine transport ATP-binding protein	SPy0183	opuAA	5		24%		1.1E+07	8.1E+06	8.5E+06	4.6E+06	6.8E+05
Peptide chain release factor 3	SPy1416	prfC	8		21%		1.2E+07	7.2E+06	4.6E+06	1.5E+06	8.8E+05
ABC transporter 2C ATP-binding protein	SPy1729		3		18%		3.4E+06	2.0E+06	5.5E+06	1.3E+06	3.5E+05
Topoisomerase IV subunit A	SPy0910	parC	7		13%		5.2E+06	1.8E+06	4.1E+06	1.2E+06	5.8E+05
GTP cyclohydrolase I (EC 3.5.4.16) type 1	SPy1097	folE	4		27%		6.7E+06	4.0E+06	2.1E+06	2.0E+06	8.1E+05
Translation initiation factor 2	SPy1721	infB	16		27%		3.5E+07	2.5E+07	1.3E+07	1.2E+07	4.4E+06
Glutamine ABC transporter 2C glutamine-binding protein	SPy1315		24		39%		9.5E+07	9.6E+07	7.0E+07	4.0E+07	1.3E+07
Phosphate transport system regulatory protein PhoU	SPy1240	phoU	5		30%		1.2E+07	4.6E+06	3.0E+06	2.0E+06	1.6E+06
N-acetylglucosamine-1-phosphate uridylyltransferase	SPy0443	gcaD	8		18%		1.4E+07	3.0E+06	5.2E+06	7.7E+05	1.9E+06
DNA binding protein starved cells-like peroxide resistance protein	SPy1531		11		66%		5.2E+08	3.8E+08	2.2E+08	3.4E+08	7.2E+07
Biotin carboxylase of acetyl-CoA carboxylase	SPy1745	accC	10		41%		3.1E+07	1.5E+07	2.0E+07	2.8E+05	4.2E+06
Catabolite control protein A	SPy0514	ccpA	8		38%		7.4E+06	4.3E+06	5.1E+06	2.5E+06	1.0E+06
Glutamine transport ATP-binding protein glnQ	SPy1316		10		52%		6.3E+07	5.3E+07	5.2E+07	2.7E+07	9.3E+06
hypothetical protein	SPy1264		3		15%		6.8E+06	7.2E+06	7.3E+06	5.3E+06	1.0E+06
S-adenosylmethionine synthetase	SPy1359	metK	5		21%		1.4E+07	1.0E+07	6.7E+06	6.7E+06	2.2E+06
<b>Increased</b>											
ATP-dependent RNA helicase 2C DEAD 2FDEAH box family	SPy1369	deaD2	1		7%		3.6E+05	2.0E+06	2.5E+06	1.6E+06	2.9E+06
Dihydroorotate dehydrogenase 2C catalytic subunit	SPy1432	pyrD	24		76%		7.9E+07	3.8E+07	2.1E+08	2.7E+08	5.5E+08
Ribonuclease R	SPy0503		11		21%		2.1E+06	1.7E+06	1.8E+06	6.7E+06	1.1E+07
Orotidine 5'-phosphate decarboxylase	SPy0900	pyrF	17		77%		1.5E+07	3.8E+06	1.5E+07	5.0E+07	6.8E+07
Deoxyguanosinetriphosphate triphosphohydrolase	SPy0621		2		9%		3.1E+05	5.1E+05	7.9E+05	8.4E+05	1.4E+06
Peptidoglycan N-acetylglucosamine deacetylase (EC 3.5.1.-)	SPy1370		6		24%		1.9E+06	1.3E+06	2.6E+06	4.1E+06	8.2E+06
hypothetical protein	SPy1304		3		44%		3.2E+05	2.5E+05	1.0E+06	1.1E+06	1.2E+06
Putative cell-cycle regulation histidine triad (HIT) protein	SPy1730		5		79%		3.1E+06	4.0E+06	8.8E+06	9.9E+06	1.1E+07
Orotate phosphoribosyltransferase	SPy0901	pyrE	10		70%		1.7E+07	3.9E+06	2.8E+07	5.6E+07	5.9E+07
Heat shock protein GrpE	SPy1761	grpE	6		48%		1.5E+07	3.4E+06	9.4E+06	2.6E+07	5.0E+07
hypothetical protein	SPy1508		1		22%		1.4E+06	3.6E+06	4.0E+06	3.2E+06	4.4E+06
Heat shock protein 60 family co-chaperone GroES	SPy2072	groES	8		96%		9.1E+07	8.7E+07	8.1E+07	1.8E+08	2.4E+08
SSU ribosomal protein S10p (S20e)	SPy0047	rpsJ	7		53%		1.9E+08	4.2E+08	1.6E+08	3.5E+08	4.6E+08
