

Article

# Supplementary Materials: Extraction of Membrane Components from *Neisseria gonorrhoeae* Using Catanionic Surfactant Vesicles: A New Approach for the Study of Bacterial Surface Molecules

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**Table S1.** Proteins identified in vesicles.

UniProtA C	Description	# of spectra identified
Q5F5V7	Major outer membrane protein porin P.IB	270
Q5F939	Pyruvate dehydrogenase E1 component	154
Q5F865	Putative peroxiredoxin family protein/glutaredoxin	153
Q5F9Q2	Cysteine synthase	116
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	109
Q5F6I1	Outer membrane protein PIII	83
Q5F7E7	Aconitate hydratase 2	52
Q5F5P4	Putative uncharacterized protein	49
Q5F905	30S ribosomal protein S1	45
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	36
Q5F942	Putative dihydrolipoamide dehydrogenase	34
Q5F501	Lipoprotein	33
Q5F724	Antibiotic resistance efflux pump component	33
Q5F5Y3	Putative ribonuclease E	32
Q5F6M3	Cell division protein FtsZ	32
Q5F725	Antibiotic resistance efflux pump component	32
Q5F7W0	Putative uncharacterized protein	31
Q5F7T8	Putative isocitrate dehydrogenase	27
Q5F5J3	Putative glyceraldehyde 3-phosphate dehydrogenase C	26
Q5F940	Putative dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex	26
Q5FA20	Putative phosphotransacetylase	26
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	25
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	22
Q5F824	Acetate kinase	22
Q5F5L5	Twitching motility/pilus retraction protein	21
Q5F649	Putative thiol:disulphide interchange protein	21
Q5F731	Glutamate dehydrogenase	21
Q5F809	Lipid modified azurin protein	21
Q5F7W9	Putative ClpB protein	20
Q5F601	Catalase	19
Q5FAI4	Putative fructose-bisphosphate aldolase	19
Q5F6N6	Outer membrane opacity protein D	18
Q5F7Y3	Putative transketolase	18
Q5F8H0	Putative GTP-binding protein	18
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	17
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	17
Q5FA34	Phosphoenolpyruvate synthase	17
Q5F6R0	Putative aspartyl-tRNA synthetase	16

Q5F6V3	Putative alcohol dehydrogenase	14
Q5F726	Multidrug efflux pump channel protein	14
Q5F815	Genome-derived Neisseria antigen 1220	14
Q5F716	Putative cytochrome c oxidase subunit	13
Q5F759	Putative cytochrome	13
Q5F7X2	Putative uncharacterized protein	13
Q5F875	Putative dihydrolipoamide succinyltransferase E2 component	13
Q5F879	Succinyl-CoA ligase [ADP-forming] subunit alpha	12
Q5FA46	Putative zinc-binding alcohol dehydrogenase	12
Q5FAH2	Carbamoyl-phosphate synthase large chain	11
Q5F598	Putative cytochrome C1	10
Q5F8H4	Inosine-5'-monophosphate dehydrogenase	10
Q5FAB8	Putative uncharacterized protein	10
Q5FAG7	Pilus-associated protein	10
Q5F5N5	Pyruvate kinase	9
Q5F5W8	Outer membrane protein assembly factor BamA	9
Q5F6F9	Glutamine synthetase	9
Q5F6M2	Cell division protein ftsA	9
Q5F9Z4	Putative malic enzyme, malate dehydrogenase/oxaloacetate-decarboxylating	9
Q5F666	Signal recognition particle protein	8
Q5F8Q3	Putative phosphogluconate dehydratase	8
Q5F9F5	Ribose-phosphate pyrophosphokinase	8
Q5F9Z8	Cell division protein ZipA	8
Q5FAC8	Putative pilus assembly protein	8
Q5F5I9	Putative electron transfer flavoprotein beta-subunit	7
Q5F798	Putative N utilisation substance protein A	7
Q5F898	Putative D-lactate dehydrogenase	7
Q5F8T2	Putative uncharacterized protein	7
Q5FAD0	Pilus assembly protein	7
Q5F4Z9	Putative chromosome segregation protein	6
Q5F693	Pilus assembly protein	6
Q5F7T9	Alpha-2,3-sialyltransferase	6
Q5F842	Aspartokinase	6
Q5F873	Citrate synthase	6
Q5F8J6	Putative DNA-binding protein Hu	6
Q5F9K8	Delta-aminolevulinic acid dehydratase	6
Q5FA28	Putative ABC transporter, periplasmic binding protein, polyamine	6
Q5FA72	Putative aminopeptidase N	6
Q5FA80	Putative ATP-dependent RNA helicase	6
Q5F697	Putative branched-chain amino acid aminotransferase	5
Q5F6A4	Putative uncharacterized protein	5
Q5F6U0	Putative aminopeptidase	5
Q5F7F1	Probable cytosol aminopeptidase	5
Q5F7Y0	Single-stranded DNA-binding protein	5
Q5F848	Putative uncharacterized protein	5
Q5F876	Dihydrolipoyl dehydrogenase	5
Q5F884	Putative uncharacterized protein	5
Q5F8D7	Putative uncharacterized protein	5
Q5F8K6	Putative peptidyl-prolyl cis-trans isomerase	5
Q5F8K8	Putative ABC-transporter, ATP-binding protein	5
Q5F8X1	Putative L-lactate dehydrogenase	5
Q5F8Y0	DNA gyrase subunit A	5
Q5F933	Putative uncharacterized protein	5
Q5F9I4	Putative cold shock protein	5
Q5FAC5	Putative cytochrome	5
Q5F4X7	Malonyl CoA-acyl carrier protein transacylase	4
Q5F533	Putative DNA polymerase I	4
Q5F5M0	DNA-binding competence protein 2	4
Q5F6I5	Putative ABC transporter, ATP-binding protein	4
Q5F7C9	Putative uncharacterized protein	4
Q5F7G1	Glutathione synthetase	4
Q5F8Q4	Putative khg/kdpg 4-hydroxy-2-oxoglutarate aldolase	4
Q5F8W0	Putative ATP-dependent RNA helicase	4

