

Supplementary Table 11. Comparison of the number of peptides of the genetic information processing proteins identified in OD 0.7 and 1.2

Transcription						Translation					
Locus name	Gene name	Protein description	Total no. peptides OD 0.7	Total no. peptides OD 1.2	OD 0.7/1.2	Locus name	Gene name	Protein description	Total no. peptides OD 0.7	Total no. peptides OD 1.2	OD 0.7/1.2
RNA polymerase						Aminoacyl-tRNA biosynthesis (continued)					
rrnAC0067	rpoN	DNA-directed RNA polymerase subunit N	2	0	∞	rrnAC1355	gatA	Glutamyl-tRNA synthetase	3	4	0.8
rrnAC2829	rpoE	DNA-directed RNA polymerase subunit E'	22	7	3.1 *	rrnAC3183	hisS	Histidyl-tRNA synthetase	9	13	0.7
rrnAC2432	rpoH	DNA-directed RNA polymerase subunit H	9	3	3.0 *	rrnAC0543	tyrS	Tyrosyl-tRNA synthetase	8	14	0.6
rrnAC2428	rpoA	DNA-directed RNA polymerase	70	41	1.7	rrnAC2634	ileS	Isoleucyl-tRNA synthetase	25	45	0.6
rrnAC2430	rpoB	DNA-directed RNA polymerase subunit B	54	34	1.6	rrnAC1729	valS	Valyl-tRNA synthetase	8	18	0.4
rrnAC2830	rpoE	DNA-directed RNA polymerase subunit E	3	2	1.5	rrnAC0517	alaS2	Alanyl-tRNA synthetase	6	14	0.4
rrnAC2429	rpoB	DNA-directed RNA polymerase beta subunit	56	40	1.4	rrnAC2701	glyS	Glycyl-tRNA synthetase	6	14	0.4
rrnAC2427	rpoC	RNA polymerase Rpb1 domain 5	22	16	1.4	rrnAC3442	asbA	L-asparaginase	0	7	0
rrnAC0259	rpb4	RNA polymerase Rpb4	20	17	1.2	rrnAC1292	cysS	Cysteinyl-tRNA synthetase	0	5	0
rrnAC1396	rpoL	DNA-directed RNA polymerase subunit L	4	4	1.0	Chaperones and folding catalysts					
rrnAC0062	rpoD	DNA-directed RNA polymerase subunit D	4	7	0.6	rrnAC1308	rrnAC130	Glutaredoxin	20	19	1.1
rrnAC0218	rpoM	DNA-directed RNA-polymerase subunit M	0	1	0	rrnAC3116	pfidA	Prefoldin alpha subunit	33	33	1.0
Basal transcription factors						rrnAC3303	ppiB1	Peptidyl-prolyl cis-trans isomerase	25	25	1.0
rrnAC0016	tfbA	Transcription initiation factor IIB	4	0	∞	rrnAC1680	pfidB	Prefoldin beta subunit	30	31	1.0
rrnAC0861	tfeA	Transcription initiation factor IIE alpha subunit	9	3	3.0 *	rrnAC2110	trxA3	Thioredoxin	26	27	1.0
rrnAC0681	thpE	TATA-box binding protein E	22	12	1.8	rrnAC3339	dnaK	Chaperone protein dnaK	57	71	0.8
Transcription factors						rrnAC1230	styD	Peptidyl-prolyl cis-trans isomerase	43	57	0.8
rrnAC2744	rrnAC274	Hypothetical protein	5	3	1.7	rrnAC3340	grpE	Heat shock protein GrpE protein	3	7	0.4
pNG2007	pNG2007	Hypothetical protein	18	11	1.6	Ubiquitin system					
rrnAC1133	rpaA	Replication protein A	12	17	0.7	rrnAC1773	psmA2	Proteasome alpha subunit	47	20	2.4
rrnAC1765	tenA	Transcriptional activator tenA	3	21	0.1 *	rrnAC0442	psmA3	Proteasome subunit alpha	6	4	1.5
rrnAC0001	birA	Biotin-(acetyl-CoA carboxylase) ligase	0	5	0	rrnAC3190	pan1	Proteasome-activating nucleotidase 1	12	8	1.5
rrnAC1767	tenA-2	Transcriptional regulator putative	0	9	0	rrnAC1174	psmA1	Proteasome alpha subunit	50	38	1.3
rrnAC0496	sirR	Transcription repressor	1	0	∞	rrnAC3546	pan2	Proteasome-activating nucleotidase 2	21	26	0.8
