

Supplementary dataset S1A. All identified proteins in *P. aeruginosa* treated with SBCL. All LFQ intensity replicates (rep.) are Log₂ transformed.

Protein name	Majority protein IDs	Gene name	Peptides	Sequence	Mol.	Score	Intensity	MS/MS count	Sequence length	LFQ Intensity Control Rep. 1	LFQ Intensity Control Rep. 2	LFQ Intensity Control Rep. 3	LFQ Intensity Control Rep. 4	LFQ Intensity	LFQ Intensity	LFQ Intensity	LFQ Intensity
				coverage [%]	weight [kDa]									SBCL Treatment Rep. 1	SBCL Treatment Rep. 2	SBCL Treatment Rep. 3	SBCL Treatment Rep. 4
criptional	G3XCW2	argR	8	41.6	36.854	34.972	4.92E+08	33	329	24.4782	23.9872	24.2421	24.4411	25.0127	25.1283	25.0573	25.0181
	G3XCW5	PA3031	2	35.6	8.0121	51.455	1.49E+09	13	73	23.1055	23.5233	22.6161	23.0348	28.4729	27.8122	27.732	27.6955
	G3XCW6	dmr	6	51.5	25.933	23.346	7.46E+08	20	227	25.6663	25.6685	25.5712	25.8873	24.1528	24.2318	22.9706	24.1863
	G3XCW7	PA1462	5	26	28.4007	16.822	5.92E+08	35	262	25.0408	25.2075	25.6259	25.3799	24.5644	24.6521	24.3574	24.6538
	G3XCX1	narG	54	63.1	140.97	323.31	4.97E+10	446	1261	29.4995	29.5339	29.3235	29.4725	28.0877	27.7781	28.1243	27.8589
	G3XCX2	PA0624	5	66.7	12.523	78.617	9.68E+08	31	114	26.429	25.6516	25.1881	26.7667	23.8771	25.34	23.6904	23.332
	G3XCX3	pilU	14	52.9	42.532	79.43	8.69E+08	61	382	25.3424	25.3163	25.4802	25.0723	24.4442	24.4228	24.2897	24.7844
	G3XCX5	PA0618	4	22	31.958	18.797	3.15E+08	15	295	24.9256	24.9544	24.9527	24.949	23.5302	22.8535	23.2724	22.1102
	G3XCY4	amrZ	5	64.8	12.333	87.246	4.43E+09	34	108	24.6446	24.5881	23.5459	25.0051	27.981	27.851	28.595	27.7735
	G3XCY9	narJ	14	56.1	27.261	144.21	6.31E+09	93	246	28.1544	28.0031	28.046	28.3921	27.3179	27.1032	27.1534	26.8216
	G3XCZ4	PA0891	10	38.4	40.213	69.913	2.64E+09	59	370	26.0254	26.1787	25.3147	26.1006	26.9901	27.0574	26.9008	27.0284
	G3XCZ8	hemO	8	50	21.953	113.58	5.25E+09	69	198	26.2842	26.2507	25.3007	26.4529	27.873	27.585	29.4201	27.6895
	G3XD16	PA2523	7	40.2	25.788	47.514	1.01E+09	30	224	23.3823	23.5233	22.5262	23.6139	26.8558	26.5833	26.1642	26.4485
	G3XD20	mucD	22	58	50.321	316.56	4.7E+10	250	474	30.0562	29.8667	29.4574	29.8807	30.3772	30.7019	30.575	30.4108
	G3XD25	mexC	22	69	40.838	323.31	3.34E+10	192	387	28.1596	28.5207	27.7099	28.5525	29.3157	28.8959	29.0788	29.2924
	G3XD28	pilM	13	47.7	37.983	77.92	2.28E+09	61	354	26.121	26.425	26.6144	26.1469	24.9251	24.8425	24.9719	24.9719
	G3XD39	PA0622	14	58.5	41.209	165.49	2.14E+09	71	386	26.4523	26.5818	26.8572	26.2553	24.9802	24.8618	25.1235	25.0534
	G3XD40	PA3925	18	73.4	40.553	314.09	1.36E+10	196	391	28.4477	28.6217	28.6235	28.4528	27.7818	27.8053	27.8256	27.6786
	G3XD49	pcrV	6	34.7	32.283	37.315	4.43E+08	27	294	25.1918	25.5583	24.7379	25.2936	21.9624	22.4288	22.4284	23.193
	G3XD80	PA0510	11	67.7	29.654	130.14	3.36E+09	61	279	27.579	27.9327	27.6788	27.7741	23.9121	24.6441	23.7583	24.4602
	G3XD87	narH	36	78.8	58.105	323.31	2.67E+10	327	513	29.8729	29.8322	29.6535	29.7883	28.6742	28.3753	28.5599	28.3677
	G3XD93	PA3842	2	22.4	13.157	21.718	1.01E+09	19	116	26.887	25.8216	25.0273	27.1923	22.1913	24.9836	23.7427	24.8584
-binding pr	G3XDA1	exoS	11	45	48.302	94.738	7.93E+08	30	453	25.8296	26.1813	26.1473	25.9096	23.2925	23.0381	22.5173	23.4628
	G3XDA8	pstS	16	72.8	34.473	201.98	6.94E+09	118	323	26.9568	27.2493	25.5384	26.9009	28.0384	27.8171	27.6466	27.3905
	moyltransf	PA0830	arcB	23	76.8	38.108	308.42	3.06E+11	541	336	32.8033	32.9313	33.1026	32.6848	30.7432	30.4517	30.9536
	rhatic amid	P11436	amiE	10	39.3	38.494	96.328	7.11E+08	43	346	25.0269	25.8158	24.8594	25.1212	23.5386	23.1654	22.9587
	nembrane	P13794	oprF	14	51.7	37.639	173.46	1.8E+10	110	350	29.3568	29.6381	28.9615	29.6052	30.5408	29.9771	30.1766
	nine delimi	P13981	arcA	39	76.6	46.435	323.31	5.03E+11	822	418	33.4859	33.5383	33.8176	33.3219	31.5189	31.2599	31.5316
	bamate rict	P13982	arcC	19	53.9	33.08	274.55	1.46E+11	219	310	32.5664	32.5131	32.4283	32.5525	30.0217	29.7994	30.1004
	rate synth	P14165	gluA	20	73.6	47.694	165.6	1.6E+10	192	428	27.9801	28.3086	27.4605	28.2249	28.7898	28.7139	28.6467
	me c551 p	P14532	ccpA	16	66.5	37.403	160.22	2.63E+10	140	346	30.4261	30.4968	30.6641	28.1208	27.545	27.7689	28.894
	ynthase c	P20580	trpE	13	38.8	54.555	82.417	1.06E+09	51	492	24.4884	24.8932	24.3344	24.345	25.1847	25.105	25.2081
	threonine	P21175	braC	24	75.6	39.769	323.31	1.02E+11	352	373	31.3977	31.5576	31.446	31.3515	30.5926	30.4749	30.5973
	no acid tra	P21630	braG	8	50.2	25.591	114.74	2.13E+09	60	233	26.1586	26.3874	26.457	25.9404	25.769	25.7321	25.5847
	nscriptio	P23747	algB	17	55.9	49.323	123.37	2.56E+09	67	449	25.5894	25.4173	25.6267	25.3316	25.8544	26.1115	26.4832
	sal activato	P23926	anr	9	38.1	27.129	66.696	2.75E+09	55	244	25.7994	25.8534	25.4536	25.8993	26.7929	26.7834	26.4895
	rite reduct	P24474	nirS	37	69.4	62.653	323.31	6.75E+10	345	568	30.3261	30.6356	30.9052	30.2525	28.1113	27.8898	27.9244
	utase/pho	P26276	algC	24	57.7	50.295	277.26	1.06E+10	149	463	26.6574	26.7222	26.7898	26.4761	27.377	27.4641	27.8933
	expression	P27017	amiC	10	48.6	42.807	41.431	6.55E+08	39	385	24.9835	25.0084	25.8822	25.038	24.0599	23.6342	22.4504
	rase sigm	P29248	flia	10	58.7	27.522	90.733	5.76E+09	58	247	28.9885	28.8869	28.7077	29.0571	28.4917	28.1286	28.3967
	rotein assi	P33641	bamD	8	39.6	38.615	35.046	6.27E+08	34	341	23.7194	24.0123	23.6651	24.2278	24.9889	24.4951	24.766
	sembly pr	P34750	pilQ	23	40.1	77.378	166.32	3.72E+09	119	714	25.3122	25.5456	25.6516	25.3905	26.331	26.1814	26.0384
	negative r	P38107	mucA	10	72.7	20.998	185.91	2.7E+09	44	194	26.2144	26.6911	26.315	26.3613	27.4027	27.1538	27.4087
U regulato	P38108	mucB	18	68	34.572	205.27	9.88E+09	141	316	26.9278	27.2521	27.1819	26.971	27.6053	27.543	27.9458	27.6014
	9nine-4-hy	P43334	phhA	8	48.5	30.321	63.31	2.14E+09	26	262	28.3761	28.1881	28.2642	28.0336	22.4816	26.8129	26.4059
	arbinolami	P43335	phhB	6	72	13.333	42.524	4.11E+09	31	118	28.5257	29.0924	28.2425	28.3037	28.2444	27.8783	27.3826
	hydrogena	P43904	aroE	12	52.6	29.484	67.534	3.11E+09	80	274	26.5338	26.8918	26.8248	26.733	26.0328	26.0297	26.049
	rase sigm	P45684	rpoS	11	44.9	38.235	155.27	4.1E+09	62	334	28.0109	27.5324	27.9635	27.5114	26.4787	26.057	26.3306
	'rotein tol	P50598	tolQ	6	28.6	25.282	46.68	8.96E+08	30	231	24.9604	25.257	24.2009	25.0595	25.9864	25.5887	25.7608
	sistance pi	P52002	mexB	12	20.9	112.79	44.063	5.61E+08	38	1046	23.2363	23.7424	23.2549	23.9439	25.149	24.5582	24.2152
	sistance pi	P52477	mexA	13	57.2	40.969	114.1	1.73E+09	61	383	25.1057	25.7881	24.732	26.478	26.7456	26.2721	26.2597
	copropor	P77915	hemN	14	43	52.488	167.68	6.13E+09	73	460	28.1824	28.2765	28.4006	28.2575	25.8727	26.3863	26.0379
	'rotein NirI	P95412	nirD	5	44	17.017	42.699	9.85E+08	24	150	26.683	26.3108	26.3935	23.0064	24.2535	23.2835	23.7359
	'rotein NirI	P95413	nirL	9	46	20.21	35.761	4.37E+08	14	174	24.7589	25.2969	25.2045	25.0244	22.567	22.1425	22.7266
	'rotein NirI	P95414	nirG	3	44.2	16.552	34.307	4.83E+08	15	147	26.1544	25.7946	25.5114	26.6424	22.7731	23.2698	22.9172
	Pycoc-S2	Q06584	pys2	4	9	73.853	16.727	1.88E+08	15	689	24.5943	23.1314	24.9.				

phosphate	Q9HV44	yedY	7	33.2	38.143	51.796	9.19E+08	41	337	25.0802	25.2492	25.1381	25.5712	24.901	24.6113	24.8036	24.1052	
	Q9HV72	PA4639	4	27.2	20.735	23.295	3.92E+08	21	195	23.9675	23.1625	23.175	24.36	25.5696	24.8238	25.0118	25.0974	
	Q9HV15	PA4616	15	63.6	36.959	152.59	7.14E+09	111	332	27.7769	27.8188	28.1983	27.893	26.4865	26.3306	25.9092	26.5362	
	Q9HV11	PA4608	4	47.2	14.573	50.619	6.5E+08	24	125	26.0701	25.9494	26.0349	25.9781	25.0775	24.6173	24.8431	25.1141	
	Q9HV12	PA4607	4	42.3	17.477	66.583	5.38E+08	22	168	25.4526	25.4115	24.8706	23.689	23.7722	22.8955	23.4088	22.0207	
cine-tRNA	Q9HV19	mexD	16	28.6	111.59	230.42	7.46E+09	131	1043	26.5831	26.9002	25.9792	27.088	27.7399	27.3903	27.2303	27.6865	
	Q9HVK6	PA4578	6	44.4	16.893	91.051	5E+09	38	162	23.3343	23.1915	23.0916	22.9586	28.7662	28.7744	29.2302	28.6787	
	Q9HVK7	PA4577	4	57.4	11.756	70.168	2.93E+09	39	108	28.5134	25.5279	25.4914	28.0664	22.9989	25.3154	22.8031	24.3325	
	Q9HV13	PA4571	14	39.6	73.386	45.992	6.23E+08	41	675	24.6132	25.285	24.2872	25.6627	23.6706	23.3006	22.9833	22.7887	
	Q9HVM4	ileS	35	58.3	105.46	262.62	8.19E+09	226	943	25.7561	26.1493	25.1815	26.2658	26.8605	26.506	26.2306	26.652	
biogenesis	Q9HVM8	pilY1	24	32.6	126.58	291.12	7.79E+09	156	1161	27.1585	27.3474	27.3359	27.1689	26.5154	26.3342	26.3179	26.3653	
	ae hydroxy	Q9HVQ7	piuC	5	31.9	25.616	27.207	4.71E+08	19	226	24.1019	24.3422	24.2364	23.8382	24.6297	24.7319	25.2261	24.9688
	Q9HVR9	PA4502	24	70.8	58.611	179.66	5.53E+09	143	531	27.0886	27.267	27.8567	26.863	25.1323	24.8768	25.0339	25.3083	
	Q9HV51	PA4500	19	41.8	59.674	81.963	1.23E+09	35	533	25.1736	26.216	27.5829	25.2356	23.399	24.0608	23.3171	23.266	
	Q9HV54	PA4497	11	44.9	59.496	80.469	5.61E+08	26	532	24.5777	25.1714	25.6225	24.4129	23.7611	23.0039	23.4027	23.5654	
32 protein i	Q9HV55	PA4496	20	52.3	60.076	176.08	4.14E+09	85	537	27.1009	27.3372	28.3758	27.2183	24.9198	23.986	23.8125	23.6914	
	Q9HV72	PA4489	25	29.9	167.43	116.32	1.48E+09	63	1516	24.9943	25.6206	25.7982	25.2025	26.0125	26.3195	26.8083	26.4219	
	Q9HV55	PA4463	8	67.6	11.739	153	8.54E+10	153	102	32.8816	32.4484	31.8925	32.9059	31.2211	30.9832	30.8793	31.2433	
	Q9HVY4	PA4431	9	69.5	20.828	67.609	1.35E+10	88	197	28.1194	27.734	26.4863	28.2692	28.9331	29.2243	28.306	29.3582	
	Q9HVY5	PA4401	6	37.4	23.789	16.234	5.5E+08	44	191	25.1104	25.0084	25.0779	25.0062	24.4121	24.4626	24.7358	24.1057	
e c reducta	Q9HW30	PA4372	13	57.9	38.323	57.19	1.29E+09	65	354	24.3219	24.796	23.4767	24.028	25.9611	25.4923	25.8643	26.2913	
	Q9HW32	icmP	17	51.1	47.23	115.25	4.25E+09	102	446	25.9348	26.3745	25.4166	26.4622	27.1807	26.5861	27.0997	27.0102	
	Q9HW37	PA4364	3	32.3	14.316	12.454	1.97E+08	8	133	24.7379	24.4882	24.6527	24.7959	23.7289	23.7602	23.0469	24.1632	
	Q9HW49	PA4352	24	72.4	30.972	323.31	4.79E+10	277	286	30.2897	30.5554	30.7205	30.3055	28.2056	28.105	28.5218	29.8751	
	Q9HW52	PA4349	7	33.9	31.671	41.701	1.39E+09	34	298	26.4564	26.4554	26.5608	26.2394	25.238	25.5529	25.8046	25.4559	
Q9HW53	Q9HW53	PA4348	7	52.5	29.475	42.735	2.57E+09	33	261	28.1445	27.2484	26.8127	28.1302	25.6558	26.3158	23.5181	25.857	
	Q9HW56	PA4345	7	50.5	22.161	28.116	4.95E+08	27	196	24.0897	24.1693	24.2044	23.8162	25.4012	24.957	26.0913	25.2345	
	Q9HW73	PA4328	17	66.1	34.419	167.56	5.93E+09	120	304	27.1521	27.4689	27.7045	27.1596	24.9745	23.9809	25.1147	24.78	
	Q9HW85	PA4115	12	44.9	51.13	70.979	2.12E+09	65	461	25.7148	26.1	25.6332	25.5626	26.5574	26.4587	26.4448	26.6621	
	Q9HW58	PA4100	19	51.9	60.354	105.83	1.24E+09	90	559	25.18	25.7592	25.3808	25.3926	24.7181	24.4729	24.5457	24.7069	
Q9HW59	Q9HW59	PA4073	19	62.2	52.094	181.13	1.96E+10	186	495	29.9203	30.1167	30.2285	29.8164	29.1927	28.9608	29.1611	29.0752	
	Q9HWX3	ribC	7	29.2	23.469	53.203	1.08E+09	35	219	25.8806	25.9064	26.0047	24.1255	24.9499	24.738	24.9258	24.9258	
	Q9HWX7	thiL	5	29.5	32.911	19.835	2.37E+08	13	322	23.6072	23.778	22.9515	23.0282	24.2164	24.5317	23.5679	24.3462	
	Q9HX01	PA4026	5	38.6	18.049	22.014	9.61E+08	28	153	26.0466	26.057	26.5539	26.7287	26.0896	25.595	25.3325	25.7866	
	Q9HX05,Q9I2aC,PA402		22	56.9	54.979	323.31	2.34E+10	230	506	29.062	29.1626	29.6094	28.7079	27.8555	27.743	28.063	27.9726	
yladenine i	Q9HX12	PA4015	10	72.8	16.7	122.78	5.79E+09	76	151	27.1241	27.2954	27.3271	27.4985	26.8823	26.6668	26.6678	26.4253	
	Q9HX17	PA4010	8	49	26.949	45.375	1.11E+09	35	239	25.3141	25.7733	25.6141	25.3548	26.2919	26.5098	26.3227	26.2408	
	Q9HX32	IptE	5	31.9	22.883	29.354	6.75E+08	28	207	24.0109	24.4739	23.3007	24.6613	26.013	25.1848	25.5897	25.4134	
	Q9HX76	PA3940	5	49.5	8.9923	87.376	7.25E+10	108	93	31.4442	31.3172	30.9321	31.7137	32.1306	32.0505	32.1217	31.8489	
	Q9HX91	PA3922	23	57.1	51.229	320.83	9.12E+09	156	455	27.6429	27.751	28.6231	26.1157	25.5564	26.1999	26.225	26.1999	
rized prot	Q9HX94	PA3919	18	63.7	51.699	224.73	8.51E+09	112	463	28.5214	28.341	28.425	27.889	26.8522	26.6956	27.3909	26.8675	
	Q9HXA0	PA3913	4	23.3	36.024	29.424	2.33E+08	16	331	23.9519	24.59	25.078	24.0675	24.2933	23.1905	22.7393	23.3795	
	Q9HXB1	ivy	6	62.1	16.905	74.318	3.64E+09	46	153	27.4955	26.911	26.0702	27.5881	27.8077	28.334	27.7926	28.0911	
	Q9HXC2	PA3891	6	36.2	43.303	62.391	5.8E+08	24	387	24.3278	24.1862	22.2273	23.3289	25.0151	25.2238	25.6405	25.1391	
	Q9HXC2	PA3880	5	67.2	14.38	57.343	5.21E+08	21	131	25.4554	25.546	24.9406	25.6865	23.9634	23.9398	23.085	22.3885	
/lprolyl iso	Q9HXC3	narL	11	68.9	24.255	113.2	3.98E+09	79	219	27.2841	27.0263	27.3875	27.3324	25.9896	26.059	26.0111	26.1879	
	Q9HXC5	PA3871	9	37.1	30.13	206.49	2.55E+09	64	272	27.1419	26.7405	25.8684	27.2713	25.5565	25.4847	25.7552	25.7027	
	Q9HXC1	PA3865	9	43.7	28.433	68.893	1.47E+09	47	263	25.755	25.9455	26.3109	25.9731	25.0057	24.8351	24.8467	24.3811	
	Q9HXC8	PA3858	10	46.9	37.042	58.842	1.18E+09	54	341	25.6541	26.1431	25.7995	26.0448	25.3076	24.8192	25.3523	25.0258	
	Q9HXG0	PA3846	4	37.2	19.892	17.412	4.74E+08	18	180	25.9194	25.9912	26.4858	25.9877	23.9668	24.4384	24.8622	23.3156	
Q9HXC8	Q9HXC8	PA3836	19	75.1	34.22	268.07	4.63E+10	207	325	30.1392	30.3997	30.1174	30.2235	29.4807	29.3919	29.3162	29.3923	
	Q9HXH0	valS	31	44.4	107.71	286.26	9.34E+09	171	950	27.3074	27.0955	26.5641	27.2807	27.872	27.6116	27.5673	27.8553	
	Q9HXH3	PA3819	13	80.2	18.972	234.24	1.34E+10	126	182	27.899	28.0215	27.175	28.0812	28.8224	28.2522	28.6832	28.361	
	Q9HXJ5	hisS	13	39.9	47.512	162.68	5.76E+09	90	429	27.2303	27.0221	26.6251	27.0975	27.6505	27.6306	27.6174	27.5823	
	Q9HXJ7	bamB	9	45.8	40.396	49.493	6.51E+08	31	380	23.6508	24.0284	23.0123	24.5118	25.8457	24.5811	24.9303	25.1581	
Q9HXK2	Q9HXK2	PA3795	9	50	34.803	113.74	4.4E+09	70	316	26.8486	26.638	27.026	26.7832	28.0655	27.6761	27.8536	27.5713	
	Q9HXK5																	