Q5F8Z6	Ribonucleoside-diphosphate reductase	4
Q5F9L7	Peptidyl-prolyl cis-trans isomerase	4
Q5F9P7	Putative twitching motility-like protein	4
Q5F9S3	Putative uncharacterized protein	4
Q5F9W7	Putative ABC transporter, ATP-binding protein, amino acid	4
Q5FA35	Transcription termination factor Rho	4
Q5FA55	Putative two-component system transcriptional response regulator	4
Q5FAG0	Putative GTP-binding protein	4
Q5FAH6	Acetyl-CoA carboxylase, biotin carboxylase	4
Q5F571	Putative peptide methionine sulfoxide reductase	3
Q5F573	Putative uncharacterized protein	3
Q5F5L4	Putative twitching motility-like protein	3
Q5F668	Phospho-2-dehydro-3-deoxyheptonate aldolase	3
Q5F7E1	Putative uncharacterized protein	3
Q5F7J5	Putative nitrogen regulatory protein P-II	3
Q5F7X0	Tryptophan--tRNA ligase	3
Q5F839	Putative uncharacterized protein	3
Q5F870	Putative succinate dehydrogenase flavoprotein subunit	3
Q5F8C2	Putative uncharacterized protein	3
Q5F8Q1	Putative uncharacterized protein	3
Q5F8S1	Putative threonine synthase	3
Q5F8V3	Pseudouridine synthase	3
Q5F9Y5	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	3
Q5FA17	ABC transporter, periplasmic binding protein, iron related	3
Q5F574	Putative ABC transporter, thiamine-binding periplasmic protein	2
Q5F591	Phosphoenolpyruvate-protein phosphotransferase	2
Q5F5D2	Aspartate-semialdehyde dehydrogenase	2
Q5F5E4	Putative uncharacterized protein	2
Q5F5E6	Methionine aminopeptidase	2
Q5F5I8	Putative electron transfer flavoprotein alpha-subunit	2
Q5F5R0	Transcription antitermination protein nusG	2
Q5F5X8	Putative parA family protein-putative ATPase	2
Q5F5Z8	Putative oligopeptidase A	2
Q5F621	Putative NADH dehydrogenase I chain G	2
Q5F655	Putative adenylosuccinate lyase	2
Q5F696	Enoyl-[acyl-carrier-protein] reductase [NADH]	2
Q5F6K2	Putative uncharacterized protein	2
Q5F6Y6	Aminomethyltransferase	2
Q5F766	Putative paraquat-inducible protein B	2
Q5F7M1	Putative O-succinylhomoserine sulfhydrylase	2
Q5F866	Putative dihydrolipoamide dehydrogenase	2
Q5F8D2	Putative cell-division protein	2
Q5F8Q2	Glucose-6-phosphate 1-dehydrogenase	2
Q5F8S3	Putative ferredoxin-NADP reductase	2
Q5F930	Carbonic anhydrase	2
Q5F950	Putative TonB-dependent receptor	2
Q5F9D9	Putative aminotransferases	2
Q5F9P8	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	2
Q5F9Q9	Putative reductase	2
Q5F9W0	Outer membrane protein assembly factor BamD	2

**Table S2.** Peptides identified by Mass Spectrometry.

UniProtA C	Description	Peptide	Right t AA	E-value
Q5F905	30S ribosomal protein S1	NAQGEIEVK	V	0.002
Q5F905	30S ribosomal protein S1	VGDFVTVTIESVENGFGETK	L	2.9E-06
Q5F905	30S ribosomal protein S1	GGLTVMISSIR	A	0.00006 7
Q5F905	30S ribosomal protein S1	AFLPGSLVDVRPVK	D	0.00000 2

Q5F905	30S ribosomal protein S1	AFLPGSLVDVVRPVKDTSHFEKG	E	0.014
Q5F905	30S ribosomal protein S1	RAVLEATLGEER	K	0.00028
Q5F905	30S ribosomal protein S1	AVLEATLGEERK	A	0.00008 2
Q5F905	30S ribosomal protein S1	KALLENLQEGSVIK	G	8.6E-08
Q5F905	30S ribosomal protein S1	ALLENLQEGSVIK	G	0.00001 1
Q5F905	30S ribosomal protein S1	RVKHPSEVLEVGQEVEAK	V	0.00009 6
Q5F905	30S ribosomal protein S1	VKHPSEVLEVGQEVEAK	V	1.6E-08
Q5F905	30S ribosomal protein S1	QLGEDPWSGLTR	R	0.00004 9
Q5F905	30S ribosomal protein S1	RYPQATR	L	0.022
Q5F905	30S ribosomal protein S1	QLEGDPFGNFISVNDKGS�VK	G	0.00018
Q5F905	30S ribosomal protein S1	LKEGDEVEAVIVTVDRK	N	1.2E-07
Q5F905	30S ribosomal protein S1	EALNSVNAAANANAGTTSGLDLLK	A	6.2E-12
Q5F9P8	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	GQVPQLPAR	F	0.036
Q5F9P8	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase	FASDGILLETAKR	A	0.00047
Q5FA17	ABC transporter, periplasmic binding protein, iron related	GDQLAGQIKEEGSR	S	0.00006 8
Q5FA17	ABC transporter, periplasmic binding protein, iron related	LEAPQVSATTVSEKEHATR	L	9.3E-07
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	VASNAEFAPFESLDSK	G	0.00001 6
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	GNVEGFDVDLMNAMAK	A	4.5E-08
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	AGNFKIEFK	H	0.012
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	QSMDFSDPYFEITQVVLPK	G	2.9E-06
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	VGVVTGHTGDFSVsK	L	0.00039
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	LLGNDNPK	I	0.0019
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	FENVPLIIK	E	0.0022
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	ELENGGLDSVSDSAVIANYYK	N	0.016
Q5F7L8	ABC transporter, periplasmic histidine-binding protein	GMDFVTLPDFTTEHYGI AVR	K	0.0031

Q5F824	Acetate kinase	LILVLNCGSSSLK	G	0.00003 2
Q5F824	Acetate kinase	VVSGGELYNESILVDDEVIAGIEK	C	1E-07
Q5F824	Acetate kinase	CIPLAPLHNPAPHLGLR	A	2.4E-07
Q5F824	Acetate kinase	GLPNVVVFDTSFHQTMPEVAYK	Y	0.00000 4
Q5F824	Acetate kinase	YGAHGTSYR	F	0.00011
Q5F824	Acetate kinase	FVADETAHFLGK	D	0.00012
Q5F824	Acetate kinase	FVADETAHFLGKDKK	D	0.0073
Q5F824	Acetate kinase	DTSMGLTPLEGLVMGTR	S	0.00009 5
Q5F824	Acetate kinase	TIEEEAAKGHKGAK	L	0.00008
Q5F824	Acetate kinase	FGNAGVITTADSK	A	3.7E-09
Q5F824	Acetate kinase	AVAVVIPTNEELMIAHDTAR	L	3.8E-06
Q5F9Y5	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	CNHHNPLSAR	Q	0.024
Q5F9Y5	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	FIGGSMGSVVGGER	F	0.00021
Q5F9Y5	Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	TSAALHLLTEK	R	0.0056
Q5F7E7	Aconitate hydratase 2	AALGIPALPLNAQQTADLVELLK	N	0.00002 5
Q5F7E7	Aconitate hydratase 2	NPPAGEGEFLVELLAHR	V	8.8E-06
Q5F7E7	Aconitate hydratase 2	VKASFLAAVAEGSASSPLVSPK	Y	3.5E-08
Q5F7E7	Aconitate hydratase 2	ASFLAAVAEGSASSPLVSPK	Y	0.00006 1
Q5F7E7	Aconitate hydratase 2	AKVPEKITVTVFK	V	0.0092
Q5F7E7	Aconitate hydratase 2	DGITPDKPGEVGPPIK	L	0.007
Q5F7E7	Aconitate hydratase 2	DGITPDKPGEVGPPIKLEELK	A	0.021
Q5F7E7	Aconitate hydratase 2	AKGHPVAYVGDVVGTGSSR	K	0.00001 3
Q5F7E7	Aconitate hydratase 2	GHPVAYVGDVVGTGSSR	K	1.2E-09
Q5F7E7	Aconitate hydratase 2	GHPVAYVGDVVGTGSSRK	S	0.00001 5
Q5F7E7	Aconitate hydratase 2	KSATNSVIWHTGEDIPFVPNKR	F	0.00029
Q5F7E7	Aconitate hydratase 2	SATNSVIWHTGEDIPFVPNKR	F	0.0034
Q5F7E7	Aconitate hydratase 2	IAPIFFNTQEDSGALPIEVDVSALK	M	1.8E-07
Q5F7E7	Aconitate hydratase 2	SOVLLDEVQAGGR	I	2.7E-08
Q5F7E7	Aconitate hydratase 2	ACGLPEGQGVPRPGTYCEPR	M	0.013
Q5F7E7	Aconitate hydratase 2	MTTVGSQDTTGPMTR	D	0.00005 6
Q5F7E7	Aconitate hydratase 2	THKELPAFISTR	G	0.00084
Q5F7E7	Aconitate hydratase 2	GGVSLRPGDGVIIHSLNLR	L	0.014
Q5F7E7	Aconitate hydratase 2	DLVNAIPLYAIK	Q	0.0011
Q5F7E7	Aconitate hydratase 2	LNKEPIIEYMK	S	0.0031
Q5F7E7	Aconitate hydratase 2	LLEGKSDIPVR	L	0.00009 9
Q5F7E7	Aconitate hydratase 2	ELSDEGHYGVLGR	A	0.00012
Q5F7E7	Aconitate hydratase 2	EGATVMSTSTR	N	2.5E-06
Q5F7E7	Aconitate hydratase 2	NTFVYLGSAELAAICSK	L	0.00075
Q5F7E7	Aconitate hydratase 2	LGKIPTVEEYQANIGIINEQGDKIYR	Y	0.0013
Q5F7E7	Aconitate hydratase 2	IPTVEEYQANIGIINEQGDKIYR	Y	1.6E-07
Q5F7T9	Alpha-2,3- sialyltransferase	NASDEHYTIFK	G	0.0012
Q5F7T9	Alpha-2,3- sialyltransferase	KMTYLPLFDASELKAGDETGGTVR	I	0.00001 2
Q5F7T9	Alpha-2,3- sialyltransferase	ILLGSPDKEMKEISEK	A	0.00018
Q5F7T9	Alpha-2,3- sialyltransferase	NFNIQYVAPHPR	Q	0.00001 7