rrnAC1715	cspD1	Cold shock protein	1	0	∞	rrnAC1772	psmA	Proteasome subunit alpha	5	9	0.6
rrnAC2339	cspD3	Cold shock protein	50	12	4.2	RNA degradation					
rrnAC1714	cspD5	Cold shock protein	3	1	3.0	rrnAC0069	eno	Enolase	24	23	1.0
rrnAC1269	asnC2	Transcription regulator AsnC family	1	2	2.5	rrnAC2072	vacB	Ribonuclease R	10	12	0.8
rrnAC3264	rrnAC326	Putative molybdenum-binding protein	5	2	0.5	rrnAC3339	dnaK	Chaperone protein dnaK	57	71	0.8
rrnAC2283	copG1	Transcriptional regulator CopG family	0	1	0	pNG7302	ppk	Polyphosphate kinase	0	8	0
Ribosome						DNA replication					
rrnAC1596	rpl6p	50S ribosomal protein L6P	5	0	∞	rrnAC2744	rrnAC274	Hypothetical protein	5	3	1.7
rrnAC1418	rpl12p	50S ribosomal protein L12P	3	0	∞	pNG2007	pNG2007	Hypothetical protein	18	11	1.6
rrnAC1607	rps19p	30S ribosomal protein S19P	12	2	6.0 *	rrnAC2851	pcn	DNA polymerase sliding clamp	24	33	0.7
rrnAC1604	rpl29p	50S ribosomal protein L29P	5	1	5.0 *	rrnAC1133	rpaA	Replication protein A	12	17	0.7
rrnAC0059	rps4p	30S ribosomal protein S4P	27	7	3.9 *	DNA replication proteins					
rrnAC0061	rps11p	30S ribosomal protein S11P	23	6	3.8 *	rrnAC0455	gyrA	DNA gyrase subunit A	13	4	3.2 *
rrnAC1598	rpl5p	50S ribosomal protein L5P	13	4	3.3 *	rrnAC2691	polC	DNA polymerase II large subunit	3	1	3.0 *
rrnAC0058	rps13p	30S ribosomal protein S13P	21	8	2.6	rrnAC1645	topA	DNA topoisomerase I	4	2	2.0
rrnAC2488	rps24e	30S ribosomal protein S24e	16	6	2.7	rrnAC2565	rfeS	Replication factor C small subunit	12	7	1.7
rrnAC1605	rps3p	30S ribosomal protein S3P	53	21	2.5	rrnAC0457	top6B	Type II DNA topoisomerase VI subunit B	37	24	1.5
rrnAC1417	rplP0	50S ribosomal protein L10E	17	8	2.1	rrnAC0456	gyrB	DNA gyrase subunit B	7	5	1.4
rrnAC1429	rps3Ae	30S ribosomal protein S3Ae	80	39	2.1	rrnAC2487	rfeC2	Replication factor C small subunit	5	4	1.3
rrnAC1600	rps4e	30S ribosomal protein S4e	34	17	2.0	rrnAC1831	polB1	DNA polymerase B elongation subunit	1	2	0.5
rrnAC2212	rps6e	30S ribosomal protein S6e	14	7	2.0	rrnAC0459	top6A	Type II DNA topoisomerase VI subunit A	2	5	0.4
rrnAC1610	rpl4p	50S ribosomal protein L4P	2	1	2.0	rrnAC2762	mcm2	Cell division control protein 21	1	1	1.0
rrnAC2357	rpl10e	50S ribosomal protein L10e	14	7	2.0	rrnAC0292	priA	Probable DNA primase small subunit	0	1	0
rrnAC1592	rps5p	30S ribosomal protein S5P	63	35	1.8	Chromosome					
rrnAC1611	rpl3p	50S ribosomal protein L3P	91	57	1.6	rrnB0062	parA3	Chromosome partitioning protein ParA family	2	0	∞
rrnAC0064	rpl18e	50S ribosomal protein L18e	41	26	1.6	rrnAC0974	rrnAC097	Hypothetical protein	3	0	∞
rrnAC1595	rpl32e	50S ribosomal protein L32e	8	5	1.6	rrnAC2004	ftsZ3	Cell division protein FtsZ	9	5	1.8
rrnAC1426	rps15p	30S ribosomal protein S15P/S13e	18	12	1.5	rrnAC0665	abcP-2	ABC transporter permease protein	5	5	1.0
rrnAC3179	rps19e	30S ribosomal protein S19e	22	15	1.5	rrnAC0703	ftsZ1	Cell division protein FtsZ	19	23	0.8