sterchange interchang	Q9I0W1	czcb	12	36.8	50.715	17.417	4.59E+08	20	484	22.4907	23.112	23.941	23.319	25.5346	24.8915	24.2793	25.0436
	Q9I0X8	PA2504	4	26.8	22.822	16.418	3.6E+08	13	205	25.2655	25.6778	25.2194	25.3541	24.7396	23.0667	22.9579	23.0558
	Q9I101	PA2481	9	38.8	31.249	40.981	1E+09	39	291	26.226	25.6333	25.3441	26.1662	24.5838	24.8783	24.7605	24.9128
	Q9I103	PA2479	13	72.6	24.747	146.59	4.23E+09	59	226	24.1781	23.7147	23.986	23.5154	28.0624	28.1769	28.1306	27.9774
anchcd-ch dehydroge lehydroger	Q9I104	dsbD2	5	14	62.093	24.972	4.75E+08	17	587	22.4965	22.7508	22.8471	24.3038	25.9388	25.5468	25.3049	25.8577
	Q9I106	dsbG	16	70.7	28.053	245.91	4.64E+10	136	256	24.1786	23.897	22.9366	24.0345	30.9852	30.889	30.9478	30.8522
	Q9I120	PA2462	22	7.9	573.17	91.146	6.68E+09	35	5627	29.5927	30.0688	29.7366	29.9499	23.0756	28.9771	23.5019	23.0955
	Q9I171	PA2410	4	26.2	31.732	18.921	5.38E+08	18	305	23.549	22.8963	24.2996	23.0954	25.8341	25.9682	26.525	25.8783
riohemery	Q9I1C6	PA2352	21	82.5	41.13	157.86	8.66E+09	149	375	27.8817	28.0117	27.9679	28.0154	27.4859	27.1815	27.1015	27.2492
	Q9I1F7	PA2318	6	74.3	12.889	103.06	2.28E+10	108	121	30.2616	29.8897	28.976	29.9818	28.562	28.8963	28.8529	29.8813
	Q9I1K7	PA2266	14	48.7	46.74	87.758	1.67E+09	67	439	26.4411	26.315	26.0466	26.3949	25.4322	25.4009	25.3951	25.4498
	Q9I1K8	PA2265	16	36.9	64.715	69.568	2.29E+09	85	591	26.1435	26.2217	26.1164	26.0966	25.4234	25.1599	25.1796	25.2586
n regulator	Q9I1L0	PA2263	6	26.8	35.615	37.292	3.56E+08	25	328	24.2891	24.809	25.479	24.1584	23.4184	23.2333	23.131	23.5913
	Q9I1M0	bkbD	20	58.2	45.774	190.61	4.25E+09	112	428	26.9233	27.3746	27.1115	27.1784	25.8595	25.4732	25.5123	25.6367
	Q9I1M1	bkdA2	15	58.3	38.324	111.67	6.81E+09	100	350	28.0484	27.9253	28.6892	27.4346	25.848	26.0665	26.3433	26.2138
	Q9I1M2	bkdA1	17	60	45.256	226.09	6.08E+09	89	410	28.046	27.8733	28.9325	27.3457	26.0342	25.7602	26.1962	26.4287
n regulator	Q9I1N7	pslB	9	32	53.515	35.166	4.76E+08	30	488	24.8537	25.4621	25.2679	24.4579	23.7508	24.3514	24.1941	24.4692
	Q9I1Y9	PA2126	10	63	23.677	62.791	1.19E+09	36	211	26.2458	26.7922	27.0329	26.5052	24.2466	24.3194	24.538	24.322
	Q9I1Z6	PA2119	16	66.9	38.561	222.98	1.76E+10	151	366	29.3304	29.3677	29.6578	29.0973	27.4181	27.2716	27.374	26.9779
	Q9I295	liuR	6	53.7	15.631	68.074	9.69E+08	31	134	25.7744	25.621	25.7911	25.3901	24.7663	24.9604	24.9939	25.0632
l-CoA/hyd	Q9I296	liuA	23	72.6	42.209	200.19	8.07E+09	160	387	28.1615	27.9876	28.5097	27.5707	27.2637	27.0921	27.6727	27.2166
	Q9I298	liuC	4	23.4	28.947	29.054	7.28E+08	24	265	26.0864	25.5988	26.0831	25.9122	25.5207	24.7845	25.3952	25.199
	Q9I2A0	liuC	8	35.7	31.837	34.702	4.79E+08	33	300	24.3441	24.459	24.7566	24.3189	23.9954	23.3245	23.9946	23.6981
	Q9I2A9	dhcB	6	40.8	23.187	38.841	1.11E+09	32	218	26.7656	26.1621	26.4369	25.3748	25.3784	25.236	25.6699	24.9129
yglucosam	Q9I2B0	dhcA	7	51.3	25.243	41.458	1.53E+09	50	232	26.8516	26.5075	26.4389	25.8431	25.2391	24.851	25.4603	24.6081
	Q9I2F8	rbsB	6	28.5	33.86	16	4.38E+08	21	319	24.9257	25.2133	25.5649	24.9758	22.5341	22.29	23.8255	22.6323
	Q9I2N2	modA	6	32.3	26.377	28.242	1.26E+09	47	251	26.353	26.4662	26.616	26.4242	25.3381	25.302	25.2741	25.0026
	Q9I2P9	cti	16	30.4	86.517	68.806	5.92E+08	48	762	25.1784	24.8166	23.5804	25.4624	23.467	23.7747	23.312	23.5743
n regulator	Q9I2Q4	PA1841	5	37.8	18.654	15.412	4.47E+08	16	165	23.5024	25.0269	24.243	24.6007	25.4285	25.3464	25.1055	25.0123
	Q9I2I7	PA1807	4	13.6	59.074	26.018	1.41E+08	16	536	22.6152	23.1115	22.746	24.1887	24.1164	24.2085	24.1204	24.1204
	Q9I2V0	lpxH	3	22.5	27.554	14.839	2E+08	11	240	23.0898	23.3118	23.9942	23.6145	23.9257	24.172	24.1592	24.2874
	Q9I2V3	PA1789	19	76.7	31.273	293.01	2.54E+10	162	287	29.4952	29.7649	30.0377	29.2986	27.3936	27.3918	27.4358	27.1832
n regulator	Q9I2X1	PA1768	10	56.4	19.72	24.433	3.41E+09	39	179	27.4608	28.2158	27.8924	27.8479	27.0889	27.2551	27.3993	27.2602
	Q9I2X2	PA1767	9	28.1	56.812	83.114	7.35E+08	35	508	24.6264	24.691	23.7052	24.727	25.3673	25.3411	25.1073	25.439
	Q9I2Z1	PA1746	9	76.2	18.189	170.52	4.45E+10	142	168	31.9753	31.7242	31.6615	32.0006	29.2495	29.323	29.3899	29.321
	Q9I311	bgIX	9	17.9	83.002	16.979	2.05E+08	20	764	24.2282	24.2804	24.67	23.9065	23.0966	23.4895	23.0691	22.7239
n regulator	Q9I321	exsD	8	35.1	31.365	31.478	1.25E+09	35	276	26.3228	26.4124	26.512	26.508	25.7972	25.5017	25.6297	25.7839
	Q9I323	popD	6	33.6	33.609	72.343	9.88E+08	20	295	26.2412	26.2918	26.4796	26.1577	27.0373	24.0123	24.2377	23.3662
	Q9I324	popB	6	29.5	40.061	55.474	1.52E+09	30	390	26.9486	26.2535	27.1765	26.5527	25.0098	22.1896	24.117	24.5696
	Q9I338	PA1689	12	28.7	77.984	68.226	1.9E+09	53	700	24.5656	24.8095	22.9164	24.9507	26.2292	26.1846	26.3548	26.3548
n regulator	Q9I352	PA1673	10	52.9	17.853	167.92	1.38E+10	89	153	25.6705	29.7944	29.0998	29.8122	28.0515	28.0278	27.4538	27.4925
	Q9I371	PA1654	8	41.8	43.311	55.308	7.87E+08	33	388	24.7604	24.6254	24.6321	24.6535	25.0838	25.3857	25.5765	25.7125
	Q9I3D3	sucA	42	59	105.88	323.31	3.69E+10	380	943	28.3962	28.7707	27.9604	28.8741	29.3576	29.2786	28.8893	29.3155
	Q9I3F7	PA1560	4	37.3	15.667	35.892	7.6E+08	18	142	23.3268	24.2344	22.4476	22.1661	26.032	26.1133	25.9939	26.6663
n regulator	Q9I3F8	PA1559	12	71.2	26.551	93.168	1.67E+09	44	203	24.2576	23.9655	22.8709	24.5681	26.7915	26.4501	26.2134	27.0452
	Q9I3F1	ccoD2	7	37.1	22.778	26.711	1.94E+09	38	202	27.2537	27.3116	26.693	27.5404	23.4866	25.9691	23.8817	26.358
	Q9I3G1	ccoP2	9	45.2	33.812	52.42	9.74E+08	43	308	25.4322	25.1046	26.3084	26.1892	23.966	23.0134	24.214	24.214
	Q9I3G3	ccoP1	3	10.9	53.108	12.092	5.04E+08	23	175	24.5308	25.1502	24.0124	25.0907	26.0629	25.6101	24.9455	25.7147
n regulator	Q9I3G6	ccoP4	5	23.6	32.236	99.766	1.35E+09	58	289	24.4315	24.9583	24.4033	25.4335	25.1324	25.4288	25.4953	25.4953
	Q9I4A1	glaA	5	53.4	44.18	23.312	3.01E+08	19	427	24.0623	23.0121	22.1044	22.9582	24.3947	24.6506	24.4605	24.777
	Q9I353	gbaA	11	43.6	34.727	75.716	4.2E+09	63	319	27.7834	28.1165	28.3921	27.1923	27.3229	26.9046	27.1369	27.1369
	Q9I402	PA1342	23	75.5	33.054	323.31	3.76E+10	275	302	30.6585	30.7228	30.6132	30.5969	29.8658	29.8636	29.9048	29.8102
nase-aspar	Q9I407	ansB	16	61.9	38.644	203.75	3.22E+10	195	362	29.1375	29.3461	29.7983	29.142	28.6228	28.6471	28.6507	28.5707
	Q9I448	PA1296	9	52.6	33.729	55.531	1.11E+09	37	310	22.1919	23.7642	24.1738	23.3407	26.3892	26.2027	27.2422	25.893
	Q9I457	PA1287	6	46.7	20.217	34.49	1.23E+09	31	184	26.7898	26.3455	25.7429	26.7877	25.5619	25.7864	25.2541	25.9128
	Q9I484	PA1260	7	39.9	29.142	34.693	3.89E+08	18	273	24.8551	24.5758	25.5418	24.6421	22.9149	23.8575	22.896	23.177
hione pero	Q9I480	PA1228	3	38.8	12.362	22.057	1.27E+09	24	116	25.929	26.3129	25.692	26.4434	26.9663	26.751	26.7666	26.3178
	Q9I483	PA1225	7	48.1	22.551	56.301	2.71E+08	21	208	24.5427	24.8542	23.8437	24.9344	24.3955	22.9458	22.2895	22.5657
	Q9I4G6	PA1171	10	37.9	42.682	61.409	1.6E+09	41	398	26.0401	26.4557	26.501	26.2718	25.5587	25.7179	25.6971	25.5334
	Q9I4I0	PA1157	3	22.5	26.405	17.076	2.7E+08	12	236	23.4376	22.7872	23.4217	22.4025	24.3487	24.7678	25.2624	23.0396
e-diphosph	Q9I4I1	nrDA	48	60.6	107.11	323.31	2.03E+10	337	963	27.0145	27.4913	26.577	27.5083	28.0822	27.7331	27.7689	28.1267
	Q9I4I8	PA1137	12	40.9	34.731	59.446	9.49E+08	42	328	26.1633	25.6714	26.4066	25.6007	24.5086	24.3147	24.6097	24.3818
	Q9I4K0	hchA	5	26.5	31.898	30.229	5.5E+08	22	291	25.729	26.0067	26.2157	26.0115	25.1806	23.6008	25.4045	24.8575
	Q9I4I2	PA1123	7	86.8	12.167	57.915	1.08E+09	37	106	26.7629	26.3135	26.729	26.917	24.9066	24.9623	25.8562	24.9076
nase S ⁺	Q9I4O3	PA1076	5	52.5	13.743	64.311	1.43E+10	57	120	30.3958	29.7947	29.0953	30.3537	27.9672	28.8187	28.1718	28.8035
	Q9I455	pdxH	12	60	24.86	163.17	1.36E+10	88	215	29.3945	29.4135	29.0343	29.6455	28.1962	27.944	27.7856	27.8785
	Q9I4W2	PA1011	11	53	43												

	G3XD71	PA0620	2	6.2	72.292	8.7943	99903000	9	691	23.9443	23.1724	24.1046	24.2349	22.8476	23.152	24.1566	24.5852
rotein ass- ntaining pr rotein Niri	O68562	bamE	3	38.6	19.395	11.234	1.8E+08	12	176	23.3836	22.4799	24.0626	23.1813	22.0182	24.5603	24.0074	24.4109
	P42810	PA4667	4	11.2	66.29	16.453	1.9E+08	12	590	23.7435	23.3562	21.9493	23.3001	23.905	22.8825	24.1107	23.8962
	P59415	nirH	5	30.4	19.582	10.704	1.54E+08	11	171	23.9793	24.4736	24.2834	22.844	22.9079	24.1475	21.6921	22.9597
	Q9HT29	PA5545	3	16.3	33.627	14.163	1.38E+08	13	319	24.168	23.9832	24.0584	24.2337	22.5911	24.451	22.523	22.7838
	Q9HT84	PA5487	5	12.1	73.998	32.499	1.25E+08	9	671	23.1412	22.907	23.0499	24.2399	23.6155	23.3123	23.8582	23.5807
	Q9HU40	PA5083	3	35.3	12.558	8.0832	92849000	11	116	24.3219	22.4803	22.923	23.3342	23.4585	22.5558	23.9555	24.1379
	Q9HUU0	PA4873	4	20	46.299	12.437	1.02E+08	17	421	24.3988	23.0892	24.4001	23.3679	24.4136	24.1945	23.443	24.3209
	Q9HUW7	PA4843	9	31	61.599	42.612	2.48E+08	13	542	24.1246	24.6103	24.2104	24.2719	22.9727	23.4995	24.3372	24.7239
	Q9HVQ6	PA4516	4	19.9	29.587	11.523	1.16E+08	11	271	23.501	24.1566	23.0246	23.1832	23.879	22.9053	24.4736	23.9676
	Q9HW12	PA4394	2	13.7	29.817	14.725	1.99E+08	13	278	23.3538	23.5774	23.6334	24.511	24.1115	24.0838	24.0563	24.4668
	Q9HX60	PA3956	8	97.9	15.453	44.921	7.88E+08	15	144	27.0345	23.3294	23.9155	26.6043	23.3884	24.397	23.2672	22.3217
	Q9HX50	nalC	2	20.2	23.533	14.921	1.42E+08	8	213	23.0928	23.6149	22.8989	24.5709	24.3118	24.6448	23.1077	23.8055
	Q9HXW8	PA3672	2	7.8	33.499	6.3282	98465000	8	307	23.4421	23.1036	22.1023	22.3713	23.8367	23.0026	23.845	23.7831
	Q9HY18	PA3417	6	30.7	40.414	22.437	2.42E+08	11	365	24.7621	22.6769	25.0435	24.4863	23.9803	22.466	23.2142	22.8264
	Q9HY19	PA3416	2	11.4	36.143	15.821	1.18E+08	8	333	24.2478	23.6242	24.898	23.7743	22.3133	23.7863	23.2264	23.2025
	Q9HY10	PA3415	8	43.8	39.52	53.42	3.79E+08	16	370	24.1697	24.7907	25.724	23.9246	23.1673	22.2322	23.8652	23.9246
stidine kins	Q9I0X9	PA2503	7	29	45.895	19.642	1.96E+08	13	417	23.528	23.2151	23.4309	23.0523	23.4406	24.1696	23.9214	23.8252
	Q9I102	PA2480	4	15.5	47.692	13.62	89224000	13	440	23.5845	22.7875	22.8826	23.0709	23.2017	22.7999	22.7503	23.2288
	Q9I124	PA2458	3	18.2	41.261	17.124	1.18E+08	12	373	23.4032	24.5829	24.53	24.3773	22.5288	22.6007	23.0236	23.558
	Q9I126	PA2457	2	8.5	36.102	11.77	63192000	7	326	23.9004	22.64	23.6874	23.7335	22.7085	22.9965	23.1599	22.8947
	Q9I2A6	bdnA	3	23	26.727	10.916	1.69E+08	11	256	24.0358	24.0812	24.347	23.8633	23.8712	22.9458	22.5005	23.7952
	Q9I2B2	PA1997	5	14.4	71.929	22.19	1.98E+08	11	651	23.2659	23.6937	24.3663	24.0237	23.3438	22.1843	22.9991	23.767
	Q9I2R3	PA1832	4	24.9	38.069	16.557	90460000	7	341	23.1738	23.221	22.4082	24.0265	24.4197	22.7283	23.7534	23.0149
	Q9I4E5	PA1193	6	37.2	25.292	11.464	1.95E+08	14	223	23.2358	23.1737	23.4675	23.8009	24.2938	24.1453	23.0679	24.4847
ic nitrate r	Q9I4X8	napA	8	14.5	92.974	16.184	1.52E+08	13	829	23.6871	23.7825	24.4678	23.5758	23.842	23.6159	24.1229	23.0353
	Q9I4X8	PA0991	3	32.8	13.286	14.686	1.66E+08	11	125	23.6261	23.6694	21.8314	24.2406	23.2372	23.2467	22.9562	23.6464
zyme inh	Q9I574	mIc	3	37	13.695	9.1778	1.47E+08	13	127	23.7923	23.9375	23.4898	22.4457	24.266	24.0108	23.8714	24.2295
	Q9I673	PA0444	6	25.3	45.265	31.49	2.5E+08	18	427	24.927	24.7157	23.5246	24.6553	22.7871	23.3418	23.242	24.5654
	Q9I6W5	PA0167	2	12.2	24.533	7.0685	1.99E+08	12	221	23.1775	24.1683	23.8381	22.7863	24.7482	24.5886	23.3677	24.6565
hain releas	E1U18	prfB	19	63.7	41.17	323.31	1.43E+10	176	364	27.9361	27.8251	28.0347	27.7251	27.9997	28.2035	28.3476	28.3124
/Cys-tRNA	G3XC74	PA3580	3	25.6	16.493	14.589	3.9E+08	15	156	25.4654	23.2886	23.3611	25.3132	25.239	25.4686	25.1506	25.4955
stidine kins	G3XC76	PA1458	24	50.3	79.737	291.08	1.14E+10	216	753	27.8241	27.6987	27.9216	27.6816	27.5128	27.6	27.5542	27.8555
	G3XCU6	cysB	11	47.2	36.109	115.06	3.11E+09	69	324	26.8287	27.0522	27.3016	26.5566	26.5997	26.7242	26.7549	26.6333
	G3XCU9	PA2020	3	16.7	23.727	6.2049	1.98E+08	13	210	23.8758	23.2683	24.0793	23.0481	24.1825	24.5225	23.1737	24.2598
	G3XCVO	fleQ	20	52.7	55.276	190.36	7.2E+09	120	490	27.5167	27.4882	27.8449	27.0377	27.1957	27.2481	27.3319	27.6062
	G3XCX8	PA0900	2	31.2	10.641	84.031	1.24E+09	20	96	27.038	26.5381	25.1162	26.4655	26.7411	26.9651	26.8856	26.6812
	G3XCZ3	pilZ	6	66.9	12.904	25.183	1.6E+09	41	118	26.1709	26.0573	25.4096	26.5909	25.9605	26.3026	25.7733	25.9569
carrier prc	G3XCZ6	fabD	16	56.1	32.444	261.1	2.97E+10	158	312	30.2119	29.9901	29.711	29.9851	29.837	30.0924	29.7635	29.9321
	G3XD09	gltD	7	27.9	52.624	62.423	9.51E+08	42	477	25.1736	25.0445	25.2215	25.1134	25.3292	25.6778	25.7864	25.2762
	G3XD11	oprH	7	44.5	21.574	130.87	2.26E+09	39	200	26.3424	26.3771	26.2555	26.4407	26.7675	26.146	26.8116	26.5644
	G3XD13	PA0902	11	55.7	35.462	118.17	2.34E+09	72	334	26.2988	26.5132	26.4495	26.2246	26.4049	26.5735	26.1579	26.2961
ding trans	G3XD14	dksA	12	73.6	17.344	129.96	5.48E+10	182	148	30.6173	30.5716	29.1893	30.7827	31.0477	30.9611	30.8665	30.9178
	G3XD17	dsbC	8	57	26.095	153.33	8.31E+09	74	242	28.037	28.1333	27.6019	28.232	28.6806	28.4458	28.6533	28.5122
ig chemota	G3XD24	PA4915;p	12	30	68.016	36.405	1.25E+08	12	629	24.1733	24.3713	23.0133	23.7894	23.1186	23.0799	24.2486	23.4002
	G3XD27	PA5055	7	81.3	13.653	55.029	1.74E+09	40	123	26.7474	26.3005	25.111	26.6647	26.1458	26.6968	25.8728	26.2219
	G3XD36	ptsP	15	36.6	83.606	81.35	1.12E+09	60	759	25.134	25.0301	24.9974	24.917	24.7977	24.6031	24.9953	25.2787
	G3XD47	aotJ	23	81.1	28.01	273.55	4.54E+10	212	259	29.4673	29.684	29.1103	29.2139	29.3783	29.7768	30.0765	29.7544
	G3XD52	PA3302	8	78.2	16.901	84.965	7.09E+09	102	156	28.4571	28.058	28.1445	28.4649	28.1809	28.0045	28.2517	28.3307
	G3XD54	dnaQ	10	54.1	26.814	132.99	5.46E+09	97	246	26.9891	26.9553	26.7938	27.0164	27.2709	27.2331	27.2005	27.1977
	G3XD55	pilY2	3	30.4	12.986	11.776	2.77E+08	11	115	22.6199	22.8323	23.0688	25.1424	23.5643	25.0405	24.9552	25.1195
amate met	G3XD63	chpB	5	34.7	37.237	24.755	5.21E+08	18	343	23.3867	25.8004	25.6565	26.3151	20.7874	25.6261	22.8453	25.5457
termining j	G3XD64	fleN	10	41.1	30.037	71.401	2.74E+09	69	280	26.1004	26.1032	26.5579	25.8439	25.6312	25.7506	25.8433	25.7574
	G3XD70	PA5279	4	33	25.767	68.789	3.93E+09	41	233	27.5816	27.7142	27.6054	27.7667	27.6815	27.5296	27.5627	27.5163
	G3XD72	PA1464	11	83.6	17.536	169.8	1.66E+10	102	159	28.8174	28.7533	28.6972	28.8264	27.8877	28.4935	28.5668	28.5038
	G3XD74	dacC	11	45.6	42.457	126.37	5.83E+09	92	386	27.163	27.782	27.31	27.6079	27.8517	27.5694	27.8008	27.9684
1,6-dicarbo	G3XD76	dapD	12	43.6	35.973	116.97	1.74E+10	115	344	28.7223	28.6541	28.9196	28.6708	28.7293	28.6528	28.5597	28.5091
	G3XD95	chpC	9	71.4	17.625	137.62	1.75E+09	71	168	26.1561	25.859	24.9312	26.0387	25.1984	25.6468	24.6616	25.5011
	G3XD97	ptsX	14	56.8	37.391	111.39	2.12E+09	47	340	27.9941	27.253	27.6497	27.1426	27.3271	23.2165	25.5157	27.7621
carrier-pro	G3XD12	fabF1	13	62.1	43.497	323.31	2.94E+10	142	414	29.4288	29.4111	29.5327	29.2632	29.5505	29.5503	29.4318	29.469
	G3XD44	PA0653	10	83.6	15.236	81.348	4.57E+09	77	140	27.3038	27.4587	27.3566	27.4667	27.2773	27.3283	27.177	27.1366
	G3XD45	oprE	5	18.7	49.666	88.226	9.36E+08	30	460	26.3655	26.7082	25.8542	26.6596	25.8715	25.9009	25.9232	25.9422
	G3XD80	crc	13	70.7	29.844	98.78	5.06E+09	101	259	27.2611	26.9506	27.2689	27.1166	26.8795	27.1358	27.1584	26.9898
	G3XD82	PA0974	15	61.3	29.997	168.53	1.69E+10	150	274	28.7895	27.9668	28.9022	28.8497	28.6986	29.2425	28.4677	29.2596
ie phospho	Q05927	cysH	8	41.9	30.215	86.202	2.38E+09	52	267	26.424	26.7114	26.8389	26.7134	26.2854	26.2204	26.4078	26.2857
nsport act	Q30525	aotP	8	41.7	27.956	15.026											

