

Bait	Prey (Unipro	MIST	Compass	Protein.names
PiIG	P46384	0.94756483	533.120937	Protein PiIG
PiIG	Q9HVVU3	0.92980307	442.797676	Maf-like protein PA4478
PiIG	Q9HVVH2	0.90073391	2158.29052	Probable c-type cytochrome
PiIG	Q9I4E1	0.89799766	199.613144	NAD-dependent protein deacylase 2 (E
PiIG	Q9HTZ6	0.89690122	135.494044	33 kDa chaperonin (Heat shock protein
PiIG	Q9I6V0	0.89157802	169.520896	Probable short-chain dehydrogenase
PiIG	Q9X6V8	0.85480747	84.5944088	UPF0250 protein PA3998
PiIG	Q9HVL7	0.83948028	58.0947502	50S ribosomal protein L27
PiIG	Q51465	0.83947855	19.7924499	Flagellar motor switch protein FliM
PiIG	P37452	0.83801107	123.237575	LexA repressor (EC 3.4.21.88)
PiIG	Q9HVVH1	0.83357547	91.8558654	Uncharacterized protein
PiIG	Q9HZ62	0.83272804	93.9719614	Phosphoglycolate phosphatase 2 (PGP :
PiIG	Q9HVF5	0.82343211	20.474287	Uncharacterized protein
PiIG	Q9I3U7	0.82297904	72.1463488	Probable two-component response reg
PiIG	G3XD63	0.81907656	153.441014	Probable methylesterase
PiIG	Q9I513	0.81240588	23.7246789	Phosphoribosylformylglycinamide cyc
PiIG	Q9HVVH0	0.80842148	2471.26913	Probable oxidoreductase
PiIG	Q9I6D5	0.79868119	52.3422138	Uncharacterized protein
PiIG	Q9HY39	0.79835541	91.8558654	Transcriptional regulator MetR
PiIG	Q9HXI9	0.7823838	6.38749814	Probable iron-binding protein IscU
PiIG	G3XD36	0.77242154	43.172251	Phosphoenolpyruvate-protein phospho
PiIG	Q9I0M7	0.77198877	75.8385471	Siroheme synthase [Includes: Uroporph
PiIG	Q9HZI5	0.77023575	62.5397089	Uncharacterized protein
PiIG	P07344	0.76905965	59.1853513	Tryptophan synthase alpha chain (EC 4.
PiIG	Q9HY55	0.730858	24.7937924	Phosphotransferase system transporter
PiIG	Q9HVC9	0.72848652	38.9131072	Molybdopterin biosynthesis MoeB prot
PiIG	Q9I405	0.7247461	18.0027946	Amino acid ABC transporter ATP bindin
PiIG	Q9I7B0	0.72265623	99.2148672	Potassium uptake protein TrkA
PiIG	Q51373	0.71457022	14.995475	Response regulator GacA (Global activa
PiIG	Q51382	0.71073047	8.09575782	Chaperone protein HscA homolog
PiIG	Q9I1S2	0.69942845	14.2795746	Hydrogen cyanide synthase subunit Hcr
PiIG	Q9HVV6	0.68907521	9.95924195	Probable ATP-binding component of AB
PiIG	Q9HY14	0.68551168	10.7791234	Uncharacterized protein
PiIG	Q9I446	0.6855114	10.7791234	Uncharacterized protein
PiIG	Q9I6K8	0.68551096	15.2439824	Sulfate transport protein CysT
PiIG	Q9HUU6	0.68551092	7.62199122	Urease subunit beta (EC 3.5.1.5) (Urea :
PiIG	Q9I5A0	0.68551048	10.7791234	Probable oxidoreductase
PiIG	Q9HZM1	0.68551047	4.44887063	Probable tolQ-type transport protein
PiIG	Q9HUI2	0.6855104	7.62199122	Transcriptional regulatory protein AruR
PiIG	Q9HXT6	0.68551039	7.62199122	Uncharacterized protein
PiIG	Q9I364	0.68551036	3.66067043	Uncharacterized protein
PiIG	Q9I2A1	0.68551035	7.62199122	Probable transcriptional regulator
PiIG	Q9HUE0	0.68551032	7.62199122	Probable transcriptional regulator
PiIG	Q9I5V7	0.68551027	7.62199122	tRNA N6-adenosine threonylcarbamoyl

PiIG	Q9HZM3	0.68551026	7.62199122	Tetraacyldisaccharide 4'-kinase (EC 2.7.
PiIG	Q9HY20	0.68551026	7.62199122	Uncharacterized protein
PiIG	Q9HZN7	0.68551025	3.33621278	Uncharacterized protein
PiIG	Q9I6V2	0.68551023	7.62199122	Chemotactic transducer for trichloroeth
PiIG	Q9I746	0.68551023	7.62199122	Uncharacterized protein
PiIG	Q9HYK0	0.6855102	7.62199122	Probable outer membrane protein
PiIG	G3XCU2	0.68551019	7.62199122	Transcriptional regulator ArgR
PiIG	Q9I280	0.68551018	7.62199122	Probable decarboxylase
PiIG	Q51463	0.68551017	7.62199122	Flagellar M-ring protein
PiIG	Q9HX73	0.68551017	7.62199122	Uncharacterized protein
PiIG	Q9I238	0.68551015	7.62199122	Uncharacterized protein
PiIG	Q9I751	0.68551013	7.62199122	Fha1
PiIG	Q9HTC2	0.68551013	7.62199122	Probable coenzyme A transferase
PiIG	Q9HVA7	0.68551013	7.62199122	Iron (III)-transport system permease Hii
PiIG	G3XD14	0.67847643	13.31661	RNA polymerase-binding transcription f
PiIG	Q9HXR3	0.67769377	22.9714212	Uncharacterized protein
PiIG	Q9HZP9	0.67580693	19.7924499	Precorrin-4 C(11)-methyltransferase (EC
PiIG	Q9HVP8	0.67574976	27.990751	Dephospho-CoA kinase (EC 2.7.1.24) (D
PiIG	P22008	0.66771021	21.2314821	Pyrroline-5-carboxylate reductase (P5C
PiIG	P13982	0.66691581	10.6818345	Carbamate kinase (EC 2.7.2.2)
PiIG	Q9HXJ4	0.66309695	12.9866672	4-hydroxy-3-methylbut-2-en-1-yl diph
PiIG	Q9I2F4	0.65881715	9.97205918	Phosphofructokinase
PiIG	Q9I0D5	0.65631009	8.32316491	Uncharacterized protein
PiIG	Q9I2S3	0.65605595	96.6202958	Uncharacterized protein
PiIG	Q9I4Z9	0.64598481	8.20971855	Protein SlyX homolog
PiIG	Q9I5A5	0.64487191	9.61140501	Phosphate acetyltransferase (EC 2.3.1.8
PiIG	Q9HXB5	0.64415146	22.3903703	Probable transcriptional regulator
PiIG	Q9I0F4	0.63988557	11.0326955	Uncharacterized protein
PiIG	Q9HZA6	0.63045828	30.2068784	Motility protein FimV
PiIG	Q9HUN3	0.62517859	75.323603	Replicative DNA helicase
PiIG	P23747	0.62044557	4.10255212	Alginate biosynthesis transcriptional req
PiIG	Q9HV13	0.61878101	6.94365075	Uncharacterized protein
PiIG	Q9HV99	0.61802009	18.0981661	Uncharacterized protein
PiIG	Q9I0L2	0.61707788	4.44887063	tRNA-specific 2-thiouridylase MnmA (EC
PiIG	Q9I2Z2	0.61604612	3.12031088	Uncharacterized protein
PiIG	Q9HXD3	0.6113251	4.44887063	Two-component response regulator Na
PiIG	P15275	0.60932026	2.7862587	Transcriptional regulatory protein AlgQ
PiIG	Q9RQ16	0.60712528	12.2749649	UPF0301 protein AlgH
PiIG	Q9I5U4	0.60620823	19.9529337	4-hydroxythreonine-4-phosphate dehyd
PiIG	Q9I3D4	0.59185634	10.3664445	Succinate dehydrogenase (B subunit)
PiIG	Q9I4V8	0.59007909	8.20971855	Probable transcriptional regulator
PiIG	P34750	0.58829498	44.9409887	Fimbrial assembly protein PilQ
PiIG	Q9HU53	0.58780665	14.3708974	2,3-bisphosphoglycerate-independent p
PiIG	Q9HVV1	0.58523979	8.09575782	Probable oxidoreductase
PiIG	Q9I400	0.58511853	11.0309007	Probable short-chain dehydrogenase

