Supplementary Table 2

(this table contains all original protein data, used to calculate most statistics throughout this study)

content: **page**

descriptions:

hit	MASCOT protein hit no.
peptides	no. of matched peptides
accession	database accession no.
description	protein desccription

hit	**peptides**	**accession**	**description**
I. Corynebacterium glutamicum; elastase digest; nLC-ESI MS/MS; no search specificity			
1	144	Cg1537	(ptsG) [M]: GLUCOSE-SPECIFIC ENZYME II BC COMPONENT OF PTS (EC 2.7.1.69)
2	97	P00772|ELA1	Elastase-1 precursor - Sus scrofa
3	74	Cg0446	(sdhA) [C]: succinate dehydrogenase A (EC 1.3.99.1)
4	71	Cg2705	(amyE) [S]: MALTOSE-BINDING PROTEIN PRECURSOR
5	65	Cg3009	[C]: hypothetical protein predicted by Glimmer/Critica
6	62	Cg2181	[S]: ABC-type peptide transport system, secreted component
7	47	Cg2120	(ptsF) [M]: SUGAR SPECIFIC PTS SYSTEM, FRUCTOSE/MANNITOL-SPECIFIC TRANSPORT PROTEIN (EC 2.7.1.69)
8	44	Cg2911	[S]: ABC-type Mn/Zn transport system, secreted Mn/Zn-binding (lipo)protein (surface adhesin)
11	41	Cg0447	(sdhB) [C]: succinate dehydrogenase B
9	39	Cg2925	(ptsS) [M]: ENZYME II SUCROSE PROTEIN (EC 2.7.1.69)
10	39	Cg2409	(ctaC) [M]: CYTOCHROME C OXIDASE CHAIN II (EC 1.9.3.1)
16	30	Cg2404	(qcrA1) [M]: RIESKE IRON-SULFUR PROTEIN
14	29	Cg1366	(atpA) [C]: PROBABLE ATP SYNTHASE ALPHA CHAIN PROTEIN (EC 3.6.1.34)
13	28	Cg3138	[M]: Membrane protease subunit, stomatin/prohibitin homolog
15	27	Cg2780	(ctaD) [M]: PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE SUBUNIT (EC 1.9.3.1)
19	27	Cg2403	(qcrB) [M]: CYTOCHROME B, MEMBRANE PROTEIN (EC 1.10.2.2)
12	26	Cg2708	(msiK1) [C]: ABC-type sugar transport system, ATPase component
17	25	Cg2875	[C]: hypothetical protein predicted by Glimmer
21	23	Cg1332	[S]: PUTATIVE SECRETED HYDROLASE
18	22	Cg3182	(cop1) [S]: Trehalose corynomycolyl transferase (EC 2.3.1.122)
23	22	Cg1363	(atpE) [M]: ATP SYNTHASE C CHAIN (EC 3.6.1.34)
27	22	Cg0413	(cmt1) [S]: Trehalose corynomycolyl transferase (EC 2.3.1.122)
24	19	Cg0683	[M]: permease
20	18	Cg0953	[M]: Na+/proline, Na+/panthothenate symporter or related permease
30	18	Cg0737	[S]: ABC-type transport system, secreted lipoprotein component
31	17	Cg1368	(atpD) [C]: ATP SYNTHASE ALPHA SUBUNIT (EC 3.6.1.34)
22	16	Cg1656	(ndh) [MS]: NADH DEHYDROGENASE (EC 1.6.99.3)
38	16	Cg3008	(porA) [M]: PORIN
25	15	Cg1603	[MS]: CONSERVED MEMBRANE PROTEIN
26	15	Cg3186	(cmt2) [S]: Trehalose corynomycolyl transferase (EC 2.3.1.122)
28	15	Cg3365	(rmpC) [M]: putative ribitol transport membrane protein
35	14	Cg1314	(putP) [M]: PROLINE TRANSPORT SYSTEM
39	14	Cg0834	[S]: Bacterial extracellular solute-binding protein, fa
29	13	Cg1081	[C]: ABC-type multidrug transport system, ATPase component
44	13	Cg1556	[C]: conserved hypothetical protein
78	13	Cg1362	(atpB) [M]: ATP SYNTHASE F0 SUBUNIT 6 (EC 3.6.1.34)
33	12	Cg2843	(pstB) [C]: ABC-type phosphate transport system, ATPase component

hit	peptides	accession	description
34	12	Cg0924	[S]: ABC-type cobalamin/Fe3+-siderophores transport sys
37	12	Cg0756	(cstA) [M]: PUTATIVE CARBON STARVATION PROTEIN A
41	12	Cg1082	[M]: putative membrane protein
64	12	Cg0359	[M]: PUTATIVE MEMBRANE PROTEIN
52	11	Cg2262	(ftsY) [S]: Signal recognition particle GTPase
61	11	Cg2361	[C]: Cell division initiation protein - Antigen 84 homolog
36	10	Cg2810	[M]: Na+/H+-dicarboxylate symporter family
43	10	Cg2195	[M]: putative secreted or membrane protein
53	10	Cg3368	[M]: ABC-transporter permease protein
54	10	Cg2912	[C]: ABC-type cobalamin/Fe3+-siderophores transport system, ATPase component
85	10	Cg0445	(sdhCD) [M]: succinate dehydrogenase CD
42	9	Cg2845	(pstC) [M]: ABC-type phosphate transport system, permease component
63	9	Cg2704	[M]: ABC-type sugar transport system, permease component
68	9	Cg0753	[S]: secreted protein
70	9	Cg2211	[M]: putative membrane protein
123	9	Cg1238	[M]: putative membrane protein
45	8	Cg1228	[C]: ABC-type cobalt transport system, ATPase component
47	8	Cg0587	(tuf) [C]: ELONGATION FACTOR TU
48	8	Cg2184	[C]: ATPase component of peptide ABC-type transport system, contains duplicated ATPase domains
49	8	Cg3395	(proP) [M]: PROLINE/ECTOINE CARRIER
55	8	Cg1791	(gap) [C]: GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
56	8	Cg2844	(pstA) [M]: ABC-type phosphate transport system, permease component
58	8	Cg1169	[M]: Na+-dependent transporters of the SNF family
59	8	Cg1001	(mscL) [M]: LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL
79	8	Cg2405	(qcrC) [M]: CYTOCHROME C1
101	8	Cg2157	(terC) [M]: TELLURIUM RESISTANCE MEMBRANE PROTEIN
88	7	Cg1429	[M]: putative membrane protein
100	7	Cg2052	[S]: putative secreted protein
137	7	Cg2949	[S]: putative secreted protein
152	7	Cg1312	[M]: putative membrane protein
257	7	Cg3244	[C]: conserved hypothetical protein
46	6	Cg1345	(narK) [M]: PUTATIVE NITRATE/NITRITE TRANSPORTER
51	6	Cg0780	[M]: membrane protein ribonuclease BN-like family
62	6	Cg2703	[M]: Sugar permease
67	6	Cg2137	(gluB) [S]: GLUTAMATE SECRETED BINDING PROTEIN
73	6	Cg0545	(pitA) [M]: PUTATIVE LOW-AFFINITY PHOSPHATE TRANSPORT PROTEIN
81	6	Cg1624	[M]: NhaP-type Na+/H+ and K+/H+ antiporter
106	6	Cg3255	(uspA3) [C]: UNIVERSAL STRESS PROTEIN FAMILY
109	6	Cg0040	[S]: PUTATIVE SECRETED PROTEIN
146	6	Cg2684	[M]: membrane protein DedA family

hit	peptides	accession	description
153	6	Cg2196	[M]: putative secreted or membrane protein
235	6	Cg0047	[M]: conserved hypothetical protein
265	6	Cg2406	(ctaE) [M]: CYTOCHROME C OXIDASE SUBUNIT 3 (EC 1.9.3.1)
71	5	Cg0944	[M]: Xanthine/uracil permeases family
86	5	Cg1604	[S]: putative secreted protein
98	5	Cg0229	(gltB) [C]: GLUTAMINE 2-OXOGLUTARATE AMINOTRANSFERASE LARGE SU (EC 1.4.1.13)
104	5	Cg1367	(atpG) [C]: ATP SYNTHASE GAMMA SUBUNIT (EC 3.6.1.34)
110	5	Cg2425	[M]: Predicted permease
127	5	Cg1661	[M]: Arsenite efflux pump ACR3 or related permease
132	5	Cg1579	[S]: putative secreted protein
164	5	Cg2958	(butA) [C]: L-2,3-butanediol dehydrogenase/acetoin reductase (EC 1.1.1.5)
191	5	Cg0314	(brnF) [M]: branched chain amino acid exporter, large subunit
192	5	Cg2812	[C]: ABC-type transport system, involved in lipoprotein release, ATPase component
208	5	Cg2893	[M]: Permease of the major facilitator superfamily
209	5	Cg1364	(atpF) [MS]: ATP synthase B chain (EC 3.6.1.34)
217	5	Cg0561	(secE) [M]: SecE subunit of protein translocation complex
260	5	Cg2735	[M]: putative membrane protein
348	5	Cg2424	[M]: putative membrane protein
491	5	Cg2151	[C]: Similar to phage shock protein A
575	5	Cg3237	(sod) [C]: MANGANESE SUPEROXIDE DISMUTASE (EC 1.15.1.1)
40	4	Cg2743	(fas-IA) [C]: FATTY ACID SYNTHASE (EC 2.3.1.85, 2.3.1.38, 2.3.1.39, 2.3.1.41, 1.1.1.100, 4.2.1.60, 4.2.1.61, 1.3.1.10, 3.1.2.14)
57	4	Cg2984	(ftsH) [M]: CELL-DIVISION PROTEIN (ATP-DEPENDENT ZN METALLOPEPTIDASE) (EC 3.4.24.)
65	4	Cg0647	(secY) [M]: preprotein translocase subunit SecY
72	4	Cg3024	(mrpA) [M]: NADH ubiquinone oxidoreductase subunit 5 (chain L)/Multisubunit Na+/H+ antiporter, A subunit
76	4	Cg0326	(nuoL) [M]: NADH-QUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)
84	4	Cg0456	[M]: permease, major facilitator superfamily
91	4	Cg3356	[M]: Na+/H+-dicarboxylate symporter
105	4	Cg0583	(fusA) [C]: ELONGATION FACTOR G
112	4	Cg2677	[M]: ABC-type dipeptide/oligopeptide/nickel transport system, permease component
113	4	Cg1730	[S]: secreted protease subunit, stomatin/prohibitin homolog
119	4	Cg2546	[M]: putative membrane protein
131	4	Cg0414	(wzz) [M]: cell surface polysaccharide biosynthesis / Chain length determinant protein
148	4	Cg0336	(ponA) [S]: PENICILLIN-BINDING PROTEIN 1B (EC 2.4.2.-)
151	4	Cg2846	(pstS) [S]: ABC-type phosphate transport system, secreted component
154	4	Cg2568	(dctM) [M]: PUTATIVE C4-DICARBOXYLATE TRANSPORT SYSTEM (PERMEASE LARGE PROTEIN)
158	4	Cg3060	(cgtS6) [M]: probable two component sensor kinase
161	4	Cg0286	[M]: CONSERVED HYPOTHETICAL membrane PROTEIN
165	4	Cg1658	[M]: Permease of the major facilitator superfamily
169	4	Cg0324	(mnhD) [M]: hydrogenlyase subunit 3/Multisubunit Na+/H+ antipoter, MnhD subunit
195	4	Cg3301	[M]: Permease of the major facilitator superfamily

hit	peptides	accession	description
202	4	Cg0736	[C]: ABC-type transporter, ATPase component
220	4	Cg1247	[S]: putative secreted protein
252	4	Cg1867	(secD) [M]: Preprotein translocase subunit SecD
298	4	Cg0061	(rodA) [M]: PUTATIVE FTSW/RODA/SPOVE FAMILY CELL CYCLE PROTEIN
313	4	Cg0980	[S]: secreted protein related to metalloendopeptidases
340	4	Cg2799	(pknE) [S]: putative secreted protein
410	4	Cg1229	[M]: ABC-type cobalt transport system, permease component CbiQ
457	4	Cg2154	(pgsA2) [M]: CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
508	4	Cg0952	[M]: PUTATIVE INTEGRAL MEMBRANE PROTEIN
542	4	Cg2913	[M]: ABC-type Mn2+/Zn2+ transport system, permease component
557	4	Cg1109	(porB) [S]: Anion-specific porin precursor
588	4	Cg0935	[C]: conserved hypothetical protein
592	4	Cg2362	[M]: putative membrane protein
620	4	Cg0982	[M]: membrane protein
716	4	Cg2325	[C]: hypothetical protein predicted by Glimmer/Critica
66	3	Cg3187	[M]: putative membrane protein
77	3	Cg0577	(rpoC) [C]: DNA-DIRECTED RNA POLYMERASE BETA~ CHAIN (EC 2.7.7.6)
87	3	Cg0284	[M]: drug exporter of the RND superfamily
92	3	Cg2590	[M]: Xanthine/uracil permease
99	3	Cg2496	[S]: putative secreted protein
107	3	Cg3019	[M]: putative secreted protein
115	3	Cg3161	[M]: putative membrane protein
117	3	Cg0486	[M]: PUTATIVE ABC TRANSPORTER INTEGRAL MEMBRANE PROTEIN
120	3	Cg1664	[M]: Sulfate permease or related transporter (MFS superfamily)
128	3	Cg0732	[M]: PUTATIVE ABC TRANSPORT SYSTEM INTEGRAL MEMBRANE PR
134	3	Cg3026	(mrpD) [M]: NADH-ubiquinone oxidoreductase/Multisubunit Na+/H+ antiporter, D subunit
141	3	Cg1359	[M]: membrane protein, UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N- acetylglucosamine-1-pho
144	3	Cg1111	(eno) [C]: ENOLASE (EC 4.2.1.11)
168	3	Cg1227	[M]: putative membrane protein
173	3	Cg1231	(chaA) [M]: Ca2+/H+ antiporter
179	3	Cg2739	[M]: Permease of the major facilitator superfamily
180	3	Cg0417	(capD) [M]: PROBABLE DTDP-GLUCOSE 4,6-DEHYDRATASE TRANSMEMBRANE PROTEIN (EC 4.2.1.46)
182	3	Cg0082	[M]: Voltage gated chloride channel
186	3	Cg2393	[M]: putative membrane protein
194	3	Cg2675	[C]: ATPase component of ABC-type transport system, contains duplicated ATPase domains
203	3	Cg3335	(mez) [C]: MALIC ENZYME (EC 1.1.1.40)
207	3	Cg0508	[S]: iron/thiamine transport system, secreted component
210	3	Cg0165	[M]: ABC-2 type transporter
225	3	Cg1883	[S]: putative secreted protein
228	3	Cg0489	[M]: hypothetical membrane protein

hit	peptides	accession	description
240	3	Cg2539	(ectP) [M]: ectoine/proline/glycine betaine carrier EctP
241	3	Cg1864	(dciAE) [S]: ABC-type dipeptide/oligopeptide/nickel transport systems, secreted component
243	3	Cg2183	[M]: ABC-type peptide transport system, permease component
246	3	Cg2173	(dinF) [M]: PUTATIVE DNA-DAMAGE-INDUCIBLE MEMBRANE PROTEIN
248	3	Cg2563	(lcoP) [M]: ECTOINE BETAINE TRANSPORTER
259	3	Cg2408	[M]: putative membrane protein
261	3	Cg0752	[S]: PUTATIVE secreted or MEMBRANE PROTEIN
264	3	Cg3371	[M]: Na+-dependent transporter
266	3	Cg2884	[M]: Dipeptide/tripeptide permease
272	3	Cg1225	(benK3) [M]: putative benzoate transport transmembrane protein
273	3	Cg0831	[M]: SUGAR ABC TRANSPORTER, PERMEASE PROTEIN
305	3	Cg3367	[C]: ABC-type multidrug transport system, ATPase component
347	3	Cg0568	[M]: Permease for amino acids and related compounds, fa
355	3	Cg0470	[M]: conserved secreted protein
357	3	Cg2370	(ftsW) [M]: Bacterial cell division membrane protein
358	3	Cg3068	(fda) [C]: fructose-bisphosphate aldolase (EC 4.1.2.13)
364	3	Cg1479	(glgP1) [C]: PUTATIVE GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
371	3	Cg1483	[M]: putative membrane protein
395	3	Cg3413	(azlC) [M]: branched-chain amino acid permease (azaleucine resistance)
398	3	Cg1665	[S]: putative secreted protein
421	3	Cg2166	(gpsI) [C]: PUTATIVE POLYRIBONUCLEOTIDE PHOSPHORYLASE / GUANOSINE PENTAPHOSPHATESYNTHETASE (EC 2.7.7.8)
437	3	Cg2777	[M]: putative membrane protein
438	3	Cg0327	[M]: membrane protein
452	3	Cg3227	(lldA) [C]: PUTATIVE L-LACTATE DEHYDROGENASE (EC 1.1.2.3)
469	3	Cg0018	[M]: HYPOTHETICAL MEMBRANE PROTEIN
500	3	Cg0735	[M]: ABC transporter, transmembrane component
507	3	Cg2412	[M]: putative membrane protein
513	3	Cg1350	(mob) [C]: PUTATIVE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS PROTEIN
533	3	Cg0769	[M]: ABC-type cobalamin/Fe3+-siderophores transport system, permease component
752	3	Cg0914	(ftsE) [C]: CELL DIVISION ATP-BINDING PROTEIN
754	3	Cg1685	(tatX) [M]: Sec-independent protein secretion pathway component
876	3	Cg0514	[M]: hypothetical membrane protein
901	3	Cg2096	[M]: putative membrane protein
910	3	Cg1387	(fixB) [C]: PUTATIVE ELECTRON TRANSFER FLAVOPROTEIN, ALPHA SUBUNIT
914	3	Cg0016	[M]: PUTATIVE INTEGRAL MEMBRANE PROTEIN
1068	3	Cg0923	[M]: membrane protein
1122	3	Cg1741	[M]: putative membrane protein
1275	3	Cg3366	(rmpA) [C]: putative ribitol-specific enzyme II of PTS system
32	2	Cg0957	(fas-IB) [C]: FATTY ACID SYNTHASE (EC 2.3.1.85, 2.3.1.38, 2.3.1.39, 2.3.1.41, 1.1.1.100, 4.2.1.60, 4.2.1.61, 1.3.1.10, 3.1.2.14))
50	2	Cg1995	[C]: hypothetical protein predicted by Glimmer/Critica

hit	peptides	accession	description
74	2	Cg0668	[MS]: segregation ATPase FtsK/SpoIIIE family
75	2	Cg0968	[C]: PUTATIVE ATP-DEPENDENT HELICASE (EC 3.6.1.)
80	2	Cg0455	[M]: permease, major facilitator superfamily
82	2	Cg0133	[M]: p-aminobenzoyl-glutamate transporter
83	2	Cg1281	[M]: ABC-type multidrug/protein/lipid transport system, ATPase component
89	2	Cg0738	(dnaE2) [C]: PUTATIVE DNA POLYMERASE III ALPHA CHAIN (EC 2.7.7.6)
94	2	Cg0275	(mgtE2) [M]: MG2+ TRANSPORTER
95	2	Cg2811	[M]: ABC-type transport system, involved in lipoprotein release, permease component
97	2	Cg2111	(hrpA) [C]: PROBABLE ATP-DEPENDENT RNA HELICASE PROTEIN (EC 3.-.-.-)
121	2	Cg0835	(msiK2) [C]: ABC-type sugar transport systems, ATPase component
135	2	Cg0468	[M]: cobalamin/Fe3+-siderophores transport systems, permease component
143	2	Cg0235	(embC) [M]: Probable arabinosyltransferase, membrane protein
149	2	Cg2641	[C]: Bacterial regulatory protein, LuxR family
150	2	Cg0236	[M]: membrane protein
156	2	Cg2095	[M]: putative membrane protein
159	2	Cg3346	(leuS) [C]: LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4)
160	2	Cg0161	[M]: putative secreted or membrane protein
162	2	Cg0206	[M]: PROBABLE TRANSPORTER
163	2	Cg0992	[M]: Sulfate permease or related transporter (MFS superfamily)
166	2	Cg3245	[M]: Permease of the major facilitator superfamily
170	2	Cg2388	(pknL) [M]: PUTATIVE SERINE/THREONINE PROTEIN KINASE (EC 2.7.1.37)
171	2	Cg3216	(gntP) [M]: GLUCONATE PERMEASE
172	2	Cg1399	[M]: Permease of the major facilitator superfamily
181	2	Cg2279	[M]: ABC-type multidrug/protein/lipid transport system, transmembrane ATPase component
183	2	Cg3079	(clpB) [C]: PROBABLE ATP-DEPENDENT PROTEASE (HEAT SHOCK PROTEIN) (EC 3.-.-.-)
185	2	Cg0868	(secA) [C]: PREPROTEIN TRANSLOCASE SUBUNIT SECA
187	2	Cg0238	[C]: L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
188	2	Cg0998	[M]: Trypsin-like serine protease
190	2	Cg3252	[M]: putative preprotein translocase subunit YidC, SpoIIIJ homolog
197	2	Cg0896	[M]: membrane protein
212	2	Cg3179	(fadD2) [C]: PUTATIVE ACYL-COA SYNTHETASE (EC 6.2.1.3)
213	2	Cg1016	(betP) [M]: glycine betaine transporter
215	2	Cg1506	[M]: putative membrane protein
219	2	Cg1456	[C]: Predicted signal-transduction protein containing cAMP-binding and CBS domain
221	2	Cg0722	[M]: drug exporter, RND superfamily
222	2	Cg2939	[M]: ABC-type dipeptide/oligopeptide/nickel transport system, fused permease and ATPase components
224	2	Cg2971	(lmrB) [M]: LINCOMYCIN RESISTANCE PROTEIN LMRB
231	2	Cg0864	(mtrB) [M]: Signal transduction histidine kinase
236	2	Cg1280	(odhA) [C]: 2-OXOGLUTARATE DEHYDROGENASE (EC 1.2.4.2)
237	2	Cg1424	(lysE) [M]: Lysine efflux permease

hit	peptides	accession	description
238	2	Cg2201	[M]: signal transduction histidine kinase
244	2	Cg2212	[M]: putative membrane protein
262	2	Cg0790	(lpdA) [C]: DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4)
263	2	Cg2077	[M]: putative membrane protein
269	2	Cg1545	[M]: Permease of the major facilitator superfamily
270	2	Cg1212	[M]: Permease of the major facilitator superfamily
276	2	Cg3165	[M]: putative membrane protein
277	2	Cg1299	(cydD) [M]: ABC-type multidrug/protein/lipid transport system, ATPase component
284	2	Cg1412	[M]: Ribose/xylose/arabinose/galactoside ABC-type transport system, permease component
286	2	Cg2466	(aceE) [C]: PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
287	2	Cg2158	(ftsK) [M]: CELL DIVISION PROTEIN, REQUIRED FOR CELL DIVISION AND CHROMOSOMEPARTITIONING
288	2	Cg2192	(mqo) [C]: MALATE:QUINONE OXIDOREDUCTASE OXIDOREDUCTASE (EC 1.1.99.16)
290	2	Cg2372	(mraY) [M]: PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.13)
291	2	Cg3132	[M]: putative membrane protein
307	2	Cg2258	(glnD) [C]: PROBABLE PROTEIN-PII URIDYLYLTRANSFERASE (EC 2.7.7.59)
310	2	Cg0057	(pknB) [C]: EUKARYOTIC-TYPE SERINE/THREONINE KINASE (EC 2.7.1.)
312	2	Cg2110	[M]: putative membrane protein
314	2	Cg3334	[M]: putative arabinose efflux permease
322	2	Cg2643	(benE) [M]: BENZOATE MEMBRANE TRANSPORT PROTEIN
325	2	Cg2552	[C]: ATPase component of ABC-type transport system, contains duplicated ATPase domain
333	2	Cg1142	[M]: Na+/proline, Na+/panthothenate symporter
334	2	Cg2680	[C]: Aminotransferase class-III, pyridoxal-phosphate dependent
341	2	Cg0331	(cgtS1) [M]: PROBABLE TWO-COMPONENT SENSOR HISTIDINE KINASE (EC 2.7.3.-)
349	2	Cg1289	[M]: Permease of the major facilitator superfamily
359	2	Cg1577	[S]: putative secreted hydrolase
361	2	Cg1365	(atpH) [C]: H+-ATPASE DELTA SUBUNIT
363	2	Cg2618	(vanK) [M]: VANILLATE TRANSPORTER VANK
377	2	Cg1673	(ppmN) [M]: polyprenol-phosphate-mannose synthase domain 2 (EC 2.3.1.-)
382	2	Cg1086	[M]: putative membrane protein
386	2	Cg1880	(thrS) [C]: THREONYL-TRNA SYNTHETASE (EC 6.1.1.3)
407	2	Cg2695	[C]: ABC-type transport system, ATPase component
416	2	Cg0781	[M]: membrane protein
418	2	Cg2301	[M]: Permease of the major facilitator superfamily
419	2	Cg1305	[M]: Amino acid permease
420	2	Cg1672	(ppmC) [C]: polyprenol-phosphate-mannose synthase domain 1
422	2	Cg1546	(rbsK1) [C]: PUTATIVE RIBOKINASE PROTEIN (EC 2.7.1.15)
423	2	Cg0396	[M]: Glycosyl transferase
430	2	Cg2470	[S]: SECRETED ABC TRANSPORTER SUBSTRATE-BINDING PROTEIN
431	2	Cg2891	(poxB) [C]: PYRUVATE DEHYDROGENASE (EC 1.2.2.2)
432	2	Cg0469	[C]: cobalamin/Fe3+-siderophores transport system, ATPase component

