Supplementary Table 10. Summary of MS/MS detected proteins in KEGG metabolic networks and cellular processes.

01100 Metabolism

01101 Carbohydrate Metabolism

	No. unique peptide(s)	**Gene name**	**Protein description**	**No. peptides (OD 0.7)**	**No. peptides (OD 1.2)**	**Total no. peptides**	**OD: 0.7/1.2**	**No. peptides (membrane)**	**No. peptides (soluble)**	**% membrane / total**	***TMHMM***
00010 Glycolysis / Gluconeogenesis [PATH:hma00010]											
rrnB0199	> 2 unique peptides	*pdhB2*	Pyruvate dehydrogenase (EC 1.2.4.1)	22	3	**25**	7.33	5	20	20	0
rrnB0217	> 2 unique peptides	*acs2*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	11	2	**13**	5.5	0	13	0	0
rrnAC0545	> 2 unique peptides	*pfk1*	Phosphofructokinase (EC 2.7.1.11)	8	5	**13**	1.6	0	13	0	0
rrnAC0546	> 2 unique peptides	*pykA*	Pyruvate kinase (EC 2.7.1.40)	19	12	**31**	1.58	0	31	0	0
rrnAC1138	> 2 unique peptides	*fbp1*	Fructose-16-bisphosphatase (EC 3.1.3.11)	7	5	**12**	1.4	0	12	0	0
rrnAC1881	> 2 unique peptides	*deoC2*	Deoxyribose-phosphate aldolase	21	15	**36**	1.4	0	36	0	0
rrnAC0537	> 2 unique peptides	*tpiA*	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphateisomerase)	20	15	**35**	1.33	0	35	0	0
rrnB0265	> 2 unique peptides	*acs4*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	106	87	**193**	1.22	8	185	4.15	0
rrnAC2957	> 2 unique peptides	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	31	27	**58**	1.15	0	58	0	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC0012	> 2 unique peptides	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	18	17	**35**	1.06	1	34	2.86	0
rrnAC0069	> 2 unique peptides	*eno*	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	24	23	**47**	1.04	0	47	0	0
rrnAC2262	> 2 unique peptides	*gap*	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.59) (GAPDH)(NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase)	19	19	**38**	1	17	21	44.74	0
rrnAC2363	> 2 unique peptides	*gapA*	Glyceraldehyde 3-phosphate dehydrogenase (EC 1.2.1.59)	4	4	**8**	1	0	8	0	0
rrnAC3381	> 2 unique peptides	*lpdA1*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	5	5	**10**	1	0	10	0	0
rrnB0197	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	3	3	**6**	1	0	6	0	0
rrnAC0345	> 2 unique peptides	*fba*	Fructose-bisphosphate aldolase (EC 4.1.2.13)	88	89	**177**	0.99	71	106	40.11	0
rrnAC3210	> 2 unique peptides	*pgi*	Probable glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)(Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)	18	19	**37**	0.95	0	37	0	0
rrnAC0772	> 2 unique peptides	*fbp2*	Fructose-16-bisphosphatase (EC 3.1.3.11)	18	19	**37**	0.95	0	37	0	0
rrnAC2956	> 2 unique peptides	*pdhB1*	Pyruvate dehydrogenase (EC 1.2.4.1)	59	69	**128**	0.86	20	108	15.63	0
rrnAC2953	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	30	37	**67**	0.81	0	67	0	0
rrnAC2955	> 2 unique peptides	*pdhC2*	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenasecomplex (EC 2.3.1.12)	36	46	**82**	0.78	12	70	14.63	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnB0198	> 2 unique peptides	*pdhC1*	Dihydrolipoamide S-acetyltransferase component of pyruvatedehydrogenase complex E2	3	4	**7**	0.75	0	7	0	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
pNG7289	> 2 unique peptides	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	9	13	**22**	0.69	0	22	0	0
rrnAC1402	> 2 unique peptides	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	5	8	**13**	0.63	0	13	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC0650	> 2 unique peptides	*acs1*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	13	21	**34**	0.62	1	33	2.94	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
pNG7278	> 2 unique peptides	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	4	7	**11**	0.57	0	11	0	0
rrnAC2364	> 2 unique peptides	*pgk*	Phosphoglycerate kinase (EC 2.7.2.3)	18	32	**50**	0.56	3	47	6	0
rrnAC0191	> 2 unique peptides	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	6	11	**17**	0.55	1	16	5.88	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC3228	> 2 unique peptides	*acs5*	Putative acetyl-coenzyme A synthetase (EC 6.2.1.1)	64	134	**198**	0.48	5	193	2.53	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
pNG7032	> 2 unique peptides	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	3	3	0	0	3	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
rrnAC3403	single hit	*gpmI*	2,3-bisphosphoglycerate-independent phosphoglycerate mutase(EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (iPGM)	1	1	2	1	0	2	0	0
rrnB0200	single hit	*pdhA2*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	2	2	4	1	0	4	0	0
pNG7314	single hit	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	1	1	2	1	0	2	0	0
rrnAC2064	single hit	*aor1*	Aldehyde ferredoxin oxidoreductase	1	1	2	1	0	2	0	0
rrnAC0547	single hit	*glcK*	Glucokinase (EC 2.7.1.2)	0	1	1	0	0	1	0	0
pNG7351	single hit	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	2	2	0	0	2	0	0
rrnAC3230	single hit	*acs3*	Acyl-coenzyme A synthetase (EC 6.2.1.1)	0	1	1	0	0	1	0	0
rrnAC0249	ND										
rrnAC0342	ND										
rrnAC2859	ND										
rrnAC0149	ND										
pNG7022	ND										
pNG7101	ND										
pNG7103	ND										
rrnAC1300	ND										
rrnAC1975	ND										
rrnAC2172	ND										
rrnAC3506	ND										
pNG7352	ND										
rrnAC2631	ND										

rrnB0092	ND										
rrnB0095	ND										
rrnAC1341	ND										
rrnAC2781	ND										
rrnAC3274	ND										
rrnAC1318	ND										
00020 Citrate cycle (TCA cycle) [PATH:hma00020]											
rrnAC1092	> 2 unique peptides	*rrnAC1092*	Hypothetical protein	3	0	3	#DIV/0!	3	0	100	3
rrnB0199	> 2 unique peptides	*pdhB2*	Pyruvate dehydrogenase (EC 1.2.4.1)	22	3	**25**	7.33	5	20	20	0
rrnB0263	> 2 unique peptides	*accC1*	Carbamoyl phosphate synthase L chain	32	21	**53**	1.52	0	53	0	0
rrnAC2706	> 2 unique peptides	*mdh*	Malate dehydrogenase (EC 1.1.1.37)	267	219	**486**	1.22	3	483	0.62	0
rrnAC0718	> 2 unique peptides	*porA*	Pyruvate ferredoxin oxidoreductase subunit alpha (EC 1.2.7.3)(EC 1.2.7.1)	83	69	**152**	1.2	1	151	0.66	0
rrnAC0028	> 2 unique peptides	*fumC*	Fumarate hydratase class-II (EC 4.2.1.2)	101	84	**185**	1.2	8	177	4.32	0
rrnAC2957	> 2 unique peptides	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	31	27	**58**	1.15	0	58	0	0
rrnAC2511	> 2 unique peptides	*citZ*	Citrate synthase II (EC 2.3.3.1)	51	47	**98**	1.09	4	94	4.08	0
rrnAC2158	> 2 unique peptides	*acnB*	Aconitate hydratase (EC 4.2.1.3)	247	228	**475**	1.08	88	387	18.53	0
rrnAC3419	> 2 unique peptides	*icd*	Isocitrate dehydrogenase (EC 1.1.1.42)	96	90	**186**	1.07	11	175	5.91	0
rrnAC3381	> 2 unique peptides	*lpdA1*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	5	5	**10**	1	0	10	0	0
rrnB0197	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	3	3	**6**	1	0	6	0	0
rrnAC0719	> 2 unique peptides	*porB*	Pyruvate ferredoxin oxidoreductase subunit beta (EC 1.2.7.3)(EC 1.2.7.1)	27	28	**55**	0.96	1	54	1.82	0
rrnAC1267	> 2 unique peptides	*korA*	2-oxoglutarate ferredoxin oxidoreductase subunit alpha (EC 1.2.7.3)(EC 1.2.7.1)	126	137	**263**	0.92	19	244	7.22	0
rrnAC0474	> 2 unique peptides	*sucD*	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)	62	69	**131**	0.9	13	118	9.92	0
rrnAC1093	> 2 unique peptides	*sdhB*	Succinate dehydrogenase iron-sulfur protein subunit(EC 1.3.99.1)	72	83	**155**	0.87	153	2	98.71	0
rrnAC2956	> 2 unique peptides	*pdhB1*	Pyruvate dehydrogenase (EC 1.2.4.1)	59	69	**128**	0.86	20	108	15.63	0
rrnAC1268	> 2 unique peptides	*korB*	Putative 2-ketoglutarate ferredoxin oxidoreductase (Beta) (EC 1.2.7.3)(EC 1.2.7.1)	63	75	**138**	0.84	7	131	5.07	0
rrnAC2953	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	30	37	**67**	0.81	0	67	0	0
rrnAC2955	> 2 unique peptides	*pdhC2*	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenasecomplex (EC 2.3.1.12)	36	46	**82**	0.78	12	70	14.63	0
rrnAC0472	> 2 unique peptides	*sucC*	Succinyl-CoA synthetase beta chain (EC 6.2.1.5)	137	177	**314**	0.77	18	296	5.73	0
rrnB0198	> 2 unique peptides	*pdhC1*	Dihydrolipoamide S-acetyltransferase component of pyruvatedehydrogenase complex E2	3	4	**7**	0.75	0	7	0	0
rrnAC1097	> 2 unique peptides	*sdhA1*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	121	180	**301**	0.67	292	9	97.01	0
rrnB0200	single hit	*pdhA2*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	2	2	4	1	0	4	0	0
rrnAC0141	single hit	*sdhA2*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	0	3	3	0	0	3	0	0
pNG6049	ND										
rrnAC1091	ND										
rrnAC0690	ND										
rrnAC0149	ND										
00030 Pentose phosphate pathway [PATH:hma00030]											
pNG7073	> 2 unique peptides	*qgd*	Quinoprotein glucose dehydrogenase (EC 1.1.5.2)	2	0	2	#DIV/0!	2	0	100	0
rrnAC0011	> 2 unique peptides	*ywfD1*	Glucose 1-dehydrogenase (EC 1.1.1.47)	7	3	**10**	2.33	0	10	0	0
rrnAC2741	> 2 unique peptides	*ywfD2*	Glucose dehydrogenase (EC 1.1.1.47)	12	6	**18**	2	0	18	0	0
rrnAC2180	> 2 unique peptides	*gnd*	6-phosphogluconate dehydrogenase (EC 1.1.1.44)	5	3	**8**	1.67	0	8	0	0
rrnAC0545	> 2 unique peptides	*pfk1*	Phosphofructokinase (EC 2.7.1.11)	8	5	**13**	1.6	0	13	0	0
rrnAC1881	> 2 unique peptides	*deoC2*	Deoxyribose-phosphate aldolase	21	15	**36**	1.4	0	36	0	0
rrnAC1138	> 2 unique peptides	*fbp1*	Fructose-16-bisphosphatase (EC 3.1.3.11)	7	5	**12**	1.4	0	12	0	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC0345	> 2 unique peptides	*fba*	Fructose-bisphosphate aldolase (EC 4.1.2.13)	88	89	**177**	0.99	71	106	40.11	0
rrnAC3210	> 2 unique peptides	*pgi*	Probable glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)(Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)	18	19	**37**	0.95	0	37	0	0
rrnAC0772	> 2 unique peptides	*fbp2*	Fructose-16-bisphosphatase (EC 3.1.3.11)	18	19	**37**	0.95	0	37	0	0
rrnAC3121	> 2 unique peptides	*eda*	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutaratealdolase (EC 4.1.2.14)	14	17	**31**	0.82	0	31	0	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
rrnAC3429	> 2 unique peptides	*deoC*	Probable deoxyribose-phosphate aldolase (EC 4.1.2.4)(Phosphodeoxyriboaldolase) (Deoxyriboaldolase) (DERA)	5	8	**13**	0.63	0	13	0	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC0575	> 2 unique peptides	*dgoA4*	Mandelate racemase/muconate lactonizing enzyme family	9	29	**38**	0.31	0	38	0	0
rrnAC2630	single hit	*prsA*	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	1	0	1	#DIV/0!	0	1	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
rrnAC2551	single hit	*kdgK*	2-keto-3-deoxygluconate kinase (EC 2.7.1.45)	1	1	2	1	0	2	0	0
rrnAC2064	single hit	*aor1*	Aldehyde ferredoxin oxidoreductase	1	1	2	1	0	2	0	0
rrnAC2572	ND										
rrnAC1318	ND										
rrnAC0249	ND										
rrnAC0342	ND										
00040 Pentose and glucuronate interconversions [PATH:hma00040]											
rrnAC3239	> 2 unique peptides	*ugd2*	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	6	3	**9**	2	0	9	0	0
rrnAC3121	> 2 unique peptides	*eda*	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutaratealdolase (EC 4.1.2.14)	14	17	**31**	0.82	0	31	0	0
rrnAC2551	single hit	*kdgK*	2-keto-3-deoxygluconate kinase (EC 2.7.1.45)	1	1	2	1	0	2	0	0
rrnAC0616	ND										
pNG7029	ND										
00051 Fructose and mannose metabolism [PATH:hma00051]											
rrnAC0545	> 2 unique peptides	*pfk1*	Phosphofructokinase (EC 2.7.1.11)	8	5	**13**	1.6	0	13	0	0

rrnAC1432	> 2 unique peptides	*dpm5*	Dolichyl-phosphate-mannose-protein mannosyltransferase (EC 2.4.1.-)(EC 2.4.1.109)	32	20	**52**	1.6	52	0	100	10
rrnAC1138	> 2 unique peptides	*fbp1*	Fructose-16-bisphosphatase (EC 3.1.3.11)	7	5	**12**	1.4	0	12	0	0
rrnAC1881	> 2 unique peptides	*deoC2*	Deoxyribose-phosphate aldolase	21	15	**36**	1.4	0	36	0	0
rrnAC0537	> 2 unique peptides	*tpiA*	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphateisomerase)	20	15	**35**	1.33	0	35	0	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC2742	> 2 unique peptides	*manC*	Mannose-1-phosphate guanylyltransferase	3	3	**6**	1	0	6	0	0
rrnAC0345	> 2 unique peptides	*fba*	Fructose-bisphosphate aldolase (EC 4.1.2.13)	88	89	**177**	0.99	71	106	40.11	0
rrnAC0772	> 2 unique peptides	*fbp2*	Fructose-16-bisphosphatase (EC 3.1.3.11)	18	19	**37**	0.95	0	37	0	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC0917	single hit	*sorD*	Sorbitol dehydrogenase (EC 1.1.1.140)	1	0	1	#DIV/0!	0	1	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
pNG7027	ND										
pNG7029	ND										
rrnAC0249	ND										
rrnAC0342	ND										
pNG7012	ND										
pNG7008	ND										
pNG7388	ND										
pNG7392	ND										
pNG7387	ND										
00052 Galactose metabolism [PATH:hma00052]											
rrnAC0545	> 2 unique peptides	*pfk1*	Phosphofructokinase (EC 2.7.1.11)	8	5	**13**	1.6	0	13	0	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC0452	> 2 unique peptides	*galE*	UDP-glucose 4-epimerase (EC 5.1.3.2)	6	7	**13**	0.86	0	13	0	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC2897	> 2 unique peptides	*galE2*	UDP-glucose 4-epimerase (EC 5.1.3.2)	3	6	**9**	0.5	0	9	0	0
rrnAC0855	> 2 unique peptides	*galE4*	UDP-glucose 4-epimerase (EC 5.1.3.2)	7	15	**22**	0.47	0	22	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
rrnAC1479	single hit	*scrB*	Sucrose-6-phosphate hydrolase	1	1	2	1	0	2	0	0
rrnAC0224	single hit	*aglA1*	Alpha-glucosidase (EC 3.2.1.20)	1	1	2	1	0	2	0	0
rrnAC0547	single hit	*glcK*	Glucokinase (EC 2.7.1.2)	0	1	1	0	0	1	0	0
pNG7014	ND										
rrnAC3259	ND										
rrnAC2781	ND										
rrnAC3274	ND										
rrnAC0249	ND										
rrnAC0342	ND										
rrnAC3069	ND										
00053 Ascorbate and aldarate metabolism [PATH:hma00053]											
rrnAC3239	> 2 unique peptides	*ugd2*	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	6	3	**9**	2	0	9	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00500 Starch and sucrose metabolism [PATH:hma00500]											
rrnAC3239	> 2 unique peptides	*ugd2*	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	6	3	**9**	2	0	9	0	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC3210	> 2 unique peptides	*pgi*	Probable glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)(Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)	18	19	**37**	0.95	0	37	0	0
rrnAC0799	> 2 unique peptides	*cdlM*	Endoglucanase	25	28	**53**	0.89	0	53	0	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC1957	> 2 unique peptides	*malQ*	4-alpha-glucanotransferase (EC 2.4.1.25)	2	12	**14**	0.17	0	14	0	0
rrnAC1113	> 2 unique peptides	*bglX-2*	Beta-D-glucosidase	0	4	4	0	0	4	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
rrnAC1479	single hit	*scrB*	Sucrose-6-phosphate hydrolase	1	1	2	1	0	2	0	0
rrnAC0224	single hit	*aglA1*	Alpha-glucosidase (EC 3.2.1.20)	1	1	2	1	0	2	0	0
rrnAC0547	single hit	*glcK*	Glucokinase (EC 2.7.1.2)	0	1	1	0	0	1	0	0
rrnAC1478	ND										
rrnAC0173	ND										
rrnAC0237	ND										
rrnAC0616	ND										
rrnAC2781	ND										
rrnAC3274	ND										

rrnAC2353	ND										
00520 Amino sugar and nucleotide sugar metabolism [PATH:hma00520]											
rrnAC3239	> 2 unique peptides	*ugd2*	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)	6	3	**9**	2	0	9	0	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC2742	> 2 unique peptides	*manC*	Mannose-1-phosphate guanylyltransferase	3	3	**6**	1	0	6	0	0
rrnAC3210	> 2 unique peptides	*pgi*	Probable glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI)(Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI)	18	19	**37**	0.95	0	37	0	0
rrnAC0452	> 2 unique peptides	*galE*	UDP-glucose 4-epimerase (EC 5.1.3.2)	6	7	**13**	0.86	0	13	0	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC1081	> 2 unique peptides	*rffH1*	Glucose-1-phosphate thymidylyltransferase	6	11	**17**	0.55	0	17	0	0
rrnAC2897	> 2 unique peptides	*galE2*	UDP-glucose 4-epimerase (EC 5.1.3.2)	3	6	**9**	0.5	0	9	0	0
rrnAC0855	> 2 unique peptides	*galE4*	UDP-glucose 4-epimerase (EC 5.1.3.2)	7	15	**22**	0.47	0	22	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
rrnAC0470	single hit	*npdA*	NAD-dependent deacetylase (EC 3.5.1.-) (Regulatory protein SIR2homolog)	0	1	1	0	0	1	0	0
rrnAC0547	single hit	*glcK*	Glucokinase (EC 2.7.1.2)	0	1	1	0	0	1	0	0
pNG7011	ND										
rrnAC1587	ND										
rrnAC3235	ND										
pNG7014	ND										
rrnAC3259	ND										
00620 Pyruvate metabolism [PATH:hma00620]											
rrnB0199	> 2 unique peptides	*pdhB2*	Pyruvate dehydrogenase (EC 1.2.4.1)	22	3	**25**	7.33	5	20	20	0
rrnB0217	> 2 unique peptides	*acs2*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	11	2	**13**	5.5	0	13	0	0
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnAC2162	> 2 unique peptides	*mgsA*	Methylglyoxal synthase (EC 4.2.3.3)	6	3	**9**	2	0	9	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnAC0329	> 2 unique peptides	*leuA2*	2-isopropylmalate synthase 2 (EC 2.3.3.13)	5	3	**8**	1.67	0	8	0	0
rrnAC0546	> 2 unique peptides	*pykA*	Pyruvate kinase (EC 2.7.1.40)	19	12	**31**	1.58	0	31	0	0
rrnB0263	> 2 unique peptides	*accC1*	Carbamoyl phosphate synthase L chain	32	21	**53**	1.52	0	53	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC0903	> 2 unique peptides	*accA*	Acetyl-CoA carboxylase alpha subunit	16	12	**28**	1.33	0	28	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnB0265	> 2 unique peptides	*acs4*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	106	87	**193**	1.22	8	185	4.15	0
rrnAC2706	> 2 unique peptides	*mdh*	Malate dehydrogenase (EC 1.1.1.37)	267	219	**486**	1.22	3	483	0.62	0
rrnAC0562	> 2 unique peptides	*pepC*	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)	52	44	**96**	1.18	3	93	3.13	0
rrnAC2957	> 2 unique peptides	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	31	27	**58**	1.15	0	58	0	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnAC1795	> 2 unique peptides	*ppsA*	Phosphoenolpyruvate synthase (EC 2.7.9.2)	54	50	**104**	1.08	14	90	13.46	0
rrnAC3381	> 2 unique peptides	*lpdA1*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	5	5	**10**	1	0	10	0	0
rrnB0197	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	3	3	**6**	1	0	6	0	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1754	> 2 unique peptides	*maeB*	NAD-dependent malate dehydrogenase (EC 1.1.1.40)	53	56	**109**	0.95	3	106	2.75	0
rrnAC2956	> 2 unique peptides	*pdhB1*	Pyruvate dehydrogenase (EC 1.2.4.1)	59	69	**128**	0.86	20	108	15.63	0
rrnAC2953	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	30	37	**67**	0.81	0	67	0	0
rrnAC2955	> 2 unique peptides	*pdhC2*	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenasecomplex (EC 2.3.1.12)	36	46	**82**	0.78	12	70	14.63	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnB0198	> 2 unique peptides	*pdhC1*	Dihydrolipoamide S-acetyltransferase component of pyruvatedehydrogenase complex E2	3	4	**7**	0.75	0	7	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC0650	> 2 unique peptides	*acs1*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	13	21	**34**	0.62	1	33	2.94	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC3228	> 2 unique peptides	*acs5*	Putative acetyl-coenzyme A synthetase (EC 6.2.1.1)	64	134	**198**	0.48	5	193	2.53	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC1409	> 2 unique peptides	*gloA1*	Lactoylglutathione lyase (EC 4.4.1.5)	5	29	**34**	0.17	0	34	0	0
rrnB0200	single hit	*pdhA2*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	2	2	4	1	0	4	0	0
rrnAC3230	single hit	*acs3*	Acyl-coenzyme A synthetase (EC 6.2.1.1)	0	1	1	0	0	1	0	0
rrnAC1341	ND										
rrnAC0149	ND										
rrnAC1167	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
rrnAC1966	ND										
rrnAC2504	ND										
00630 Glyoxylate a											
rrnAC2706	> 2 unique peptides	*mdh*	Malate dehydrogenase (EC 1.1.1.37)	267	219	**486**	1.22	3	483	0.62	0
rrnAC2511	> 2 unique peptides	*citZ*	Citrate synthase II (EC 2.3.3.1)	51	47	**98**	1.09	4	94	4.08	0
rrnAC2158	> 2 unique peptides	*acnB*	Aconitate hydratase (EC 4.2.1.3)	247	228	**475**	1.08	88	387	18.53	0
rrnAC0996	> 2 unique peptides	*folD 1*	Bifunctional protein folD 1 [Includes: Methylenetetrahydrofolatedehydrogenase (EC 1.5.1.5)	14	15	**29**	0.93	0	29	0	0