Q5F6Y6	Aminomethyltransferase	AFFRKLIVANDVAK	L	0.037
Q5F6Y6	Aminomethyltransferase	ALQTAGVQCGLGAR	D	0.041
Q5F724	Antibiotic resistance efflux pump component	AQVGGIIQK	R	0.023
Q5F724	Antibiotic resistance efflux pump component	AQVGGIIQKR	L	0.000097
Q5F724	Antibiotic resistance efflux pump component	AGQPLYQIDSSTYEAGLESAR	A	5.2E-10
Q5F724	Antibiotic resistance efflux pump component	AQLATAQATLAK	A	0.00037
Q5F724	Antibiotic resistance efflux pump component	SAEAGVKAAQAAIK	S	0.0094
Q5F724	Antibiotic resistance efflux pump component	SAGINLNR	S	0.00099
Q5F724	Antibiotic resistance efflux pump component	SRITAPISGFIGQSK	V	0.00016
Q5F724	Antibiotic resistance efflux pump component	ITAPISGFIGQSK	V	3.9E-06
Q5F724	Antibiotic resistance efflux pump component	VSEGTLLNAGDTTVLATIR	Q	5E-08
Q5F724	Antibiotic resistance efflux pump component	QTNPMYVNVTSASEVMK	L	1.3E-08
Q5F724	Antibiotic resistance efflux pump component	AAVSNDQNILMPGLYVR	V	2.9E-07
Q5F724	Antibiotic resistance efflux pump component	VLMDQVAADNAFIVPQQAVTR	G	0.00013
Q5F724	Antibiotic resistance efflux pump component	GAKDVMIVNAQGGMEPR	E	1.7E-07
Q5F724	Antibiotic resistance efflux pump component	EWAPSENQAAAPQAGVQTASEAKPASEAK	-	0.00073
Q5F725	Antibiotic resistance efflux pump component	LSEVLSTLPATVQQYGVTVSK	A	0.0012
Q5F725	Antibiotic resistance efflux pump component	ANTDGSNIYLKDVAK	V	0.000014
Q5F725	Antibiotic resistance efflux pump component	TDATLAQVTQLAK	S	8.4E-07
Q5F725	Antibiotic resistance efflux pump component	TASGSDAVAVAGK	L	0.0051
Q5F725	Antibiotic resistance efflux pump component	ASGLFDPSTVR	A	0.0026
Q5F725	Antibiotic resistance efflux pump component	AGGLEDSPQLK	I	0.0019

Q5F725	Antibiotic resistance efflux pump component	AAAAAQGISFADIR	T	3E-08
Q5F725	Antibiotic resistance efflux pump component	TALASALSSSYVSDFPNQGR	L	8.5E-09
Q5F725	Antibiotic resistance efflux pump component	MQPADILNLTVPNK	S	1.1E-06
Q5F725	Antibiotic resistance efflux pump component	SGVAVPLSTIATVSWENGTEQSVR	F	0.0079
Q5F725	Antibiotic resistance efflux pump component	LSASPATGVSTGQAMAAVQK	M	6.9E-10
Q5F725	Antibiotic resistance efflux pump component	AGITGSDDKQY	-	0.012
Q5F842	Aspartokinase	YGGTSVGSPPER	I	0.01
Q5F842	Aspartokinase	AAVTGIAFDKNQAR	I	0.00001
Q5FAH2	Carbamoyl-phosphate synthase large chain	TPASFEPSIDYVVTK	I	0.00063
Q5FAH2	Carbamoyl-phosphate synthase large chain	ELANPGPER	M	0.0066
Q5FAH2	Carbamoyl-phosphate synthase large chain	VLNDLGLRQPPNR	I	0.016
Q5FAH2	Carbamoyl-phosphate synthase large chain	IAHNEEEALVK	A	0.004
Q5FAH2	Carbamoyl-phosphate synthase large chain	AEEIGYPLVVRPSYVLGGR	A	0.01
Q5FAH2	Carbamoyl-phosphate synthase large chain	VPQYTTTAGGEAMSEGA	S	5.5E-07
Q5F601	Catalase	TTSKCPVTHLTMNNGAPVADNQNSLTAGPR	G	4.6E-06
Q5F601	Catalase	CPVTHLTMNNGAPVADNQNSLTAGPR	G	0.0049
Q5F601	Catalase	GPLLTQDLWLNEK	L	0.00057
Q5F601	Catalase	EVIPERR	M	0.0025
Q5F601	Catalase	FTTVAGER	G	0.049
Q5F601	Catalase	LFNYADAQR	Y	0.00003
Q5F601	Catalase	QIPVNRPR	C	0.0053
Q5F601	Catalase	ALFNLMNDAQK	Q	0.00003 8
Q5F601	Catalase	QALFDNTAAAMGDAPDFIK	Y	0.00001 3
Q5F601	Catalase	QALFDNTAAAMGDAPDFIKYR	H	5.7E-06
Q5F601	Catalase	CDPAYGEGVAK	A	0.0019
Q5F6M2	Cell division protein ftsA	ITHVTTGIAGNHIR	S	1.2E-07
Q5F6M2	Cell division protein ftsA	VHIITGASTAVQNVQK	C	1.6E-08
Q5F6M3	Cell division protein FtsZ	MEFVYDVAESA VSPAVIK	V	5.2E-06
Q5F6M3	Cell division protein FtsZ	VIGLGGGGCNAINNMVANNVR	S	2E-07
Q5F6M3	Cell division protein FtsZ	SVEFISANTDAQSLAK	N	2.3E-07
Q5F6M3	Cell division protein FtsZ	RIQLGTNLTR	G	0.00084
Q5F6M3	Cell division protein FtsZ	IQLGTNLTR	G	0.00057
Q5F6M3	Cell division protein FtsZ	GLGAGANPDIGR	A	0.00001 5
Q5F6M3	Cell division protein FtsZ	GIAMMGSGYAQGIDR	A	6.8E-07