hit	peptides	accession	description
439	2	Cg0088	(citP) [M]: Citrate transporter
451	2	Cg3027	(mrpE) [S]: Multisubunit Na+/H+ antiporter, subunit E
463	2	Cg1020	[C]: double-stranded beta-helix domain
464	2	Cg1245	[M]: putative membrane protein
471	2	Cg2139	(gluD) [M]: GLUTAMATE PERMEASE
476	2	Cg0926	[M]: ABC-type cobalamin/Fe3+-siderophores transport system, permease component
482	2	Cg0480	(fadD5) [C]: LONG-CHAIN-FATTY-ACID-COA LIGASE (EC 6.2.1.3)
495	2	Cg0893	[S]: secreted protein containing a PDZ domain
497	2	Cg2291	(pyk) [C]: PYRUVATE KINASE (EC 2.7.1.40)
502	2	Cg1064	[M]: Branched-chain amino acid ABC-type transport system, permease component
517	2	Cg2558	[C]: related to aldose 1-epimerase
518	2	Cg1115	(ppx2) [C]: EXOPOLYPHOSPHATASE (EC 3.6.1.11)
532	2	Cg1657	(ufaA) [C]: PUTATIVE CYCLOPROPANE FATTY ACID SYNTHASE (CYCLOPROPANE-FATTY-ACYL-PHOSPHOLIPID SYNTHASE)
536	2	Cg0249	[M]: polysaccharide/polyol phosphate export systems, permease component
539	2	Cg0262	(modB) [M]: sulfate/molybdate transport system, permease component
541	2	Cg0390	[M]: permease, major facilitator family
560	2	Cg2487	[C]: conserved hypothetical protein
563	2	Cg1474	[C]: putative ATP/GTP-binding protein
570	2	Cg1643	(gnd) [C]: 6-PHOSPHOGLUCONATE DEHYDROGENASE (EC 1.1.1.44)
574	2	Cg3135	[M]: putative membrane protein
577	2	Cg2577	[M]: Predicted multitransmembrane, metal-binding protein
585	2	Cg1203	[C]: Mg-chelatase subunit ChlI
595	2	Cg3226	[M]: permease of the major facilitator superfamily
597	2	Cg1505	[S]: putative secreted protein
600	2	Cg0334	[S]: secreted phosphohydrolase
619	2	Cg2657	[MS]: putative membrane protein - fragment
627	2	Cg1650	(pctC) [M]: ABC-type phosphate/phosphonate transport system, permease component
647	2	Cg0004	(dnaN) [C]: DNA POLYMERASE III, BETA SUBUNIT (EC 2.7.7.7)
660	2	Cg1868	(secN) [MS]: Preprotein translocase subunit YajC homolog
661	2	Cg2719	[C]: PUTATIVE ENTEROCHELIN ESTERASE
665	2	Cg1354	(rho) [C]: Transcription termination factor Rho
700	2	Cg1647	[M]: ABC-type multidrug transport system, permease component
703	2	Cg1282	[M]: conserved hypothetical protein
719	2	Cg2809	[M]: putative membrane protein
721	2	Cg2535	[S]: putative secreted protein
727	2	Cg0362	[C]: PUTATIVE SEPTUM SITE DETERMINING PROTEIN
741	2	Cg1623	[M]: Predicted divalent heavy-metal cations transporter
743	2	Cg0475	[C]: conserved hypothetical protein
761	2	Cg0064	[C]: conserved hypothetical protein
763	2	Cg3312	[M]: putative membrane protein

hit	**peptides**	**accession**	**description**
765	2	Cg2334	(ilvA) [C]: THREONINE DEHYDRATASE (EC 4.2.1.16)
769	2	Cg1806	(metK) [C]: S-Adenosylmethionine Synthetase (EC 2.5.1.6)
777	2	Cg2215	[M]: putative membrane protein
806	2	Cg2701	[M]: putative membrane protein
822	2	Cg1540	[S]: putative secreted protein
834	2	Cg0759	(prpD2) [C]: PROPIONATE CATABOLISM PROTEIN PRPD
856	2	Cg1343	(narH) [C]: PROBABLE RESPIRATORY NITRATE REDUCTASE OXIDOREDUCT (EC 1.7.99.4)
857	2	Cg0124	(amn) [C]: AMP NUCLEOSIDASE (EC 3.2.2.4)
867	2	Cg1528	(dkgX) [C]: putative 2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)
881	2	Cg3119	(cysJ) [C]: Probable Sulfite Reductase (Flavoprotein) (EC 1.8.1.2)
884	2	Cg0448	[M]: conserved hypothetical membrane protein
887	2	Cg0216	[M]: hypothetical memebrane protein
892	2	Cg0727	[M]: nucleoside-diphosphate-sugar epimerase
903	2	Cg2762	(murI) [C]: GLUTAMATE RACEMASE (EC 5.1.1.3)
916	2	Cg1128	[MS]: similar to ribosomal protein S2
953	2	Cg1277	[M]: conserved hypothetical membrane protein
964	2	Cg1165	[M]: Gamma-aminobutyrate permease or related permease
970	2	Cg1865	(secF) [M]: Preprotein translocase subunit SecF
971	2	Cg2294	[M]: putative membrane protein
985	2	Cg0534	[M]: PUTATIVE INTEGRAL MEMBRANE PROTEIN
997	2	Cg0862	(mtrA) [C]: Response regulator
1042	2	Cg0389	[C]: short chain dehydrogenase
1047	2	Cg0092	[M]: PUTATIVE MEMBRANE PROTEIN
1123	2	Cg3399	[M]: Permease of the major facilitator superfamily
1194	2	Cg2973	[C]: conserved hypothetical protein
1202	2	Cg2457	[C]: conserved hypothetical protein
1260	2	Cg1190	[C]: hypothetical protein predicted by Glimmer/Critica
1267	2	Cg2128	[MS]: putative secreted or membrane protein
1280	2	Cg2186	[C]: conserved hypothetical protein
1341	2	Cg0355	[C]: pyrophosphohydrolase
1371	2	Cg3338	[M]: putative membrane protein
1419	2	Cg2010	[M]: Permease of the major facilitator superfamily
1462	2	Cg2620	(clpX) [C]: PROBABLE ATP-DEPENDENT PROTEASE (ATP-BINDING SPECIFICITY SUBUNIT) (EC 3.4.-.-)
1464	2	Cg3308	(rpsF) [C]: RIBOSOMAL PROTEIN S6
1534	2	Cg2806	[M]: putative membrane protein
1550	2	Cg2350	[C]: conserved hypothetical protein
1662	2	Cg0530	[M]: hypothetical protein
1801	2	Cg3357	(trpP) [M]: tryptophan-specific permease, 5-methyltryptophan resistance
1823	2	Cg2547	[M]: putative membrane protein
2249	2	Cg0612	(dkg) [C]: 2,5-DIKETO-D-GLUCONIC ACID REDUCTASE (EC 1.1.1.-)

hit	peptides	accession	description
2331	2	Cg2071	(int2~) [C]: putative phage Integrase (N-terminal fragment)
60	1	Cg2032	[M]: putative membrane protein
69	1	Cg0129	(putA) [C]: PROLINE DEHYDROGENASE/DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (EC 1.5.99.8)
90	1	Cg3178	(pks) [C]: POLYKETIDE SYNTHASE
93	1	Cg1701	(metH) [C]: Homocysteine Methyltransferase (EC 2.1.1.13)
102	1	Cg0507	[M]: ABC TRANSPORT SYSTEM PERMEASE PROTEIN
103	1	Cg3100	(dnaK) [C]: Heat shock protein hsp70
111	1	Cg0015	(gyrA) [C]: DNA TOPOISOMERASE (ATP-HYDROLYSING) (EC 5.99.1.3)
114	1	Cg2338	(dnaE1) [C]: PUTATIVE DNA POLYMERASE III, ALPHA CHAIN (EC 2.7.7.7)
116	1	Cg2323	(treY) [C]: MALTOOLIGOSYL TREHALOSE SYNTHASE (EC 5.4.99.15)
118	1	Cg3398	[C]: DNA or RNA helicase of superfamily II
122	1	Cg1054	(mmpL2) [M]: drug exporter of the RND superfamily
126	1	Cg3125	[M]: putative membrane protein
129	1	Cg3174	(mmpL1) [M]: exporter of the MMPL family
130	1	Cg0845	[C]: Superfamily II DNA/RNA helicase, SNF2 family
133	1	Cg3419	[M]: Uncharacterized membrane protein, virulence factor homolog
136	1	Cg1790	(pgk) [C]: PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
142	1	Cg1744	(pacL) [M]: CATION-TRANSPORTING ATPASE (EC 3.6.1.)
157	1	Cg2990	(speE) [M]: PUTATIVE SPERMIDINE SYNTHASE TRANSMEMBRANE PROTEIN (EC 2.5.1.16)
174	1	Cg0885	[C]: HELICASE, UVRD/REP FAMILY
175	1	Cg2243	[M]: PUTATIVE DICARBOXYLASE TRANSLOCATOR
176	1	Cg2263	[C]: conserved hypothetical protein
177	1	Cg1795	(uvrC) [C]: Nuclease subunit of the excinuclease ABC complex
184	1	Cg1103	[M]: putative membrane protein
198	1	Cg2678	[S]: ABC-type dipeptide/oligopeptide/nickel transport systems, secreted component
199	1	Cg0972	[M]: Cyanate permease
201	1	Cg3015	[C]: hypothetical protein predicted by Glimmer/Critica
206	1	Cg3281	[M]: PROBABLE CATION-TRANSPORTING ATPASE TRANSMEMBRANE PROTEIN (EC 3.6.1.-)
214	1	Cg2521	(fadD15) [C]: LONG-CHAIN FATTY ACID COA LIGASE (EC 6.2.1.3)
218	1	Cg3046	(pknG) [C]: Serine/threonine protein kinase (EC 2.7.1.)
227	1	Cg0766	(icd) [C]: ISOCITRATE DEHYDROGENASE (EC 1.1.1.42)
229	1	Cg2699	[M]: putative membrane protein
232	1	Cg3418	[S]: putative secreted protein
242	1	Cg0202	(iolD) [C]: PUTATIVE ACETOLACTATE SYNTHASE PROTEIN (EC 4.1.3.18)
247	1	Cg1498	[C]: RecG-like helicase
256	1	Cg0934	[C]: conserved hypothetical protein
267	1	Cg2840	(actA) [C]: BUTYRYL-COA:ACETATE COENZYME A TRANSFERASE (EC 2.8.3.8)
268	1	Cg2642	(benK1) [M]: PUTATIVE BENZOATE TRANSPORT PROTEIN
274	1	Cg2339	[M]: Predicted permease
280	1	Cg2537	(brnQ) [M]: Branched-Chain Amino Acid Uptake Carrier

hit	peptides	accession	description
281	1	Cg1709	(cysS2) [C]: PUTATIVE CYSTEINE TRNA SYNTHETASE (EC 6.1.1.16)
282	1	Cg3096	[C]: ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
283	1	Cg3387	[M]: Permease of the major facilitator superfamily
292	1	Cg1419	[M]: putative Na+-dependent transporter
295	1	Cg1787	(ppc) [C]: PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
297	1	Cg2125	(uraA) [M]: PUTATIVE URACYL PERMEASE
299	1	Cg1234	[C]: putative excinuclease ATPase subunit - UvrA-like protein
301	1	Cg2359	(ileS) [C]: ISOLEUCINE-TRNA LIGASE-LIKE PROTEIN (EC 6.1.1.5)
303	1	Cg1219	[M]: putative membrane protein
304	1	Cg0158	[M]: PUTATIVE MEMBRANE TRANSPORT PROTEIN
308	1	Cg1784	(ocd) [C]: PROBABLE ORNITHINE CYCLODEAMINASE PROTEIN (EC 4.3.1.12)
309	1	Cg3382	[M]: Dipeptide/tripeptide permease
311	1	Cg1435	(ilvB) [C]: ACETOLACTATE SYNTHASE (EC 4.1.3.18)
317	1	Cg2356	[M]: Permease of the drug/metabolite transporter (DMT) superfamily
319	1	Cg1832	[M]: ABC-type cobalamin/Fe3+-siderophores transport system, permease component
320	1	Cg1768	[M]: ABC-type multidrug transport system, permease component
323	1	Cg3101	[M]: Predicted permease
326	1	Cg1395	[C]: conserved hypothetical protein
328	1	Cg1195	[M]: Sulfate permease or related transporter (MFS superfamily)
337	1	Cg2571	(lepA) [C]: Membrane GTPase LepA
338	1	Cg2419	(pepB) [C]: LEUCINE AMINOPEPTIDASE (EC 3.4.11.1)
342	1	Cg0886	[C]: PROBABLE DNA HELICASE II PROTEIN (EC 3.6.1.-)
351	1	Cg2916	(ksdD) [MS]: 3-KETOSTEROID-1-DEHYDROGENASE (EC 1.3.99.4)
353	1	Cg0522	(ccsA) [M]: Cytochrome c biogenesis protein transmembrane prot
354	1	Cg3169	(pck) [C]: PROBABLE PHOSPHOENOLPYRUVATE CARBOXYKINASE PROTEIN (EC 4.1.1.32)
362	1	Cg1121	[M]: Permease of the major facilitator superfamily
369	1	Cg2371	(murD) [C]: UDP-N-ACETYLMURAMOYLALANINE D-GLUTAMATE LIGASE (EC 6.3.2.9)
374	1	Cg3248	(cgtS11) [M]: probable two component sensor kinase
375	1	Cg1726	(mcmA) [C]: METHYLMALONYL-COA MUTASE SMALL SUBUNIT (EC 5.4.99.2)
378	1	Cg2147	[M]: membrane protein, BioY family
380	1	Cg3157	[S]: putative secreted protein
381	1	Cg1654	(thiD1) [C]: PHOSPHOMETHYLPYRIMIDINE KINASE / HYDROXYMETHYLPYRI (EC 2.7.4.7,2.5.1.3)
387	1	Cg0915	(ftsX) [M]: PUTATIVE CELL DIVISION PROTEIN
388	1	Cg1090	(ggtB) [C]: PROBABLE GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR PR (EC 2.3.2.2)
394	1	Cg2267	[M]: putative membrane protein
396	1	Cg1526	[M]: Permease of the major facilitator superfamily
399	1	Cg1690	[C]: Putative proteasome component
400	1	Cg0437	[M]: membrane protein
403	1	Cg0565	[C]: PUTATIVE TRANSCRIPTIONAL REGULATOR
404	1	Cg3242	[M]: putative membrane protein

hit	**peptides**	**accession**	**description**
406	1	Cg1959	(priP) [C]: PROPHAGE DNA PRIMASE
408	1	Cg0552	(menD) [C]: 2-OXOGLUTARATE DECARBOXYLASE (EC 4.1.1.71)
409	1	Cg2008	[M]: putative membrane protein
413	1	Cg2833	(cysK) [C]: O-Acetylserine (Thiol)-Lyase (EC 4.2.99.8)
424	1	Cg0808	(wbpC) [M]: LIPOPOLYSACCHARIDE BIOSYNTHESIS ACYLTRANSFERASE, m
425	1	Cg0375	(cyaB) [M]: putative ADENYLATE CYCLASE (EC 4.6.1.1)
426	1	Cg0887	[M]: Kef-type K+ transport systems, predicted NAD-binding component
427	1	Cg2109	(oxyR) [C]: HYDROGEN PEROXIDE SENSING REGULATOR
428	1	Cg0318	(arsC1) [M]: PUTATIVE HEAVY METAL RESISTANCE MEMBRANE PROTEIN
435	1	Cg2557	[M]: Predicted Na+-dependent transporter
441	1	Cg1341	(narI) [M]: RESPIRATORY NITRATE REDUCTASE 2 GAMMA CHAIN (EC 1.7.99.4)
442	1	Cg3322	[S]: putative secreted membrane-fusion protein
445	1	Cg1774	(tkt) [C]: TRANSKETOLASE (EC 2.2.1.1)
447	1	Cg0623	[M]: cobalt transport system, permease component
449	1	Cg1737	(acn) [C]: ACONITASE (EC 4.2.1.3)
456	1	Cg1411	[C]: ABC-type sugar (aldose) transport system, ATPase component
462	1	Cg1451	(serA) [C]: Phosphoglycerate Dehydrogenase (EC 1.1.1.95)
465	1	Cg3153	[M]: putative membrane protein
466	1	Cg2673	[M]: Permease of the major facilitator superfamily
467	1	Cg0755	(metY) [C]: O-Acetylhomoserine (Thiol)-Lyase (EC 4.2.99.10)
468	1	Cg0997	(cgtS2) [M]: probable two component sensor kinase
470	1	Cg2314	[S]: transcriptional regulator, LacI family
478	1	Cg2610	[S]: ABC-type dipeptide/oligopeptide/nickel transport system, secreted component
481	1	Cg2206	(ispG) [C]: involved in the nonmevalonate pathway of terpenoid biosynthesis
483	1	Cg0370	[C]: DEAD/DEAH box helicase
487	1	Cg2001	[C]: conserved hypothetical protein
493	1	Cg0195	[M]: membrane protein
506	1	Cg0688	[C]: Uncharacterized protein family UPF0031
512	1	Cg0340	[M]: PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN
519	1	Cg2598	[M]: putative membrane protein
522	1	Cg0083	[M]: mononucleotide transporter
524	1	Cg2292	(lgt) [M]: PUTATIVE PROLIPOPROTEIN DIACYLGLYCEROL TRANSFERASE (EC 2.4.99.)
525	1	Cg3017	[M]: putative membrane protein
531	1	Cg1578	[M]: Acyltransferase family, membrane protein
535	1	Cg2369	(murG) [C]: peptidoglycan biosynthesis protein (EC 2.4.1.-)
537	1	Cg1855	(hisS) [C]: HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21)
543	1	Cg2559	(aceB) [C]: MALATE SYNTHASE (EC 4.1.3.2)
544	1	Cg2289	(glgP2) [C]: ALPHA-GLUCAN PHOSPHORYLASE, GLYCOGEN PHOSPHORYLASE (EC 2.4.1.1)
552	1	Cg2390	[M]: putative membrane protein
553	1	Cg1569	(ugpE) [M]: sn-glycerol-3-phosphate transport system permease protein

hit	peptides	accession	description
561	1	Cg1353	(fadD4) [C]: ACYL-COA SYNTHETASE (EC 6.2.1.3)
565	1	Cg0824	(tnp5a(ISCg5a)) [C]: Transposase
569	1	Cg0701	[M]: drug/metabolite transporter DMT superfamily
572	1	Cg0025	[M]: (Q93JD3) PUTATIVE INTEGRAL MEMBRANE CYTOCHROME BIO
573	1	Cg1101	[M]: ABC-type multidrug/protein/lipid transport system, membrane component
578	1	Cg1274	(mrp) [C]: ATPases involved in chromosome partitioning
579	1	Cg0444	(ramB) [C]: transcriptional regulator, MerR family
580	1	Cg0948	(serC) [C]: Phosphoserine Transaminase (EC 2.6.1.52)
581	1	Cg1609	[C]: ATPase component of ABC transporter with duplicated ATPase domains
583	1	Cg0776	[S]: ABC-type cobalamin/Fe3+-siderophores transport system, secreted component
584	1	Cg0042	[M]: ABC TRANSPORTER PROTEIN, INTEGRAL MEMBRANE SUBUNIT
586	1	Cg2524	[M]: putative BETA (1-->2) GLUCAN EXPORT COMPOSITE TRANSMEMBRANE/ATP-BINDING PROTEIN
589	1	Cg2878	(purD) [C]: PHOSPHORIBOSYLAMINE-GLYCINE LIGASE (EC 6.3.4.13)
591	1	Cg0397	[M]: PROBABLE 5~-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5)
593	1	Cg0648	(adk) [C]: ADENYLATE KINASE (EC 2.7.4.3)
596	1	Cg1669	[S]: putative secreted protein
598	1	Cg1292	[S]: FLAVIN-CONTAINING MONOOXYGENASE 3 (EC 1.14.13.8)
599	1	Cg2447	(glnA2) [C]: GLUTAMINE SYNTHETASE 2 (EC 6.3.1.2)
604	1	Cg2731	(uxaC) [C]: PUTATIVE GLUCURONATE ISOMERASE (EC 5.3.1.12)
608	1	Cg1802	(fmu) [C]: PUTATIVE 16S RRNA M(5)C 967 METHYLTRANSFERASE (EC 2.1.1.-)
611	1	Cg0363	[C]: PROBABLE SECRETION ATPASE PROTEIN
613	1	Cg2511	[M]: putative membrane protein containing CBS domain
614	1	Cg2421	(sucB) [C]: DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (EC 2.3.1.61)
615	1	Cg1164	(lytB) [C]: Penicillin tolerance protein
617	1	Cg1307	[C]: Superfamily II DNA and RNA helicase
623	1	Cg2611	(hscA) [C]: Molecular chaperone, HSP70 family
626	1	Cg0554	[C]: GLYCOSYL TRANSFERASE
628	1	Cg1904	[M]: putative membrane protein
629	1	Cg3042	[C]: ABC-type multidrug transport system, ATPase component
631	1	Cg2970	[C]: conserved hypothetical protein
635	1	Cg3362	(trpCF) [C]: INDOLE-3-GGLYCEROL-PHOSPHATE SYNTHASE/PHOSPHORIBOSYLANTHRANILATE ISOMERASE (EC 4.1.1.48, 5.3.1.24)
637	1	Cg1798	(ribA) [C]: PUTATIVE GTP CYCLOHYDROLASE II/3,4-DIHYDROXY-2-BUTANONE-4-PHOSPHATESYNTHASE (EC 3.5.4.25)
639	1	Cg2397	[M]: putative membrane protein
641	1	Cg2796	[C]: MMGE/PRPD FAMILY PROTEIN
644	1	Cg0308	[M]: putative membrane protein
646	1	Cg3114	(cysN) [C]: Sulfate Adenyltransferase Subunit 1 (EC 2.7.7.4)
648	1	Cg0794	[C]: Cobalamin synthesis protein/P47K
658	1	Cg2304	(hisC) [C]: PROBABLE HISTIDINOL-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.9)
663	1	Cg0559	(ispB) [C]: PUTATIVE OCTAPRENYL-DIPHOSPHATE SYNTHASE PROTEIN ((EC 2.5.1.)
664	1	Cg1527	[C]: transcriptional regulator

hit	peptides	accession	description
671	1	Cg2776	(dinG) [C]: PROBABLE ATP-DEPENDENT DNA HELICASE-RELATED PROTEIN (EC 3.6.1.-)
676	1	Cg1163	(xseA) [C]: EXODEOXYRIBONUCLEASE VII LARGE SUBUNIT (EC 3.1.11.6)
677	1	Cg2194	(gor) [C]: PUTATIVE GLUTATHIONE REDUCTASE (EC 1.6.4.2)
681	1	Cg0400	(adhC) [C]: ALCOHOL DEHYDROGENASE, CLASS C (EC 1.1.1.2)
682	1	Cg1697	(aspA) [C]: ASPARTATE AMMONIA-LYASE (ASPARTASE) (EC 4.3.1.1)
685	1	Cg1089	[M]: ABC-type multidrug/protein/lipid transport system, ATPase component
686	1	Cg1466	[S]: putative secreted protein
688	1	Cg1434	(yggB) [M]: Small-conductance mechanosensitive channel
696	1	Cg0783	[C]: conserved hypothetical protein
697	1	Cg0041	[S]: PUTATIVE SOLUTE-BINDING LIPOPROTEIN, signal peptid
704	1	Cg2856	(purM) [C]: PHOSPHORIBOSYL AMINOIMIDAZOLE SYNTHETASE (EC 6.3.3.1)
707	1	Cg1582	(argB) [C]: ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
709	1	Cg2550	[M]: ABC-type dipeptide/oligopeptide/nickel transport system, permease component
713	1	Cg2208	(dxr) [S]: PROBABLE 1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE (EC 1.1.1.)
717	1	Cg2504	[C]: conserved hypothetical protein
723	1	Cg0221	[C]: PROBABLE LACI-FAMILY TRANSCRIPTIONAL REGULATOR
726	1	Cg2659	[M]: putative membrane protein
728	1	Cg1753	[C]: ATPase component of ABC transporters with duplicated ATPase domains
729	1	Cg0524	(ccsB) [M]: Cytochrome c assembly membrane protein
730	1	Cg2485	(phoD) [S]: SECRETED ALKALINE PHOSPHATASE PRECURSOR (EC 3.1.3.1)
733	1	Cg0873	(aroA) [C]: 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
734	1	Cg1794	[C]: Uncharacterised P-loop ATPase protein
735	1	Cg0062	(ppp) [M]: PROTEIN PHOSPHATASE (EC 3.1.3.16)
737	1	Cg0123	[C]: PUTATIVE HEAT SHOCK PROTEIN (HSP90-FAMILY)
740	1	Cg1503	[M]: ABC-type amino acid transport system, permease component
746	1	Cg3197	(psp5) [S]: Putative secreted protein
750	1	Cg1776	(tal) [C]: TRANSALDOLASE (EC 2.2.1.2)
755	1	Cg0007	(gyrB) [C]: DNA GYRASE SUBUNIT B (EC 5.99.1.3)
756	1	Cg1452	[C]: hypothetical protein predicted by Glimmer/Critica
760	1	Cg1836	[S]: secreted solute-binding protein, aminodeoxychorismate lyase-like
762	1	Cg0198	[C]: conserved hypothetical protein
767	1	Cg1648	[C]: transcriptional regulator, rpiR family
774	1	Cg2418	(ilvE) [C]: BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
781	1	Cg1727	[M]: putative membrane protein
782	1	Cg0510	(hemD) [C]: UROPORPHYRINOGEN III SYNTHASE/METHYLTRANSFERASE (EC 4.2.1.75)
784	1	Cg1713	(pyrD) [C]: DIHYDROOROTATE DEHYDROGENASE (EC 1.3.3.1)
791	1	Cg3134	[M]: ABC-type cobalt transport system, permease component
792	1	Cg2767	[M]: membrane protein (homolog of Drosophila rhomboid)
798	1	Cg2313	(idhA3) [C]: MYO-INOSITOL 2-DEHYDROGENASE (EC 1.1.1.18)
802	1	Cg0531	(menA) [M]: 1,4-DIHYDROXY-2-NAPHTHOATE OCTAPRENYLTRANSFERASE ((EC 2.5.1.-)