rrnAC3121	> 2 unique peptides	*eda*	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutaratealdolase (EC 4.1.2.14)	14	17	**31**	0.82	0	31	0	0
rrnAC3272	> 2 unique peptides	*purU*	Formyltetrahydrofolate deformylase (EC 3.5.1.10) (EC 2.1.2.2)	4	8	**12**	0.5	0	12	0	0
pNG7060	> 2 unique peptides	*fmdA*	Formamidase	2	10	**12**	0.2	0	12	0	0
pNG7380	> 2 unique peptides	*fhs*	Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolatesynthetase) (FHS) (FTHFS)	2	27	**29**	0.07	1	28	3.45	0
pNG7318	> 2 unique peptides	*fdhG*	Formate dehydrogenase alpha subunit	0	3	3	0	1	2	33.33	0
pNG7328	> 2 unique peptides	*folD 2*	Bifunctional protein folD 2 [Includes: Methylenetetrahydrofolatedehydrogenase (EC 1.5.1.5)	0	5	**5**	0	0	5	0	0
pNG6049	ND										
pNG7015	ND										
pNG7151	ND										
rrnAC1332	ND										
rrnAC1333	ND										
00640 Propanoate metabolism [PATH:hma00640]											
rrnB0217	> 2 unique peptides	*acs2*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	11	2	**13**	5.5	0	13	0	0
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnB0261	> 2 unique peptides	*pccB*	Propionyl-CoA carboxylase beta subunit	40	20	**60**	2	0	60	0	0
rrnAC0637	> 2 unique peptides	*mcmA1*	Methylmalonyl-CoA mutase subunit alpha	4	2	**6**	2	0	6	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC0903	> 2 unique peptides	*accA*	Acetyl-CoA carboxylase alpha subunit	16	12	**28**	1.33	0	28	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnB0265	> 2 unique peptides	*acs4*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	106	87	**193**	1.22	8	185	4.15	0
rrnB0264	> 2 unique peptides	*acdH*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	37	31	**68**	1.19	0	68	0	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC0474	> 2 unique peptides	*sucD*	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)	62	69	**131**	0.9	13	118	9.92	0
rrnAC0382	> 2 unique peptides	*gabT*	4-aminobutyrate aminotransferase	66	79	**145**	0.84	8	137	5.52	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnAC0472	> 2 unique peptides	*sucC*	Succinyl-CoA synthetase beta chain (EC 6.2.1.5)	137	177	**314**	0.77	18	296	5.73	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC1983	> 2 unique peptides	*acdI*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	4	6	**10**	0.67	0	10	0	0
rrnAC0934	> 2 unique peptides	*mcmA3*	Putative methylmalonyl-CoA mutase	5	8	**13**	0.63	0	13	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC0650	> 2 unique peptides	*acs1*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	13	21	**34**	0.62	1	33	2.94	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC3228	> 2 unique peptides	*acs5*	Putative acetyl-coenzyme A synthetase (EC 6.2.1.1)	64	134	**198**	0.48	5	193	2.53	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
rrnAC1275	> 2 unique peptides	*mcmA2*	Methylmalonyl-CoA mutase subunit alpha	0	4	4	0	0	4	0	0
rrnAC3230	single hit	*acs3*	Acyl-coenzyme A synthetase (EC 6.2.1.1)	0	1	1	0	0	1	0	0
rrnAC1341	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00650 Butanoate metabolism [PATH:hma00650]											
rrnAC1092	> 2 unique peptides	*rrnAC1092*	Hypothetical protein	3	0	3	#DIV/0!	3	0	100	3
rrnAC0331	> 2 unique peptides	*ilvN*	Acetolactate synthase small subunit (EC 2.2.1.6)	2	0	2	#DIV/0!	0	2	0	0
rrnB0219	> 2 unique peptides	*gabD*	Succinate-semialdehyde dehydrogenase	9	1	**10**	9	0	10	0	0
rrnAC2886	> 2 unique peptides	*phaC*	Poly(3-hydroxyalkanoate) synthase	7	1	**8**	7	8	0	100	0
rrnB0199	> 2 unique peptides	*pdhB2*	Pyruvate dehydrogenase (EC 1.2.4.1)	22	3	**25**	7.33	5	20	20	0
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnAC0330	> 2 unique peptides	*ilvB2*	Acetolactate synthase (EC 2.2.1.6)	8	3	**11**	2.67	4	7	36.36	0
rrnB0209	> 2 unique peptides	*ilvB3*	Acetolactate synthase large subunit (EC 2.2.1.6)	7	3	**10**	2.33	0	10	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC2957	> 2 unique peptides	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	31	27	**58**	1.15	0	58	0	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1093	> 2 unique peptides	*sdhB*	Succinate dehydrogenase iron-sulfur protein subunit(EC 1.3.99.1)	72	83	**155**	0.87	153	2	98.71	0
rrnAC2956	> 2 unique peptides	*pdhB1*	Pyruvate dehydrogenase (EC 1.2.4.1)	59	69	**128**	0.86	20	108	15.63	0
rrnAC0382	> 2 unique peptides	*gabT*	4-aminobutyrate aminotransferase	66	79	**145**	0.84	8	137	5.52	0

rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC0134	> 2 unique peptides	*ilvB1*	Acetolactate synthase large subunit (EC 2.2.1.6)	16	22	**38**	0.73	1	37	2.63	0
rrnAC1097	> 2 unique peptides	*sdhA1*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	121	180	**301**	0.67	292	9	97.01	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
rrnAC1740	> 2 unique peptides	*mvaS*	Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	1	10	**11**	0.1	0	11	0	0
rrnB0200	single hit	*pdhA2*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	2	2	4	1	0	4	0	0
rrnAC2874	single hit	*phaJ1*	(R)-specific enoyl-CoA hydratase (EC 4.2.1.-)	0	1	1	0	0	1	0	0
rrnAC0141	single hit	*sdhA2*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	0	3	3	0	0	3	0	0
rrnAC0648	single hit	*bdhA*	D-beta-hydroxybutyrate dehydrogenase	0	2	2	0	0	2	0	0
pNG7012	ND										
rrnAC1091	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
rrnAC0149	ND										
00660 C5-Branched dibasic acid metabolism [PATH:hma00660]											
rrnAC0331	> 2 unique peptides	*ilvN*	Acetolactate synthase small subunit (EC 2.2.1.6)	2	0	2	#DIV/0!	0	2	0	0
rrnAC0330	> 2 unique peptides	*ilvB2*	Acetolactate synthase (EC 2.2.1.6)	8	3	**11**	2.67	4	7	36.36	0
rrnB0209	> 2 unique peptides	*ilvB3*	Acetolactate synthase large subunit (EC 2.2.1.6)	7	3	**10**	2.33	0	10	0	0
rrnAC0474	> 2 unique peptides	*sucD*	Succinyl-CoA synthetase alpha chain (EC 6.2.1.5)	62	69	**131**	0.9	13	118	9.92	0
rrnAC0472	> 2 unique peptides	*sucC*	Succinyl-CoA synthetase beta chain (EC 6.2.1.5)	137	177	**314**	0.77	18	296	5.73	0
rrnAC0336	> 2 unique peptides	*leuD*	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	3	4	**7**	0.75	0	7	0	0
rrnAC0134	> 2 unique peptides	*ilvB1*	Acetolactate synthase large subunit (EC 2.2.1.6)	16	22	**38**	0.73	1	37	2.63	0
rrnAC0334	> 2 unique peptides	*leuC*	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI)	2	9	**11**	0.22	0	11	0	0
rrnAC0687	ND										
rrnAC0684	ND										
rrnAC0984	ND										
00562 Inositol phosphate metabolism [PATH:hma00562]											
rrnAC1004	> 2 unique peptides	*suhB1*	Inositol-1-monophosphatase (EC 3.1.3.25)	3	2	**5**	1.5	0	5	0	0
rrnAC0537	> 2 unique peptides	*tpiA*	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphateisomerase)	20	15	**35**	1.33	0	35	0	0
rrnB0102	single hit	*suhB2*	Inositol-1-monophosphatase (EC 3.1.3.25)	0	1	1	0	0	1	0	0
01102 Energy Metabolism											
00190 Oxidative phosphorylation [PATH:hma00190]											
rrnAC1092	> 2 unique peptides	*rrnAC1092*	Hypothetical protein	3	0	3	#DIV/0!	3	0	100	3
rrnAC3162	> 2 unique peptides	*atpD*	V-type ATP synthase subunit D (EC 3.6.3.14)	32	16	**48**	2	5	43	10.42	0
rrnAC3530	> 2 unique peptides	*nuoL1*	NADH dehydrogenase I L subunit	22	14	**36**	1.57	36	0	100	12
rrnAC3156	> 2 unique peptides	*atpE*	V-type ATP synthase subunit E (EC 3.6.3.14)	65	46	**111**	1.41	39	72	35.14	0
rrnAC1456	> 2 unique peptides	*ndhD*	NADH dehydrogenase subunit 4	22	17	**39**	1.29	39	0	100	14
rrnAC3152	> 2 unique peptides	*atpG*	Vacuolar (H+)-ATPase G subunit (EC 3.6.3.14)	15	13	**28**	1.15	12	16	42.86	0
rrnAC1450	> 2 unique peptides	*ndhG4*	NADH dehydrogenase/oxidoreductase	25	22	**47**	1.14	47	0	100	9
rrnAC1448	> 2 unique peptides	*nuoB*	NADH dehydrogenase I B subunit	27	24	**51**	1.13	51	0	100	0
rrnAC1301	> 2 unique peptides	*yjlD2*	NADH dehydrogenase	29	26	**55**	1.12	30	25	54.55	0
rrnAC3155	> 2 unique peptides	*atpC1*	H+ ATP synthase sununit C (EC 3.6.3.14)	940	871	**1811**	1.08	1811	0	100	2
rrnAC3160	> 2 unique peptides	*ntpB*	V-type sodium ATP synthase subunit B (EC 3.6.3.14)	180	183	**363**	0.98	118	245	32.51	0
rrnAC1154	> 2 unique peptides	*coxA3*	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	74	76	**150**	0.97	150	0	100	13
rrnAC0043	> 2 unique peptides	*coxB1*	Cytochrome c oxidase polypeptide II (EC 1.9.3.1)	24	25	**49**	0.96	49	0	100	3
rrnAC3154	> 2 unique peptides	*atpI*	V-type ATP synthase subunit I (EC 3.6.3.14)	48	50	**98**	0.96	98	0	100	7
rrnAC1278	> 2 unique peptides	*coxA1*	Cytochrome c oxidase polypeptide I (EC 1.9.3.1)	26	29	**55**	0.9	55	0	100	13
rrnAC3159	> 2 unique peptides	*ntpA*	V-type sodium ATP synthase subunit A (EC 3.6.3.14)	65	73	**138**	0.89	26	112	18.84	0
rrnAC3157	> 2 unique peptides	*ntpC*	V-type ATP synthase subunit C (EC 3.6.3.14)	50	57	**107**	0.88	78	29	72.9	0
rrnAC1093	> 2 unique peptides	*sdhB*	Succinate dehydrogenase iron-sulfur protein subunit(EC 1.3.99.1)	72	83	**155**	0.87	153	2	98.71	0
rrnAC1449	> 2 unique peptides	*ndHG5*	NADH dehydrogenase/oxidoreductase	90	104	**194**	0.87	189	5	97.42	0
rrnAC1458	> 2 unique peptides	*ndhG3*	NADH dehydrogenase/oxidoreductase	24	31	**55**	0.77	55	0	100	13
rrnAC1451	> 2 unique peptides	*nolD*	NADH dehydrogenase/oxidoreductase-like protein	10	13	**23**	0.77	23	0	100	0
rrnAC3285	> 2 unique peptides	*nolA*	NADH dehydrogenase/oxidoreductase-like protein	27	38	**65**	0.71	32	33	49.23	0
rrnAC1455	> 2 unique peptides	*nuoL2*	NADH dehydrogenase I L subunit	44	63	**107**	0.7	107	0	100	16
rrnAC1097	> 2 unique peptides	*sdhA1*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	121	180	**301**	0.67	292	9	97.01	0
rrnAC1485	> 2 unique peptides	*yjlD4*	NADH dehydrogenase (EC 1.6.99.3)	4	6	**10**	0.67	0	10	0	0

rrnAC3323	> 2 unique peptides	*ipp*	Inorganic pyrophosphatase (EC 3.6.1.1)	18	31	**49**	0.58	0	49	0	0
rrnAC2023	> 2 unique peptides	*nuoC*	NADH dehydrogenase I chain C D	2	4	**6**	0.5	6	0	100	0
rrnAC1153	> 2 unique peptides	*coxB2*	Cytochrome c oxidase subunit II (EC 1.9.3.1)	35	79	**114**	0.44	114	0	100	1
pNG7302	> 2 unique peptides	*ppk*	Polyphosphate kinase (EC 2.7.4.1)	0	8	**8**	0	0	8	0	0
rrnAC1454	single hit	*nolC*	NADH dehydrogenase/oxidoreductase-like protein	2	0	2	#DIV/0!	2	0	100	1
rrnAC1447	single hit	*nolB*	NAD(P)H-quinone oxidoreductase chain 3 (EC 1.6.5.-)	2	4	6	0.5	6	0	100	3
rrnAC1453	single hit	*rrnAC1453*	Hypothetical protein	1	3	4	0.33	4	0	100	2
rrnAC1399	single hit	*cyoC*	Cytochrome c oxidase polypeptide III (EC 1.9.3.1)	1	3	4	0.33	4	0	100	7
rrnAC3158	single hit	*atpF*	V-type ATP synthase subunit F (EC 3.6.3.14)	1	3	4	0.33	3	1	75	0
rrnAC1435	single hit	*atpC2*	ATP synthase subunit C (EC 3.6.3.14)	8	45	53	0.18	53	0	100	2
rrnAC0141	single hit	*sdhA2*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	0	3	3	0	0	3	0	0
pNG7189	ND										
pNG7319	ND										
rrnAC1452	ND										
pNG7037	ND										
rrnAC1091	ND										
rrnAC0882	ND										
rrnAC0880	ND										
rrnAC2311	ND										
rrnAC0879	ND										
rrnAC2310	ND										
00680 Methane metabolism [PATH:hma00680]											
rrnAC0999	> 2 unique peptides	*glyA*	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)(SHMT)	20	16	**36**	1.25	0	36	0	0
rrnAC1171	> 2 unique peptides	*perA*	Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase)	161	155	**316**	1.04	3	313	0.95	0
rrnAC1616	> 2 unique peptides	*mch*	N(5)N(10)-methenyltetrahydromethanopterin cyclohydrolase(EC 3.5.4.27)	2	9	**11**	0.22	0	11	0	0
pNG7318	> 2 unique peptides	*fdhG*	Formate dehydrogenase alpha subunit	0	3	3	0	1	2	33.33	0
pNG7363	> 2 unique peptides	*metF*	5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	0	4	4	0	4	0	100	0
pNG7151	ND										
rrnAC1332	ND										
rrnAC1333	ND										
pNG7247	ND										
rrnAC2018	ND										
00910 Nitrogen metabolism [PATH:hma00910]											
rrnAC0384	> 2 unique peptides	*gdhA1*	NADP-specific glutamate dehydrogenase (EC 1.4.1.3)	76	51	**127**	1.49	25	102	19.69	0
rrnAC2780	> 2 unique peptides	*glnA*	Glutamine synthetase (EC 6.3.1.2)	99	83	**182**	1.19	18	164	9.89	0
pNG7157	> 2 unique peptides	*gudB*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	76	75	**151**	1.01	19	132	12.58	0
rrnAC0958	> 2 unique peptides	*icfA2*	Carbonic anhydrase	3	3	**6**	1	0	6	0	0
rrnAC2486	> 2 unique peptides	*nadE1*	NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	8	9	**17**	0.89	0	17	0	0
rrnAC0775	> 2 unique peptides	*gdhA2*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	52	64	**116**	0.81	1	115	0.86	0
rrnAC1791	> 2 unique peptides	*hutH*	Histidine ammonia-lyase (EC 4.3.1.3)	23	55	**78**	0.42	8	70	10.26	0
rrnAC1500	> 2 unique peptides	*gcvT*	Probable aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage systemT protein)	1	3	4	0.33	0	4	0	0
pNG7361	> 2 unique peptides	*gcvT5*	Probable aminomethyltransferase (EC 2.1.2.10)	32	104	**136**	0.31	5	131	3.68	0
pNG7366	> 2 unique peptides	*gcvT3*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	9	40	**49**	0.23	0	49	0	0
pNG7060	> 2 unique peptides	*fmdA*	Formamidase	2	10	**12**	0.2	0	12	0	0
rrnAC2439	> 2 unique peptides	*tnaA*	Tryptophanase (EC 4.1.99.1)	12	68	**80**	0.18	14	66	17.5	0
pNG7370	> 2 unique peptides	*gcvT1*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	0	9	**9**	0	1	8	11.11	0
rrnAC0169	single hit	*gltB*	Glutamate synthase large subunit (EC 1.4.1.13)	1	0	1	#DIV/0!	0	1	0	0
rrnAC2992	single hit	*nirA2*	Ferredoxin-nitrite reductase	5	3	8	1.67	0	8	0	0
rrnAC0751	ND										
rrnAC1199	ND										
rrnAC1200	ND										
rrnAC2627	ND										
rrnAC2625	ND										
pNG7227	ND										
rrnAC2552	ND										
rrnAC0687	ND										
rrnAC3420	ND										
rrnAC0884	ND										
rrnAC1359	ND										
pNG7354	ND										
rrnAC2272	ND										
rrnAC0390	ND										
rrnAC3102	ND										
00920 Sulfur metabolism [PATH:hma00920]											
rrnAC0653	> 2 unique peptides	*cysH*	Phospho-adenylyl-sulfate Reductase (EC 1.8.4.8)	63	59	**122**	1.07	17	105	13.93	0
rrnAC1236	> 2 unique peptides	*cysK1*	Cysteine synthase (EC 2.5.1.47)	2	3	**5**	0.67	0	5	0	0
rrnAC2414	> 2 unique peptides	*metB*	Cystathionine gamma-synthase (EC 2.5.1.48)	30	46	**76**	0.65	1	75	1.32	0
pNG7330	single hit	*cysE1*	Serine acetyltransferase (EC 2.3.1.30)	1	0	1	#DIV/0!	0	1	0	0
pNG2036	ND										
rrnAC3064	ND										
rrnAC1087	ND										

rrnAC0137	ND										
01103 Lipid Metabolism											
00061 Fatty acid biosynthesis [PATH:hma00061]											
rrnAC0903	> 2 unique peptides	*accA*	Acetyl-CoA carboxylase alpha subunit	16	12	**28**	1.33	0	28	0	0
rrnAC0904	> 2 unique peptides	*fabG1*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	22	18	**40**	1.22	0	40	0	0
rrnAC0002	> 2 unique peptides	*accC2*	Carbamoyl phosphate synthase L chain (EC 6.3.4.16)	47	56	**103**	0.84	6	97	5.83	0
rrnAC1984	> 2 unique peptides	*fabG4*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	8	10	**18**	0.8	0	18	0	0
pNG7335	single hit	*fabG5*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	2	0	2	#DIV/0!	0	2	0	0
00062 Fatty acid elongation in mitochondria [PATH:hma00062]											
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
00071 Fatty acid metabolism [PATH:hma00071]											
rrnAC1074	> 2 unique peptides	*fadD3*	Long-chain fatty-acid-CoA ligase	4	1	**5**	4	4	1	80	0
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnB0264	> 2 unique peptides	*acdH*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	37	31	**68**	1.19	0	68	0	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnAC0012	> 2 unique peptides	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	18	17	**35**	1.06	1	34	2.86	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC1972	> 2 unique peptides	*gcdH*	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)	46	63	**109**	0.73	3	106	2.75	0
pNG7289	> 2 unique peptides	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	9	13	**22**	0.69	0	22	0	0
rrnAC1983	> 2 unique peptides	*acdI*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	4	6	**10**	0.67	0	10	0	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC0717	> 2 unique peptides	*rrnAC0717*	FAD/NAD binding oxidoreductase (EC 1.18.1.3)	5	8	**13**	0.63	0	13	0	0
rrnAC1402	> 2 unique peptides	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	5	8	**13**	0.63	0	13	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
pNG7278	> 2 unique peptides	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	4	7	**11**	0.57	0	11	0	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0191	> 2 unique peptides	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	6	11	**17**	0.55	1	16	5.88	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0073	> 2 unique peptides	*cyc*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	2	3	0.5	1	2	33.33	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC3312	> 2 unique peptides	*cyp1*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	3	4	0.33	4	0	100	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
rrnAC0929	> 2 unique peptides	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	1	10	**11**	0.1	0	11	0	0
pNG7032	> 2 unique peptides	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	3	3	0	0	3	0	0
pNG7314	single hit	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	1	1	2	1	0	2	0	0
pNG7351	single hit	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	2	2	0	0	2	0	0
pNG7022	ND										
pNG7101	ND										
pNG7103	ND										
rrnAC1300	ND										
rrnAC1975	ND										
rrnAC2172	ND										
rrnAC3506	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00072 Synthesis and degradation of ketone bodies [PATH:hma00072]											
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0

rrnAC1740	> 2 unique peptides	*mvaS*	Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	1	10	**11**	0.1	0	11	0	0
rrnAC0648	single hit	*bdhA*	D-beta-hydroxybutyrate dehydrogenase	0	2	2	0	0	2	0	0
00100 Steroid biosynthesis [PATH:hma00100]											
rrnAC1477	ND										
pNG6036	ND										
00561 Glycerolipid metabolism [PATH:hma00561]											
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC0550	> 2 unique peptides	*glpK*	Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)(Glycerokinase) (GK)	8	32	**40**	0.25	0	40	0	0
rrnAC0175	single hit	*gldA*	Glycerol-1-phosphate dehydrogenase [NAD(P)] (EC 1.1.1.6)(EC 1.1.1.261)	0	2	2	0	0	2	0	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
pNG7101	ND										
00564 Glycerophospholipid metabolism [PATH:hma00564]											
rrnAC0532	> 2 unique peptides	*pgsA*	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase(EC 2.7.8.5)	2	0	2	#DIV/0!	2	0	100	3
rrnAC1438	> 2 unique peptides	*taqD*	Glycerol-3-phosphate cytidyltransferase	6	5	**11**	1.2	0	11	0	0
rrnAC1955	> 2 unique peptides	*glpA*	Glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.99.5)	6	9	**15**	0.67	0	15	0	0
rrnAC0554	> 2 unique peptides	*gpdA*	Glycerol-3-phosphate dehydrogenase (EC 1.1.99.5)	1	2	3	0.5	3	0	100	0
rrnAC0555	> 2 unique peptides	*gpdB*	Glycerol-3-phosphate dehydrogenase chain B	1	5	**6**	0.2	6	0	100	0
rrnAC1917	> 2 unique peptides	*glpQ2*	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)	0	6	**6**	0	0	6	0	0
rrnAC0788	single hit	*pssA*	CDP-diacylglycerol-serine O phosphatidyltransferase	1	0	1	#DIV/0!	1	0	100	5
rrnAC0556	single hit	*gpdC*	Glycerol-3-phosphate dehydrogenase chain C	0	1	1	0	1	0	100	0
rrnB0316	ND										
00565 Ether lipid metabolism											
00600 Sphingolipid metabolism [PATH:hma00600]											
rrnAC0858	single hit	*rrnAC0858*	Arylsulfatase (EC 3.1.6.8)	1	1	2	1	1	1	50	0
pNG5066	ND										
00591 Linoleic acid metabolism											
pNG7012	ND										
00592 alpha-Linolenic acid metabolism [PATH:hma00592]											
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC0929	> 2 unique peptides	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	1	10	**11**	0.1	0	11	0	0
01040 Biosynthesis of unsaturated fatty acids [PATH:hma01040]											
rrnAC0904	> 2 unique peptides	*fabG1*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	22	18	**40**	1.22	0	40	0	0
rrnAC1984	> 2 unique peptides	*fabG4*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	8	10	**18**	0.8	0	18	0	0
pNG7335	single hit	*fabG5*	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100)	2	0	2	#DIV/0!	0	2	0	0
01004 Lipid biosynthesis proteins											
rrnB0217	> 2 unique peptides	*acs2*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	11	2	**13**	5.5	0	13	0	0
rrnAC1074	> 2 unique peptides	*fadD3*	Long-chain fatty-acid-CoA ligase	4	1	**5**	4	4	1	80	0
rrnB0265	> 2 unique peptides	*acs4*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	106	87	**193**	1.22	8	185	4.15	0
rrnAC1259	> 2 unique peptides	*alkK2*	Medium-chain-fatty-acid-CoA ligase	45	50	**95**	0.9	1	94	1.05	0
rrnAC0847	> 2 unique peptides	*alkK3*	Medium-chain acyl-CoA ligase	35	49	**84**	0.71	2	82	2.38	0
rrnAC0650	> 2 unique peptides	*acs1*	Acyl-coenzyme A synthetases (EC 6.2.1.1)	13	21	**34**	0.62	1	33	2.94	0
rrnAC1977	> 2 unique peptides	*alkK4*	Medium-chain fatty acid-CoA ligase	5	10	**15**	0.5	0	15	0	0
rrnAC3228	> 2 unique peptides	*acs5*	Putative acetyl-coenzyme A synthetase (EC 6.2.1.1)	64	134	**198**	0.48	5	193	2.53	0
rrnAC3230	single hit	*acs3*	Acyl-coenzyme A synthetase (EC 6.2.1.1)	0	1	1	0	0	1	0	0
rrnAC1341	ND										
01104 Nucleotide Metabolism											
00230 Purine metabolism [PATH:hma00230]											
rrnAC2139	> 2 unique peptides	*imd3*	Inosine monophosphate dehydrogenase (EC 1.1.1.205)	2	0	2	#DIV/0!	2	0	100	3
rrnAC1694	> 2 unique peptides	*guaAA*	GMP synthase [glutamine-hydrolyzing] subunit A (EC 6.3.5.2) (Glutamineamidotransferase)	3	0	3	#DIV/0!	0	3	0	0
rrnAC0067	> 2 unique peptides	*rpoN*	DNA-directed RNA polymerase subunit N (EC 2.7.7.6)	2	0	2	#DIV/0!	0	2	0	0
rrnAC2829	> 2 unique peptides	*rpoE'*	DNA-directed RNA polymerase subunit E'	22	7	**29**	3.14	0	29	0	0
rrnAC0797	> 2 unique peptides	*purF*	Amidophosphoribosyl transferase (EC 2.4.2.14)	3	1	4	3	0	4	0	0
rrnAC2432	> 2 unique peptides	*rpoH*	DNA-directed RNA polymerase subunit H (EC 2.7.7.6)	9	3	**12**	3	0	12	0	0
rrnAC2691	> 2 unique peptides	*polC*	DNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: HmapolC intein (Hma pol II intein)]	3	1	4	3	0	4	0	0
rrnB0175	> 2 unique peptides	*imd2*	Inosine monophosphate dehydrogenase (EC 1.1.1.205)	13	6	**19**	2.17	19	0	100	3
rrnAC2428	> 2 unique peptides	*rpoA*	DNA-directed RNA polymerase (EC 2.7.7.6)	70	41	**111**	1.71	35	76	31.53	0
rrnAC0546	> 2 unique peptides	*pykA*	Pyruvate kinase (EC 2.7.1.40)	19	12	**31**	1.58	0	31	0	0
rrnAC2430	> 2 unique peptides	*rpoB*	DNA-directed RNA polymerase subunit B	54	34	**88**	1.59	28	60	31.82	0
rrnAC2830	> 2 unique peptides	*rpoE''*	DNA-directed RNA polymerase subunit E''	3	2	**5**	1.5	0	5	0	0
rrnAC2429	> 2 unique peptides	*rpoB*	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	56	40	**96**	1.4	3	93	3.13	0
rrnAC2427	> 2 unique peptides	*rpoC*	RNA polymerase Rpb1 domain 5 (EC 2.7.7.6)	22	16	**38**	1.38	13	25	34.21	0
rrnAC3472	> 2 unique peptides	*guaAB*	GMP synthase [glutamine-hydrolyzing] subunit B (EC 6.3.5.2) (GMPsynthetase)	27	20	**47**	1.35	0	47	0	0