Q5F6M3	Cell division protein FtsZ	MATDQAISSPLDDVTLDGAR	G	8.8E-08
Q5F6M3	Cell division protein FtsZ	GVLVNITTAPGCLK	M	1.9E-08
Q5F6M3	Cell division protein FtsZ	IVNQSAHPDLECK	F	0.0016
Q5F6M3	Cell division protein FtsZ	ITIIATGLKEK	G	0.00056
Q5F6M3	Cell division protein FtsZ	GAVDPTPAR	E	0.0055
Q5F6M3	Cell division protein FtsZ	GAVDPTPAREVEAVAPSKQEQSHNVEGMIR	T	0.017
Q5F6M3	Cell division protein FtsZ	EVEAVAPSKQEQSHNVEGMIR	T	0.000015
Q5F9Z8	Cell division protein ZipA	VRDQFGHSDKDALLNSK	T	1.6E-06
Q5F9Z8	Cell division protein ZipA	TSHVRDGGKPSGGPVMMPKQPQPAVK	K	0.00088
Q5F9Z8	Cell division protein ZipA	KPAKPQDSAMR	N	0.011
Q5F9Z8	Cell division protein ZipA	NLQEQDAVYIAK	Q	0.00012
Q5F873	Citrate synthase	SKSIKLNVPGR	A	0.0033
Q5F873	Citrate synthase	SIKLNVPGR	A	0.0022
Q5F873	Citrate synthase	AGLELPVLEASIGHDVVDIR	G	8.5E-06
Q5F873	Citrate synthase	IFILHADHEQNASTSTVR	L	1.2E-06
Q5F873	Citrate synthase	RDYVPAGER	-	0.0098
Q5F9Q2	Cysteine synthase	MKIANSITELIGNTPLVK	L	3.4E-09
Q5F9Q2	Cysteine synthase	IANSITELIGNTPLVK	L	0.0029
Q5F9Q2	Cysteine synthase	GLKAEVAVK	L	0.0059
Q5F9Q2	Cysteine synthase	TFGAELILTPAAEGMAGAIK	A	3.7E-07
Q5F9Q2	Cysteine synthase	AQSLVDAHPTDYFMPR	Q	1E-07
Q5F9Q2	Cysteine synthase	QFDNEANPEVHR	K	0.00042
Q5F9Q2	Cysteine synthase	QFDNEANPEVHRK	T	0.00021
Q5F9Q2	Cysteine synthase	GPHPIQGIGAGFIPTVLNTK	I	1E-08
Q5F9Q2	Cysteine synthase	IYDSIAKVPNEAAFETAR	A	1.8E-06
Q5F9Q2	Cysteine synthase	VPNEAAFETAR	A	5.1E-07
Q5F9Q2	Cysteine synthase	EGILAGISSGAAVWSALQLAK	Q	5.3E-07
Q5F9Q2	Cysteine synthase	QPENEGKLIVVLLPSYGER	Y	3.1E-06
Q5F9Q2	Cysteine synthase	LIVVLLPSYGER	Y	0.000076
Q5F9K8	Delta-aminolevulinic acid dehydratase	LGIPMLALFPVVTANK	T	9.6E-06
Q5F9K8	Delta-aminolevulinic acid dehydratase	AQEAYNPEGLVPSTVR	A	0.000028
Q5F876	Dihydrolipoyl dehydrogenase	SQYDVVVIGAGPGGYVAAIR	A	3.7E-08
Q5F876	Dihydrolipoyl dehydrogenase	TNLPNVWAIGDVVR	G	4.2E-06
Q5F876	Dihydrolipoyl dehydrogenase	ASDEGVAVAER	I	2.7E-06
Q5F8Y0	DNA gyrase subunit A	IVGDVIGK	Y	0.049
Q5F8Y0	DNA gyrase subunit A	IIDFVDILSKPER	I	0.000023
Q5F8Y0	DNA gyrase subunit A	KNKGGQGSIAINTGER	N	0.0023
Q5F8Y0	DNA gyrase subunit A	LINLDEGETLVSLER	V	0.00024
Q5F5M0	DNA-binding competence protein 2	VKGIGPAVLAK	L	0.00015
Q5F5M0	DNA-binding competence protein 2	LKDQASVGAPAPK	G	1.8E-06
Q5F696	Enoyl-[acyl-carrier- protein] reductase [NADH]	EAFNTAHEISAYSLPALAK	A	0.000045



Q5F696	Enoyl-[acyl-carrier-protein] reductase [NADH]	TLAASGIADFGK	L	0.023
Q5F8I5	Genome-derived Neisseria antigen 1220	AMQAQITAER	E	0.00008 4
Q5F8I5	Genome-derived Neisseria antigen 1220	AMQAQITAEREK	R	0.00027
Q5F8I5	Genome-derived Neisseria antigen 1220	IAESEGRKIEQINLASGQR	E	0.0047
Q5F8I5	Genome-derived Neisseria antigen 1220	KIEQINLASGQR	E	2.2E-06
Q5F8I5	Genome-derived Neisseria antigen 1220	IEQINLASGQR	E	0.039
Q5F8I5	Genome-derived Neisseria antigen 1220	EAEIQQSEGEAQAAVNASNAEK	I	1E-07
Q5F8I5	Genome-derived Neisseria antigen 1220	QIAAALQTQGGADAVNLK	I	6.8E-12
Q5F8I5	Genome-derived Neisseria antigen 1220	IAEQYVAAFNNLAK	E	0.00001 2
Q5F731	Glutamate dehydrogenase	TDLNTLFANLK	Q	1.4E-06
Q5F731	Glutamate dehydrogenase	TDLNTLFANLKQR	N	0.00023
Q5F731	Glutamate dehydrogenase	NPKYTQQSLER	I	0.0057
Q5F731	Glutamate dehydrogenase	YTQQSLER	I	9.6E-06
Q5F731	Glutamate dehydrogenase	FLAFEQVFK	N	0.043
Q5F731	Glutamate dehydrogenase	VLISGSGNVAQYAAEK	A	7.1E-09
Q5F731	Glutamate dehydrogenase	ASNAGGVATSGLEMSQNAIR	L	3E-11
Q5F731	Glutamate dehydrogenase	VGDKVNYYNGANIAGFVK	V	2.1E-06
Q5F6F9	Glutamine synthetase	GGYAPVAPIDCGQDLR	S	0.00027
Q5F6F9	Glutamine synthetase	FATLVKR	A	0.0026
Q5F6F9	Glutamine synthetase	ALNAITNPSTNSYK	R	0.0074
Q5F6F9	Glutamine synthetase	ALNAITNPSTNSYKR	L	0.00001
Q5F6F9	Glutamine synthetase	LVPHFAPTK	L	0.027
Q5F6F9	Glutamine synthetase	LVPHFAPTKLAYSAK	N	0.0006
Q5F6F9	Glutamine synthetase	SASIRIPSVNSSK	A	0.0019
Q5F7G1	Glutathione synthetase	AADKVQTALK	E	0.015
Q5F7G1	Glutathione synthetase	FTAPTLVTTR	S	0.00002 6
Q5F7G1	Glutathione synthetase	YIPEIVHGDKR	I	0.046
Q5F7G1	Glutathione synthetase	ILIIGGEVVPYALAR	I	0.00009 5
Q5F8H4	Inosine-5'- monophosphate dehydrogenase	AYTFDDVLLVPAHSTVLPR	D	2.9E-07
Q5F8H4	Inosine-5'- monophosphate dehydrogenase	EITLNLPLLSAAMDTVTEAR	L	1.6E-07
Q5F8H4	Inosine-5'- monophosphate dehydrogenase	RHESGVVKDPVTVAPTTLIR	E	0.0025
Q5F8H4	Inosine-5'- monophosphate dehydrogenase	HESGVVKDPVTVAPTTLIR	E	0.00001 5
Q5F8H4	Inosine-5'- monophosphate dehydrogenase	TTEFPNANKDSEGR	L	0.0012