PiIG	Q9HXE5	0.58510912	18.55951	ATP-dependent RNA helicase RhlB (EC 3.6.1.15)
PiIG	Q9HTV1	0.58449056	10.7124518	Transcription termination factor Rho (E
PiIG	Q9I495	0.58303263	17.5099061	Probable sensor/response regulator hyl
PiIG	Q9I012	0.58274503	6.48428048	Uncharacterized protein
PiIG	Q9I0B2	0.58180613	21.5059254	Uncharacterized protein
PiIG	Q9HZQ2	0.58058876	9.69647516	Protein CobW
PiIG	Q9HVZ4	0.57992927	8.08023382	Protein MraZ
PiIG	Q9I1E9	0.579915	30.5748042	Probable ATP-binding component of AB
PiIG	Q9HT35	0.57322984	24.2890443	GTP cyclohydrolase FolE2 (EC 3.5.4.16)
PiIG	Q9HZI3	0.57131189	5.51026733	Probable lipid kinase YegS-like (EC 2.7.1
PiIG	Q9HT76	0.56969468	16.5538079	NrdJa
PiIG	Q9HVW6	0.56502204	4.44887063	Uncharacterized protein
PiIG	Q9HT22	0.56422401	4.44887063	Bifunctional protein GlnU [Includes: Uf
PiIG	Q9I0J4	0.56302588	14.5160508	NADH-quinone oxidoreductase subunit
PiIG	Q9HXJ0	0.55904233	2.97585032	Probable iron-binding protein IscA
PiIG	Q9HVT2	0.55831808	3.33621278	UPF0192 protein PA4489
PiIG	Q9I524	0.55778488	11.9962047	GTP pyrophosphokinase
PiIG	Q9I6Z8	0.55186351	6.48428048	Probable guanine deaminase
PiIG	Q9HUB8	0.55156778	4.5850787	Probable protein kinase UbiB (EC 2.7.-.-
PiIG	Q9HVX5	0.54473756	8.09575782	Uncharacterized protein
PiIG	Q9I2U0	0.54351088	7.17277725	ATP-dependent Clp protease ATP-bindin
PiIG	Q9HYU6	0.54217095	14.3435304	Probable ATP-dependent helicase
PiIG	Q9HYC8	0.5418642	7.57212329	Uncharacterized protein
PiIG	Q9HWK1	0.53552876	15.2706616	Probable acetolactate synthase large su
PiIG	Q9HVQ4	0.53436935	90.9571517	Uncharacterized protein
PiIG	Q9I325	0.53008708	8.68064398	Regulatory protein PcrH
PiIG	Q9HYT2	0.52524115	34.3498959	Probable 3-hydroxyisobutyrate dehydr
PiIG	Q9HY41	0.52429211	8.20844332	Glycerol kinase 1 (EC 2.7.1.30) (ATP:glyc
PiIG	Q9HXY6	0.52287899	24.8399866	UDP-3-O-acylglucosamine N-acyltransfe
PiIG	Q9HW01	0.52183514	4.78530505	UDP-N-acetylglucosamine--N-acetylmur
PiIG	Q9HXU4	0.51679176	4.44887063	Uncharacterized protein
PiIG	Q9HUM9	0.51563621	13.9534729	30S ribosomal protein S6
PiIG	G3XCT6	0.51374654	3.57947766	Probable two-component sensor
PiIG	Q9HT80	0.51339726	6.88789721	DNA polymerase I (POL I) (EC 2.7.7.7)
PiIG	Q9HVQ2	0.51296143	3.3731643	Probable chemotaxis transducer
PiIG	Q9I383	0.5127067	7.67487253	Selenide, water dikinase (EC 2.7.9.3) (Se
PiIG	Q9HT73	0.51179938	12.9225457	Zinc import ATP-binding protein ZnuC (I
PiIG	Q9HUD4	0.51128275	4.92213549	Uncharacterized protein
PiIG	Q9I5A8	0.51086287	11.4968435	Uncharacterized protein
PiIG	Q9HTD5	0.50775936	4.71811737	Probable transcriptional regulator
PiIG	Q9HVU0	0.49692172	4.78748919	Rod shape-determining protein MreB
PiIG	Q9I4Y1	0.49375978	4.44887063	Uncharacterized protein
PiIG	Q9I1W2	0.49257785	32.8319777	1,4-alpha-glucan branching enzyme Glg
PiIG	Q9HV42	0.49081996	10.0555624	Protein GrpE (HSP-70 cofactor)
PiIG	P08280	0.48171765	6.4757254	Protein RecA (Recombinase A)

PiIG	Q9HXZ4	0.47863369	3.24323395	CTP synthase (EC 6.3.4.2) (CTP syntheta
PiIG	Q9HZ68	0.47792003	5.84249194	Histidinol-phosphate aminotransferase
PiIG	Q9HT39	0.47764434	22.0422655	Uncharacterized protein
PiIG	Q9HTU9	0.47602888	7.6849198	Uncharacterized protein
PiIG	G3XDA1	0.47394998	38.0803572	Exoenzyme S
PiIG	G3XCV0	0.47210708	4.59302294	Transcriptional regulator FleQ
PiIG	P30718	0.47067436	34.1289584	60 kDa chaperonin (GroEL protein) (Pro
PiIG	Q9K3C5	0.46955805	5.08342894	B-type flagellar hook-associated proteir
PiIG	Q9I4W4	0.46809269	11.1303157	Uncharacterized protein
PiIG	Q9I179	0.46802176	23.6568396	Probable non-ribosomal peptide synthe
PiIG	Q9HXZ1	0.46662215	12.5183323	DNA polymerase III subunit alpha (EC 2.
PiIG	Q9HV43	0.46461929	25.84745	Chaperone protein DnaK (HSP70) (Heat
PiIG	Q9HXP1	0.4641752	7.70566996	Uncharacterized protein
PiIG	Q9HZT5	0.46350424	4.71811737	Probable ATP-binding component of AB
PiIG	Q9I689	0.46289417	21.4235091	ATP-dependent RNA helicase RhlE (EC 3
PiIG	P47204	0.46287069	5.13637249	Cell division protein FtsZ
PiIG	Q9I5Q6	0.46092645	4.55628412	Iron-sulfur cluster insertion protein Erp.
PiIG	Q9HW21	0.46069207	3.21729442	Probable two-component response reg
PiIG	Q9IOV0	0.46069198	4.44887063	Probable transcriptional regulator
PiIG	Q9HXE4	0.46069198	4.44887063	NAD(P)H-dependent anabolic L-arginine
PiIG	Q9I6I9	0.46023542	4.94087877	Polyamine transport protein PotG
PiIG	P15276	0.46006345	7.99005196	Transcriptional regulatory protein AlgP
PiIG	Q9I003	0.45927916	20.4839278	ATP-dependent RNA helicase DeaD (EC
PiIG	P57112	0.45925985	7.46156038	Soluble pyridine nucleotide transhydrog
PiIG	Q9I3C5	0.459043	10.8049748	Chaperone protein HtpG (Heat shock pr
PiIG	Q9HT77	0.45828172	6.61898993	NrdJb
PiIG	Q51422	0.4531545	2.56259958	Aspartate--tRNA ligase (EC 6.1.1.12) (As
PiIG	Q9HUX5	0.45266218	9.92675428	Uncharacterized protein
PiIG	Q9HZM8	0.45264361	9.11121196	Ribonuclease E (RNase E) (EC 3.1.26.12)
PiIG	Q9HZK4	0.45082506	3.48205474	Probable glyceraldehyde-3-phosphate c
PiIG	Q9I5F6	0.45068447	6.42593119	Proline dehydrogenase PutA
PiIG	Q9HVS8	0.45057018	2.42971869	RoxR
PiIG	Q9I5P0	0.44859318	4.5850787	Probable type II secretion system prote
PiIG	Q9I2V5	0.44725161	6.82296069	Aconitate hydratase 2 (Aconitase 2) (EC
PiIG	Q9I239	0.44652223	9.38630862	Probable transcriptional regulator
PiIG	P48372	0.44521876	6.63891856	DNA gyrase subunit A (EC 5.99.1.3)
PiIG	Q9I5H1	0.44362923	6.86252263	Uncharacterized protein
PiIG	G3XD93	0.44333976	13.388187	Probable chaperone
PiIG	Q51466	0.44212118	5.91617964	Flagellar motor switch protein FliN
PiIG	G3XD61	0.44128517	4.50776052	UDP-2,3-diacetamido-2,3-dideoxy-D-glu
PiIG	Q9I4L9	0.44104356	4.44887063	Uncharacterized protein
PiIG	Q9I6A1	0.43995692	8.62743894	Cystathionine beta-synthase
PiIG	Q9HX38	0.43809606	17.7698173	Uncharacterized protein
PiIG	Q9HT12	0.43662766	15.7039676	Chromosome partitioning protein Spo0.
PiIG	Q9LCT3	0.43620776	5.34591409	Protein translocase subunit SecA