rrnAC0267	> 2 unique peptides	*imd1*	Inosine monophosphate dehydrogenase (EC 1.1.1.205)	10	8	**18**	1.25	0	18	0	0
rrnAC2699	> 2 unique peptides	*rrnAC2699*	Putative inosine monophosphate dehydrogenase (EC 1.1.1.205)	19	16	**35**	1.19	0	35	0	0
rrnAC1622	> 2 unique peptides	*nrdA*	Ribonucleoside-diphosphate reductase alpha chain(EC 1.17.4.1)	108	91	**199**	1.19	5	194	2.51	0
rrnAC0259	> 2 unique peptides	*rpb4*	RNA polymerase Rpb4	20	17	**37**	1.18	1	36	2.7	0
rrnAC3269	> 2 unique peptides	*rrnAC3269*	Hypothetical protein	11	10	**21**	1.1	0	21	0	0
rrnAC1109	> 2 unique peptides	*purD2*	Phosphoribosylamine-glycine ligase (EC 6.3.4.13)	33	32	**65**	1.03	2	63	3.08	0
rrnAC0192	> 2 unique peptides	*purB*	Adenylosuccinate lyase (EC 4.3.2.2)	11	11	**22**	1	0	22	0	0
rrnAC1396	> 2 unique peptides	*rpoL*	DNA-directed RNA polymerase subunit L (EC 2.7.7.6)	4	4	**8**	1	0	8	0	0
rrnAC0748	> 2 unique peptides	*guaB3*	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	35	36	**71**	0.97	1	70	1.41	0
rrnAC3346	> 2 unique peptides	*adk*	Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)	39	40	**79**	0.98	0	79	0	0
rrnAC1283	> 2 unique peptides	*purA*	Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)(AdSS) (AMPSase)	48	50	**98**	0.96	1	97	1.02	0
rrnAC0189	> 2 unique peptides	*purH*	Bifunctional purine biosynthesis protein PurH (EC 3.5.4.10)(EC 2.1.2.3) (EC 2.1.2.2)	28	33	**61**	0.85	0	61	0	0
rrnAC2659	> 2 unique peptides	*rrnAC2659*	Hypothetical protein	18	22	**40**	0.82	0	40	0	0
rrnAC2153	> 2 unique peptides	*mutT2*	Mut/nudix family protein	4	5	**9**	0.8	0	9	0	0
rrnAC0438	> 2 unique peptides	*purM*	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	12	15	**27**	0.8	0	27	0	0
rrnAC0106	> 2 unique peptides	*ndk*	Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)(Nucleoside-2-P kinase)	17	22	**39**	0.77	0	39	0	0
rrnAC0514	> 2 unique peptides	*surE*	5'-nucleotidase surE (EC 3.1.3.5) (Nucleoside 5'-monophosphatephosphohydrolase)	3	4	**7**	0.75	0	7	0	0
rrnAC1446	> 2 unique peptides	*purE*	Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21)	8	11	**19**	0.73	0	19	0	0
rrnAC0062	> 2 unique peptides	*rpoD*	DNA-directed RNA polymerase subunit D (EC 2.7.7.6)	4	7	**11**	0.57	0	11	0	0
rrnAC3272	> 2 unique peptides	*purU*	Formyltetrahydrofolate deformylase (EC 3.5.1.10) (EC 2.1.2.2)	4	8	**12**	0.5	0	12	0	0
rrnAC1390	> 2 unique peptides	*purL*	Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAMsynthase II)	5	10	**15**	0.5	0	15	0	0
rrnAC3268	> 2 unique peptides	*purQ*	Phosphoribosylformylglycinamidine synthase I (EC 6.3.5.3)	2	4	**6**	0.5	0	6	0	0
rrnAC1431	> 2 unique peptides	*purK*	Phosphoribosylaminoimidazole carboxylase ATP binding subunit (EC 4.1.1.21)	1	2	3	0.5	0	3	0	0
rrnAC1831	> 2 unique peptides	*polB1*	DNA polymerase B elongation subunit (EC 2.7.7.7)	1	2	3	0.5	0	3	0	0
rrnAC3275	> 2 unique peptides	*purC*	Phosphoribosylaminoimidazole-succinocarboxamide synthase(EC 6.3.2.6)	2	5	**7**	0.4	0	7	0	0
rrnAC3523	> 2 unique peptides	*apt*	Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT)	2	6	**8**	0.33	0	8	0	0
rrnAC2630	single hit	*prsA*	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)	1	0	1	#DIV/0!	0	1	0	0
rrnAC3256	single hit	*rrnAC3256*	Hypothetical protein	0	1	1	0	0	1	0	0
rrnAC0218	single hit	*rpoM*	DNA-directed RNA-polymerase subunit M	0	1	1	0	0	1	0	0
rrnAC0307	ND										
rrnAC1903	ND										
rrnAC0226	ND										
pNG7153	ND										
rrnAC1274	ND										
rrnAC2924	ND										
rrnB0283	ND										
rrnAC0068	ND										
rrnAC0313	ND										
rrnAC1668	ND										
pNG6176	ND										
rrnAC2714	ND										
rrnAC1232	ND										
rrnAC0282	ND										
rrnAC0894	ND										
rrnAC2493	ND										
rrnAC1504	ND										
pNG7124	ND										
pNG7123	ND										
pNG7125	ND										
00240 Pyrimidine metabolism [PATH:hma00240]											
rrnAC0067	> 2 unique peptides	*rpoN*	DNA-directed RNA polymerase subunit N (EC 2.7.7.6)	2	0	2	#DIV/0!	0	2	0	0
rrnAC2829	> 2 unique peptides	*rpoE'*	DNA-directed RNA polymerase subunit E'	22	7	**29**	3.14	0	29	0	0
rrnAC2432	> 2 unique peptides	*rpoH*	DNA-directed RNA polymerase subunit H (EC 2.7.7.6)	9	3	**12**	3	0	12	0	0
rrnAC2691	> 2 unique peptides	*polC*	DNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: HmapolC intein (Hma pol II intein)]	3	1	4	3	0	4	0	0
rrnAC2969	> 2 unique peptides	*pyrD*	Dihydroorotate dehydrogenase (EC 1.3.3.1) (Dihydroorotate oxidase)(DHOdehase) (DHODase) (DHOD)	32	15	**47**	2.13	47	0	100	0
rrnAC3363	> 2 unique peptides	*carA*	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	10	5	**15**	2	0	15	0	0
rrnAC3343	> 2 unique peptides	*cmk*	Cytidylate kinase (EC 2.7.4.14) (CK) (Cytidine monophosphate kinase)(CMP kinase)	4	2	**6**	2	0	6	0	0
rrnAC2159	> 2 unique peptides	*dcd3*	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase(EC 3.6.1.23)	2	1	3	2	0	3	0	0
rrnAC3360	> 2 unique peptides	*carB*	Carbamoylphosphate synthetase large subunit (EC 6.3.5.5)	17	9	**26**	1.89	0	26	0	0
rrnAC1121	> 2 unique peptides	*thyX*	Thymidylate synthase thyX (EC 2.1.1.148) (TS) (TSase)	19	11	**30**	1.73	0	30	0	0
rrnAC2428	> 2 unique peptides	*rpoA*	DNA-directed RNA polymerase (EC 2.7.7.6)	70	41	**111**	1.71	35	76	31.53	0
rrnAC2430	> 2 unique peptides	*rpoB*	DNA-directed RNA polymerase subunit B	54	34	**88**	1.59	28	60	31.82	0
rrnAC3434	> 2 unique peptides	*udp1*	Uridine phosphorylase (EC 2.4.2.3)	11	7	**18**	1.57	0	18	0	0
rrnAC2577	> 2 unique peptides	*upp*	Probable uracil phosphoribosyltransferase (EC 2.4.2.9) (UMPpyrophosphorylase) (UPRTase)	29	19	**48**	1.53	3	45	6.25	0
rrnAC2521	> 2 unique peptides	*pyrE1*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	6	4	**10**	1.5	0	10	0	0
rrnAC2830	> 2 unique peptides	*rpoE''*	DNA-directed RNA polymerase subunit E''	3	2	**5**	1.5	0	5	0	0
rrnAC1776	> 2 unique peptides	*dcd*	Probable deoxycytidine triphosphate deaminase (EC 3.5.4.13) (dCTPdeaminase)	3	2	**5**	1.5	0	5	0	0
rrnAC3471	> 2 unique peptides	*pyrG*	CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) (CTP synthetase)	24	17	**41**	1.41	0	41	0	0
rrnAC2429	> 2 unique peptides	*rpoB*	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	56	40	**96**	1.4	3	93	3.13	0

rrnAC2427	> 2 unique peptides	*rpoC*	RNA polymerase Rpb1 domain 5 (EC 2.7.7.6)	22	16	**38**	1.38	13	25	34.21	0
rrnAC3174	> 2 unique peptides	*pyrH*	Probable uridylate kinase (EC 2.7.4.-)	4	3	**7**	1.33	0	7	0	0
rrnAC0927	> 2 unique peptides	*pyrE2*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	15	12	**27**	1.25	2	25	7.41	0
rrnAC1622	> 2 unique peptides	*nrdA*	Ribonucleoside-diphosphate reductase alpha chain(EC 1.17.4.1)	108	91	**199**	1.19	5	194	2.51	0
rrnAC0259	> 2 unique peptides	*rpb4*	RNA polymerase Rpb4	20	17	**37**	1.18	1	36	2.7	0
rrnAC2232	> 2 unique peptides	*pyrC*	Dihydroorotase (EC 3.5.2.3)	6	6	**12**	1	0	12	0	0
rrnAC1396	> 2 unique peptides	*rpoL*	DNA-directed RNA polymerase subunit L (EC 2.7.7.6)	4	4	**8**	1	0	8	0	0
rrnAC0448	> 2 unique peptides	*udp2*	Uridine phosphorylase (EC 2.4.2.3)	15	15	**30**	1	0	30	0	0
rrnAC1225	> 2 unique peptides	*pyrB*	Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartatetranscarbamylase) (ATCase)	33	34	**67**	0.97	6	61	8.96	0
rrnAC0106	> 2 unique peptides	*ndk*	Nucleoside diphosphate kinase (EC 2.7.4.6) (NDK) (NDP kinase)(Nucleoside-2-P kinase)	17	22	**39**	0.77	0	39	0	0
rrnAC0514	> 2 unique peptides	*surE*	5'-nucleotidase surE (EC 3.1.3.5) (Nucleoside 5'-monophosphatephosphohydrolase)	3	4	**7**	0.75	0	7	0	0
rrnAC0062	> 2 unique peptides	*rpoD*	DNA-directed RNA polymerase subunit D (EC 2.7.7.6)	4	7	**11**	0.57	0	11	0	0
rrnAC1224	> 2 unique peptides	*pyrI*	Aspartate carbamoyltransferase regulatory chain	3	6	**9**	0.5	0	9	0	0
rrnAC1831	> 2 unique peptides	*polB1*	DNA polymerase B elongation subunit (EC 2.7.7.7)	1	2	3	0.5	0	3	0	0
rrnAC1515	> 2 unique peptides	*pyrF*	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)	2	7	**9**	0.29	0	9	0	0
rrnAC1129	> 2 unique peptides	*trxB3*	Thioredoxin reductase (EC 1.8.1.9)	1	6	**7**	0.17	0	7	0	0
rrnAC2670	single hit	*ort*	Orotate phosphoribosyltransferase (EC 2.4.2.10)	1	0	1	#DIV/0!	0	1	0	0
rrnAC1470	single hit	*trxB2*	Thioredoxin reductase (EC 1.8.1.9)	1	0	1	#DIV/0!	0	1	0	0
rrnAC0446	single hit	*cdd*	Cytidine deaminase (EC 3.5.4.5)	3	3	6	1	0	6	0	0
rrnAC3286	single hit	*tmk*	Probable thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	1	1	2	1	0	2	0	0
rrnAC0218	single hit	*rpoM*	DNA-directed RNA-polymerase subunit M	0	1	1	0	0	1	0	0
pNG7248	single hit	*amaB*	N-carbamoyl-L-amino acid amidohydrolase (EC 3.5.1.-)	0	1	1	0	0	1	0	0
pNG7078	single hit	*trxB1*	Thioredoxin reductase (EC 1.8.1.9)	0	2	2	0	0	2	0	0
pNG7258	ND										
rrnAC0068	ND										
rrnAC0313	ND										
rrnAC1668	ND										
pNG6176	ND										
rrnAC2714	ND										
rrnAC0052	ND										
rrnAC0282	ND										
rrnAC0894	ND										
01105 Amino Acid Metabolism											
00250 Alanine, aspartate and glutamate metabolism [PATH:hma00250]											
rrnB0219	> 2 unique peptides	*gabD*	Succinate-semialdehyde dehydrogenase	9	1	**10**	9	0	10	0	0
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC0797	> 2 unique peptides	*purF*	Amidophosphoribosyl transferase (EC 2.4.2.14)	3	1	4	3	0	4	0	0
rrnAC3363	> 2 unique peptides	*carA*	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)	10	5	**15**	2	0	15	0	0
rrnAC3360	> 2 unique peptides	*carB*	Carbamoylphosphate synthetase large subunit (EC 6.3.5.5)	17	9	**26**	1.89	0	26	0	0
rrnAC0384	> 2 unique peptides	*gdhA1*	NADP-specific glutamate dehydrogenase (EC 1.4.1.3)	76	51	**127**	1.49	25	102	19.69	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC2780	> 2 unique peptides	*glnA*	Glutamine synthetase (EC 6.3.1.2)	99	83	**182**	1.19	18	164	9.89	0
pNG7157	> 2 unique peptides	*gudB*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	76	75	**151**	1.01	19	132	12.58	0
rrnAC0192	> 2 unique peptides	*purB*	Adenylosuccinate lyase (EC 4.3.2.2)	11	11	**22**	1	0	22	0	0
rrnAC1225	> 2 unique peptides	*pyrB*	Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartatetranscarbamylase) (ATCase)	33	34	**67**	0.97	6	61	8.96	0
rrnAC1283	> 2 unique peptides	*purA*	Adenylosuccinate synthetase (EC 6.3.4.4) (IMP--aspartate ligase)(AdSS) (AMPSase)	48	50	**98**	0.96	1	97	1.02	0
rrnAC2683	> 2 unique peptides	*argG*	Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartateligase)	20	22	**42**	0.91	0	42	0	0
rrnAC0382	> 2 unique peptides	*gabT*	4-aminobutyrate aminotransferase	66	79	**145**	0.84	8	137	5.52	0
rrnAC0775	> 2 unique peptides	*gdhA2*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	52	64	**116**	0.81	1	115	0.86	0
rrnAC1224	> 2 unique peptides	*pyrI*	Aspartate carbamoyltransferase regulatory chain	3	6	**9**	0.5	0	9	0	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
rrnAC2681	single hit	*argH*	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL)	1	0	1	#DIV/0!	0	1	0	0
rrnAC0169	single hit	*gltB*	Glutamate synthase large subunit (EC 1.4.1.13)	1	0	1	#DIV/0!	0	1	0	0
rrnAC3409	ND										
rrnAC3420	ND										
rrnAC1359	ND										
rrnAC0884	ND										
rrnAC1587	ND										
rrnAC3235	ND										
00260 Glycine, serine and threonine metabolism [PATH:hma00260]											
rrnAC1884	> 2 unique peptides	*trpA*	Tryptophan synthase alpha chain (EC 4.2.1.20)	5	1	**6**	5	0	6	0	0
rrnAC2717	> 2 unique peptides	*serB1*	Phosphoserine phosphatase (EC 3.1.3.3)	3	1	4	3	0	4	0	0
rrnAC2667	> 2 unique peptides	*thrC3*	Threonine synthase	75	38	**113**	1.97	106	7	93.81	0
rrnAC0365	> 2 unique peptides	*asd*	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	14	9	**23**	1.56	0	23	0	0
rrnAC2408	> 2 unique peptides	*hom*	Homoserine dehydrogenase (EC 1.1.1.3)	15	10	**25**	1.5	0	25	0	0
rrnAC1820	> 2 unique peptides	*rrnAC1820*	Hypothetical protein	44	33	**77**	1.33	0	77	0	0
rrnAC1497	> 2 unique peptides	*nifS*	Selenocysteine lyase (EC 4.4.1.16)	14	11	**25**	1.27	0	25	0	0
rrnAC0999	> 2 unique peptides	*glyA*	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)(SHMT)	20	16	**36**	1.25	0	36	0	0
rrnAC1231	> 2 unique peptides	*ilvA1*	Threonine dehydratase (EC 4.3.1.19)	12	10	**22**	1.2	5	17	22.73	0
rrnAC2663	> 2 unique peptides	*lysC*	Aspartokinase (EC 2.7.2.4)	14	12	**26**	1.17	0	26	0	0

rrnAC3348	> 2 unique peptides	*thrB*	Homoserine kinase (EC 2.7.1.39) (HSK) (HK)	2	2	4	1	0	4	0	0
rrnAC3381	> 2 unique peptides	*lpdA1*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	5	5	**10**	1	0	10	0	0
rrnB0197	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	3	3	**6**	1	0	6	0	0
rrnAC2953	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	30	37	**67**	0.81	0	67	0	0
rrnAC2056	> 2 unique peptides	*serA3*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	3	4	**7**	0.75	0	7	0	0
rrnAC2696	> 2 unique peptides	*serA1*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	17	26	**43**	0.65	0	43	0	0
rrnAC3505	> 2 unique peptides	*thrC1*	Threonine synthase (EC 4.2.3.1)	5	10	**15**	0.5	0	15	0	0
rrnAC1498	> 2 unique peptides	*gcvP1*	Glycine dehydrogenase subunit 1 (EC 1.4.4.2)	2	5	**7**	0.4	0	7	0	0
rrnAC1500	> 2 unique peptides	*gcvT*	Probable aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage systemT protein)	1	3	4	0.33	0	4	0	0
rrnAC2508	> 2 unique peptides	*ilvA2*	Threonine dehydratase (EC 4.3.1.19)	1	3	4	0.33	0	4	0	0
pNG7361	> 2 unique peptides	*gcvT5*	Probable aminomethyltransferase (EC 2.1.2.10)	32	104	**136**	0.31	5	131	3.68	0
pNG7366	> 2 unique peptides	*gcvT3*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	9	40	**49**	0.23	0	49	0	0
pNG7370	> 2 unique peptides	*gcvT1*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	0	9	**9**	0	1	8	11.11	0
rrnAC0788	single hit	*pssA*	CDP-diacylglycerol-serine O phosphatidyltransferase	1	0	1	#DIV/0!	1	0	100	5
rrnAC1762	single hit	*serA2*	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)	0	2	2	0	0	2	0	0
pNG7257	ND										
rrnAC2515	ND										
pNG7333	ND										
rrnAC0362	ND										
rrnAC2451	ND										
pNG7015	ND										
rrnAC2552	ND										
rrnAC1865	ND										
pNG7371	ND										
rrnAC1885	ND										
00270 Cysteine and methionine metabolism [PATH:hma00270]											
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC0365	> 2 unique peptides	*asd*	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	14	9	**23**	1.56	0	23	0	0
rrnAC2408	> 2 unique peptides	*hom*	Homoserine dehydrogenase (EC 1.1.1.3)	15	10	**25**	1.5	0	25	0	0
rrnAC2840	> 2 unique peptides	*ahcY*	Adenosylhomocysteinase (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-homocysteine hydrolase)	15	11	**26**	1.36	0	26	0	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC1233	> 2 unique peptides	*mat*	S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionineadenosyltransferase) (AdoMet synthetase)	10	8	**18**	1.25	0	18	0	0
rrnAC2663	> 2 unique peptides	*lysC*	Aspartokinase (EC 2.7.2.4)	14	12	**26**	1.17	0	26	0	0
rrnAC2716	> 2 unique peptides	*cysD*	O-acetylhomoserine (Thiol)-lyase (EC 2.5.1.49)	31	42	**73**	0.74	5	68	6.85	0
rrnAC1236	> 2 unique peptides	*cysK1*	Cysteine synthase (EC 2.5.1.47)	2	3	**5**	0.67	0	5	0	0
rrnAC2414	> 2 unique peptides	*metB*	Cystathionine gamma-synthase (EC 2.5.1.48)	30	46	**76**	0.65	1	75	1.32	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
pNG7330	single hit	*cysE1*	Serine acetyltransferase (EC 2.3.1.30)	1	0	1	#DIV/0!	0	1	0	0
rrnAC0254	single hit	*metE*	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase(EC 2.1.1.14)	2	0	2	#DIV/0!	0	2	0	0
rrnAC1087	ND										
rrnAC0137	ND										
rrnAC0255	ND										
rrnB0070	ND										
rrnAC3064	ND										
rrnAC3063	ND										
00280 Valine, leucine and isoleucine degradation [PATH:hma00280]											
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnB0261	> 2 unique peptides	*pccB*	Propionyl-CoA carboxylase beta subunit	40	20	**60**	2	0	60	0	0
rrnAC0637	> 2 unique peptides	*mcmA1*	Methylmalonyl-CoA mutase subunit alpha	4	2	**6**	2	0	6	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnB0264	> 2 unique peptides	*acdH*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	37	31	**68**	1.19	0	68	0	0
rrnAC2957	> 2 unique peptides	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	31	27	**58**	1.15	0	58	0	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnAC3381	> 2 unique peptides	*lpdA1*	Dihydrolipoamide dehydrogenase (EC 1.8.1.4)	5	5	**10**	1	0	10	0	0
rrnB0197	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	3	3	**6**	1	0	6	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC2953	> 2 unique peptides	*lpdA2*	Dihydrolipoyl dehydrogenase 2 (EC 1.8.1.4) (Dihydrolipoamidedehydrogenase 2)	30	37	**67**	0.81	0	67	0	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC1983	> 2 unique peptides	*acdI*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	4	6	**10**	0.67	0	10	0	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC0934	> 2 unique peptides	*mcmA3*	Putative methylmalonyl-CoA mutase	5	8	**13**	0.63	0	13	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC3071	> 2 unique peptides	*ilvE1*	Branched-chain amino acid aminotransferase	20	35	**55**	0.57	0	55	0	0

rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
rrnAC0929	> 2 unique peptides	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	1	10	**11**	0.1	0	11	0	0
rrnAC1740	> 2 unique peptides	*mvaS*	Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	1	10	**11**	0.1	0	11	0	0
rrnAC1275	> 2 unique peptides	*mcmA2*	Methylmalonyl-CoA mutase subunit alpha	0	4	4	0	0	4	0	0
rrnAC0711	ND										
rrnAC0149	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00290 Valine, leucine and isoleucine biosynthesis [PATH:hma00290]											
rrnAC0331	> 2 unique peptides	*ilvN*	Acetolactate synthase small subunit (EC 2.2.1.6)	2	0	2	#DIV/0!	0	2	0	0
rrnB0199	> 2 unique peptides	*pdhB2*	Pyruvate dehydrogenase (EC 1.2.4.1)	22	3	**25**	7.33	5	20	20	0
rrnAC0330	> 2 unique peptides	*ilvB2*	Acetolactate synthase (EC 2.2.1.6)	8	3	**11**	2.67	4	7	36.36	0
rrnB0209	> 2 unique peptides	*ilvB3*	Acetolactate synthase large subunit (EC 2.2.1.6)	7	3	**10**	2.33	0	10	0	0
rrnAC0329	> 2 unique peptides	*leuA2*	2-isopropylmalate synthase 2 (EC 2.3.3.13)	5	3	**8**	1.67	0	8	0	0
rrnAC0332	> 2 unique peptides	*ilvC*	Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acidisomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase)	8	6	**14**	1.33	0	14	0	0
rrnAC1231	> 2 unique peptides	*ilvA1*	Threonine dehydratase (EC 4.3.1.19)	12	10	**22**	1.2	5	17	22.73	0
rrnAC2957	> 2 unique peptides	*pdhA3*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)(EC 1.2.4.4)	31	27	**58**	1.15	0	58	0	0
rrnAC2650	> 2 unique peptides	*leuS1*	Leucyl-tRNA synthetase (EC 6.1.1.4)	16	14	**30**	1.14	0	30	0	0
rrnAC2956	> 2 unique peptides	*pdhB1*	Pyruvate dehydrogenase (EC 1.2.4.1)	59	69	**128**	0.86	20	108	15.63	0
rrnAC0302	> 2 unique peptides	*ilvD*	Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD)	26	32	**58**	0.81	0	58	0	0
rrnAC2947	> 2 unique peptides	*leuS2*	Leucyl-tRNA synthetase (EC 6.1.1.4)	35	46	**81**	0.76	0	81	0	0
rrnAC0336	> 2 unique peptides	*leuD*	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)	3	4	**7**	0.75	0	7	0	0
rrnAC0134	> 2 unique peptides	*ilvB1*	Acetolactate synthase large subunit (EC 2.2.1.6)	16	22	**38**	0.73	1	37	2.63	0
rrnAC0340	> 2 unique peptides	*ipmD*	3-isopropylmalate dehydrogenase (EC 1.1.1.85)	10	15	**25**	0.67	0	25	0	0
rrnAC3071	> 2 unique peptides	*ilvE1*	Branched-chain amino acid aminotransferase	20	35	**55**	0.57	0	55	0	0
rrnAC2634	> 2 unique peptides	*ileS*	Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)(IleRS)	25	45	**70**	0.56	0	70	0	0
rrnAC1729	> 2 unique peptides	*valS*	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS)	8	18	**26**	0.44	0	26	0	0
rrnAC2508	> 2 unique peptides	*ilvA2*	Threonine dehydratase (EC 4.3.1.19)	1	3	4	0.33	0	4	0	0
rrnAC0334	> 2 unique peptides	*leuC*	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)(Isopropylmalate isomerase) (Alpha-IPM isomerase) (IPMI)	2	9	**11**	0.22	0	11	0	0
rrnAC1690	single hit	*leuA1*	2-isopropylmalate synthase 2 (EC 2.3.3.13)	1	0	1	#DIV/0!	0	1	0	0
rrnB0200	single hit	*pdhA2*	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	2	2	4	1	0	4	0	0
pNG7371	ND										
rrnAC0711	ND										
rrnAC0149	ND										
00300 Lysine biosynthesis [PATH:hma00300]											
rrnAC2679	> 2 unique peptides	*rimK*	Ribosomal protein S6 modification protein	9	1	**10**	9	0	10	0	0
rrnAC2674	> 2 unique peptides	*gltCP*	Glutamate carboxypeptidase (EC 3.4.17.11)	6	2	**8**	3	0	8	0	0
rrnAC2678	> 2 unique peptides	*argC*	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	10	4	**14**	2.5	0	14	0	0
rrnAC0132	> 2 unique peptides	*rrnAC0132*	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (EC 1.5.1.7)(EC 1.5.1.10)	7	4	**11**	1.75	0	11	0	0
rrnAC2675	> 2 unique peptides	*argD*	Acetylornithine aminotransferase (EC 2.6.1.11)	19	12	**31**	1.58	0	31	0	0
rrnAC0365	> 2 unique peptides	*asd*	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)	14	9	**23**	1.56	0	23	0	0
rrnAC2408	> 2 unique peptides	*hom*	Homoserine dehydrogenase (EC 1.1.1.3)	15	10	**25**	1.5	0	25	0	0
rrnAC0204	> 2 unique peptides	*dapD*	23,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase(EC 2.3.1.117)	27	21	**48**	1.29	0	48	0	0
rrnAC2663	> 2 unique peptides	*lysC*	Aspartokinase (EC 2.7.2.4)	14	12	**26**	1.17	0	26	0	0
rrnAC0206	> 2 unique peptides	*dapB*	Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR)	6	6	**12**	1	0	12	0	0
rrnAC0207	> 2 unique peptides	*dapA*	Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPS)	9	10	**19**	0.9	0	19	0	0
rrnAC2676	single hit	*argB2*	Acetylglutamate kinase (EC 2.7.2.8)	3	4	7	0.75	0	7	0	0
rrnAC0198	single hit	*odc*	Diaminopimelate decarboxylase (EC 4.1.1.20)	0	1	1	0	0	1	0	0
rrnAC0960	ND										
rrnAC0196	ND										
rrnAC2680	ND										
00310 Lysine degradation [PATH:hma00310]											
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnAC0132	> 2 unique peptides	*rrnAC0132*	Lysine-ketoglutarate reductase/saccharopine dehydrogenase (EC 1.5.1.7)(EC 1.5.1.10)	7	4	**11**	1.75	0	11	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0

rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC1972	> 2 unique peptides	*gcdH*	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)	46	63	**109**	0.73	3	106	2.75	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00330 Arginine and proline metabolism [PATH:hma00330]											
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC0383	> 2 unique peptides	*arg2*	Arginase (EC 3.5.3.1)	16	4	**20**	4	0	20	0	0
rrnAC2678	> 2 unique peptides	*argC*	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38) (AGPR) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	10	4	**14**	2.5	0	14	0	0
rrnAC0223	> 2 unique peptides	*camH3*	Creatinine amidohydrolase (EC 3.5.2.10)	2	1	3	2	0	3	0	0
rrnAC2675	> 2 unique peptides	*argD*	Acetylornithine aminotransferase (EC 2.6.1.11)	19	12	**31**	1.58	0	31	0	0
rrnAC0384	> 2 unique peptides	*gdhA1*	NADP-specific glutamate dehydrogenase (EC 1.4.1.3)	76	51	**127**	1.49	25	102	19.69	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC2780	> 2 unique peptides	*glnA*	Glutamine synthetase (EC 6.3.1.2)	99	83	**182**	1.19	18	164	9.89	0
pNG7157	> 2 unique peptides	*gudB*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	76	75	**151**	1.01	19	132	12.58	0
pNG7165	> 2 unique peptides	*hyuB*	N-methylhydantoinase B (EC 3.5.2.9)	4	4	**8**	1	0	8	0	0
rrnAC2683	> 2 unique peptides	*argG*	Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartateligase)	20	22	**42**	0.91	0	42	0	0
rrnAC2471	> 2 unique peptides	*yusM*	Proline dehydrogenase	9	10	**19**	0.9	7	12	36.84	0
rrnAC0227	> 2 unique peptides	*ocd3*	Ornithine cyclodeaminase (EC 4.3.1.12)	21	24	**45**	0.88	0	45	0	0
rrnAC3121	> 2 unique peptides	*eda*	2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxoglutaratealdolase (EC 4.1.2.14)	14	17	**31**	0.82	0	31	0	0
rrnAC0775	> 2 unique peptides	*gdhA2*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	52	64	**116**	0.81	1	115	0.86	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
pNG7164	> 2 unique peptides	*hyuA*	N-methylhydaintoinase A (EC 3.5.2.9)	6	8	**14**	0.75	0	14	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC0038	> 2 unique peptides	*ocd1*	Ornithine cyclodeaminase (EC 4.3.1.12)	5	8	**13**	0.63	0	13	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
rrnAC0453	> 2 unique peptides	*arg1*	Arginase (EC 3.5.3.1)	0	2	2	0	0	2	0	0
rrnAC2470	single hit	*prr*	Proline racemase (EC 5.1.1.4)	1	0	1	#DIV/0!	0	1	0	0
rrnAC2681	single hit	*argH*	Argininosuccinate lyase (EC 4.3.2.1) (Arginosuccinase) (ASAL)	1	0	1	#DIV/0!	0	1	0	0
rrnAC2676	single hit	*argB2*	Acetylglutamate kinase (EC 2.7.2.8)	3	4	7	0.75	0	7	0	0
rrnAC0198	single hit	*odc*	Diaminopimelate decarboxylase (EC 4.1.1.20)	0	1	1	0	0	1	0	0
pNG7096	ND										
pNG7341	ND										
rrnAC3199	ND										
pNG7067	ND										
rrnAC1927	ND										
rrnB0070	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
rrnAC2941	ND										
pNG7124	ND										
pNG7123	ND										
pNG7125	ND										
rrnAC0884	ND										
rrnAC2095	ND										
00340 Histidine metabolism [PATH:hma00340]											
rrnAC2371	> 2 unique peptides	*hisE*	Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31) (PRA-PH)	4	1	**5**	4	0	5	0	0
rrnAC0529	> 2 unique peptides	*hisC*	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	6	7	**13**	0.86	0	13	0	0
rrnAC1789	> 2 unique peptides	*hutG*	Probable formimidoylglutamase (EC 3.5.3.8)	9	11	**20**	0.82	0	20	0	0
rrnAC0272	> 2 unique peptides	*hisD*	Histidinol dehydrogenase (EC 1.1.1.23) (HDH)	10	13	**23**	0.77	0	23	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0

rrnAC2835	> 2 unique peptides	*hisG*	ATP phosphoribosyltransferase (EC 2.4.2.17) (ATP-PRTase) (ATP-PRT)	7	10	**17**	0.7	0	17	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC1787	> 2 unique peptides	*hutU*	Urocanate hydratase (EC 4.2.1.49)	57	115	**172**	0.5	13	159	7.56	0
rrnAC1790	> 2 unique peptides	*hutI*	Imidazolonepropionase (EC 3.5.2.7)	15	35	**50**	0.43	0	50	0	0
rrnAC1791	> 2 unique peptides	*hutH*	Histidine ammonia-lyase (EC 4.3.1.3)	23	55	**78**	0.42	8	70	10.26	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC2529	> 2 unique peptides	*hisA*	1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase (EC 5.3.1.16)(Phosphoribosylformimino-5-aminoimidazole carboxamide ribotideisomerase)	1	4	**5**	0.25	0	5	0	0
rrnAC1394	> 2 unique peptides	*hisF*	Imidazole glycerol phosphate synthase subunit hisF (EC 4.1.3.-) (IGPsynthase cyclase subunit) (IGP synthase subunit hisF) (ImGP synthasesubunit hisF)	0	3	3	0	0	3	0	0
rrnAC2524	ND										
rrnAC2794	ND										
rrnAC2555	ND										
rrnAC1934	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
rrnAC0542	ND										
rrnAC3101	ND										
00350 Tyrosine metabolism [PATH:hma00350]											
rrnB0219	> 2 unique peptides	*gabD*	Succinate-semialdehyde dehydrogenase	9	1	**10**	9	0	10	0	0
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC0012	> 2 unique peptides	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	18	17	**35**	1.06	1	34	2.86	0
rrnAC0529	> 2 unique peptides	*hisC*	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	6	7	**13**	0.86	0	13	0	0
pNG7289	> 2 unique peptides	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	9	13	**22**	0.69	0	22	0	0
rrnAC1402	> 2 unique peptides	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	5	8	**13**	0.63	0	13	0	0
pNG7278	> 2 unique peptides	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	4	7	**11**	0.57	0	11	0	0
rrnAC0191	> 2 unique peptides	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	6	11	**17**	0.55	1	16	5.88	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
pNG7032	> 2 unique peptides	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	3	3	0	0	3	0	0
pNG7314	single hit	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	1	1	2	1	0	2	0	0
pNG7351	single hit	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	2	2	0	0	2	0	0
rrnAC1934	ND										
rrnAC1798	ND										
pNG7022	ND										
pNG7101	ND										
pNG7103	ND										
rrnAC1300	ND										
rrnAC1975	ND										
rrnAC2172	ND										
rrnAC3506	ND										
rrnAC0542	ND										
rrnAC3101	ND										
00360 Phenylalanine metabolism [PATH:hma00360]											
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC0529	> 2 unique peptides	*hisC*	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	6	7	**13**	0.86	0	13	0	0
rrnAC0717	> 2 unique peptides	*rrnAC0717*	FAD/NAD binding oxidoreductase (EC 1.18.1.3)	5	8	**13**	0.63	0	13	0	0
rrnB0243	> 2 unique peptides	*paaK1*	Phenylacetyl-coenzyme A ligase	5	15	**20**	0.33	0	20	0	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
rrnB0231	ND										
rrnAC1934	ND										
00380 Tryptophan metabolism [PATH:hma00380]											
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnAC1171	> 2 unique peptides	*perA*	Peroxidase/catalase (EC 1.11.1.6) (Catalase-peroxidase)	161	155	**316**	1.04	3	313	0.95	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC2965	> 2 unique peptides	*trpS*	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	11	11	**22**	1	0	22	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0

rrnAC1972	> 2 unique peptides	*gcdH*	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)	46	63	**109**	0.73	3	106	2.75	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0073	> 2 unique peptides	*cyc*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	2	3	0.5	1	2	33.33	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC3312	> 2 unique peptides	*cyp1*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	3	4	0.33	4	0	100	0
rrnAC2439	> 2 unique peptides	*tnaA*	Tryptophanase (EC 4.1.99.1)	12	68	**80**	0.18	14	66	17.5	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
pNG7354	ND										
rrnAC2018	ND										
00400 Phenylalanine, tyrosine and tryptophan biosynthesis [PATH:hma00400]											
rrnAC1884	> 2 unique peptides	*trpA*	Tryptophan synthase alpha chain (EC 4.2.1.20)	5	1	**6**	5	0	6	0	0
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC0752	> 2 unique peptides	*rrnAC0752*	Hypothetical protein	10	3	**13**	3.33	0	13	0	0
rrnAC0124	> 2 unique peptides	*aroC*	Chorismate synthase (EC 4.2.3.5) (5-enolpyruvylshikimate-3-phosphatephospholyase)	12	7	**19**	1.71	0	19	0	0
rrnAC0709	> 2 unique peptides	*trpE1*	Anthranilate synthase component 1 1 (EC 4.1.3.27) (Anthranilatesynthase component I 1)	4	3	**7**	1.33	0	7	0	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC0127	> 2 unique peptides	*aroA*	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)	3	3	**6**	1	0	6	0	0
rrnAC3306	> 2 unique peptides	*trpD1*	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	51	53	**104**	0.96	1	103	0.96	0
rrnAC2950	> 2 unique peptides	*pheA*	Prephenate dehydratase (EC 4.2.1.51)	9	10	**19**	0.9	0	19	0	0
rrnAC0529	> 2 unique peptides	*hisC*	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	6	7	**13**	0.86	0	13	0	0
rrnAC1877	> 2 unique peptides	*aroD*	3-dehydroquinate dehydratase (EC 4.2.1.10)	3	5	**8**	0.6	0	8	0	0
rrnAC1879	> 2 unique peptides	*aroB*	3-dehydroquinate synthase (EC 4.2.3.4)	7	12	**19**	0.58	0	19	0	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
rrnAC1520	single hit	*trpD*	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	3	2	5	1.5	1	4	20	0
rrnAC0707	single hit	*aroE*	Shikimate 5-dehydrogenase (EC 1.1.1.25)	1	1	2	1	0	2	0	0
rrnAC0753	single hit	*aroK*	Shikimate kinase (EC 2.7.1.71)	1	1	2	1	0	2	0	0
pNG7327	single hit	*trpE3*	Anthranilate synthase component 1 3 (EC 4.1.3.27)	0	1	1	0	0	1	0	0
rrnAC1518	ND										
pNG7325	ND										
rrnAC0710	ND										
rrnAC1517	ND										
rrnAC1519	ND										
rrnAC1886	ND										
rrnAC1885	ND										
rrnAC0512	ND										
rrnAC1934	ND										
01106 Metabolism of Other Amino Acids											
00410 beta-Alanine metabolism [PATH:hma00410]											
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnB0264	> 2 unique peptides	*acdH*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	37	31	**68**	1.19	0	68	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC0382	> 2 unique peptides	*gabT*	4-aminobutyrate aminotransferase	66	79	**145**	0.84	8	137	5.52	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC1983	> 2 unique peptides	*acdI*	Acyl-CoA dehydrogenase (EC 1.3.99.3)	4	6	**10**	0.67	0	10	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
pNG7248	single hit	*amaB*	N-carbamoyl-L-amino acid amidohydrolase (EC 3.5.1.-)	0	1	1	0	0	1	0	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
rrnB0070	ND										

rrnAC0052	ND										
00440 Phosphonate and phosphinate metabolism [PATH:hma00440]											
pNG7088	> 2 unique peptides	*qad*	Quinohemoprotein alcohol dehydrogenase (EC 1.1.99.-)	17	9	**26**	1.89	26	0	100	0
pNG7099	single hit	*cpt*	CDP-alcohol phosphatidyltransferase (EC 2.7.8.-)	1	0	1	#DIV/0!	1	0	100	5
00450 Selenoamino acid metabolism [PATH:hma00450]											
rrnAC2840	> 2 unique peptides	*ahcY*	Adenosylhomocysteinase (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-homocysteine hydrolase)	15	11	**26**	1.36	0	26	0	0
rrnAC1233	> 2 unique peptides	*mat*	S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionineadenosyltransferase) (AdoMet synthetase)	10	8	**18**	1.25	0	18	0	0
rrnAC1800	> 2 unique peptides	*metG*	Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)(MetRS)	24	20	**44**	1.2	0	44	0	0
rrnAC1236	> 2 unique peptides	*cysK1*	Cysteine synthase (EC 2.5.1.47)	2	3	**5**	0.67	0	5	0	0
rrnAC2414	> 2 unique peptides	*metB*	Cystathionine gamma-synthase (EC 2.5.1.48)	30	46	**76**	0.65	1	75	1.32	0
rrnAC3104	> 2 unique peptides	*csd1*	Probable cysteine desulfurase (EC 4.4.1.-)	3	7	**10**	0.43	1	9	10	0
rrnAC0542	ND										
rrnAC3101	ND										
rrnAC0137	ND										
pNG7239	ND										
00460 Cyanoamino acid metabolism [PATH:hma00460]											
rrnAC0999	> 2 unique peptides	*glyA*	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)(SHMT)	20	16	**36**	1.25	0	36	0	0
rrnAC1113	> 2 unique peptides	*bglX-2*	Beta-D-glucosidase	0	4	4	0	0	4	0	0
pNG7354	ND										
rrnAC0173	ND										
rrnAC3420	ND										
00471 D-Glutamine and D-glutamate metabolism											
rrnAC0384	> 2 unique peptides	*gdhA1*	NADP-specific glutamate dehydrogenase (EC 1.4.1.3)	76	51	**127**	1.49	25	102	19.69	0
pNG7157	> 2 unique peptides	*gudB*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	76	75	**151**	1.01	19	132	12.58	0
rrnAC0775	> 2 unique peptides	*gdhA2*	NAD(P)-specific glutamate dehydrogenase (EC 1.4.1.3)	52	64	**116**	0.81	1	115	0.86	0
00480 Glutathione metabolism [PATH:hma00480]											
rrnAC3419	> 2 unique peptides	*icd*	Isocitrate dehydrogenase (EC 1.1.1.42)	96	90	**186**	1.07	11	175	5.91	0
rrnAC2180	> 2 unique peptides	*gnd*	6-phosphogluconate dehydrogenase (EC 1.1.1.44)	5	3	**8**	1.67	0	8	0	0
rrnAC0198	single hit	*odc*	Diaminopimelate decarboxylase (EC 4.1.1.20)	0	1	1	0	0	1	0	0
rrnB0070	ND										
01107 Glycan Biosynthesis and Metabolism											
00514 O-Mannosyl glycan biosynthesis											
rrnAC1432	> 2 unique peptides	*dpm5*	Dolichyl-phosphate-mannose-protein mannosyltransferase (EC 2.4.1.-)(EC 2.4.1.109)	32	20	**52**	1.6	52	0	100	10
01005 Lipopolysaccharide biosynthesis proteins											
pNG7011	ND										
00511 Other glycan degradation [PATH:hma00511]											
pNG5066	ND										
01003 Glycosyltransferases											
rrnAC1432	> 2 unique peptides	*dpm5*	Dolichyl-phosphate-mannose-protein mannosyltransferase (EC 2.4.1.-)(EC 2.4.1.109)	32	20	**52**	1.6	52	0	100	10
rrnAC0431	> 2 unique peptides	*tot*	Transmembrane oligosaccharyl transferase	55	35	**90**	1.57	90	0	100	13
rrnAC3242	> 2 unique peptides	*rrnAC3242*	Hypothetical protein	3	2	**5**	1.5	5	0	100	11
rrnAC0419	> 2 unique peptides	*gtl*	Glycosyl transferase-like	15	11	**26**	1.36	26	0	100	2
01108 Biosynthesis of Polyketides and Nonribosomal Peptides											
00523 Polyketide sugar unit biosynthesis [PATH:hma00523]											
rrnAC0633	> 2 unique peptides	*rffH2*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	35	23	**58**	1.52	0	58	0	0
rrnAC2178	> 2 unique peptides	*rfbB3*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	4	3	**7**	1.33	7	0	100	0
rrnAC1572	> 2 unique peptides	*rfbB2*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	27	23	**50**	1.17	2	48	4	0
rrnAC1011	> 2 unique peptides	*rffG*	DTDP-glucose dehydratase (EC 4.2.1.46)	3	4	**7**	0.75	1	6	14.29	0
rrnAC1010	> 2 unique peptides	*rfbB1*	DTDP-glucose 4-6-dehydratase (EC 4.2.1.46)	29	39	**68**	0.74	13	55	19.12	0
rrnAC3238	> 2 unique peptides	*rffH3*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	10	18	**28**	0.56	3	25	10.71	0
rrnAC1960	> 2 unique peptides	*graD4b*	Glucose-1-phosphate thymidylyltransferase	7	13	**20**	0.54	0	20	0	0
rrnAC3232	> 2 unique peptides	*graD4c*	Glucose-1-phosphate thymidylyltransferase	3	7	**10**	0.43	0	10	0	0
pNG7218	ND										
rrnAC2343	ND										
01053 Biosynthesis of siderophore group nonribosomal peptides [PATH:hma01053]											
rrnAC0837	ND										
rrnAC2100	ND										
01055 Biosynthesis of vancomycin group antibiotics											
rrnAC2178	> 2 unique peptides	*rfbB3*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	4	3	**7**	1.33	7	0	100	0
rrnAC1572	> 2 unique peptides	*rfbB2*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	27	23	**50**	1.17	2	48	4	0
rrnAC1011	> 2 unique peptides	*rffG*	DTDP-glucose dehydratase (EC 4.2.1.46)	3	4	**7**	0.75	1	6	14.29	0
rrnAC1010	> 2 unique peptides	*rfbB1*	DTDP-glucose 4-6-dehydratase (EC 4.2.1.46)	29	39	**68**	0.74	13	55	19.12	0
01109 Metabolism of Cofactors and Vitamins											
00730 Thiamine metabolism [PATH:hma00730]											
rrnAC2449	> 2 unique peptides	*thiD*	Phosphomethylpyrimidine kinase (EC 2.7.4.7)	5	1	**6**	5	0	6	0	0
rrnAC3104	> 2 unique peptides	*csd1*	Probable cysteine desulfurase (EC 4.4.1.-)	3	7	**10**	0.43	1	9	10	0
rrnAC1765	> 2 unique peptides	*tenA*	Transcriptional activator tenA	3	21	**24**	0.14	1	23	4.17	0