rrnAC0070	rps2p	30S ribosomal protein S2P	26	18	1.4	pNG6012	parA2	Partition protein	7	9	0.8
rrnAC2065	rpl15e	50S ribosomal protein L15e	16	11	1.5	rrnAC0056	mrp1	Mrp protein-like	5	7	0.7
rrnAC1608	rpl2p	50S ribosomal protein L2P	24	17	1.4	rrnAC1639	smc2	Chromosome segregation protein	1	0	∞
rrnAC3112	rpl39e	50S ribosomal protein L39e	7	5	1.4	pNG2014	sojC	Chromosome partitioning protein	0	2	0
rrnAC1511	rps8e	30S ribosomal protein S8e	12	9	1.3	Base excision repair					
rrnAC1591	rpl30p	50S ribosomal protein L30P	9	7	1.3	rrnAC2015	nfo	Probable endonuclease 4	3	2	1.5
rrnAC1603	rps17p	30S ribosomal protein S17P	10	8	1.3	pNG7116	nthC	Endonuclease III	4	4	1.0
rrnAC0260	rpl21e	50S ribosomal protein L21e	5	4	1.3	rrnAC2851	pcn	DNA polymerase sliding clamp	24	33	0.7
rrnAC0055	rps17e	30S ribosomal protein S17e	6	5	1.2	rrnAC0265	apl	AP-endonuclease/AP-lyase	4	7	0.6
rrnAC1606	rpl22p	50S ribosomal protein L22P	12	10	1.2	rrnAC0739	nthA	Endonuclease III	1	1	1.0
rrnAC0065	rpl13p	50S ribosomal protein L13P	30	27	1.1	rrnAC1088	alkA	DNA-3-methyladenine glycosylase	0	2	0
rrnAC1597	rps8p	30S ribosomal protein S8P	7	7	1.0	Nucleotide excision repair					
rrnAC2424	rps12p	30S ribosomal protein S12P	15	15	1.0	rrnAC2996	uvrB	UvrABC system protein B	2	0	∞
rrnAC0103	rpl7ae	50S ribosomal protein L7Ae	16	16	1.0	rrnAC2267	uvrD	Repair helicase	27	9	3.0 *
rrnAC2423	rps7p	30S ribosomal protein S7P	35	40	0.9	rrnAC2116	uvrA	Excinuclease ABC subunit A	14	8	1.8
rrnAC1602	rpl4p	50S ribosomal protein L14P	21	29	0.7	rrnAC2744	rrnAC274	Hypothetical protein	5	3	1.7
rrnAC3113	rpl31e	50S ribosomal protein L31e	4	6	0.7	pNG2007	pNG2007	Hypothetical protein	18	11	1.6
rrnAC1415	rpl1p5	50S ribosomal protein L1P	1	2	0.5	rrnAC2851	pcn	DNA polymerase sliding clamp	24	33	0.7
rrnAC1594	rpl19e	50S ribosomal protein L19e	2	5	0.4	rrnAC1133	rpaA	Replication protein A	12	17	0.7
rrnAC1590	rpl15p	50S ribosomal protein L15P	10	28	0.4	Mismatch repair					
rrnAC2405	rps10p	30S ribosomal protein S10P	1	3	0.3 *	rrnB0041	xseA2	Probable exodeoxyribonuclease VII large subunit	3	0	∞
rrnAC3513	rps27E	30S ribosomal protein S27e	1	3	0.3 *	rrnAC2267	uvrD	Repair helicase	27	9	3.0 *
rrnAC1609	rpl23p	50S ribosomal protein L23P	1	0	∞	rrnAC2532	mutS1	DNA mismatch repair protein mutS 1	2	1	2.0
rrnAC0066	rps9p	30S ribosomal protein S9P	6	3	2.0	rrnAC2744	rrnAC274	Hypothetical protein	5	3	1.7
rrnAC1414	rpl11p	50S ribosomal protein L11P	2	1	2.0	pNG2007	pNG2007	Hypothetical protein	18	11	1.6
rrnAC1593	rpl18p	50S ribosomal protein L18P	3	3	1.0	rrnAC2851	pcn	DNA polymerase sliding clamp	24	33	0.7
rrnAC2489	rps27ae	30S ribosomal protein S27ae	0	1	0	rrnAC1133	rpaA	Replication protein A	12	17	0.7
rrnAC1601	rpl24p	50S ribosomal protein L24P	0	1	0	rrnAC2550	mutL	DNA mismatch repair protein mutL	2	3	0.7
Translation factors						pNG6094	xseA1	Probable exodeoxyribonuclease VII large subunit	0	2	0
rrnAC0261	ef1b	Elongation factor 1-beta	13	6	2.2	Homologous recombination					