l-phosphat	P27726	gap	8	39.8	36.17	131.66	2.38E+09	60	334	26.3	26.4803	26.6894	26.1031	26.5953	25.9152	26.5169	26.1749
utratrde	P28811	mms8	4	26.8	30.486	23.562	2.91E+08	19	298	25.4738	24.6272	23.2904	25.0516	22.4925	23.2347	24.194	23.4892
onine synt	P29363	thrC	24	62.7	51.795	196.45	8.75E+09	147	469	27.2285	27.4463	26.7603	27.43	27.7561	27.7628	27.7563	27.9462
ioserine kin	P29364	thrB	8	31	35.374	53.833	1.64E+09	53	316	26.6471	26.6316	25.9126	26.7581	26.3782	26.6918	26.6154	26.4625
'ine dehydi	P29365	hom	13	48.2	46.223	194.8	2.09E+10	140	434	28.747	28.7891	28.862	28.411	28.7576	28.7063	28.9203	28.9519
Da chapen	P30718	groL	49	78.2	57.085	323.31	1.11E+12	2194	547	33.9094	33.897	34.2853	33.9213	34.1123	33.9289	34.0901	33.8527
Da chapen	P30720	groS	5	51.5	10.267	158.36	1.23E+11	130	97	32.8403	32.8567	31.8623	33.0513	32.8378	32.7505	32.5501	32.9423
nyrophosph	P30819	nadC	11	44.7	30.551	147.04	6.81E+09	110	282	26.9345	27.069	27.1173	26.9891	26.7222	26.9325	26.8539	26.7806
uconate de	P31961	edd	18	49.7	65.182	245.49	8.6E+09	136	608	26.9913	27.0368	27.1324	26.7787	27.4022	27.181	27.5513	27.212
scriptional	P32265	nfxB	5	44.9	21.077	66.227	9.76E+09	42	187	28.8633	29.0118	28.9101	29.0729	29.3509	29.4205	29.3831	29.057
unit pseud	P33640	riuD	6	22.5	35.625	27.109	6.4E+08	23	320	25.0074	25.0517	25.1994	25.0899	25.2752	24.9982	24.7919	25.0696
nino acid o	P33642	PA4548	8	41.8	39.445	34.993	1.24E+09	44	364	25.479	25.163	25.7155	25.1252	25.7349	25.6535	25.5852	25.8212
main prote	P33663	PA4543	5	43.4	26.047	40.285	4.97E+08	23	242	25.402	22.7704	23.8031	25.4543	24.8806	26.0583	22.3054	25.5323
roquinat	P34002	aroB	15	54.6	40.109	119.9	1.03E+10	134	368	27.2862	27.2297	27.3795	27.3306	27.2568	27.2047	27.2812	27.1548
kimate kin	P34003	aroK	5	40.1	19.237	40.375	4.1E+08	14	172	24.7367	24.9018	25.253	24.8054	24.7934	24.8879	23.2266	25.2885
tion syste	P35818	xcpQ	6	24.6	69.952	12.565	1.67E+08	20	658	23.7931	23.5156	23.4796	23.7242	23.9215	24.4484	23.8444	22.9444
xA repress	P37452	lexA	5	35.3	22.506	33.332	2.59E+09	39	204	26.6656	27.0824	27.2845	26.9596	26.9214	26.875	26.7456	26.5123
in carboxy	P37798	accB	22	56.3	48.887	301.02	5.93E+10	230	449	29.7835	29.957	29.9999	29.5339	29.7159	29.9137	29.9414	29.9083
rotein of .	P37799	accC	7	57.7	16.455	255.93	5.67E+10	166	156	30.9322	30.6934	29.5659	31.1882	31.0952	31.3965	30.6121	31.236
phate synt	P38098	carA	16	62.7	40.828	225.78	2.49E+10	169	378	29.2697	29.3682	29.2289	29.0599	29.0599	29.3103	29.1696	29.2766
phate synt	P38100	carB	53	65.4	117.33	323.31	1.91E+10	304	547	27.8495	27.6802	26.8945	27.6374	27.6046	27.6046	27.472	27.9075
ydrolyticp	P38103	capB	14	68.3	28.324	153.17	8.45E+09	89	268	27.679	27.9036	27.7877	27.6965	28.0082	27.9052	27.8838	28.0844
ed DNA-bi	P40947	ssb	12	67.9	18.557	143.73	1.1E+10	122	165	30.0761	30.305	29.7118	29.8987	30.3538	30.2785	30.4571	30.1701
Protein PilI	P42257	pilI	10	24.8	72.527	144.61	1.05E+09	46	682	25.1925	25.7823	24.8191	25.3431	24.9457	24.6114	24.524	25.0303
2-C-methy	P42805	ispE	3	21.3	30.843	13.305	3.86E+08	20	282	24.4953	24.6515	24.4664	24.5321	24.8709	24.4965	24.25	24.8683
hain reles	P42806	prfA	17	51.9	40.04	271.81	1.39E+10	102	360	29.8843	29.8963	30.158	30.0045	30.0345	30.0562	30.0342	30.0387
yl-rRNA re	P42807	hemA	7	30.8	46.123	80.432	8.09E+08	46	422	25.1704	24.9352	24.998	24.7535	25.1376	25.3185	25.1257	25.5699
io-acid am	P43336	phhC	13	50.4	43.273	72.182	2.42E+09	88	399	25.926	25.7841	25.773	26.0933	26.0708	25.7866	25.8661	25.851
rotein PilH	P43501	pilH	5	60.3	13.273	28.633	8.98E+09	40	121	29.7576	28.8207	27.7519	29.9762	28.221	29.0897	27.5583	28.9023
Protein PilI	P43502	pilI	5	46.1	19.934	42.613	5.13E+08	30	178	24.8137	24.7481	24.8665	24.7348	24.5292	24.6008	24.1248	24.4728
o:poroprot	P43898	hemF	15	63.6	34.806	119.95	1.11E+10	169	305	27.7637	27.9297	27.8289	27.9407	27.4251	27.4385	27.4152	27.2405
ie oxidorec	P43903	qor	12	56.6	35.094	103	3.47E+09	89	325	26.5392	26.5414	26.5932	26.2386	26.1601	26.0199	26.0509	25.9779
artate O-m	P45683	pcm	9	56.9	23.407	103.06	4.97E+09	72	211	27.2521	27.4899	27.5424	27.3455	27.5594	27.5754	27.5272	27.6053
rotein PilC	P46384	pilG	7	59.3	14.718	49.757	7.71E+09	63	135	28.503	28.2226	27.4073	28.6754	27.1022	27.8001	26.8708	27.7077
ision prote	P47203	ftsA	26	74.3	44.646	323.31	2.74E+10	245	417	28.6588	28.8428	28.9273	28.5127	28.7582	28.8723	29.0518	28.8625
ision prote	P47204	ftsZ	28	87.3	41.218	323.31	5.29E+10	281	394	29.6467	29.8914	29.9445	29.6951	29.3393	29.2502	29.3875	29.1781
oyl] N-acet	P47205	lpwC	17	54.8	33.435	160.56	4.01E+10	165	303	29.4679	29.7516	29.8098	29.4354	29.2915	29.4353	29.3734	29.4407
yrinogen-I	P48246	hemD	5	42.6	27.279	31.611	4.33E+08	28	251	25.1	25.0954	24.5975	24.8821	24.7884	24.6101	24.9901	24.9323
ialdehyde	P48247	hemL	24	74.5	45.397	316.96	2.09E+10	224	427	28.8353	28.9236	29.0236	28.4326	28.5235	28.7098	28.8593	28.9701
gyrase subi	P48372	gyrA	33	48.1	101.13	301.01	1.05E+10	208	923	26.7093	27.3125	26.5266	27.4113	27.465	27.1653	27.1735	27.5986
erage sigm	P49988	rpoN	16	46.3	56.054	153.96	3.95E+09	91	497	26.3895	26.4654	26.6812	26.1065	26.2713	26.4136	26.3453	26.2646
sphoribios	P50587	pyrE	12	62.4	23.32	144.49	1.15E+10	112	213	28.837	28.5314	28.6053	28.4572	28.5175	28.3358	28.1515	28.0873
onuclease	P50597	rph	5	34.7	25.654	97.391	3.19E+09	44	239	27.8991	27.9897	27.9909	28.1215	27.3831	27.6121	27.672	27.4635
'rotein Toll	P50601	tolB	29	75.7	47.752	302.81	3.21E+10	239	432	28.5544	28.8549	28.975	28.5925	29.0387	28.9936	29.2456	28.8946
'osuccinat	P50987	argH	17	41.2	51.64	150.89	8.08E+09	120	464	27.0488	27.0375	26.84	27.0116	27.2465	27.3503	27.1678	27.3124
stance ope	P52003	mexR	4	38.1	16.964	14.821	3.51E+08	17	147	24.821	24.2237	23.2972	24.7166	24.085	25.0579	24.3821	24.8923
erage III su	P52024	holB	5	25.9	35.746	35.435	2.35E+08	18	328	22.6922	24.0534	23.7723	22.4309	23.8644	24.0924	24.2575	24.3657
osphate de	P52111	glpD	29	74.6	57.134	311.43	1.48E+10	218	512	27.9371	28.1015	28.0672	28.1111	28.1864	27.7911	27.9673	27.6615
] ADP-forr	P53593	sucC	24	64.4	41.542	323.31	2.76E+11	578	388	32.0321	32.1183	32.2942	31.8641	31.9316	32.0947	32.1651	31.8273
ide dismut	P53641	sodB	10	66.3	21.351	135.96	3.56E+10	155	193	31.0503	30.1255	28.8081	30.8314	30.7924	30.9928	29.3704	30.6771
moserine :	P55218	metZ	17	52.9	43.184	150.2	4.59E+09	91	403	26.8703	27.1382	26.8959	27.1478	27.2172	27.4049	27.1682	27.0001
'receptor-l	P55222	vfr	9	41.6	24.225	83.065	3.43E+09	65	214	26.5999	27.1609	26.5125	26.7419	26.531	26.6017	26.2286	26.5122
ucleotide :	P57112	sthA	27	71.6	51.16	323.31	4.04E+10	297	464	28.6563	28.8003	28.5731	28.5256	29.1376	29.0259	29.0357	28.8405
oribonucle	P57665	orn	10	41.7	20.826	69.64	3.34E+09	89	180	26.8874	26.8006	26.4761	26.8376	26.4852	26.4122	26.4102	26.6157
le thiol per	P57668	tpx	14	91.5	17.234	289.98	4.1E+10	163	165	29.6357	29.4479	29.0694	29.7033	29.7011	29.6249	29.705	29.5345
I4-phosph	P57707	ispD	6	41.5	25.613	67.942	1.07E+09	45	234	25.4297	25.3592	25.3293	25.513	25.5033	25.5134	25.7006	25.7722
e O-acetyl	P57714	metX	8	38.3	41.834	87.004	1.37E+09	37	379	25.1319	25.6302	25.1646	25.3094	25.7633	25.8881	25.5024	25.9779
i Initiation	P65116	infA	4	69.4	8.3025	114.05	2.99E+10	80	72	30.5963	30.7656	29.5996	30.7727	30.9645	30.931	30.6957	30.7782
type flagell	P72151	flhC	2	8.2	49.242	85.116	6.63E+10	56	488	32.1246	32.2569	32.1697	32.4051	31.8739	31.7392	31.6461	31.7386
douridine :	P72154	truD	13	57.2	33.41	193.33	8.61E+09	120	304	27.7963	27.8804	27.8995	27.6695	27.4782	27.7457	27.5364	27.6631
idazole rib	P72157	purE	8	62.6	16.889	95.159	1.68E+10	104	163	28.6283	28.2238	27.4658	28.5285	28.5161	28.9047	28.739	28.9452
idazole rib	P72158	purK	7	33.9	38.495	66.937	9.6E+09	84	360	27.6622	27.6522	27.9935	28.1488	27.9299	27.9299	27.8551	27.8208
hydroxoru	P72170	pyrC	21	66.1	38.406	215.34	1.38E+10	168	348	28.085	27.68	26.7119	28.1111	27.813	27.9663	27.3284	27.9734
e aminotra	P72173	aspC	21	73.9	43.315	256.91	1.47E+10	153	398	27.5596	27.8477	27.4978	27.5607	27.8423	27.8506	27.7698	28.254
.system pr	P72174	uvrB	23	51.2	76.065	169.82	2.43E+09	94	670	26.3406	26.3342	2					