rrnAC1182	> 2 unique peptides	*thiC*	Thiamine biosynthesis protein thiC	0	59	**59**	0	2	57	3.39	0
rrnAC1767	> 2 unique peptides	*tenA-2*	Transcriptional regulator putative	0	9	**9**	0	0	9	0	0
rrnAC1234	ND										
rrnAC2143	ND										
rrnAC3177	ND										
rrnAC2493	ND										
00740 Riboflavin metabolism [PATH:hma00740]											
rrnAC3074	> 2 unique peptides	*rrnAC3074*	Hypothetical protein	1	2	3	0.5	0	3	0	0
rrnAC2367	> 2 unique peptides	*ribC*	Ribiflavin synthase alpha chain (EC 2.5.1.9)	2	9	**11**	0.22	0	11	0	0
rrnAC1131	single hit	*ribG*	25-diamino-6-hydroxy-4-(5-phosphoribosylamino)pyrimidine 1-reductase(EC 1.1.1.-)	2	2	4	1	0	4	0	0
rrnAC3073	ND										
rrnAC1433	ND										
00750 Vitamin B6 metabolism [PATH:hma00750]											
rrnAC2667	> 2 unique peptides	*thrC3*	Threonine synthase	75	38	**113**	1.97	106	7	93.81	0
rrnAC1732	> 2 unique peptides	*pdxS*	Pyridoxal biosynthesis lyase pdxS (EC 4.-.-.-)	46	44	**90**	1.05	4	86	4.44	0
rrnAC2369	> 2 unique peptides	*pdxT*	Glutamine amidotransferase subunit pdxT (EC 2.6.-.-) (Glutamineamidotransferase glutaminase subunit pdxT)	10	12	**22**	0.83	0	22	0	0
rrnAC3505	> 2 unique peptides	*thrC1*	Threonine synthase (EC 4.2.3.1)	5	10	**15**	0.5	0	15	0	0
pNG7257	ND										
rrnAC2515	ND										
00760 Nicotinate and nicotinamide metabolism [PATH:hma00760]											
rrnAC2241	> 2 unique peptides	*rrnAC2241*	Quinolinate phosphoribosyl transferase (EC 2.4.2.19)	9	2	**11**	4.5	0	11	0	0
rrnAC2486	> 2 unique peptides	*nadE1*	NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	8	9	**17**	0.89	0	17	0	0
rrnAC0514	> 2 unique peptides	*surE*	5'-nucleotidase surE (EC 3.1.3.5) (Nucleoside 5'-monophosphatephosphohydrolase)	3	4	**7**	0.75	0	7	0	0
rrnAC3391	> 2 unique peptides	*ppnK*	Probable inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23)(Poly(P)/ATP NAD kinase)	1	2	3	0.5	0	3	0	0
rrnAC1913	single hit	*rrnAC1913*	Nicotinamide-nucleotide adenylyltransferase (EC 2.7.7.1) (NAD(+)pyrophosphorylase) (NAD(+) diphosphorylase) (NMN adenylyltransferase)	0	1	1	0	0	1	0	0
rrnAC3409	ND										
rrnAC3410	ND										
rrnAC3408	ND										
pNG7227	ND										
rrnAC0226	ND										
rrnAC0727	ND										
rrnAC0821	ND										
00770 Pantothenate and CoA biosynthesis [PATH:hma00770]											
rrnAC0331	> 2 unique peptides	*ilvN*	Acetolactate synthase small subunit (EC 2.2.1.6)	2	0	2	#DIV/0!	0	2	0	0
rrnAC0330	> 2 unique peptides	*ilvB2*	Acetolactate synthase (EC 2.2.1.6)	8	3	**11**	2.67	4	7	36.36	0
rrnB0209	> 2 unique peptides	*ilvB3*	Acetolactate synthase large subunit (EC 2.2.1.6)	7	3	**10**	2.33	0	10	0	0
rrnAC0332	> 2 unique peptides	*ilvC*	Ketol-acid reductoisomerase (EC 1.1.1.86) (Acetohydroxy-acidisomeroreductase) (Alpha-keto-beta-hydroxylacil reductoisomerase)	8	6	**14**	1.33	0	14	0	0
rrnAC0868	> 2 unique peptides	*coaD2*	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	8	6	**14**	1.33	0	14	0	0
rrnAC0878	> 2 unique peptides	*panB*	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)	4	4	**8**	1	0	8	0	0
rrnAC0302	> 2 unique peptides	*ilvD*	Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD)	26	32	**58**	0.81	0	58	0	0
rrnAC0134	> 2 unique peptides	*ilvB1*	Acetolactate synthase large subunit (EC 2.2.1.6)	16	22	**38**	0.73	1	37	2.63	0
rrnAC3071	> 2 unique peptides	*ilvE1*	Branched-chain amino acid aminotransferase	20	35	**55**	0.57	0	55	0	0
rrnAC2278	single hit	*coaD1*	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)	1	0	1	#DIV/0!	0	1	0	0
rrnAC3539	single hit	*dfp*	Pantothenate metabolism flavoprotein	0	1	1	0	0	1	0	0
pNG7248	single hit	*amaB*	N-carbamoyl-L-amino acid amidohydrolase (EC 3.5.1.-)	0	1	1	0	0	1	0	0
rrnAC3068	ND										
rrnAC0711	ND										
rrnAC0052	ND										
00780 Biotin metabolism [PATH:hma00780]											
rrnAC0001	> 2 unique peptides	*birA*	Biotin-(Acetyl-CoA carboxylase) ligase	0	5	**5**	0	0	5	0	0
rrnAC0885	ND										
rrnAC0883	ND										
00785 Lipoic acid metabolism [PATH:hma00785]											
rrnAC2019	single hit	*lpl*	Lipoate protein ligase (EC 6.3.4.-)	0	1	1	0	0	1	0	0
rrnAC2959	ND										
00790 Folate biosynthesis [PATH:hma00790]											
rrnAC0246	> 2 unique peptides	*folP3*	Dihydropteroate synthase (EC 2.5.1.15)	11	15	**26**	0.73	1	25	3.85	0
rrnAC1616	> 2 unique peptides	*mch*	N(5)N(10)-methenyltetrahydromethanopterin cyclohydrolase(EC 3.5.4.27)	2	9	**11**	0.22	0	11	0	0
pNG7379	single hit	*folP2*	Dihydropteroate synthase (EC 2.5.1.15)	0	3	3	0	0	3	0	0
rrnAC2437	single hit	*mer1*	F420-dependent N5N10-methylene-tetrahydromethanopterin reductase	0	2	2	0	0	2	0	0
pNG7382	ND										
rrnAC0184	ND										
pNG7359	ND										
rrnAC0859	ND										
rrnAC2166	ND										
00670 One carbon pool by folate [PATH:hma00670]											
rrnAC1121	> 2 unique peptides	*thyX*	Thymidylate synthase thyX (EC 2.1.1.148) (TS) (TSase)	19	11	**30**	1.73	0	30	0	0
rrnAC0999	> 2 unique peptides	*glyA*	Serine hydroxymethyltransferase (EC 2.1.2.1) (Serine methylase)(SHMT)	20	16	**36**	1.25	0	36	0	0

rrnAC0996	> 2 unique peptides	*folD 1*	Bifunctional protein folD 1 [Includes: Methylenetetrahydrofolatedehydrogenase (EC 1.5.1.5)	14	15	**29**	0.93	0	29	0	0
rrnAC0189	> 2 unique peptides	*purH*	Bifunctional purine biosynthesis protein PurH (EC 3.5.4.10)(EC 2.1.2.3) (EC 2.1.2.2)	28	33	**61**	0.85	0	61	0	0
rrnAC3272	> 2 unique peptides	*purU*	Formyltetrahydrofolate deformylase (EC 3.5.1.10) (EC 2.1.2.2)	4	8	**12**	0.5	0	12	0	0
rrnAC1500	> 2 unique peptides	*gcvT*	Probable aminomethyltransferase (EC 2.1.2.10) (Glycine cleavage systemT protein)	1	3	4	0.33	0	4	0	0
pNG7361	> 2 unique peptides	*gcvT5*	Probable aminomethyltransferase (EC 2.1.2.10)	32	104	**136**	0.31	5	131	3.68	0
pNG7366	> 2 unique peptides	*gcvT3*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	9	40	**49**	0.23	0	49	0	0
pNG7380	> 2 unique peptides	*fhs*	Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolatesynthetase) (FHS) (FTHFS)	2	27	**29**	0.07	1	28	3.45	0
pNG7328	> 2 unique peptides	*folD 2*	Bifunctional protein folD 2 [Includes: Methylenetetrahydrofolatedehydrogenase (EC 1.5.1.5)	0	5	**5**	0	0	5	0	0
pNG7370	> 2 unique peptides	*gcvT1*	Sacrosine dehydrogenase/glycine cleavage T-protein (EC 1.5.3.1)(EC 2.1.2.10)	0	9	**9**	0	1	8	11.11	0
pNG7363	> 2 unique peptides	*metF*	5,10-methylenetetrahydrofolate reductase (EC 1.7.99.5)	0	4	4	0	4	0	100	0
rrnAC3378	single hit	*rrnAC3378*	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)	1	0	1	#DIV/0!	0	1	0	0
pNG7359	ND										
rrnAC0859	ND										
rrnAC2552	ND										
pNG7381	ND										
00860 Porphyrin and chlorophyll metabolism [PATH:hma00860]											
rrnAC3000	> 2 unique peptides	*cbiL*	Precorrin-2 C20-methyltransferase	5	0	**5**	#DIV/0!	2	3	40	0
rrnAC3001	> 2 unique peptides	*cbiF*	Cobalamin biosynthesis precorrin-3 methylase	7	0	**7**	#DIV/0!	0	7	0	0
rrnAC3019	> 2 unique peptides	*cobN*	Cobalamin biosynthesis protein	111	40	**151**	2.78	0	151	0	0
rrnAC3018	> 2 unique peptides	*hmcA*	Protporphyrin IX magnesium chelatase	4	2	**6**	2	0	6	0	0
rrnAC3003	> 2 unique peptides	*cbiG*	Cobalamin biosynthesis protein G	12	7	**19**	1.71	0	19	0	0
rrnAC1102	> 2 unique peptides	*cobB*	Probable cobyrinic acid A,C-diamide synthase	5	3	**8**	1.67	3	5	37.5	0
rrnAC3020	> 2 unique peptides	*cbiC*	Precorrin-8X methylmutase (EC 5.4.1.2)	36	24	**60**	1.5	3	57	5	0
rrnAC3021	> 2 unique peptides	*cbiJ*	Precorrin-3 methylase	38	26	**64**	1.46	1	63	1.56	0
rrnAC1936	> 2 unique peptides	*cobI*	Cobalamin adenosyltransferase (EC 2.5.1.17)	5	4	**9**	1.25	1	8	11.11	0
rrnAC3005	> 2 unique peptides	*cobH*	Precorrin-3B C17-methyltransferase (EC 2.1.1.131)	14	12	**26**	1.17	0	26	0	0
rrnAC2628	> 2 unique peptides	*hemL*	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) (GSA)(Glutamate-1-semialdehyde aminotransferase) (GSA-AT)	10	9	**19**	1.11	0	19	0	0
rrnAC3086	> 2 unique peptides	*hemC*	Porphobilinogen deaminase (EC 2.5.1.61)	7	7	**14**	1	0	14	0	0
rrnAC3008	> 2 unique peptides	*cbiH*	Precorrin-3B C17-methyltransferase (EC 2.1.1.131)	24	25	**49**	0.96	6	43	12.24	0
rrnAC0085	> 2 unique peptides	*gltX*	Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)(GluRS)	10	11	**21**	0.91	0	21	0	0
rrnAC2610	> 2 unique peptides	*hemB*	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24)	10	12	**22**	0.83	0	22	0	0
rrnAC1289	> 2 unique peptides	*rrnAC1289*	Chelatase	8	14	**22**	0.57	1	21	4.55	0
rrnAC1709	single hit	*hemX*	Uroporphyrin-III C-methyltransferase	1	0	1	#DIV/0!	0	1	0	0
rrnAC2998	single hit	*cbiT*	Precorrin-8W decarboxylase (EC 1.-.-.-)	1	1	2	1	2	0	100	0
rrnAC3088	single hit	*cysG1*	Uroporphyrin-III C-methyltransferase	0	2	2	0	0	2	0	0
rrnAC1938	single hit	*cobQ*	Probable cobyric acid synthase	0	1	1	0	0	1	0	0
rrnAC1935	single hit	*rrnAC1935*	Hypothetical protein	0	1	1	0	0	1	0	0
rrnAC1708	ND										
rrnAC3087	ND										
rrnAC1930	ND										
rrnAC1931	ND										
00130 Ubiquinone and other terpenoid-quinone biosynthesis [PATH:hma00130]											
rrnAC0841	> 2 unique peptides	*ech1*	Enoyl-CoA hydratase (EC 4.2.1.17)	15	16	**31**	0.94	0	31	0	0
rrnAC3151	> 2 unique peptides	*ubiE1*	Ubiquinone/menaquinone biosynthesis methyltransferase	10	12	**22**	0.83	17	5	77.27	0
rrnAC0845	single hit	*menA*	14-dihydroxy-2-naphthoate octaprenyltransferase	2	1	3	2	3	0	100	7
rrnB0266	ND										
rrnB0267	ND										
rrnAC0837	ND										
rrnAC0838	ND										
rrnAC0843	ND										
01110 Biosynthesis of Secondary Metabolites											
00900 Terpenoid backbone biosynthesis [PATH:hma00900]											
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC0081	> 2 unique peptides	*idsA*	Geranylgeranyl diphosphate synthase (EC 2.5.1.1) (EC 2.5.1.10)	19	16	**35**	1.19	0	35	0	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1489	> 2 unique peptides	*dmd*	Diphosphomevalonate decarboxylase (EC 4.1.1.33)	8	8	**16**	1	1	15	6.25	0
rrnAC3484	> 2 unique peptides	*idi*	Isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) (IPP isomerase)(Isopentenyl pyrophosphate isomerase) (IPP:DMAPP isomerase)	7	9	**16**	0.78	0	16	0	0
rrnAC0077	> 2 unique peptides	*mvk*	Mevalonate kinase (EC 2.7.1.36)	3	4	**7**	0.75	0	7	0	0
rrnAC1740	> 2 unique peptides	*mvaS*	Hydroxymethylglutaryl-CoA synthase (EC 2.3.3.10)	1	10	**11**	0.1	0	11	0	0
rrnAC1932	ND										
rrnAC3412	ND										
rrnAC1716	ND										
00903 Limonene and pinene degradation [PATH:hma00903]											
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0

pNG7088	> 2 unique peptides	*qad*	Quinohemoprotein alcohol dehydrogenase (EC 1.1.99.-)	17	9	**26**	1.89	26	0	100	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC1925	> 2 unique peptides	*mhpC*	2-hydroxy-6-ketonona-24-dienedioic acid hydrolase (EC 3.7.1.-)	5	17	**22**	0.29	22	0	100	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
rrnAC2874	single hit	*phaJ1*	(R)-specific enoyl-CoA hydratase (EC 4.2.1.-)	0	1	1	0	0	1	0	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
rrnAC1384	ND										
00906 Carotenoid biosynthesis [PATH:hma00906]											
rrnAC2069	> 2 unique peptides	*crtB*	Phytoene synthase (EC 2.5.1.32) (EC 2.5.1.21)	8	5	**13**	1.6	13	0	100	0
rrnAC0321	> 2 unique peptides	*crtI2*	Phytoene dehydrogenase (EC 1.3.99.-)	1	2	3	0.5	3	0	100	0
00311 Penicillin and cephalosporin biosynthesis											
rrnB0229	ND										
rrnB0230	ND										
00521 Streptomycin biosynthesis [PATH:hma00521]											
rrnAC0633	> 2 unique peptides	*rffH2*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	35	23	**58**	1.52	0	58	0	0
rrnAC1004	> 2 unique peptides	*suhB1*	Inositol-1-monophosphatase (EC 3.1.3.25)	3	2	**5**	1.5	0	5	0	0
rrnAC2178	> 2 unique peptides	*rfbB3*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	4	3	**7**	1.33	7	0	100	0
rrnAC1572	> 2 unique peptides	*rfbB2*	DTDP-glucose-46-dehydratase (EC 4.2.1.46)	27	23	**50**	1.17	2	48	4	0
rrnAC2522	> 2 unique peptides	*manB3*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	15	13	**28**	1.15	0	28	0	0
rrnAC1011	> 2 unique peptides	*rffG*	DTDP-glucose dehydratase (EC 4.2.1.46)	3	4	**7**	0.75	1	6	14.29	0
rrnAC1010	> 2 unique peptides	*rfbB1*	DTDP-glucose 4-6-dehydratase (EC 4.2.1.46)	29	39	**68**	0.74	13	55	19.12	0
rrnAC0444	> 2 unique peptides	*manB2*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	18	25	**43**	0.72	0	43	0	0
rrnAC2568	> 2 unique peptides	*pmm*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	22	37	**59**	0.59	3	56	5.08	0
rrnAC3238	> 2 unique peptides	*rffH3*	Glucose-1-phosphate thymidylyltransferase (EC 2.7.7.24)	10	18	**28**	0.56	3	25	10.71	0
rrnAC1960	> 2 unique peptides	*graD4b*	Glucose-1-phosphate thymidylyltransferase	7	13	**20**	0.54	0	20	0	0
rrnAC3232	> 2 unique peptides	*graD4c*	Glucose-1-phosphate thymidylyltransferase	3	7	**10**	0.43	0	10	0	0
rrnAC2574	single hit	*manB1*	Phosphoglucomutase/phosphomannomutase (EC 5.4.2.2) (EC 5.4.2.8)	2	1	3	2	0	3	0	0
rrnAC0547	single hit	*glcK*	Glucokinase (EC 2.7.1.2)	0	1	1	0	0	1	0	0
rrnB0102	single hit	*suhB2*	Inositol-1-monophosphatase (EC 3.1.3.25)	0	1	1	0	0	1	0	0
pNG7218	ND										
rrnAC2343	ND										
00253 Tetracycline biosynthesis											
rrnAC0903	> 2 unique peptides	*accA*	Acetyl-CoA carboxylase alpha subunit	16	12	**28**	1.33	0	28	0	0
00401 Novobiocin biosynthesis [PATH:hma00401]											
rrnB0206	> 2 unique peptides	*aspC1*	Aspartate aminotransferase (EC 2.6.1.1)	28	6	**34**	4.67	4	30	11.76	0
rrnAC3495	> 2 unique peptides	*aspB2*	Aspartate aminotransferase (EC 2.6.1.1)	26	20	**46**	1.3	1	45	2.17	0
rrnAC0529	> 2 unique peptides	*hisC*	Histidinol-phosphate aminotransferase (EC 2.6.1.9) (Imidazole acetol-phosphate transaminase)	6	7	**13**	0.86	0	13	0	0
rrnAC1434	> 2 unique peptides	*aspC3*	Aspartate aminotransferase (EC 2.6.1.1)	10	31	**41**	0.32	0	41	0	0
rrnAC0512	ND										
rrnAC1934	ND										
01111 Xenobiotics Biodegradation and Metabolism											
00930 Caprolactam degradation [PATH:hma00930]											
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC1925	> 2 unique peptides	*mhpC*	2-hydroxy-6-ketonona-24-dienedioic acid hydrolase (EC 3.7.1.-)	5	17	**22**	0.29	22	0	100	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
pNG7101	ND										
00361 gamma-Hexachlorocyclohexane degradation [PATH:hma00361]											
rrnAC0073	> 2 unique peptides	*cyc*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	2	3	0.5	1	2	33.33	0
rrnAC3312	> 2 unique peptides	*cyp1*	Cytochrome P450 (EC 1.14.14.1) (EC 1.6.2.4)	1	3	4	0.33	4	0	100	0
rrnAC0241	> 2 unique peptides	*hadL*	2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	1	3	4	0.33	0	4	0	0

00641 3-Chloroacrylic acid degradation [PATH:hma00641]											
rrnAC0012	> 2 unique peptides	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	18	17	**35**	1.06	1	34	2.86	0
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
pNG7289	> 2 unique peptides	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	9	13	**22**	0.69	0	22	0	0
rrnAC1402	> 2 unique peptides	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	5	8	**13**	0.63	0	13	0	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
pNG7278	> 2 unique peptides	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	4	7	**11**	0.57	0	11	0	0
rrnAC0191	> 2 unique peptides	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	6	11	**17**	0.55	1	16	5.88	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
pNG7032	> 2 unique peptides	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	3	3	0	0	3	0	0
pNG7314	single hit	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	1	1	2	1	0	2	0	0
pNG7351	single hit	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	2	2	0	0	2	0	0
pNG7022	ND										
pNG7101	ND										
pNG7103	ND										
rrnAC1300	ND										
rrnAC1975	ND										
rrnAC2172	ND										
rrnAC3506	ND										
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00351 1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation											
rrnAC1925	> 2 unique peptides	*mhpC*	2-hydroxy-6-ketonona-24-dienedioic acid hydrolase (EC 3.7.1.-)	5	17	**22**	0.29	22	0	100	0
00623 2,4-Dichlorobenzoate degradation											
rrnAC0359	> 2 unique peptides	*rrnAC0359*	4-hydroxybenzoate 3-monooxygenase (EC 1.14.13.2)	8	8	**16**	1	16	0	100	0
rrnAC0657	> 2 unique peptides	*rrnAC0657*	P-hydroxybenzoate hydroxylase (EC 1.14.13.2)	4	6	**10**	0.67	9	1	90	0
00631 1,2-Dichloroethane degradation [PATH:hma00631]											
rrnB0246	> 2 unique peptides	*aldY5*	Aldehyde dehydrogenase (EC 1.2.1.3)	47	62	**109**	0.76	1	108	0.92	0
rrnAC3036	> 2 unique peptides	*aldY3*	Aldehyde dehydrogenase	10	16	**26**	0.63	0	26	0	0
rrnAC2473	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	83	140	**223**	0.59	17	206	7.62	0
rrnAC1973	> 2 unique peptides	*aldY4*	Aldehyde dehydrogenase (EC 1.2.1.3)	21	42	**63**	0.5	1	62	1.59	0
rrnAC0201	> 2 unique peptides	*aldY2*	Aldehyde dehydrogenase (EC 1.2.1.3)	39	94	**133**	0.41	12	121	9.02	0
rrnAC0241	> 2 unique peptides	*hadL*	2-haloalkanoic acid dehalogenase (EC 3.8.1.2)	1	3	4	0.33	0	4	0	0
pNG7352	ND										
rrnAC2631	ND										
rrnB0092	ND										
rrnB0095	ND										
00625 Tetrachloroethene degradation											
pNG7012	ND										
00643 Styrene degradation											
pNG7354	ND										
00626 Naphthalene and anthracene degradation [PATH:hma00626]											
rrnAC1384	ND										
rrnAC0542	ND										
rrnAC3101	ND										
00642 Ethylbenzene degradation											
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC0929	> 2 unique peptides	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	1	10	**11**	0.1	0	11	0	0
00632 Benzoate degradation via CoA ligation [PATH:hma00632]											
rrnAC1092	> 2 unique peptides	*rrnAC1092*	Hypothetical protein	3	0	3	#DIV/0!	3	0	100	3
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1093	> 2 unique peptides	*sdhB*	Succinate dehydrogenase iron-sulfur protein subunit(EC 1.3.99.1)	72	83	**155**	0.87	153	2	98.71	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnAC1972	> 2 unique peptides	*gcdH*	Glutaryl-CoA dehydrogenase (EC 1.3.99.7)	46	63	**109**	0.73	3	106	2.75	0
rrnAC1097	> 2 unique peptides	*sdhA1*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	121	180	**301**	0.67	292	9	97.01	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC1925	> 2 unique peptides	*mhpC*	2-hydroxy-6-ketonona-24-dienedioic acid hydrolase (EC 3.7.1.-)	5	17	**22**	0.29	22	0	100	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0

rrnAC2874	single hit	*phaJ1*	(R)-specific enoyl-CoA hydratase (EC 4.2.1.-)	0	1	1	0	0	1	0	0
rrnAC0141	single hit	*sdhA2*	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	0	3	3	0	0	3	0	0
pNG7354	ND										
rrnAC1167	ND										
rrnAC1091	ND										
00362 Benzoate degradation via hydroxylation [PATH:hma00362]											
pNG7088	> 2 unique peptides	*qad*	Quinohemoprotein alcohol dehydrogenase (EC 1.1.99.-)	17	9	**26**	1.89	26	0	100	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC0359	> 2 unique peptides	*rrnAC0359*	4-hydroxybenzoate 3-monooxygenase (EC 1.14.13.2)	8	8	**16**	1	16	0	100	0
rrnAC0657	> 2 unique peptides	*rrnAC0657*	P-hydroxybenzoate hydroxylase (EC 1.14.13.2)	4	6	**10**	0.67	9	1	90	0
rrnAC1925	> 2 unique peptides	*mhpC*	2-hydroxy-6-ketonona-24-dienedioic acid hydrolase (EC 3.7.1.-)	5	17	**22**	0.29	22	0	100	0
rrnAC0929	> 2 unique peptides	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	1	10	**11**	0.1	0	11	0	0
rrnAC2874	single hit	*phaJ1*	(R)-specific enoyl-CoA hydratase (EC 4.2.1.-)	0	1	1	0	0	1	0	0
rrnAC0572	ND										
00791 Atrazine degradation											
pNG7124	ND										
pNG7123	ND										
pNG7125	ND										
00363 Bisphenol A degradation											
pNG7012	ND										
00624 1- and 2-Methylnaphthalene degradation [PATH:hma00624]											
rrnAC1261	> 2 unique peptides	*acdD*	Acyl-coA dehydrogenase (EC 1.3.99.-)	11	3	**14**	3.67	0	14	0	0
rrnAC0012	> 2 unique peptides	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	18	17	**35**	1.06	1	34	2.86	0
rrnAC0770	> 2 unique peptides	*acdB*	Acyl-coA dehydrogenase (EC 1.3.99.-)	74	76	**150**	0.97	8	142	5.33	0
rrnAC0874	> 2 unique peptides	*acdA*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	20	21	**41**	0.95	0	41	0	0
pNG7289	> 2 unique peptides	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	9	13	**22**	0.69	0	22	0	0
rrnAC1402	> 2 unique peptides	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	5	8	**13**	0.63	0	13	0	0
pNG7278	> 2 unique peptides	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	4	7	**11**	0.57	0	11	0	0
rrnAC0191	> 2 unique peptides	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	6	11	**17**	0.55	1	16	5.88	0
rrnAC1084	> 2 unique peptides	*acdG*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	2	7	**9**	0.29	0	9	0	0
pNG7032	> 2 unique peptides	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	3	3	0	0	3	0	0
rrnAC1986	> 2 unique peptides	*acdC*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	0	3	3	0	0	3	0	0
pNG7314	single hit	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	1	1	2	1	0	2	0	0
rrnAC2874	single hit	*phaJ1*	(R)-specific enoyl-CoA hydratase (EC 4.2.1.-)	0	1	1	0	0	1	0	0
pNG7351	single hit	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	2	2	0	0	2	0	0
rrnAC1384	ND										
pNG7022	ND										
pNG7101	ND										
pNG7103	ND										
rrnAC1300	ND										
rrnAC1975	ND										
rrnAC2172	ND										
rrnAC3506	ND										
rrnAC0779	ND										
rrnAC0780	ND										
00633 Trinitrotoluene degradation											
pNG7247	ND										
00281 Geraniol degradation [PATH:hma00281]											
rrnAC1261	> 2 unique peptides	*acdD*	Acyl-coA dehydrogenase (EC 1.3.99.-)	11	3	**14**	3.67	0	14	0	0
rrnB0254	> 2 unique peptides	*ech6*	Enoyl-CoA hydratase (EC 4.2.1.17)	6	3	**9**	2	0	9	0	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC1979	> 2 unique peptides	*ech5*	Enoyl-CoA hydratase/isomerase (EC 4.2.1.17)	4	4	**8**	1	0	8	0	0
rrnAC0770	> 2 unique peptides	*acdB*	Acyl-coA dehydrogenase (EC 1.3.99.-)	74	76	**150**	0.97	8	142	5.33	0
rrnAC0874	> 2 unique peptides	*acdA*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	20	21	**41**	0.95	0	41	0	0
rrnAC1083	> 2 unique peptides	*hbd1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	122	136	**258**	0.9	6	252	2.33	0
rrnAC1982	> 2 unique peptides	*hbd2*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35) (EC 4.2.1.17)	17	22	**39**	0.77	0	39	0	0
rrnB0238	> 2 unique peptides	*hbd3*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	9	14	**23**	0.64	4	19	17.39	0
rrnAC0833	> 2 unique peptides	*ech2*	Enoyl-CoA hydratase (EC 4.2.1.17)	13	23	**36**	0.57	3	33	8.33	0
rrnAC0771	> 2 unique peptides	*paaH*	3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.35)	31	58	**89**	0.53	0	89	0	0
rrnAC2484	> 2 unique peptides	*ech3*	Enoyl-CoA hydratase (EC 4.2.1.17)	2	4	**6**	0.5	0	6	0	0
rrnAC0264	> 2 unique peptides	*hbd-1*	3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35)	2	4	**6**	0.5	0	6	0	0
rrnAC1084	> 2 unique peptides	*acdG*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	2	7	**9**	0.29	0	9	0	0
rrnB0237	> 2 unique peptides	*ech4*	Enoyl-CoA hydratase (EC 4.2.1.17)	1	6	**7**	0.17	0	7	0	0
rrnAC0929	> 2 unique peptides	*acaB4*	3-ketoacyl-CoA thiolase (EC 2.3.1.16)	1	10	**11**	0.1	0	11	0	0
rrnAC1986	> 2 unique peptides	*acdC*	Acyl-CoA dehydrogenase (EC 1.3.99.-)	0	3	3	0	0	3	0	0
rrnAC1384	ND										
rrnAC0779	ND										
rrnAC0780	ND										
00980 Metabolism of xenobiotics by cytochrome P450											
rrnAC0012	> 2 unique peptides	*adh11*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	18	17	**35**	1.06	1	34	2.86	0
pNG7289	> 2 unique peptides	*adh6*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	9	13	**22**	0.69	0	22	0	0