PiIG	Q9I181	0.43564134	36.0976536	PvdJ
PiIG	Q9I7C2	0.43510652	2.64296591	DNA gyrase subunit B (EC 5.99.1.3)
PiIG	Q9I1F5	0.43418264	9.1552543	Probable glyceraldehyde-3-phosphate c
PiIG	Q9I323	0.43346716	16.5118922	Translocator outer membrane protein F
PiIG	P09591	0.43251226	6.20839855	Elongation factor Tu (EF-Tu)
PiIG	Q9HWW7	0.43023697	18.6737066	Probable thioredoxin
PiIG	P38100	0.42833574	5.39185453	Carbamoyl-phosphate synthase large ct
PiIG	Q9I0J6	0.42828254	3.63524536	NADH-quinone oxidoreductase subunit
PiIG	Q9HYG4	0.42684135	9.08905892	Aliphatic sulfonates import ATP-binding
PiIG	Q9I403	0.42629412	3.21729442	Amino acid ABC transporter membrane
PiIG	P52024	0.42593596	3.21729442	DNA polymerase III subunit delta' (EC 2.
PiIG	O50274	0.42462522	6.98104741	Bifunctional enzyme CysN/CysC [Includ
PiIG	Q9I762	0.42373042	6.30567143	Uncharacterized protein
PiIG	Q9HWW1	0.42356394	5.5802973	Outer membrane protein OprG
PiIG	Q9I0K0	0.42351173	3.57543165	NADH-quinone oxidoreductase subunit
PiIG	Q9I157	0.42209996	28.6396372	PvdL
PiIG	Q9HVU7	0.42163195	2.20169366	Uncharacterized protein
PiIG	Q9I2U2	0.42109325	8.30889935	Trigger factor (TF) (EC 5.2.1.8) (PPlase)
PiIG	Q9HV59	0.41946529	9.81401559	Polyribonucleotide nucleotidyltransfera
PiIG	Q9HTZ7	0.41924014	13.4819876	Phosphoenolpyruvate carboxykinase [A
PiIG	Q9HXC2	0.41881216	27.5109263	Probable ATP-binding component of AE
PiIG	Q9HVC5	0.41772584	5.07234143	Ribose-phosphate pyrophosphokinase (
PiIG	Q9HWC7	0.4172971	2.70970433	50S ribosomal protein L10
PiIG	Q9I2A0	0.41716918	17.9064941	3-hydroxy-3-methylglutaryl-CoA lyase
PiIG	G3XD17	0.41682292	5.97574764	Thiol:disulfide interchange protein DsbI
PiIG	Q9HW15	0.41678875	2.23053521	Probable short-chain dehydrogenase
PiIG	Q9I3D5	0.41616448	2.61796551	Succinate dehydrogenase (A subunit)
PiIG	Q9HTW7	0.41465865	4.75668749	UbiH protein
PiIG	Q9HUT4	0.41447944	6.06154651	Uncharacterized protein
PiIG	Q9I278	0.41328462	4.44887063	Uncharacterized protein
PiIG	Q9I022	0.41002479	4.84242558	Probable glutathione S-transferase
PiIG	Q9HZM9	0.40981588	11.1907226	Ribosomal large subunit pseudouridine
PiIG	Q9I182	0.40923967	20.6256856	Pyoverdine synthetase D
PiIG	Q9HWP6	0.40881553	11.6102953	Probable transcriptional regulator
PiIG	Q9HYZ5	0.40696	6.89620385	Cell division topological specificity factc
PiIG	Q9I4Q5	0.40682833	5.59740513	Uncharacterized protein
PiIG	Q9HV53	0.40574454	3.85277931	Ribosome maturation factor RimP
PiIG	Q9HT19	0.40497547	1.44244081	ATP synthase gamma chain (ATP syntha
PiIG	Q9HTZ9	0.40465468	5.59072296	Probable nitroreductase
PiIG	Q9HV96	0.40450367	11.1365789	Uncharacterized protein
PiIG	G3XD23	0.40428652	3.90097364	UDP-N-acetyl-2-amino-2-deoxy-D-glucu
PiIG	Q9I0A7	0.40124167	10.8195884	Probable restriction-modification syste
PiIG	Q9I0J7	0.40099259	4.53421893	NADH-quinone oxidoreductase subunit
PiIG	Q9HZG8	0.40093035	3.94999118	Uncharacterized protein
PiIG	Q9HWC6	0.40033454	8.65826517	50S ribosomal protein L1

PiIG	Q9HVC4	0.40030231	3.25941846	50S ribosomal protein L25 (General stre
PiIG	Q9I1V0	0.39926339	11.0833408	Glycogen synthase (EC 2.4.1.21) (Starch
PiIG	Q9I2T9	0.39887231	6.66273779	Lon protease (EC 3.4.21.53) (ATP-deper
PiIG	Q9HZA7	0.39802895	2.78908024	Acetyl-coenzyme A carboxylase carboxy
PiIG	Q9HY77	0.39774542	1.77667556	Glutaredoxin
PiIG	Q9HXR1	0.39658006	15.0779675	Uncharacterized protein
PiIG	P37799	0.39612222	4.13576481	Biotin carboxyl carrier protein of acetyl-
PiIG	Q9I6B4	0.39470889	3.72374231	Thiazole synthase (EC 2.8.1.10)
PiIG	Q9HZ71	0.39203281	2.62569261	30S ribosomal protein S1
PiIG	Q9I0L8	0.39194766	3.83945686	ATP-binding protease component ClpA
PiIG	Q9HYE0	0.39056175	11.666044	Probable ATP-dependent RNA helicase
PiIG	Q9HX16	0.38799372	4.82594163	Uncharacterized protein
PiIG	Q9I0A0	0.38743065	3.02424168	Translation initiation factor IF-3
PiIG	Q9I0Z9	0.38668435	1.76240797	Uncharacterized protein
PiIG	Q9I1V4	0.38613621	6.24911552	Uncharacterized protein
PiIG	Q9HWF0	0.38475178	3.59750601	50S ribosomal protein L6
PiIG	Q9HUD0	0.38460432	1.10114806	50S ribosomal protein L31
PiIG	Q9HYT5	0.38433195	4.54471286	Universal stress protein
PiIG	Q9I3I1	0.38428137	11.1232972	DNA polymerase subunits gamma and t
PiIG	Q9HVV2	0.38424332	2.69570399	50S ribosomal protein L13
PiIG	Q9HWC8	0.38424094	4.96543975	50S ribosomal protein L7/L12
PiIG	Q9HWC5	0.38409281	2.1529275	50S ribosomal protein L11
PiIG	Q9HV40	0.38389613	5.37739678	SsrA-binding protein
PiIG	Q9HUK1	0.38247825	3.87598091	DNA topoisomerase 4 subunit A (EC 5.9
PiIG	Q9I5Q7	0.38187736	2.53711185	Uncharacterized protein
PiIG	Q9I291	0.38163822	3.21274722	UTP--glucose-1-phosphate uridylyltrans
PiIG	P65116	0.38156887	7.53914836	Translation initiation factor IF-1
PiIG	Q9HXJ8	0.38022932	3.38251858	GTPase Der (GTP-binding protein EngA)
PiIG	Q9HX76	0.37972464	5.18856308	Probable DNA binding protein
PiIG	Q9HVN5	0.37865695	6.89477272	Chaperone protein ClpB
PiIG	Q9I6D9	0.3779004	9.64499379	Uncharacterized protein
PiIG	Q9HVV7	0.37650915	2.06407013	UDP-N-acetylglucosamine 1-carboxyvin
PiIG	Q9HY25	0.37548393	3.97997722	50S ribosomal protein L31 type B
PiIG	Q9HWE7	0.37476507	1.64119887	50S ribosomal protein L5
PiIG	Q9HWD2	0.37455595	3.22448862	Elongation factor G 1 (EF-G 1)
PiIG	P05384	0.37451737	7.61068668	DNA-binding protein HU-beta
PiIG	Q9HVV4	0.37420657	0.4082862	Ubiquinol-cytochrome c reductase iron-
PiIG	Q9HUU1	0.3739482	11.0244277	Oxaloacetate decarboxylase (EC 4.1.1.3
PiIG	Q9HUC5	0.37188841	5.18097591	ATP-dependent protease ATPase subun
PiIG	Q9HUM7	0.37089907	8.34948488	Ribonuclease R (RNase R) (EC 3.1.13.1)
PiIG	Q9HWE0	0.3707914	1.264735	50S ribosomal protein L22
PiIG	Q9I4W9	0.36950221	3.33621278	Quinolate synthase A (EC 2.5.1.72)
PiIG	Q9HUC3	0.36931328	1.00457501	Polyhydroxyalkanoate synthesis proteir
PiIG	Q9HZ55	0.3687225	3.05625711	Ribosomal large subunit pseudouridine
PiIG	Q51561	0.36868467	7.31635296	DNA-directed RNA polymerase subunit