hit	peptides	accession	description
804	1	Cg1761	(nifS2) [C]: CYSTEINE DESULFHYDRASE / SELENOCYSTEINE LYASE (EC 4.4.1.-)
805	1	Cg2896	[S]: putative secreted protein, hypothetical endoglucanase
816	1	Cg3190	[C]: Membrane-associated phospholipid phosphatase
817	1	Cg0045	[M]: PROBABLE ABC TRANSPORT PROTEIN, MEMBRANE COMPONENT
825	1	Cg3047	(ackA) [C]: ACETATE KINASE (EC 2.7.2.1)
830	1	Cg0412	[M]: membrane protein
831	1	Cg0193	(pepO) [C]: ENDOPEPTIDASE O (EC 3.4.24.)
832	1	Cg0265	[C]: ABC TRANSPORTER ATP-BINDING PROTEIN
840	1	Cg2836	(sucD) [C]: SUCCINYL-COA SYNTHETASE ALPHA SUBUNIT (EC 6.2.1.5)
841	1	Cg0296	(dnaZX) [C]: DNA POLYMERASE III GAMMA AND TAU SUBUNITS (EC 2.7.7.7)
846	1	Cg2498	[M]: conserved hypothetical protein
847	1	Cg2255	[M]: ABC-type multidrug transport system, permease component
848	1	Cg3106	[C]: conserved hypothetical protein
854	1	Cg0778	[M]: ABC-type cobalamin/Fe3+-siderophores transport system, permease component
859	1	Cg1696	[M]: Permease of the major facilitator superfamily
864	1	Cg0928	[C]: ABC-type cobalamin/Fe3+-siderophores transport system, ATPase component
865	1	Cg3403	[M]: Permease of the major facilitator superfamily
866	1	Cg0368	[S]: conserved secreted protein
868	1	Cg0143	(mtlD) [C]: MANNITOL 2-DEHYDROGENASE (EC 1.1.1.67)
869	1	Cg2135	(miaB) [C]: TRNA METHYLTHIOTRANSFERASE
872	1	Cg2784	[C]: metal-dependent transcriptional regulator
883	1	Cg3396	[C]: Membrane protease subunit, stomatin/prohibitin homologs
885	1	Cg0167	[M]: permease
889	1	Cg0945	[C]: 23S RIBOSOMAL RNA METHYLTRANSFERASE (EC 2.1.1.-)
893	1	Cg1166	[M]: putative membrane protein
907	1	Cg2374	(murE) [C]: PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2 (EC 6.3.2.13)
919	1	Cg1298	(cydC) [M]: ABC-type multidrug/protein/lipid transport system, ATPase component
929	1	Cg0422	(murA) [C]: UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
932	1	Cg1458	[C]: 2-HYDROXYHEPTA-2,4-DIENE- 1,7-DIOATE ISOMERASE (EC 5.3.3.-)
934	1	Cg0263	(modA) [S]: MOLYBDATE-BINDING secreted PROTEIN
935	1	Cg0405	[S]: cobalamin/Fe3+-siderophores transport system, secreted component
940	1	Cg3177	(pccB) [C]: PROPIONYL-COA CARBOXYLASE BETA CHAIN (EC 6.4.1.3)
942	1	Cg0624	[M]: secreted oxidoreductase
947	1	Cg3426	(parB) [C]: Predicted transcriptional regulator involved in chromosome patitioning
949	1	Cg3133	[C]: ABC-type cobalt transport system, ATPase component
957	1	Cg3336	(gntK) [C]: PUTATIVE GLUCONATE KINASE (EC 2.7.1.12)
958	1	Cg2908	[S]: putative membrane protein
962	1	Cg1890	[C]: hypothetical protein predicted by Glimmer/Critica
965	1	Cg2549	[S]: ABC-type dipeptide/oligopeptide/nickel transport system, secreted component
968	1	Cg1369	(atpC) [C]: PROBABLE ATP SYNTHASE EPSILON CHAIN PROTEIN (EC 3.6.1.34)

hit	peptides	accession	description
969	1	Cg1482	[C]: Zn-dependent hydrolases, including glyoxylases
981	1	Cg3389	[C]: Predicted dehydrogenase
994	1	Cg1035	[C]: TatD related DNase
1001	1	Cg3407	[M]: putative membrane protein
1005	1	Cg1649	(pctD) [M]: ABC-type phosphate/phosphonate transport system, permease component
1010	1	Cg0091	[C]: D-isomer specific 2-hydroxyacid dehydrogenase
1011	1	Cg0932	[M]: membrane protein
1018	1	Cg1104	[M]: Predicted esterase, membrane protein
1019	1	Cg2900	(ddh) [C]: MESO-DIAMINOPIMELATE DEHYDROGENASE (EC 1.4.1.16)
1021	1	Cg0244	[M]: membrane protein
1025	1	Cg3170	[M]: Tellurite resistance protein or related permease
1028	1	Cg0010	[C]: conserved hypothetical protein
1029	1	Cg2938	[M]: ABC-type dipeptide/oligopeptide/nickel transport system, permease component
1033	1	Cg1122	[S]: putative secreted protein
1038	1	Cg2160	[C]: HYDROLASE OF METALLO-BETA-LACTAMASE SUPERFAMILY
1039	1	Cg0742	[M]: PUTATIVE INTEGRAL MEMBRANE PROTEIN
1040	1	Cg0291	[C]: 3,4-dioxygenase beta subunit
1051	1	Cg0472	[C]: conserved hypothetical protein
1055	1	Cg2955	(mutY) [C]: A/G-SPECIFIC ADENINE GLYCOSYLASE (EC 3.2.2.-)
1060	1	Cg2994	[S]: putative secreted or membrane protein
1061	1	Cg2894	[C]: Bacterial regulatory protein, TetR family
1062	1	Cg2342	[C]: Dehydrogenase
1064	1	Cg1522	[M]: putative membrane protein
1065	1	Cg3163	[M]: PROBABLE ACYLTRANSFERASE (EC 2.3.1.-)
1076	1	Cg0879	[M]: membrane protein
1077	1	Cg3116	(cysH) [C]: Phosphoadenosine-Phosphosulfate Reductase (EC 1.8.99.4)
1080	1	Cg3316	[C]: Universal stress protein UspA or related nucleotide-binding protein
1087	1	Cg0230	(gltD) [C]: (Q9Z464) GLUTAMINE 2-OXOGLUTARATE AMINOTRANSFERASE (EC 1.4.1.13)
1090	1	Cg3264	[C]: conserved hypothetical protein
1101	1	Cg1226	(pobB) [C]: 4-HYDROXYBENZOATE 3-MONOOXYGENASE (EC 1.14.13.2)
1104	1	Cg0001	(dnaA) [C]: CHROMOSOMAL REPLICATION INITIATOR PROTEIN
1107	1	Cg1002	[S]: putative secreted protein
1112	1	Cg2127	[C]: conserved hypothetical protein
1117	1	Cg2049	[C]: hypothetical protein predicted by Glimmer/Critica
1129	1	Cg3025	(mrpC) [M]: MULTISUBUNIT NA+/H+ ANTIPORTER INVOLVED IN PH REGULATION
1134	1	Cg0970	[M]: membrane protein
1137	1	Cg0432	[M]: PROBABLE LIPOPOLYSACCHARIDE MODIFICATION ACYLTRANS
1141	1	Cg0523	[M]: membrane protein required for cytochrome c biosynthesis
1145	1	Cg2510	(bex) [C]: BEX PROTEIN (GTP-BINDING PROTEIN ERA HOMOLOG)
1147	1	Cg1799	(ribC) [C]: PUTATIVE RIBOFLAVIN SYNTHASE (EC 2.5.1.9)

hit	peptides	accession	description
1151	1	Cg2114	(lexA) [C]: PUTATIVE LEXA REPRESSOR TRANSCRIPTION REGULATOR PROTEIN (EC 3.4.21.88)
1156	1	Cg2410	(ltsA) [C]: glutamine-dependent amidotransferase involved in formation of cell wall and L-glutamate biosynthesis (EC 6.3.5.4)
1159	1	Cg2650	[M]: putative membrane protein
1166	1	Cg1051	[C]: hypothetical protein predicted by Glimmer/Critica
1167	1	Cg0401	(rmlA1) [C]: TDP-GLUCOSE PYROPHOSPHORYLASE (EC 2.7.7.24)
1172	1	Cg2936	[C]: Bacterial regulatory proteins, GntR family
1176	1	Cg1129	(aroF) [C]: PROBABLE PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
1180	1	Cg2402	[S]: NPL/P60 FAMILY SECRETED PROTEIN
1185	1	Cg2554	(rbsK2) [C]: PROBABLE RIBOKINASE PROTEIN (EC 2.7.1.15)
1186	1	Cg2286	[M]: putative membrane protein
1187	1	Cg2482	[C]: hypothetical protein predicted by Glimmer/Critica
1199	1	Cg2664	[C]: Predicted type IV restriction endonuclease
1203	1	Cg2429	(glnA) [C]: GLUTAMINE SYNTHETASE I (EC 6.3.1.2)
1205	1	Cg1355	(prfA) [C]: PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)
1211	1	Cg2022	[MS]: putative secreted protein
1215	1	Cg2318	[S]: ABC-type cobalamin/Fe3+-siderophores transport system component
1219	1	Cg2271	[M]: Co/Zn/Cd efflux system component
1221	1	Cg0352	[S]: putative secreted protein
1223	1	Cg0310	(katA) [C]: CATALASE (EC 1.11.1.6)
1225	1	Cg1881	[S]: Predicted iron-dependent peroxidase, secreted protein
1234	1	Cg2348	[S]: putative secreted protein
1236	1	Cg1568	(ugpA) [M]: sn-Glycerol-3-phosphate transport system permease protein
1247	1	Cg1494	[S]: putative secreted protein
1251	1	Cg1733	[C]: conserved hypothetical protein
1259	1	Cg0649	(map1) [C]: METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
1262	1	Cg2000	[M]: putative membrane protein
1263	1	Cg1158	[S]: putative secreted protein
1269	1	Cg1859	[S]: putative secreted protein
1270	1	Cg3099	(grpE) [C]: Molecular chaperone GrpE (heat shock protein)
1288	1	Cg2226	[C]: Predicted Rossmann fold nucleotide-binding protein involved in DNA uptake
1290	1	Cg0786	(upp) [C]: PUTATIVE URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9)
1301	1	Cg0353	(nth) [C]: PROBABLE ENDONUCLEASE III PROTEIN (EC 4.2.99.18)
1303	1	Cg1300	(cydB) [M]: CYTOCHROME D TERMINAL OXIDASE POLYPEPTIDE SUBUNIT (EC 1.10.3.-)
1313	1	Cg0899	[C]: glutamine amidotransferase involved in pyridoxine biosynthesis
1317	1	Cg0237	[C]: PUTATIVE OXIDOREDUCTASE
1318	1	Cg3172	[C]: SAM-dependent methyltransferase
1322	1	Cg2517	(hemN) [C]: PUTATIVE ANAEROBIC COPROPORPHYRINOGEN III OXIDASE (EC 1.3.3.3)
1327	1	Cg1738	[C]: (AAK45786) TRANSCRIPTIONAL REGULATOR, TETR FAMILY
1332	1	Cg0596	(rplD) [C]: 50S RIBOSOMAL PROTEIN L4
1337	1	Cg2428	[M]: putative membrane protein

hit	peptides	accession	description
1340	1	Cg0721	(crtB2) [C]: PHYTOENE SYNTHETASE (EC 2.5.1.)
1343	1	Cg2977	[M]: putative membrane protein
1345	1	Cg0046	[C]: PROBABLE ABC TRANSPORT PROTEIN, ATP-BINDING COMPON
1346	1	Cg1811	(ihf) [C]: putative integration host factor cIHF
1350	1	Cg0548	(menB) [C]: DIHYDROXYNAPHTHONIC ACID SYNTHASE (EC 4.1.3.36)
1354	1	Cg1180	[M]: Glycosyltransferases, probably involved in cell wall biogenesis
1370	1	Cg0330	(cgtR1) [C]: PUTATIVE TWO COMPONENT RESPONSE REGULATOR
1372	1	Cg3317	[M]: putative membrane protein
1375	1	Cg0562	(nusG) [C]: TRANSCRIPTION ANTITERMINATION PROTEIN NUSG
1378	1	Cg0128	[S]: secreted protein, Signal peptide
1381	1	Cg0696	(sigD) [C]: PUTATIVE RNA POLYMERASE SIGMA FACTOR, ECF family
1397	1	Cg1056	[M]: putative membrane protein
1398	1	Cg2099	[M]: putative membrane protein
1402	1	Cg3214	[C]: conserved hypothetical protein
1407	1	Cg0684	(papA) [C]: PROLYL AMINOPEPTIDASE A (EC 3.4.11.5)
1414	1	Cg1405	[C]: Siderophore-interacting protein
1418	1	Cg1242	[M]: putative membrane protein
1421	1	Cg1260	(dapE) [C]: SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18)
1429	1	Cg0602	(rplP) [C]: 50S RIBOSOMAL PROTEIN L16
1430	1	Cg3299	(trxB1) [C]: THIOREDOXIN
1431	1	Cg2578	[MS]: secreted DNA uptake protein or related DNA-binding protein
1433	1	Cg1236	(tpx) [C]: THIOL PEROXIDASE (EC 1.11.1.-)
1437	1	Cg1291	[M]: putative membrane protein
1442	1	Cg2625	(pcaF) [C]: PUTATIVE ACETYL-COA:ACETYLTRANSFERASE (EC 2.3.1.9)
1447	1	Cg3211	[S]: putative secreted protein
1456	1	Cg1490	[C]: NTP pyrophosphohydrolases including oxidative damage repair enzymes
1459	1	Cg2935	(nanP) [C]: NEURAMINIDASE NANP
1467	1	Cg0153	(hde) [C]: PROBABLE ESTERASE/LIPASE PROTEIN (EC 3.1.1.-)
1468	1	Cg1176	[C]: short chain dehydrogenase
1476	1	Cg0154	[C]: haloacid dehalogenase-like hydrolase
1479	1	Cg0650	[S]: secreted protein
1488	1	Cg1675	[M]: putative membrane protein
1498	1	Cg0156	[C]: Bacterial regulatory proteins, Crp family
1505	1	Cg1206	[C]: PEP phosphonomutase or related enzyme
1506	1	Cg1842	[S]: putative secreted metalloprotease
1508	1	Cg1962	[M]: putative membrane protein
1509	1	Cg2952	[S]: putative secreted protein
1523	1	Cg0946	[C]: conserved hypothetical protein
1532	1	Cg2567	[C]: hypothetical protein predicted by Glimmer/Critica
1539	1	Cg0109	[C]: TRIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.3)

hit	peptides	accession	description
1542	1	Cg3209	[M]: Predicted metal-dependent membrane protease
1547	1	Cg0620	[S]: secreted protein
1549	1	Cg2134	[M]: putative membrane protein
1565	1	Cg3155	(dcd) [C]: DEOXYCYTIDINE TRIPHOSPHATE DEAMINASE (EC 3.5.4.13)
1568	1	Cg0680	[C]: conserved hypothetical protein
1571	1	Cg1514	[S]: secreted protein
1572	1	Cg3277	[C]: Uncharacterized ACR, double-stranded beta-helix domain
1579	1	Cg1370	[MS]: conserved hypothetical protein
1584	1	Cg3249	[S]: putative secreted protein
1585	1	Cg2720	(lppS) [S]: secreted lipoprotein ErfK/YbiS/YcfS/YnhG family
1590	1	Cg3280	[S]: putative secreted protein
1605	1	Cg0179	[M]: membrane protein
1617	1	Cg3293	[C]: hypothetical protein predicted by Glimmer/Critica
1634	1	Cg0325	[M]: Na+/H+ antiporter
1643	1	Cg0415	(ptpA2) [C]: Low molecular weight phosphotyrosine protein phosp
1645	1	Cg1597	[C]: conserved hypothetical protein
1649	1	Cg1033	[M]: Cadmium resistance transporter
1650	1	Cg2623	(scoA) [C]: PROBABLE FESUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE SUBUNIT (EC 2.8.3.5)
1670	1	Cg0795	[MS]: FAD-dependent pyridine nucleotide-disulphide oxidoreductase
1675	1	Cg0292	(tnp16a(ISCg16a)) [C]: TRANSPOSASE
1681	1	Cg1893	[C]: acetyltransferase
1696	1	Cg2113	[C]: hypothetical protein predicted by Glimmer/Critica
1699	1	Cg2315	[C]: ABC-type cobalamin/Fe3+-siderophores transport systems, ATPase component
1704	1	Cg1130	(uppS1) [C]: PUTATIVE UNDECAPRENYL PYROPHOSPHATE SYNTHETASE (EC 2.5.1.31)
1709	1	Cg2207	[M]: Predicted membrane-embedded Zn-dependent protease
1710	1	Cg0465	[M]: conserved hypothetical membrane protein
1712	1	Cg2861	[M]: membrane protein, hemolysin III homolog
1720	1	Cg1682	[C]: Trypsin-like serine protease
1728	1	Cg3412	(azlD) [M]: Predicted branched-chain amino acid permease (azaleucine resistance)
1741	1	Cg3223	[C]: NADPH-dependent FMN reductase
1748	1	Cg2942	[C]: Bacterial regulatory proteins, AsnC family
1750	1	Cg1652	(pctA) [S]: ALKYLPHOSPHONATE ABC TRANPORTER (SECRETED PHOSPHATE-BINDING PROTEIN)
1751	1	Cg1630	[C]: PUTATIVE SIGNAL TRANSDUCTION PROTEIN, FHA DOMAIN
1770	1	Cg1884	[M]: putative membrane protein
1771	1	Cg2765	[S]: putative secreted protein
1783	1	Cg2344	(cysY) [C]: hyp. Cystathionine beta-Synthase
1803	1	Cg0852	[C]: conserved hypothetical protein
1824	1	Cg0240	[M]: membrane protein
1827	1	Cg1167	[S]: putative secreted protein
1832	1	Cg1612	[C]: Acetyltransferase

hit	peptides	accession	description
1833	1	Cg3129	[C]: ABC-type transport system, ATPase component
1837	1	Cg1834	[C]: ABC-type cobalamin/Fe3+-siderophores transport system, ATPase component
1840	1	Cg1783	(soxA~) [C]: sarcosine oxidase - N-terminal fragment
1846	1	Cg2053	[M]: putative membrane protein
1847	1	Cg3139	[C]: conserved hypothetical protein
1866	1	Cg1348	[M]: membrane protein containing CBS domain
1871	1	Cg3345	[C]: hypothetical protein predicted by Glimmer/Critica
1875	1	Cg0374	[C]: conserved hypothetical protein
1879	1	Cg3127	[MS]: putative membrane protein
1886	1	Cg0599	(rpsS) [C]: 30S RIBOSOMAL PROTEIN S19
1892	1	Cg3324	[S]: putative secreted protein
1900	1	Cg3331	(ogt) [C]: METHYLATED-DNA--PROTEIN-CYSTEINE METHYLTRANSFERASE (EC 2.1.1.63)
1901	1	Cg0337	(whiB4) [C]: PUTATIVE REGULATORY PROTEIN (WHIB-RELATED PROTEIN)
1902	1	Cg2607	[M]: putative membrane protein
1904	1	Cg1796	(ribX) [M]: putative membrane protein - C. ammoniagenes RibX homolog
1907	1	Cg1706	[C]: Low molecular weight phosphotyrosine protein phosphatase
1911	1	Cg3052	[S]: putative secreted protein
1925	1	Cg1326	[C]: hypothetical protein predicted by Glimmer/Critica
1930	1	Cg1874	[M]: putative membrane protein
1937	1	Cg2824	[C]: SAM-dependent methyltransferase
1949	1	Cg2981	(folX) [C]: DIHYDRONEOPTERIN ALDOLASE (EC 4.1.2.25)
1954	1	Cg2121	(ptsH) [C]: PHOSPHOCARRIER PROTEIN HPR
1959	1	Cg2785	[M]: putative membrane protein
1991	1	Cg3105	[C]: hypothetical protein predicted by Glimmer/Critica
1993	1	Cg1181	[M]: Glycosyltransferase, probably involved in cell wall biogenesis
1998	1	Cg2572	[C]: conserved hypothetical protein
2001	1	Cg0983	(purN) [C]: (Q9RHX7) 5~-PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSF (EC 2.1.2.2)
2036	1	Cg1804	(def2) [C]: POLYPEPTIDE DEFORMYLASE (EC 3.5.1.31)
2048	1	Cg2582	[C]: conserved hypothetical protein
2049	1	Cg3257	[C]: conserved hypothetical protein
2051	1	Cg2839	[C]: conserved hypothetical protein
2078	1	Cg1469	[S]: putative secreted protein
2110	1	Cg2033	[S]: putative secreted protein
2119	1	Cg2850	[C]: conserved hypothetical protein
2120	1	Cg0246	[M]: GLYCOSYL TRANSFERASE
2123	1	Cg0500	[C]: Bacterial regulatory protein, LysR family
2137	1	Cg0297	[C]: Uncharacterized BCR, YbaB family COG0718
2138	1	Cg0107	[S]: secreted protein
2148	1	Cg3110	[C]: SLIGHTLY SIMILAR TO AQUAPORIN
2162	1	Cg0582	(rpsG) [C]: 30S RIBOSOMAL PROTEIN S7

hit	peptides	accession	description
2163	1	Cg1635	[M]: putative membrane protein
2191	1	Cg3423	(trxC) [C]: THIOREDOXIN
2202	1	Cg1085	[C]: hypothetical protein predicted by Glimmer/Critica
2223	1	Cg1894	[C]: hypothetical protein predicted by Glimmer/Critica
2225	1	Cg0588	[C]: hypothetical protein
2232	1	Cg1072	(rplY) [C]: Ribosomal protein L25 (general stress protein Ctc)
2239	1	Cg0155	[C]: PUTATIVE ACETYLTRANSFERASE (EC 2.3.1.)
2271	1	Cg2443	[M]: Permease of the major facilitator superfamily
2281	1	Cg2996	(~ptsX~) [M]: Phosphotransferase system IIC components - fragment
2292	1	Cg1241	[C]: hypothetical protein predicted by Glimmer/Critica
2295	1	Cg1708	[C]: conserved hypothetical protein
2301	1	Cg2340	[S]: ABC-type amino acid transport system, secreted component
2336	1	Cg0358	[C]: hydrolase or acyltransferase
2346	1	Cg3267	[MS]: putative membrane protein
2435	1	Cg0321	[M]: Na+/H+ antiporter subunit
2443	1	Cg1201	[C]: hypothetical protein predicted by Glimmer/Critica
2447	1	Cg0366	[M]: conserved hypothetical protein, membrane
2457	1	Cg0087	[M]: probable transmembrane transport protein
2468	1	Cg3433	[C]: hypothetical protein predicted by Glimmer/Critica
2497	1	Cg2710	(int3) [C]: putative phage-type integrase
2632	1	Cg0380	[C]: hypothetical protein
2635	1	Cg2988	(ppa) [C]: INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
2716	1	Cg0606	[M]: hypothetical membrane protein