rrnAC1402	> 2 unique peptides	*adh4*	Alcohol dehydrogenase (EC 1.1.1.1)	5	8	**13**	0.63	0	13	0	0
pNG7278	> 2 unique peptides	*adh12*	Alcohol dehydrogenase (EC 1.1.1.1)	4	7	**11**	0.57	0	11	0	0
rrnAC0191	> 2 unique peptides	*adh3*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	6	11	**17**	0.55	1	16	5.88	0
pNG7032	> 2 unique peptides	*adh10*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	3	3	0	0	3	0	0
pNG7314	single hit	*adhC*	Formaldehyde dehydrogenase (EC 1.1.1.1)	1	1	2	1	0	2	0	0
pNG7351	single hit	*adh13*	Zinc-binding dehydrogenase (EC 1.1.1.1) (EC 1.6.5.5)	0	2	2	0	0	2	0	0
pNG7022	ND										
pNG7101	ND										
pNG7103	ND										
rrnAC1300	ND										
rrnAC1975	ND										
rrnAC2172	ND										
rrnAC3506	ND										
01112 Enzyme Families											
01001 Protein kinases											
rrnAC2205	> 2 unique peptides	*cheA3*	Chemotaxis protein CheA (EC 2.7.3.-)	4	2	**6**	2	0	6	0	0
rrnAC2476	single hit	*prk2*	Protein kinase	1	0	1	#DIV/0!	0	1	0	0
rrnAC2036	single hit	*pkn*	Serine/threonine protein kinase	0	1	1	0	0	1	0	0
rrnAC2193	ND										
01002 Peptidases											
pNG7291	> 2 unique peptides	*htpX2*	Probable protease HtpX-like (EC 3.4.24.-)	5	1	**6**	5	6	0	100	4
rrnAC1773	> 2 unique peptides	*psmA2*	Proteasome alpha subunit (EC 3.4.25.1) (Multicatalytic endopeptidasecomplex alpha subunit)	47	20	**67**	2.35	0	67	0	0
rrnAC1914	> 2 unique peptides	*lon*	ATP-dependent protease LA (EC 3.4.21.53)	174	105	**279**	1.66	278	1	99.64	1
rrnAC0442	> 2 unique peptides	*psmA3*	Proteasome subunit alpha	6	4	**10**	1.5	0	10	0	0
rrnAC1174	> 2 unique peptides	*psmA1*	Proteasome alpha subunit (EC 3.4.25.1) (Multicatalytic endopeptidasecomplex alpha subunit)	50	38	**88**	1.32	1	87	1.14	0
rrnAC2712	> 2 unique peptides	*sec11a*	Signal sequence peptidase	9	7	**16**	1.29	16	0	100	1
rrnAC3189	> 2 unique peptides	*pepF*	Oligoendopeptidase F (EC 3.4.24.-)	38	31	**69**	1.23	2	67	2.9	0
rrnAC2906	> 2 unique peptides	*htpX1*	Probable protease htpX-like (EC 3.4.24.-)	13	11	**24**	1.18	24	0	100	4
rrnAC0489	> 2 unique peptides	*pip*	Putative intracellular protease (EC 3.2.-.-)	11	11	**22**	1	0	22	0	0
rrnAC3421	> 2 unique peptides	*map*	Methionine aminopeptidase (EC 3.4.11.18)	4	4	**8**	1	0	8	0	0
rrnAC0630	> 2 unique peptides	*sppA*	Putative signal peptide peptidase SppA (EC 3.4.21.-)	25	27	**52**	0.93	52	0	100	1
rrnAC2047	> 2 unique peptides	*sppA*	Protease IV-like (EC 3.4.21.-)	11	13	**24**	0.85	24	0	100	1
rrnAC0322	> 2 unique peptides	*pepQ*	Xaa-Pro aminopeptidase (EC 3.4.11.9)	15	21	**36**	0.71	0	36	0	0
rrnAC3544	> 2 unique peptides	*htpX4*	Protease heat shock protein HtpX (EC 3.4.24.-)	4	7	**11**	0.57	10	1	90.91	4
rrnAC2092	> 2 unique peptides	*cxp*	Probable carboxypeptidase	22	39	**61**	0.56	5	56	8.2	0
rrnAC1772	> 2 unique peptides	*psmA1*	Proteasome subunit alpha	5	9	**14**	0.56	0	14	0	0
rrnAC2490	single hit	*gcp*	Putative O-sialoglycoprotein endopeptidase (EC 3.4.24.57)(Glycoprotease)	2	1	3	2	0	3	0	0
rrnAC3038	single hit	*htpX3*	Heat shock protein X	1	1	2	1	2	0	100	4
rrnB0229	ND										
rrnB0230	ND										
rrnAC2713	ND										
rrnAC2982	ND										
00199 Cytochrome P450											
01120 Genetic Information Processing											
01121 Transcription											
03020 RNA polymerase [PATH:hma03020]											
rrnAC0067	> 2 unique peptides	*rpoN*	DNA-directed RNA polymerase subunit N (EC 2.7.7.6)	2	0	2	#DIV/0!	0	2	0	0
rrnAC2829	> 2 unique peptides	*rpoE'*	DNA-directed RNA polymerase subunit E'	22	7	**29**	3.14	0	29	0	0
rrnAC2432	> 2 unique peptides	*rpoH*	DNA-directed RNA polymerase subunit H (EC 2.7.7.6)	9	3	**12**	3	0	12	0	0
rrnAC2428	> 2 unique peptides	*rpoA*	DNA-directed RNA polymerase (EC 2.7.7.6)	70	41	**111**	1.71	35	76	31.53	0
rrnAC2430	> 2 unique peptides	*rpoB*	DNA-directed RNA polymerase subunit B	54	34	**88**	1.59	28	60	31.82	0
rrnAC2830	> 2 unique peptides	*rpoE''*	DNA-directed RNA polymerase subunit E''	3	2	**5**	1.5	0	5	0	0
rrnAC2429	> 2 unique peptides	*rpoB*	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)	56	40	**96**	1.4	3	93	3.13	0
rrnAC2427	> 2 unique peptides	*rpoC*	RNA polymerase Rpb1 domain 5 (EC 2.7.7.6)	22	16	**38**	1.38	13	25	34.21	0
rrnAC0259	> 2 unique peptides	*rpb4*	RNA polymerase Rpb4	20	17	**37**	1.18	1	36	2.7	0
rrnAC1396	> 2 unique peptides	*rpoL*	DNA-directed RNA polymerase subunit L (EC 2.7.7.6)	4	4	**8**	1	0	8	0	0
rrnAC0062	> 2 unique peptides	*rpoD*	DNA-directed RNA polymerase subunit D (EC 2.7.7.6)	4	7	**11**	0.57	0	11	0	0
rrnAC0218	single hit	*rpoM*	DNA-directed RNA-polymerase subunit M	0	1	1	0	0	1	0	0
rrnAC0068	ND										
rrnAC0313	ND										
rrnAC1668	ND										
03022 Basal transcription factors [PATH:hma03022]											
rrnAC0016	> 2 unique peptides	*tfbA*	Transcription initiation factor IIB	4	0	4	#DIV/0!	0	4	0	0
rrnAC0861	> 2 unique peptides	*tfeA*	Transcription initiation factor IIE alpha subunit	9	3	**12**	3	0	12	0	0
rrnAC0681	> 2 unique peptides	*tbpE*	TATA-box binding protein E	22	12	**34**	1.83	7	27	20.59	0
pNG6072	ND										
pNG6123	ND										

rrnAC1126	ND										
rrnAC1357	ND										
rrnAC1875	ND										
rrnAC2051	ND										
rrnAC2769	ND										
rrnB0148	ND										
03000 Transcription factors											
rrnAC2744	> 2 unique peptides	*rrnAC2744*	Hypothetical protein	5	3	**8**	1.67	0	8	0	0
pNG2007	> 2 unique peptides	*pNG2007*	Hypothetical protein	18	11	**29**	1.64	0	29	0	0
rrnAC1133	> 2 unique peptides	*rpaA*	Replication protein A	12	17	**29**	0.71	0	29	0	0
rrnAC1765	> 2 unique peptides	*tenA*	Transcriptional activator tenA	3	21	**24**	0.14	1	23	4.17	0
rrnAC0001	> 2 unique peptides	*birA*	Biotin-(Acetyl-CoA carboxylase) ligase	0	5	**5**	0	0	5	0	0
rrnAC1767	> 2 unique peptides	*tenA-2*	Transcriptional regulator putative	0	9	**9**	0	0	9	0	0
rrnAC0496	single hit	*sirR*	Transcription repressor	1	0	1	#DIV/0!	0	1	0	0
rrnAC1715	single hit	*cspD1*	Cold shock protein	1	0	1	#DIV/0!	0	1	0	0
rrnAC2339	single hit	*cspD3*	Cold shock protein	50	12	62	4.17	0	62	0	0
rrnAC1714	single hit	*cspD5*	Cold shock protein	3	1	4	3	0	4	0	0
rrnAC1269	single hit	*asnC2*	Transcription regulator AsnC family	5	2	7	2.5	0	7	0	0
rrnAC3264	single hit	*rrnAC3264*	Putative molybdenum-binding protein	1	2	3	0.5	0	3	0	0
rrnAC2283	single hit	*copG1*	Transcriptional regulator CopG family	0	1	1	0	0	1	0	0
rrnAC2302	ND										
rrnAC2037	ND										
rrnAC1238	ND										
rrnAC3447	ND										
rrnAC2519	ND										
rrnAC1742	ND										
rrnAC2338	ND										
rrnAC2900	ND										
01122 Translation											
03010 Ribosome [PATH:hma03010]											
rrnAC1596	> 2 unique peptides	*rpl6p*	50S ribosomal protein L6P (Hmal6) (Hl10)	5	0	**5**	#DIV/0!	0	5	0	0
rrnAC1418	> 2 unique peptides	*rpl12p*	50S ribosomal protein L12P (Hmal12)	3	0	3	#DIV/0!	0	3	0	0
rrnAC1607	> 2 unique peptides	*rps19p*	30S ribosomal protein S19P (HmaS19) (HS18)	12	2	**14**	6	3	11	21.43	0
rrnAC1604	> 2 unique peptides	*rpl29p*	50S ribosomal protein L29P (Hmal29) (Hl33)	5	1	**6**	5	0	6	0	0
rrnAC0059	> 2 unique peptides	*rps4p*	30S ribosomal protein S4P (HmaS4)	27	7	**34**	3.86	0	34	0	0
rrnAC0061	> 2 unique peptides	*rps11p*	30S ribosomal protein S11P (HmaS11) (HS19)	23	6	**29**	3.83	4	25	13.79	0
rrnAC1598	> 2 unique peptides	*rpl5p*	50S ribosomal protein L5P (Hmal5) (Hl13)	13	4	**17**	3.25	11	6	64.71	0
rrnAC0058	> 2 unique peptides	*rps13p*	30S ribosomal protein S13P (HmaS13)	21	8	**29**	2.63	6	23	20.69	0
rrnAC2488	> 2 unique peptides	*rps24e*	30S ribosomal protein S24e (HS15) (E1.2)	16	6	**22**	2.67	3	19	13.64	0
rrnAC1605	> 2 unique peptides	*rps3p*	30S ribosomal protein S3P (HmaS3) (HS1)	53	21	**74**	2.52	1	73	1.35	0
rrnAC1417	> 2 unique peptides	*rplP0*	50S ribosomal protein L10E (Ribosomal protein L10) (Acidic ribosomalprotein P0 homolog) (L10E) (HMal10)	17	8	**25**	2.13	3	22	12	0
rrnAC1429	> 2 unique peptides	*rps3Ae*	30S ribosomal protein S3Ae	80	39	**119**	2.05	52	67	43.7	0
rrnAC1600	> 2 unique peptides	*rps4e*	30S ribosomal protein S4E (HS3)	34	17	**51**	2	9	42	17.65	0
rrnAC2212	> 2 unique peptides	*rps6e*	30S ribosomal protein S6e (HS13)	14	7	**21**	2	0	21	0	0
rrnAC1610	> 2 unique peptides	*rpl4p*	50S ribosomal protein L4P (Hmal4) (Hl6)	2	1	3	2	0	3	0	0
rrnAC2357	> 2 unique peptides	*rpl10e*	50S ribosomal protein L10e	14	7	**21**	2	21	0	100	0
rrnAC1592	> 2 unique peptides	*rps5p*	30S ribosomal protein S5P (HmaS5)	63	35	**98**	1.8	16	82	16.33	0
rrnAC1611	> 2 unique peptides	*rpl3p*	50S ribosomal protein L3P (Hmal3) (Hl1)	91	57	**148**	1.6	148	0	100	0
rrnAC0064	> 2 unique peptides	*rpl18e*	50S ribosomal protein L18e (Hl29) (L19)	41	26	**67**	1.58	63	4	94.03	0
rrnAC1595	> 2 unique peptides	*rpl32e*	50S ribosomal protein L32e (Hl5)	8	5	**13**	1.6	6	7	46.15	0
rrnAC1426	> 2 unique peptides	*rps15p*	30S ribosomal protein S15P/S13e (HmaS15) (HS11)	18	12	**30**	1.5	8	22	26.67	0
rrnAC3179	> 2 unique peptides	*rps19e*	30S ribosomal protein S19e (HS12) (E1.3)	22	15	**37**	1.47	5	32	13.51	0
rrnAC0070	> 2 unique peptides	*rps2p*	30S ribosomal protein S2P (HS2) (ORFMSG)	26	18	**44**	1.44	0	44	0	0
rrnAC2065	> 2 unique peptides	*rpl15e*	50S ribosomal protein L15e (50S ribosomal protein LC12)	16	11	**27**	1.45	27	0	100	0
rrnAC1608	> 2 unique peptides	*rpl2p*	50S ribosomal protein L2P (Hmal2) (Hl4)	24	17	**41**	1.41	38	3	92.68	0
rrnAC3112	> 2 unique peptides	*rpl39e*	50S ribosomal protein L39e (Hl39e) (Hl46e)	7	5	**12**	1.4	12	0	100	0
rrnAC1511	> 2 unique peptides	*rps8e*	30S ribosomal protein S8e (HS23)	12	9	**21**	1.33	12	9	57.14	0
rrnAC1591	> 2 unique peptides	*rpl30p*	50S ribosomal protein L30P (Hmal30) (Hl20) (Hl16)	9	7	**16**	1.29	0	16	0	0
rrnAC1603	> 2 unique peptides	*rps17p*	30S ribosomal protein S17P (HmaS17) (HS14)	10	8	**18**	1.25	1	17	5.56	0
rrnAC0260	> 2 unique peptides	*rpl21e*	50S ribosomal protein L21e (Hl31)	5	4	**9**	1.25	6	3	66.67	0
rrnAC0055	> 2 unique peptides	*rps17e*	30S ribosomal protein S17e (Ribosomal protein HS26)	6	5	**11**	1.2	0	11	0	0
rrnAC1606	> 2 unique peptides	*rpl22p*	50S ribosomal protein L22P (Hmal22) (Hl23)	12	10	**22**	1.2	15	7	68.18	0
rrnAC0065	> 2 unique peptides	*rpl13p*	50S ribosomal protein L13P (Hmal13)	30	27	**57**	1.11	56	1	98.25	0
rrnAC1597	> 2 unique peptides	*rps8p*	30S ribosomal protein S8P (HmaS8) (HS16)	7	7	**14**	1	3	11	21.43	0
rrnAC2424	> 2 unique peptides	*rps12p*	30S ribosomal protein S12P	15	15	**30**	1	18	12	60	0
rrnAC0103	> 2 unique peptides	*rpl7ae*	50S ribosomal protein L7Ae (Hs6)	16	16	**32**	1	3	29	9.38	0
rrnAC2423	> 2 unique peptides	*rps7p*	30S ribosomal protein S7P (HmaS7)	35	40	**75**	0.88	35	40	46.67	0
rrnAC1602	> 2 unique peptides	*rpl14p*	50S ribosomal protein L14P (Hmal14) (Hl27)	21	29	**50**	0.72	48	2	96	0
rrnAC3113	> 2 unique peptides	*rpl31e*	50S ribosomal protein L31e (L34) (Hl30)	4	6	**10**	0.67	7	3	70	0

rrnAC1415	> 2 unique peptides	*rpl1p*	50S ribosomal protein L1P (Hmal1) (HL8)	1	2	3	0.5	2	1	66.67	0
rrnAC1594	> 2 unique peptides	*rpl19e*	50S ribosomal protein L19e (Hmal19) (Hl24)	2	5	**7**	0.4	5	2	71.43	0
rrnAC1590	> 2 unique peptides	*rpl15p*	50S ribosomal protein L15P (Hmal15) (Hl9)	10	28	**38**	0.36	33	5	86.84	0
rrnAC2405	> 2 unique peptides	*rps10p*	30S ribosomal protein S10P (HmaS10)	1	3	4	0.33	0	4	0	0
rrnAC3513	> 2 unique peptides	*rps27E*	30S ribosomal protein S27e	1	3	4	0.33	0	4	0	0
rrnAC1609	single hit	*rpl23p*	50S ribosomal protein L23P (Hmal23) (Hl25) (L21)	1	0	1	#DIV/0!	0	1	0	0
rrnAC0066	single hit	*rps9p*	30S ribosomal protein S9P (HmaS9) (HS3) (F1)	6	3	9	2	2	7	22.22	0
rrnAC1414	single hit	*rpl11p*	50S ribosomal protein L11P (Hmal11)	2	1	3	2	0	3	0	0
rrnAC1593	single hit	*rpl18p*	50S ribosomal protein L18P (Hmal18) (Hl12)	3	3	6	1	6	0	100	0
rrnAC2489	single hit	*rps27ae*	30S ribosomal protein S27ae (HSH)	0	1	1	0	0	1	0	0
rrnAC1601	single hit	*rpl24p*	50S ribosomal protein L24P (Hmal24) (Hl16) (Hl15)	0	1	1	0	1	0	100	0
pNG7228	ND										
rrnAC0104	ND										
rrnAC1669	ND										
rrnAC2802	ND										
rrnAC3514	ND										
rrlB-4											
rrlB-1											
rrlB-2											
rrlB-3											
rrs-1											
rrs-2											
rrs-3											
rrlA-1											
rrlA-2											
rrlA-3											
03011 Ribosome											
03012 Translation factors											
rrnAC0261	> 2 unique peptides	*ef1b*	Elongation factor 1-beta (EF-1-beta) (aEF-1beta)	13	6	**19**	2.17	0	19	0	0
rrnAC3164	> 2 unique peptides	*prf1*	Peptide chain release factor subunit 1 (Translation termination factoraRF1)	11	6	**17**	1.83	0	17	0	0
rrnAC1956	> 2 unique peptides	*eif2BD2*	Translation initiation factor eIF-2B subunit delta	10	7	**17**	1.43	0	17	0	0
rrnAC2413	> 2 unique peptides	*fusA*	Elongation factor 2 (EF-2)	148	141	**289**	1.05	9	280	3.11	0
rrnAC2474	> 2 unique peptides	*eif1a*	Translation initiation factor 1A (aIF-1A)	19	19	**38**	1	3	35	7.89	0
rrnAC2827	> 2 unique peptides	*eif2g*	Translation initiation factor 2 gamma subunit (eIF-2-gamma) (aIF2-gamma)	11	11	**22**	1	0	22	0	0
rrnAC1929	> 2 unique peptides	*eif5a*	Translation initiation factor 5A (eIF-5A) (Hypusine-containingprotein)	13	13	**26**	1	0	26	0	0
rrnAC2445	> 2 unique peptides	*sui1*	Protein translation factor SUI1 homolog	9	9	**18**	1	0	18	0	0
rrnAC0289	> 2 unique peptides	*eif2BD1*	Translation initiation factor eIF-2B subunit delta	16	19	**35**	0.84	0	35	0	0
rrnAC2406	> 2 unique peptides	*tuf*	Elongation factor 1-alpha (EF-1-alpha) (Elongation factor Tu) (EF-Tu)	141	222	**363**	0.64	40	323	11.02	0
rrnAC3512	> 2 unique peptides	*eif2a*	Translation initiation factor 2 alpha subunit (eIF-2-alpha) (aIF2-alpha)	8	13	**21**	0.62	0	21	0	0
rrnAC0138	> 2 unique peptides	*eif2B1*	Probable translation initiation factor 2 beta subunit	4	7	**11**	0.57	0	11	0	0
rrnAC1619	> 2 unique peptides	*gbp2*	GTP-binding protein-like	2	5	**7**	0.4	0	7	0	0
rrnAC3203	> 2 unique peptides	*infB*	Probable translation initiation factor IF-2	3	10	**13**	0.3	0	13	0	0
rrnAC1241	ND										
rrnAC1124	ND										
00970 Aminoacyl-tRNA biosynthesis [PATH:hma00970]											
rrnAC2967	> 2 unique peptides	*pheT*	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--tRNA ligase beta chain) (PheRS)	20	15	**35**	1.33	1	34	2.86	0
rrnAC3462	> 2 unique peptides	*thrS*	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase)(ThrRS)	15	12	**27**	1.25	0	27	0	0
rrnAC1800	> 2 unique peptides	*metG*	Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)(MetRS)	24	20	**44**	1.2	0	44	0	0
rrnAC3173	> 2 unique peptides	*lysS*	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)	6	5	**11**	1.2	0	11	0	0
rrnAC2966	> 2 unique peptides	*pheS*	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)	7	6	**13**	1.17	0	13	0	0
rrnAC2650	> 2 unique peptides	*leuS1*	Leucyl-tRNA synthetase (EC 6.1.1.4)	16	14	**30**	1.14	0	30	0	0
rrnAC2808	> 2 unique peptides	*serS*	Seryl-tRNA synthetase (EC 6.1.1.11) (Seryl-tRNA(Ser/Sec) synthetase)(Serine--tRNA ligase) (SerRS)	19	17	**36**	1.12	0	36	0	0
rrnAC0166	> 2 unique peptides	*proS*	Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase) (ProRS)	19	18	**37**	1.06	0	37	0	0
rrnAC3169	> 2 unique peptides	*argS*	Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS)	25	24	**49**	1.04	0	49	0	0
rrnAC0023	> 2 unique peptides	*gatE*	Glutamyl-tRNA(Gln) amidotransferase subunit E (EC 6.3.5.-)	12	12	**24**	1	0	24	0	0
rrnAC2965	> 2 unique peptides	*trpS*	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)	11	11	**22**	1	0	22	0	0
rrnAC0085	> 2 unique peptides	*gltX*	Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)(GluRS)	10	11	**21**	0.91	0	21	0	0
rrnAC1356	> 2 unique peptides	*gatC*	Glutamyl-tRNA(Gln) amidotransferase subunit C (EC 6.3.5.-)	9	11	**20**	0.82	0	20	0	0
rrnAC2561	> 2 unique peptides	*alaS*	Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS)	12	15	**27**	0.8	0	27	0	0
rrnAC1642	> 2 unique peptides	*gatB*	Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B(EC 6.3.5.-) (Asp/Glu-ADT subunit B)	15	19	**34**	0.79	0	34	0	0
rrnAC1657	> 2 unique peptides	*aspS*	Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase)(AspRS)	40	52	**92**	0.77	2	90	2.17	0
rrnAC2947	> 2 unique peptides	*leuS2*	Leucyl-tRNA synthetase (EC 6.1.1.4)	35	46	**81**	0.76	0	81	0	0
rrnAC1355	> 2 unique peptides	*gatA*	Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) (Glu-ADTsubunit A)	3	4	**7**	0.75	0	7	0	0
rrnAC3183	> 2 unique peptides	*hisS*	Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)(HisRS)	9	13	**22**	0.69	0	22	0	0
rrnAC0543	> 2 unique peptides	*tyrS*	Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosine--tRNA ligase) (TyrRS)	8	14	**22**	0.57	0	22	0	0
rrnAC2634	> 2 unique peptides	*ileS*	Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)(IleRS)	25	45	**70**	0.56	0	70	0	0
rrnAC1729	> 2 unique peptides	*valS*	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS)	8	18	**26**	0.44	0	26	0	0
rrnAC0517	> 2 unique peptides	*alaS2*	Alanyl-tRNA synthetase (EC 6.1.1.7)	6	14	**20**	0.43	0	20	0	0
rrnAC2701	> 2 unique peptides	*glyS*	Glycyl-tRNA synthetase (EC 6.1.1.14)	6	14	**20**	0.43	0	20	0	0
rrnAC3442	> 2 unique peptides	*asbA*	L-asparaginase (EC 3.5.1.1)	0	7	**7**	0	0	7	0	0