PiIG	Q9I4K8	0.3676529	16.6001401	Probable oxidoreductase
PiIG	Q9HWF8	0.36713916	0.53404105	30S ribosomal protein S11
PiIG	Q9HTQ3	0.36656158	5.54406053	Probable transcriptional regulator
PiIG	Q9HWD6	0.36638342	3.76314782	50S ribosomal protein L4
PiIG	Q9HWE5	0.36584946	0.62229596	50S ribosomal protein L14
PiIG	O68822	0.36535254	7.68518513	Cytosol aminopeptidase (EC 3.4.11.1) (L
PiIG	Q9HW72	0.36449823	8.05234589	Pyruvate kinase (EC 2.7.1.40)
PiIG	Q9I3D2	0.36432026	2.65490727	Dihydrolipoyllysine-residue succinyltrar
PiIG	Q9I0A2	0.3639347	0.67349756	50S ribosomal protein L20
PiIG	Q9HU56	0.36306755	2.01511949	Protein-export protein SecB
PiIG	Q59637	0.36286306	4.32593904	Pyruvate dehydrogenase E1 componen
PiIG	Q9HWD4	0.36273549	0.6123171	30S ribosomal protein S10
PiIG	Q9HWE3	0.36214155	1.84369678	50S ribosomal protein L29
PiIG	Q9HWF7	0.35861621	0.70956175	30S ribosomal protein S13
PiIG	Q9I4H3	0.35845467	3.21729442	Uncharacterized protein
PiIG	Q9I0G3	0.35718978	4.39155033	Probable type II secretion system prote
PiIG	Q9I4F5	0.35709082	7.76323754	C4-dicarboxylate transport protein 2
PiIG	Q9HUN2	0.35697965	4.86819241	50S ribosomal protein L9
PiIG	Q9HYC7	0.35626648	4.65213645	Methionine--tRNA ligase (EC 6.1.1.10) (I
PiIG	Q9HVL2	0.35526901	6.357882	Peptidyl-prolyl cis-trans isomerase (EC 5
PiIG	Q9HWE4	0.35490764	0.86171631	30S ribosomal protein S17
PiIG	Q9HX15	0.35454938	3.21729442	Uncharacterized protein
PiIG	Q9HWC9	0.35215582	3.78020176	DNA-directed RNA polymerase subunit
PiIG	Q9HVA1	0.35211369	6.13200106	Acetolactate synthase isozyme III small
PiIG	Q9HWE2	0.35155354	0.30036213	50S ribosomal protein L16
PiIG	Q9HUJ8	0.35128824	7.58859881	DNA topoisomerase 4 subunit B (EC 5.9
PiIG	P72131	0.35104483	5.36375254	HTH-type transcriptional regulator PtxR
PiIG	Q9HY81	0.35003727	1.5614082	Probable peroxidase
PiIG	Q9HWZ6	0.35002724	3.48833584	Inorganic pyrophosphatase (EC 3.6.1.1)
PiIG	Q9HVM1	0.34999221	0.41561019	30S ribosomal protein S20
PiIG	Q9HUD3	0.34997396	2.55360911	Malic enzyme
PiIG	Q9HWD1	0.34970993	1.14720312	30S ribosomal protein S7
PiIG	Q9HUM8	0.34917708	3.6824269	23S rRNA (guanosine-2'-O-)-methyltran
PiIG	Q9I749	0.34868369	2.98399943	Uncharacterized protein
PiIG	Q9I0J9	0.34851728	5.15309184	NADH-quinone oxidoreductase subunit
PiIG	Q9HWF1	0.34837638	0.4772659	50S ribosomal protein L18
PiIG	P96963	0.34749381	33.5579911	DNA repair protein RadA homolog (DN/
PiIG	Q9I3D3	0.34742973	6.11048934	2-oxoglutarate dehydrogenase (E1 subu
PiIG	O54438	0.34729823	4.74402742	3-oxoacyl-[acyl-carrier-protein] reducta
PiIG	Q9HVV3	0.34698767	0.42771487	30S ribosomal protein S9
PiIG	O54439	0.34587813	0.51419938	Acyl carrier protein 1 (ACP 1)
PiIG	O30506	0.34573535	2.25245857	Arginine/ornithine transport ATP-bindir
PiIG	Q9I6H5	0.34544341	3.64533126	D-3-phosphoglycerate dehydrogenase
PiIG	Q9I6Z3	0.34473707	1.52021043	Alkyl hydroperoxide reductase subunit
PiIG	P30720	0.34413814	1.56061581	10 kDa chaperonin (GroES protein) (Pro

PiIG	Q9HWG0	0.34322183	5.82033573	UvrABC system protein A (UvrA protein
PiIG	Q9HUM2	0.34250304	4.35594233	Protease subunit HflK
PiIG	Q9HVD1	0.34225841	4.66450427	Lipid A deacylase PagL (EC 3.1.1.77) (LP:
PiIG	P72151	0.34224988	4.39544164	B-type flagellin
PiIG	Q9HXP9	0.34188154	0.68215231	30S ribosomal protein S16
PiIG	Q9I0Z1	0.34140694	2.38296685	Probable oxidoreductase
PiIG	Q59638	0.34135291	4.21270659	Dihydrolipoyllysine-residue acetyltransl
PiIG	Q9HZ98	0.34019674	5.537958	Heat-shock protein IbpA
PiIG	Q9HUT5	0.3401809	10.2981482	Probable transcriptional regulator
PiIG	Q9HXF7	0.33994049	3.82441487	Nucleoid-associated protein PA3849
PiIG	Q9HXT4	0.33990317	4.44887063	Uncharacterized protein
PiIG	Q9HUJ2	0.33981492	3.92420654	Phosphomethylpyrimidine synthase (EC
PiIG	Q9HZ97	0.33932008	11.8279682	Uncharacterized protein
PiIG	Q9HWF3	0.33875088	0.21565409	50S ribosomal protein L30
PiIG	Q9HWE9	0.33837416	4.00481341	30S ribosomal protein S8
PiIG	Q9HZP0	0.33829716	4.5850787	Uncharacterized protein
PiIG	G3XD20	0.33772224	3.44143506	Serine protease MucD
PiIG	G3XD12	0.33754822	3.97919086	Hydrogen cyanide synthase subunit Hcr
PiIG	Q9I4F9	0.33751977	3.52434581	Two-component response regulator Ph
PiIG	Q51472	0.33700202	4.84165934	Integration host factor subunit alpha (Ih
PiIG	P33642	0.33547714	15.281475	Probable D-amino acid oxidase PA4548
PiIG	Q9HT20	0.3344876	1.95642513	ATP synthase subunit beta (EC 3.6.3.14)
PiIG	Q9HWF2	0.33441432	0.71864132	30S ribosomal protein S5
PiIG	Q9HTQ4	0.33419311	1.6853726	Cytochrome c5
PiIG	O82850	0.33343247	1.25220596	30S ribosomal protein S2
PiIG	Q9HXK2	0.33317741	8.02742175	Probable oxidoreductase
PiIG	Q51567	0.33293574	2.04928099	Succinyl-CoA ligase [ADP-forming] subu
PiIG	Q9HVL6	0.33263593	2.25768967	50S ribosomal protein L21
PiIG	P48247	0.33210476	1.8616468	Glutamate-1-semialdehyde 2,1-aminorr
PiIG	Q9HXQ2	0.33205978	0.76362336	50S ribosomal protein L19
PiIG	Q9HWE1	0.3320344	0.49966804	30S ribosomal protein S3
PiIG	Q9I5Z0	0.33125071	2.98574723	S-adenosylmethionine synthase (AdoM
PiIG	Q9HT17	0.33118098	1.36565935	ATP synthase subunit delta (ATP syntha
PiIG	P47203	0.3302693	4.70036311	Cell division protein FtsA
PiIG	Q9I0K4	0.32941955	3.07994213	Isocitrate lyase (ICL) (Isocitrase) (Isocitr:
PiIG	Q9HWF4	0.32877326	0.26972166	50S ribosomal protein L15
PiIG	Q9HU38	0.32784706	4.19494622	Uncharacterized protein
PiIG	Q9I2U9	0.3273439	1.94260312	Peptidyl-prolyl cis-trans isomerase (EC 5
PiIG	Q9I692	0.32727533	3.42825254	Uncharacterized protein
PiIG	Q9HV58	0.32707598	1.43422939	30S ribosomal protein S15
PiIG	Q9I2U6	0.32684857	41.597673	Bifunctional protein FofD [Includes: Me
PiIG	Q9I2X1	0.32663773	6.3630255	Uncharacterized protein
PiIG	Q9HX60	0.32642064	1.57187479	Uncharacterized protein
PiIG	P04739	0.32601528	2.28548554	Fimbrial protein (Pilin) (Strain PAO)
PiIG	G3XCY4	0.32525108	4.79611304	Alginate and motility regulator Z



PiIG	Q9HWD9	0.32425273	0.44006906	30S ribosomal protein S19
PiIG	Q9HV44	0.32225762	4.93835768	Chaperone protein DnaJ
PiIG	Q9HUN0	0.32182882	1.78259889	30S ribosomal protein S18
PiIG	Q9HV01	0.32164856	12.293094	L-seryl-tRNA(Sec) selenium transferase
PiIG	P53593	0.32126503	2.39820476	Succinyl-CoA ligase [ADP-forming] subu
PiIG	Q9HYR9	0.32068641	2.76980766	ATP-dependent Clp protease proteolyti
PiIG	Q9I4Z4	0.32031797	0.32958759	Peptidoglycan-associated lipoprotein
PiIG	Q9HWE8	0.31884398	2.18367957	30S ribosomal protein S14
PiIG	O52760	0.31827608	10.110317	DNA-directed RNA polymerase subunit
PiIG	Q9I3N0	0.31814078	4.44887063	Cytochrome c-type biogenesis protein C
PiIG	Q9I2T8	0.31670163	7.25022206	Peptidyl-prolyl cis-trans isomerase D
PiIG	P55222	0.3157161	3.27747148	Cyclic AMP receptor-like protein
PiIG	Q9HW86	0.31560099	4.87869251	MvaT (Transcriptional regulator MvaT, I
PiIG	Q9I685	0.31464034	4.29583134	Adenosylhomocysteinase (EC 3.3.1.1) (S
PiIG	Q9HWD8	0.31352661	8.98574378	50S ribosomal protein L2
PiIG	Q9I0M2	0.31239988	3.01546976	Thioredoxin reductase (EC 1.8.1.9)
PiIG	O52759	0.3103844	0.7255428	30S ribosomal protein S4
PiIG	P11221	0.30995482	0.77972324	Major outer membrane lipoprotein (Ou
PiIG	Q9HWD5	0.30971058	1.03742264	50S ribosomal protein L3
PiIG	Q9HYZ0	0.30949375	4.5850787	Uncharacterized protein
PiIG	Q03456	0.30930507	1.8885993	Ferric uptake regulation protein (Ferric
PiIG	Q9I3D1	0.30704485	3.46551151	Dihydrolipoyl dehydrogenase (EC 1.8.1.
PiIG	Q9HUF1	0.3069318	3.43351549	Peptide methionine sulfoxide reductase
PiIG	P57703	0.30672258	5.57070279	5-methyltetrahydropteroyltriglutamate
PiIG	Q9I2W9	0.30646491	4.05217261	Phosphoenolpyruvate synthase (PEP sy
PiIG	Q9HXU8	0.30638141	3.04042594	Lipotoxon F, LptF
PiIG	Q9HWW4	0.30589636	4.4320263	Probable ATP-binding component of AB
PiIG	Q9I7B7	0.30430071	4.26995225	Glycine--tRNA ligase alpha subunit (EC C
PiIG	Q9HVA0	0.30375683	4.28127058	Acetolactate synthase large subunit
PiIG	Q9HWI1	0.30308985	6.48428048	Uncharacterized protein
PiIG	Q9HT18	0.3015563	1.15267676	ATP synthase subunit alpha (EC 3.6.3.14
PiIG	Q9I690	0.29967471	0.70811723	UPF0312 protein PA0423
PiIG	O52761	0.29946822	2.19468111	50S ribosomal protein L17
PiIG	Q9HXU9	0.29873526	2.36360691	Uncharacterized protein
PiIG	Q9HWD7	0.29862288	0.31713229	50S ribosomal protein L23
PiIG	P13794	0.29822177	2.108345	Outer membrane porin F
PiIG	Q9I0H1	0.29660549	2.56035456	Uncharacterized protein
PiIG	Q9HTN8	0.29648616	4.74651151	50S ribosomal protein L28
PiIG	Q9I553	0.29645518	5.5635442	Alanine--tRNA ligase (EC 6.1.1.7) (Alany
PiIG	Q9HVV1	0.29595095	4.30477844	Probable ATP-binding component of AB
PiIG	Q9I788	0.2955694	10.8533112	Exoenzyme T
PiIG	Q9I5F9	0.29470997	3.47194017	Lon protease (EC 3.4.21.53) (ATP-deper
PiIG	Q9HV73	0.29459224	6.04465887	Two-component response regulator Cb
PiIG	Q9I659	0.2944795	2.48686043	Probable ClpA/B protease ATP binding c
PiIG	Q9I6X4	0.29340308	6.29792373	Probable Resistance-Nodulation-Cell Di