END OF LIST I

hit	peptides	accession	description
II. Purple membrane; elastase digest; nLC-ESI MS/MS, no search specificity			
1	295	P02945|BACR	Bacteriorhodopsin
2	214	P00772|ELA1	Elastase-1 precursor - Sus scrofa
3	83	Q9HM69|CSG	Cell surface glycoprotein
4	45	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
5	38	Q9HQA6|Q9HQA6	Putative uncharacterized protein
6	38	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
7	33	Q9HRU5|Q9HRU5	Immunogenic protein
11	26	Q9HR99|Q9HR99	Halocyanin-like
10	24	Q9HNI7|Q9HNI7	Possible phosphate binding protein
12	24	P16102|BACH	Halorhodopsin
9	23	Q9HR20|Q9HR20	Putative uncharacterized protein
14	19	Q9HHN1|Q9HHN1	Na+/H+ antiporter
16	16	Q48302|Q48302	Precursor proteolipid
17	16	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
13	15	Q9HS51|Q9HS51	Putative uncharacterized protein
15	14	Q9HMW4|Q9HMW	Oligopeptide binding protein
18	14	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
19	13	Q9HPQ5|Q9HPQ5	Htr8 transducer
22	11	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
21	10	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
24	9	Q9HMH4|Q9HMH4	Putative uncharacterized protein
25	9	O54610|O54610	CydA
26	8	Q9HNV1|Q9HNV1	Putative uncharacterized protein
29	8	Q9HHR4|Q9HHR4	Vng6268c
30	8	Q9HMU9|Q9HMU9	Nitrite/nitrate reduction protein
34	8	Q9HN94|Q9HN94	Cytochrome c oxidase subunit II
23	7	Q9HPB1|SECY	Preprotein translocase subunit secY
28	7	Q9HS10|Q9HS10	Phosphate ABC transporter periplasmic phosphate-binding
33	7	Q9HML5|Q9HML5	Phosphate ABC transporter binding
40	7	Q9HQF4|Q9HQF4	Membrane protein
20	6	P33741|HTR1	Sensory rhodopsin I transducer
31	6	Q9HR04|Q9HR04	Iron-binding protein
48	6	P57684|ATKA	Potassium-transporting ATPase A chain
51	6	O54596|O54596	CydB
35	5	Q9HRR2|Q9HRR2	Cytochrome b6
44	5	P33518|COX1	Cytochrome c oxidase polypeptide 1
52	5	Q9HN25|Q9HN25	Putative uncharacterized protein

hit	peptides	accession	description
53	5	P25964|BACS1	Sensory rhodopsin-1
57	5	Q9HRR1|Q9HRR1	Putative uncharacterized protein
65	5	Q9HRR3|Q9HRR3	Putative uncharacterized protein
83	5	Q9HME2|Q9HME2	Putative uncharacterized protein
88	5	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
93	5	Q9HN93|Q9HN93	Halocyanin-like
27	4	Q9HRL2|Q9HRL2	F420H2:quinone oxidoreductase chain M
36	4	Q9HND8|VATI	V-type ATP synthase subunit I
43	4	Q9HS47|Q9HS47	Putative uncharacterized protein
46	4	Q9HHP3|Q9HHP3	Vng6297c
62	4	O54523|O54523	Putative uncharacterized protein
76	4	Q9HRS9|Q9HRS9	Putative uncharacterized protein
77	4	Q9HNB9|Q9HNB9	Putative uncharacterized protein
118	4	Q9HHE7|Q9HHE7	Vng6441h
128	4	Q9HRF2|Q9HRF2	Putative uncharacterized protein
248	4	Q9HQ64|Q9HQ64	Membrane anchor
32	3	Q9HRT0|Q9HRT0	Putative uncharacterized protein
38	3	Q9HMY1|Q9HMY1	Sensor protein
39	3	Q9HHI2|Q9HHI2	L-lactate permease
47	3	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
50	3	Q9HN37|Q9HN37	Protein export
60	3	Q9HR23|Q9HR23	Ribose ABC transporter permease
67	3	Q9HQY4|Q9HQY4	Flagella accessory protein J
82	3	P82857|P82857	Cytochrome-like protein
84	3	Q9HNY2|Q9HNY2	Putative uncharacterized protein
89	3	Q9HNN6|Q9HNN6	Putative uncharacterized protein
91	3	Q9HMS7|Q9HMS7	DNA damage-inducible protein
95	3	Q9HMW2|Q9HMW	Oligopeptide transport permease protein
121	3	O54662|O54662	Putative uncharacterized protein
123	3	Q9HS59|Q9HS59	Putative uncharacterized protein
127	3	Q9HP49|Q9HP49	Putative uncharacterized protein
145	3	Q9HQA7|Q9HQA7	Putative uncharacterized protein
153	3	Q9HMT5|Q9HMT5	Putative uncharacterized protein
155	3	Q9HI34|Q9HI34	Vng6345h
157	3	Q9HSC3|LONH	Putative protease La homolog type
212	3	Q9HP06|Q9HP06	Cation efflux system protein
224	3	Q9HRR0|Q9HRR0	Putative uncharacterized protein
303	3	O51978|O51978	Putative uncharacterized protein
312	3	Q9HRL4|Q9HRL4	NADH dehydrogenase/oxidoreductase-like protein
445	3	Q9HML1|Q9HML1	Putative uncharacterized protein

hit	peptides	accession	description
8	2	Q9HH34|Q9HH34	Rhodopsin
41	2	Q9HRU7|Q9HRU7	Putative uncharacterized protein
42	2	Q9HS86|Q9HS86	Htr14 transducer
55	2	O52005|O52005	Putative uncharacterized protein
56	2	Q9HS26|Q9HS26	Na+/H+ antiporter
58	2	Q9HN17|Q9HN17	4-hydroxybutyrate CoA transferase
64	2	Q9HML7|Q9HML7	Phosphate ABC transporter permease
69	2	Q9HP66|Q9HP66	Putative uncharacterized protein
75	2	Q9HPT7|Q9HPT7	Putative uncharacterized protein
85	2	Q9HNR2|Q9HNR2	Putative uncharacterized protein
87	2	Q9HNF6|Q9HNF6	Putative uncharacterized protein
97	2	Q9HNB6|Q9HNB6	Putative uncharacterized protein
98	2	Q9HN36|Q9HN36	Protein export
103	2	Q9HNQ2|IF2P	Probable translation initiation factor IF-2
104	2	Q9HNQ5|Q9HNQ5	Putative uncharacterized protein
105	2	Q9HSW6|CDC61	Cell division control protein 6 homolog 1
111	2	Q9HQT5|Q9HQT5	Htr13 transducer
122	2	Q9HRN3|Q9HRN3	Proteinase IV homolog
124	2	Q9HMG7|Q9HMG7	Ferrichrome ABC transporter permease
135	2	Q9HP32|PYRG	CTP synthase
137	2	Q9HNS6|Q9HNS6	Putative uncharacterized protein
139	2	Q9HSQ7|Q9HSQ7	ABC transport protein
147	2	Q9HS33|Q9HS33	Multidrug resistance protein homolog
152	2	Q9HSB1|Q9HSB1	Dolichol-P-glucose synthetase
172	2	Q9HPX5|Q9HPX5	Htr-like protein
174	2	Q9HNT7|Q9HNT7	Subtilisin homolog
187	2	Q9HPF9|Q9HPF9	Putative uncharacterized protein
199	2	O73955|CATA	Peroxidase/catalase
205	2	P71411|BACS2	Sensory rhodopsin-2
209	2	Q9HRJ3|Q9HRJ3	Putative uncharacterized protein
225	2	Q9HQ63|DHSD	Succinate dehydrogenase hydrophobic membrane anchor subunit
226	2	Q9HQN5|Q9HQN5	Glycine betaine transporter
232	2	Q9HQQ5|Q9HQQ5	Probable transport protein
239	2	Q9HRT5|Q9HRT5	Putative uncharacterized protein
246	2	Q9HM75|Q9HM75	Cytochrome oxidase subunit I homolog
251	2	Q9HRW7|Q9HRW7	Putative uncharacterized protein
254	2	Q9HN92|Q9HN92	Putative uncharacterized protein
263	2	Q9HM70|Q9HM70	Putative uncharacterized protein
270	2	Q9HSF1|Q9HSF1	Putative uncharacterized protein
271	2	Q9HMM6|CSD	Probable cysteine desulfurase

hit	**peptides**	**accession**	**description**
272	2	Q9HRJ8|Q9HRJ8	Heme synthase
293	2	Q9HQP1|Q9HQP1	Putative uncharacterized protein
304	2	Q9HSG5|TRUD	Probable tRNA pseudouridine synthase D
306	2	Q9HP92|Q9HP92	GTP-binding protein homolog
309	2	Q9HRC9|Q9HRC9	Putative uncharacterized protein
311	2	Q9HPU7|Q9HPU7	Bacteriorhodopsin related protein
327	2	Q9HQV9|Q9HQV9	Putative uncharacterized protein
328	2	Q9HR50|Q9HR50	Putative uncharacterized protein
329	2	Q9HMZ1|Q9HMZ1	Delta-aminolevulinic acid dehydratase
337	2	Q9HMD8|Q9HMD8	Putative uncharacterized protein
349	2	Q9HRZ5|Q9HRZ5	Pyruvate ferredoxin oxidoreductase, subunit alpha
385	2	Q9HQ25|Q9HQ25	Putative uncharacterized protein
388	2	Q9HQF0|Q9HQF0	Acyl-CoA dehydrogenase
393	2	Q9HRB8|Q9HRB8	Putative uncharacterized protein
398	2	Q9HNG3|Q9HNG3	Putative uncharacterized protein
399	2	Q9HS00|Q9HS00	Putative uncharacterized protein
403	2	Q9HMW6|Q9HMW	Putative uncharacterized protein
415	2	Q9HSY7|Q9HSY7	Putative uncharacterized protein
417	2	Q9HQU0|Q9HQU0	Putative uncharacterized protein
425	2	P05971|RL15	50S ribosomal protein L15P
440	2	Q9HRW2|Q9HRW	Putative uncharacterized protein
451	2	Q9HQV6|Q9HQV6	Putative uncharacterized protein
487	2	Q9HQ91|Q9HQ91	Putative uncharacterized protein
518	2	Q9HMW1|Q9HMW	Oligopeptide ABC transporter ATP-binding
558	2	Q9HRR5|Q9HRR5	Putative uncharacterized protein
585	2	Q9HRB9|Q9HRB9	Phosphate regulatory protein homolog
604	2	Q9HHP9|Q9HHP9	Vng6290h
628	2	Q9HHJ7|CDC66	Cell division control protein 6 homolog 6
670	2	Q9HQV2|Q9HQV2	Putative uncharacterized protein
739	2	Q9HPZ6|Y1401	UPF0179 protein VNG1401C
859	2	Q9HPK2|Y1595	UPF0100 protein VNG1595C
45	1	Q9HP84|HTR4	Halobacterial transducer protein 4
49	1	Q9HR41|Q9HR41	Possible signaling protein
61	1	Q9HNG4|Q9HNG4	Putative uncharacterized protein
63	1	Q9HS95|Q9HS95	Chromosome segregation
68	1	P57699|ATKB	Potassium-transporting ATPase B chain
70	1	Q9HNT5|Q9HNT5	Putative uncharacterized protein
71	1	P71414|P71414	Transducer HtC protein
72	1	Q9HSL5|Q9HSL5	Cationic amino acid transporter
73	1	Q9HNR0|Q9HNR0	Protein-export membrane protein

hit	peptides	accession	description
74	1	Q9HPQ1|Q9HPQ1	Sodium-and chloride-dependent transporter
79	1	Q9HSJ6|Q9HSJ6	Putative uncharacterized protein
80	1	Q9HSM2|MUTS1	DNA mismatch repair protein mutS 1
81	1	Q9HP01|Q9HP01	Spermidine/putrescine ABC transporter permease
92	1	Q9HNK5|Q9HNK5	Putative uncharacterized protein
94	1	Q9HR54|Q9HR54	Putative uncharacterized protein
96	1	Q9HRS0|Q9HRS0	Putative uncharacterized protein
99	1	Q9HMI2|Q9HMI2	Dipeptide ABC transporter permease
100	1	Q9HT01|Q9HT01	Putative uncharacterized protein
101	1	Q9HQ54|Q9HQ54	Putative uncharacterized protein
102	1	O51965|O51965	RepH
106	1	Q9HP81|HTR2	Sensory rhodopsin II transducer
107	1	Q9HMV6|HELS	Putative ski2-type helicase
108	1	Q9HR16|Q9HR16	Proline permease
110	1	Q9HS12|Q9HS12	Phosphate ABC transporter permease
113	1	Q9HPN8|Q9HPN8	Chloride channel
114	1	Q9HHP2|Q9HHP2	Vng6298c
115	1	Q9HR05|Q9HR05	Iron transporter-like protein
119	1	Q9HR13|Q9HR13	Putative uncharacterized protein
125	1	Q9HNH6|Q9HNH6	Threonine dehydratase
126	1	Q9HSV6|Q9HSV6	Putative uncharacterized protein
129	1	Q9HR62|Q9HR62	Putative uncharacterized protein
130	1	Q9HRT4|Q9HRT4	Putative uncharacterized protein
131	1	Q9HQ23|Q9HQ23	Putative uncharacterized protein
133	1	Q9HNQ9|Q9HNQ9	Protein-export membrane protein
136	1	Q9HS71|Q9HS71	Cell division protein ftsZ
141	1	Q9HSN5|Q9HSN5	Zinc-transporting ATPase
142	1	Q9HS03|Q9HS03	Putative uncharacterized protein
143	1	Q9HQJ9|Q9HQJ9	Putative 2-ketoglutarate ferredoxin oxidoreductase
144	1	Q9HQZ0|Q9HQZ0	Acetyl-CoA synthetase
160	1	Q9HI06|Q9HI06	Vng6135c
163	1	Q9HRD0|Q9HRD0	Anion permease
165	1	Q9HPV6|Q9HPV6	Putative uncharacterized protein
167	1	Q9HSM6|MUTL	DNA mismatch repair protein mutL
168	1	Q9HN16|Q9HN16	Putative uncharacterized protein
171	1	Q9HP43|CARB	Carbamoyl-phosphate synthase large chain
176	1	Q9HRM4|Q9HRM4	Putative uncharacterized protein
177	1	Q9HM71|Q9HM71	Putative uncharacterized protein
178	1	O54630|O54630	Putative uncharacterized protein
185	1	Q9HN44|Q9HN44	Na+/Ca2+-exchanging protein

hit	peptides	accession	description
186	1	Q9HHU7|Q9HHU7	Cationic amino acid transporter
192	1	Q9HRT3|Q9HRT3	Succinoglycan biosynthesis transport protein
193	1	Q9HQ81|Q9HQ81	TRK potassium uptake system protein
197	1	Q9HNK9|IF2G	Translation initiation factor 2 subunit gamma
200	1	Q9HMX2|Q9HMX2	Oligopeptide ABC transporter
201	1	Q9HN70|THSA	Thermosome subunit alpha
206	1	Q9HQD6|HUTI	Probable imidazolonepropionase
207	1	O52009|O52009	RepJ
211	1	Q9HMU6|Q9HMU6	Putative uncharacterized protein
214	1	Q9HQ03|Q9HQ03	Putative uncharacterized protein
215	1	Q9HPA2|Q9HPA2	Htr17 transducer
216	1	Q9HNG6|Q9HNG6	Putative uncharacterized protein
218	1	Q9HRE4|Q9HRE4	Sensor protein
219	1	Q9HRH7|Q9HRH7	Putative uncharacterized protein
236	1	Q9HRN5|Q9HRN5	Putative uncharacterized protein
244	1	Q9HP89|Q9HP89	Photolyase/cryptochrome
245	1	Q9HPD9|Q9HPD9	Putative uncharacterized protein
247	1	Q9HNC9|Q9HNC9	Putative uncharacterized protein
249	1	Q9HHR2|Q9HHR2	Sn-glycerol-1-phosphate dehydrogenase
252	1	Q9HN22|Q9HN22	Putative uncharacterized protein
258	1	Q9HPR5|Q9HPR5	Cell division protein pelota
266	1	Q9HR01|Q9HR01	Putative uncharacterized protein
267	1	Q9HSL4|Q9HSL4	TRK potassium uptake system protein
268	1	O51984|O51984	Putative uncharacterized protein
273	1	Q9HPQ4|Q9HPQ4	Putative uncharacterized protein
276	1	Q9HPL9|Q9HPL9	Putative uncharacterized protein
277	1	Q9HRM6|Q9HRM6	Aspartate aminotransferase
278	1	Q9HNI3|Q9HNI3	Putative uncharacterized protein
283	1	Q9HN79|Q9HN79	DNA damage-inducible protein
286	1	Q9HSA1|Q9HSA1	Phosphoenolpyruvate synthase
287	1	Q9HQI5|Q9HQI5	Ornithine carbamoyltransferase
289	1	Q9HNP8|Q9HNP8	Oligopeptidase
291	1	Q9HPD4|RL3	50S ribosomal protein L3P
297	1	Q9HSR4|Q9HSR4	Oxidoreductase
298	1	Q9HRJ7|Q9HRJ7	ABC transporter, ATP-binding protein homolog
301	1	Q9HMK3|SYFB	Phenylalanyl-tRNA synthetase beta chain
308	1	Q9HP12|Q9HP12	Putative uncharacterized protein
314	1	Q9HN02|Q9HN02	Hemolysin protein
316	1	Q9HSC1|TRPC	Indole-3-glycerol phosphate synthase
317	1	Q9HMK5|Q9HMK5	Putative uncharacterized protein

hit	peptides	accession	description
318	1	O51963|O51963	Putative uncharacterized protein
319	1	Q9HRN6|Q9HRN6	Htr16 transducer
320	1	Q9HQT0|Q9HQT0	Putative uncharacterized protein
322	1	Q9HMG3|Q9HMG3	Putative uncharacterized protein
323	1	Q9HMB7|Q9HMB7	Probable carboxypeptidase
335	1	Q9HPQ2|Q9HPQ2	Daunorubicin resistance ABC transporter ATP-binding protein
339	1	Q9HHQ6|Q9HHQ6	Sn-glycerol-3-phosphate transport system permease
343	1	Q9HQI9|ENO	Enolase
350	1	Q9HR72|Q9HR72	Molybdopterin oxidoreductase
353	1	Q9HNE5|Q9HNE5	Geranylgeranyl-diphosphate geranylgeranyltransferase
355	1	Q9HMC6|Q9HMC6	Hydroxymethylpyrimidine phosphate kinase
357	1	Q9HRF8|Q9HRF8	Putative uncharacterized protein araL
360	1	Q9HQS6|Q9HQS6	Putative uncharacterized protein
362	1	P13077|FLAB2	Flagellin B2
364	1	Q9HM89|EF1A	Elongation factor 1-alpha
365	1	Q9HSG1|Q9HSG1	Putative uncharacterized protein
367	1	Q9HHR9|Q9HHR9	Sodium-dependent transporter
370	1	O52039|O52039	Putative uncharacterized protein
371	1	Q9HP02|Q9HP02	Spermidine/putrescine ABC transporter permease
372	1	Q9HMP2|Q9HMP2	Aminopeptidase homolog
373	1	P50562|RL18	50S ribosomal protein L18P
378	1	Q9HP11|Q9HP11	Translation initiation factor eIF-2B subunit alpha
384	1	Q9HRE2|Q9HRE2	Putative uncharacterized protein
387	1	Q9HR91|Q9HR91	Succinate-semialdehyde dehydrogenase
390	1	Q9HSA2|Q9HSA2	Zinc metalloproteinase homolog
394	1	Q9HRL5|Q9HRL5	Putative uncharacterized protein
401	1	P13078|FLAB3	Flagellin B3
404	1	Q9HRD4|Q9HRD4	Protein kinase
411	1	Q9HRV6|Q9HRV6	Putative uncharacterized protein
423	1	Q9HMK2|PYRD	Dihydroorotate dehydrogenase
424	1	Q9HQP8|Q9HQP8	Rhamnosyl transferase
426	1	Q9HMH9|PYRC	Dihydroorotase
427	1	Q9HPR3|Q9HPR3	Putative uncharacterized protein
428	1	Q9HR79|Q9HR79	Type II secretion system protein
432	1	Q9HR30|Q9HR30	DNA gyrase subunit B
433	1	Q9HRF4|Q9HRF4	Putative uncharacterized protein
436	1	Q9HNA5|Q9HNA5	MCM / cell division control protein 21
439	1	Q9HHY0|Q9HHY0	Cationic amino acid transporter
442	1	Q9HHR8|Q9HHR8	ABC transporter, permease protein
446	1	Q9HMR2|Q9HMR2	Glycolate oxidase subunit

hit	peptides	accession	description
455	1	Q9HMB8|Q9HMB8	Putative uncharacterized protein
459	1	Q9HNB5|Q9HNB5	Alcohol dehydrogenase
461	1	Q9HN35|Q9HN35	Mismatch repair protein
462	1	Q9HNT1|ATGT	7-cyano-7-deazaguanine tRNA-ribosyltransferase
465	1	Q9HQB9|Q9HQB9	Sensor protein
468	1	Q9HS08|Q9HS08	Nodulation protein
474	1	Q9HPD1|RL2	50S ribosomal protein L2P
480	1	Q9HSI4|Q9HSI4	Putative uncharacterized protein
490	1	Q9HQZ1|Q9HQZ1	GufA protein
494	1	Q9HQ12|Q9HQ12	Extragenic suppressor homolog
497	1	Q9HHQ7|Q9HHQ7	Sn-glycerol-3-phosphate transport system permease
500	1	Q9HRK1|Q9HRK1	Cytochrome c oxidase subunit III
506	1	Q9HRA7|Q9HRA7	CDP-diacylglycerol-serine O-phosphatidyltransferase
512	1	Q9HNH3|Q9HNH3	Potassium channel homolog
517	1	Q9HS50|Q9HS50	Putative uncharacterized protein
522	1	Q9HP58|Q9HP58	Putative uncharacterized protein
524	1	Q9HMZ0|Q9HMZ0	Putative uncharacterized protein
525	1	Q9HQV1|Q9HQV1	Putative uncharacterized protein
526	1	Q9HS82|Q9HS82	Putative uncharacterized protein
528	1	Q9HN50|SAHH	Adenosylhomocysteinase
530	1	Q9HQQ6|Q9HQQ6	Glycosyl transferase-like
533	1	Q9HN47|PRIL	Probable DNA primase large subunit
537	1	Q9HRJ0|Q9HRJ0	Putative uncharacterized protein
541	1	Q9HPS5|Q9HPS5	Putative uncharacterized protein
545	1	Q9HPN1|Q9HPN1	Cobalamin biosynthesis
546	1	O51994|O51994	Putative uncharacterized protein
551	1	Q9HQ85|Q9HQ85	Putative uncharacterized protein
553	1	Q9HNS4|Q9HNS4	Glycerol-3-phosphate dehydrogenase chain A
556	1	Q9HPP8|Q9HPP8	Biotin carboxylase
560	1	Q9HMZ4|Y2317	Putative ABC transporter ATP-binding protein VNG2317G
563	1	Q9HMW3|Q9HMW	Oligopeptide ABC permease
565	1	Q9HRC1|Q9HRC1	Putative uncharacterized protein
566	1	Q9HQW6|CHEB	Chemotaxis response regulator protein-glutamate methylesterase
584	1	Q9HSV2|Q9HSV2	LPS biosynthesis protein
586	1	Q9HP54|Q9HP54	Putative uncharacterized protein
589	1	Q9HRL0|Q9HRL0	Putative uncharacterized protein
593	1	Q9HPA3|Q9HPA3	Putative uncharacterized protein
594	1	Q9HQX0|Q9HQX0	Chemotaxis protein
597	1	Q9HRZ2|Q9HRZ2	Probable oxidoreductase
598	1	Q9HMH3|Q9HMH3	Putative uncharacterized protein

hit	peptides	accession	description
599	1	Q9HHG1|Q9HHG1	Vng6416h
606	1	P08959|GVPA2	Gas vesicle structural protein 2
616	1	Q9HSG4|Q9HSG4	Putative uncharacterized protein
617	1	Q9HNV3|Q9HNV3	NADH dehydrogenase/oxidoreductase-like protein
618	1	Q9HSG2|Q9HSG2	Putative uncharacterized protein
619	1	O54654|O54654	Putative uncharacterized protein
620	1	Q9HSW4|Q9HSW4	Glucose-1-phosphate thymidylyltransferase
623	1	Q9HSR9|Q9HSR9	Type I restriction modification enzyme, M subunit
632	1	Q9HPZ7|Q9HPZ7	Putative uncharacterized protein
633	1	Q9HRJ5|Q9HRJ5	Putative uncharacterized protein
635	1	Q9HN45|PCNA	DNA polymerase sliding clamp
640	1	P15756|RS12	30S ribosomal protein S12P
642	1	Q9HSR5|Q9HSR5	Putative uncharacterized protein
647	1	Q9HSQ2|HTPX	Probable protease htpX homolog
655	1	Q9HQE5|Q9HQE5	Putative uncharacterized protein
660	1	Q9HPQ7|Q9HPQ7	Putative uncharacterized protein
664	1	Q9HSK1|Q9HSK1	Putative uncharacterized protein
665	1	Q9HHX5|Q9HHX5	Cationic amino acid transporter
669	1	Q9HMT1|Q9HMT1	Putative uncharacterized protein
677	1	Q9HQH4|Q9HQH4	Putative uncharacterized protein
679	1	Q9HSW8|Q9HSW8	Putative uncharacterized protein
683	1	Q9HN66|SYW2	Tryptophanyl-tRNA synthetase 2
689	1	Q9HR96|Q9HR96	Putative uncharacterized protein
707	1	Q9HPT8|Q9HPT8	Putative uncharacterized protein
712	1	Q9HQ62|Q9HQ62	3-methyladenine DNA glycosylase
719	1	Q9HR47|Q9HR47	Asparagine synthetase
720	1	Q9HSE6|Q9HSE6	Putative uncharacterized protein
730	1	Q9HNG1|Y2119	UPF0290 protein VNG2119C
731	1	Q9HS84|Q9HS84	Putative uncharacterized protein
742	1	Q9HMQ2|ASSY	Argininosuccinate synthase
745	1	Q9HQ19|Q9HQ19	Iron
748	1	Q9HNW9|Q9HNW9	Putative uncharacterized protein
750	1	Q9HS91|Q9HS91	Putative uncharacterized protein
752	1	P57697|PSMA	Proteasome subunit alpha
753	1	Q9HPR9|Q9HPR9	Putative uncharacterized protein
754	1	Q9HQF7|Q9HQF7	Heme biosynthesis protein
762	1	Q9HRL6|Q9HRL6	Putative uncharacterized protein
769	1	Q9HNX6|Y1901	UPF0343 protein VNG1901C
773	1	Q9HPR7|Q9HPR7	Putative uncharacterized protein
774	1	Q9HSQ5|Q9HSQ5	Putative uncharacterized protein

hit	**peptides**	**accession**	**description**
776	1	Q9HS66|TRPE2	Anthranilate synthase component 1 2
778	1	Q9HHV9|Q9HHV9	Vng6204h
795	1	Q9HQP0|Q9HQP0	Glycerol-3-phosphate dehydrogenase chain A
805	1	Q9HQJ4|RPOD	DNA-directed RNA polymerase subunit D
811	1	Q9HS73|Q9HS73	Transcription termination-antitermination factor
814	1	Q9HMC5|Q9HMC5	Putative uncharacterized protein
817	1	Q9HME6|Q9HME6	Putative uncharacterized protein
818	1	Q9HSV1|Q9HSV1	UDP-glucose 4-epimerase
820	1	Q9HSF8|PCRB	Protein pcrB homolog
824	1	Q9HQF5|Q9HQF5	Coenzyme PQQ synthesis protein
828	1	Q9HPN5|Q9HPN5	Putative uncharacterized protein
831	1	Q9HQT2|Q9HQT2	Putative uncharacterized protein
832	1	Q9HSZ9|Q9HSZ9	Glucose-1-phosphate thymidylyltransferase
834	1	Q9HP41|Q9HP41	Transcription regulator
837	1	Q9HNX1|Q9HNX1	Putative uncharacterized protein
846	1	Q9HRM1|Q9HRM1	NADH dehydrogenase/oxidoreductase-like protein
876	1	Q9HQ46|PHR	Deoxyribodipyrimidine photo-lyase
879	1	Q9HT00|GLMS	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
885	1	Q9HMH2|Y2543	Protein VNG2543C
886	1	Q9HNK7|Q9HNK7	ATP-binding protein
894	1	Q9HR70|Q9HR70	Putative uncharacterized protein
906	1	Q9HNH8|Q9HNH8	Putative uncharacterized protein
919	1	Q9HHU8|Q9HHU8	TRK potassium uptake system protein
924	1	O54605|O54605	Putative uncharacterized protein
953	1	Q9HQS8|Q9HQS8	Putative uncharacterized protein
954	1	Q9HHK7|Q9HHK7	Vng6348h
958	1	Q9HN71|Q9HN71	Ornithine cyclodeaminase
959	1	Q9HHL5|Q9HHL5	Spo0A activation inhibitor
965	1	Q9HPH2|Q9HPH2	Putative uncharacterized protein
977	1	Q9HQY9|Q9HQY9	Putative uncharacterized protein
978	1	Q9HHF3|Q9HHF3	Vng6431h
985	1	Q9HNH1|Q9HNH1	Succinate dehydrogenase subunit
986	1	P33963|GVPK2	Protein gvpK 2
1009	1	Q9HHZ7|Q9HHZ7	Spo0A activation inhibitor
1010	1	Q9HSV9|Q9HSV9	Putative uncharacterized protein
1024	1	Q9HSB5|Q9HSB5	Putative uncharacterized protein
1027	1	Q9HSG7|Q9HSG7	Putative uncharacterized protein
1040	1	Q9HSA9|Q9HSA9	Putative uncharacterized protein
1041	1	Q9HPH8|Q9HPH8	Putative uncharacterized protein
1060	1	Q9HMD5|Q9HMD5	Putative uncharacterized protein