Q5F8H4	Inosine-5'- monophosphate dehydrogenase	VGAAVGTGGDTERVK	A	0.00072
Q5F8H4	Inosine-5'- monophosphate dehydrogenase	IVAGVGVQLTAIHNVAEALK	G	0.001
Q5F809	Lipid modified azurin protein	ACKEFTITLK	H	0.013
Q5F809	Lipid modified azurin protein	ASMGHNLVIAK	A	0.00008 6
Q5F809	Lipid modified azurin protein	LIGGGEESLTLDDPAK	L	2.2E-06
Q5F809	Lipid modified azurin protein	FACTFPGHGALMNGK	V	0.00001 7
Q5F809	Lipid modified azurin protein	FACTFPGHGALMNGKVTLVD	-	0.0016
Q5F501	Lipoprotein	DSAPAASAAAPSADNGAAK	K	0.0045
Q5F501	Lipoprotein	DSAPAASAAAPSADNGAAKK	E	0.00005 7
Q5F501	Lipoprotein	EIVFGTTVGDGDMVK	E	0.00013
Q5F501	Lipoprotein	EQIQAELEKK	G	0.018
Q5F501	Lipoprotein	EHNLDITEAFQVPTAPLGLYPGK	L	0.00043
Q5F501	Lipoprotein	LKSLEEVKDGSTVSAPNDPSNFAR	A	5.9E-06
Q5F501	Lipoprotein	SLEEVKDGSTVSAPNDPSNFAR	A	0.00001 4
Q5F501	Lipoprotein	DGSTVSAPNDPSNFAR	A	0.0021
Q5F501	Lipoprotein	ALVMLNELGWIK	L	0.00013
Q5F501	Lipoprotein	LKDGINPLTASK	A	0.00014
Q5F501	Lipoprotein	IVELEAAQLPR	S	0.00007 5
Q5F501	Lipoprotein	LTEALFQEPSFAYVNWSAVK	T	2.8E-06
Q5F501	Lipoprotein	TADKDSQWLKDVTEAYNSDAFK	A	6.3E-07
Q5F501	Lipoprotein	RFEGYKYPAAWNEGAAK	-	5.7E-06
Q5F501	Lipoprotein	FEGYKYPAAWNEGAAK	-	0.00000 1
Q5F5V7	Major outer membrane protein porin P.IB	AGVQTYRSVEHTDGK	V	0.031
Q5F5V7	Major outer membrane protein porin P.IB	AGVQTYRSVEHTDGKVS	V	0.007
Q5F5V7	Major outer membrane protein porin P.IB	AGVQTYRSVEHTDGKSVK	I	2.2E-06
Q5F5V7	Major outer membrane protein porin P.IB	SVEHTDGKVS	V	0.00007
Q5F5V7	Major outer membrane protein porin P.IB	SVEHTDGKSVKSVETGSEIADFGSK	I	3.3E-06
Q5F5V7	Major outer membrane protein porin P.IB	VSKVETGSEIADFGSK	I	1.6E-07
Q5F5V7	Major outer membrane protein porin P.IB	VETGSEIADFGSK	I	1.2E-07
Q5F5V7	Major outer membrane protein porin P.IB	IGFKGQEDLGNGLK	A	7.8E-06
Q5F5V7	Major outer membrane protein porin P.IB	GQEDLGNGLK	A	0.00005 8
Q5F5V7	Major outer membrane protein porin P.IB	AVWQLEQGASVAGTNTGWGNK	Q	3E-10
Q5F5V7	Major outer membrane protein porin P.IB	AVWQLEQGASVAGTNTGWGNKQSFVGLK	G	0.03
Q5F5V7	Major outer membrane protein porin P.IB	QSFVGLKGGFGTIR	A	0.00001 1
Q5F5V7	Major outer membrane protein porin P.IB	AGSLNSPLK	N	0.00083
Q5F5V7	Major outer membrane protein porin P.IB	FTGNVLEISGMAQR	E	0.00055

Q5F5V7	Major outer membrane protein porin P.IB	YDSPEFAGFSGSVQYAPK	D	1.2E-09
Q5F5V7	Major outer membrane protein porin P.IB	LVGGYDNNALYVSVAAQQQDAK	L	6.2E-11
Q5F5V7	Major outer membrane protein porin P.IB	VSYAHGFK	G	0.000027
Q5F5V7	Major outer membrane protein porin P.IB	GTVDSANHDNTYDQVVVGAEYDFSKR	T	0.00001
Q5F5V7	Major outer membrane protein porin P.IB	RTSALVSAGWLQEGK	G	3.2E-08
Q5F5V7	Major outer membrane protein porin P.IB	TSALVSAGWLQEGK	G	2.1E-06
Q5F5V7	Major outer membrane protein porin P.IB	TSALVSAGWLQEGKGADK	I	8.9E-07
Q5F5V7	Major outer membrane protein porin P.IB	TSALVSAGWLQEGKGADKIVSTASAVVLR	H	0.000006
Q5F5V7	Major outer membrane protein porin P.IB	GADKIVSTASAVVLR	H	2E-07
Q5F5V7	Major outer membrane protein porin P.IB	IVSTASAVVLR	H	3.4E-06
Q5F4X7	Malonyl CoA-acyl carrier protein transacylase	TVEIKQPQIR	V	0.018
Q5F4X7	Malonyl CoA-acyl carrier protein transacylase	VIHNADVAAYDDAGK	I	0.000055
Q5F4X7	Malonyl CoA-acyl carrier protein transacylase	IKDALVR	Q	0.023
Q5F726	Multidrug efflux pump channel protein	NNLLPTLAANANGSR	Q	0.0037
Q5F726	Multidrug efflux pump channel protein	AGVISAVALRQQEALIESAK	A	1.4E-07
Q5F726	Multidrug efflux pump channel protein	NALATLINRPIPEDLPAGLPLDK	Q	0.002
Q5F726	Multidrug efflux pump channel protein	LPAGLSSEVLLDRPDIR	A	0.000051
Q5F726	Multidrug efflux pump channel protein	AAEHALKQANANIGAAR	A	9.1E-06
Q5F726	Multidrug efflux pump channel protein	QANANIGAAR	A	0.0023
Q5F726	Multidrug efflux pump channel protein	LTGSGVTGSVELGGLFK	S	4.4E-06
Q5F726	Multidrug efflux pump channel protein	YKHGVS GALDLLDAER	I	1.6E-06
Q5F6N6	Outer membrane opacity protein D	NKISTVSDYFR	N	0.0017
Q5F6N6	Outer membrane opacity protein D	ISTVSDYFR	N	0.00018
Q5F6N6	Outer membrane opacity protein D	VSVG YDFGGWR	I	8.5E-06
Q5F6N6	Outer membrane opacity protein D	VAYGHVR	H	0.0018
Q5F5W8	Outer membrane protein assembly factor BamA	TEPSTVFNYLPVK	V	0.00035
Q5F5W8	Outer membrane protein assembly factor BamA	VGD TYNDTHGSAIK	S	0.0051
Q5F5W8	Outer membrane protein assembly factor BamA	GKLNIQITPK	V	0.003