PiIG	Q9HV97	0.29257297	2.63508079	Uncharacterized protein
PiIG	Q9HZN4	0.29220547	0.57871996	50S ribosomal protein L32
PiIG	Q9HXT9	0.29146551	4.91091249	Probable two-component response reg
PiIG	G3XD11	0.29130849	5.00832715	PhoP/Q and low Mg <sup>2+</sup> inducible outer r
PiIG	Q9I3B2	0.29079653	1.77652967	Beta-ketoacyl-ACP synthase I
PiIG	Q9HYG2	0.29059599	4.37395605	Alkanesulfonate monooxygenase (EC 1.
PiIG	Q9I5Y1	0.29047814	2.81388962	Fructose-bisphosphate aldolase (FBP ali
PiIG	P23189	0.28946215	3.79320685	Glutathione reductase (GR) (GRase) (EC
PiIG	O82851	0.288968	3.09850445	Elongation factor Ts (EF-Ts)
PiIG	G3XD01	0.28879885	1.98809068	UDP-2-acetamido-3-amino-2,3-dideoxy
PiIG	Q9I317	0.28862545	2.09560262	Type III export protein PscE (Pseudomo
PiIG	Q9HUC8	0.2856222	5.90408563	Arginine--tRNA ligase (EC 6.1.1.19) (Arg
PiIG	Q9I3F5	0.2853438	3.78589981	Aconitate hydratase 1 (Aconitase 1) (EC
PiIG	Q9HTT7	0.28449209	4.80810864	Uncharacterized protein
PiIG	Q9HT21	0.28378223	1.27990898	ATP synthase epsilon chain (ATP syntha
PiIG	Q9HX85	0.28362008	9.12001073	Uncharacterized protein
PiIG	P26276	0.28330774	2.62902235	Phosphomannomutase/phosphoglucon
PiIG	Q9HTP6	0.28326629	2.68278727	Leucine-responsive regulatory protein
PiIG	P40947	0.28224942	1.53128457	Single-stranded DNA-binding protein (S
PiIG	Q9HWW2	0.28173751	4.57026215	Uncharacterized protein
PiIG	Q9HVJ1	0.28159289	2.46517601	Probable ATP-binding component of AB
PiIG	Q9HTY9	0.28146797	2.79426185	AmgR
PiIG	Q9HX51	0.28119189	2.70499256	Probable transcriptional regulator
PiIG	P13981	0.2810154	3.55236746	Arginine deiminase (ADI) (EC 3.5.3.6) (A
PiIG	G3XD28	0.28069682	6.07099458	Type 4 fimbrial biogenesis protein PilM
PiIG	Q9I4Z7	0.27888916	3.12872719	Probable dna-binding stress protein
PiIG	Q9HZX5	0.27877618	8.50358757	Uncharacterized protein
PiIG	P29365	0.27728898	3.47423983	Homoserine dehydrogenase (HDH) (EC
PiIG	Q9HXY0	0.27715596	3.59920153	Probable aminotransferase
PiIG	Q9HV55	0.27715268	4.72122596	Translation initiation factor IF-2
PiIG	Q9X2T1	0.27639904	2.4964604	Thioredoxin (Trx)
PiIG	Q9I5X4	0.27589056	4.72455591	Probable hydrolase
PiIG	O33877	0.27341546	2.13374742	3-hydroxydecanoyl-[acyl-carrier-proteir
PiIG	Q9HWH2	0.27315232	2.6103355	Probable phenazine-specific methyltrar
PiIG	Q9HW73	0.27226143	3.57465666	Uncharacterized protein
PiIG	Q9HUE2	0.27222371	4.33939857	Uncharacterized protein
PiIG	Q9HVL8	0.27103137	2.17793859	GTPase Obg (GTP-binding protein Obg)
PiIG	Q51551	0.2710059	2.39084471	Dihydroorotase-like protein (Aspartate
PiIG	O68823	0.27019875	3.21729442	DNA polymerase III subunit chi (EC 2.7.:
PiIG	Q9HW49	0.26989045	3.0241391	Uncharacterized protein
PiIG	Q9HUM6	0.26958499	2.03027158	Adenylosuccinate synthetase (AMPSase
PiIG	Q9I4I1	0.2691906	5.12932626	Ribonucleoside-diphosphate reductase
PiIG	O50273	0.26914374	2.20800952	Sulfate adenylyltransferase subunit 2 (E
PiIG	Q9HYG6	0.26789276	2.66537182	Uncharacterized protein
PiIG	Q9I402	0.26670305	2.22865462	Probable binding protein component of

PiIG	Q9HX25	0.2665426	6.79283285	Lipoyl synthase (EC 2.8.1.8) (Lip-syn) (L
PiIG	Q9HTL4	0.26645321	1.78187231	OxyR
PiIG	Q9HU11	0.26635294	1.12825364	Uncharacterized protein
PiIG	Q9HYX8	0.2658127	2.02498148	Peptidyl-prolyl cis-trans isomerase (EC 5
PiIG	Q9HTI8	0.26504995	4.73988322	Probable ATP-binding component of AB
PiIG	Q9HXW7	0.26443575	4.44887063	Glycerol-3-phosphate acyltransferase (C
PiIG	Q9HXI8	0.26436951	2.2280136	Cysteine desulfurase IscS (EC 2.8.1.7)
PiIG	Q9IOL5	0.2638017	2.67338459	Isocitrate dehydrogenase [NADP] (EC 1.
PiIG	Q9I340	0.26335504	3.28180133	Enolase-phosphatase E1 (EC 3.1.3.77) (;
PiIG	Q9HV67	0.26274561	5.43334201	Glucose-6-phosphate isomerase (GPI) (I
PiIG	Q9I585	0.26234072	2.07624285	Uncharacterized protein
PiIG	Q9HWQ1	0.26159744	3.73183542	Probable sulfite or nitrite reductase
PiIG	Q9HT16	0.26146153	1.66915086	ATP synthase subunit b (ATP synthase F
PiIG	Q9I494	0.26138321	2.93526954	Uncharacterized protein
PiIG	Q9I7C4	0.26114571	1.32266252	DNA polymerase III subunit beta (EC 2.7
PiIG	P32722	0.26099316	5.61461568	Porin D (EC 3.4.21.-) (Imipenem/basic a
PiIG	P00282	0.25970155	4.14120045	Azurin
PiIG	Q9I2Q2	0.25857035	9.28135368	Methionine synthase (EC 2.1.1.13) (5-m
PiIG	Q9I2U7	0.25764421	3.33621278	Cysteine--tRNA ligase (EC 6.1.1.16) (Cys
PiIG	Q9I662	0.25545256	1.97441134	Probable cold-shock protein
PiIG	Q9I4S1	0.25460841	2.53423635	Uncharacterized protein
PiIG	Q9HWE6	0.254193	6.01660118	50S ribosomal protein L24
PiIG	Q9I4Q8	0.2539311	8.12255554	Probable short-chain dehydrogenase
PiIG	Q9HZ66	0.25299002	2.19666882	Phosphoserine aminotransferase (EC 2.
PiIG	Q9IOM6	0.25182183	4.36733577	Serine--tRNA ligase (EC 6.1.1.11) (Seryl-
PiIG	Q9I6K6	0.25160925	4.02058945	Uncharacterized protein
PiIG	Q9HVQ7	0.24966141	2.63508079	PKHD-type hydroxylase PiuC (EC 1.14.1:
PiIG	Q9I406	0.2493516	3.85065975	Gamma-glutamyltranspeptidase (EC 2.3
PiIG	Q9HT25	0.24932311	1.92221996	Glutamine--fructose-6-phosphate amin
PiIG	Q9I588	0.24926043	3.6424178	Probable oxidoreductase
PiIG	Q9HZP6	0.24910606	1.584242	Electron transfer flavoprotein subunit b
PiIG	Q9HUP3	0.24797306	2.87337775	NH(3)-dependent NAD(+) synthetase (E
PiIG	Q9HZU4	0.24755053	6.42250662	Precorrin-3 methylase CobJ
PiIG	Q9HZJ2	0.24694704	2.07577214	Fatty acid oxidation complex subunit al
PiIG	Q9HUC0	0.24680531	3.16890244	Ubiquinone/menaquinone biosynthesis
PiIG	Q9HYX7	0.2455747	4.07876989	Recombination-associated protein RdgC
PiIG	Q9I6J5	0.24524438	3.44222802	Probable glutamine synthetase
PiIG	Q9HVX6	0.24491764	4.53999671	Tryptophan--tRNA ligase (EC 6.1.1.2) (T
PiIG	Q9HV48	0.24439018	2.42282671	ATP-dependent zinc metalloprotease Ft
PiIG	Q9HV60	0.2442737	3.13413957	Uncharacterized protein
PiIG	Q9HWJ1	0.24412741	2.73160939	Probable FAD-dependent monooxygena
PiIG	Q9HY12	0.24368671	11.337654	Uncharacterized protein
PiIG	Q9HYY4	0.24339569	10.5760614	Probable oxidoreductase
PiIG	Q9HZE0	0.2431276	10.8882664	NAD-specific glutamate dehydrogenase
PiIG	Q9I3Q7	0.24223733	2.92366127	Uncharacterized protein