hit	peptides	accession	description
1062	1	Q9HR40|Q9HR40	Putative uncharacterized protein
1070	1	Q9HQR3|Q9HQR3	Putative uncharacterized protein
1076	1	O54608|Y3061	UPF0033 protein VNG5061C/VNG5236C/VNG6059C/VNG6467C
1085	1	Q9HS14|Q9HS14	Transcriptional regulator
1090	1	Q9HML3|Q9HML3	Putative uncharacterized protein
1094	1	Q9HMI5|Q9HMI5	Putative uncharacterized protein
1096	1	Q9HPB8|RL6	50S ribosomal protein L6P
1100	1	Q9HR94|Q9HR94	Putative uncharacterized protein
1105	1	Q9HPD8|Q9HPD8	Phytoene dehydrogenase
1107	1	Q9HMF0|Q9HMF0	Pab N-terminal acetyltransferase
1109	1	Q9HMI7|Q9HMI7	Putative uncharacterized protein
1113	1	Q9HMJ1|Q9HMJ1	Putative uncharacterized protein
1120	1	P15008|RL22	50S ribosomal protein L22P
1128	1	Q9HRY0|GRPE	Protein grpE
1149	1	Q9HHN6|Q9HHN6	Vng6306c
1153	1	Q9HS42|Q9HS42	Adenylosuccinate lyase
1154	1	Q9HRU9|Q9HRU9	Putative uncharacterized protein
1159	1	O54646|O54646	Putative uncharacterized protein
1163	1	Q9HMJ9|Q9HMJ9	Putative uncharacterized protein
1167	1	P15763|RS7	30S ribosomal protein S7P
1170	1	Q9HRZ7|Q9HRZ7	Putative uncharacterized protein
1191	1	P13044|GVPE1	Protein gvpE 1
1193	1	O52020|O52020	Putative uncharacterized protein
1204	1	Q9HPT5|Q9HPT5	Putative uncharacterized protein
1210	1	Q9HHL1|Q9HHL1	Vng6343h
1216	1	Q9HRK5|Q9HRK5	Putative uncharacterized protein
1225	1	Q9HQC2|AROC	Chorismate synthase
1227	1	Q9HN85|Q9HN85	Phosphomannomutase
1233	1	Q9HQ04|Q9HQ04	Putative uncharacterized protein
1246	1	Q9HPE9|RS8E	30S ribosomal protein S8e
1254	1	Q9HQV5|Q9HQV5	Putative uncharacterized protein
1256	1	Q9HQK8|Q9HQK8	Glyoxalase
1264	1	Q9HR06|Q9HR06	Spermidine/putrescine ABC transporter ATP-binding
1267	1	Q9HMD3|Q9HMD3	Putative uncharacterized protein
1280	1	Q9HQ35|Q9HQ35	Putative uncharacterized protein
1294	1	Q9HQC3|Q9HQC3	Putative uncharacterized protein
1298	1	Q9HN39|Q9HN39	Putative uncharacterized protein
1345	1	O52038|O52038	Putative uncharacterized protein
1363	1	Q9HN99|Q9HN99	Putative uncharacterized protein
1384	1	Q9HRS3|Q9HRS3	Putative uncharacterized protein

hit	peptides	accession	description
1402	1	Q9HHH6|Q9HHH6	Vng6393h
1419	1	Q9HQV0|Q9HQV0	Putative uncharacterized protein
1425	1	Q9HSN8|Q9HSN8	Putative uncharacterized protein
1466	1	Q9HPI3|Q9HPI3	Cytochrome aa3 controlling protein
1490	1	Q9HPQ9|KITH	Thymidine kinase
1548	1	Q9HHS4|Q9HHS4	Vng6254c
1588	1	Q9HSE3|Q9HSE3	Putative uncharacterized protein
1633	1	Q9HNR9|Q9HNR9	Putative uncharacterized protein
1647	1	Q9HHL8|Q9HHL8	Vng6332h
1665	1	Q9V2W4|RS13	30S ribosomal protein S13P
1668	1	Q9HHG7|Q9HHG7	Vng6407h
1677	1	Q9HM72|Q9HM72	Putative uncharacterized protein
1680	1	Q9HPG0|Q9HPG0	Putative uncharacterized protein
1707	1	Q9HR95|Q9HR95	Putative uncharacterized protein

END OF LIST II

hit	**peptides**	**accession**	**description**
III. Corynebacterium glutamicum membranes; elatsase digest; nLC-MALDI MS/MS; no search specificity			
1	166	P00772|ELA1	Elastase-1 - Sus scrofa (Pig).
2	72	Cg0446	(sdhA) [C]: succinate dehydrogenase A (EC 1.3.99.1)
3	61	Cg1537	(ptsG) [M]: GLUCOSE-SPECIFIC ENZYME II BC COMPONENT OF PTS (EC 2.7.1.69)
5	47	Cg2409	(ctaC) [M]: CYTOCHROME C OXIDASE CHAIN II (EC 1.9.3.1)
4	46	Cg2705	(amyE) [S]: MALTOSE-BINDING PROTEIN PRECURSOR
6	46	Cg0587	(tuf) [C]: ELONGATION FACTOR TU
7	26	Cg3138	[M]: Membrane protease subunit, stomatin/prohibitin homolog
8	22	Cg2911	[S]: ABC-type Mn/Zn transport system, secreted Mn/Zn-binding (lipo)protein (surface adhesin)
9	22	Cg3009	[C]: hypothetical protein predicted by Glimmer/Critica
10	22	Cg0447	(sdhB) [C]: succinate dehydrogenase B
12	21	Cg2780	(ctaD) [M]: PROBABLE CYTOCHROME C OXIDASE POLYPEPTIDE SUBUNIT (EC 1.9.3.1)
15	19	Cg2403	(qcrB) [M]: CYTOCHROME B, MEMBRANE PROTEIN (EC 1.10.2.2)
13	18	Cg1656	(ndh) [MS]: NADH DEHYDROGENASE (EC 1.6.99.3)
11	17	Cg0583	(fusA) [C]: ELONGATION FACTOR G
16	17	Cg2843	(pstB) [C]: ABC-type phosphate transport system, ATPase component
17	17	Cg2404	(qcrA1) [M]: RIESKE IRON-SULFUR PROTEIN
14	14	Cg0957	(fas-IB) [C]: FATTY ACID SYNTHASE (EC 2.3.1.85, 2.3.1.38, 2.3.1.39, 2.3.1.41, 1.1.1.100, 4.2.1.60, 4.2.1.61, 1.3.1.10, 3.1.2.14))
18	13	Cg2708	(msiK1) [C]: ABC-type sugar transport system, ATPase component
19	12	Cg1787	(ppc) [C]: PHOSPHOENOLPYRUVATE CARBOXYLASE (EC 4.1.1.31)
21	12	Cg0791	(pyc) [C]: PYRUVATE CARBOXYLASE (EC 6.4.1.1)
22	12	Cg2875	[C]: hypothetical protein predicted by Glimmer
20	11	Cg1368	(atpD) [C]: ATP SYNTHASE ALPHA SUBUNIT (EC 3.6.1.34)
27	11	Cg0445	(sdhCD) [M]: succinate dehydrogenase CD
23	10	Cg2181	[S]: ABC-type peptide transport system, secreted component
28	10	Cg0924	[S]: ABC-type cobalamin/Fe3+-siderophores transport sys
29	10	Cg2196	[M]: putative secreted or membrane protein
26	9	Cg3186	(cmt2) [S]: Trehalose corynomycolyl transferase (EC 2.3.1.122)
31	9	Cg1437	(ilvC) [C]: KETOL-ACID REDUCTOISOMERASE (EC 1.1.1.86)
33	9	Cg0756	(cstA) [M]: PUTATIVE CARBON STARVATION PROTEIN A
37	9	Cg1790	(pgk) [C]: PHOSPHOGLYCERATE KINASE (EC 2.7.2.3)
38	9	Cg1366	(atpA) [C]: PROBABLE ATP SYNTHASE ALPHA CHAIN PROTEIN (EC 3.6.1.34)
40	9	Cg2958	(butA) [C]: L-2,3-butanediol dehydrogenase/acetoin reductase (EC 1.1.1.5)
32	8	Cg3227	(lldA) [C]: PUTATIVE L-LACTATE DEHYDROGENASE (EC 1.1.2.3)
42	8	Cg1429	[M]: putative membrane protein
45	8	Cg2211	[M]: putative membrane protein
50	8	Cg1685	(tatX) [M]: Sec-independent protein secretion pathway component
51	8	Cg2444	[C]: hypothetical protein predicted by Glimmer/Critica

hit	peptides	accession	description
24	7	Cg1081	[C]: ABC-type multidrug transport system, ATPase component
25	7	Cg1111	(eno) [C]: ENOLASE (EC 4.2.1.11)
30	7	Cg2405	(qcrC) [M]: CYTOCHROME C1
34	7	Cg0766	(icd) [C]: ISOCITRATE DEHYDROGENASE (EC 1.1.1.42)
36	7	Cg1290	(metE) [C]: Homocysteine methyltransferase (EC 2.1.1.14)
54	7	Cg1880	(thrS) [C]: THREONYL-TRNA SYNTHETASE (EC 6.1.1.3)
39	6	Cg2523	(malQ) [C]: 4-ALPHA-GLUCANOTRANSFERASE (EC 2.4.1.25)
41	6	Cg2499	(glyS) [C]: GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (EC 6.1.1.14)
43	6	Cg1791	(gap) [C]: GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
44	6	Cg1001	(mscL) [M]: LARGE CONDUCTANCE MECHANOSENSITIVE CHANNEL
46	6	Cg1737	(acn) [C]: ACONITASE (EC 4.2.1.3)
47	6	Cg0953	[M]: Na+/proline, Na+/panthothenate symporter or related permease
53	6	Cg3079	(clpB) [C]: PROBABLE ATP-DEPENDENT PROTEASE (HEAT SHOCK PROTEIN) (EC 3.-.-.-)
55	6	Cg0647	(secY) [M]: preprotein translocase subunit SecY
56	6	Cg2291	(pyk) [C]: PYRUVATE KINASE (EC 2.7.1.40)
57	6	Cg2840	(actA) [C]: BUTYRYL-COA:ACETATE COENZYME A TRANSFERASE (EC 2.8.3.8)
58	6	Cg1169	[M]: Na+-dependent transporters of the SNF family
62	6	Cg3365	(rmpC) [M]: putative ribitol transport membrane protein
73	6	Cg2558	[C]: related to aldose 1-epimerase
49	5	Cg0737	[S]: ABC-type transport system, secreted lipoprotein component
59	5	Cg2845	(pstC) [M]: ABC-type phosphate transport system, permease component
60	5	Cg2949	[S]: putative secreted protein
61	5	Cg1586	(argG) [C]: ARGININOSUCCINATE SYNTHASE (EC 6.3.4.5)
65	5	Cg1556	[C]: conserved hypothetical protein
70	5	Cg0935	[C]: conserved hypothetical protein
76	5	Cg1363	(atpE) [M]: ATP SYNTHASE C CHAIN (EC 3.6.1.34)
94	5	Cg3008	(porA) [M]: PORIN
99	5	Cg1121	[M]: Permease of the major facilitator superfamily
120	5	Cg2703	[M]: Sugar permease
35	4	Cg2743	(fas-IA) [C]: FATTY ACID SYNTHASE (EC 2.3.1.85, 2.3.1.38, 2.3.1.39, 2.3.1.41, 1.1.1.100, 4.2.1.60, 4.2.1.61, 1.3.1.10, 3.1.2.14)
48	4	Cg0576	(rpoB) [C]: DNA-DIRECTED RNA POLYMERASE BETA CHAIN (EC 2.7.7.6)
52	4	Cg0545	(pitA) [M]: PUTATIVE LOW-AFFINITY PHOSPHATE TRANSPORT PROTEIN
64	4	Cg1579	[S]: putative secreted protein
66	4	Cg2137	(gluB) [S]: GLUTAMATE SECRETED BINDING PROTEIN
67	4	Cg2410	(ltsA) [C]: glutamine-dependent amidotransferase involved in formation of cell wall and L-glutamate biosynthesis (EC 6.3.5.4)
68	4	Cg2195	[M]: putative secreted or membrane protein
74	4	Cg2799	(pknE) [S]: putative secreted protein
75	4	Cg2704	[M]: ABC-type sugar transport system, permease component
78	4	Cg2192	(mqo) [C]: MALATE:QUINONE OXIDOREDUCTASE OXIDOREDUCTASE (EC 1.1.99.16)
79	4	Cg2695	[C]: ABC-type transport system, ATPase component

hit	peptides	accession	description
80	4	Cg3149	[C]: Aminotransferases class-I
81	4	Cg0834	[S]: Bacterial extracellular solute-binding protein, fa
83	4	Cg2963	(clpC) [C]: PROBABLE ATP-DEPENDENT PROTEASE (HEAT SHOCK PROTEIN) (EC 3.-.-.-)
85	4	Cg1203	[C]: Mg-chelatase subunit ChlI
89	4	Cg2157	(terC) [M]: TELLURIUM RESISTANCE MEMBRANE PROTEIN
92	4	Cg1362	(atpB) [M]: ATP SYNTHASE F0 SUBUNIT 6 (EC 3.6.1.34)
98	4	Cg2466	(aceE) [C]: PYRUVATE DEHYDROGENASE E1 COMPONENT (EC 1.2.4.1)
104	4	Cg3219	(ldh) [C]: L-LACTATE DEHYDROGENASE (EC 1.1.1.27)
117	4	Cg2096	[M]: putative membrane protein
240	4	Cg0952	[M]: PUTATIVE INTEGRAL MEMBRANE PROTEIN
63	3	Cg2120	(ptsF) [M]: SUGAR SPECIFIC PTS SYSTEM, FRUCTOSE/MANNITOL-SPECIFIC TRANSPORT PROTEIN (EC 2.7.1.69)
72	3	Cg0703	(guaA) [C]: PUTATIVE GMP SYNTHASE (EC 6.3.5.2)
77	3	Cg2900	(ddh) [C]: MESO-DIAMINOPIMELATE DEHYDROGENASE (EC 1.4.1.16)
84	3	Cg0414	(wzz) [M]: cell surface polysaccharide biosynthesis / Chain length determinant protein
86	3	Cg1813	(carB) [C]: PUTATIVE CARBAMOYL-PHOSPHATE SYNTHASE SUBUNIT (EC 6.3.5.5)
91	3	Cg0896	[M]: membrane protein
95	3	Cg1525	(polA) [C]: DNA POLYMERASE I (EC 2.7.7.7)
96	3	Cg0610	(rplE) [C]: 50S RIBOSOMAL PROTEIN L5
100	3	Cg0238	[C]: L-GULONOLACTONE OXIDASE (EC 1.1.3.8)
102	3	Cg2166	(gpsI) [C]: PUTATIVE POLYRIBONUCLEOTIDE PHOSPHORYLASE / GUANOSINE PENTAPHOSPHATESYNTHETASE (EC 2.7.7.8)
113	3	Cg3195	[C]: Flavin-containing monooxygenase (FMO)
118	3	Cg1643	(gnd) [C]: 6-PHOSPHOGLUCONATE DEHYDROGENASE (EC 1.1.1.44)
124	3	Cg1238	[M]: putative membrane protein
127	3	Cg2406	(ctaE) [M]: CYTOCHROME C OXIDASE SUBUNIT 3 (EC 1.9.3.1)
151	3	Cg0472	[C]: conserved hypothetical protein
157	3	Cg0007	(gyrB) [C]: DNA GYRASE SUBUNIT B (EC 5.99.1.3)
220	3	Cg2613	(mdh) [C]: MALATE DEHYDROGENASE OXIDOREDUCTASE PROTEIN (EC 1.1.1.37)
239	3	Cg1227	[M]: putative membrane protein
303	3	Cg4005	[S]: putative secreted protein
311	3	Cg1911	[S]: putative secreted protein
353	3	Cg1164	(lytB) [C]: Penicillin tolerance protein
475	3	Cg2325	[C]: hypothetical protein predicted by Glimmer/Critica
69	2	Cg0577	(rpoC) [C]: DNA-DIRECTED RNA POLYMERASE BETA~ CHAIN (EC 2.7.7.6)
71	2	Cg1280	(odhA) [C]: 2-OXOGLUTARATE DEHYDROGENASE (EC 1.2.4.2)
82	2	Cg1451	(serA) [C]: Phosphoglycerate Dehydrogenase (EC 1.1.1.95)
88	2	Cg1603	[MS]: CONSERVED MEMBRANE PROTEIN
105	2	Cg2496	[S]: putative secreted protein
108	2	Cg1463	(gltS) [C]: PUTATIVE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17)
110	2	Cg2492	(glmS) [C]: PROBABLE GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (EC 2.6.1.16)
114	2	Cg0047	[M]: conserved hypothetical protein

hit	peptides	accession	description
115	2	Cg0303	(leuA) [C]: 2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12)
116	2	Cg0654	(rpsD) [C]: RIBOSOMAL PROTEIN S4
121	2	Cg3100	(dnaK) [C]: Heat shock protein hsp70
122	2	Cg2333	(treZ) [C]: MALTO-OLIGOSYLTREHALOSE TREHALOHYDROLASE (EC 3.2.1.141)
123	2	Cg3154	(udgA2) [C]: UDP-GLUCOSE 6-DEHYDROGENASE (EC 1.1.1.22)
134	2	Cg1725	(mcmB) [C]: METHYLMALONYL-COA MUTASE LARGE SUBUNIT (EC 5.4.99.2)
137	2	Cg2678	[S]: ABC-type dipeptide/oligopeptide/nickel transport systems, secreted component
138	2	Cg1364	(atpF) [MS]: ATP synthase B chain (EC 3.6.1.34)
153	2	Cg0683	[M]: permease
155	2	Cg2571	(lepA) [C]: Membrane GTPase LepA
156	2	Cg3237	(sod) [C]: MANGANESE SUPEROXIDE DISMUTASE (EC 1.15.1.1)
164	2	Cg1133	(glyA) [C]: Serine Hydroxymethyltransferase (EC 2.1.2.1)
181	2	Cg2925	(ptsS) [M]: ENZYME II SUCROSE PROTEIN (EC 2.7.1.69)
193	2	Cg0326	(nuoL) [M]: NADH-QUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3)
196	2	Cg1836	[S]: secreted solute-binding protein, aminodeoxychorismate lyase-like
218	2	Cg2470	[S]: SECRETED ABC TRANSPORTER SUBSTRATE-BINDING PROTEIN
228	2	Cg3244	[C]: conserved hypothetical protein
232	2	Cg2437	(thrC) [C]: THREONINE SYNTHASE (EC 4.2.99.2)
236	2	Cg1365	(atpH) [C]: H+-ATPASE DELTA SUBUNIT
243	2	Cg0559	(ispB) [C]: PUTATIVE OCTAPRENYL-DIPHOSPHATE SYNTHASE PROTEIN ((EC 2.5.1.)
244	2	Cg3323	[C]: Myo-inositol-1-phosphate synthase
246	2	Cg1229	[M]: ABC-type cobalt transport system, permease component CbiQ
269	2	Cg2846	(pstS) [S]: ABC-type phosphate transport system, secreted component
278	2	Cg0508	[S]: iron/thiamine transport system, secreted component
284	2	Cg0153	(hde) [C]: PROBABLE ESTERASE/LIPASE PROTEIN (EC 3.1.1.-)
349	2	Cg1829	(aroC) [C]: PUTATIVE CHORISMATE SYNTHASE (EC 4.6.1.4)
351	2	Cg0040	[S]: PUTATIVE SECRETED PROTEIN
357	2	Cg0451	[M]: PUTATIVE MEMBRANE PROTEIN
360	2	Cg1128	[MS]: similar to ribosomal protein S2
372	2	Cg1005	(moeA2) [C]: MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN
416	2	Cg2052	[S]: putative secreted protein
441	2	Cg0936	(rpf1) [S]: RPF PROTEIN PRECURSOR
570	2	Cg1665	[S]: putative secreted protein
674	2	Cg3343	[M]: putative secreted membrane protein
756	2	Cg1874	[M]: putative membrane protein
857	2	Cg3257	[C]: conserved hypothetical protein
977	2	Cg1904	[M]: putative membrane protein
90	1	Cg2984	(ftsH) [M]: CELL-DIVISION PROTEIN (ATP-DEPENDENT ZN METALLOPEPTIDASE) (EC 3.4.24.)
103	1	Cg1314	(putP) [M]: PROLINE TRANSPORT SYSTEM
107	1	Cg0656	(rplQ) [C]: 50S RIBOSOMAL PROTEIN L17

hit	**peptides**	**accession**	**description**
109	1	Cg0835	(msiK2) [C]: ABC-type sugar transport systems, ATPase component
119	1	Cg0235	(embC) [M]: Probable arabinosyltransferase, membrane protein
125	1	Cg0161	[M]: putative secreted or membrane protein
143	1	Cg2586	(proA) [C]: GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (EC 1.2.1.41)
144	1	Cg2292	(lgt) [M]: PUTATIVE PROLIPOPROTEIN DIACYLGLYCEROL TRANSFERASE (EC 2.4.99.)
148	1	Cg3182	(cop1) [S]: Trehalose corynomycolyl transferase (EC 2.3.1.122)
149	1	Cg2811	[M]: ABC-type transport system, involved in lipoprotein release, permease component
150	1	Cg0658	[M]: putative membrane protein
161	1	Cg1234	[C]: putative excinuclease ATPase subunit - UvrA-like protein
165	1	Cg0062	(ppp) [M]: PROTEIN PHOSPHATASE (EC 3.1.3.16)
168	1	Cg2833	(cysK) [C]: O-Acetylserine (Thiol)-Lyase (EC 4.2.99.8)
173	1	Cg2262	(ftsY) [S]: Signal recognition particle GTPase
175	1	Cg3018	[C]: hypothetical protein predicted by Glimmer/Critica
176	1	Cg3191	[C]: Predicted glycosyltransferase
182	1	Cg1082	[M]: putative membrane protein
186	1	Cg3220	[M]: putative membrane protein
189	1	Cg0336	(ponA) [S]: PENICILLIN-BINDING PROTEIN 1B (EC 2.4.2.-)
199	1	Cg1861	(rel) [C]: PPGPP SYNTHETASE, PPGPP PYROPHOSPHORYLASE (EC 2.7.6.5, 3.1.7.2)
200	1	Cg1841	(aspS) [C]: PROBABLE ASPARTYL-TRNA SYNTHETASE PROTEIN (EC 6.1.1.12)
202	1	Cg0854	(pmmA) [C]: PHOSPHOMANNOMUTASE (EC 5.4.2.8)
203	1	Cg0410	[C]: PUTATIVE PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
204	1	Cg1195	[M]: Sulfate permease or related transporter (MFS superfamily)
207	1	Cg2657	[MS]: putative membrane protein - fragment
212	1	Cg1345	(narK) [M]: PUTATIVE NITRATE/NITRITE TRANSPORTER
215	1	Cg0783	[C]: conserved hypothetical protein
223	1	Cg1502	[C]: ABC-type polar amino acid transport system, ATPase component
224	1	Cg3161	[M]: putative membrane protein
227	1	Cg0602	(rplP) [C]: 50S RIBOSOMAL PROTEIN L16
229	1	Cg0523	[M]: membrane protein required for cytochrome c biosynthesis
235	1	Cg3429	[M]: Preprotein translocase subunit YidC
237	1	Cg2800	(pgm) [C]: PHOSPHOGLUCOMUTASE (EC 5.4.2.2)
238	1	Cg2176	(infB) [C]: Translation initiation factor 2 (GTPase)
247	1	Cg1435	(ilvB) [C]: ACETOLACTATE SYNTHASE (EC 4.1.3.18)
249	1	Cg0928	[C]: ABC-type cobalamin/Fe3+-siderophores transport system, ATPase component
251	1	Cg1456	[C]: Predicted signal-transduction protein containing cAMP-binding and CBS domain
252	1	Cg2527	(dcp) [C]: PROBABLE PEPTIDYL-DIPEPTIDASE A PROTEIN (EC 3.4.15.1)
260	1	Cg2675	[C]: ATPase component of ABC-type transport system, contains duplicated ATPase domains
263	1	Cg3011	(groEL) [C]: Chaperonin cpn60 (60Kd subunit)
264	1	Cg2092	(sigA) [S]: RNA POLYMERASE SIGMA 70 FACTOR
270	1	Cg1562	[M]: putative membrane protein

hit	peptides	accession	description
273	1	Cg3405	[C]: NADPH quinone reductase or Zn-dependent oxidoreductase
275	1	Cg2372	(mraY) [M]: PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.13)
280	1	Cg2261	(amtB) [M]: LOW AFFINITY AMMONIUM UPTAKE PROTEIN
283	1	Cg2151	[C]: Similar to phage shock protein A
287	1	Cg3189	[M]: 4-hydroxybenzoate polyprenyltransferase or related prenyltransferase
291	1	Cg0249	[M]: polysaccharide/polyol phosphate export systems, permease component
292	1	Cg3255	(uspA3) [C]: UNIVERSAL STRESS PROTEIN FAMILY
295	1	Cg0915	(ftsX) [M]: PUTATIVE CELL DIVISION PROTEIN
310	1	Cg2968	[C]: conserved hypothetical protein
314	1	Cg1794	[C]: Uncharacterised P-loop ATPase protein
321	1	Cg0250	[C]: AMINOTRANSFERASE
323	1	Cg1582	(argB) [C]: ACETYLGLUTAMATE KINASE (EC 2.7.2.8)
326	1	Cg0949	(gltA) [C]: CITRATE SYNTHASE (EC 4.1.3.7)
328	1	Cg0134	[C]: HYDROLASE, AMA/HIPO/HYUC FAMILY
335	1	Cg0327	[M]: membrane protein
343	1	Cg1109	(porB) [S]: Anion-specific porin precursor
344	1	Cg0464	(ctpA) [M]: COPPER-TRANSPORTING ATPASE (EC 3.6.1.36)
348	1	Cg2361	[C]: Cell division initiation protein - Antigen 84 homolog
350	1	Cg1268	(glgA) [C]: GLYCOSYL TRANSFERASE
359	1	Cg2300	(hisH) [C]: IMIDAZOLEGLYCEROL-PHOSPHATE SYNTHASE, AMIDOTRANSFERASE (EC 2.4.2.)
366	1	Cg1629	(secA2) [C]: Similar to preprotein translocase subunit SecA
370	1	Cg1594	(tyrS) [C]: TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1)
376	1	Cg1333	(argS) [C]: ARGINYL-TRNA SYNTHETASE (EC 6.1.1.19)
388	1	Cg1855	(hisS) [C]: HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21)
392	1	Cg0528	[S]: putative secreted protein
399	1	Cg0085	(phoH1) [C]: ATPase related to phosphate starvation-inducible protein
403	1	Cg1418	[S]: ABC-type cobalamin/Fe3+-siderophores transport system secreted component
412	1	Cg2862	(purL) [C]: PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE (EC 6.3.5.3)
413	1	Cg2474	(nagD) [C]: PUTATIVE PHOSPHATASE IN N-ACETYLGLUCOSAMINE METABOLISM
414	1	Cg3049	(fprA) [S]: PUTATIVE FERREDOXIN/FERREDOXIN-NADP REDUCTASE (EC 1.18.1.2)
419	1	Cg0291	[C]: 3,4-dioxygenase beta subunit
421	1	Cg3069	[C]: conserved hypothetical protein
422	1	Cg0237	[C]: PUTATIVE OXIDOREDUCTASE
426	1	Cg0413	(cmt1) [S]: Trehalose corynomycolyl transferase (EC 2.3.1.122)
428	1	Cg1796	(ribX) [M]: putative membrane protein - C. ammoniagenes RibX homolog
430	1	Cg2510	(bex) [C]: BEX PROTEIN (GTP-BINDING PROTEIN ERA HOMOLOG)
435	1	Cg0867	[C]: Ribosome-associated protein Y (PSrp-1)
437	1	Cg2408	[M]: putative membrane protein
438	1	Cg2235	(rplS) [C]: 50S RIBOSOMAL PROTEIN L19
443	1	Cg1859	[S]: putative secreted protein