Q5F5W8	Outer membrane protein assembly factor BamA	ILDTDIQTNEDKTR	Q	0.00024
Q5F5W8	Outer membrane protein assembly factor BamA	QQMTAVLGEIQNR	M	0.017
Q5F5W8	Outer membrane protein assembly factor BamA	IYVNEIHITGNNK	T	0.00001 1
Q5F5W8	Outer membrane protein assembly factor BamA	TKEIPFFENFYGGGLGSVR	G	0.00001 9
Q5F9W0	Outer membrane protein assembly factor BamD	GLVLFNEDQSFLNK	L	7.4E-06
Q5F9W0	Outer membrane protein assembly factor BamD	GAYIAAANR	A	0.0006
Q5F5Y8	Outer membrane protein assembly factor BamE	AVAALRPGMTKDQVLLLLGSPILR	D	0.0033
Q5F6I1	Outer membrane protein PIII	NAYFDKASQGR	V	0.00005 6
Q5F6I1	Outer membrane protein PIII	ASQGRVECGDAVAVPEPEPAPVAVVEQAPQYVDETISLS AK	T	0.00018
Q5F6I1	Outer membrane protein PIII	TLFGFDKDSLRL	A	0.01
Q5F6I1	Outer membrane protein PIII	TLFGFDKDSLRAEAQDNLK	V	0.00005 3
Q5F6I1	Outer membrane protein PIII	DSLRAEAQDNLK	V	0.00027
Q5F6I1	Outer membrane protein PIII	TNVQSVR	V	0.00031
Q5F6I1	Outer membrane protein PIII	VEGHTDFMGSEK	Y	0.0013
Q5F6I1	Outer membrane protein PIII	VEGHTDFMGSEKYNQALSER	R	3.9E-07
Q5F6I1	Outer membrane protein PIII	YNQALSER	R	0.00001 8
Q5F6I1	Outer membrane protein PIII	RAYVVANNLVSNGVPASR	I	4.1E-07
Q5F6I1	Outer membrane protein PIII	AYVVANNLVSNGVPASR	I	2.5E-09
Q5F6I1	Outer membrane protein PIII	ISAVGLGESQAQMTQVCQAEVAK	L	5.7E-09
Q5F6I1	Outer membrane protein PIII	EALIACIEPDR	R	0.0011
Q5F6I1	Outer membrane protein PIII	EALIACIEPDRRVDVK	I	0.044
Q5F6I1	Outer membrane protein PIII	IRSIVTR	Q	0.02
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	SLKQMKEQGAEIDLK	V	0.003
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	FLQEQQAK	A	0.027
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	ANKEKGEAFLKENAAK	D	0.00003 9
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	ANKEKGEAFLKENAAKDGVK	T	0.046
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	DGVKTTASGLQYK	I	0.03
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	DGVKTTASGLQYKITK	Q	0.00013

Q5F7F3	Peptidyl-prolyl cis-trans isomerase	TTASGLQYK	I	0.0036
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	TTASGLQYKITK	Q	0.000073
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	QGEGKQPTKDDIVTVEYEGR	L	0.0017
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	LIDGTVFDSSK	A	0.0018
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	ANGGPATFPLSQVIPGWTEGVR	L	1E-07
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	LLKEGGEATFYIPSNLAYREQGAGEK	I	0.00024
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	EGGEATFYIPSNLAYR	E	0.000011
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	IGPNATLVFDVK	L	2.6E-06
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	IGAPENAPAKQPDQVDIK	K	0.0023
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	IGAPENAPAKQPDQVDIKK	V	0.0044
Q5F7F3	Peptidyl-prolyl cis-trans isomerase	IGAPENAPAKQPDQVDIKKVN	-	0.0013
Q5F820	Peptidyl-prolyl cis-trans isomerase	FKATVESVR	D	0.0068
Q5F9L7	Peptidyl-prolyl cis-trans isomerase	TVVQDWGYAVFGK	V	0.000085
Q5F9L7	Peptidyl-prolyl cis-trans isomerase	VVDGFDVVDAIESV <sub>s</sub> TKR	H	1.7E-08
Q5F668	Phospho-2-dehydro-3-deoxyheptonate aldolase	ELLPPIAHLYELPISK	E	0.013
Q5F668	Phospho-2-dehydro-3-deoxyheptonate aldolase	EASGLVHR	T	0.013
Q5FA34	Phosphoenolpyruvate synthase	ADNYVIWFENLR	M	0.000016
Q5FA34	Phosphoenolpyruvate synthase	NASLGEMISQLTEK	G	0.000026
Q5FA34	Phosphoenolpyruvate synthase	VPGGFATTADAYR	A	9.6E-07
Q5FA34	Phosphoenolpyruvate synthase	AFLAHNGLNER	I	0.0033
Q5FA34	Phosphoenolpyruvate synthase	VHKGFEHDIVALSAGVQR	M	2.1E-08
Q5FA34	Phosphoenolpyruvate synthase	GFEHDIVALSAGVQR	M	0.000035
Q5FA34	Phosphoenolpyruvate synthase	MIFTDKAEAGK	S	0.0078
Q5FA34	Phosphoenolpyruvate synthase	DGLDGKLYILQARPETVK	S	0.00013
Q5FA34	Phosphoenolpyruvate synthase	LYILQARPETVK	S	0.000032
Q5FA34	Phosphoenolpyruvate synthase	VRDEMGLTNVEIMIPFVR	T	0.00066
Q5FA34	Phosphoenolpyruvate synthase	ALKENGLER	G	0.0052
Q5FAD1	Pilin assembly protein	KAELLNSSDKNTEQAAAPAAEQN	-	0.013
Q5F693	Pilus assembly protein	KITQEDITVFTR	Q	0.000012
Q5F693	Pilus assembly protein	AGLPLMQAFEIVAR	G	5.4E-08
Q5F693	Pilus assembly protein	GQVEQGSSLSR	A	0.00045
Q5FAD0	Pilus assembly protein	SIDAASLNLRDELASIR	S	0.013
Q5FAD0	Pilus assembly protein	IAQSPENGGNPDGK	S	0.035
Q5FAD0	Pilus assembly protein	SSILNLSAIATTYQAK	S	8.6E-08

Q5FAG7	Pilus-associated protein	VQMYSASVSTYPGSSSSR	I	3.1E-07
Q5FAG7	Pilus-associated protein	KDIEGNDSLAK	E	0.0078
Q5FAG7	Pilus-associated protein	TQNGKYAAFLASGYAAK	N	0.00003 3
Q5FAG7	Pilus-associated protein	YAAFLASGYAAK	N	0.00002 3
Q5FAG7	Pilus-associated protein	TIFEGDKPITSAPAVSR	L	0.00017
Q5FAG7	Pilus-associated protein	TVCPNGYVYDKPVNVR	Y	0.00071
Q5F7F1	Probable cytosol aminopeptidase	FSQAVFHSAHEAAVK	E	0.0023
Q5F7F1	Probable cytosol aminopeptidase	VAEAQVYGQSLCR	D	0.036
Q5F7F1	Probable cytosol aminopeptidase	TAKAEAEKLGAAK	I	1.2E-06
Q5F7F1	Probable cytosol aminopeptidase	GATGRPVPLLMNYLR	N	0.00039
Q5FA43	Protein translocase subunit SecD	QNITTLHNR	V	0.0002
Q5F8V3	Pseudouridine synthase	QWRDGAAPSACK	T	0.048
Q5F8V3	Pseudouridine synthase	GQFYELNPAEVANILK	W	9.5E-07
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	IASAVAGGADEAMLKK	Q	4.8E-07
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	IQGVGAAQLDPLK	R	2.6E-06
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	IQGVGAAQLDPLKR	I	0.00002 5
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	NYFESVLSTPHYNADQK	R	2.1E-06
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	ILKEMTAAETLER	Y	0.0036
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	STVHCTDIAK	M	0.015
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	EKIETGLPAADIER	L	0.00033
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	LTEKFTAVPEGFALHPTAK	R	0.00019
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	FTAVPEGFALHPTAK	R	1.3E-07
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	QAIDWGMATLAYASLLTK	G	1.1E-09
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	VVLCAGQVYDLEAGR	A	1.1E-06
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	VEQLYFPYDEVKAELAK	Y	0.011
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	NQGAFYQIR	H	0.0022
Q5F874	Putative 2-oxoglutarate dehydrogenase, E1 component	HRIEDVISEEQK	L	0.038

Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	IALVTGASR	G	0.01
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	GIGAAIADTLAAAGAK	I	7E-08
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	IIGTATGESGAAAISK	R	1.2E-06
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	IIGTATGESGAAAISKR	L	0.033
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	LAQWGGEGR	V	0.00026
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	VLNSAEPETVENLIADIEK	T	5.5E-07
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	TFGKLDILVNNAGITR	D	0.00021
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	LDILVNNAGITR	D	0.033
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	ALPEETRQFTTAQTALGR	F	0.019
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	FGDAQDIADAVLFLASDQAK	Y	4.7E-12
Q5F4Y0	Putative 3-oxoacyl-[acyl-carrier protein] reductase	YITGQTLHVNGGMLMP	-	0.00071
Q5F6I5	Putative ABC transporter, ATP-binding protein	LGNEVIEFVNVSK	S	3.5E-07
Q5F6I5	Putative ABC transporter, ATP-binding protein	VPAGAIVGIIIGPNGAGK	S	9.7E-07
Q5F6I5	Putative ABC transporter, ATP-binding protein	DILQVGQFEIPAR	Q	0.000018
Q5F9W7	Putative ABC transporter, ATP-binding protein, amino acid	KGEVVVVCGPSGSGK	S	0.037
Q5F9W7	Putative ABC transporter, ATP-binding protein, amino acid	DAFPSQLSGGQQQR	V	0.00063
Q5F9W7	Putative ABC transporter, ATP-binding protein, amino acid	AKQFLQQVMTH	-	0.017
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	INNKGTVTVGTEGTYAPFTYHDKDGK	L	0.000029
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	INNKGTVTVGTEGTYAPFTYHDKDGKLTGYDVEVTR	A	0.000055
Q5F9M1	Putative ABC transporter,	VEFKETQWDSMMAGLK	A	0.000062

	periplasmic binding protein, amino acid			
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	AGRFDVVANQVGLTSPER	Q	2.4E-08
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	FDVVANQVGLTSPER	Q	2.5E-06
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	QATFDKSEPYSWGAVLVAHNDSNIK	S	0.000015
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	SEPYSWGAVLVAHNDSNIK	S	0.000011
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	TAQSLTSNYGEK	A	0.000031
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	AKAAGAQLVPVDGLAQSLTLIEQK	R	0.00016
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	AAGAQLVPVDGLAQSLTLIEQK	R	1.1E-08
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	AAGAQLVPVDGLAQSLTLIEQKR	A	5.8E-09
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	RADATLNDELAVLDYLK	K	3.6E-08
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	RADATLNDELAVLDYLKK	N	5.7E-08
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	ADATLNDELAVLDYLK	K	4.1E-08
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	ADATLNDELAVLDYLKK	N	0.00013
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	IVWSAPADEKVGSGLIVNK	G	5.2E-08
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	IVWSAPADEKVGSGLIVNKGNDEAVAK	F	0.00019
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	VGSGLIVNK	G	0.033
Q5F9M1	Putative ABC transporter,	VGSGLIVNKGNDEAVAK	F	0.00004



	periplasmic binding protein, amino acid			
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	FSTAINELK	A	0.000099
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	FSTAINELKADGTLK	K	4.2E-06
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	FSTAINELKADGTLKK	L	0.000031
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	KLGEQFFGKDISVQ	-	3.4E-07
Q5F9M1	Putative ABC transporter, periplasmic binding protein, amino acid	LGEQFFGKDISVQ	-	0.00028
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	SGYDLVVPGIAFLPR	Q	2.6E-06
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	VNKDLIPNYKNIDPELLK	M	0.015
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	GSNPEDLKAAA EVLK	S	0.00011
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	RFSPSIIDELAR	G	0.017
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	FSPSIIDELAR	G	0.00083
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	ARSEEVKNNV GIEVLTPK	G	4.8E-06
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	SEEVKNNV GIEVLTPK	G	0.000048
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	YINYTLDP EIAAK	N	0.00074
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	NGIAVTFAPASKPAR	E	0.000044
Q5F6Q5	Putative ABC transporter, periplasmic binding protein, polyamine	EKMPAELVNTR	S	0.00041
Q5F6Q5	Putative ABC transporter,	MPAELVNTR	S	0.028

	periplasmic binding protein, polyamine			
Q5F7C5	Putative ABC transporter, periplasmic binding protein, polyamine	NGNFVTYAPSSKPAR	D	0.0064
Q5FA28	Putative ABC transporter, periplasmic binding protein, polyamine	SGYDLTAPSIANVGR	Q	3.1E-06
Q5FA28	Putative ABC transporter, periplasmic binding protein, polyamine	AQIPHYGNIDKDLLK	M	0.00022
Q5FA28	Putative ABC transporter, periplasmic binding protein, polyamine	TGVGWVDSFMIPR	D	0.00078
Q5FA28	Putative ABC transporter, periplasmic binding protein, polyamine	YIDYTLRPEVAAK	N	0.0039
Q5F8K8	Putative ABC-transporter, ATP-binding protein	FAEYDGYTAEAR	A	1.6E-07
Q5F8K8	Putative ABC-transporter, ATP-binding protein	LQELQEFVAR	F	0.025
Q5F8K8	Putative ABC-transporter, ATP-binding protein	LKQADKIKSEMVEVKPSTR	Q	0.008
Q5F8K8	Putative ABC-transporter, ATP-binding protein	SEMVEVKPSTR	Q	0.014
Q5F8K8	Putative ABC-transporter, ATP-binding protein	LAIIGPNGACK	S	0.00068
Q5F8B6	Putative ABC-type transporter, ATP-binding protein	SREDKIQTASAPK	A	0.013
Q5F655	Putative adenylosuccinate lyase	LLELTPALYVGK	A	0.0037
Q5F655	Putative adenylosuccinate lyase	LLELTPALYVGKAEALAK	R	0.000037
Q5F6V3	Putative alcohol dehydrogenase	MKMQAVVVNK	N	0.00014
Q5F6V3	Putative alcohol dehydrogenase	ETGADLVVNAAKEDAAK	V	0.00043
Q5F6V3	Putative alcohol dehydrogenase	TGGAHAHVVTAVSAAAFNSAVNCVR	A	0.015
Q5F6V3	Putative alcohol dehydrogenase	VVAVGLPPESMDLSIPR	L	0.033
Q5F6V3	Putative alcohol dehydrogenase	LVLGDGIEVVGSLVGTR	K	2.1E-07
Q5F6V3	Putative alcohol dehydrogenase	LVLGDGIEVVGSLVGTRK	D	5.8E-07
Q5F6V3	Putative alcohol dehydrogenase	ALDEAPAIFQEMR	E	0.000049
Q5F8U5	Putative aldehyde dehydrogenase	ILAAHAGANLKK	T	0.00042
Q5F758	Putative amino acid aminotransferase	IVTVQTLGGSGALK	V	0.0036
Q5F6U0	Putative aminopeptidase	LIEGINPSTFFK	S	0.00038