thase subu	Q9HT17	atpH	14	78.7	19.26	296.89	7.38E+10	279	178	31.1266	30.7251	30.1797	30.9828	30.8262	31.0266	30.9044	31.1082
hase subu	Q9HT18	atpA	33	63.2	55.393	323.31	3.8E+11	549	514	32.2536	32.3482	32.5052	32.2975	32.5686	32.4404	32.3443	32.2292
hase gamr	Q9HT19	atpG	18	75.2	31.553	204.63	4.8E+10	192	286	29.6419	29.6566	29.7396	29.8371	29.9054	29.5767	29.7256	
thase subu	Q9HT20	atpD	42	93.4	49.499	323.31	5.04E+11	1207	458	32.1375	32.1866	32.4035	31.9725	32.2967	32.2543	32.254	32.2163
thase epsil	Q9HT21	atpC	6	49.6	14.726	47.804	2.04E+10	62	141	29.9932	29.5624	29.4187	30.0279	29.9341	30.0196	29.8418	29.9441
4-acetyltrai	Q9HT22	glmU	21	54	48.851	236.84	1.32E+10	173	454	28.1571	28.4297	28.549	27.9909	28.3424	28.4235	28.519	28.5379
	Q9HT24	glmR	6	45.9	28.151	16.416	2.74E+08	16	257	24.5808	24.204	23.1354	24.1901	24.4986	24.13	24.7524	24.2203
hphate ami	Q9HT25	glmS	19	44.8	66.294	151.51	2.93E+09	106	611	25.7446	26.0733	25.6343	26.112	26.2324	26.3105	26.2957	26.6103
	Q9HT52	PA5521	9	55.2	26.894	102.62	4.83E+09	73	252	28.2107	28.2953	28.3273	28.0291	27.9366	28.1843	28.2819	28.2563
	Q9HT54	PA5519	3	23.4	21.215	7.2815	3.52E+08	14	188	25.5799	25.5822	23.4511	25.2401	24.4557	24.5501	24.4323	24.2227
oxamine k	Q9HT57	pdxY	9	46.5	31.285	42.013	2.51E+09	71	288	26.5335	25.9631	24.9869	26.53	26.2187	26.2643	25.7182	26.168
	Q9HT62	mifR	17	49.2	49.629	60.286	1.04E+09	54	447	25.5474	25.3996	25.4032	25.2613	25.3463	25.4376	25.7667	25.534
	Q9HT64	PA5509	10	59	24.841	67.174	2.7E+09	65	222	26.6761	26.7528	26.2943	26.7858	26.1591	26.5651	26.2166	26.3056
	Q9HT65	PA5508	9	44	47.9	79.352	1.62E+09	60	443	25.8994	25.9395	25.6068	25.5927	25.5435	25.9775	25.947	26.1048
	Q9HT66	PA5507	14	73.7	24.262	249.42	2.75E+10	169	217	29.7803	29.7678	29.9442	29.7571	29.2557	29.3126	29.523	29.3035
	Q9HT67	PA5506	10	42.5	32.143	102.97	1.26E+09	38	285	26.234	26.1002	26.5002	26.3047	25.8348	26.0975	26.1879	25.8634
	Q9HT68	PA5505	12	55	28.065	89.906	3.12E+09	64	260	26.7432	26.8157	22.4624	26.4164	26.6683	27.4553	26.9913	27.1719
: ATP-bindi	Q9HT70	metN2	11	65.4	36.759	95.41	2.44E+09	54	335	26.4108	26.7341	26.6902	26.1322	26.2825	26.6525	26.5936	26.702
	Q9HT74	np20	4	49.1	18.216	47.763	1.39E+09	25	167	26.3981	26.7329	26.3729	26.3889	26.3872	26.4044	26.2318	26.2054
ly polymera	Q9HT80	poIA	47	66.3	99.792	323.31	1.32E+10	303	913	26.9243	27.0243	27.0664	26.669	26.8017	27.0523	27.0393	27.0955
P-binding ;	Q9HT81	hsp70	9	57.7	23.786	55.469	2.3E+09	56	215	26.4199	26.6561	26.3538	26.3955	26.3414	26.5394	26.5498	26.3937
	Q9HT98	PA5472	12	66.5	29.148	85.572	6.63E+09	101	266	28.5093	28.1881	27.3568	28.5083	27.3204	27.9172	27.0698	27.6174
	Q9HTC5	PA5441	23	50.2	80.036	177.94	4.57E+09	137	733	26.348	26.2322	26.27	26.067	26.2591	26.4235	26.4841	26.1959
	Q9HTC8	PA5438	10	51.5	31.68	53.73	1.94E+09	44	293	26.3913	26.7433	26.6044	25.9537	26.4836	26.5086	26.3851	26.8087
	Q9HTD0	PA5436	21	55.6	51.848	144.49	2.93E+09	121	471	25.9198	26.1001	25.9386	25.9655	25.8017	25.6046	25.5151	25.7449
ite ammon	Q9HTD7	aspA	19	66.9	51.069	289.56	4.96E+10	254	474	30.4845	30.2969	30.6316	30.2202	30.1475	30.679	30.5313	30.1835
	Q9HTD8	PA5428	8	43	33.477	54.079	7.45E+08	45	302	24.8457	25.0438	24.806	25.1108	25.3718	25.2199	25.1047	24.6869
	Q9HTD1	PA5423	3	28.6	20.002	16.028	6.55E+08	22	182	25.3608	25.5705	24.894	25.5379	25.0141	25.542	25.0018	24.9445
	Q9HTD2	PA5422	12	56.9	36.139	64.409	1.52E+09	54	318	25.2322	25.2292	25.5164	24.9251	24.9802	25.2459	25.6066	25.2222
	Q9HTF0	PA5414	4	31.5	22.547	13.927	2.22E+08	15	213	24.1005	24.1723	23.7623	23.9498	24.0559	23.8864	23.8679	24.2854
ty L-theor	Q9HTF1	ItaE	13	52.6	38.213	200.86	1.56E+10	119	346	29.1398	28.9947	28.934	28.9835	29.0562	29.0753	29.0471	28.9917
ision prote	Q9HTF7	PA5407	2	32.3	10.292	24.985	4.73E+08	13	96	25.578	25.3192	23.4621	25.6103	25.0812	25.2892	25.3481	25.3962
	Q9HTF8	PA5406	2	31.8	12.445	47.35	2.85E+09	27	110	28.4184	25.9046	25.3522	28.2008	25.7026	28.309	25.7537	27.7063
	Q9HTH8	PA5376	10	36	43.721	30.957	9.64E+08	44	392	25.0393	25.415	25.2245	24.9777	25.0841	24.8745	25.1679	25.0451
scriptional	Q9HTJ0	betI	5	32.5	21.861	25.854	4.24E+08	15	197	24.5652	24.2246	24.6951	24.687	24.1801	24.5664	24.606	24.5109
betaine alk	Q9HTJ1	betB	16	57.3	53.332	172.78	7.34E+09	114	490	27.5678	27.4798	27.4947	27.316	27.0678	27.5722	27.894	27.4495
ent choline	Q9HTJ2	betA	20	51.7	61.836	115.72	1.52E+09	96	561	25.6123	25.407	25.4939	25.7312	25.3958	25.673	25.9629	25.5498
	Q9HTJ3	PA5371	5	56.7	14.555	78.361	1.5E+09	45	134	26.7459	26.3216	26.7425	26.6847	27.0754	26.8753	26.4243	26.4243
	Q9HTJ6	PA5364	12	47.7	32.401	91.821	1.74E+09	55	300	26.0565	25.9566	26.1874	25.6665	25.5551	25.4141	25.7162	25.601
in-NAD(+))	Q9HTK9	alkT	15	67.2	40.617	180.69	4.67E+09	110	384	26.891	27.1422	26.9146	26.8081	27.0727	27.1808	27.2907	27.2243
	Q9HTL4	oxyR	18	75.2	34.295	159.4	7.34E+09	119	310	27.5217	27.7776	27.8056	27.2644	27.1539	27.3483	27.5398	27.4579
	Q9HTL5	PA5343	9	46.3	30.778	82.856	3.07E+09	74	283	26.6385	26.6955	26.848	26.6079	26.2448	26.5372	26.5953	26.4665
ly polymera	Q9HTL9	PA5339	9	93.7	13.609	86.13	7.25E+10	211	126	31.0343	30.6899	29.9581	31.244	30.6614	31.4259	30.9285	31.0712
anylate kin	Q9HTM1	rpoZ	7	44.3	9.748	120.1	3.67E+10	84	88	31.2695	30.6933	29.4476	30.8714	31.454	30.6659	31.3258	
	Q9HTM2	gmk	10	59.6	23.102	115.05	9.08E+09	90	203	28.3281	28.4603	28.2486	28.5273	28.3562	28.3051	27.8994	28.0341
	Q9HTM3	PA5335	12	39.7	31.708	69.613	3.99E+09	49	287	27.6353	27.6741	28.0162	27.515	27.4812	27.7767	27.8552	
	Q9HTM5	PA5330	8	50.7	22.434	100.12	2.37E+09	48	205	27.3104	26.976	24.9325	27.3274	27.4014	27.3798	26.6495	27.1422
glutamate	Q9HTN2	argB	19	83.7	31.849	231.79	2.7E+10	195	301	28.8978	28.9063	29.0277	29.0033	29.1962	29.2301	29.417	29.1292
hosphate r	Q9HTN3	dut	4	56.3	15.92	74.429	3.02E+09	29	151	27.7815	27.2934	26.6701	27.9792	27.0288	27.5497	26.947	27.3942
	Q9HTN4	coaC	17	72.9	43.133	235.34	8.2E+09	118	402	28.0752	27.9426	28.2783	27.861	27.8377	27.7568	27.7283	27.6621
osomal pro	Q9HTN8	rpmB	5	35.9	9.0655	18.539	1.69E+10	28	78	30.4977	31.2329	30.278	30.5695	31.2434	31.057	30.8367	30.718
osomal pro	Q9HTN9	rpmG	3	35.3	6.045	61.759	7.05E+10	58	51	32.2364	32.8605	32.8177	31.7571	32.6726	32.6413	32.8667	32.6408
	Q9HTP1	PA5313	5	20.7	48.347	13.075	2.71E+08	15	444	22.9366	24.0365	22.8445	23.7952	24.5796	24.3133	24.4329	22.3614
	Q9HTP2	PA5312	29	71	53.143	323.31	6.3E+10	352	497	30.476	30.6466	30.9335	30.1439	30.2352	30.21	30.2902	30.2312
	Q9HTP5	PA5309	12	45.1	47.701	81.241	2.4E+09	78	439	26.8946	27.1381	27.3103	26.9544	26.8206	26.9509	26.9342	26.7685
	Q9HTP6	lrp	6	46.3	18.868	14.455	7.19E+08	25	162	25.0981	25.5516	25.2777	25.0407	25.1135	24.9331	24.9343	24.8845
	Q9HTP9	PA5305	4	56.1	11.527	69.895	2.18E+09	35	114	28.0072	25.1341	25.3821	27.6325	24.4817	27.1892	24.4967	26.3214
racemase, i	Q9HTQ1	PA5303	4	47	13.019	27.919	3.15E+08	20	117	25.2149	24.7445	23.1526	25.2479	24.1741	22.2826	23.8404	24.204
	Q9HTQ2	dadX	12	43.1	38.914	108.76	5.46E+09	59	357	27.5006	27.6367	27.4717	27.6471	27.5785	27.4558	27.431	27.1706
	Q9HTQ3	PA5301	10	67	19.962	79.777	5.01E+09	57	182	26.9461	27.2195	27.1749	26.9271	26.9839	27.0358	26.9238	26.8733
	Q9HTQ4	cycB	9	58.1	13.458	77.491	1.52E+10	83	136	29.9998	27.9568	27.4377	29.9478	28.9435	30.1712	28.3442	29.6538
hosphoribos	Q9HTQ6	xpt	7	36.8	20.607	40.98	4.84E+09	56	190	28.0463	28.4623	28.6061	28.2499	27.9429	28.0363	28.1021	27.9633
	Q9HTR5	PA5289	5	66.3	9.5239	35.643	1.42E+09	30	86	26.7214	26.1877	25.5321	26.9113	25.9068	26.6046	25.6633	26.4515
	Q9HTR6	glmK	11	76.8	12.828	108.3	3.31E+10	122	112	30.0238	30.1334	29.5724	30.2454	29.778	29.6832	29.9063	29.6666
	Q9HTR9	PA5285	7	81	11.168	115.39	2.7E+10	77	109	30.0318	29.4038	29.9109	30.3001	29.8318	30.1388	28.4855	30.0864
'rotein Cya	Q9HTS5	cysY	5	58.3	11.9												

-bisphosph	Q9HU73	fbp	15	66.7	37.216	249.53	2.21E+10	168	336	28.8834	29.0109	29.1598	28.8781	28.6859	28.8997	29.0153	28.7904
-iminopep	Q9HUA3	PA5080	19	77.7	36.515	201.62	1.47E+10	156	323	28.1669	28.3446	28.4348	28.112	27.9136	27.8596	27.8968	27.649
osynthesis	Q9HUA5	oggG	28	60.4	59.476	236.79	4.45E+10	287	525	28.8492	28.9787	29.0976	28.7645	28.8772	28.8577	28.954	28.8471
hesis gluco	Q9HUA6	oggH	6	13.9	96.994	35.369	4.62E+08	32	861	23.5472	24.2931	22.0489	24.2883	24.8145	24.5037	24.5784	24.7506
	Q9HUA7	PA5076	20	74.8	29.736	222.4	2.54E+10	179	266	28.8839	28.7491	28.9401	28.8006	28.9548	28.9096	28.695	28.8292
	Q9HUA9	PA5074	3	23.8	27.075	15.223	3.11E+08	20	244	24.2669	23.784	24.7014	24.1553	24.3261	24.2756	24.3748	24.1977
yl-ATP pyr	Q9HUB6	hisE	3	21.6	12.038	10.701	7.52E+08	18	111	24.2619	23.6646	23.5931	26.6819	26.0771	26.1854	23.6158	26.4058
yl-AMP cy	Q9HUB7	hisI	6	74.6	15.375	51.481	3.79E+09	47	134	27.1846	26.9969	26.2392	27.001	27.0735	26.9374	26.668	26.8978
	Q9HUB9	PA5064	3	18.8	22.767	24.017	6.83E+08	24	208	25.1296	25.1846	25.7669	26.0839	25.5247	25.6091	25.5366	25.6642
biosynthesi	Q9HUC0	ubiE	14	66.8	28.254	161.14	1.18E+10	129	256	28.0564	28.3541	28.4844	27.9508	27.7225	27.7956	27.8925	27.6719
	Q9HUC1	PA5062	3	44.8	9.8063	20.871	1.21E+09	26	91	26.4972	26.0535	25.4916	26.6299	25.8866	26.2258	25.5124	25.8794
	Q9HUC3	phaF	5	22.7	30.577	11.229	8.18E+08	22	309	23.2357	25.4232	24.476	25.4459	25.8517	25.7088	25.7567	25.8276
rotease AT	Q9HUC5	hslU	29	52.6	50.082	191.17	2.66E+10	211	447	28.9072	28.9994	29.2232	28.7692	28.6561	28.8264	28.8154	28.8133
nt protease	Q9HUC6	hslV	5	54.8	18.785	106.5	4.46E+09	46	177	27.7038	27.2111	27.4217	27.5286	27.942	28.0618	27.832	27.8496
ine-tRNA I	Q9HUC8	argS	22	43.8	65.199	164.8	8.04E+09	147	587	26.8229	27.2346	26.5565	27.1037	26.9764	26.7595	26.4557	26.8805
isomal pro	Q9HUD0	rpmE	6	74.6	7.9201	85.533	8.03E+10	145	71	32.1242	31.5366	30.9521	32.5271	31.6811	31.8053	31.7501	32.1638
	Q9HUD3	PA5046	39	85.3	45.428	323.31	3.06E+11	640	422	32.0858	31.9537	32.1641	32.1078	32.438	32.2105	32.3612	32.2145
	Q9HUD4	PA5037	15	44.6	57.446	117.56	1.74E+09	64	551	25.6587	25.8396	25.3109	25.8925	26.0967	25.6803	25.4936	25.5879
	Q9HUE1	PA5028	11	73.7	28.643	56.972	1.37E+09	42	255	26.2832	26.3132	26.2991	26.0207	25.7951	26.3597	26.2127	26.0355
te subunit i	Q9HUF0	rmlJ	8	42.8	31.882	33.469	3.53E+08	27	278	24.2069	24.6368	23.0474	24.2996	24.2848	24.3331	24.6627	24.9247
ne sulfoxid	Q9HUF1	mscA	9	59.5	23.517	63.968	8.32E+09	77	215	28.7689	28.6998	28.2155	28.8385	28.4556	28.4098	28.2873	28.1396
	Q9HUF5	waaC	4	20.6	39.746	14.269	3.66E+08	24	355	24.9153	24.6778	22.4226	24.7111	24.6631	24.7151	24.7774	24.7774
	Q9HUF6	waaG	4	23.3	42.156	14.695	1.64E+08	17	373	22.4884	23.0135	22.7593	24.6922	24.3921	23.8628	24.3697	24.5959
	Q9HUF8	PA5007	11	70.2	29.414	48.124	1.06E+09	66	252	25.0057	25.0595	25.3632	24.7231	24.6934	24.8692	25.0831	25.0215
	Q9HUG0	PA5005	18	49.6	66.079	130.26	4.33E+09	85	585	26.8913	27.4599	26.221	27.2533	27.2897	27.0622	26.8353	27.5922
	Q9HUG1	PA5004	8	33.6	42.197	35.419	4.88E+08	27	378	24.2757	24.201	24.2392	24.1045	24.6545	24.5678	24.2855	24.9596
	Q9HUG2	PA5003	6	37.2	33.849	60.434	3.22E+08	18	298	23.0818	25.0941	22.9736	23.8132	25.2816	23.6081	25.0303	25.1874
	Q9HUG7	PA4998	5	28.2	24.985	6.3834	3.36E+08	18	216	24.0819	24.3547	24.3637	23.321	24.8569	23.9869	23.764	24.0156
inding/per	Q9HUG8	msbA	5	14.3	66.431	23.945	2.05E+08	14	603	23.2395	23.8704	23.8677	23.3638	24.2674	23.8133	23.9488	24.3575
ate adeny	Q9HUG9	hldE	21	57.4	50.348	203.61	1.26E+10	151	474	29.7257	28.0054	28.0267	27.6353	27.8479	27.9288	27.8318	27.8245
	Q9HUH3	PA4992	12	59.6	29.03	113.95	1.65E+09	50	270	25.8533	26.3421	26.2961	25.9903	26.291	26.0689	26.2345	25.6675
	Q9HUH4	PA4991	15	61.1	42.109	136.15	6.19E+09	78	391	28.7263	28.7697	28.7516	28.9039	28.8604	28.7573	28.712	28.5035
	Q9HUI1	PA4974	19	48.3	53.405	142.42	2.68E+09	101	482	25.5088	25.3827	25.1288	25.5135	26.0505	25.4303	26.1951	25.5583
	Q9HUI4	aspP	10	59	23.133	112.02	3.63E+09	86	205	26.7356	26.76	26.6672	26.6224	26.6834	26.8573	26.5999	26.754
ophosphat	Q9HUI6	cpdA	9	57.7	30.516	101.6	1.37E+09	46	272	26.118	24.7087	23.3855	25.9912	25.3947	26.21	23.8071	26.2047
	Q9HUI7	PA4968	7	60.7	22.645	36.282	1.14E+09	54	206	25.2479	25.3825	25.3567	25.1375	25.3134	25.388	25.21	25.2144
somerase 4	Q9HUI8	parE	28	56.8	69.178	140.72	4.48E+09	137	629	26.1476	26.2396	26.3457	26.0691	26.6046	26.5995	26.7378	26.7146
	Q9HUI9	PA4966	13	55.8	36.483	39.519	1.41E+09	48	337	25.4488	25.4893	24.3892	25.4468	25.3496	25.2019	25.4072	25.0472
somerase 4	Q9HUK1	parC	28	52.1	83.364	187.66	7.97E+09	144	754	28.099	28.5854	27.9159	28.5382	28.9034	28.7769	28.6353	28.9356
	Q9HUK5	PA4960	8	24.7	46.438	40.507	1.49E+09	33	429	26.1212	26.3729	26.2325	26.0786	26.1876	26.1496	26.0284	26.2819
	Q9HUK6	flmX	4	9.8	75.992	60.298	3.45E+08	24	691	24.0813	24.7139	24.211	24.0964	24.9492	24.9443	24.1765	24.7108
	Q9HUK7	PA4958	20	62.6	67.828	102.32	2.3E+09	81	607	25.4592	25.805	25.2907	25.6787	25.794	25.7939	25.7157	25.8963
furtransfer	Q9HUK9	rhdA	12	70.8	29.391	101.1	8.53E+09	82	271	27.6965	27.7199	27.4959	27.8369	27.8143	27.7798	27.6486	27.6831
ne biogene	Q9HUL3	rsfA	12	54.3	37.078	102.02	2.29E+09	76	339	26.1858	26.1198	26.4147	26.0942	26.1339	26.1447	25.8793	26.0586
	Q9HUL6	PA4948	4	40.6	16.495	34.079	4.89E+08	16	155	25.2885	23.8008	24.7105	24.9338	23.1509	22.2817	25.4942	25.1286
	Q9HUL7	amiB	15	49.1	50.683	131.09	3.62E+09	89	475	26.7898	27.0027	27.2075	26.8009	26.6611	26.8403	26.7754	26.6186
ch repair r	Q9HUL8	mutL	8	28	69.747	67.303	8.33E+08	41	633	24.6618	25.1702	25.0288	24.9234	24.9962	25.088	25.2089	25.7971
TPase Hfd	Q9HUM1	hflX	15	52	48.607	111.38	1.47E+09	71	433	26.0698	25.7954	26.1644	26.0256	25.5154	25.8955	25.94	26.0935
transferasi	Q9HUM5	hisZ	15	48.7	42.546	159.99	9.89E+09	100	394	24.5523	28.614	28.7555	28.3414	28.6647	28.8764	28.9768	28.9622
uccinate s	Q9HUM6	purA	28	65.8	46.814	323.31	5.67E+10	332	430	29.834	30.0598	29.9563	29.4988	29.6017	30.0108	29.9577	30.1832
-2'-O-)-me	Q9HUM8	rhmB	11	60.1	27.081	58.602	2.91E+09	48	248	27.3305	27.6273	27.3545	27.277	27.2171	27.1841	27.328	27.2117
osomal prc	Q9HUM9	rpsF	14	69.1	16.164	323.31	2.56E+11	488	139	32.3404	32.4029	32.0348	32.3267	32.4076	32.4105	32.3763	32.3138
osomal prc	Q9HUN0	rpsI	4	40.8	8.8732	44.39	1.7E+10	50	76	29.6161	30.6092	29.8269	30.3993	30.9369	30.3557	30.609	30.6838
osomal prc	Q9HUN2	rrlR	11	73	15.532	157.41	3.42E+11	700	148	33.046	32.9952	32.6082	33.2693	33.2052	33.1098	32.9286	33.0546
	Q9HUN3	dnaB	24	67	51.589	156.35	2.64E+09	114	464	25.5624	25.6394	25.6064	25.2831	25.5276	25.6368	25.8832	26.0183
cemase, bi	Q9HUN4	air	9	38.3	38.31	101.5	3.74E+09	83	358	26.8742	26.5871	26.3447	26.8092	26.7554	26.9096	26.4658	26.7073
ndent NAD(-	Q9HUP3	nadE	17	82.9	29.696	294.38	2.11E+10	173	275	29.3738	29.1475	28.6598	29.328	28.6805	28.7813	28.5337	28.6603
osphoribos	Q9HUP4	pncB1	14	46.6	46.094	84.819	1.19E+09	45	399	25.5604	25.5516	24.753	25.6792	25.4074	25.0559	25.3222	23.2228
	Q9HUP7	PA4916	7	39.8	25.457	42.213	1.3E+09	47	231	26.1222	26.2857	26.0326	26.2337	25.797	25.9216	25.6219	25.7181
	Q9HUP6	PA4907	12	65.2	27.384	210.65	1.09E+10	99	253	27.8426	28.0648	28.3713	27.7549	27.6927	27.7679	27.8418	27.6514
	Q9HUR4	PA4899	5	23.9	52.697	37.003	4.41E+08	28	489	24.6047	24.5253	24.997	24.3407	24.0886	23.6949	24.2574	24.3025
	Q9HUS3	desT	9	60.3	22.899	23.577	6.36E+08	36	209	24.6373	24.9449	25.1398	24.9398	24.9756	25.15	24.4905	23.648
	Q9HUT3	PA4880	12	76.3	20.217	214.21	6.79E+09	85	177	27.6822	27.9877	27.6315	27.7715	28.1259	27.7787	27.8743	27.6125
	Q9HUT5	PA4878	5	36.7	31.168	41.841	1.63E+09	24	270	27.4732	25.9983	23.4214	27.5707	26.2334	27.3196	26.1321	26.9995
te subunit -	Q9HUV5	urcC	6	23.1	60.61	84.805	3.62E+08	24	566	24.4837	24.2691	23.6761	24.6261	24.4941	24.6261	24.7652	24