hit	peptides	accession	description
454	1	Cg3107	(adhA) [C]: Zn-dependent alcohol dehydrogenase (EC 1.1.1.1)
457	1	Cg1228	[C]: ABC-type cobalt transport system, ATPase component
469	1	Cg1789	(tpi) [C]: TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1)
472	1	Cg0628	(rpsH) [C]: RIBOSOMAL PROTEIN S8
477	1	Cg0779	(trpS) [C]: TRYPTOPHAN TRNA SYNTHETASE (EC 6.1.1.2)
488	1	Cg0680	[C]: conserved hypothetical protein
489	1	Cg2199	(pbp) [S]: PENICILLIN-BINDING PROTEIN, PUTATIVE D-ALANYL-D-ALANINE CARBOXYPEPTIDASE (EC 3.4.16.4)
490	1	Cg1574	(pheS) [C]: PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN (EC 6.1.1.20)
493	1	Cg2368	(murC) [C]: PROBABLE UDP-N-ACETYLMURAMATE--ALANINE LIGASE PROTEIN (EC 6.3.2.8)
512	1	Cg1436	(ilvN) [C]: ACETOHYDROXYACID SYNTHASE SMALL SUBUNIT (EC 4.1.3.18)
517	1	Cg1337	(hom) [C]: Homoserine Dehydrogenase (EC 1.1.1.3)
537	1	Cg3096	[C]: ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
539	1	Cg2841	[C]: Predicted TIM-barrel enzyme, possibly dehydrogenase, nifR3 family
543	1	Cg2876	(purB) [C]: ADENYLOSUCCINATE LYASE (EC 4.3.2.2)
557	1	Cg2154	(pgsA2) [M]: CDP-DIACYLGLYCEROL--GLYCEROL-3-PHOSPHATE 3-PHOSPHATIDYLTRANSFERASE (EC 2.7.8.5)
559	1	Cg1604	[S]: putative secreted protein
564	1	Cg2100	[C]: rRNA or tRNA methylase
565	1	Cg1247	[S]: putative secreted protein
568	1	Cg2440	[M]: Permease of the major facilitator superfamily
571	1	Cg3068	(fda) [C]: fructose-bisphosphate aldolase (EC 4.1.2.13)
590	1	Cg0939	[S]: secreted protein
592	1	Cg0655	(rpoA) [C]: DNA-DIRECTED RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.6)
595	1	Cg3325	[C]: conserved hypothetical protein
597	1	Cg0565	[C]: PUTATIVE TRANSCRIPTIONAL REGULATOR
610	1	Cg0873	(aroA) [C]: 3-PHOSPHOSHIKIMATE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.19)
616	1	Cg2418	(ilvE) [C]: BRANCHED-CHAIN AMINO ACID AMINOTRANSFERASE (EC 2.6.1.42)
625	1	Cg0489	[M]: hypothetical membrane protein
631	1	Cg0933	[C]: DNA or RNA helicase of superfamily II
642	1	Cg0564	(rplA) [C]: 50S RIBOSOMAL PROTEIN L1
644	1	Cg0442	(galU2) [C]: PUTATIVE UTP-GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERA (EC 2.7.7.9)
648	1	Cg1641	[C]: Superfamily II DNA or RNA helicase
656	1	Cg1432	(ilvD) [C]: DIHYDROXY-ACID DEHYDRATASE (EC 4.2.1.9)
662	1	Cg2342	[C]: Dehydrogenase
667	1	Cg2994	[S]: putative secreted or membrane protein
671	1	Cg2924	(cysS) [C]: CYSTEINE TRNA SYNTHETASE (EC 6.1.1.16)
692	1	Cg1129	(aroF) [C]: PROBABLE PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE (EC 4.1.2.15)
694	1	Cg2460	[M]: putative membrane protein
698	1	Cg1730	[S]: secreted protease subunit, stomatin/prohibitin homolog
703	1	Cg1069	(gapX) [C]: similar to GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12)
704	1	Cg1764	(sufB) [C]: component of an uncharacterized iron-regulated ABC-type transporter

hit	peptides	accession	description
706	1	Cg1675	[M]: putative membrane protein
709	1	Cg2890	[C]: PUTATIVE AMINO ACID PROCESSING ENZYME
710	1	Cg2676	[M]: ABC-type dipeptide/oligopeptide/nickel transport systems, permease component
714	1	Cg0594	(rplC) [C]: 50S RIBOSOMAL PROTEIN L3
735	1	Cg3387	[M]: Permease of the major facilitator superfamily
755	1	Cg1458	[C]: 2-HYDROXYHEPTA-2,4-DIENE- 1,7-DIOATE ISOMERASE (EC 5.3.3.-)
788	1	Cg2467	[C]: ABC TRANSPORTER ATP-BINDING PROTEIN
820	1	Cg1623	[M]: Predicted divalent heavy-metal cations transporter
824	1	Cg1646	[C]: ABC-type multidrug transport system, ATPase component
830	1	Cg3240	[M]: Permease of the major facilitator superfamily
834	1	Cg3304	(dnaB) [C]: PUTATIVE REPLICATIVE DNA HELICASE (EC 3.6.1.)
841	1	Cg1740	[C]: putative nucleoside-diphosphate-sugar epimerase
850	1	Cg0396	[M]: Glycosyl transferase
870	1	Cg2362	[M]: putative membrane protein
884	1	Cg0914	(ftsE) [C]: CELL DIVISION ATP-BINDING PROTEIN
887	1	Cg3160	[S]: putative secreted protein
893	1	Cg2619	[M]: Predicted permease
899	1	Cg2561	(thiX) [S]: secreted protein potentially involved into thiamin biosynthesis
958	1	Cg3215	(glpQ1) [C]: PUTATIVE GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46)
967	1	Cg0620	[S]: secreted protein
979	1	Cg0475	[C]: conserved hypothetical protein
988	1	Cg0573	(rplL) [C]: PROBABLE 50S RIBOSOMAL SUBUNIT PROTEIN L7/L12
989	1	Cg1341	(narI) [M]: RESPIRATORY NITRATE REDUCTASE 2 GAMMA CHAIN (EC 1.7.99.4)
990	1	Cg1505	[S]: putative secreted protein
1002	1	Cg3407	[M]: putative membrane protein
1010	1	Cg2954	(cynT) [C]: CARBONIC ANHYDRASE (EC 4.2.1.1)
1020	1	Cg2604	[M]: putative secreted or membrane protein
1052	1	Cg0674	(rpsI) [C]: 30S RIBOSOMAL PROTEIN S9
1057	1	Cg0359	[M]: PUTATIVE MEMBRANE PROTEIN
1058	1	Cg1731	[M]: Membrane protein implicated in regulation of membrane protease activity
1080	1	Cg0556	(ubiE) [C]: UBIQUINONE/MENAQUINONE BIOSYNTHESIS METHYLTRANSFER (EC 2.1.1.-)
1117	1	Cg1635	[M]: putative membrane protein
1121	1	Cg1092	[S]: putative secreted protein
1132	1	Cg1312	[M]: putative membrane protein
1139	1	Cg0653	(rpsK) [C]: RIBOSOMAL PROTEIN S11
1145	1	Cg3254	[M]: putative membrane protein
1148	1	Cg3361	(trpD) [C]: ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.18)
1195	1	Cg1811	(ihf) [C]: putative integration host factor cIHF
1215	1	Cg2033	[S]: putative secreted protein
1220	1	Cg0726	[S]: secreted lipoprotein

hit	**peptides**	**accession**	**description**
1231	1	Cg1072	(rplY) [C]: Ribosomal protein L25 (general stress protein Ctc)
1236	1	Cg0609	(rplX) [C]: 50S RIBOSOMAL PROTEIN L24
1276	1	Cg1672	(ppmC) [C]: polyprenol-phosphate-mannose synthase domain 1
1319	1	Cg2535	[S]: putative secreted protein
1345	1	Cg3367	[C]: ABC-type multidrug transport system, ATPase component
1346	1	Cg3353	(benK2) [M]: putative benzoate transport protein
1413	1	Cg1694	(recB) [C]: RecB family exonuclease
1414	1	Cg1568	(ugpA) [M]: sn-Glycerol-3-phosphate transport system permease protein
1426	1	Cg0412	[M]: membrane protein
1433	1	Cg3139	[C]: conserved hypothetical protein
1436	1	Cg1810	(gmk) [C]: PROBABLE GUANYLATE KINASE PROTEIN (EC 2.7.4.8)
1481	1	Cg1085	[C]: hypothetical protein predicted by Glimmer/Critica
1483	1	Cg0600	(rplV) [C]: RIBOSOMAL PROTEIN L22
1506	1	Cg1751	[M]: putative membrane protein
1525	1	Cg0561	(secE) [M]: SecE subunit of protein translocation complex
1526	1	Cg0524	(ccsB) [M]: Cytochrome c assembly membrane protein
1529	1	Cg2737	[S]: Bacterial regulatory protein, tetR family
1543	1	Cg1259	(dapD2) [C]: similar to tetrahydrodipicolinate N-succinyltransferase
1559	1	Cg0652	(rpsM) [C]: (Q9RA65) RIBOSOMAL PROTEIN S13
1582	1	Cg2773	[C]: Uncharacterized protein with SCP/PR1 domain
1698	1	Cg0966	(thyA) [C]: PROBABLE THYMIDYLATE SYNTHASE (EC 2.1.1.45)
1748	1	Cg2735	[M]: putative membrane protein

END OF LIST III

hit	peptides	accession	description
IV. Purple membrane; elastase digest; nLC-MALDI MS/MS; no search specificity			
1	120	P02945|BACR	Bacteriorhodopsin
2	72	P00772|ELA1	Elastase-1 precursor - Sus scrofa
3	54	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
4	22	Q9HR99|Q9HR99	Halocyanin-like
5	22	Q9HN93|Q9HN93	Halocyanin-like
7	22	Q48302|Q48302	Precursor proteolipid
6	20	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
8	18	Q9HHN1|Q9HHN1	Na+/H+ antiporter
10	15	Q9HM69|CSG	Cell surface glycoprotein
12	14	Q9HMG3|Q9HMG3	Putative uncharacterized protein
13	12	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
16	12	Q9HSS1|Q9HSS1	Phosphoglycerate dehydrogenase
14	10	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
15	10	Q9HRS0|Q9HRS0	Putative uncharacterized protein
17	10	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
22	7	Q9HND8|VATI	V-type ATP synthase subunit I
19	6	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
20	6	Q9HMF1|Q9HMF1	Aconitase
21	6	Q9HMT7|Q9HMT7	Probable thiosulfate sulfurtransferase
24	6	Q9HRR0|Q9HRR0	Putative uncharacterized protein
18	5	Q9HN94|Q9HN94	Cytochrome c oxidase subunit II
32	5	Q9HMW4|Q9HMW	Oligopeptide binding protein
25	4	Q9HSQ7|Q9HSQ7	ABC transport protein
26	4	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
29	4	Q9HHP3|Q9HHP3	Vng6297c
36	4	Q9HM89|EF1A	Elongation factor 1-alpha
41	4	Q9HNL7|Q9HNL7	Putative uncharacterized protein
49	4	Q9HMU9|Q9HMU9	Nitrite/nitrate reduction protein
23	3	Q9HRR1|Q9HRR1	Putative uncharacterized protein
27	3	Q9HNB9|Q9HNB9	Putative uncharacterized protein
31	3	Q9HQA6|Q9HQA6	Putative uncharacterized protein
33	3	Q9HQF4|Q9HQF4	Membrane protein
34	3	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
35	3	Q9HMX1|Q9HMX1	Dipeptide ABC transporter permease
37	3	Q9HR04|Q9HR04	Iron-binding protein
40	3	Q9HMB7|Q9HMB7	Probable carboxypeptidase
78	3	Q9HS12|Q9HS12	Phosphate ABC transporter permease

hit	peptides	accession	description
80	3	Q9HMK0|Q9HMK0	Putative uncharacterized protein
28	2	Q9HQP2|Q9HQP2	Transmembrane oligosaccharyl transferase
38	2	Q9HSM4|DHE42	NADP-specific glutamate dehydrogenase B
39	2	Q9HMB6|Q9HMB6	Alcohol dehydrogenase
42	2	Q9HP76|Q9HP76	Putative uncharacterized protein
45	2	Q9HRL9|Q9HRL9	NADH dehydrogenase/oxidoreductase
47	2	Q9HPB1|SECY	Preprotein translocase subunit secY
48	2	Q9HM85|EF2	Elongation factor 2
51	2	Q9HMH4|Q9HMH4	Putative uncharacterized protein
58	2	Q9HMX0|Q9HMX0	Dipeptide ABC transporter permease
64	2	Q9HP88|Q9HP88	Phytoene dehydrogenase
66	2	Q9HNY9|Q9HNY9	Quinolinate phosphoribosyltransferase
92	2	Q9HSQ2|HTPX	Probable protease htpX homolog
105	2	Q9HMQ2|ASSY	Argininosuccinate synthase
119	2	Q9HP48|Q9HP48	NADH oxidase
141	2	Q9HRR3|Q9HRR3	Putative uncharacterized protein
160	2	Q9HN22|Q9HN22	Putative uncharacterized protein
266	2	Q9HN92|Q9HN92	Putative uncharacterized protein
618	2	Q9HQV6|Q9HQV6	Putative uncharacterized protein
50	1	Q9HNH3|Q9HNH3	Potassium channel homolog
54	1	Q9HP84|HTR4	Halobacterial transducer protein 4
57	1	Q9HSC3|LONH	Putative protease La homolog type
61	1	Q9HQ23|Q9HQ23	Putative uncharacterized protein
62	1	Q9HNN6|Q9HNN6	Putative uncharacterized protein
63	1	Q9HT00|GLMS	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
74	1	Q9HPA6|Q9HPA6	Htr-like protein
75	1	Q9HNR0|Q9HNR0	Protein-export membrane protein
77	1	Q9HNS6|Q9HNS6	Putative uncharacterized protein
81	1	Q9HQQ9|Q9HQQ9	UDP-glucose dehydrogenase
85	1	Q9HRL2|Q9HRL2	F420H2:quinone oxidoreductase chain M
91	1	Q9HR92|HTR6	Halobacterial transducer protein 6
94	1	Q9HS26|Q9HS26	Na+/H+ antiporter
95	1	P57684|ATKA	Potassium-transporting ATPase A chain
96	1	Q9HMB4|Q9HMB4	Repair helicase
97	1	Q9HR32|TOP6A	Type II DNA topoisomerase VI subunit A
100	1	Q9HPQ2|Q9HPQ2	Daunorubicin resistance ABC transporter ATP-binding protein
104	1	Q9HR98|Q9HR98	Cystathionine gamma-synthase
109	1	Q9HMQ8|Q9HMQ8	D-lactate dehydrogenase
110	1	Q9HS00|Q9HS00	Putative uncharacterized protein
112	1	Q9HHI3|Q9HHI3	Vng6381h

hit	peptides	accession	description
115	1	Q9HQU8|Q9HQU8	Acetyl-CoA synthetase
117	1	Q9HT01|Q9HT01	Putative uncharacterized protein
122	1	Q9HPG8|Q9HPG8	Ribonucleoside-diphosphate reductase
126	1	P25964|BACS1	Sensory rhodopsin-1
128	1	Q9HN02|Q9HN02	Hemolysin protein
131	1	Q9HHP2|Q9HHP2	Vng6298c
139	1	Q9HMZ3|Q9HMZ3	Heterodisulfide reductase
144	1	Q9HN43|CAPPA	Phosphoenolpyruvate carboxylase
146	1	Q9HRJ5|Q9HRJ5	Putative uncharacterized protein
148	1	Q9HNI3|Q9HNI3	Putative uncharacterized protein
149	1	Q9HS86|Q9HS86	Htr14 transducer
166	1	Q9HNP7|Q9HNP7	Putative uncharacterized protein
173	1	Q9HRT0|Q9HRT0	Putative uncharacterized protein
174	1	Q9HP01|Q9HP01	Spermidine/putrescine ABC transporter permease
175	1	Q9HQ43|Q9HQ43	Putative uncharacterized protein
176	1	Q9HPT9|Q9HPT9	Carboxylesterase
184	1	Q48294|Q48294	Arginine deiminase
187	1	Q9HR74|Q9HR74	Dimethylsulfoxide reductase
195	1	Q9HQU4|Q9HQU4	Inosine monophosphate dehydrogenase
200	1	Q9HR22|Q9HR22	Ribose ABC transporter permease
207	1	Q9HP66|Q9HP66	Putative uncharacterized protein
211	1	Q9HRZ2|Q9HRZ2	Probable oxidoreductase
217	1	Q9HNS4|Q9HNS4	Glycerol-3-phosphate dehydrogenase chain A
222	1	Q9HSW2|Q9HSW2	Putative uncharacterized protein
239	1	Q9HPY6|Q9HPY6	Putative uncharacterized protein
246	1	Q9HQN2|Q9HQN2	Isochorismate synthase
255	1	Q9HRS9|Q9HRS9	Putative uncharacterized protein
258	1	Q9HMU8|Q9HMU8	Copper transport ATP-binding protein
264	1	Q9HN37|Q9HN37	Protein export
282	1	Q9HR54|Q9HR54	Putative uncharacterized protein
290	1	Q9HSZ8|Q9HSZ8	Glucose-1-phosphate thymidylyltransferase
301	1	Q9HNU9|COFG	FO synthase subunit 1
317	1	Q9HQU3|Q9HQU3	Putative uncharacterized protein
318	1	Q9HMU6|Q9HMU6	Putative uncharacterized protein
320	1	Q9HNW7|Q9HNW7	Phosphoribosyl transferase
323	1	Q9HQ64|Q9HQ64	Membrane anchor
325	1	Q9HN54|Q9HN54	Putative uncharacterized protein
339	1	Q9HMJ2|Q9HMJ2	Putative uncharacterized protein
362	1	Q9HST4|MOAA	Probable molybdenum cofactor biosynthesis protein A
374	1	Q9HPI6|Q9HPI6	Putative uncharacterized protein

hit	peptides	accession	description
391	1	P57697|PSMA	Proteasome subunit alpha
402	1	Q9HNQ9|Q9HNQ9	Protein-export membrane protein
412	1	Q9HQ52|THYX	Thymidylate synthase thyX
449	1	Q9HPW3|Q9HPW3	Putative uncharacterized protein
453	1	Q9HSW6|CDC61	Cell division control protein 6 homolog 1
462	1	Q9HN08|Q9HN08	Thioredoxin reductase
474	1	Q9HRL4|Q9HRL4	NADH dehydrogenase/oxidoreductase-like protein
476	1	Q9HM88|Q9HM88	Homoserine dehydrogenase
479	1	Q9HRS4|Q9HRS4	Putative uncharacterized protein
493	1	Q9HN36|Q9HN36	Protein export
519	1	Q9HNC8|Q9HNC8	Putative uncharacterized protein
542	1	Q9HMC9|Q9HMC9	Arsenite transport protein
558	1	Q9HQU7|Q9HQU7	Probable oxidoreductase
559	1	Q9HRK1|Q9HRK1	Cytochrome c oxidase subunit III
560	1	Q9HRS8|Q9HRS8	NADH dehydrogenase/oxidoreductase
564	1	Q9HPK2|Y1595	UPF0100 protein VNG1595C
585	1	Q9HQ34|Q9HQ34	Putative uncharacterized protein
599	1	Q9HQI3|Q9HQI3	Geranylgeranyl diphosphate synthase
603	1	Q9HPQ1|Q9HPQ1	Sodium-and chloride-dependent transporter
615	1	Q9HSF1|Q9HSF1	Putative uncharacterized protein
650	1	Q9HNE5|Q9HNE5	Geranylgeranyl-diphosphate geranylgeranyltransferase
684	1	O52037|O52037	Putative uncharacterized protein
704	1	O51975|O51975	Putative uncharacterized protein
717	1	Q9HML4|Q9HML4	Putative uncharacterized protein
732	1	Q9HSA0|Q9HSA0	Putative uncharacterized protein
791	1	Q9HNB8|Q9HNB8	Putative uncharacterized protein
808	1	Q9HS40|Q9HS40	Putative uncharacterized protein
830	1	Q9HQE2|Q9HQE2	Putative uncharacterized protein
861	1	Q9HP98|Q9HP98	Htr-like protein
864	1	Q9HPF2|RADB	DNA repair and recombination protein radB
880	1	Q9HRW7|Q9HRW7	Putative uncharacterized protein
894	1	Q9HRN0|Q9HRN0	Putative uncharacterized protein
899	1	Q9HME2|Q9HME2	Putative uncharacterized protein
928	1	Q9HMK6|Q9HMK6	Putative uncharacterized protein
939	1	Q9HNI4|Q9HNI4	Putative uncharacterized protein
1035	1	Q9HSP8|Q9HSP8	Archaeal histone A1
1041	1	Q9HR01|Q9HR01	Putative uncharacterized protein
1095	1	Q9HRH6|Q9HRH6	Putative uncharacterized protein
1125	1	Q9HQ91|Q9HQ91	Putative uncharacterized protein
1161	1	Q9HMB0|Q9HMB0	Putative uncharacterized protein

hit	**peptides**	**accession**	**description**
1189	1	Q9HRR5|Q9HRR5	Putative uncharacterized protein
1204	1	Q9HSJ4|Q9HSJ4	Putative uncharacterized protein
1247	1	Q9HRR2|Q9HRR2	Cytochrome b6
1287	1	Q9HNI2|GLNA	Glutamine synthetase
1414	1	Q9HQB1|Q9HQB1	Putative uncharacterized protein
1581	1	Q9HRK3|Q9HRK3	Putative uncharacterized protein
1657	1	Q9HP64|Q9HP64	Putative uncharacterized protein
1659	1	Q9HNA9|Q9HNA9	Putative uncharacterized protein