PiIG	Q9I376	0.24177242	2.56855665	Probable short-chain dehydrogenase
PiIG	Q9HUK6	0.24121399	23.5106402	FimX
PiIG	Q9I399	0.23711093	4.06729551	Uncharacterized protein
PiIG	Q9HVA2	0.23709716	6.09995445	Ketol-acid reductoisomerase (EC 1.1.1.8
PiIG	G3XD74	0.23576056	2.31790152	D-ala-D-ala-carboxypeptidase
PiIG	Q9HZ78	0.23535231	4.84836777	LPS biosynthesis protein WbpG
PiIG	Q9HTW3	0.23481267	3.21729442	Cell division protein ZapA (Z ring-associ
PiIG	Q9HTF1	0.2340372	2.81194652	Low specificity L-threonine aldolase (Lo
PiIG	Q9HY58	0.23263323	5.44475069	Probable nucleotide sugar dehydrogenase
PiIG	Q9HUP4	0.23258701	3.37512358	Nicotinate phosphoribosyltransferase 1
PiIG	Q9I418	0.2315156	3.73498866	Threonine dehydratase, biosynthetic
PiIG	Q9HYU4	0.23128917	2.00740161	Long-chain-fatty-acid--CoA ligase
PiIG	Q9HWD0	0.22971231	1.34201612	30S ribosomal protein S12
PiIG	Q9XCX8	0.22922696	4.5850787	GTPase Era
PiIG	Q9I4Q6	0.22905422	4.5850787	Probable heat shock protein (Hsp90 fan
PiIG	Q9I0Q4	0.22775918	5.37778309	Uncharacterized protein
PiIG	Q9I2R2	0.22703911	2.25231651	Probable oxidoreductase
PiIG	Q9I2Q7	0.22533222	4.15605508	Sulfite reductase
PiIG	O69077	0.22528127	4.45683155	Aspartokinase (EC 2.7.2.4) (Aspartate ki
PiIG	G3XDA5	0.22485324	3.95622258	Anaerobically-induced outer membran
PiIG	Q9I5G8	0.22467706	6.77973391	Elongation factor 4 (EF-4) (EC 3.6.5.n1)
PiIG	Q9I0T3	0.22319828	10.1370669	Probable transcriptional regulator
PiIG	Q9HUF4	0.22297756	3.29487526	Glutamate-ammonia-ligase adenylyltra
PiIG	Q9HV83	0.22291985	2.1211116	Probable aminotransferase
PiIG	Q9I3X2	0.22260617	4.34218807	Uncharacterized protein
PiIG	O82852	0.22143101	2.82929977	Uridylate kinase (UK) (EC 2.7.4.22) (Uric
PiIG	G3XCW5	0.21906259	0.76094314	Uncharacterized protein
PiIG	Q9I1A1	0.21905746	3.21729442	Probable aldehyde dehydrogenase
PiIG	Q51548	0.2183235	6.77562679	L-ornithine 5-monooxygenase (EC 1.13.
PiIG	P95453	0.21738753	2.89489925	Probable RNA-binding protein PA4753
PiIG	P38098	0.21723799	3.35742026	Carbamoyl-phosphate synthase small cl
PiIG	Q9HXP8	0.21539287	1.79011368	Signal recognition particle protein (Fifty
PiIG	Q9I2P8	0.21475913	0.64270753	Fe/S biogenesis protein NfuA
PiIG	Q9HZP8	0.21187242	3.89079858	Putative reductase PA2950 (EC 1.3.1.-)
PiIG	Q9I730	0.20966706	2.67810167	Carbonic anhydrase (EC 4.2.1.1)
PiIG	Q9HTM1	0.20829566	2.45315173	DNA-directed RNA polymerase subunit
PiIG	Q9I184	0.20572626	6.3630255	Pyoverdine synthetase F
PiIG	Q9HTD9	0.20497642	3.03391758	Alcohol dehydrogenase
PiIG	Q59643	0.20472397	2.88611844	Delta-aminolevulinic acid dehydratase (
PiIG	Q9HX32	0.20375024	1.87710734	LPS-assembly lipoprotein LptE
PiIG	Q9I2Z1	0.20234456	2.7708304	Uncharacterized protein
PiIG	Q9I6Y9	0.20198475	2.53711185	Nonspecific ribonucleoside hydrolase
PiIG	Q9HWL9	0.20107501	3.21729442	Probable short-chain dehydrogenase
PiIG	P26275	0.20026489	0.82941918	Positive alginate biosynthesis regulator
PiIG	Q9HV90	0.19995852	1.65982653	Heme-transport protein, PhuT

PiIG	Q9HV72	0.19941418	9.55203933	Poly(A) polymerase I (PAP I) (EC 2.7.7.1)
PiIG	Q9I5V8	0.19885224	1.20555386	30S ribosomal protein S21
PiIG	Q9HZC5	0.19882634	3.32471163	Aminopeptidase N
PiIG	Q9I088	0.19873673	1.73884886	Ecotin
PiIG	Q9HZ76	0.19793194	2.03660577	UDP-2-acetamido-2-deoxy-3-oxo-D-gluc
PiIG	Q9HYF6	0.19624956	1.30594323	Probable antioxidant protein
PiIG	Q51342	0.19610729	1.7386471	Amidophosphoribosyltransferase (ATas
PiIG	Q9HT40	0.19480175	4.5850787	Uncharacterized protein
PiIG	Q9HY13	0.19472983	2.52819651	Uncharacterized protein
PiIG	G3XDB0	0.1940976	2.97691127	Catabolite repression control protein
PiIG	Q9HWC4	0.19283861	1.58113883	Transcription termination/antiterminat
PiIG	Q9I5A7	0.19215491	2.50334787	Uncharacterized protein
PiIG	Q9HWX4	0.19042176	3.94101938	3,4-dihydroxy-2-butanone 4-phosphate
PiIG	Q9HXU3	0.18941326	2.71228665	Uncharacterized protein
PiIG	Q9HTE2	0.18939795	5.01703029	Uncharacterized protein
PiIG	P33640	0.18911804	4.5850787	Ribosomal large subunit pseudouridine
PiIG	O82853	0.18789782	3.75873568	Ribosome-recycling factor (RRF) (Ribosc
PiIG	Q9HVI7	0.18671753	1.99372596	Serine hydroxymethyltransferase 3 (SHI
PiIG	P26480	0.18591686	4.23533096	RNA polymerase sigma factor RpoD (Sig
PiIG	Q9HX22	0.18396354	4.53548971	Ribosomal silencing factor RsfS
PiIG	Q9HXV0	0.18333116	2.84212333	Probable metal-transporting P-type ATF
PiIG	P50601	0.18331407	3.11724932	Protein TolB
PiIG	Q9HYR2	0.18238507	3.89042451	3-oxoacyl-[acyl-carrier-protein] synthas
PiIG	Q9HW10	0.18099365	4.73988322	Probable two-component response reg
PiIG	Q9I099	0.18031633	2.35804468	Threonine--tRNA ligase (EC 6.1.1.3) (Thi
PiIG	Q9HUE1	0.18029139	3.40460757	Uncharacterized protein
PiIG	Q9HXQ0	0.18002789	3.99996946	Ribosome maturation factor RimM
PiIG	P50587	0.17998717	3.01946326	Orotate phosphoribosyltransferase (OP
PiIG	Q9I2Q5	0.17996014	4.5499414	Uncharacterized protein
PiIG	Q9I4K5	0.17925325	4.73988322	Rhamnosyltransferase 2
PiIG	Q9I645	0.17916717	4.92795923	Probable glutathione S-transferase
PiIG	Q9I5U9	0.17804192	2.04343246	Uncharacterized protein
PiIG	Q9HV61	0.17715171	1.01983145	UPF0337 protein PA4738
PiIG	Q9HXI0	0.17519277	1.25071001	Uncharacterized protein
PiIG	Q9S646	0.17240434	3.6024879	Polyphosphate kinase (EC 2.7.4.1) (ATP-
PiIG	Q9HXZ2	0.17234138	1.90528987	Acetyl-coenzyme A carboxylase carboxy
PiIG	Q9HZP7	0.17006094	1.30215323	Electron transfer flavoprotein subunit a
PiIG	Q9HZL4	0.16838579	3.84501774	Probable phosphodiesterase
PiIG	Q9HYY0	0.16746772	4.66787528	Probable transcriptional regulator
PiIG	O52762	0.16706166	0.96346813	Catalase (EC 1.11.1.6)
PiIG	Q9HXR4	0.16597794	1.99110449	Uncharacterized protein
PiIG	Q9I3I0	0.1649306	1.4426382	Nucleoid-associated protein PA1533
PiIG	P43903	0.16446423	2.88809738	Quinone oxidoreductase (EC 1.6.5.5) (N
PiIG	Q9I4H8	0.16361146	1.8381832	Probable cold-shock protein
PiIG	Q9HXM5	0.16355428	2.44345452	Inosine-5'-monophosphate dehydrogen