rrnAC1292	> 2 unique peptides	*cysS*	Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase)(CysRS)	0	5	**5**	0	0	5	0	0
01123 Folding, Sorting and Degradation											
03110 Chaperones and folding catalysts											
rrnAC1308	> 2 unique peptides	*rrnAC1308*	Glutaredoxin	20	19	**39**	1.05	0	39	0	0
rrnAC3116	> 2 unique peptides	*pfdA*	Prefoldin alpha subunit (GimC alpha subunit)	33	33	**66**	1	0	66	0	0
rrnAC3303	> 2 unique peptides	*ppiB1*	Peptidyl-prolyl cis-trans isomerase slr1251 (EC 5.2.1.8)	25	25	**50**	1	7	43	14	0
rrnAC1680	> 2 unique peptides	*pfdB*	Prefoldin beta subunit (GimC beta subunit)	30	31	**61**	0.97	1	60	1.64	0
rrnAC2110	> 2 unique peptides	*trxA3*	Thioredoxin	26	27	**53**	0.96	0	53	0	0
rrnAC3339	> 2 unique peptides	*dnaK*	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDaprotein) (HSP70)	57	71	**128**	0.8	29	99	22.66	0
rrnAC1230	> 2 unique peptides	*slyD*	Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	43	57	**100**	0.75	2	98	2	0
rrnAC3340	> 2 unique peptides	*grpE*	Heat shock protein GrpE protein	3	7	**10**	0.43	0	10	0	0
rrnAC3334	ND										
rrnAC0638	ND										
pNG7134	ND										
rrnB0277	ND										
04121 Ubiquitin system											
rrnAC1773	> 2 unique peptides	*psmA2*	Proteasome alpha subunit (EC 3.4.25.1) (Multicatalytic endopeptidasecomplex alpha subunit)	47	20	**67**	2.35	0	67	0	0
rrnAC0442	> 2 unique peptides	*psmA3*	Proteasome subunit alpha	6	4	**10**	1.5	0	10	0	0
rrnAC3190	> 2 unique peptides	*pan1*	Proteasome-activating nucleotidase 1	12	8	**20**	1.5	1	19	5	0
rrnAC1174	> 2 unique peptides	*psmA1*	Proteasome alpha subunit (EC 3.4.25.1) (Multicatalytic endopeptidasecomplex alpha subunit)	50	38	**88**	1.32	1	87	1.14	0
rrnAC3546	> 2 unique peptides	*pan2*	Proteasome-activating nucleotidase 2	21	26	**47**	0.81	1	46	2.13	0
rrnAC1772	> 2 unique peptides	*psmA1*	Proteasome subunit alpha	5	9	**14**	0.56	0	14	0	0
03018 RNA degradation [PATH:hma03018]											
rrnAC0069	> 2 unique peptides	*eno*	Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase)	24	23	**47**	1.04	0	47	0	0
rrnAC2072	> 2 unique peptides	*vacB*	Ribonuclease R (EC 3.1.-.-)	10	12	**22**	0.83	0	22	0	0
rrnAC3339	> 2 unique peptides	*dnaK*	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDaprotein) (HSP70)	57	71	**128**	0.8	29	99	22.66	0
pNG7302	> 2 unique peptides	*ppk*	Polyphosphate kinase (EC 2.7.4.1)	0	8	**8**	0	0	8	0	0
01124 Replication and Repair											
03030 DNA replication [PATH:hma03030]											
rrnAC2744	> 2 unique peptides	*rrnAC2744*	Hypothetical protein	5	3	**8**	1.67	0	8	0	0
pNG2007	> 2 unique peptides	*pNG2007*	Hypothetical protein	18	11	**29**	1.64	0	29	0	0
rrnAC2851	> 2 unique peptides	*pcn*	DNA polymerase sliding clamp (Proliferating cell nuclear antigenhomolog) (PCNA)	24	33	**57**	0.73	5	52	8.77	0
rrnAC1133	> 2 unique peptides	*rpaA*	Replication protein A	12	17	**29**	0.71	0	29	0	0
rrnAC0463	single hit	*ligA*	DNA ligase (EC 6.5.1.1)	0	1	1	0	0	1	0	0
pNG7077	ND										
rrnAC3320	ND										
rrnAC3216	ND										
rrnAC3049	ND										
rrnAC2302	ND										
rrnAC0032	ND										
03032 DNA replication proteins											
rrnAC0455	> 2 unique peptides	*gyrA*	DNA gyrase subunit A (EC 5.99.1.3)	13	4	**17**	3.25	0	17	0	0
rrnAC2691	> 2 unique peptides	*polC*	DNA polymerase II large subunit (EC 2.7.7.7) (Pol II) [Contains: HmapolC intein (Hma pol II intein)	3	1	4	3	0	4	0	0
rrnAC1645	> 2 unique peptides	*topA*	DNA topoisomerase I (EC 5.99.1.2)	4	2	**6**	2	0	6	0	0
rrnAC2565	> 2 unique peptides	*rfcS*	Replication factor C small subunit (RFC small subunit) (Clamp loadersmall subunit)	12	7	**19**	1.71	0	19	0	0
rrnAC0457	> 2 unique peptides	*top6B*	Type II DNA topoisomerase VI subunit B (EC 5.99.1.3)	37	24	**61**	1.54	17	44	27.87	0
rrnAC0456	> 2 unique peptides	*gyrB*		7	5	**12**	1.4	0	12	0	0
rrnAC2487	> 2 unique peptides	*rfcC2*	Replication factor C small subunit	5	4	**9**	1.25	0	9	0	0
rrnAC1831	> 2 unique peptides	*polB1*	DNA polymerase B elongation subunit (EC 2.7.7.7)	1	2	3	0.5	0	3	0	0
rrnAC0459	> 2 unique peptides	*top6A*	Type II DNA topoisomerase VI subunit A (EC 5.99.1.3)	2	5	**7**	0.4	0	7	0	0
rrnAC2862	single hit	*cdc6-5*	Cell division control protein 6 homolog 5 (CDC6 homolog 5)	1	0	1	#DIV/0!	0	1	0	0
rrnAC2762	single hit	*mcm2*	Cell division control protein 21	1	1	2	1	0	2	0	0
rrnAC0292	single hit	*priA*	Probable DNA primase small subunit (EC 2.7.7.-)	0	1	1	0	0	1	0	0
rrnAC2711	ND										
rrnAC2318	ND										
pNG6176	ND										
rrnAC2714	ND										
rrnAC1744	ND										
rrnAC2963	ND										
03036 Chromosome											
rrnB0062	> 2 unique peptides	*parA3*	Chromosome partitioning protein ParA family ATPase	2	0	2	#DIV/0!	0	2	0	0
rrnAC0974	> 2 unique peptides	*rrnAC0974*	Hypothetical protein	3	0	3	#DIV/0!	0	3	0	0
rrnAC2004	> 2 unique peptides	*ftsZ3*	Cell division protein FtsZ	9	5	**14**	1.8	4	10	28.57	0
rrnAC0665	> 2 unique peptides	*abcP-2*	ABC transporter permease protein	5	5	**10**	1	10	0	100	4
rrnAC0703	> 2 unique peptides	*ftsZ1*	Cell division protein FtsZ	19	23	**42**	0.83	9	33	21.43	0
pNG6012	> 2 unique peptides	*parA2*	Partition protein	7	9	**16**	0.78	0	16	0	0
rrnAC0056	> 2 unique peptides	*mrp1*	Mrp protein-like	5	7	**12**	0.71	0	12	0	0
rrnAC1639	single hit	*smc2*	Chromosome segregation protein	1	0	1	#DIV/0!	0	1	0	0

pNG2014	single hit	*sojC*	Chromosome partitioning protein	0	2	2	0	0	2	0	0
rrnAC1638	ND										
rrnAC1227	ND										
rrnAC1880	ND										
rrnAC1939	ND										
rrnAC2768	ND										
rrnAC3166	ND										
pNG4012	ND										
rrnAC1208	ND										
03410 Base excision repair [PATH:hma03410]											
rrnAC2015	> 2 unique peptides	*nfo*	Probable endonuclease 4 (EC 3.1.21.2) (Endonuclease IV)(Endodeoxyribonuclease IV)	3	2	**5**	1.5	0	5	0	0
pNG7116	> 2 unique peptides	*nthC*	Endonuclease III (EC 4.2.99.18)	4	4	**8**	1	0	8	0	0
rrnAC2851	> 2 unique peptides	*pcn*	DNA polymerase sliding clamp (Proliferating cell nuclear antigenhomolog) (PCNA)	24	33	**57**	0.73	5	52	8.77	0
rrnAC0265	> 2 unique peptides	*apl*	AP-endonuclease/AP-lyase (EC 3.1.21.2) (EC 4.2.99.18)	4	7	**11**	0.57	0	11	0	0
rrnAC0739	single hit	*nthA*	Endonuclease III (EC 4.2.99.18)	1	1	2	1	0	2	0	0
rrnAC1088	single hit	*alkA*	DNA-3-methyladenine glycosylase	0	2	2	0	0	2	0	0
rrnAC0463	single hit	*ligA*	DNA ligase (EC 6.5.1.1)	0	1	1	0	0	1	0	0
rrnAC1166	ND										
rrnAC1908	ND										
rrnAC2648	ND										
rrnAC0987	ND										
rrnAC3049	ND										
rrnAC0032	ND										
03420 Nucleotide excision repair [PATH:hma03420]											
rrnAC2996	> 2 unique peptides	*uvrB*	UvrABC system protein B (Protein uvrB) (Excinuclease ABC subunit B)	2	0	2	#DIV/0!	0	2	0	0
rrnAC2267	> 2 unique peptides	*uvrD*	Repair helicase	27	9	**36**	3	2	34	5.56	0
rrnAC2116	> 2 unique peptides	*uvrA*	Excinuclease ABC subunit A	14	8	**22**	1.75	0	22	0	0
rrnAC2744	> 2 unique peptides	*rrnAC2744*	Hypothetical protein	5	3	**8**	1.67	0	8	0	0
pNG2007	> 2 unique peptides	*pNG2007*	Hypothetical protein	18	11	**29**	1.64	0	29	0	0
rrnAC2851	> 2 unique peptides	*pcn*	DNA polymerase sliding clamp (Proliferating cell nuclear antigenhomolog) (PCNA)	24	33	**57**	0.73	5	52	8.77	0
rrnAC1133	> 2 unique peptides	*rpaA*	Replication protein A	12	17	**29**	0.71	0	29	0	0
rrnAC0463	single hit	*ligA*	DNA ligase (EC 6.5.1.1)	0	1	1	0	0	1	0	0
rrnAC3041	ND										
rrnAC3049	ND										
rrnAC2302	ND										
03430 Mismatch repair [PATH:hma03430]											
rrnB0041	> 2 unique peptides	*xseA2*	Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	3	0	3	#DIV/0!	3	0	100	1
rrnAC2267	> 2 unique peptides	*uvrD*	Repair helicase	27	9	**36**	3	2	34	5.56	0
rrnAC2532	> 2 unique peptides	*mutS1*	DNA mismatch repair protein mutS 1	2	1	3	2	0	3	0	0
rrnAC2744	> 2 unique peptides	*rrnAC2744*	Hypothetical protein	5	3	**8**	1.67	0	8	0	0
pNG2007	> 2 unique peptides	*pNG2007*	Hypothetical protein	18	11	**29**	1.64	0	29	0	0
rrnAC2851	> 2 unique peptides	*pcn*	DNA polymerase sliding clamp (Proliferating cell nuclear antigenhomolog) (PCNA)	24	33	**57**	0.73	5	52	8.77	0
rrnAC1133	> 2 unique peptides	*rpaA*	Replication protein A	12	17	**29**	0.71	0	29	0	0
rrnAC2550	> 2 unique peptides	*mutL*	DNA mismatch repair protein mutL	2	3	**5**	0.67	0	5	0	0
pNG6094	> 2 unique peptides	*xseA1*	Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	0	2	2	0	2	0	100	1
rrnAC0463	single hit	*ligA*	DNA ligase (EC 6.5.1.1)	0	1	1	0	0	1	0	0
rrnAC2937	ND										
pNG6095	ND										
rrnB0042	ND										
rrnAC3049	ND										
rrnAC2302	ND										
03440 Homologous recombination											
rrnAC2744	> 2 unique peptides	*rrnAC2744*	Hypothetical protein	5	3	**8**	1.67	0	8	0	0
pNG2007	> 2 unique peptides	*pNG2007*	Hypothetical protein	18	11	**29**	1.64	0	29	0	0
rrnAC1133	> 2 unique peptides	*rpaA*	Replication protein A	12	17	**29**	0.71	0	29	0	0
rrnAC2302	ND										
03450 Non-homologous end-joining											
rrnAC0032	ND										
03400 DNA repair and recombination proteins											
rrnAC2996	> 2 unique peptides	*uvrB*	UvrABC system protein B (Protein uvrB) (Excinuclease ABC subunit B)	2	0	2	#DIV/0!	0	2	0	0
rrnB0041	> 2 unique peptides	*xseA2*	Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	3	0	3	#DIV/0!	3	0	100	1
rrnAC0455	> 2 unique peptides	*gyrA*	DNA gyrase subunit A (EC 5.99.1.3)	13	4	**17**	3.25	0	17	0	0
rrnAC2267	> 2 unique peptides	*uvrD*	Repair helicase	27	9	**36**	3	2	34	5.56	0
rrnAC0832	> 2 unique peptides	*phrB1*	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)	2	1	3	2	0	3	0	0
rrnAC2159	> 2 unique peptides	*dcd3*	Probable deoxyuridine 5'-triphosphate nucleotidohydrolase(EC 3.6.1.23)	2	1	3	2	0	3	0	0
rrnAC2532	> 2 unique peptides	*mutS1*	DNA mismatch repair protein mutS 1	2	1	3	2	0	3	0	0
rrnAC1840	> 2 unique peptides	*smc1*	Structural maintenance of chromosomes	2	1	3	2	0	3	0	0
rrnAC2847	> 2 unique peptides	*hjr*	Holliday junction resolvase	4	2	**6**	2	0	6	0	0
rrnAC1645	> 2 unique peptides	*topA*	DNA topoisomerase I (EC 5.99.1.2)	4	2	**6**	2	0	6	0	0
rrnAC2116	> 2 unique peptides	*uvrA*	Excinuclease ABC subunit A	14	8	**22**	1.75	0	22	0	0
rrnAC2744	> 2 unique peptides	*rrnAC2744*	Hypothetical protein	5	3	**8**	1.67	0	8	0	0

pNG2007	> 2 unique peptides	*pNG2007*	Hypothetical protein	18	11	**29**	1.64	0	29	0	0
rrnAC2015	> 2 unique peptides	*nfo*	Probable endonuclease 4 (EC 3.1.21.2) (Endonuclease IV)(Endodeoxyribonuclease IV)	3	2	**5**	1.5	0	5	0	0
rrnAC0456	> 2 unique peptides	*gyrB*	DNA gyrase subunit B (EC 5.99.1.3)	7	5	**12**	1.4	0	12	0	0
rrnAC1622	> 2 unique peptides	*nrdA*	Ribonucleoside-diphosphate reductase alpha chain(EC 1.17.4.1)	108	91	**199**	1.19	5	194	2.51	0
rrnAC0669	> 2 unique peptides	*polX*	DNA polymerase IV	9	8	**17**	1.13	0	17	0	0
pNG7116	> 2 unique peptides	*nthC*	Endonuclease III (EC 4.2.99.18)	4	4	**8**	1	0	8	0	0
rrnAC2910	> 2 unique peptides	*radA*	DNA repair and recombination protein RadA	25	27	**52**	0.93	1	51	1.92	0
rrnAC2851	> 2 unique peptides	*pcn*	DNA polymerase sliding clamp (Proliferating cell nuclear antigenhomolog) (PCNA)	24	33	**57**	0.73	5	52	8.77	0
rrnAC1133	> 2 unique peptides	*rpaA*	Replication protein A	12	17	**29**	0.71	0	29	0	0
rrnAC2550	> 2 unique peptides	*mutL*	DNA mismatch repair protein mutL	2	3	**5**	0.67	0	5	0	0
rrnAC0265	> 2 unique peptides	*apl*	AP-endonuclease/AP-lyase (EC 3.1.21.2) (EC 4.2.99.18)	4	7	**11**	0.57	0	11	0	0
pNG6094	> 2 unique peptides	*xseA1*	Probable exodeoxyribonuclease VII large subunit (EC 3.1.11.6)	0	2	2	0	2	0	100	1
rrnAC1532	single hit	*radB*	DNA repair and recombination protein RadB	1	0	1	#DIV/0!	0	1	0	0
rrnAC0739	single hit	*nthA*	Endonuclease III (EC 4.2.99.18)	1	1	2	1	0	2	0	0
rrnAC0463	single hit	*ligA*	DNA ligase (EC 6.5.1.1)	0	1	1	0	0	1	0	0
rrnAC1088	single hit	*alkA*	DNA-3-methyladenine glycosylase	0	2	2	0	0	2	0	0
rrnAC1943	ND										
rrnAC0987	ND										
rrnAC1166	ND										
rrnAC1908	ND										
rrnAC2648	ND										
rrnAC2302	ND										
rrnAC2704	ND										
rrnAC1180	ND										
rrnAC0676	ND										
rrnAC3049	ND										
rrnAC3041	ND										
rrnAC2937	ND										
pNG6095	ND										
rrnB0042	ND										
rrnAC2963	ND										
rrnAC0540	ND										
rrnAC0959	ND										
rrnAC1139	ND										
01130 Environmental Information Processing											
01131 Membrane Transport											
02000 Transporters											
rrnAC2868	> 2 unique peptides	*potD2*	Spermidine/putrescine ABC transporter spermidine/putrescine bindingprotein	2	0	2	#DIV/0!	2	0	100	1
rrnAC0029	> 2 unique peptides	*rrnAC0029*	Sugar ABC transporter permease protein	2	0	2	#DIV/0!	2	0	100	6
rrnB0321	> 2 unique peptides	*phnE*	Phosphonates ABC tranporter permease protein	22	3	**25**	7.33	25	0	100	5
rrnB0322	> 2 unique peptides	*phnD2*	Phosphonates ABC transporter permease protein	12	2	**14**	6	14	0	100	5
rrnAC1505	> 2 unique peptides	*pstB1*	Phosphate import ATP-binding protein pstB 1 (EC 3.6.3.27) (Phosphate-transporting ATPase 1) (ABC phosphate transporter 1)	18	4	**22**	4.5	22	0	100	0
rrnB0320	> 2 unique peptides	*phnC2*	Phosphonates import ATP-binding protein phnC 2 (EC 3.6.3.28)	34	9	**43**	3.78	42	1	97.67	0
rrnB0319	> 2 unique peptides	*phnD1*	ABC tranporter phosphate-binding protein	250	73	**323**	3.42	323	0	100	0
rrnB0207	> 2 unique peptides	*rrnB0207*	Putative extracellular ligand binding protein	59	19	**78**	3.11	78	0	100	0
rrnAC0147	> 2 unique peptides	*tppA*	Thiamine-binding periplasmic protein-like	21	7	**28**	3	28	0	100	0
rrnB0204	> 2 unique peptides	*livM-7*	High-affinity branched-chain amino acid transport protein	5	2	**7**	2.5	7	0	100	8
rrnAC0906	> 2 unique peptides	*ibp*	Iron-binding protein	52	22	**74**	2.36	74	0	100	0
rrnAC1745	> 2 unique peptides	*yckA-2*	Amino acid ABC transporter permease protein	11	5	**16**	2.2	16	0	100	5
rrnAC2084	> 2 unique peptides	*nosF-3*	ABC transporter ATP-binding protein	4	2	**6**	2	6	0	100	0
rrnAC2230	> 2 unique peptides	*oppC1*	Oligopeptide transport system permease protein OppC	21	12	**33**	1.75	33	0	100	6
rrnAC3297	> 2 unique peptides	*oppC*	Oligopeptide ABC transporter permease protein	65	39	**104**	1.67	104	0	100	8
rrnAC1507	> 2 unique peptides	*pstA2*	Phosphate ABC transporter permease protein	59	37	**96**	1.59	96	0	100	14
rrnAC0915	> 2 unique peptides	*rrnAC0915*	Hypothetical protein	29	19	**48**	1.53	48	0	100	0
pNG7253	> 2 unique peptides	*rbsC-1*	Sugar ABC transporter permease protein	12	8	**20**	1.5	20	0	100	8
rrnAC0825	> 2 unique peptides	*livM*	High-affinity branched-chain amino acid transport protein	9	6	**15**	1.5	15	0	100	8
rrnAC1029	> 2 unique peptides	*rrnAC1029*	ABC transporter ATP-binding protein	6	4	**10**	1.5	10	0	100	0
rrnAC1509	> 2 unique peptides	*phoX*	Phosphate ABC transporter phosphate-binding protein	20	14	**34**	1.43	34	0	100	0
rrnAC2228	> 2 unique peptides	*dppD*	Dipeptide ABC transporter ATP-binding	551	392	**943**	1.41	943	0	100	0
rrnAC3052	> 2 unique peptides	*nosY2*	ABC-type transport system involved in multi-copper enzyme maturation permease component	24	17	**41**	1.41	41	0	100	6
rrnAC0381	> 2 unique peptides	*glnH1*	Glutamine ABC transporter permease protein	43	31	**74**	1.39	74	0	100	0
rrnAC3053	> 2 unique peptides	*rrnAC3053*	ABC transporter ATP-binding protein	43	31	**74**	1.39	74	0	100	0
rrnAC0252	> 2 unique peptides	*abcS-2*	ABC transporter permease protein	22	17	**39**	1.29	39	0	100	4
rrnAC0829	> 2 unique peptides	*livF-4*	Branched-chain amino acid ABC transporter ATP-binding protein	5	4	**9**	1.25	8	1	88.89	0
rrnAC2469	> 2 unique peptides	*rrnAC2469*	Hypothetical protein	21	17	**38**	1.24	38	0	100	0
rrnAC3299	> 2 unique peptides	*dppA*	Dipeptide ABC transporter dipeptide-binding	437	355	**792**	1.23	791	1	99.87	0
rrnAC2229	> 2 unique peptides	*dppB1*	Dipeptide ABC transporter permease	47	38	**85**	1.24	85	0	100	6