quinone c	Q9HVFO	PA4642	3	43.8	10.8	28.353	6.03E+09	40	96	28.6376	27.8802	26.7858	28.8302	28.0677	28.768	27.6693	28.6299
	Q9HVF1	mqo2	14	37.9	55.498	97.961	7.44E+09	94	507	28.1857	28.1169	28.2765	27.6217	27.5942	28.048	28.1451	28.3209
	Q9HVF5	PA4636	10	43	43.779	58.857	1.35E+09	47	386	25.427	25.6603	25.684	25.544	25.3673	25.8034	25.7775	26.27
	Q9HVF9	PA4632	6	37.4	29.159	47.577	4.35E+08	26	273	24.3602	24.6154	22.3779	24.8521	24.9439	24.739	24.6423	24.9384
il subunit r	Q9HVG0	PA4631	9	46	37.263	69.493	7.56E+08	40	341	24.9257	25.1748	25.3078	25.1456	25.022	25.029	24.9823	24.9298
	Q9HVG4	rsmc	7	28.9	35.937	22.733	3.28E+08	23	332	24.0825	24.5403	23.3347	23.7602	24.2637	23.9932	24.5269	24.0488
	Q9HVG5	hprA	6	27.9	34.285	21.924	6.11E+08	33	323	24.681	25.1829	24.9974	24.5112	25.0377	25.3289	25.2466	25.182
	Q9HVI1	PA4620	3	21.2	19.918	21.723	3.06E+08	21	179	24.6485	24.3471	22.5739	24.7894	24.6396	24.5979	24.0127	24.231
Q9HVI2	PA4619	11	41	44.71	141.03	1.16E+09	73	415	25.3598	25.2966	24.8355	25.4939	24.9744	24.7798	23.521	24.8332	
	Q9HVI6	PA4615	11	56.2	29.377	72.136	2.69E+09	75	258	25.5938	26.0019	25.9364	25.7254	26.1046	25.5655	25.8272	25.4933
	Q9HVI9	PA4611	4	60.7	9.7158	55.783	7.69E+09	44	84	30.0844	28.9018	27.9325	30.7592	26.4082	28.9882	27.1323	28.4211
	Q9HVI5	PA4604	4	20.1	37.256	14.443	2.89E+08	19	334	23.749	24.6567	24.57	22.9966	24.7302	24.6658	23.7713	24.7945
xymethylt	Q9HVI7	glyA2	13	52.8	45.157	144.21	2.63E+10	149	417	30.8324	30.4392	30.7372	30.5818	31.0211	31.0615	30.9854	30.9339
	Q9HVI1	PA4595	36	63.2	61.32	323.31	5.63E+10	356	554	29.6756	29.7911	29.8243	29.3769	29.6899	29.866	29.8494	29.9004
	Q9HVK8	PA4576	22	36.4	90.222	195.48	3.02E+09	104	817	25.4043	25.6508	25.3107	25.4523	25.6354	25.5283	25.6838	26.0378
	Q9HVL2	fkfB	7	36.6	21.795	163.93	1.58E+10	71	205	30.0563	29.4382	28.5499	30.0321	29.1574	29.8458	29.1827	29.8565
isomal pro	Q9HVL5	ispB	14	62.7	34.851	143.28	3.57E+09	86	322	26.8352	26.7953	26.9114	26.461	26.7883	26.9659	26.9711	27.2526
	Q9HVL6	rplU	14	77.7	11.653	96.902	9.22E+10	189	103	30.9321	31.2967	31.1509	30.9802	31.2029	31.0961	31.1338	31.0714
	Q9HVL7	rpmA	5	51.8	8.9903	10.174	2.46E+09	19	85	27.0534	27.6252	23.6087	27.1681	27.6911	27.346	27.8418	27.6363
	Q9HVL8	otg	20	64	44.338	217.66	1.26E+10	127	406	28.1216	28.2414	28.405	27.9874	27.9874	28.044	28.1098	27.9539
amate 5-ki	Q9HVL9	proB	8	33.9	39.845	91.226	1.36E+09	60	372	25.4182	25.3272	25.6866	25.4934	25.4664	25.8013	25.6684	25.9397
	Q9HVM0	PA4564	7	55.2	16.724	48.998	1.63E+09	39	154	26.4176	26.4461	26.459	25.879	26.0003	26.2084	25.9354	25.9403
	isomal pro	Q9HVM1	rpsT	1	15.4	9.9175	9.4061	8.54E+09	15	91	29.4262	30.2405	22.7422	30.2771	30.6414	30.3719	30.4749
	biosynthe	Q9HVM3	ribF	11	44.6	34.34	49.437	8.8E+08	27	312	25.8108	25.4401	25.8629	25.9841	26.6034	25.6132	26.2534
lyl cis-tran	Q9HVM6	PA4558	7	68.5	15.984	115.2	1.47E+10	75	146	29.3125	28.6543	27.5819	29.3909	29.9821	29.5365	28.8952	29.431
	Q9HVM7	ispB	14	51	34.762	99.852	4.27E+09	86	314	24.9274	26.9875	26.5187	27.0686	27.1724	27.1468	27.1367	26.9397
	Q9HVN5	clpB	66	74.4	95.004	323.31	6.37E+10	550	854	29.2904	29.2782	29.497	29.0888	28.7367	28.9675	28.9697	28.8575
	Q9HVP4	PA4533	5	32.1	17.645	14.498	9.52E+08	27	156	26.2337	26.3825	26.6539	26.3933	26.2148	26.3564	26.4373	26.4375
ispho-CoA	Q9HVP8	coaE	8	66	22.843	77.075	2.33E+09	46	203	26.3041	26.3103	25.7418	26.5458	26.2559	26.3599	26.1215	26.2028
	Q9HVL3	speC	19	66.7	43.559	216.69	7.76E+09	142	387	26.895	26.8418	27.0985	26.824	27.0995	27.0432	27.28	27.0049
	Q9HVR5	PA4506	6	28.5	36.339	31.284	4.06E+08	23	323	24.4728	24.6792	25.1755	24.0435	24.5082	22.6432	23.9714	23.105
	Q9HVR6	PA4505	7	38	35.429	30.371	3.55E+08	23	324	25.0152	24.6097	25.4346	24.2005	24.2266	24.32	24.2414	23.699
Q9HVS2	PA4499	4	41.7	20.435	9.111	2.5E+08	14	187	24.6734	24.6574	22.8141	23.4409	24.5146	24.8157	23.0691	24.8941	
	Q9HVS3	PA4498	10	40	44.126	74.519	4.5E+08	34	405	24.674	24.6845	24.5242	24.744	24.3947	23.9142	23.8245	24.3909
	Q9HVS6	PA4495	11	54.7	24.879	191.25	2.34E+10	113	236	29.2942	29.4281	28.9605	29.4447	29.3474	29.1631	29.888	29.0055
	Q9HVS8	roxR	8	71	20.616	93.854	1.58E+10	71	186	29.0087	29.0918	29.3541	28.9759	28.7415	28.8527	28.9134	28.8672
Q9HVT4	PA4487	5	42.2	28.145	48.71	5.46E+08	13	263	23.7879	25.9502	23.2361	23.4937	22.3225	25.3943	25.7635	25.5523	
	Q9HVT5	PA4486	7	76.6	13.947	21.311	1.04E+09	17	128	26.3173	22.693	23.7782	26.3439	25.3157	26.0595	25.7606	25.9685
	Q9HVT7	gatB	26	60.5	53.081	260.59	1.67E+10	228	481	28.062	28.1006	28.0321	28.0145	28.0002	28.2179	28.1604	28.2611
	Q9HVT8	gatA	24	71.7	51.862	256.58	2E+10	180	484	28.5553	28.4613	28.6736	28.2335	28.4336	28.8051	28.7354	28.9561
Q9HVT9	gatC	4	79.2	10.53	41.041	2.51E+09	42	96	27.4793	24.18	24.3083	27.0728	24.0416	27.4564	24.5642	25.8477	
	Q9HVU0	mreB	21	57.4	36.976	312.1	2.73E+10	184	345	28.5402	28.7226	28.7318	28.292	28.5942	28.8017	28.8873	28.9946
	Q9HVU4	caF	7	20.6	54.665	42.097	3.69E+08	27	485	23.5908	24.0841	23.8222	24.0939	24.1844	24.245	24.1782	23.7241
	Q9HVU6	PA4475	7	34	30.724	17.197	3.41E+08	16	282	24.3692	24.0723	24.6094	23.7928	23.902	23.0227	24.3909	23.7713
Q9HVU7	PA4474	16	51.2	50.266	226.16	9.34E+09	123	480	27.4075	27.5413	27.664	27.4032	27.5647	27.3796	27.6	27.2288	
	Q9HVU8	pmbA	7	52.3	20.21	42.234	2.12E+09	31	174	26.9166	27.0879	27.0925	26.7782	26.732	26.6339	26.8054	26.7247
	Q9HVU9	PA4473	30	82	47.908	323.31	1.99E+10	218	449	29.0344	29.0575	29.3775	29.1381	29.1756	29.0164	29.1496	28.6863
	Q9HVU2	ptsH	4	60	9.7021	64.744	1.8E+09	29	90	26.9291	26.7738	26.4915	27.0784	26.5567	26.5835	26.6324	26.5091
inding pro	Q9HVU3	PA4465	8	45.1	32.218	88.438	2.45E+09	53	286	26.4677	26.2906	26.7917	26.3083	26.155	26.1994	26.6224	26.3521
	Q9HVU4	ptsN	6	48.1	16.73	69.981	2.38E+09	41	154	27.0001	26.0958	25.46	27.1726	26.1544	27.0149	25.716	26.7762
	Q9HVU6	PA4461	12	56.8	26.45	106.01	1.04E+10	116	241	27.5888	27.7521	28.0553	27.5053	27.6386	27.8574	27.6992	27.634
	Q9HVU7	lptA	8	56	19.126	128.37	1.3E+10	79	175	29.3588	29.3086	29.0213	29.1867	29.5444	29.3724	24.9493	29.1207
e export sy	Q9HVU8	lptC	4	28.9	21.353	11.622	2.29E+08	15	190	24.1515	24.1349	24.2087	23.5276	24.5911	24.2881	24.2064	24.7101
	Q9HVU9	PA4458	8	44.7	19.334	59.748	4.04E+09	66	179	27.1142	26.8259	26.947	27.0149	27.244	27.4279	27.0132	27.2592
	Q9HVU0	kdsD	16	63.8	34.197	165.18	1.24E+10	136	326	28.058	28.2143	28.2364	28.0368	28.0227	28.0448	28.2525	28.1657
	Q9HVW1	PA4456	13	48.3	29.621	88.198	4.2E+09	77	269	26.1941	26.3828	26.4468	26.0448	26.3471	26.6387	26.5789	26.6033
Q9HVW3	PA4454	5	47.8	16.557	29.798	8.45E+08	28	157	25.7871	22.7857	24.4047	25.5488					

isomal pro	Q9HWE2	rpIP	6	41.6	15.401	35.096	3.49E+10	87	137	29.6306	30.2621	29.2805	30.2661	30.2178	30.1016	29.8279	30.2909
isomal pro	Q9HWE3	rpmC	5	60.3	7.2013	191.72	1.17E+11	85	63	32.4	32.0597	31.7511	32.7082	32.4799	32.7833	32.0875	32.5481
isomal pro	Q9HWE4	rsPQ	6	43.2	10.086	23.4	6.99E+10	75	88	31.5964	31.9711	31.9617	31.8891	31.8569	31.9343	32.0672	31.6616
isomal pro	Q9HWE5	rpIN	11	61.5	13.412	177.65	3.56E+10	149	122	30.0158	30.4626	30.1252	30.2732	30.4324	30.1988	30.2321	30.1781
isomal pro	Q9HWE6	rpIX	15	67.3	11.47	323.31	2.16E+11	270	104	32.2615	32.6388	32.3941	32.5467	32.9098	32.5163	32.8097	32.4663
osomal prc	Q9HWE7	rpIE	17	61.7	20.392	127.38	1.56E+11	263	179	31.8288	32.1013	32.3037	32.273	32.0391	31.8204	31.7659	31.7556
isomal pro	Q9HWE8	rpsN	3	31.7	11.565	7.9815	9.77E+09	22	101	29.0046	29.7872	28.7391	29.343	30.2199	29.8308	29.6406	29.5402
osomal prc	Q9HWE9	rpsH	9	65.4	14.17	77.788	2E+11	382	130	32.7832	32.8557	32.6416	32.9271	32.7888	32.7598	32.7948	32.5462
osomal prc	Q9HWF0	rpIF	15	73.4	19.099	117.37	2.36E+11	247	177	32.4366	32.6614	32.8596	32.5945	32.7246	32.6282	32.6161	32.4161
isomal pro	Q9HWF1	rpIR	4	36.2	12.661	43.512	5.26E+10	44	116	30.5625	31.1121	30.4883	30.9727	31.3403	31.2408	31.0237	31.0952
osomal prc	Q9HWF2	rpsE	10	65.7	17.625	182.69	1.39E+11	369	166	32.3205	32.625	32.7011	32.5518	32.5927	32.4906	32.6118	32.4038
isomal pro	Q9HWF3	rpmD	2	25.9	6.4775	162.67	5.38E+10	36	58	31.6809	31.7832	31.925	31.7079	31.6493	31.8042	31.5882	31.5357
isomal pro	Q9HWF4	rpIO	10	54.9	15.174	107.35	6.13E+10	89	144	30.65	31.1223	30.7171	31.0894	31.4224	31.2433	31.2417	31.1056
isomal pro	Q9HWF7	rpsM	13	65.3	13.265	184.92	3.54E+10	139	118	29.7182	30.4181	29.4601	30.2541	30.6584	30.4157	30.3445	30.6057
isomal pro	Q9HWF8	rpsK	6	49.6	13.629	67.244	7.64E+10	76	129	32.4851	32.9703	31.8785	33.2046	33.1189	33.1221	32.809	33.1019
cterioferri	Q9HWF9	bfr	9	78.6	17.94	93.695	3.07E+09	47	154	27.5972	27.2398	26.4027	27.9066	25.9965	27.2318	26.2538	26.9096
:system pr	Q9HWF0	uvrA	26	48.9	104.49	118.08	2.41E+09	106	945	25.8687	26.0141	23.7296	26.4076	26.4786	26.2844	26.3357	26.6753
	Q9HWR2	aph	18	64.9	29.812	323.31	2.15E+10	181	268	28.7813	28.7935	28.4319	28.6401	28.7092	28.8429	29.0024	28.8729
	Q9HWR9	PA4069	6	30.3	32.939	27.225	4.3E+08	19	294	25.1682	23.4793	24.8526	23.168	25.2279	25.1931	25.0206	24.9024
	Q9HWR0	PA4068	11	57.8	33.31	98.535	3.66E+09	72	309	27.0628	26.9929	27.1224	26.9687	27.1671	27.2828	27.3673	27.2488
	Q9HWW1	optA	4	22.8	25.193	34.431	5.54E+08	12	232	26.5688	26.5161	22.8711	25.6594	25.6117	23.7583	25.6555	25.6555
	Q9HWW5	PA4063	7	46.4	21.235	22.025	9.82E+08	31	196	26.5849	25.5159	23.0757	26.7389	25.3582	26.3511	25.3132	25.7308
	Q9HWW7	PA4061	13	47.4	31.878	210.74	1.27E+10	110	289	28.4551	28.0203	27.1324	28.5704	28.1473	28.3786	27.8344	28.2825
ional repre	Q9HWX1	nrdR	7	45.5	17.925	48.953	2.03E+09	50	154	26.2886	26.6176	26.3064	26.3655	26.3926	26.4048	26.5107	26.115
ynthesis	Q9HWX2	ribD	16	60.9	39.764	148.57	2.49E+09	89	373	26.4673	26.629	26.8699	26.3665	26.4023	26.3852	26.4321	26.432
tanone 4-g	Q9HWX4	ribB	16	66	39.438	222.66	2.35E+10	151	365	29.2569	29.4307	29.5352	29.1817	28.7144	28.9544	29.0661	28.9876
istance prc	Q9HWX6	nusB	7	55.3	17.707	42.348	6.25E+09	51	159	28.385	28.6194	28.6618	28.6412	28.3991	28.2209	28.4007	28.2742
yclohydrol	Q9HWY1	ribA	9	68.3	22.099	83.308	4.09E+09	67	205	26.9538	27.3252	26.9572	27.0206	27.0519	27.0907	27.0397	27.0924
	Q9HWY4	ispA	13	59	31.464	101.75	2.89E+09	90	295	26.2728	26.3266	25.7892	26.2559	26.2698	26.399	26.5265	26.3944
nuclease 7	Q9HWY5	xseB	4	75	8.9728	118.1	2.69E+09	48	80	26.8191	26.1663	25.7431	27.0082	26.8591	26.9345	26.6847	26.8406
	Q9HWZ2	PA4035	11	46.8	35.895	80.897	1.47E+09	51	333	26.2572	26.2331	26.0776	26.3322	25.8502	25.8019	25.7453	25.9321
	Q9HWZ5	PA4032	2	25.6	27.422	23.714	5.9E+08	15	238	25.5183	23.7051	23.1445	25.3182	25.2833	25.4906	25.9807	26.04
c pyrophos	Q9HWZ6	ppa	13	60	19.396	151.9	7.14E+10	194	175	31.4744	30.5477	29.8871	31.3076	30.8416	31.3232	30.3966	31.2517
	Q9HX07	mpl	10	36.8	48.469	123.03	5.72E+09	87	451	27.4448	27.4059	27.3544	27.436	27.8265	27.689	28.108	27.7226
	Q9HX10	PA4017	11	52.1	23.164	51.858	2.98E+09	77	213	26.7316	26.8539	26.5401	26.717	26.5772	26.466	26.6559	26.4129
myl phosph	Q9HX20	proA	23	74.1	45.044	323.31	2.18E+10	181	421	28.2735	28.2515	28.4482	28.2237	28.2776	28.4576	28.6255	28.4668
nucleotide	Q9HX21	nadD	6	44.4	23.801	67.995	1.12E+09	30	214	25.4142	25.8763	25.8291	25.7769	25.7576	26.1076	26.2425	25.7018
silencing f	Q9HX22	rsfS	7	83.9	13.054	81.313	6.09E+09	63	118	28.2283	27.8407	27.7203	28.3748	27.3995	28.2026	27.9819	28.1818
e subunit r	Q9HX23	rlmH	6	50.3	17.79	39.477	7.37E+08	24	155	25.1267	25.0753	25.4298	25.1807	25.4507	25.4122	25.5323	25.2367
	Q9HX24	sltB1	16	65	37.867	134.22	3.44E+09	84	340	26.4907	26.5388	26.8964	26.7106	26.9912	26.788	26.8153	26.3701
oyl syntha	Q9HX25	lipA	19	63.3	37.763	187.19	1.13E+10	158	327	27.9282	27.916	28.0266	27.8598	28.0079	28.0618	28.2336	28.0653
	Q9HX28	PA3992	13	47.8	47.73	85.448	1.06E+09	46	448	24.892	24.9736	25.1394	24.8167	24.8492	24.7959	24.834	24.8256
	Q9HX31	holA	8	43.2	37.378	47.155	9.72E+08	50	345	24.5869	24.4209	24.3685	24.7239	24.8311	24.8293	24.9478	24.9525
ne--tRNA I	Q9HX33	leuS	42	59.7	97.647	323.31	2.42E+10	330	873	27.6941	27.7628	27.2875	28.0009	28.4847	28.4122	28.134	28.0121
	Q9HX36	PA3983	12	47.3	31.548	74.32	3.49E+09	90	279	26.3786	26.4862	26.77	26.2303	26.6798	26.6688	26.292	26.2681
bonuclease	Q9HX37	ybeY	6	49.4	17.981	50.99	7.75E+08	21	160	25.9972	25.1673	22.6203	24.9842	25.398	25.3324	25.3741	25.3741
	Q9HX38	PA3981	11	50.6	38.424	62.953	1.95E+09	47	340	26.068	26.4617	26.6345	25.9547	26.0807	26.1398	26.3928	26.8522
	Q9HX39	PA3979	4	46.4	12.624	26.519	1.35E+09	26	110	26.1081	25.9665	25.6172	26.0211	26.2543	26.4801	25.896	26.2328
phosphate	Q9HX40	thiE	8	64.6	22.146	135.55	1.68E+09	37	209	26.6701	26.3118	27.0948	26.9459	26.6929	26.7974	26.9067	26.6818
	Q9HX41	thiD	9	56.6	27.979	127.73	3.7E+09	76	265	27.1305	26.8827	26.6992	26.975	26.8147	27.0802	26.8397	27.0666
	Q9HX44	PA3972	18	55.9	60.338	127.58	1.92E+09	76	549	25.7743	26.1357	25.8017	26.0046	25.4601	25.4336	25.3743	25.4573
P nucleosic	Q9HX46	amn	9	29.7	56.225	50.431	5.94E+08	32	499	24.0858	24.8733	24.3578	24.448	24.368	24.228	24.3506	24.5873
	Q9HX49	PA3967	4	51.5	14.705	31.339	1.99E+09	22	130	27.4261	27.3252	27.3583	27.5926	27.5311	27.2527	27.3931	27.1539
	Q9HX51	PA3965	8	48.5	19.289	23.345	1.43E+09	29	169	27.1349	27.3533	27.6802	26.9363	26.8053	27.1354	26.7473	26.5099
	Q9HX64	PA3952	4	42.9	19.793	102.88	2.53E+09	44	191	26.6822	25.8747	24.2875	26.4039	26.8212	27.5078	26.7439	27.3427
	Q9HX66	PA3950	5	15.4	48.6	16.871	1.51E+08	16	449	23.5343	23.906	22.1072	23.7021	23.939	23.8188	23.3261	23.7622
	Q9HX68	rocA1	6	34.9	22.995	24.912	8.59E+08	25	209	25.7395	25.71	26.1043	25.7115	25.7487	25.6061	25.6917	25.4196
	Q9HX71	PA3945	3	21.9	22.403	10.961	3.18E+08	21	196	24.6232	24.6404	24.6491	24.5732	24.5259	24.5639	25.2736	24.15
	Q9HX72	PA3944	4	28.6	21.857	27.772	6.54E+08	24	192	25.0842	24.9306	24.9191	25.0258	25.1035	25.0812	25.1701	25.0923
	Q9HX74	tesB	7	40.1	32.934	56.143	1.76E+09	58	289	26.4714	26.5126	26.3437	26.4352	26.718	26.2827	26.1694	26.1679
	Q9HX85	PA3931	15	54.4	28.101	103.19	1.16E+10	109	259	28.2736	28.7439	27.4263	28.5195	28.6175	28.2969	28.1365	28.5416
hosphate :	Q9HX95	moaC	6	41.2	17.338	32.286	4.46E+09	51	160	27.3395	27.3388	26.7953	27.5252	26.9281	27.0028	26.8993	26.9838
ynthase sul	Q9HX96	moaD	3	43.4	9.2153	34.751	1.61E+09	32	83	27.3493	26.7591	26.6842	27.7043	26.58	27.4082	26.9099	26.6494
	Q9HX97	moaE	5	58	16.886	26.829	6.55E+08	28	150	26.3439	25.6604	25.4952	26.2006	25.4669	24.9007	25.2842	25.634
actor bios	Q9HX98	moaB1	11	88.6	19.669	98.495	2.11E+09	63	185	26.8987	26.7195	27.0412	26.8219	26.6444	26.9131	26.5292	26.7433
hain rleas	Q9HX80	rpfC															