PiIG	Q9I4N9	0.1623339	2.56855665	Uncharacterized protein
PiIG	Q9I1U2	0.16140231	2.94911153	Uncharacterized protein
PiIG	Q9HUG0	0.16066594	2.4048569	Probable carbamoyl transferase
PiIG	G3XD94	0.15926428	1.6390495	UDP-N-acetyl-D-glucosamine 6-dehydr
PiIG	P37798	0.15905412	2.16689673	Biotin carboxylase (EC 6.3.4.14) (Acetyl-
PiIG	Q9HWX1	0.15794369	2.03706284	Transcriptional repressor NrdR
PiIG	Q9I3R8	0.15779951	4.01006354	Uncharacterized protein
PiIG	Q9I589	0.15571205	4.45410663	Chitin-binding protein CbpD
PiIG	Q9HX48	0.15554771	3.21729442	Ribosomal large subunit pseudouridine
PiIG	P57668	0.15505213	1.72643423	Probable thiol peroxidase (EC 1.11.1.-)
PiIG	Q9I0F3	0.15469861	3.34965649	Uncharacterized protein
PiIG	Q9I6Z1	0.15467839	3.61130128	Uncharacterized protein
PiIG	Q9I7A7	0.1543109	4.8001749	Uncharacterized protein
PiIG	Q9HYP7	0.15144042	3.20377509	Probable chemotaxis protein
PiIG	Q9HZX0	0.14995007	2.85476825	Probable transcriptional regulator
PiIG	P53641	0.14823031	1.93200094	Superoxide dismutase [Fe] (EC 1.15.1.1)
PiIG	Q9I500	0.14808934	2.56855665	Uncharacterized protein
PiIG	Q9I4Q3	0.1472743	1.84819023	Uncharacterized protein
PiIG	Q9HW90	0.14554563	3.81477075	Uncharacterized protein
PiIG	Q9I347	0.14474997	2.22033831	50S ribosomal protein L3 glutamine me
PiIG	Q9I696	0.14438169	16.8460778	Component of chemotactic signal trans
PiIG	Q9I671	0.14385852	2.56773958	Glutaryl-CoA dehydrogenase
PiIG	Q9I344	0.1431612	2.64541463	Chorismate synthase (EC 4.2.3.5) (5-enc
PiIG	Q9HU65	0.1419529	1.75533299	Glutamine synthetase (EC 6.3.1.2) (Glut
PiIG	Q9HUG1	0.14160729	2.13907731	Probable glycosyl transferase
PiIG	Q9I747	0.14003129	2.24966924	Protein hcp1
PiIG	Q9HVU9	0.13618958	2.58116517	PmbA protein
PiIG	Q9HVW9	0.13456887	1.84553338	Histidinol dehydrogenase (HDH) (EC 1.1
PiIG	Q9HW02	0.13100521	2.59357022	UDP-N-acetylmuramate--L-alanine ligas
PiIG	Q9HZI1	0.12888077	2.17793859	Probable FAD-dependent glycerol-3-ph
PiIG	Q51473	0.12815308	1.90300731	Integration host factor subunit beta (IH
PiIG	Q9HZG0	0.12715925	3.79896131	Ribosomal RNA large subunit methyltra
PiIG	Q9HWQ0	0.1238933	2.23248165	Probable iron-sulfur protein
PiIG	Q9HTY8	0.12384671	2.72400442	Uncharacterized protein
PiIG	Q9HZJ5	0.12161946	4.1462397	DNA topoisomerase 1 (EC 5.99.1.2) (DN
PiIG	Q9HT70	0.11960179	4.9339714	Methionine import ATP-binding protein
PiIG	Q9I6M1	0.11874851	9.444315	Uncharacterized protein
PiIG	Q9HV50	0.11656991	3.46004706	Phosphoglucosamine mutase (EC 5.4.2.
PiIG	Q9HXA0	0.11536797	2.53711185	Probable protease
PiIG	Q9I2U1	0.11525359	1.94626959	ATP-dependent Clp protease proteolyti
PiIG	Q9I352	0.11523686	3.49963551	Bacteriohemerythrin
PiIG	Q9HV06	0.11332286	3.21729442	Uncharacterized protein
PiIG	POC2B2	0.11202495	2.7466854	Thiol:disulfide interchange protein Dsb/
PiIG	Q9HZG2	0.11178168	2.29062661	Uncharacterized protein
PiIG	Q9HTW5	0.1111763	2.26768137	UPF0149 protein PA5225

PiIG	Q9I709	0.10992524	2.63508079	Probable transcriptional regulator
PiIG	Q9I1E8	0.10958342	3.12018962	Uncharacterized protein
PiIG	Q9HYJ2	0.10910913	3.85382251	Uncharacterized protein
PiIG	Q9H XK5	0.10774446	2.28574915	2-isopropylmalate synthase (EC 2.3.3.13)
PiIG	Q9HYE5	0.10548454	3.44317679	Uncharacterized protein
PiIG	Q9I6J2	0.10534019	2.23105996	Putrescine aminotransferase
PiIG	Q9HTT8	0.10533512	1.88379415	Uncharacterized protein
PiIG	Q9I748	0.1033329	2.23034973	Uncharacterized protein
PiIG	Q9I753	0.10303897	2.16568183	Uncharacterized protein
PiIG	Q9I324	0.10270648	2.85775929	Translocator protein PopB
PiIG	G3XD39	0.10165557	2.71228665	Probable bacteriophage protein
PiIG	P52477	0.09790164	2.14961086	Multidrug resistance protein MexA
PiIG	Q9HZ52	0.09777022	3.21729442	Uncharacterized protein
PiIG	Q9HVQ3	0.09736125	3.18826686	Ornithine decarboxylase
PiIG	Q9I151	0.09624362	1.90884751	Uncharacterized protein
PiIG	Q9HY01	0.0956173	1.61080271	Alcohol dehydrogenase class III
PiIG	Q9I363	0.09551148	5.66599793	Probable ClpA/B-type protease
PiIG	Q9HTY0	0.09219394	4.68054897	Probable secretion pathway ATPase
PiIG	Q9I4I2	0.09158164	1.9357718	Ribonucleoside-diphosphate reductase
PiIG	Q9HVZ2	0.08972646	1.64820122	Uncharacterized protein
PiIG	Q9HUT2	0.08951288	2.63508079	Uncharacterized protein
PiIG	Q9HYF1	0.08787272	2.22796327	Uncharacterized protein
PiIG	Q9HUG9	0.08632417	2.03772826	Bifunctional protein HldE [Includes: D-b
PiIG	Q9HTV6	0.08552582	2.7096243	Probable oxidoreductase
PiIG	Q9HTW6	0.08110424	2.22560855	Aminopeptidase P
PiIG	Q9HVC2	0.08098448	2.42270589	Ribosome-binding ATPase YchF
PiIG	Q9HYZ6	0.07890867	2.59407302	Site-determining protein
PiIG	Q9I742	0.07802128	4.80937283	Protein ClpV1
PiIG	Q9HTK9	0.07775079	2.34428203	Rubredoxin-NAD(+) reductase (RdxR) (E
PiIG	Q9I046	0.07756449	1.10090228	Uncharacterized protein
PiIG	Q9I198	0.07744347	1.5673278	Uncharacterized protein
PiIG	Q9HYV7	0.07602238	2.66311669	Uncharacterized protein
PiIG	Q9I0Q1	0.07015695	2.18583266	UvrABC system protein C (Protein UvrC)
PiIG	Q59653	0.07008728	2.85883464	Aspartate carbamoyltransferase (EC 2.1
PiIG	Q9HX79	0.06967954	3.52028322	Taurine import ATP-binding protein Tau
PiIG	Q9HYP2	0.06918637	1.48517987	Uncharacterized protein
PiIG	Q9HVG0	0.06890372	2.22500546	Uncharacterized protein
PiIG	P23926	0.06785558	1.92749	Transcriptional activator protein anr
PiIG	Q9HZF5	0.06774265	4.69076471	Probable hydrolytic enzyme
PiIG	Q9HYR5	0.06736197	1.75553791	Probable short chain dehydrogenase
PiIG	G3XD43	0.06621961	2.29959276	Type 4 fimbrial biogenesis protein PilE
PiIG	Q9HTY4	0.06504943	2.40194306	Acetylornithine deacetylase
PiIG	Q9HZI6	0.0650067	2.00866325	Probable soluble lytic transglycosylase
PiIG	Q9HXI2	0.06462244	1.55784128	Protein translocase subunit SecF
PiIG	Q9HT33	0.06119422	3.06073894	Dihydroorotase