C3-degrading proteinase	SPy1851		9		39%		1.1E+07	6.8E+06	1.6E+07	3.2E+07	2.7E+07
LSU ribosomal protein L15p (L27Ae)	SPy0072	rplO	7		48%		1.6E+08	4.5E+08	3.7E+08	5.0E+08	3.8E+08
Neutral endopeptidase O	SPy2095	pepO	29		49%		1.4E+08	2.0E+08	2.4E+08	3.0E+08	3.0E+08
Xanthine phosphoribosyltransferase	SPy1136		3		23%		9.1E+05	0.0E+00	1.6E+06	2.4E+06	1.9E+06
SSU ribosomal protein S18p	SPy1829	rpsR	7		30%		4.8E+07	7.6E+07	8.5E+07	1.1E+08	9.2E+07
Ribosylhomocysteine (EC 3.2.1.148)	SPy1642	luxS	3		36%		4.4E+06	5.8E+06	4.8E+06	7.0E+06	8.4E+06
Transcriptional regulator 2C repressor of the glutamine synthetase	SPy1878		6		67%		7.6E+06	4.2E+06	4.0E+06	7.4E+06	1.4E+07
<b>No detectable levels in 20%</b>											
D-alanine--poly(phosphoribitol) ligase subunit 2	SPy1310	ditC	1		14%		2.6E+06	1.8E+06	3.5E+05	0.0E+00	0.0E+00
Spermidine Putrescine transport ATP-binding protein	SPy1102	potA	1		4%		1.4E+06	1.2E+06	8.5E+05	0.0E+00	0.0E+00
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase	SPy1746	fabZ	4		28%		6.4E+06	3.5E+06	1.0E+06	0.0E+00	0.0E+00
ABC transporter ATP-binding protein	SPy1674		1		5%		1.4E+06	1.5E+06	1.3E+06	9.2E+05	0.0E+00
L-proline Glycine Betaine ABC transport system permease protein proW	SPy0184	opuABC	4		10%		6.0E+06	7.2E+06	4.3E+06	9.6E+05	0.0E+00
UDP-N-acetylmuramoylalanine--D-glutamate ligase	SPy1525	murD	3		16%		3.8E+06	2.0E+06	2.9E+06	1.1E+06	0.0E+00
Integral membrane protein	SPy1828		2		17%		3.6E+06	3.1E+06	3.2E+06	2.1E+06	0.0E+00
Hydrolase (HAD superfamily)	SPy1633		8		24%		3.7E+06	1.8E+06	2.1E+06	5.3E+05	0.0E+00
PTS system 2C mannose 2Fructose family IIB component	SPy1058		4		47%		6.0E+06	7.5E+06	2.4E+06	6.5E+05	0.0E+00
3-oxoacyl-[acyl-carrier-protein] synthase 3	SPy1754	fabH	3		22%		5.3E+06	4.8E+06	2.7E+06	1.1E+06	0.0E+00
<b>No detectable levels in TH</b>											
Hyaluronan synthase	SPy2200	hasA	3		10%		0.0E+00	0.0E+00	0.0E+00	2.9E+06	5.8E+06
hypothetical protein	SPy2060		2		27%		0.0E+00	0.0E+00	7.0E+05	9.9E+05	3.7E+06
Streptokinase	SPy1979	ska	1		5%		0.0E+00	0.0E+00	0.0E+00	0.0E+00	3.0E+06
SSE esterase (nmpd )	SPy1718	sse	3		21%		0.0E+00	0.0E+00	0.0E+00	5.9E+05	2.5E+06
Peptide methionine sulfoxide reductase	SPy0466	msrA.2	1		16%		0.0E+00	0.0E+00	0.0E+00	0.0E+00	1.1E+06
L-asparaginase	SPy1782	asnB	1		7%		0.0E+00	0.0E+00	0.0E+00	8.1E+05	7.7E+05
hypothetical protein	SPy1875		1		21%		0.0E+00	0.0E+00	0.0E+00	0.0E+00	6.7E+05
hypothetical protein	SPy0864		2		37%		0.0E+00	0.0E+00	0.0E+00	0.0E+00	4.7E+05
Phosphate starvation-inducible protein PhoH 2C predicted ATPase	SPy0471	phoH	2		9%		0.0E+00	0.0E+00	0.0E+00	3.6E+05	3.7E+05
Putative regulator of the mannose operon 2C ManO	SPy1741		2		20%		0.0E+00	0.0E+00	0.0E+00	3.2E+05	2.3E+05

n\_u\_pep, number of unique peptides; seq\_cov, sequence coverage