END OF LIST IV

hit	peptides	accession	description
V. Purple membrane; elastase digest; nLC-MALDI MS/MS; AVLISTG search specificity			
1	86	P02945|BACR	Bacteriorhodopsin
2	48	P00772|ELA1	Elastase-1 precursor - Sus scrofa
3	30	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
6	19	Q48302|Q48302	Precursor proteolipid
4	13	Q9HR99|Q9HR99	Halocyanin-like
5	13	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
7	11	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
8	11	Q9HN93|Q9HN93	Halocyanin-like
9	10	Q9HHN1|Q9HHN1	Na+/H+ antiporter
10	10	Q9HRS0|Q9HRS0	Putative uncharacterized protein
11	8	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
12	7	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
13	6	Q9HM69|CSG	Cell surface glycoprotein
14	6	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
15	6	Q9HND8|VATI	V-type ATP synthase subunit I
16	5	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
17	5	Q9HMF1|Q9HMF1	Aconitase
18	4	Q9HRR0|Q9HRR0	Putative uncharacterized protein
19	4	Q9HMW4|Q9HMW	Oligopeptide binding protein
21	4	Q9HMG3|Q9HMG3	Putative uncharacterized protein
24	4	Q9HSS1|Q9HSS1	Phosphoglycerate dehydrogenase
25	4	Q9HQP2|Q9HQP2	Transmembrane oligosaccharyl transferase
20	3	Q9HMT7|Q9HMT7	Probable thiosulfate sulfurtransferase
22	3	Q9HNL7|Q9HNL7	Putative uncharacterized protein
23	3	Q9HHP3|Q9HHP3	Vng6297c
26	3	Q9HQF4|Q9HQF4	Membrane protein
27	3	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
28	3	Q9HMX1|Q9HMX1	Dipeptide ABC transporter permease
29	3	Q9HS12|Q9HS12	Phosphate ABC transporter permease
68	3	Q9HN92|Q9HN92	Putative uncharacterized protein
30	2	Q9HMX0|Q9HMX0	Dipeptide ABC transporter permease
31	2	Q9HR04|Q9HR04	Iron-binding protein
32	2	Q9HP48|Q9HP48	NADH oxidase
33	2	Q9HMH4|Q9HMH4	Putative uncharacterized protein
34	2	Q9HRR1|Q9HRR1	Putative uncharacterized protein
35	2	Q9HNY2|Q9HNY2	Putative uncharacterized protein
37	2	Q9HM85|EF2	Elongation factor 2

hit	peptides	accession	description
38	2	Q9HM89|EF1A	Elongation factor 1-alpha
39	2	Q9HNS6|Q9HNS6	Putative uncharacterized protein
45	2	Q9HP88|Q9HP88	Phytoene dehydrogenase
58	2	Q9HR32|TOP6A	Type II DNA topoisomerase VI subunit A
72	2	P16102|BACH	Halorhodopsin
74	2	Q9HHI2|Q9HHI2	L-lactate permease
99	2	Q9HQ23|Q9HQ23	Putative uncharacterized protein
103	2	Q9HN43|CAPPA	Phosphoenolpyruvate carboxylase
118	2	Q9HMU9|Q9HMU9	Nitrite/nitrate reduction protein
126	2	Q9HS00|Q9HS00	Putative uncharacterized protein
289	2	O51975|O51975	Putative uncharacterized protein
36	1	Q9HPG8|Q9HPG8	Ribonucleoside-diphosphate reductase
40	1	Q9HP84|HTR4	Halobacterial transducer protein 4
41	1	Q9HMS7|Q9HMS7	DNA damage-inducible protein
43	1	Q9HT00|GLMS	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
47	1	Q9HRL2|Q9HRL2	F420H2:quinone oxidoreductase chain M
48	1	Q9HMB4|Q9HMB4	Repair helicase
49	1	Q9HNN6|Q9HNN6	Putative uncharacterized protein
50	1	Q9HPB1|SECY	Preprotein translocase subunit secY
52	1	Q9HPQ2|Q9HPQ2	Daunorubicin resistance ABC transporter ATP-binding protein
54	1	Q9HS26|Q9HS26	Na+/H+ antiporter
56	1	Q9HMU6|Q9HMU6	Putative uncharacterized protein
57	1	Q9HRJ5|Q9HRJ5	Putative uncharacterized protein
59	1	Q9HQQ9|Q9HQQ9	UDP-glucose dehydrogenase
60	1	Q9HSM2|MUTS1	DNA mismatch repair protein mutS 1
61	1	Q9HMU8|Q9HMU8	Copper transport ATP-binding protein
62	1	Q9HMZ3|Q9HMZ3	Heterodisulfide reductase
63	1	Q9HSM4|DHE42	NADP-specific glutamate dehydrogenase B
66	1	Q9HHR4|Q9HHR4	Vng6268c
69	1	Q9HNW7|Q9HNW7	Phosphoribosyl transferase
70	1	Q9HSJ6|Q9HSJ6	Putative uncharacterized protein
76	1	Q9HRS4|Q9HRS4	Putative uncharacterized protein
77	1	Q9HRS9|Q9HRS9	Putative uncharacterized protein
80	1	Q9HS72|SECE	Preprotein translocase subunit secE
81	1	Q9HNR0|Q9HNR0	Protein-export membrane protein
84	1	Q9HQ64|Q9HQ64	Membrane anchor
85	1	Q9HS86|Q9HS86	Htr14 transducer
87	1	Q9HPA9|Q9HPA9	TRK potassium uptake system protein
93	1	Q9HNQ9|Q9HNQ9	Protein-export membrane protein
96	1	Q9HNK1|Q9HNK1	Putative uncharacterized protein

hit	peptides	accession	description
97	1	Q9HN02|Q9HN02	Hemolysin protein
100	1	Q9HSA0|Q9HSA0	Putative uncharacterized protein
105	1	Q9HHI3|Q9HHI3	Vng6381h
110	1	Q9HQE2|Q9HQE2	Putative uncharacterized protein
116	1	O54610|O54610	CydA
119	1	Q9HPT9|Q9HPT9	Carboxylesterase
123	1	Q9HPG5|TRPE1	Anthranilate synthase component 1 1
127	1	Q9HRU7|Q9HRU7	Putative uncharacterized protein
128	1	Q9HN22|Q9HN22	Putative uncharacterized protein
132	1	Q9HN79|Q9HN79	DNA damage-inducible protein
140	1	Q9HMV1|Q9HMV1	Aspartokinase
142	1	Q9HPM1|Q9HPM1	Precorrin isomerase
145	1	Q9HMB7|Q9HMB7	Probable carboxypeptidase
150	1	Q9HPY6|Q9HPY6	Putative uncharacterized protein
151	1	Q9HMY7|Q9HMY7	Putative uncharacterized protein
152	1	Q9HRL4|Q9HRL4	NADH dehydrogenase/oxidoreductase-like protein
155	1	Q9HQU8|Q9HQU8	Acetyl-CoA synthetase
156	1	Q9HSW2|Q9HSW2	Putative uncharacterized protein
158	1	Q9HR62|Q9HR62	Putative uncharacterized protein
161	1	Q9HMQ8|Q9HMQ8	D-lactate dehydrogenase
162	1	Q9HRA8|Q9HRA8	Putative uncharacterized protein
164	1	Q9HP98|Q9HP98	Htr-like protein
165	1	Q9HRJ0|Q9HRJ0	Putative uncharacterized protein
175	1	P25964|BACS1	Sensory rhodopsin-1
177	1	Q9HP66|Q9HP66	Putative uncharacterized protein
182	1	P33518|COX1	Cytochrome c oxidase polypeptide 1
183	1	Q9HR22|Q9HR22	Ribose ABC transporter permease
185	1	Q9HN36|Q9HN36	Protein export
186	1	Q9HPK2|Y1595	UPF0100 protein VNG1595C
188	1	Q9HS30|Q9HS30	Putative uncharacterized protein
189	1	Q9HNY9|Q9HNY9	Quinolinate phosphoribosyltransferase
205	1	Q9HN37|Q9HN37	Protein export
221	1	Q9HSQ7|Q9HSQ7	ABC transport protein
234	1	Q9HP76|Q9HP76	Putative uncharacterized protein
236	1	Q9HPQ6|Q9HPQ6	A/G specific adenine glycosylase, repair protein
239	1	Q9HMQ2|ASSY	Argininosuccinate synthase
248	1	Q9HSJ4|Q9HSJ4	Putative uncharacterized protein
258	1	Q9HQE1|Q9HQE1	Glutamate dehydrogenase
260	1	Q9HPQ1|Q9HPQ1	Sodium-and chloride-dependent transporter
266	1	Q9HQU3|Q9HQU3	Putative uncharacterized protein

hit	peptides	accession	description
270	1	Q9HMC9|Q9HMC9	Arsenite transport protein
288	1	Q9HST9|Q9HST9	Putative uncharacterized protein
294	1	Q9HNI3|Q9HNI3	Putative uncharacterized protein
299	1	Q9HQ90|Q9HQ90	Putative uncharacterized protein
303	1	Q9HQ63|DHSD	Succinate dehydrogenase hydrophobic membrane anchor subunit
309	1	Q9HMC7|THI4	Putative thiazole biosynthetic enzyme
325	1	Q9HQZ3|Q9HQZ3	Putative uncharacterized protein
343	1	Q9HMB0|Q9HMB0	Putative uncharacterized protein
345	1	Q48325|TBPB	TATA-box-binding protein B
348	1	Q9HRW7|Q9HRW7	Putative uncharacterized protein
361	1	Q9HSW6|CDC61	Cell division control protein 6 homolog 1
363	1	Q9HMJ2|Q9HMJ2	Putative uncharacterized protein
371	1	Q9HQH2|Q9HQH2	Putative uncharacterized protein
392	1	Q9HNB8|Q9HNB8	Putative uncharacterized protein
395	1	Q9HRR3|Q9HRR3	Putative uncharacterized protein
398	1	Q9HRR2|Q9HRR2	Cytochrome b6
408	1	Q9HNJ2|Q9HNJ2	Putative uncharacterized protein
411	1	Q9HM88|Q9HM88	Homoserine dehydrogenase
433	1	Q9HME2|Q9HME2	Putative uncharacterized protein
460	1	Q9HMY1|Q9HMY1	Sensor protein
488	1	Q9HN08|Q9HN08	Thioredoxin reductase
493	1	Q9HRH6|Q9HRH6	Putative uncharacterized protein
495	1	Q9HRR5|Q9HRR5	Putative uncharacterized protein
499	1	Q9HS52|SYP	Prolyl-tRNA synthetase
512	1	Q9HRK3|Q9HRK3	Putative uncharacterized protein
520	1	Q9HSE5|Q9HSE5	Putative uncharacterized protein
525	1	Q9HQV6|Q9HQV6	Putative uncharacterized protein
537	1	Q9HMK6|Q9HMK6	Putative uncharacterized protein
545	1	Q9HR54|Q9HR54	Putative uncharacterized protein
558	1	Q9HQW3|Q9HQW3	Putative uncharacterized protein
587	1	Q9HPI6|Q9HPI6	Putative uncharacterized protein
632	1	Q9HRR7|Q9HRR7	Putative uncharacterized protein
633	1	Q9HQB1|Q9HQB1	Putative uncharacterized protein
651	1	Q9HRR6|Q9HRR6	Putative uncharacterized protein
668	1	Q9HN96|Q9HN96	Putative uncharacterized protein
689	1	Q9HRP9|Q9HRP9	Putative uncharacterized protein
721	1	Q9HRE8|RTCA	Probable RNA 3~-terminal phosphate cyclase
737	1	Q9HRP5|Q9HRP5	Putative uncharacterized protein
743	1	Q9HPV1|Q9HPV1	Putative uncharacterized protein
755	1	Q9HS03|Q9HS03	Putative uncharacterized protein

hit	**peptides**	**accession**	**description**
981	1	Q9HHQ7|Q9HHQ7	Sn-glycerol-3-phosphate transport system permease
1081	1	Q9HNX9|Q9HNX9	Putative uncharacterized protein
1082	1	Q9HRF3|Q9HRF3	Putative uncharacterized protein

END OF LIST III

hit	peptides	accession	description
VI. Purple membrane; elastase digest; nLC-MALDI MS/MS; AVLIST search specificity			
1	86	P02945|BACR	Bacteriorhodopsin
2	48	P00772|ELA1	Elastase-1 precursor - Sus scrofa
3	29	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
6	22	Q48302|Q48302	Precursor proteolipid
4	18	Q9HR99|Q9HR99	Halocyanin-like
5	17	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
7	12	Q9HN93|Q9HN93	Halocyanin-like
8	12	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
10	9	Q9HHN1|Q9HHN1	Na+/H+ antiporter
11	9	Q9HMG3|Q9HMG3	Putative uncharacterized protein
12	9	Q9HRS0|Q9HRS0	Putative uncharacterized protein
13	8	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
14	8	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
15	6	Q9HND8|VATI	V-type ATP synthase subunit I
16	5	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
17	5	Q9HM69|CSG	Cell surface glycoprotein
18	5	Q9HMF1|Q9HMF1	Aconitase
20	5	Q9HSS1|Q9HSS1	Phosphoglycerate dehydrogenase
25	5	Q9HR04|Q9HR04	Iron-binding protein
19	4	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
23	4	Q9HMW4|Q9HMW	Oligopeptide binding protein
28	4	Q9HQP2|Q9HQP2	Transmembrane oligosaccharyl transferase
21	3	Q9HMT7|Q9HMT7	Probable thiosulfate sulfurtransferase
22	3	Q9HMX1|Q9HMX1	Dipeptide ABC transporter permease
24	3	Q9HHP3|Q9HHP3	Vng6297c
26	3	Q9HM89|EF1A	Elongation factor 1-alpha
27	3	Q9HQF4|Q9HQF4	Membrane protein
30	3	Q9HS12|Q9HS12	Phosphate ABC transporter permease
31	3	Q9HRR0|Q9HRR0	Putative uncharacterized protein
63	3	Q9HN92|Q9HN92	Putative uncharacterized protein
29	2	Q9HNL7|Q9HNL7	Putative uncharacterized protein
32	2	Q9HMX0|Q9HMX0	Dipeptide ABC transporter permease
33	2	Q9HRR1|Q9HRR1	Putative uncharacterized protein
34	2	Q9HM85|EF2	Elongation factor 2
35	2	Q9HP48|Q9HP48	NADH oxidase
37	2	Q9HNS6|Q9HNS6	Putative uncharacterized protein
39	2	Q9HP88|Q9HP88	Phytoene dehydrogenase

hit	peptides	accession	description
45	2	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
46	2	Q9HNY2|Q9HNY2	Putative uncharacterized protein
57	2	Q9HR32|TOP6A	Type II DNA topoisomerase VI subunit A
69	2	Q9HNK1|Q9HNK1	Putative uncharacterized protein
78	2	P16102|BACH	Halorhodopsin
83	2	Q9HHI2|Q9HHI2	L-lactate permease
90	2	Q9HN43|CAPPA	Phosphoenolpyruvate carboxylase
138	2	Q9HP66|Q9HP66	Putative uncharacterized protein
162	2	Q9HS00|Q9HS00	Putative uncharacterized protein
258	2	O51975|O51975	Putative uncharacterized protein
36	1	Q9HHR4|Q9HHR4	Vng6268c
38	1	Q9HPG8|Q9HPG8	Ribonucleoside-diphosphate reductase
41	1	Q9HRU7|Q9HRU7	Putative uncharacterized protein
42	1	Q9HRJ5|Q9HRJ5	Putative uncharacterized protein
43	1	Q9HMS7|Q9HMS7	DNA damage-inducible protein
44	1	Q9HP84|HTR4	Halobacterial transducer protein 4
49	1	Q9HRL2|Q9HRL2	F420H2:quinone oxidoreductase chain M
50	1	Q9HPB1|SECY	Preprotein translocase subunit secY
53	1	Q9HS26|Q9HS26	Na+/H+ antiporter
54	1	Q9HRL9|Q9HRL9	NADH dehydrogenase/oxidoreductase
55	1	Q9HPA9|Q9HPA9	TRK potassium uptake system protein
56	1	Q9HQQ9|Q9HQQ9	UDP-glucose dehydrogenase
58	1	Q9HSM2|MUTS1	DNA mismatch repair protein mutS 1
60	1	Q9HQ54|Q9HQ54	Putative uncharacterized protein
61	1	Q9HMU8|Q9HMU8	Copper transport ATP-binding protein
66	1	Q9HSM4|DHE42	NADP-specific glutamate dehydrogenase B
68	1	Q9HPQ2|Q9HPQ2	Daunorubicin resistance ABC transporter ATP-binding protein
73	1	Q9HRS4|Q9HRS4	Putative uncharacterized protein
74	1	P25964|BACS1	Sensory rhodopsin-1
76	1	Q9HS86|Q9HS86	Htr14 transducer
80	1	Q9HS72|SECE	Preprotein translocase subunit secE
82	1	Q9HR22|Q9HR22	Ribose ABC transporter permease
84	1	Q9HQ64|Q9HQ64	Membrane anchor
89	1	Q9HSA0|Q9HSA0	Putative uncharacterized protein
91	1	Q9HN02|Q9HN02	Hemolysin protein
94	1	Q9HNQ9|Q9HNQ9	Protein-export membrane protein
95	1	Q9HMZ3|Q9HMZ3	Heterodisulfide reductase
98	1	Q9HHI3|Q9HHI3	Vng6381h
99	1	Q9HPM1|Q9HPM1	Precorrin isomerase
102	1	Q9HR62|Q9HR62	Putative uncharacterized protein

hit	peptides	accession	description
104	1	Q9HPG5|TRPE1	Anthranilate synthase component 1 1
105	1	Q9HN22|Q9HN22	Putative uncharacterized protein
115	1	Q9HNY9|Q9HNY9	Quinolinate phosphoribosyltransferase
118	1	Q9HSL1|Q9HSL1	Putative uncharacterized protein
119	1	Q9HP01|Q9HP01	Spermidine/putrescine ABC transporter permease
122	1	Q9HRS9|Q9HRS9	Putative uncharacterized protein
128	1	Q9HMB7|Q9HMB7	Probable carboxypeptidase
131	1	Q9HQE2|Q9HQE2	Putative uncharacterized protein
135	1	Q9HMY7|Q9HMY7	Putative uncharacterized protein
136	1	Q9HRL4|Q9HRL4	NADH dehydrogenase/oxidoreductase-like protein
137	1	Q9HSW2|Q9HSW2	Putative uncharacterized protein
139	1	Q9HPT9|Q9HPT9	Carboxylesterase
143	1	Q9HMQ8|Q9HMQ8	D-lactate dehydrogenase
145	1	Q9HRA8|Q9HRA8	Putative uncharacterized protein
148	1	Q9HMH4|Q9HMH4	Putative uncharacterized protein
150	1	Q9HN79|Q9HN79	DNA damage-inducible protein
155	1	P33518|COX1	Cytochrome c oxidase polypeptide 1
157	1	Q9HN37|Q9HN37	Protein export
160	1	Q07971|Q07971	RepH protein
169	1	Q9HN36|Q9HN36	Protein export
173	1	Q9HMB4|Q9HMB4	Repair helicase
174	1	Q9HS30|Q9HS30	Putative uncharacterized protein
178	1	Q9HMU6|Q9HMU6	Putative uncharacterized protein
179	1	O54610|O54610	CydA
187	1	Q9HRJ8|Q9HRJ8	Heme synthase
190	1	Q9HMV1|Q9HMV1	Aspartokinase
192	1	Q9HHV2|Q9HHV2	Iron transport protein A
193	1	Q9HMC9|Q9HMC9	Arsenite transport protein
204	1	Q9HP76|Q9HP76	Putative uncharacterized protein
206	1	Q9HPQ6|Q9HPQ6	A/G specific adenine glycosylase, repair protein
211	1	Q9HPY6|Q9HPY6	Putative uncharacterized protein
213	1	Q9HQB8|Q9HQB8	Putative uncharacterized protein
220	1	Q9HMJ2|Q9HMJ2	Putative uncharacterized protein
228	1	Q9HNJ2|Q9HNJ2	Putative uncharacterized protein
229	1	Q9HMU9|Q9HMU9	Nitrite/nitrate reduction protein
232	1	Q9HPQ1|Q9HPQ1	Sodium-and chloride-dependent transporter
233	1	Q9HPQ5|Q9HPQ5	Htr8 transducer
237	1	Q9HM88|Q9HM88	Homoserine dehydrogenase
239	1	Q9HQU3|Q9HQU3	Putative uncharacterized protein
255	1	Q9HRJ0|Q9HRJ0	Putative uncharacterized protein

hit	peptides	accession	description
260	1	Q9HME2|Q9HME2	Putative uncharacterized protein
264	1	Q9HQU8|Q9HQU8	Acetyl-CoA synthetase
265	1	Q9HQE1|Q9HQE1	Glutamate dehydrogenase
273	1	Q9HQ63|DHSD	Succinate dehydrogenase hydrophobic membrane anchor subunit
277	1	Q9HNE6|Q9HNE6	Brp-like homolog
278	1	Q9HQ90|Q9HQ90	Putative uncharacterized protein
279	1	Q9HMQ2|ASSY	Argininosuccinate synthase
304	1	Q9HMB0|Q9HMB0	Putative uncharacterized protein
307	1	Q48325|TBPB	TATA-box-binding protein B
310	1	Q9HRW7|Q9HRW7	Putative uncharacterized protein
319	1	Q9HRR2|Q9HRR2	Cytochrome b6
323	1	Q9HSW6|CDC61	Cell division control protein 6 homolog 1
324	1	Q9HML8|PSTB2	Phosphate import ATP-binding protein pstB 2
328	1	Q9HQH2|Q9HQH2	Putative uncharacterized protein
331	1	Q9HRJ7|Q9HRJ7	ABC transporter, ATP-binding protein homolog
344	1	Q9HQV2|Q9HQV2	Putative uncharacterized protein
354	1	Q9HNB8|Q9HNB8	Putative uncharacterized protein
387	1	Q9HSQ7|Q9HSQ7	ABC transport protein
401	1	Q9HQ23|Q9HQ23	Putative uncharacterized protein
432	1	Q9HRH6|Q9HRH6	Putative uncharacterized protein
433	1	Q9HSE5|Q9HSE5	Putative uncharacterized protein
441	1	Q9HS52|SYP	Prolyl-tRNA synthetase
458	1	Q9HRK3|Q9HRK3	Putative uncharacterized protein
471	1	Q9HMW6|Q9HMW	Putative uncharacterized protein
472	1	Q9HQV6|Q9HQV6	Putative uncharacterized protein
482	1	Q9HMK6|Q9HMK6	Putative uncharacterized protein
490	1	Q9HR54|Q9HR54	Putative uncharacterized protein
534	1	Q9HPI6|Q9HPI6	Putative uncharacterized protein
576	1	Q9HRR3|Q9HRR3	Putative uncharacterized protein
595	1	Q9HRR7|Q9HRR7	Putative uncharacterized protein
596	1	Q9HQB1|Q9HQB1	Putative uncharacterized protein
609	1	Q9HRR6|Q9HRR6	Putative uncharacterized protein
632	1	Q9HRE8|RTCA	Probable RNA 3~-terminal phosphate cyclase
650	1	Q9HRP9|Q9HRP9	Putative uncharacterized protein
652	1	Q48295|ARCC	Carbamate kinase
654	1	Q9HSE7|Q9HSE7	Putative uncharacterized protein
689	1	Q9HRP5|Q9HRP5	Putative uncharacterized protein
694	1	Q9HPV1|Q9HPV1	Putative uncharacterized protein
719	1	O54633|O54633	Putative uncharacterized protein
748	1	Q9HR26|Q9HR26	Putative uncharacterized protein

hit	peptides	accession	description
768	1	Q9HPH6|Q9HPH6	Cobalt transport protein
901	1	Q9HHQ7|Q9HHQ7	Sn-glycerol-3-phosphate transport system permease
1001	1	Q9HRF3|Q9HRF3	Putative uncharacterized protein

END OF LIST VI

hit	peptides	accession	description
VII. Purple membrane; elastase digest; nLC-MALDI MS/MS; AVLI search specificity			
1	50	P02945|BACR	Bacteriorhodopsin
2	38	P00772|ELA1	Elastase-1 precursor - Sus scrofa
4	15	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
5	15	Q48302|Q48302	Precursor proteolipid
3	13	Q9HR99|Q9HR99	Halocyanin-like
6	11	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
7	10	Q9HN93|Q9HN93	Halocyanin-like
9	6	Q9HMG3|Q9HMG3	Putative uncharacterized protein
10	6	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
12	5	Q9HSS1|Q9HSS1	Phosphoglycerate dehydrogenase
11	4	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
17	4	Q9HMW4|Q9HMW	Oligopeptide binding protein
13	3	Q9HMF1|Q9HMF1	Aconitase
14	3	Q9HRS0|Q9HRS0	Putative uncharacterized protein
15	3	Q9HM89|EF1A	Elongation factor 1-alpha
16	3	Q9HS26|Q9HS26	Na+/H+ antiporter
20	3	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
21	3	Q9HM69|CSG	Cell surface glycoprotein
24	3	Q9HMX1|Q9HMX1	Dipeptide ABC transporter permease
47	3	Q9HN92|Q9HN92	Putative uncharacterized protein
18	2	Q9HRR1|Q9HRR1	Putative uncharacterized protein
22	2	Q9HM85|EF2	Elongation factor 2
23	2	Q9HP48|Q9HP48	NADH oxidase
27	2	Q9HS12|Q9HS12	Phosphate ABC transporter permease
28	2	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
34	2	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
39	2	Q9HP76|Q9HP76	Putative uncharacterized protein
53	2	Q9HN43|CAPPA	Phosphoenolpyruvate carboxylase
59	2	Q9HHI2|Q9HHI2	L-lactate permease
98	2	Q9HP01|Q9HP01	Spermidine/putrescine ABC transporter permease
19	1	Q9HHR4|Q9HHR4	Vng6268c
26	1	Q9HMT7|Q9HMT7	Probable thiosulfate sulfurtransferase
29	1	Q9HSM4|DHE42	NADP-specific glutamate dehydrogenase B
33	1	Q9HPA9|Q9HPA9	TRK potassium uptake system protein
36	1	Q9HRJ5|Q9HRJ5	Putative uncharacterized protein
37	1	Q9HNY2|Q9HNY2	Putative uncharacterized protein
38	1	Q9HP84|HTR4	Halobacterial transducer protein 4

hit	peptides	accession	description
40	1	Q9HR98|Q9HR98	Cystathionine gamma-synthase
43	1	Q9HRS4|Q9HRS4	Putative uncharacterized protein
44	1	Q9HS72|SECE	Preprotein translocase subunit secE
45	1	Q9HPG8|Q9HPG8	Ribonucleoside-diphosphate reductase
46	1	Q9HHN1|Q9HHN1	Na+/H+ antiporter
48	1	Q9HSM2|MUTS1	DNA mismatch repair protein mutS 1
50	1	Q9HQ64|Q9HQ64	Membrane anchor
51	1	Q9HR22|Q9HR22	Ribose ABC transporter permease
52	1	Q9HPQ2|Q9HPQ2	Daunorubicin resistance ABC transporter ATP-binding protein
54	1	P25964|BACS1	Sensory rhodopsin-1
55	1	Q9HNK1|Q9HNK1	Putative uncharacterized protein
57	1	Q9HSB5|Q9HSB5	Putative uncharacterized protein
61	1	Q9HMZ3|Q9HMZ3	Heterodisulfide reductase
66	1	P16102|BACH	Halorhodopsin
67	1	Q9HRL9|Q9HRL9	NADH dehydrogenase/oxidoreductase
69	1	Q9HQP2|Q9HQP2	Transmembrane oligosaccharyl transferase
71	1	Q9HNR0|Q9HNR0	Protein-export membrane protein
76	1	Q9HN02|Q9HN02	Hemolysin protein
80	1	Q9HPM1|Q9HPM1	Precorrin isomerase
83	1	Q9HMB7|Q9HMB7	Probable carboxypeptidase
84	1	Q9HMY7|Q9HMY7	Putative uncharacterized protein
86	1	Q9HN37|Q9HN37	Protein export
87	1	Q9HND8|VATI	V-type ATP synthase subunit I
88	1	Q9HPT9|Q9HPT9	Carboxylesterase
89	1	Q9HRN3|Q9HRN3	Proteinase IV homolog
90	1	Q9HQB8|Q9HQB8	Putative uncharacterized protein
91	1	Q9HHV1|Q9HHV1	Iron transport protein B
92	1	Q9HN47|PRIL	Probable DNA primase large subunit
95	1	Q9HN22|Q9HN22	Putative uncharacterized protein
96	1	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
103	1	Q9HME2|Q9HME2	Putative uncharacterized protein
106	1	Q9HQ90|Q9HQ90	Putative uncharacterized protein
108	1	Q9HSA0|Q9HSA0	Putative uncharacterized protein
110	1	Q9HQ63|DHSD	Succinate dehydrogenase hydrophobic membrane anchor subunit
113	1	Q9HSW2|Q9HSW2	Putative uncharacterized protein
114	1	Q9HRJ8|Q9HRJ8	Heme synthase
115	1	Q9HRT4|Q9HRT4	Putative uncharacterized protein
119	1	Q9HNP7|Q9HNP7	Putative uncharacterized protein
125	1	Q9HP66|Q9HP66	Putative uncharacterized protein
127	1	Q9HPQ1|Q9HPQ1	Sodium-and chloride-dependent transporter