mylate kin	Q9HXV4	adk	12	65.1	23.107	238.3	5.75E+10	219	215	30.6777	30.5848	29.6854	30.979	30.6473	30.7243	30.3047	30.4881
	Q9HXV5	PA3685	5	38.5	24.18	61.636	1E+09	35	226	25.8892	25.6339	25.9545	26.1415	25.5274	25.8761	26.0338	25.8946
ill subunit i	Q9HXW0	rsmj	6	34.5	27.904	27.186	4.18E+08	13	261	25.117	24.6756	24.0591	25.3128	25.0197	25.0394	24.8346	25.3199
	Q9HXW2	PA3678	7	52.8	23.15	30.699	5.04E+08	28	212	24.5094	23.9977	23.3718	24.6188	24.6044	24.6549	24.6396	24.3133
	Q9HXW6	PA3674	4	47	14.393	30.204	9.18E+08	14	132	23.5942	22.9637	23.1853	25.3798	23.1023	26.8055	27.2072	26.8777
	Q9HXK2	PA3668	6	62.1	15.927	57.786	6.63E+08	36	140	25.0465	24.9157	24.6091	25.1283	24.9855	24.8491	24.8385	24.6759
cysteine de	Q9HXK3	csd	10	37.9	43.274	74.441	1.34E+09	56	401	25.107	25.3023	25.5021	25.1943	25.4073	25.4663	25.4368	25.2106
	Q9HXK5	PA3664	9	77.4	13.111	52.324	4.85E+09	58	115	27.7784	27.4028	27.0728	27.895	27.4826	27.6259	27.3375	27.6016
ine aminop	Q9HXY1	map	15	75.1	29.086	154.82	2.74E+10	139	261	29.4073	29.3934	29.374	29.3121	29.1173	29.3451	29.3623	29.2788
te synthasi	Q9HXY2	upp5	4	22.7	28.04	104.48	1.67E+09	24	251	26.4618	27.2405	27.4249	26.9554	26.9977	27.2964	27.7496	27.2733
p-like prot	Q9HXY5	PA3647	7	38.7	19.09	46.408	4.7E+10	87	168	30.4054	30.6863	30.3372	30.5898	30.9268	30.8585	30.9813	30.8318
cosamine f	Q9HYX6	lpxD	7	31.7	36.191	40.024	1.84E+09	31	353	26.0875	26.136	26.15	26.0611	26.093	26.3131	26.002	26.186
saccharide	Q9HYX8	lpxB	8	32	41.294	30.549	2.8E+08	24	378	24.0408	23.5937	23.1583	24.1998	23.4422	23.9927	23.6806	24.3556
onuclease	Q9HYX9	rnhB	9	49.3	21.771	28.041	8.36E+08	26	201	25.9436	22.9005	23.3581	25.4773	24.3265	25.5367	25.2662	25.9707
erage III su	Q9HXZ1	dnaE	16	21.7	130.9	47.363	3.26E+08	36	1173	23.5179	23.2202	23.2697	23.3847	24.4264	23.3062	23.5092	24.4633
ase carbox	Q9HXZ2	accA	21	66.8	34.947	323.31	4.21E+10	231	316	29.4423	29.5416	29.4317	29.3693	29.1913	29.3788	29.4393	29.4718
TP synthas	Q9HXZ4	pyrG	32	75.3	59.617	323.31	2.04E+10	252	542	27.7137	28.0049	27.7055	27.7294	28.1425	28.2833	28.179	28.561
Enolase	Q9HXZ5	eno	22	63.4	45.195	323.31	1.59E+11	356	429	30.9481	30.9338	31.0093	31.0262	31.1725	31.2794	31.3605	31.137
	Q9HXZ8	PA3632	5	79.3	9.1152	30.86	1.54E+09	25	82	27.1709	25.6926	24.7867	27.1374	25.1411	26.7953	25.0888	26.2982
[glutathion	Q9HY01	adhC	12	46.5	39.208	123.22	2.08E+10	127	370	29.2038	29.1518	29.4209	28.973	29.377	29.5182	29.4924	29.5118
	Q9HY02	PA3628	11	60.4	31.275	133.6	6.87E+09	100	283	27.5861	27.4723	27.6101	27.7596	28.2714	27.9687	27.9524	27.6366
	Q9HY05	surF	6	37.8	26.368	70.64	3.2E+09	56	249	26.7647	26.7265	26.4861	26.768	26.8322	26.7783	26.7008	26.747
iclotidase	Q9HY07	fdxA	3	24.3	12.159	22.31	1.03E+10	39	107	29.2362	28.7599	26.9895	29.4381	28.7675	29.2052	27.7236	29.0797
erredoxin	Q9HY08	mutS	18	32.6	94.977	80.082	4.81E+08	55	855	23.2415	24.0042	23.746	24.2214	25.118	24.2005	23.8422	24.8299
ch repair p	Q9HY10	PA3618	6	59.5	17.715	51.348	6.28E+08	27	168	25.1055	25.6185	25.4103	25.1021	25.8254	25.5337	25.5381	25.3713
Q9HY11	PA3615	7	26.1	40.465	28.288	5.05E+08	25	356	25.3581	25.4844	25.0918	25.3474	24.9859	24.2962	24.644	24.6292	24.6836
	PA3611	3	47.5	14.986	82.416	1.45E+10	19	136	30.4683	29.9858	28.6254	30.2675	30.0258	30.3328	29.9942	30.3544	30.7648
	import ATP	potA2	8	33.8	40.044	58.643	9.64E+08	32	363	26.4848	25.8003	26.2404	26.3382	25.7575	26.0505	25.3836	25.3656
Q9HY22	erfR	10	69.1	23.531	98.525	6.66E+09	91	217	27.6237	27.7335	27.3849	27.6116	27.5466	27.4916	27.5307	27.5446	27.5446
	Q9HY50	PA3567	13	64.7	36.677	157.65	8.03E+09	77	337	28.2614	28.5552	28.7506	28.1468	28.2681	28.2838	28.386	28.2308
	Q9HY51	PA3566	4	68	11.167	28.248	2.47E+09	17	97	28.4898	24.1753	26.3927	28.0512	22.361	28.4957	27.5699	28.6189
Q9HY54	fruI	11	39.5	36.387	76.712	6.35E+08	51	329	24.6189	24.8823	25.0605	24.4069	24.4425	24.4874	24.5526	24.564	24.564
	Q9HY55	fruI	16	32.5	101.57	107.48	1.27E+09	71	956	25.094	24.8951	24.9683	24.9203	24.6682	25.2857	24.9331	25.2029
	Q9HY56	fruK	7	33.8	33.381	40.382	1.25E+09	42	314	26.2781	26.1863	26.8075	26.2509	25.5422	25.9338	26.0176	25.8335
phofructo	Q9HY58	PA3559	19	50.2	51.795	169.11	6.52E+09	139	464	26.8478	26.9076	27.2715	26.3449	26.9537	27.3541	27.4096	27.6398
	Q9HY64	arnC	9	39.8	37.296	22.454	6.07E+08	30	339	23.7872	24.4013	23.4363	24.2319	24.6442	24.7746	24.0616	24.9339
	oxyl-4-form	Q9HY65	arnB	20	60.2	41.866	248.54	4.85E+10	205	382	30.0581	30.1026	30.189	30.1305	30.7252	30.5273	30.5827
binose-ox	Q9HY72	PA3539	11	62.9	29.56	110.61	3.17E+09	59	259	26.8391	26.9431	27.0908	26.3888	26.8304	27.0151	27.2039	26.8677
16 protein i	Q9HY73	PA3538	9	46.7	39.189	48.229	1.15E+09	31	360	25.7553	26.2624	25.8637	25.6024	25.9666	26.1859	26.194	26.1312
	Q9HY77	PA3533	7	61.1	11.843	31.402	1.25E+10	50	108	30.7425	29.0689	28.5093	30.3806	28.2746	30.0469	28.1747	29.1308
	Q9HY81	PA3529	14	89.5	21.822	165.43	1.29E+11	198	200	31.8066	32.1234	32.0253	31.8769	31.8999	31.946	32.1036	31.8926
ilutaredoxi	Q9HY82	rnt	10	62.9	24.723	148.34	6.3E+09	74	224	27.5186	27.5253	27.417	27.4153	27.2005	27.2426	27.306	27.1973
	Q9HY84	argG	30	82.7	45.297	323.31	3.11E+10	259	405	29.4262	29.6438	29.674	29.1864	29.0504	29.3793	29.2686	29.2836
	succinate i	Q9HY83	PA3496	5	79.7	6.8834	22.389	1.94E+09	27	59	27.8232	27.4476	24.6614	28.1568	27.8993	27.5125	27.0432
donuclease	Q9HY84	nth	8	42.9	23.737	40.025	9.16E+08	34	212	25.8207	26.0677	26.0213	25.9496	26.0882	26.089	25.8083	25.9534
nine--trnU	Q9HYC7	metG	32	65.7	74.903	323.31	1.61E+10	219	677	27.2338	27.3767	26.9709	27.4754	27.8919	27.7976	27.522	27.5574
	Q9HYC8	PA3481	12	54.4	38.888	104.77	5.48E+09	69	364	27.697	27.7421	27.7286	27.3678	27.5138	27.6816	27.9229	27.9586
	triphosphi	Q9HYC9	dcd	6	46.3	21.154	69.637	3.76E+09	53	188	27.21	27.3432	27.5362	27.3148	27.3281	27.3783	27.3822
ndent mal	Q9HYD5	maeA	22	64.4	62.42	323.31	1.14E+10	142	564	27.8737	27.7087	27.7079	27.7016	28.0107	28.3515	28.519	28.3335
	Q9HYE0	PA3466	13	43.5	48.989	56.076	1.21E+09	72	446	24.761	25.0326	24.5472	25.159	24.9764	24.8506	25.0124	25.2991
	12 protein i	Q9HYF3	PA3453	8	57.5	24.16	82.422	4.15E+09	59	221	26.6572	26.8094	26.9337	26.6039	27.1695	26.9461	27.0572
:quinone c	Q9HYF4	mqoI	11	32.1	57.21	53.234	1.36E+09	56	523	25.0805	25.4162	25.0513	25.5946	25.63	25.2667	25.0705	25.5787
	Q9HYF6	PA3450	13	73.1	24.164	115.29	9.74E+09	93	212	28.0901	29.0376	27.9351	28.2022	28.2386	27.8805	28.123	28.0756
	Q9HYG6	PA3440	7	63.1	11.637	104.31	8.18E+09	60	103	29.0489	27.1092	26.4176	28.9626	27.2109	29.0309	27.0091	28.3543
c/hydrolyz	Q9HYG8	foiE1	9	53.8	20.833	22.816	4.64E+08	27	186	24.2958	24.5998	24.34.					