rrnAC3164	prf1	Peptide chain release factor subunit 1	11	6	1.8	rrnAC2744	rrnAC274	Hypothetical protein	5	3	1.7
rrnAC1956	ef2BD2	Translation initiation factor eIF-2B subunit delta	10	7	1.4	pNG2007	pNG2007	Hypothetical protein	18	11	1.6
rrnAC2413	fusA	Elongation factor 2	148	141	1.1	rrnAC1133	rpaA	Replication protein A	12	17	0.7
rrnAC2474	ef1A	Translation initiation factor 1A	19	19	1.0	DNA repair and recombination proteins					
rrnAC2827	ef2g	Translation initiation factor 2 gamma subunit	11	11	1.0	rrnAC2996	uvrB	UvrABC system protein B	2	0	∞
rrnAC1929	ef5a	Translation initiation factor 5A	13	13	1.0	rrnB0041	xseA2	Probable exodeoxyribonuclease VII large subunit	3	0	∞
rrnAC2445	sui1	Protein translation factor SUI1 homolog	9	9	1.0	rrnAC0455	gyrA	DNA gyrase subunit A	13	4	3.3 *
rrnAC0289	ef2BD1	Translation initiation factor eIF-2B subunit delta	16	19	0.8	rrnAC2267	uvrD	Repair helicase	27	9	3.0 *
rrnAC2406	tuf	Elongation factor 1-alpha	141	222	0.6	rrnAC0832	phrB1	Deoxyribodipyrimidine photolyase	2	1	2.0
rrnAC3512	ef2a	Translation initiation factor 2 alpha subunit	8	13	0.6	rrnAC2159	dcd3	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase	2	1	2.0
rrnAC0138	ef2B1	Probable translation initiation factor 2 beta	4	7	0.6	rrnAC2532	mutS1	DNA mismatch repair protein mutS 1	2	1	2.0
rrnAC1619	gbb2	GTP-binding protein-like	2	5	0.4	rrnAC1840	smc1	Structural maintenance of chromosomes	2	1	2.0
rrnAC3203	infB	Probable translation initiation factor IF-2	3	10	0.3 *	rrnAC2847	hjr	Holliday junction resolvase	4	2	2.0
Aminoacyl-tRNA biosynthesis						rrnAC1645	topA	DNA topoisomerase I	4	2	2.0
rrnAC2967	pheT	Phenylalanyl-tRNA synthetase beta chain	20	15	1.3	rrnAC2116	uvrA	Excinuclease ABC subunit A	14	8	1.8
rrnAC3462	thrS	Threonyl-tRNA synthetase	15	12	1.3	rrnAC2744	rrnAC274	Hypothetical protein	5	3	1.7
rrnAC1800	metG	Methionyl-tRNA synthetase	24	20	1.2	pNG2007	pNG2007	Hypothetical protein	18	11	1.6
rrnAC3173	lysS	Lysyl-tRNA synthetase	6	5	1.2	rrnAC2015	nfo	Probable endonuclease 4	3	2	1.5
rrnAC2966	pheS	Phenylalanyl-tRNA synthetase alpha chain	7	6	1.2	rrnAC0456	gyrB	DNA gyrase subunit B	7	5	1.4
rrnAC2650	leuS1	Leucyl-tRNA synthetase	16	14	1.1	rrnAC1622	rrdA	Ribonucleoside-diphosphate reductase alpha chain	108	91	1.2
rrnAC2808	serS	Seryl-tRNA synthetase	19	17	1.1	rrnAC0669	polX	DNA polymerase IV	9	8	1.1
rrnAC0166	proS	Prolyl-tRNA synthetase	19	18	1.1	pNG7116	nthC	Endonuclease III	4	4	1.0
rrnAC3169	argS	Arginyl-tRNA synthetase	25	24	1.0	rrnAC2910	radA	DNA repair and recombination protein RadA	25	27	0.9
rrnAC0023	gatE	Glutamyl-tRNA synthetase	12	12	1.0	rrnAC2851	pcn	DNA polymerase sliding clamp	24	33	0.7
rrnAC2965	trpS	Tryptophanyl-tRNA synthetase	11	11	1.0	rrnAC1133	rpaA	Replication protein A	12	17	0.7
rrnAC0085	gluX	Glutamyl-tRNA synthetase	10	11	0.9	rrnAC2550	mutL	DNA mismatch repair protein mutL	2	3	0.7
rrnAC1356	gatC	Glutamyl-tRNA synthetase	9	11	0.8	rrnAC					