Q5F6U0	Putative aminopeptidase	VVPVGTPTAEQKR	D	0.0049
Q5F6U0	Putative aminopeptidase	RLEPLTEGAAK	A	0.004
Q5FA72	Putative aminopeptidase N	YLKDYQTPAYR	I	0.013
Q5FA72	Putative aminopeptidase N	LKNNVFELTIK	Q	0.02
Q5FA72	Putative aminopeptidase N	RSDTLQVQVQTALQHPK	F	1.7E-06
Q5FA72	Putative aminopeptidase N	NVPHFHAQDGSQYR	F	0.0089
Q5F9D9	Putative aminotransferases	TYHGSAMSIPVQR	A	0.0084
Q5F9D9	Putative aminotransferases	AAIQVLPGR	F	0.0011
Q5F6R0	Putative aspartyl-tRNA synthetase	LRYQVATGVR	R	0.0083
Q5F6R0	Putative aspartyl-tRNA synthetase	VHPGFEFFALPQSPQLFK	Q	0.00027
Q5F6R0	Putative aspartyl-tRNA synthetase	QVFKDALNVDLGDFPR	M	0.000001
Q5F6R0	Putative aspartyl-tRNA synthetase	VVALRVPNGAK	F	0.0008
Q5F6R0	Putative aspartyl-tRNA synthetase	VNDAGNLSNGEDSGLQSPIVK	F	0.00049
Q5F6R0	Putative aspartyl-tRNA synthetase	YVAVHHPFTAPK	E	0.026
Q5F6R0	Putative aspartyl-tRNA synthetase	EGHEDLMVSDPANCLAR	A	0.002
Q5F6R0	Putative aspartyl-tRNA synthetase	FGLLDNLK	F	0.00046
Q5F6R0	Putative aspartyl-tRNA synthetase	FGAPPHGGLAFGLDR	L	0.00014
Q5F6R0	Putative aspartyl-tRNA synthetase	LVTLMTGAESIRDVIAFPK	T	0.039
Q5F6R0	Putative aspartyl-tRNA synthetase	AQCLLDAPNSVDDK	Q	8.8E-07
Q5F6R0	Putative aspartyl-tRNA synthetase	AQCLLDAPNSVDDKQLR	E	0.017
Q5FAG6	Putative atpase	TLLDTVAVPNTAR	T	0.0022
Q5FAG6	Putative atpase	LNVPLLGQLPLSLPVR	E	0.000068
Q5F9I6	Putative ATP-dependent C1p protease	QKKVIGK	A	0.00085
Q5F8W0	Putative ATP-dependent RNA helicase	GIDVPTITHVINYLDPK	Q	0.0029
Q5F8W0	Putative ATP-dependent RNA helicase	RGDHKPGKEGFGGK	T	0.00087
Q5FA80	Putative ATP-dependent RNA helicase	ALAGHDLLAAAQTGTGK	T	3.9E-07
Q5FA80	Putative ATP-dependent RNA helicase	YATASTSPAMHPVR	M	0.0004
Q5F697	Putative branched-chain amino acid aminotranferase	IVLFRPTANIAR	M	0.00094
Q5F697	Putative branched-chain amino acid aminotranferase	AADEIPDAPAALYLRPTLIGTDPVIGK	A	0.0029

Q5F697	Putative branched-chain amino acid aminotranferase	AGSPSETALLYILASPVGDYFK	V	0.000026
Q5FAB9	Putative carboxypeptidase, penicillin binding protein	RSDNLIAR	S	0.025
Q5F932	Putative carboxy-terminal processing protease	AVIVGTQSF GK	G	0.0029
Q5F8D2	Putative cell-division protein	SPDVSQGSVSDGTAVR	D	0.00013
Q5F8D2	Putative cell-division protein	APHLLVAGTTGSGK	S	0.000059
Q5F4Z9	Putative chromosome segregation protein	AAQIAGLSEIPAVIK	T	0.0031
Q5F4Z9	Putative chromosome segregation protein	TISDE TALAMGLIENLQR	E	3.7E-06
Q5F4Z9	Putative chromosome segregation protein	LADEFGLTHETIAQAVGK	S	8.8E-09
Q5F4Z9	Putative chromosome segregation protein	LLSLPESVQEMLYQR	R	0.000003
Q5F4Z9	Putative chromosome segregation protein	ALLTLPVVEQLELAQK	A	0.0019
Q5F4Z9	Putative chromosome segregation protein	SQAALQNKRPPEK	K	0.0007
Q5F7W9	Putative ClpB protein	QRLQQHLNSLPK	V	0.032
Q5F7W9	Putative ClpB protein	VSGQGGEILPSR	E	0.0015
Q5F7W9	Putative ClpB protein	EAGATEQNINAAIDAVR	G	0.00011
Q5F7W9	Putative ClpB protein	TKNNPVLIGEPGVGK	T	0.00057
Q5F7W9	Putative ClpB protein	LLVLDLAALIAGAK	Y	3E-09
Q5F7W9	Putative ClpB protein	VLVGEPVVEDTIAILR	G	2.1E-07
Q5F7W9	Putative ClpB protein	FLPDKAIDLIDEAASR	V	0.0002
Q5F7W9	Putative ClpB protein	AISDGAANIKK	Q	0.0029
Q5F7W9	Putative ClpB protein	IKIEQAKR	Q	0.05
Q5F7W9	Putative ClpB protein	NNVGAEIEAEVVSR	M	3.2E-06
Q5F7W9	Putative ClpB protein	SGLADPNKPYGSFLFLGPTGVGK	T	0.004
Q5F7W9	Putative ClpB protein	ALAGFLFDS EDHLIR	I	0.000012
Q5F7W9	Putative ClpB protein	AIQSEIENPLAK	A	0.0011
Q5F9I4	Putative cold shock protein	GFGFITPDEGGEDLFAHFSAINMEGFK	T	0.000079
Q5F9I4	Putative cold shock protein	GFGFITPDEGGEDLFAHFSAINMEGFKTLK	E	0.0032
Q5F9I4	Putative cold shock protein	VSFDVTTGPK	G	0.0019
Q5F9I4	Putative cold shock protein	GKQAANIQAA	-	0.018
Q5F759	Putative cytochrome	IQPVGQLTMGDGIPVGER	Q	1.9E-07
Q5F759	Putative cytochrome	GGAADLTDQELKR	A	0.0011
Q5F759	Putative cytochrome	AEDKGAAAPAVGVDGK	K	0.00017
Q5F759	Putative cytochrome	AEDKGAAAPAVGVDGKK	V	0.0013
Q5F759	Putative cytochrome	HALEGFNAMPK	G	0.0092
Q5FAC5	Putative cytochrome	SGEANPKENPELGAK	I	0.0001
Q5FAC5	Putative cytochrome	MSEEDLKAVANFIQGLR	-	2.5E-07
Q5F716	Putative cytochrome c oxidase subunit	AATQPAPGVKPYNALQVAGR	D	0.000023