	Q9HZG8	PA3040	5	39.4	11.916	49.167	9.67E+08	35	109	25.1909	25.7694	25.6401	25.7986	25.9317	25.5476	26.3254	25.8337
	Q9HZH4	PA3034	3	20.5	20.988	7.259	1.37E+08	13	185	22.9409	23.797	23.7966	22.986	22.0784	22.7906	23.8848	22.4625
	Q9HZH8	moeA2	7	28.6	43.39	49.966	7.98E+08	27	405	24.832	25.0487	25.1614	24.6661	24.888	25.0233	25.1787	25.4557
	Q9HZI4	PA3022	11	50.7	29.579	47.059	1.19E+09	43	268	26.0146	26.2912	26.49	26.3842	26.0236	25.8074	25.9745	25.4681
	Q9HZI5	PA3021	9	56.2	14.206	87.737	1.61E+09	54	128	26.0806	25.5174	24.687	26.3427	25.4952	25.7001	25.4694	25.7683
	Q9HZI7	PA3019	17	37.8	71.155	91.792	1.65E+09	107	640	24.937	25.1255	24.8912	25.0434	25.0471	24.9994	25.143	25.4768
sal stress p	Q9HZI9	PA3017	5	69	15.844	72.881	1.71E+09	39	145	26.8803	26.1102	26.2586	26.8602	25.2642	26.0847	25.8746	25.4688
oyl-CoA is	Q9HZI2	fadB	30	51	76.953	246.46	1.54E+10	276	715	27.413	27.506	27.4217	27.1675	27.1176	27.3579	27.3434	27.3093
acyl-CoA t	Q9HZJ3	fadA	13	61.6	41.643	171.65	2.45E+10	132	391	29.9661	30.0839	30.21	29.8637	29.717	29.6787	29.8929	29.6597
opoisomeri	Q9HZJ5	topA	37	52.5	97.282	264.86	6.94E+09	168	868	26.0926	26.4775	25.9282	26.434	26.5613	26.676	26.4402	26.7204
	Q9HZJ6	PA3010	5	44.8	19.071	22.912	6.99E+08	30	172	25.0304	24.0951	25.3373	25.1319	24.9629	25.0636	25.1106	24.9564
	Q9HZJ9	psrA	12	70.8	25.784	80.299	3.87E+09	70	233	27.5507	27.3762	27.4312	27.3716	27.3571	27.2281	27.4233	27.0736
hexosamin	Q9HZK0	nagZ	13	50.9	36.101	98.981	6.58E+09	107	332	27.6612	27.7327	27.6435	27.5871	27.7799	27.6286	27.7776	27.6441
	Q9HZK2	PA3003	9	72.2	22.474	63.103	8.09E+09	91	209	28.9062	28.7137	27.7991	28.8678	28.8847	28.9386	28.678	28.8287
lDH-quinor	Q9HZK6	nqrA	18	58	48.081	205.76	6.22E+09	115	445	27.2029	27.3561	27.2257	27.1544	27.3984	27.4937	27.3183	27.446
lDH-quinor	Q9HZK8	nqrC	6	37.2	27.779	18.73	5.8E+08	22	261	23.7995	24.9441	23.1289	24.9583	24.8611	25.1505	24.7696	25.3104
	Q9HZL4	PA2990	9	38.3	26.887	68.986	1.06E+09	47	240	25.2097	25.4468	25.2666	25.277	24.7263	24.6867	25.1226	24.8585
	Q9HZL5	PA2989	3	10.2	28.376	11.672	1.91E+08	14	254	24.215	24.0653	24.2831	24.1165	23.8883	23.9635	23.7759	23.0788
system ATI	Q9HZL7	loId	4	48	24.65	92.148	1.95E+09	33	227	26.9076	27.0694	26.997	26.997	27.0224	26.9298	27.3388	27.3081
14 protein I	Q9HZM4	PA2980	5	77	6.7208	40.865	5.69E+09	35	61	29.1363	27.5088	26.7242	28.8542	27.2333	28.7784	27.4868	27.9398
ulosonate	Q9HZM5	kdsB	10	44.5	27.546	94.232	3.99E+09	59	254	26.976	26.9898	27.1856	26.6495	26.9121	26.9045	27.0789	26.9339
	Q9HZM6	qtdA	6	52.6	17.152	48.289	3.92E+08	28	154	24.5824	21.9792	24.5699	24.7665	24.3109	23.8563	24.4049	24.818
bonuclease	Q9HZM8	rme	38	39.4	117.46	323.31	5.13E+10	346	1057	29.3661	29.6506	29.2775	29.4417	29.7782	29.7446	29.8216	29.873
unit pseud	Q9HZM9	rluC	8	26.7	35.641	28.968	4.75E+08	30	318	24.3816	24.5141	24.3769	24.2585	24.2898	24.6277	24.4245	24.5343
	Q9HZN0	PA2974	9	54.8	25.322	46.418	9.67E+08	35	230	24.5718	25.1887	25.0778	24.4678	24.7912	25.1036	25.2745	24.895
	Q9HZN1	PA2973	5	24.2	36.063	56.577	5.93E+08	23	326	24.9419	25.3695	23.2682	25.1472	25.6718	25.405	25.43	25.7693
æ protein F	Q9HZN2	PA2972	8	58.3	21.054	53.154	1.93E+09	49	192	26.4332	26.7095	25.7432	26.571	26.8028	26.8082	26.7547	26.7927
	Q9HZN3	PA2971	6	50.6	19.569	33.006	1.72E+09	32	178	27.1245	26.9623	21.8184	27.059	26.9205	27.3021	26.8496	27.2135
isomal pro	Q9HZN4	rpmF	4	55	6.7914	46.994	8.62E+10	69	60	32.2442	32.2333	31.5283	32.2188	32.3711	32.1846	32.3851	32.1124
ste acyltra	Q9HZN5	plxX	4	19	35.549	25.084	2.27E+08	19	336	24.0587	23.6917	24.0774	22.9629	22.539	23.9194	24.128	23.9043
	Q9HZN6	pabC	3	15.1	29.886	7.8268	3.79E+08	20	271	23.9971	24.2086	24.4687	24.1377	24.046	24.1781	24.0595	23.8073
nidylate ki	Q9HZN8	tmk	7	50.5	23.109	59.816	1.35E+09	38	210	25.5314	25.5034	25.039	25.4723	25.5577	25.6921	25.4765	25.5263
	Q9HZN9	PA2959	12	77.9	28.114	150.8	5.62E+09	84	258	27.2027	26.9029	26.6734	27.2763	27.0769	27.2687	26.8134	27.1615
	Q9HZP0	PA2958	7	30	42.109	29.442	4.58E+08	20	377	24.4405	25.0819	22.9645	24.77	25.3898	25.1368	25.9351	25.3946
	Q9HZP4	PA2954	7	57.7	21.24	27.207	4.77E+08	25	189	25.157	25.1542	24.918	25.3424	23.5891	25.0531	24.923	24.6756
rotein-ubiq	Q9HZP5	PA2953	32	70.8	59.928	284.94	4.37E+10	324	551	29.0065	29.1324	28.9512	28.8337	28.9864	24.914	29.0163	29.0914
r flavoprot	Q9HZP6	etfB	13	74.7	26.376	204.77	1.23E+11	236	249	31.3362	31.3783	31.6877	31.4112	31.2621	31.3364	31.3765	31.1592
flavoprote	Q9HZP7	etfA	17	76.7	31.422	309.48	1.59E+11	411	309	32.2302	32.2127	32.5427	32.3695	32.2502	32.1927	32.3386	32.0494
eductase	Q9HZP8	PA2950	26	60.6	43.528	323.31	4.65E+10	245	398	29.6535	29.973	29.9262	29.5046	29.3534	29.5155	29.4915	29.6114
rotein Cobl	Q9HZQ2	cobW	15	51.5	41.206	323.31	9.25E+09	115	375	27.4834	27.4466	27.4045	27.2593	27.322	27.5041	27.8028	27.5295
	Q9HZQ5	PA2942	4	20.1	36.545	36.118	4.03E+08	23	338	24.3382	24.347	24.8615	24.122	24.4455	24.6165	24.2635	24.6423
	Q9HZR5	morB	9	47.7	39.631	85.21	1.03E+09	62	369	24.9862	24.642	24.9239	25.1251	24.9612	24.8683	24.8822	24.7845
	Q9HZS9	PA2918	3	22.2	26.738	18.165	4.82E+08	27	257	24.9592	24.9802	25.1548	24.7625	25.2915	25.2158	25.1843	24.9703
	Q9HZT2	PA2915	8	49.3	32.013	74.381	1.01E+09	43	288	25.1832	25.2888	25.7112	25.1629	25.4669	25.6225	25.9597	25.7235
1-8X methy	Q9HZU2	cobH	5	24	21.65	30.371	1.07E+09	31	208	25.4974	25.6483	25.6282	25.5576	25.6955	25.6186	25.9496	25.6834
[20]-methy	Q9HZU3	cobI	7	42.4	27.274	38.398	9.25E+08	35	250	25.7839	25.8072	25.8225	25.6621	25.51	25.887	25.7661	25.6209
	Q9HZU4	cobJ	3	8.4	58.982	11.907	79832000	12	559	23.8387	22.9542	22.3334	22.9796	22.2879	23.1738	23.0468	23.3131
	Q9HZU5	PA2902	8	35.5	30.448	62.753	7.95E+08	16	282	25.9929	26.2204	23.0691	26.6439	21.829	25.5516	23.4946	25.6729
	Q9HZW2	atuA	4	29.3	22.057	47.444	1.14E+09	33	198	26.0255	26.2189	26.6305	25.8384	25.9013	25.5593	23.3364	25.4384
	Q9HZX5	PA2871	8	44.2	28.695	53.46	1.57E+09	50	265	25.3073	25.5934	25.4565	25.5394	25.8893	25.4251	25.6529	25.4282
	Q9HZY0	mttC	5	30.3	29.544	75.008	6.54E+08	23	267	25.1471	25.1531	23.1771	25.4389	25.4791	25.4023	25.1198	25.0593
elongatio	Q9HZY5	greB	6	42.9	19.144	37.176	6.16E+08	22	168	25.1148	23.1957	24.8592	25.2134	25.5744	25.5047	25.6444	25.1958
	Q9HZY7	PA2857	7	46.3	24.585	63.884	1.47E+09	48	227	25.5533	25.8423	26.2661	25.5105	26.2609	26.3997	26.3036	25.9971
terase Tes	Q9HZY8	tesA	5	51.2	21.037	55.471	1.28E+09	45	201	26.3699	25.3785	25.1471	26.2427	25.3275	25.9718	25.8227	25.94
	Q9HZZ0	PA2854	16	59.8	34.799	116.22	1.49E+10	147	323	28.1609	28.419	28.3034	28.1182	27.9432	27.9783	28.0472	28.0169
gation fact	Q9HZZ2	efp	9	38.3	20.985	80.928	9.93E+10	119	188	31.5017	31.7483	31.4751	31.6815	31.7598	31.6797	31.558	31.5754
	Q9HZZ3	ohr	5	54.2	14.522	98.69	6.43E+09	40	142	28.1998	27.9718	27.4882	28.1851	28.2197	28.5638	28.542	28.6352
ent RNA h	Q9I000	PA2843	11	35.9	49.851	30.947	4.71E+08	23	448	24.9428	24.8766	23.0302	25.4438	23.6146	25.1236	24.843	25.3104
: S-methylt	Q9I003	deaD	26	54.9	62.107	190.04	1.3E+10	186	567	27.7622	28.0878	27.8946	27.7085	27.7739	27.9001	27.9041	28.0161
	Q9I011	tpm	6	49.5	24.875	14.035	5.22E+08	22	218	25.2902	23.0612	25.3819	25.1424	25.1322	25.2859	25.4558	25.166
	Q9I012	PA2831	12	49.2	42.933	89.604	1.67E+09	59	375	26.1102	26.2791	26.2832	26.2164	26.207	26.0252	25.968	25.9239
	Q9I014	PA2829	6	56.7	16.431	27.592	3.84E+08	23	150	24.4372	24.1316	24.4244	24.3927	24.7485	24.5867	24.8094	24.5049
	Q9I015	PA2828	13	53.8	44.799	113.22	6.89E+09	100	403	27.3151	26.9408	26.9283	27.4771	27.7879	27.6191	27.4114	27.3774
hione pero	Q9I017	PA2826	6	53.4	17.659	35.335	1.6E+09	38	161	26.5456	26.9409	26.9797	26.5071	26.5483	26.7566	26.8339	26.575
	Q9I020	PA2823	12	50	33.792	118.1	5.49E+09	82	26	27.5433	27.7291	27.9856	27.4322	27.6473	27.8035	27.8888	27.8149
	Q9I021</																

age system genase (de ase 1;Serin nethlytran	Q9I0V3	PA20250	9	37.2	48.959	79.317	9.55E+08	45	441	25.7907	25.5357	25.8453	25.2715	26.1856	25.8123	25.8687	25.9544
	Q9I0Z0	mexT	3	12.7	38.222	18.058	2.2E+08	14	347	22.2821	24.4896	24.6342	24.2621	23.0266	24.1063	24.5928	24.3527
	Q9I0Z9	PA2483	9	57.1	36.102	47.687	7.35E+08	48	333	25.0704	24.1521	24.7448	24.5808	24.5456	24.6923	24.6545	25.0705
	Q9I118	PA2464	5	47.1	17.626	14.585	5.65E+08	16	174	24.8516	24.7566	24.1738	25.2107	25.4906	25.1319	24.9509	24.9977
	Q9I127	PA2455	3	22.3	20.332	9.3627	1.85E+08	10	175	23.2455	23.9746	23.542	24.0913	24.3125	23.9538	23.6013	22.8691
	Q9I136	gcvH1	3	22.8	13.793	11.284	5.21E+09	29	127	28.7609	28.3069	27.1654	28.6564	27.297	28.4705	27.0848	28.1027
	Q9I137	gcvP1	30	46	103.92	286.25	5.56E+09	167	959	26.197	26.7832	25.5809	26.6041	26.4213	26.4268	25.9185	26.7484
	Q9I138	glyA1,glyA2	11	37.6	44.973	143.52	2.83E+09	82	418	26.5257	26.487	26.5922	26.1168	25.6888	26.2123	25.6894	25.851
	Q9I140	gcvT2	18	65.7	39.882	157.51	2.65E+10	166	373	29.0345	29.1477	29.29	29.0827	28.833	28.9134	28.7915	28.6642
	Q9I192	fpvR	3	15.1	37.022	18.899	3.46E+08	16	331	24.1716	24.3267	24.2908	24.628	24.6189	24.782	24.8057	24.6359
l7 protein i '1 protein i	Q9I1A0	PA2379	6	58.3	16.618	54.083	7.62E+08	34	156	25.1128	24.9608	23.4526	24.8318	25.6325	25.4382	25.4165	25.3217
	Q9I1A1	PA2378	20	42.8	83.665	152	3.49E+09	88	771	26.2319	26.2063	24.5283	26.1066	26.8879	26.5853	26.577	26.5943
	Q9I1F5	PA2323	16	49.5	59.96	107.24	1.98E+09	78	541	26.1361	26.4881	26.1	26.3193	25.6751	25.6439	25.7719	26.1588
	Q9I1F6	gntR	9	32.7	37.147	26.859	4.12E+08	24	343	23.0806	24.7342	25.0573	24.7984	24.3437	24.6901	24.4541	24.6811
	Q9I1F8	PA2317	6	24.5	47.855	30.961	5.71E+08	28	432	25.3604	25.3253	25.1671	24.7271	24.4893	24.4324	22.5685	24.7766
	Q9I1H4	PA2301	6	42.2	19.33	23.787	3.19E+08	25	180	24.2821	24.2122	24.298	24.1017	24.1165	24.3117	24.4012	24.0632
	Q9I1I5	gcd	8	16.6	86.217	45.453	5.19E+08	33	803	24.2431	25.0158	23.6977	24.9942	24.5647	23.0348	23.7121	24.5181
	Q9I1K9	PA2264	10	64.3	26.358	53.068	2.84E+09	40	238	28.0097	27.4373	26.2961	28.1827	26.3749	26.6832	26.1317	26.7574
	Q9I1L6	ansA	7	30.5	34.755	36.784	8.34E+08	32	328	25.212	25.2006	25.1587	25.0187	24.8291	25.3747	25.272	25.5023
	Q9I1I9	lpdV	29	81	48.588	323.31	6.34E+09	97	464	25.2096	27.0905	28.9368	24.61	24.623	23.1696	25.586	23.7051
poyl dehyd	Q9I1P0	PA2229	6	33.5	26.56	53.083	1.37E+09	30	239	26.2076	26.1108	26.0889	26.552	26.3701	26.4874	26.0746	26.4317
	Q9I1R3	PA2204	22	74.6	29.308	173.37	1.03E+10	141	268	27.6846	27.7954	27.3361	27.7952	27.5688	27.5181	27.5523	27.5261
	Q9I1R8	PA2199	5	26.8	30.886	53.44	8.86E+08	34	291	25.1191	25.1289	25.6795	25.438	25.7147	25.0948	25.1261	25.2246
	Q9I1S0	PA2197	14	54.2	37.135	81.716	1.99E+09	84	345	25.9912	25.9237	26.1648	25.8022	25.6666	25.6213	25.793	25.4734
	Q9I1Z9	PA2116	8	38.1	29.221	57.867	4.12E+09	76	265	27.4819	27.7818	27.9646	27.0689	27.141	27.374	27.6002	27.3418
	Q9I203	PA2112	14	82.2	26.334	191.66	1.47E+10	131	247	28.5538	28.5455	28.5458	28.3522	28.1278	28.6722	28.6792	28.5412
	Q9I204	PA2111	10	47.7	26.218	81.769	2.57E+09	62	237	25.6971	26.0111	26.0052	25.8046	25.9836	25.8951	25.8665	25.5984
	Q9I205	PA2110	3	11.8	33.06	13.48	5.96E+08	19	313	24.7717	25.3443	25.4161	24.9424	24.9645	25.2386	25.5399	25.5759
	Q9I244	fusB	32	65.7	77.573	196.28	6.4E+09	144	702	26.7166	26.8868	27.0842	26.6804	27.4638	27.1896	27.6299	27.1168
	Q9I271	PA2044	33	67.3	70.083	323.31	1.32E+10	218	624	27.776	27.814	28.0698	27.9166	27.6287	27.4101	27.6079	27.4628
nosphate u	Q9I275	PA2040	9	42.1	50.931	22.956	5.29E+08	15	458	24.9121	24.7487	24.3675	24.9514	25.5606	26.0557	23.4181	26.0321
	Q9I291	galU	17	69.9	31.236	195.25	2.22E+10	144	279	29.1758	29.1903	29.1551	29.1685	29.3948	29.574	29.8511	29.7061
	Q9I297	liuB	8	25.6	57.433	28.574	5.44E+08	28	535	24.5101	24.6567	24.5758	24.5896	24.5297	24.2897	24.5102	24.3535
	Q9I299	liuD	13	30.8	71.282	53.263	9.83E+08	35	655	25.6392	25.9642	26.2999	22.5565	25.348	25.1618	25.652	25.4297
	Q9I2A2	fahA	4	16	46.341	25.574	4.88E+08	22	432	24.8962	24.9694	24.9144	24.6105	24.8001	24.8948	24.9835	24.7482
	Q9I2A8	atoB	20	75.1	40.405	269.78	8.96E+09	168	393	27.2095	27.0705	27.4822	26.8054	26.9144	26.5708	26.8861	26.5057
	Q9I2E0	PA1964	14	48.4	57.917	86.026	1.72E+09	45	521	26.9802	27.2361	26.5482	26.2462	26.2577	27.6952	26.895	27.4311
	Q9I2F4	rbtK	6	27.9	31.846	41.434	3.07E+08	26	308	24.1166	24.3978	24.364	24.2405	23.8949	23.9553	24.1514	23.9222
	Q9I2P3	PA1852	3	52.7	9.97	46.929	5.35E+08	21	91	24.573	23.7877	22.9871	24.9169	24.7117	25.6216	24.9343	25.7335
	Q9I2P8	nfuA	6	44.3	21.136	103.42	5.16E+09	51	194	28.5655	28.7706	27.2825	28.8686	27.9725	28.2943	27.8359	28.4545
enesis prot ionine syn	Q9I2Q2	metH	22	31.4	135.06	89.763	1E+09	78	1234	25.3419	25.073	22.546	25.0926	25.7741	25.6806	25.1891	25.24
	Q9I2Q7	cysI	26	59.2	62.132	189.69	6.14E+09	145	552	26.6417	26.7021	26.2736	26.9575	27.1213	26.9989	26.7419	26.7064
	Q9I2Q8	PA1837	7	57	18.765	150.17	2.5E+09	53	165	26.8707	27.0434	27.163	27.0954	27.4506	27.2749	27.3246	26.9113
	Q9I2R2	PA1833	14	58.5	34.551	120.75	8E+09	100	330	27.6394	27.6466	27.9331	27.4927	27.2893	27.1514	27.2749	27.0376
	Q9I2R5	PA1830	5	63.5	11.11	28.27	1.02E+10	46	104	29.9074	28.2792	27.5519	29.9109	27.6152	29.727	28.7862	29.5747
	Q9I2R7	PA1828	9	49.4	26.919	74.277	2.85E+09	51	255	26.6661	26.8449	26.6407	26.4819	26.3306	26.207	26.4297	26.4816
	Q9I2S3	fimL	16	47.9	60.868	84.927	2.31E+09	87	562	26.1565	25.9268	26.0071	25.8324	25.9651	26.1355	26.0068	26.4558
	Q9I2S4	PA1821	8	41.9	29.989	72.215	1.44E+09	53	270	25.4713	25.6619	25.705	25.0573	25.8998	25.5848	25.6147	25.5965
	Q9I2S7	ldcA	16	33.4	82.756	72.976	9.66E+08	75	751	24.7491	24.8042	24.542	25.0338	24.8819	25.0048	25.0292	25.165
	Q9I2S9	rmhA	8	58.1	16.697	67.95	1.18E+09	37	148	25.6251	25.5553	25.5847	25.4986	25.5262	25.6308	26.5266	25.636
xonuclease lglutathion	Q9I2T1	glbB	8	45	28.865	41.275	1.12E+09	46	258	25.9131	24.8486	25.3861	25.9331	25.4495	25.5395	25.8472	25.3864
	Q9I2T4	PA1810	27	56.1	70.473	167.73	4.88E+09	148	615	26.2847	26.4328	26.5416	26.5084	26.9543	26.615	26.6026	26.2677
	Q9I2T8	ppdI	29	55.7	68.741	290.96	9.96E+09	158	621	27.2728	27.4441	26.9023	27.5318	27.526	27.4103	27.3135	27.631
	Q9I2T9	lon	51	60.8	88.646	323.31	1.61E+10	332	798	27.3853	27.5126	27.309	27.4601	27.5443	27.4566	27.5774	27.5774
	Q9I2U0	clpX	24	66	46.991	217.62	3.64E+10	256	426	29.5141	29.6672	29.6633	29.2883	29.521	29.655	29.7338	29.609
	Q9I2U1	clpP1	2	18.8	23.502	46.733	1.64E+10	44	213	29.425	30.0884	28.8562	29.8796	30.0948	30.0549	29.8054	30.0718
	Q9I2U2	tig	41	87.4	48.58												