hit	**peptides**	**accession**	**description**
130	1	Q9HQH2|Q9HQH2	Putative uncharacterized protein
132	1	Q9HQU3|Q9HQU3	Putative uncharacterized protein
135	1	Q9HM88|Q9HM88	Homoserine dehydrogenase
137	1	Q9HQ19|Q9HQ19	Iron
142	1	Q9HP88|Q9HP88	Phytoene dehydrogenase
149	1	Q9HMH4|Q9HMH4	Putative uncharacterized protein
151	1	Q9HRJ0|Q9HRJ0	Putative uncharacterized protein
156	1	Q9HMQ2|ASSY	Argininosuccinate synthase
161	1	Q9HNE6|Q9HNE6	Brp-like homolog
166	1	Q9HHV2|Q9HHV2	Iron transport protein A
170	1	Q9HPN9|Q9HPN9	CTAG modification methylase
174	1	Q9HPQ3|Q9HPQ3	Putative uncharacterized protein
178	1	Q9HSW6|CDC61	Cell division control protein 6 homolog 1
182	1	Q48325|TBPB	TATA-box-binding protein B
187	1	Q07971|Q07971	RepH protein
188	1	P33518|COX1	Cytochrome c oxidase polypeptide 1
189	1	Q9HS30|Q9HS30	Putative uncharacterized protein
190	1	Q9HR04|Q9HR04	Iron-binding protein
192	1	Q9HRR2|Q9HRR2	Cytochrome b6
193	1	Q9HMJ2|Q9HMJ2	Putative uncharacterized protein
195	1	Q9HMU6|Q9HMU6	Putative uncharacterized protein
198	1	O54559|O54559	Putative uncharacterized protein
208	1	Q9HNB8|Q9HNB8	Putative uncharacterized protein
212	1	Q9HRJ7|Q9HRJ7	ABC transporter, ATP-binding protein homolog
232	1	Q9HSQ7|Q9HSQ7	ABC transport protein
236	1	Q9HR54|Q9HR54	Putative uncharacterized protein
241	1	Q9HN79|Q9HN79	DNA damage-inducible protein
246	1	Q9HQU8|Q9HQU8	Acetyl-CoA synthetase
254	1	Q9HSE1|Q9HSE1	Phytoene dehydrogenase
260	1	Q9HRP5|Q9HRP5	Putative uncharacterized protein
271	1	Q9HRH6|Q9HRH6	Putative uncharacterized protein
273	1	Q9HR62|Q9HR62	Putative uncharacterized protein
282	1	Q9HRK3|Q9HRK3	Putative uncharacterized protein
286	1	O54662|O54662	Putative uncharacterized protein
289	1	O54610|O54610	CydA
294	1	Q9HMW6|Q9HMW	Putative uncharacterized protein
296	1	Q9HQV6|Q9HQV6	Putative uncharacterized protein
303	1	Q9HNW7|Q9HNW7	Phosphoribosyl transferase
309	1	Q9HPF1|Q9HPF1	Putative uncharacterized protein
332	1	Q9HPY6|Q9HPY6	Putative uncharacterized protein

hit	peptides	accession	description
375	1	Q9HQY5|Q9HQY5	Cell division inhibitor
382	1	Q9HRS8|Q9HRS8	NADH dehydrogenase/oxidoreductase
385	1	Q9HQZ0|Q9HQZ0	Acetyl-CoA synthetase
388	1	Q9HRR7|Q9HRR7	Putative uncharacterized protein
397	1	Q9HHW5|Q9HHW5	Sodium-dependent phosphate transporter
405	1	Q9HRR6|Q9HRR6	Putative uncharacterized protein
420	1	Q9HRC9|Q9HRC9	Putative uncharacterized protein
421	1	Q9HQ23|Q9HQ23	Putative uncharacterized protein
433	1	Q48295|ARCC	Carbamate kinase
447	1	Q9HS52|SYP	Prolyl-tRNA synthetase
458	1	Q9HMQ8|Q9HMQ8	D-lactate dehydrogenase
462	1	Q9HNS6|Q9HNS6	Putative uncharacterized protein
463	1	Q9HMT5|Q9HMT5	Putative uncharacterized protein
469	1	Q9HPV1|Q9HPV1	Putative uncharacterized protein
508	1	Q9HRK2|Q9HRK2	Putative uncharacterized protein
548	1	Q9HQM2|Q9HQM2	Putative uncharacterized protein
553	1	Q9HP32|PYRG	CTP synthase
647	1	Q9HS38|Q9HS38	Putative uncharacterized protein
661	1	Q9HHQ7|Q9HHQ7	Sn-glycerol-3-phosphate transport system permease
670	1	Q9HQB1|Q9HQB1	Putative uncharacterized protein

END OF LIST VII

hit	peptides	accession	description
VIII. Purple membrane; trypsin digest; nLC-MALDI MS/MS; KR search specificity			
1	8	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
4	6	Q9HMW4|Q9HMW	Oligopeptide binding protein
7	6	Q9HMZ3|Q9HMZ3	Heterodisulfide reductase
11	6	Q9HMX1|Q9HMX1	Dipeptide ABC transporter permease
5	5	Q9HHN1|Q9HHN1	Na+/H+ antiporter
6	5	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
8	5	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
10	5	Q9HP76|Q9HP76	Putative uncharacterized protein
15	5	Q9HPB1|SECY	Preprotein translocase subunit secY
9	4	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
12	4	Q9HRR3|Q9HRR3	Putative uncharacterized protein
14	4	Q9HNQ9|Q9HNQ9	Protein-export membrane protein
20	4	P02945|BACR	Bacteriorhodopsin
2	3	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
3	3	Q9HHP3|Q9HHP3	Vng6297c
16	3	Q9HS26|Q9HS26	Na+/H+ antiporter
18	3	Q9HRF2|Q9HRF2	Putative uncharacterized protein
21	3	Q9HS72|SECE	Preprotein translocase subunit secE
23	3	Q9HSQ7|Q9HSQ7	ABC transport protein
27	3	Q9HRS0|Q9HRS0	Putative uncharacterized protein
30	3	Q9HHR4|Q9HHR4	Vng6268c
32	3	Q9HQP2|Q9HQP2	Transmembrane oligosaccharyl transferase
33	3	Q9HP89|Q9HP89	Photolyase/cryptochrome
45	3	Q9HMU9|Q9HMU9	Nitrite/nitrate reduction protein
13	2	Q9HN93|Q9HN93	Halocyanin-like
17	2	Q9HRL4|Q9HRL4	NADH dehydrogenase/oxidoreductase-like protein
19	2	P33518|COX1	Cytochrome c oxidase polypeptide 1
22	2	Q9HN94|Q9HN94	Cytochrome c oxidase subunit II
25	2	Q9HRJ0|Q9HRJ0	Putative uncharacterized protein
26	2	Q9HSQ2|HTPX	Probable protease htpX homolog
28	2	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
29	2	Q9HRR1|Q9HRR1	Putative uncharacterized protein
31	2	Q9HR99|Q9HR99	Halocyanin-like
34	2	Q9HNE6|Q9HNE6	Brp-like homolog
35	2	Q9HQ04|Q9HQ04	Putative uncharacterized protein
36	2	Q9HRM1|Q9HRM1	NADH dehydrogenase/oxidoreductase-like protein
37	2	Q9HSC3|LONH	Putative protease La homolog type

hit	peptides	accession	description
38	2	Q9HRT0|Q9HRT0	Putative uncharacterized protein
39	2	Q9HSC9|Q9HSC9	N-methyltransferase homolog
40	2	Q9HS12|Q9HS12	Phosphate ABC transporter permease
41	2	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
46	2	P25964|BACS1	Sensory rhodopsin-1
47	2	Q9HMX0|Q9HMX0	Dipeptide ABC transporter permease
54	2	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
55	2	Q9HMK7|Q9HMK7	Glutaryl-CoA dehydrogenase
56	2	Q9HR16|Q9HR16	Proline permease
61	2	Q9HPU7|Q9HPU7	Bacteriorhodopsin related protein
62	2	Q9HR80|Q9HR80	Putative uncharacterized protein
63	2	Q9HNN6|Q9HNN6	Putative uncharacterized protein
64	2	P33741|HTR1	Sensory rhodopsin I transducer
76	2	Q9HRC5|Q9HRC5	Putative uncharacterized protein
82	2	P16102|BACH	Halorhodopsin
24	1	Q9HND9|Q9HND9	H+-transporting ATP synthase subunit K
42	1	Q9HMG3|Q9HMG3	Putative uncharacterized protein
43	1	Q9HR22|Q9HR22	Ribose ABC transporter permease
44	1	Q9HPD4|RL3	50S ribosomal protein L3P
48	1	Q9HRN3|Q9HRN3	Proteinase IV homolog
49	1	Q9HRR2|Q9HRR2	Cytochrome b6
50	1	Q9HN07|Q9HN07	Acylaminoacyl-peptidase
51	1	Q9HN25|Q9HN25	Putative uncharacterized protein
52	1	Q9HHS5|Q9HHS5	Vng6251h
53	1	Q9HQU7|Q9HQU7	Probable oxidoreductase
57	1	Q9HSF7|TF2B7	Transcription initiation factor IIB 7
58	1	Q9HMD1|SECG	Preprotein translocase subunit secG
59	1	Q9HRZ2|Q9HRZ2	Probable oxidoreductase
60	1	Q9HQ64|Q9HQ64	Membrane anchor
65	1	Q9HPA6|Q9HPA6	Htr-like protein
66	1	Q9HRR0|Q9HRR0	Putative uncharacterized protein
67	1	O51960|O51960	Putative uncharacterized protein
68	1	Q9HND8|VATI	V-type ATP synthase subunit I
69	1	Q9HQ63|DHSD	Succinate dehydrogenase hydrophobic membrane anchor subunit
70	1	Q9HRC9|Q9HRC9	Putative uncharacterized protein
71	1	Q9HT02|Q9HT02	Putative uncharacterized protein
72	1	Q9HQ52|THYX	Thymidylate synthase thyX
73	1	Q9HT01|Q9HT01	Putative uncharacterized protein
74	1	Q9HR62|Q9HR62	Putative uncharacterized protein
75	1	Q9HRL2|Q9HRL2	F420H2:quinone oxidoreductase chain M

hit	peptides	accession	description
77	1	Q9HPQ5|Q9HPQ5	Htr8 transducer
78	1	Q9HRL9|Q9HRL9	NADH dehydrogenase/oxidoreductase
79	1	Q9HSL5|Q9HSL5	Cationic amino acid transporter
80	1	Q9HQU6|Q9HQU6	Putative uncharacterized protein
81	1	Q9HN76|Q9HN76	Pyruvate dehydrogenase beta subunit
83	1	Q48290|FTSZ	Cell division protein ftsZ homolog
84	1	P57699|ATKB	Potassium-transporting ATPase B chain
85	1	Q9HN02|Q9HN02	Hemolysin protein
86	1	Q9HR92|HTR6	Halobacterial transducer protein 6
87	1	Q9HRM0|Q9HRM0	NADH dehydrogenase/oxidoreductase
88	1	Q9HNK1|Q9HNK1	Putative uncharacterized protein
89	1	Q9HRQ7|Q9HRQ7	Putative uncharacterized protein
90	1	Q9HQ81|Q9HQ81	TRK potassium uptake system protein
91	1	Q9HN58|Q9HN58	Putative uncharacterized protein
92	1	Q9HQQ6|Q9HQQ6	Glycosyl transferase-like
93	1	Q9HS60|Q9HS60	Putative uncharacterized protein
94	1	Q9HQP7|Q9HQP7	Putative uncharacterized protein
95	1	Q9HSE0|Q9HSE0	Putative uncharacterized protein
96	1	Q9HSA3|MFNA	L-tyrosine decarboxylase
97	1	Q9HPJ9|GCSPA	Probable glycine dehydrogenase [decarboxylating] subunit 1
98	1	Q9HNI9|Q9HNI9	Transport protein
99	1	Q9HRC1|Q9HRC1	Putative uncharacterized protein
100	1	Q9HSE1|Q9HSE1	Phytoene dehydrogenase
101	1	O52005|O52005	Putative uncharacterized protein
102	1	Q9HNG0|Q9HNG0	Proline dehydrogenase
103	1	Q9HPX5|Q9HPX5	Htr-like protein
104	1	Q9HR54|Q9HR54	Putative uncharacterized protein
105	1	Q9HMH6|Q9HMH6	Putative uncharacterized protein
106	1	Q9HPT0|Q9HPT0	Putative uncharacterized protein
107	1	Q9HHH4|Q9HHH4	Vng6397h
108	1	Q9HRS2|Q9HRS2	Putative uncharacterized protein
109	1	Q9HR04|Q9HR04	Iron-binding protein
110	1	Q9HNM8|Q9HNM8	Putative uncharacterized protein
111	1	Q9HQV1|Q9HQV1	Putative uncharacterized protein
112	1	Q9HNS2|Q9HNS2	Glycerol-3-phosphate dehydrogenase chain C
113	1	Q9HP84|HTR4	Halobacterial transducer protein 4
114	1	Q9HMW2|Q9HMW	Oligopeptide transport permease protein
115	1	Q9HPR5|Q9HPR5	Cell division protein pelota
116	1	Q9HRK2|Q9HRK2	Putative uncharacterized protein
117	1	Q9HRY6|Q9HRY6	Probable acetyltransferase

hit	**peptides**	**accession**	**description**
118	1	Q9HNB2|Q9HNB2	DNA repair protein
119	1	Q9HHI4|Q9HHI4	Vng6379c
120	1	Q9HSJ6|Q9HSJ6	Putative uncharacterized protein
121	1	Q9HHS8|GVPO2	Protein gvpO 2
123	1	Q9HMY6|Q9HMY6	Putative uncharacterized protein
124	1	Q9HP19|Q9HP19	Putative uncharacterized protein
125	1	Q9HNT0|Q9HNT0	Putative uncharacterized protein
126	1	Q9HQS2|Q9HQS2	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase
127	1	Q9HQS6|Q9HQS6	Putative uncharacterized protein
128	1	Q9HQ42|Q9HQ42	Putative uncharacterized protein
129	1	Q9HHW0|Q9HHW	Vng6203h
130	1	Q9HQS5|Q9HQS5	Putative uncharacterized protein
131	1	Q9HQZ6|Q9HQZ6	NADH-dependent flavin oxidoreductase
132	1	Q9HRH2|Q9HRH2	Molybdenum-binding protein
133	1	Q9HRF4|Q9HRF4	Putative uncharacterized protein
134	1	Q9HN17|Q9HN17	4-hydroxybutyrate CoA transferase
135	1	Q9HQ56|Q9HQ56	Putative uncharacterized protein
136	1	O51999|O51999	RepI
137	1	Q9HN83|SYW1	Tryptophanyl-tRNA synthetase 1
138	1	Q9HQM4|Q9HQM4	Putative uncharacterized protein
139	1	Q9HMS7|Q9HMS7	DNA damage-inducible protein
140	1	Q9HQB1|Q9HQB1	Putative uncharacterized protein
141	1	Q9HRS1|Q9HRS1	Pantothenate metabolism flavoprotein
142	1	Q9HPN3|Q9HPN3	Cobalamin biosynthesis
143	1	Q9HM88|Q9HM88	Homoserine dehydrogenase
144	1	Q9HR33|Q9HR33	Putative uncharacterized protein
145	1	Q9HSS1|Q9HSS1	Phosphoglycerate dehydrogenase
146	1	Q9HSS0|Q9HSS0	Putative uncharacterized protein
147	1	Q9HS67|Q9HS67	Putative uncharacterized protein
148	1	Q9HRH6|Q9HRH6	Putative uncharacterized protein
149	1	Q9HI31|Q9HI31	Vng6391h
150	1	Q9HRA1|Q9HRA1	Htr6 transducer
151	1	Q9HQ54|Q9HQ54	Putative uncharacterized protein
152	1	Q9HP79|Q9HP79	Agmatinase
153	1	Q9HSL0|Q9HSL0	Putative uncharacterized protein
155	1	Q9HQD7|HUTG	Probable formimidoylglutamase
160	1	Q9HNA3|Q9HNA3	Putative uncharacterized protein
161	1	Q9HS87|Q9HS87	Putative uncharacterized protein
163	1	Q9HPK0|GCSPB	Probable glycine dehydrogenase [decarboxylating] subunit 2
167	1	Q9HRU7|Q9HRU7	Putative uncharacterized protein

hit	peptides	accession	description
168	1	Q9HN78|LIPA	Probable lipoyl synthase
176	1	Q9HRT5|Q9HRT5	Putative uncharacterized protein
178	1	Q9HMG7|Q9HMG7	Ferrichrome ABC transporter permease

END OF LIST VIII

hit	**peptides**	**accession**	**description**
IX. Purple membrane; trypsin digest; nLC-MALDI MS/MS; no search specificity			
1	39	P02945|BACR	Bacteriorhodopsin
2	22	Q9HMW9|Q9HMW	Dipeptide ABC transporter dipeptide-binding
4	10	Q9HHN1|Q9HHN1	Na+/H+ antiporter
6	10	Q9HMW4|Q9HMW	Oligopeptide binding protein
8	9	Q9HSA8|Q9HSA8	Bifunctional short chain isoprenyl diphosphate synthase
5	8	Q9HN95|Q9HN95	Cytochrome c oxidase subunit I
7	8	Q9HRR3|Q9HRR3	Putative uncharacterized protein
3	7	Q9HN93|Q9HN93	Halocyanin-like
12	7	Q9HMX1|Q9HMX1	Dipeptide ABC transporter permease
9	6	Q48302|Q48302	Precursor proteolipid
10	6	Q9HNQ9|Q9HNQ9	Protein-export membrane protein
13	5	Q9HMI3|Q9HMI3	Dipeptide ABC transporter ATP-binding
16	5	Q9HM69|CSG	Cell surface glycoprotein
21	5	Q9HP76|Q9HP76	Putative uncharacterized protein
11	4	Q9HHP3|Q9HHP3	Vng6297c
15	4	Q9HMK0|Q9HMK0	Putative uncharacterized protein
18	4	Q9HMZ3|Q9HMZ3	Heterodisulfide reductase
19	4	Q9HSQ7|Q9HSQ7	ABC transport protein
20	4	Q9HMG3|Q9HMG3	Putative uncharacterized protein
24	4	Q9HQP2|Q9HQP2	Transmembrane oligosaccharyl transferase
35	4	Q9HHR4|Q9HHR4	Vng6268c
14	3	Q9HRQ9|Q9HRQ9	Putative uncharacterized protein
17	3	Q9HRS0|Q9HRS0	Putative uncharacterized protein
25	3	Q9HPB1|SECY	Preprotein translocase subunit secY
28	3	Q9HRU5|Q9HRU5	Immunogenic protein
29	3	Q9HRL3|Q9HRL3	F420H2:quinone oxidoreductase chain L
30	3	Q9HSQ2|HTPX	Probable protease htpX homolog
31	3	Q9HRR1|Q9HRR1	Putative uncharacterized protein
36	3	Q9HS72|SECE	Preprotein translocase subunit secE
41	3	Q9HQ04|Q9HQ04	Putative uncharacterized protein
22	2	P33518|COX1	Cytochrome c oxidase polypeptide 1
23	2	Q9HRM1|Q9HRM1	NADH dehydrogenase/oxidoreductase-like protein
26	2	Q9HRL4|Q9HRL4	NADH dehydrogenase/oxidoreductase-like protein
27	2	Q9HN94|Q9HN94	Cytochrome c oxidase subunit II
32	2	Q9HRF2|Q9HRF2	Putative uncharacterized protein
33	2	Q9HRJ0|Q9HRJ0	Putative uncharacterized protein
37	2	Q9HS26|Q9HS26	Na+/H+ antiporter

hit	peptides	accession	description
38	2	Q9HNN6|Q9HNN6	Putative uncharacterized protein
39	2	Q9HQV3|Q9HQV3	Putative uncharacterized protein
40	2	Q9HQF4|Q9HQF4	Membrane protein
43	2	Q9HQA6|Q9HQA6	Putative uncharacterized protein
44	2	Q9HP89|Q9HP89	Photolyase/cryptochrome
45	2	O59634|O59634	Methyl-accepting aerotaxis transducer protein
46	2	Q9HS51|Q9HS51	Putative uncharacterized protein
47	2	Q9HRT0|Q9HRT0	Putative uncharacterized protein
49	2	Q9HR99|Q9HR99	Halocyanin-like
51	2	Q9HSC3|LONH	Putative protease La homolog type
52	2	Q9HNE6|Q9HNE6	Brp-like homolog
64	2	Q9HMX0|Q9HMX0	Dipeptide ABC transporter permease
34	1	Q9HS12|Q9HS12	Phosphate ABC transporter permease
42	1	P25964|BACS1	Sensory rhodopsin-1
48	1	Q9HR22|Q9HR22	Ribose ABC transporter permease
50	1	Q9HNR0|Q9HNR0	Protein-export membrane protein
54	1	Q9HPU7|Q9HPU7	Bacteriorhodopsin related protein
55	1	Q9HRN3|Q9HRN3	Proteinase IV homolog
56	1	Q9HMU9|Q9HMU9	Nitrite/nitrate reduction protein
57	1	Q9HN07|Q9HN07	Acylaminoacyl-peptidase
58	1	Q9HN92|Q9HN92	Putative uncharacterized protein
59	1	Q9HRL8|Q9HRL8	NADH dehydrogenase/oxidoreductase
60	1	Q9HRJ9|Q9HRJ9	Cytochrome c oxidase subunit 2
61	1	Q9HHJ8|Q9HHJ8	DNA polymerase B2
62	1	Q9HR16|Q9HR16	Proline permease
63	1	Q9HT01|Q9HT01	Putative uncharacterized protein
68	1	Q9HND8|VATI	V-type ATP synthase subunit I
69	1	Q9HQU7|Q9HQU7	Probable oxidoreductase
71	1	Q9HPD4|RL3	50S ribosomal protein L3P
72	1	Q9HRL1|Q9HRL1	NADH dehydrogenase/oxidoreductase
74	1	Q9HSF7|TF2B7	Transcription initiation factor IIB 7
75	1	Q9HT00|GLMS	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
78	1	Q9HQ63|DHSD	Succinate dehydrogenase hydrophobic membrane anchor subunit
81	1	Q9HN25|Q9HN25	Putative uncharacterized protein
87	1	Q9HSL5|Q9HSL5	Cationic amino acid transporter
88	1	Q9HNB2|Q9HNB2	DNA repair protein
93	1	Q9HHS5|Q9HHS5	Vng6251h
94	1	Q9HT02|Q9HT02	Putative uncharacterized protein
105	1	Q9HP72|HEM1	Glutamyl-tRNA reductase
107	1	Q9HRL9|Q9HRL9	NADH dehydrogenase/oxidoreductase

hit	peptides	accession	description
110	1	P00772|ELA1	Elastase-1 precursor - Sus scrofa
111	1	P71416|P71416	Transducer HtF protein
112	1	Q9HQW0|Q9HQW	Putative uncharacterized protein
113	1	Q9HQ64|Q9HQ64	Membrane anchor
114	1	Q9HMK7|Q9HMK7	Glutaryl-CoA dehydrogenase
117	1	Q9HSJ6|Q9HSJ6	Putative uncharacterized protein
118	1	Q9HP32|PYRG	CTP synthase
125	1	Q9HPA6|Q9HPA6	Htr-like protein
126	1	Q9HNK1|Q9HNK1	Putative uncharacterized protein
128	1	Q9HRD0|Q9HRD0	Anion permease
129	1	Q9HP01|Q9HP01	Spermidine/putrescine ABC transporter permease
130	1	Q9HRC9|Q9HRC9	Putative uncharacterized protein
132	1	Q9HMD1|SECG	Preprotein translocase subunit secG
134	1	Q9HRU7|Q9HRU7	Putative uncharacterized protein
136	1	Q9HQQ5|Q9HQQ5	Probable transport protein
139	1	Q9HQ03|Q9HQ03	Putative uncharacterized protein
150	1	P16102|BACH	Halorhodopsin
158	1	Q9HNT9|Q9HNT9	Putative uncharacterized protein
159	1	Q9HPX0|Q9HPX0	Aspartate-semialdehyde dehydrogenase
160	1	Q9HRZ2|Q9HRZ2	Probable oxidoreductase
163	1	Q9HR62|Q9HR62	Putative uncharacterized protein
164	1	Q9HRY9|Q9HRY9	Putative uncharacterized protein
169	1	Q9HMS1|Q9HMS1	Putative uncharacterized protein
170	1	Q9HR07|Q9HR07	Putative uncharacterized protein
197	1	O51960|O51960	Putative uncharacterized protein
199	1	Q9HS48|Q9HS48	Putative uncharacterized protein
202	1	Q9HQW3|Q9HQW	Putative uncharacterized protein
213	1	Q9HS33|Q9HS33	Multidrug resistance protein homolog
220	1	Q9HSA0|Q9HSA0	Putative uncharacterized protein
230	1	Q9HN82|ENDA	tRNA-splicing endonuclease
234	1	Q9HN85|Q9HN85	Phosphomannomutase
285	1	Q9HNZ0|NADB	L-aspartate oxidase
301	1	Q9HSJ5|Q9HSJ5	Putative uncharacterized protein
339	1	Q9HQ52|THYX	Thymidylate synthase thyX
344	1	Q9HN76|Q9HN76	Pyruvate dehydrogenase beta subunit
375	1	Q48290|FTSZ	Cell division protein ftsZ homolog
394	1	Q9HQQ6|Q9HQQ6	Glycosyl transferase-like
395	1	Q9HNU0|Q9HNU0	Formyltetrahydrofolate deformylase
454	1	P17103|Y1111	Uncharacterized GTP-binding protein VNG1111G
508	1	Q9HRM0|Q9HRM0	NADH dehydrogenase/oxidoreductase

hit	peptides	accession	description
536	1	O51958|O51958	Putative uncharacterized protein
635	1	Q9HSM8|Q9HSM8	Oxalate/formate antiporter

END OF LIST IX