rrnAC0379	> 2 unique peptides	*glnQ2*	Glutamine ABC transporter	6	5	**11**	1.2	8	3	72.73	0
rrnAC3298	> 2 unique peptides	*dppB*	Dipeptide ABC transporter permease	20	18	**38**	1.11	38	0	100	6
rrnAC2227	> 2 unique peptides	*dppF*	Dipeptide ABC transporter ATP-binding	68	65	**133**	1.05	129	4	96.99	0
rrnAC3295	> 2 unique peptides	*ykfD*	Oligopeptide ABC transporter ATP-binding	43	42	**85**	1.02	85	0	100	0
rrnAC2349	> 2 unique peptides	*malE1*	Maltose ABC transporter maltose-binding protein	11	11	**22**	1	22	0	100	0
pNG7252	> 2 unique peptides	*rbsA*	Ribose ABC transporter ATP-binding	3	3	**6**	1	6	0	100	0
rrnAC0380	> 2 unique peptides	*glnP*	Glutamine-binding periplasmic protein of glutamine ABCtransporter	9	9	**18**	1	18	0	100	4
rrnAC0048	> 2 unique peptides	*rrnAC0048*	ABC transporter ATP-binding protein	2	2	4	1	4	0	100	0
rrnAC0665	> 2 unique peptides	*abcP-2*	ABC transporter permease protein	5	5	**10**	1	10	0	100	4
rrnAC2656	> 2 unique peptides	*yufN*	ABC transporter	125	127	**252**	0.98	252	0	100	0
rrnAC1830	> 2 unique peptides	*yurF*	ABC transporter ATP-binding protein	50	51	**101**	0.98	2	99	1.98	0
rrnAC2464	> 2 unique peptides	*livF-6*	Branched-chain amino acid ABC transporter ATP-binding protein	11	12	**23**	0.92	22	1	95.65	0
rrnAC0251	> 2 unique peptides	*yvrO-2*	ABC transporter ATP-binding protein	9	10	**19**	0.9	19	0	100	0
pNG5001	> 2 unique peptides	*abcP-1*	ABC transporter permease protein	8	9	**17**	0.89	17	0	100	4
rrnAC0502	> 2 unique peptides	*ycdH*	Adhesion protein	26	31	**57**	0.84	57	0	100	0
rrnAC3128	> 2 unique peptides	*livG-9*	Branched-chain amino acid ABC transporter ATP-binding protein	5	6	**11**	0.83	11	0	100	0
rrnAC2073	> 2 unique peptides	*trp2*	ABC transporter ATP-binding protein	8	10	**18**	0.8	18	0	100	0
rrnAC3296	> 2 unique peptides	*oppD2*	Oligopeptide ABC transporter ATPase component	31	40	**71**	0.78	71	0	100	0
rrnAC2468	> 2 unique peptides	*livH-6*	Branched chain amino acid transporter permease protein	3	4	**7**	0.75	7	0	100	8
rrnAC2280	> 2 unique peptides	*cbiQ1*	Cobalt transport protein	3	4	**7**	0.75	7	0	100	5
pNG5003	> 2 unique peptides	*yvrO-1*	ABC transporter ATP-binding protein	12	17	**29**	0.71	29	0	100	0
rrnAC1749	> 2 unique peptides	*glnH2*	Glutamine ABC transporter permease protein	2	3	**5**	0.67	5	0	100	3
rrnAC1747	> 2 unique peptides	*glnQ1*	Glutamine ABC transporter ATP-binding protein	4	6	**10**	0.67	10	0	100	0
rrnAC2465	> 2 unique peptides	*livG-6*	Branched-chain amino acid ABC transporter ATP-binding protein	4	6	**10**	0.67	10	0	100	0
rrnAC3129	> 2 unique peptides	*livM-6*	Branched-chain amino acid ABC transporter permease protein	7	11	**18**	0.64	18	0	100	9
rrnB0225	> 2 unique peptides	*livG-10*	Branched-chain amino acid ABC transporter ATP-binding protein	1	2	3	0.5	3	0	100	0
rrnAC2147	> 2 unique peptides	*pstA1*	Phosphate ABC transporter permease protein	14	39	**53**	0.36	53	0	100	24
rrnAC3127	> 2 unique peptides	*livF-7*	Branched-chain amino acid ABC transporter ATP-binding protein	3	9	**12**	0.33	12	0	100	0
pNG7346	> 2 unique peptides	*potD1*	Spermidine/putrescine transporter substrate binding protein	2	7	**9**	0.29	9	0	100	0
rrnAC2149	> 2 unique peptides	*yqgG*	Phosphate ABC transporter binding	79	726	**805**	0.11	802	3	99.63	0
rrnAC2148	> 2 unique peptides	*pstC2*	Phosphate ABC transporter permease protein	1	11	**12**	0.09	12	0	100	8
rrnB0312	> 2 unique peptides	*ugpA*	ABC transporter permease protein	0	9	**9**	0	9	0	100	6
rrnB0314	> 2 unique peptides	*ugpE*	Sn-glycerol-3-phosphate transport system permease	0	23	**23**	0	23	0	100	6
rrnB0315	> 2 unique peptides	*msmX-3*	Sugar ABC transporter ATP-binding protein	0	24	**24**	0	24	0	100	0
rrnAC2146	> 2 unique peptides	*pstB2*	Phosphate import ATP-binding protein pstB 2 (EC 3.6.3.27) (Phosphate-transporting ATPase 2) (ABC phosphate transporter 2)	0	37	**37**	0	37	0	100	0
pNG7254	single hit	*rbsC-2*	Sugar ABC transporter permease protein	1	0	1	#DIV/0!	1	0	100	9
rrnAC2651	single hit	*rbsC*	Ribose ABC transporter permease	1	0	1	#DIV/0!	1	0	100	9
rrnAC3130	single hit	*livH-7*	Branched-chain amino acid ABC transporter permease protein	1	0	1	#DIV/0!	1	0	100	4
rrnB0275	single hit	*rrnB0275*	Putative-iron binding protein	1	0	1	#DIV/0!	1	0	100	0
rrnAC2083	single hit	*yadH*	ABC transporter permease protein	1	0	1	#DIV/0!	1	0	100	6
pNG7275	single hit	*fhuG1*	Ferrichrome ABC transporter permease protein	3	1	4	3	4	0	100	8
rrnAC2282	single hit	*cbiM*	Cobalamin biosynthesis protein CbiM	2	1	3	2	3	0	100	6
rrnAC0030	single hit	*yurM*	ABC transporter permease protein	1	1	2	1	2	0	100	7
rrnAC3374	single hit	*hemU*	Iron(III) dicitrate transport system permease protein FecD	2	2	4	1	4	0	100	8
rrnAC0049	single hit	*rrnAC0049*	ABC transporter ATP-binding domain	2	2	4	1	4	0	100	6
rrnAC2088	single hit	*rrnAC2088*	Hypothetical protein	1	2	3	0.5	0	3	0	0
rrnB0227	single hit	*livH-9*	Branched-chain amino acid ABC transporter permease protein	1	3	4	0.33	4	0	100	16
pNG7025	single hit	*malFG-1*	Sugar ABC transporter permease protein	0	2	2	0	2	0	100	6
rrnAC0922	single hit	*malFG-5*	Putative ABC transporter permease protein	0	1	1	0	1	0	100	8
rrnAC1183	ND										
rrnAC1184	ND										
rrnAC0907	ND										
rrnAC0908	ND										
rrnAC0146	ND										
pNG7350	ND										
rrnAC2873	ND										
pNG7349	ND										
rrnAC2872	ND										
pNG7347	ND										
rrnAC2870	ND										
rrnAC2347	ND										
rrnAC2346	ND										
rrnAC0552	ND										
pNG7339	ND										
rrnAC3196	ND										
rrnB0104	ND										
pNG7338	ND										
rrnAC0921	ND										
rrnAC3195	ND										
rrnB0105	ND										

pNG7342	ND										
rrnAC2352	ND										
rrnAC3194	ND										
rrnB0106	ND										
rrnAC2653	ND										
rrnAC2655	ND										
rrnAC1508	ND										
pNG7234	ND										
pNG7231	ND										
pNG7233	ND										
pNG7122	ND										
rrnAC0702	ND										
pNG7121	ND										
rrnAC0569	ND										
rrnAC0646	ND										
rrnAC0824	ND										
rrnAC1989	ND										
rrnB0205	ND										
pNG7120	ND										
pNG7119	ND										
rrnAC0567	ND										
rrnAC0642	ND										
rrnB0203	ND										
pNG7118	ND										
rrnAC0641	ND										
rrnAC1993	ND										
rrnB0202	ND										
rrnB0224	ND										
rrnAC2040	ND										
rrnAC2041	ND										
rrnAC2042	ND										
rrnAC2043	ND										
pNG7041	ND										
rrnAC3375	ND										
pNG7276	ND										
rrnAC3372	ND										
rrnAC0500	ND										
rrnAC0501	ND										
rrnAC2418	ND										
rrnAC0396	ND										
rrnAC2536	ND										
pNG7050	ND										
rrnAC0394	ND										
rrnAC0479	ND										
rrnAC2535	ND										
rrnAC0666	ND										
rrnAC1369	ND										
pNG7391	ND										
pNG7389	ND										
pNG7388	ND										
pNG7392	ND										
pNG7387	ND										
02010 ABC transporters [PATH:hma02010]											
rrnB0321	> 2 unique peptides	*phnE*	Phosphonates ABC tranporter permease protein	22	3	**25**	7.33	25	0	100	5
rrnB0322	> 2 unique peptides	*phnD2*	Phosphonates ABC transporter permease protein	12	2	**14**	6	14	0	100	5
rrnAC1505	> 2 unique peptides	*pstB1*	Phosphate import ATP-binding protein pstB 1 (EC 3.6.3.27) (Phosphate-transporting ATPase 1) (ABC phosphate transporter 1)	18	4	**22**	4.5	22	0	100	0
rrnB0320	> 2 unique peptides	*phnC2*	Phosphonates import ATP-binding protein phnC 2 (EC 3.6.3.28)	34	9	**43**	3.78	42	1	97.67	0
rrnB0319	> 2 unique peptides	*phnD1*	ABC tranporter phosphate-binding protein	250	73	**323**	3.42	323	0	100	0
rrnB0207	> 2 unique peptides	*rrnB0207*	Putative extracellular ligand binding protein	59	19	**78**	3.11	78	0	100	0
rrnAC0147	> 2 unique peptides	*tppA*	Thiamine-binding periplasmic protein-like	21	7	**28**	3	28	0	100	0
rrnB0204	> 2 unique peptides	*livM-7*	High-affinity branched-chain amino acid transport protein	5	2	**7**	2.5	7	0	100	8
rrnAC0906	> 2 unique peptides	*ibp*	Iron-binding protein	52	22	**74**	2.36	74	0	100	0
rrnAC2084	> 2 unique peptides	*nosF-3*	ABC transporter ATP-binding protein	4	2	**6**	2	6	0	100	0
rrnAC2230	> 2 unique peptides	*oppC1*	Oligopeptide transport system permease protein OppC	21	12	**33**	1.75	33	0	100	6
rrnAC3297	> 2 unique peptides	*oppC*	Oligopeptide ABC transporter permease protein	65	39	**104**	1.67	104	0	100	8
rrnAC1507	> 2 unique peptides	*pstA2*	Phosphate ABC transporter permease protein	59	37	**96**	1.59	96	0	100	14
rrnAC0825	> 2 unique peptides	*livM*	High-affinity branched-chain amino acid transport protein	9	6	**15**	1.5	15	0	100	8
rrnAC1509	> 2 unique peptides	*phoX*	Phosphate ABC transporter phosphate-binding protein	20	14	**34**	1.43	34	0	100	0
rrnAC2228	> 2 unique peptides	*dppD*	Dipeptide ABC transporter ATP-binding	551	392	**943**	1.41	943	0	100	0
rrnAC0829	> 2 unique peptides	*livF-4*	Branched-chain amino acid ABC transporter ATP-binding protein	5	4	**9**	1.25	8	1	88.89	0

rrnAC2469	> 2 unique peptides	*rrnAC2469*	Hypothetical protein	21	17	**38**	1.24	38	0	100	0
rrnAC3299	> 2 unique peptides	*dppA*	Dipeptide ABC transporter dipeptide-binding	437	355	**792**	1.23	791	1	99.87	0
rrnAC2229	> 2 unique peptides	*dppB1*	Dipeptide ABC transporter permease	47	38	**85**	1.24	85	0	100	6
rrnAC3298	> 2 unique peptides	*dppB*	Dipeptide ABC transporter permease	20	18	**38**	1.11	38	0	100	6
rrnAC2227	> 2 unique peptides	*dppF*	Dipeptide ABC transporter ATP-binding	68	65	**133**	1.05	129	4	96.99	0
rrnAC3295	> 2 unique peptides	*ykfD*	Oligopeptide ABC transporter ATP-binding	43	42	**85**	1.02	85	0	100	0
rrnAC2349	> 2 unique peptides	*malE1*	Maltose ABC transporter maltose-binding protein	11	11	**22**	1	22	0	100	0
rrnAC0665	> 2 unique peptides	*abcP-2*	ABC transporter permease protein	5	5	**10**	1	10	0	100	4
rrnAC2464	> 2 unique peptides	*livF-6*	Branched-chain amino acid ABC transporter ATP-binding protein	11	12	**23**	0.92	22	1	95.65	0
rrnAC0502	> 2 unique peptides	*ycdH*	Adhesion protein	26	31	**57**	0.84	57	0	100	0
rrnAC3128	> 2 unique peptides	*livG-9*	Branched-chain amino acid ABC transporter ATP-binding protein	5	6	**11**	0.83	11	0	100	0
rrnAC3296	> 2 unique peptides	*oppD2*	Oligopeptide ABC transporter ATPase component	31	40	**71**	0.78	71	0	100	0
rrnAC2468	> 2 unique peptides	*livH-6*	Branched chain amino acid transporter permease protein	3	4	**7**	0.75	7	0	100	8
rrnAC2280	> 2 unique peptides	*cbiQ1*	Cobalt transport protein	3	4	**7**	0.75	7	0	100	5
rrnAC2465	> 2 unique peptides	*livG-6*	Branched-chain amino acid ABC transporter ATP-binding protein	4	6	**10**	0.67	10	0	100	0
rrnAC3129	> 2 unique peptides	*livM-6*	Branched-chain amino acid ABC transporter permease protein	7	11	**18**	0.64	18	0	100	9
rrnB0225	> 2 unique peptides	*livG-10*	Branched-chain amino acid ABC transporter ATP-binding protein	1	2	3	0.5	3	0	100	0
rrnAC2147	> 2 unique peptides	*pstA1*	Phosphate ABC transporter permease protein	14	39	**53**	0.36	53	0	100	24
rrnAC3127	> 2 unique peptides	*livF-7*	Branched-chain amino acid ABC transporter ATP-binding protein	3	9	**12**	0.33	12	0	100	0
rrnAC2149	> 2 unique peptides	*yqgG*	Phosphate ABC transporter binding	79	726	**805**	0.11	802	3	99.63	0
rrnAC2148	> 2 unique peptides	*pstC2*	Phosphate ABC transporter permease protein	1	11	**12**	0.09	12	0	100	8
rrnB0312	> 2 unique peptides	*ugpA*	ABC transporter permease protein	0	9	**9**	0	9	0	100	6
rrnB0314	> 2 unique peptides	*ugpE*	Sn-glycerol-3-phosphate transport system permease	0	23	**23**	0	23	0	100	6
rrnAC2146	> 2 unique peptides	*pstB2*	Phosphate import ATP-binding protein pstB 2 (EC 3.6.3.27) (Phosphate-transporting ATPase 2) (ABC phosphate transporter 2)	0	37	**37**	0	37	0	100	0
rrnAC3130	single hit	*livH-7*	Branched-chain amino acid ABC transporter permease protein	1	0	1	#DIV/0!	1	0	100	4
rrnB0275	single hit	*rrnB0275*	Putative-iron binding protein	1	0	1	#DIV/0!	1	0	100	0
rrnAC2083	single hit	*yadH*	ABC transporter permease protein	1	0	1	#DIV/0!	1	0	100	6
pNG7275	single hit	*fhuG1*	Ferrichrome ABC transporter permease protein	3	1	4	3	4	0	100	8
rrnAC2282	single hit	*cbiM*	Cobalamin biosynthesis protein CbiM	2	1	3	2	3	0	100	6
rrnAC3374	single hit	*hemU*	Iron(III) dicitrate transport system permease protein FecD	2	2	4	1	4	0	100	8
rrnAC2088	single hit	*rrnAC2088*	Hypothetical protein	1	2	3	0.5	0	3	0	0
rrnB0227	single hit	*livH-9*	Branched-chain amino acid ABC transporter permease protein	1	3	4	0.33	4	0	100	16
pNG7025	single hit	*malFG-1*	Sugar ABC transporter permease protein	0	2	2	0	2	0	100	6
rrnAC1183	ND										
rrnAC1184	ND										
rrnAC0907	ND										
rrnAC0908	ND										
rrnAC0146	ND										
rrnAC2347	ND										
rrnAC2346	ND										
rrnAC0552	ND										
rrnAC1508	ND										
pNG7234	ND										
pNG7231	ND										
pNG7233	ND										
pNG7122	ND										
rrnAC0702	ND										
pNG7121	ND										
rrnAC0569	ND										
rrnAC0646	ND										
rrnAC0824	ND										
rrnAC1989	ND										
rrnB0205	ND										
pNG7120	ND										
pNG7119	ND										
rrnAC0567	ND										
rrnAC0642	ND										
rrnB0203	ND										
pNG7118	ND										
rrnAC0641	ND										
rrnAC1993	ND										
rrnB0202	ND										
rrnB0224	ND										
rrnAC2040	ND										
rrnAC2041	ND										
rrnAC2042	ND										
rrnAC2043	ND										
pNG7041	ND										
rrnAC3375	ND										
pNG7276	ND										

rrnAC3372	ND										
rrnAC0500	ND										
rrnAC0501	ND										
rrnAC2418	ND										
rrnAC1369	ND										
02060 Phosphotransferase system (PTS) [PATH:hma02060]											
pNG7391	ND										
pNG7388	ND										
pNG7392	ND										
pNG7387	ND										
03070 Bacterial secretion system [PATH:hma03070]											
rrnAC3118	> 2 unique peptides	*dpa*	Signal recognition particle receptor	2	0	2	#DIV/0!	0	2	0	0
rrnAC3124	> 2 unique peptides	*srp54*	Signal recognition 54 kDa protein	8	2	**10**	4	2	8	20	0
rrnAC2858	> 2 unique peptides	*tatC2*	SEC independent protein translocase TatC	4	2	**6**	2	6	0	100	10
rrnAC0524	> 2 unique peptides	*rrnAC0524*	Putative sEC independent transolcation prot	16	11	**27**	1.45	27	0	100	1
rrnAC3215	> 2 unique peptides	*secD*	Protein-export membrane protein SecD	59	47	**106**	1.26	106	0	100	6
rrnAC1589	> 2 unique peptides	*secY*	Preprotein translocase subunit secY (Protein transport protein SEC61subunit alpha homolog)	62	51	**113**	1.22	113	0	100	9
rrnAC3214	> 2 unique peptides	*secF*	Protein-export membrane protein SecF	8	10	**18**	0.8	18	0	100	6
rrnAC2857	single hit	*tatC1*	SEC independent protein translocase protein TatC	2	1	3	2	3	0	100	14
02044 Secretion system											
rrnAC0041	> 2 unique peptides	*srp19*	Signal recognition particle 19 kDa protein	5	3	**8**	1.67	0	8	0	0
rrnAC0700	> 2 unique peptides	*secE*	Preprotein translocase subunit secE (Protein transport protein SEC61gamma subunit homolog)	12	9	**21**	1.33	21	0	100	1
pNG1026	> 2 unique peptides	*flaA2*	Flagellin A protein	5	6	**11**	0.83	11	0	100	1
rrnAC0466	ND										
rrnB0018	ND										
rrnAC2198	ND										
rrnAC1482	ND										
rrnAC2191	ND										
rrnAC2190	ND										
rrnAC2187	ND										
rrnAC2186	ND										
rrnAC2184	ND										
rrnAC2183	ND										
rrnAC2645	ND										
03060 Protein export [PATH:hma03060]											
rrnAC3118	> 2 unique peptides	*dpa*	Signal recognition particle receptor	2	0	2	#DIV/0!	0	2	0	0
rrnAC3124	> 2 unique peptides	*srp54*	Signal recognition 54 kDa protein	8	2	**10**	4	2	8	20	0
rrnAC2858	> 2 unique peptides	*tatC2*	SEC independent protein translocase TatC	4	2	**6**	2	6	0	100	10
rrnAC0041	> 2 unique peptides	*srp19*	Signal recognition particle 19 kDa protein	5	3	**8**	1.67	0	8	0	0
rrnAC0524	> 2 unique peptides	*rrnAC0524*	Putative sEC independent transolcation prot	16	11	**27**	1.45	27	0	100	1
rrnAC0700	> 2 unique peptides	*secE*	Preprotein translocase subunit secE (Protein transport protein SEC61gamma subunit homolog)	12	9	**21**	1.33	21	0	100	1
rrnAC2712	> 2 unique peptides	*sec11a*	Signal sequence peptidase	9	7	**16**	1.29	16	0	100	1
rrnAC3215	> 2 unique peptides	*secD*	Protein-export membrane protein SecD	59	47	**106**	1.26	106	0	100	6
rrnAC1589	> 2 unique peptides	*secY*	Preprotein translocase subunit secY (Protein transport protein SEC61subunit alpha homolog)	62	51	**113**	1.22	113	0	100	9
rrnAC3214	> 2 unique peptides	*secF*	Protein-export membrane protein SecF	8	10	**18**	0.8	18	0	100	6
rrnAC2857	single hit	*tatC1*	SEC independent protein translocase protein TatC	2	1	3	2	3	0	100	14
rrnAC2713	ND										
rrnAC2982	ND										
01132 Signal Transduction											
02020 Two-component system [PATH:hma02020]											
rrnAC0067	> 2 unique peptides	*rpoN*	DNA-directed RNA polymerase subunit N (EC 2.7.7.6)	2	0	2	#DIV/0!	0	2	0	0
rrnAC1884	> 2 unique peptides	*trpA*	Tryptophan synthase alpha chain (EC 4.2.1.20)	5	1	**6**	5	0	6	0	0
rrnAC3497	> 2 unique peptides	*yqeF*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	3	1	4	3	0	4	0	0
rrnAC2205	> 2 unique peptides	*cheA3*	Chemotaxis protein CheA (EC 2.7.3.-)	4	2	**6**	2	0	6	0	0
rrnAC0896	> 2 unique peptides	*acaB3*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	30	16	**46**	1.88	0	46	0	0
rrnAC1509	> 2 unique peptides	*phoX*	Phosphate ABC transporter phosphate-binding protein	20	14	**34**	1.43	34	0	100	0
rrnB0242	> 2 unique peptides	*acaB2*	3-ketoacyl-CoA thiolase (EC 2.3.1.9) (EC 2.3.1.16)	7	5	**12**	1.4	0	12	0	0
rrnAC0709	> 2 unique peptides	*Anthranilate synthase component 11*	Anthranilate synthase component 1 1 (EC 4.1.3.27)	4	3	**7**	1.33	0	7	0	0
rrnB0240	> 2 unique peptides	*aca1*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	31	25	**56**	1.24	2	54	3.57	0
rrnAC2780	> 2 unique peptides	*glnA*	Glutamine synthetase (EC 6.3.1.2)	99	83	**182**	1.19	18	164	9.89	0
rrnAC2815	> 2 unique peptides	*aca2*	Acetyl-coA acetyltransferase (EC 2.3.1.9)	57	51	**108**	1.12	2	106	1.85	0
rrnB0309	> 2 unique peptides	*acaB1*	3-ketoacyl-CoA thiolase (EC 2.3.1.9)	2	2	4	1	0	4	0	0
rrnAC3306	> 2 unique peptides	*trpD1*	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	51	53	**104**	0.96	1	103	0.96	0
rrnAC2149	> 2 unique peptides	*yqgG*	Phosphate ABC transporter binding	79	726	**805**	0.11	802	3	99.63	0
rrnAC1520	single hit	*trpD*	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)	3	2	5	1.5	1	4	20	0
pNG7327	single hit	*trpE3*	Anthranilate synthase component 1 3 (EC 4.1.3.27)	0	1	1	0	0	1	0	0
rrnAC0053	single hit	*citG*	CitG family protein	0	1	1	0	0	1	0	0
rrnAC2621	single hit	*glnB*	Nitrogen regulatory protein P-II	0	1	1	0	0	1	0	0

rrnAC1478	ND										
rrnAC1885	ND										
rrnAC1886	ND										
rrnAC1518	ND										
rrnAC0690	ND										
rrnAC1199	ND										
rrnAC1200	ND										
rrnAC1761	ND										
rrnAC2206	ND										
rrnAC1484	ND										
rrnAC2203	ND										
rrnAC2193	ND										
rrnAC2194	ND										
rrnAC2204	ND										
01133 Signaling Molecules and Interaction											
04000 Receptors and channels											
rrnAC3161	> 2 unique peptides	*bop*	Bacteriorhodopsin	32	55	**87**	0.58	87	0	100	7
rrnAC2030	> 2 unique peptides	*xop1*	Bacteriorhodopsin	7	20	**27**	0.35	27	0	100	7
rrnAC1659	single hit	*hop*	Halorhodopsin	0	1	1	0	1	0	100	7
02042 Bacterial toxins											
rrnAC2600	> 2 unique peptides	*rrnAC2600*	Hypothetical protein	49	38	**87**	1.29	87	0	100	2
pNG5066	ND										
01141 Cell Motility											
02030 Bacterial chemotaxis [PATH:hma02030]											
rrnAC2205	> 2 unique peptides	*cheA3*	Chemotaxis protein CheA (EC 2.7.3.-)	4	2	**6**	2	0	6	0	0
rrnAC1258	single hit	*cheC2*	Chemotaxis protein CheC	0	1	1	0	0	1	0	0
rrnAC2425	ND										
rrnAC2633	ND										
rrnAC2193	ND										
rrnAC1484	ND										
rrnAC2203	ND										
rrnAC2194	ND										
rrnAC0528	ND										
rrnAC2204	ND										
rrnAC2192	ND										
rrnAC2206	ND										
02035 Bacterial motility proteins											
pNG1026	> 2 unique peptides	*flaA2*	Flagellin A protein	5	6	**11**	0.83	11	0	100	1
rrnB0018	ND										
rrnAC2198	ND										
rrnAC1482	ND										
rrnAC2191	ND										
rrnAC2190	ND										
rrnAC2187	ND										
rrnAC2186	ND										
rrnAC2184	ND										
rrnAC2183	ND										
rrnAC0466	ND										
04812 Cytoskeleton proteins											
rrnB0062	> 2 unique peptides	*parA3*	Chromosome partitioning protein ParA family ATPase	2	0	2	#DIV/0!	0	2	0	0
rrnAC2004	> 2 unique peptides	*ftsZ3*	Cell division protein FtsZ	9	5	**14**	1.8	4	10	28.57	0
rrnAC0703	> 2 unique peptides	*ftsZ1*	Cell division protein FtsZ	19	23	**42**	0.83	9	33	21.43	0
pNG6012	> 2 unique peptides	*parA2*	Partition protein	7	9	**16**	0.78	0	16	0	0
pNG2014	single hit	*sojC*	Chromosome partitioning protein	0	2	2	0	0	2	0	0
rrnAC1227	ND										
rrnAC1880	ND										
rrnAC1939	ND										
rrnAC2768	ND										
rrnAC3166	ND										
pNG4012	ND										

ND: Not detected