PiIG	O87125	0.06070471	1.76976436	Chemotaxis response regulator protein
PiIG	Q9HTY1	0.05883341	1.90971917	Uncharacterized protein
PiIG	P00106	0.05300439	1.91154098	Cytochrome c4
PiIG	Q9I7B8	0.05263035	2.45412904	Glycine--tRNA ligase beta subunit (EC 6.
PiIG	Q9I149	0.0493613	1.89044002	Uncharacterized protein
PiIG	Q9HVF2	0.0482796	1.50316295	Uncharacterized protein
PiIG	Q9HXJ9	0.04794358	3.02407505	Probable aminotransferase
PiIG	Q9HVV5	0.0464613	2.79545652	Uncharacterized protein
PiIG	Q9HVV8	0.04497886	4.15103457	UPF0307 protein PA4473
PiIG	Q9HUA5	0.04320476	3.22162899	Glucans biosynthesis protein G
PiIG	Q9I2N2	0.04244328	2.70500009	Molybdate-binding periplasmic protein
PiIG	Q9I4W5	0.04161726	1.52744332	Bacterioferritin comigratory protein
PiIG	Q9HXJ7	0.04100716	1.32684952	Outer membrane protein assembly fact
PiIG	Q9HYU8	0.04059544	1.7114203	Probable HIT family protein
PiIG	Q9HWX5	0.04043368	2.89410938	6,7-dimethyl-8-ribityllumazine synthase
PiIG	Q9I6X7	0.03782155	4.06482619	Transcriptional regulator PcaR
PiIG	Q9HXY4	0.03725691	1.99502562	Outer membrane protein assembly fact
PiIG	Q9HXZ5	0.03610002	2.40135145	Enolase (EC 4.2.1.11) (2-phospho-D-glyc
PiIG	Q9HY15	0.03412079	1.5519286	Uncharacterized protein
PiIG	Q9HTD1	0.03390434	1.74955932	Probable transcarboxylase subunit
PiIG	O68281	0.03352067	6.00237921	HTH-type transcriptional regulator HexI
PiIG	P45684	0.03153309	1.74872201	RNA polymerase sigma factor RpoS (Sig
PiIG	Q9I407	0.03124571	2.50758792	Glutaminase-asparaginase (EC 3.5.1.38)
PiIG	Q9I0A3	0.03055967	2.08574171	Phenylalanine--tRNA ligase alpha subur
PiIG	P33883	0.03016442	3.11570624	Acyl-homoserine-lactone synthase (EC ;
PiIG	Q9HVA9	0.03005723	3.2579568	Uncharacterized protein
PiIG	Q9I0L4	0.02979188	3.00771781	Isocitrate dehydrogenase
PiIG	O69078	0.02848371	2.62243894	Carbon storage regulator homolog
PiIG	P52111	0.02834875	2.02461809	Glycerol-3-phosphate dehydrogenase (l
PiIG	Q9HWU9	0.02810934	1.50078548	Probable dehydrogenase
PiIG	Q9HZ90	0.02761607	3.33621278	Probable transcriptional regulator
PiIG	Q9HTL0	0.02606602	2.94600652	DNA-binding protein HU-alpha
PiIG	Q9I1E7	0.02569665	1.33398596	Uncharacterized protein
PiIG	Q9HUV9	0.02560649	2.28744549	Bifunctional purine biosynthesis proteir
PiIG	Q9I6J1	0.02555923	1.43899664	Putrescine-binding periplasmic protein
PiIG	Q9HT95	0.02551315	1.68507539	Uncharacterized protein
PiIG	Q9HUL8	0.02529141	4.44807693	DNA mismatch repair protein MutL
PiIG	Q9I5Q3	0.0252342	2.80719033	Tyrosine--tRNA ligase 2 (EC 6.1.1.1) (Tyr
PiIG	Q9HVVH9	0.0243695	1.13167483	Uncharacterized protein
PiIG	Q9I1N7	0.02386837	2.04716849	PslB
PiIG	Q9HUC6	0.02349924	1.59459299	ATP-dependent protease subunit HslV (
PiIG	Q9I5L3	0.02331047	3.25677781	Uncharacterized protein
PiIG	Q9I3J3	0.02308355	2.72678512	Probable transcriptional regulator
PiIG	Q9HUF6	0.02266115	2.29104923	UDP-glucose:(Heptosyl) LPS alpha 1,3-g
PiIG	Q9HXI1	0.0218855	1.28345203	Protein translocase subunit SecD



PiIG	Q9HY84	0.02165565	1.22077005	Argininosuccinate synthase (EC 6.3.4.5)
PiIG	Q9HUT7	0.02115458	1.97980301	Osmotically inducible lipoprotein OsmE
PiIG	Q9I3E5	0.02065901	3.61073265	Uncharacterized protein
PiIG	Q9HUL5	0.02030092	2.16598994	Uncharacterized protein
PiIG	G3XCU6	0.01962645	2.08222769	Transcriptional regulator CysB
PiIG	Q9HV76	0.01924725	1.77594778	Probable aminotransferase
PiIG	Q9I773	0.01785587	1.83797167	Osmotically inducible protein OsmC
PiIG	Q9HZJ3	0.01691384	1.66609394	3-ketoacyl-CoA thiolase (EC 2.3.1.16) (A
PiIG	Q9I636	0.01685719	2.28285357	Malate synthase G (EC 2.3.3.9)
PiIG	Q9I3L9	0.01669029	2.01290837	Sulfate-binding protein of ABC transpor
PiIG	Q9HWK5	0.0161651	1.71578005	Peptidyl-prolyl cis-trans isomerase C2
PiIG	Q9I3L8	0.01441813	1.37294388	Uncharacterized protein
PiIG	P38103	0.01423082	1.17385669	4-hydroxy-tetrahydrodipicolinate reduc
PiIG	Q9HVM4	0.01378674	1.40780661	Isoleucine--tRNA ligase (EC 6.1.1.5) (Iso
PiIG	Q51390	0.01328726	1.11166835	Glycerol kinase 2 (EC 2.7.1.30) (ATP:glyc
PiIG	Q9HT11	0.01307915	2.84692475	Chromosome partitioning protein Soj
PiIG	Q9I658	0.01249245	1.71921551	Uncharacterized protein
PiIG	Q9HYK7	0.01199945	1.70747482	Ferredoxin--NADP+ reductase
PiIG	Q9HY63	0.01189065	2.97305935	Bifunctional polymyxin resistance prote
PiIG	Q9I1R3	0.01188926	2.42791556	Probable binding protein component of
PiIG	Q9HVS6	0.01090368	1.2300281	Uncharacterized protein
PiIG	Q9HUT3	0.00985403	1.94563536	Probable bacterioferritin
PiIG	Q9HV54	0.00978946	1.3724245	N utilization substance protein A
PiIG	Q9I5A3	0.00948917	2.54227149	Peptidyl-prolyl cis-trans isomerase (EC :
PiIG	P43502	0.00876714	3.61350777	Protein Pill
PiIG	Q9I1W4	0.00837876	1.28847853	Alpha-1,4-glucan:maltose-1-phosphate
PiIG	G3XCX8	0.00831661	1.3574618	Uncharacterized protein
PiIG	Q9X6P4	0.0082566	3.16791268	Acyl-[acyl-carrier-protein]--UDP-N-acet
PiIG	G3XCZ3	0.00822773	4.76884539	Type 4 fimbrial biogenesis protein PilZ
PiIG	Q9I083	0.00719593	2.07377118	Probable outer membrane protein
PiIG	Q9HYE7	0.00666251	2.04486654	Asparagine synthetase (EC 6.3.5.4)
PiIG	Q51391	0.00585707	5.11539597	Glycerol-3-phosphate regulon represso
PiIG	Q9HW32	0.00578887	1.0269344	Insulin-cleaving metalloproteinase oute
PiIG	Q9HX94	0.00544198	1.95303988	Uncharacterized protein
PiIG	Q9HUM0	0.00398867	2.08406699	RNA-binding protein Hfq
PiIG	Q9HYR8	0.00398422	1.24246997	Probable non-ribosomal peptide synthe
PiIG	Q9HWP9	0.00397492	1.88844338	Uncharacterized protein
PiIG	Q9HZ61	0.00372722	1.5791943	Probable short-chain dehydrogenase
PiIG	Q9I120	0.00259636	4.37097938	Uncharacterized protein
PiIG	G3XCX3	0.00250125	2.08211233	Twitching motility protein PilU
PiIG	Q9HW65	0.00183774	1.81431875	Uncharacterized protein
PiIG	Q9HW87	0.00087719	1.29348874	Formyltetrahydrofolate deformylase
PiIG	P14165	0.0006251	6.86717759	Citrate synthase (EC 2.3.3.16)
PiIG	P43501	0.00043405	2.7514448	Protein PilH
PiIG	Q9HWW5	0.0002456	1.40130184	Uncharacterized protein

PiG

P22608

0.0001896 2.61147882 Type 4 fimbrial assembly protein PilB

Gene.names

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