pyruvate is	Q9I3K8	PA1504	5	31	24.179	21.556	3E+08	13	216	24.293	24.5967	24.5134	23.6687	24.5598	23.8824	24.1926	24.4329
	Q9I3L1	PA1501	4	27.7	29.203	4.4535	86237000	15	260	23.8058	23.1161	23.4936	24.1089	23.2818	23.4504	22.8969	23.5341
	Q9I3L8	PA1494	21	50.3	60.65	156.75	4.14E+09	112	551	26.1124	26.1685	26.4059	26.3697	26.4065	26.1813	26.9909	26.0447
	Q9I3I9	cysP	12	50.9	36.517	110.04	1.69E+09	76	332	25.7083	25.3836	22.8155	25.7582	26.123	25.789	24.015	25.5947
s ATP-bindi	Q9I3N7	ccmA	6	39.5	24.995	72.111	8.21E+08	37	233	24.9798	25.027	24.4601	24.803	25.2933	25.1131	25.0752	25.3772
	Q9I3N8	PA1474	10	42.3	52.688	71.004	4.64E+08	49	492	25.1181	24.5594	24.9839	24.0464	23.5919	24.5373	24.2997	24.5628
	Q9I3Q7	PA1440	5	51.8	22.382	61.935	5.84E+09	57	195	28.7281	28.1593	28.5463	28.8119	28.4836	28.47	28.2763	28.6698
	Q9I3S7	PA1417	11	39.2	57.29	36.609	6.01E+08	34	533	24.4042	23.9764	24.5784	24.3898	24.6147	24.6031	24.2148	24.5974
r phosphate	Q9I3T4	PA1410	8	32	40.451	27.164	4.88E+08	32	363	24.8465	24.7507	24.937	24.6003	24.6822	24.8224	25.028	25.0097
	Q9I3T5	aphA	10	51.2	37.953	56.679	8.44E+08	35	346	24.8274	24.9948	24.7743	24.8543	25.3613	25.3555	25.0107	25.2341
	Q9I3U2	PA1402	8	53.4	23.753	27.311	1.06E+09	36	221	26.5189	26.47	26.5881	26.4399	26.1585	26.3937	26.8765	26.0479
	Q9I3W9	pdxB	7	26.6	41.001	35.805	1.32E+09	40	380	25.5914	25.6851	25.8743	25.9463	26.2538	26.0736	26.2519	25.8396
carrier-pro	Q9I3X1	fabF2	8	34.6	43.485	27.118	4.39E+08	25	422	25.3005	24.8237	25.1523	24.4212	25.0344	24.7343	24.9588	25.0457
	Q9I400	PA1344	11	48.1	27.397	81.45	2.52E+09	51	264	26.2632	26.7551	26.9866	26.2448	26.5437	26.3536	26.9504	26.2117
	Q9I405	I339;PA41	10	52.9	26.916	47.219	1.83E+09	54	244	26.3073	26.4709	26.5613	26.0378	26.1472	26.0755	25.985	26.4598
	Q9I406	ggT	24	50.4	59.873	181.51	1.01E+10	168	557	28.111	27.9919	27.5444	28.1736	27.9468	27.9276	27.5404	27.8437
peptidase	Q9I437	PA1307	8	43.6	28.544	80.707	1.83E+09	45	257	26.6655	26.8087	26.7461	26.6621	26.8227	26.5224	26.6406	26.4057
	Q9I445	PA1299	3	36.2	17.234	15.535	1.84E+08	14	149	24.0685	22.4678	23.9876	24.6201	24.1642	23.8425	23.1396	24.047
	Q9I446	PA1298	2	38.5	10.023	11.652	2.53E+08	12	91	24.8587	23.1192	25.0678	23.3229	24.304	24.1272	24.679	24.6585
	Q9I449	PA1295	2	49.5	11.361	20.929	1.86E+09	17	97	27.2933	26.3401	25.4938	27.2527	26.572	27.3016	26.7222	27.6438
sonuclease	Q9I450	rml	16	61.8	43.098	141.08	3.55E+09	90	374	25.8967	26.0097	26.0165	25.9933	26.1139	26.4599	26.2059	26.3059
	Q9I451	PA1293	5	28.6	38.794	24.365	1.77E+08	16	353	22.652	22.7405	24.0559	24.1665	24.1945	24.0017	24.1439	24.3111
	Q9I452	sseA	7	45.8	30.597	70.935	1.44E+09	36	284	26.807	26.5464	26.4409	26.5154	23.0418	26.1128	26.0031	26.2962
	Q9I461	PA1283	3	24.7	20.307	7.6533	2.51E+08	15	186	22.8064	24.7967	25.0167	24.7366	25.3664	25.2515	22.9477	23.0452
bala min bi	Q9I466	cobP	8	64.2	18.862	60.848	8.8E+08	35	173	24.6857	24.5306	24.6447	24.8831	24.9725	25.0559	24.9408	24.8582
	Q9I472	cobO	5	36.5	22.292	31.866	2.29E+09	27	203	26.5901	26.8924	26.9702	26.7191	26.9633	27.1385	27.1083	26.8937
	Q9I4A4	PA1234	3	33.5	18.46	13.724	5.56E+08	20	167	25.7486	25.4152	25.4853	25.7889	25.5318	23.4713	25.4957	25.4949
	Q9I482	PA1226	7	50	22.308	44.483	5.86E+08	40	202	24.4849	24.6965	24.3331	24.4839	24.3502	24.5092	24.4656	24.649
in 2,3-diox	Q9I4D2	PA1206	9	79.6	17.69	84.821	3.85E+09	73	157	26.5966	26.5777	26.0081	26.4695	26.4074	26.6262	26.5474	26.5598
	Q9I4D3	PA1205	6	31.4	34.455	34.388	7.03E+08	30	315	25.8718	26.069	26.0157	26.1397	25.3683	25.4782	25.7404	23.8187
	Q9I4D4	PA1204	4	40.5	20.224	47.987	1.34E+09	21	185	26.2767	26.0395	26.4083	26.1724	26.1578	25.7421	25.6786	25.5395
	Q9I4D5	PA1203	3	26.7	14.681	13.362	5.86E+08	18	135	23.2713	25.4981	22.9827	26.2299	24.8758	25.6307	24.5437	25.5728
ent protei	Q9I4E1	cobB2	4	27	27.686	28.846	2.69E+08	17	256	24.3481	24.3075	23.8557	24.0624	24.7994	24.2912	24.1553	23.9847
	Q9I4E6	ttcA	6	27.7	31.26	30.696	7.89E+08	40	274	24.9029	24.8074	25.242	24.6537	25.1231	25.311	25.1032	25.4147
	Q9I4F8	phoQ	4	12.7	50.28	17.185	84879000	15	448	23.1251	23.4832	23.6455	22.5679	23.2236	23.6534	23.1262	22.9372
	Q9I4F9	phoP	18	75.1	25.65	323.31	4.73E+10	216	225	29.7703	29.6675	29.9369	29.64	30.1879	30.2748	30.4041	30.1587
noplimate	Q9I4H3	PA1164	4	27.4	28.898	29.615	5.3E+08	21	270	25.1474	25.1756	25.1493	25.0452	24.9458	25.0257	22.3095	25.176
	Q9I4H5	dapE	13	53.3	41.077	128.53	1.02E+10	119	383	27.5207	27.6707	27.5833	27.611	27.7507	27.8669	27.9872	27.7323
	Q9I4H6	rrmA	8	36.7	29.644	16.209	4.34E+08	20	267	24.5689	24.376	24.5666	24.3968	24.4717	24.3244	24.6733	24.3815
	Q9I4H7	PA1160	6	79.5	14.042	53.816	1.49E+09	34	127	26.5212	26.0957	25.6019	26.6893	26.2552	26.3656	25.9451	26.256
osphate rei	Q9I4I8	PA1159	4	50.7	7.7246	40.226	2.12E+10	44	69	29.6866	29.727	29.4484	29.7408	29.9562	29.9839	30.1019	29.7582
	Q9I4I2	nrdB	20	69.9	47.386	252.44	1.54E+10	141	415	28.5579	28.5455	27.8782	28.9056	29.0811	28.9691	28.8284	28.8371
	Q9I4J5	PA1140	6	43.9	31.614	58.921	1.84E+09	43	278	25.7937	26.2375	25.9709	25.3868	26.1024	25.9624	25.9736	25.8734
	Q9I4J6	PA1139	4	32.6	29.336	28.53	4.16E+08	14	282	25.9375	23.9299	23.0807	25.8824	22.287	24.8363	23.809	24.5616
specific AT	Q9I4K8	PA1127	22	76.6	36.474	275.62	2.3E+10	202	329	29.4182	29.5193	29.8739	29.6292	29.4535	29.2982	29.5299	28.9969
	Q9I4L8	PA1117	5	72.6	13.589	20.361	2.46E+08	21	124	23.8236	23.7692	23.2204	24.347	24.1885	24.2483	23.6431	23.7296
	Q9I4L9	PA1116	6	29	31.308	23.884	3.84E+08	20	279	24.6928	24.2552	24.9419	24.9581	24.8207	25.0196	25.0092	24.5939
	Q9I4N1	filI	11	36.4	48.38	33.706	3.6E+08	25	451	22.5848	24.5393	24.6537	24.4154	24.732	24.7307	23.5937	24.1806
lar P-ring p	Q9I4N3	fleR	17	51.8	51.234	83.763	1.93E+09	83	473	25.7942	25.8224	26.0961	25.6743	25.8134	25.9552	25.891	25.9083
	Q9I4P5	flgI	14	57.2	38.18	72.387	2.26E+09	78	369	25.5801	25.6291	25.4228	25.7382	25.4432	25.7118	25.4105	25.6837
	Q9I4P9	flgE	9	50.4	48.335	113.93	1.44E+09	55	462	25.4602	25.6532	25.3303	25.9012	25.9917	25.9397	26.1108	25.9392
	Q9I4Q0	flgD	4	38.8	24.85	42.265	4.53E+08	25	237	25.1871	25.0089	23.844	25.1911	25.2177	24.7987	25.2215	25.2025
lazole-succ	Q9I4Q4	PA1075	3	58.1	11.337	17.359	5.76E+08	25	105	25.6107	23.2683	23.7947	26.2314	24.4008	25.7601	24.9137	25.5242
	Q9I4Q5	PA1069	12	25.4	86.114	35.952	3.75E+08	37	764	23.6312	23.9046	24.377	24.1056	24.9862	24.3296	24.7095	24.

	Q9IS77	PA0601	7	55.7	22.9	25.107	3.07E+08	21	210	23.9538	24.454	24.4723	24.1725	23.5834	24.0023	23.35	23.931
	Q9IS79	PA0599	3	14.2	37.979	15.382	4.83E+08	16	353	25.4032	25.7658	22.6316	23.1989	23.6117	25.4332	25.1656	25.4255
	Q9ISU0	PA0597	3	36.6	24.149	35.129	2.53E+09	43	224	27.0747	26.6779	26.014	26.8918	26.5317	26.689	26.5262	26.955
	Q9ISU1	PA0596	13	50	38.185	127.78	7.78E+09	112	338	27.0854	27.092	27.1293	27.4319	27.2232	27.1088	27.3256	26.9937
aperoene Si-4-phosphat	Q9ISU3	surA	28	71.7	46.953	323.31	3.92E+10	288	417	29.3845	29.444	28.5672	29.4552	29.5226	29.442	29.5494	29.4393
	Q9ISU4	pdxA1	7	43	34.923	46.967	9.13E+08	40	328	25.3236	25.4265	25.5736	25.1847	24.8648	25.4031	25.8979	25.4795
	Q9ISU5	rsmA	7	45.5	30.058	61.528	1.84E+09	54	268	26.0928	26.0087	26.1609	26.1005	25.8885	26.3579	26.3285	26.3116
	Q9ISU6	apaG	3	48.4	13.622	51.355	2.19E+09	32	126	27.993	27.2791	26.738	27.9811	27.9372	27.4968	27.3626	27.9161
rotein apA-traphosph	Q9ISU7	apaH	14	61.8	32.018	61.108	1.83E+09	64	283	25.7243	25.9207	25.876	25.7179	25.7571	25.6452	25.7518	25.7096
	Q9ISV3	cca	10	36.1	45.639	58.179	4.41E+08	41	410	24.3976	24.211	24.5281	24.7035	23.9086	23.7382	24.0386	23.9612
A-adding e	Q9ISV4	PA0583	7	53.3	20.091	30.596	3.97E+08	19	180	24.2392	23.8186	23.8908	24.5364	23.2581	24.559	22.8166	24.3455
	Q9ISV7	tsaD	6	28.7	36.561	40.475	5.52E+08	28	341	24.2636	24.6684	24.3018	24.2801	24.715	24.7058	24.9475	24.7853
threonylcaisomal pro	Q9ISV8	rpsU	6	46.5	8.4848	48.034	1.71E+10	83	71	29.1701	29.5367	28.8689	29.5754	30.1347	29.8021	29.5643	29.9246
	Q9ISV9	PA0578	3	22.8	16.842	20.136	8.68E+08	23	149	25.4743	25.9632	24.7388	25.6038	25.9275	25.8397	25.9801	25.8
nA primas	Q9ISW0	dnaG	8	19.6	74.175	25.353	1.29E+08	20	664	22.5641	23.7606	23.8966	22.353	23.929	24.0199	23.8631	23.4807
	Q9ISX4	PA0562	8	45.5	24.232	97.125	1.66E+09	56	224	25.8426	25.9703	25.9217	25.6896	26.0551	25.8671	26.0177	25.7664
	Q9ISX7	PA0559	7	21.4	42.618	35.682	9.37E+08	37	392	25.1952	25.2128	25.1439	25.4514	25.5251	25.2247	25.4015	25.0739
isphosphatoglycerate	Q9ISY1	fba	24	64.7	38.573	323.31	8.36E+10	323	354	30.4805	30.7633	30.6889	30.3853	30.7102	30.8141	30.772	30.6466
	Q9ISY4	pgk	20	69.3	40.404	278.67	6.49E+10	258	387	29.6175	29.7232	29.8875	29.6972	30.0733	30.0287	30.1822	29.895
	Q9ISY5	epd	11	67	38.743	139.42	1.97E+09	62	353	25.8173	25.6735	25.63	25.8016	26.2859	26.2606	26.5172	26.1647
	Q9ISY6	pyruvate	11	67	29.834	54.922	9.04E+08	40	265	24.9108	24.9344	24.9048	24.9071	24.8367	24.6216	24.6889	24.6121
ranksketol	Q9ISY8	tkdA	35	73.1	72.219	323.31	1.12E+10	262	665	27.7123	27.9528	27.2295	28.3417	28.5504	28.4608	28.1385	28.3515
	Q9ISZ0	metK	27	85.4	42.709	299.53	1.15E+11	361	396	30.9925	31.01	31.082	30.8672	31.1995	31.1226	31.0723	30.9536
methionin	Q9ISZ4	PA0542	4	23	14.767	85.396	4.72E+09	37	139	27.9586	28.464	28.8915	28.2546	28.0576	27.5297	28.5342	28.542
	Q9I610	8,9,PA4199,f	13	34.6	63.628	48.913	2.19E+09	66	592	26.2556	26.3857	25.981	26.1987	26.2988	26.2531	26.3783	25.9484
	Q9I612	PA0506	23	50.7	65.358	219.55	9.06E+09	140	601	28.1562	28.1567	27.7983	27.9482	27.967	28.0016	27.8789	28.0353
ethiobiotri	Q9I614	bioD	4	28.9	23.337	23.965	5.39E+08	25	228	25.6994	25.589	25.2681	25.307	25.4918	25.6802	25.2259	25.5334
	Q9I616	PA0502	5	26.4	26.949	53.148	6.91E+08	28	240	25.4377	24.3916	24.8204	25.0895	25.2224	25.0725	24.588	24.871
xononano	Q9I617	bioF	10	50.6	42.237	68.691	4.96E+08	36	401	24.9458	23.5966	24.3677	24.8134	24.6169	24.7409	24.6488	25.2326
	Q9I618	bioB	21	71.3	39.113	270.04	1.17E+10	167	352	27.9853	28.0508	28.1502	28.0292	28.5399	28.3476	28.4956	28.3669
ctin syntha	Q9I622	PA0496	12	59.7	34.635	143.3	2.03E+09	68	325	25.75	25.7871	26.4475	25.4042	25.2281	25.0312	25.5542	25.2141
	Q9I623	PA0495	3	18.5	32.951	15.295	3.43E+08	15	292	23.8993	24.9864	25.1751	24.3635	22.1316	22.7538	24.8713	24.8713
I1 protein i	Q9I624	PA0494	10	40.8	50.07	46.89	3.31E+08	35	458	23.3295	24.0817	25.0819	22.3689	24.0172	24.0949	23.5677	23.8214
	Q9I626	PA0492	8	50	27.559	36.002	7.7E+08	47	252	25.0646	24.9575	25.0655	24.8615	25.1128	24.8032	25.145	24.648
ate syntha:	Q9I631	PA0487	6	29.4	26.948	29.108	7.28E+08	25	252	25.2899	25.3045	25.8382	25.5514	24.855	25.2617	25.3354	25.3065
	Q9I632	PA0486	3	16	36.968	16.574	1.91E+08	17	324	24.0603	23.7203	23.832	23.7654	23.6749	23.8502	23.9296	24.0529
glcB	Q9I636	glcB	31	64.4	78.659	323.31	3.16E+10	261	725	29.3333	29.4352	29.5647	29.296	29.5737	29.4084	29.4751	29.2839
	Q9I645	PA0473	6	39	28.326	27.539	7.54E+08	29	249	25.6699	25.9871	25.9129	25.6929	25.842	25.9633	25.8549	25.6548
Q9I649	PA0469	19	68.4	32.137	224.26	4.65E+09	107	285	26.4297	26.5332	26.7242	26.3961	26.0401	26.0596	26.3013	25.9234	
	Q9I650	PA0468	9	53.8	33.594	121.29	2.65E+09	71	316	26.5244	26.1227	25.6672	26.7849	25.666	25.7414	25.2484	26.0738
Q9I651	PA0467	9	61.2	23.301	64.532	9.39E+08	38	206	25.3171	25.5838	25.3304	25.6474	25.5463	25.3695	25.2422	25.2407	
	Q9I655	creB	7	38.9	25.573	61.837	7.43E+08	30	229	25.2341	25.3756	25.4581	25.329	24.9867	25.1372	25.0354	25.9038
Q9I656	PA0462	5	21.8	26.262	15.538	9.71E+08	19	234	23.2085	25.9894	25.748	25.8279	26.6683	26.0499	26.6808	26.2991	
	Q9I658	PA0460	8	77.6	18.727	69.193	1.14E+10	80	192	28.7929	27.7093	27.2045	28.1478	29.3726	28.6938	28.9425	
Q9I662	PA0456	7	82.6	7.7066	82.635	2.36E+11	100	69	34.6019	34.1945	33.1272	34.57	34.0861	34.3375	34.2926	34.167	
	Q9I663	dbpA	6	24	49.784	30.143	3.27E+08	19	458	24.7385	24.3657	24.5446	24.1192	23.9379	22.4701	23.9501	
yIhomocys	Q9I685	ahcY	35	80.6	51.399	323.31	9.56E+10	390	469	30.4843	30.6287	30.6476	30.3925	30.3453	30.4495	30.4996	30.4124
	Q9I686	PA0431	5	63.6	20.639	16.905	4.74E+08	36	184	24.8322	24.631	23.9072	25.0595	25.1711	24.9477	24.6649	24.9196
rahydrofol	Q9I687	metF	16	66.6	32.228	132	1.52E+10	142	290	28.9474	29.0653	29.0519	28.8248	28.7964	28.9832	28.8641	28.7722
	Q9I689	rhlE	26	49.9	70.111	220.45	6.77E+09	166	639	26.6285	27.1533	26.4339	27.155	27.3776	27.081	26.8627	27.3612
N(7)-)-met	Q9I692	PA0421	26	63.1	54.207	285.88	6.48E+09	155	496	27.1694	27.3133	27.4701	27.1297	27.1251	27.2311	27.2752	27.2587
	Q9I693	bioA	19	59.3	52.477	83.102	2.31E+09	90	467	26.2009	26.2426	26.0621	26.179	25.7187	25.6037	25.6167	25.6967
no-7-oxoni	Q9I694	PA0419	6	42.1	26.468	108.57	2.26E+09	51	240	27.0447	27.1152	27.0057	26.9796	26.9283	27.0199	26.7948	26.9378
	Q9I695	PA0418	7	25.1	52.172	23.636											

	Q9I777	PA0055	5	44.6	18.433	56.346	1.84E+09	38	168	25.9139	26.2003	26.4769	26.4108	26.0687	25.5993	25.8459	25.5812
	Q9I793	PA0039	5	52	7.9233	15.099	1.18E+09	21	75	27.1886	24.7741	22.441	27.0389	23.2179	26.6051	23.8016	26.0596
bamoyl-AH	Q9I7A5	tsaC	6	58.9	20.371	75	8.24E+08	30	185	25.1804	25.1025	25.2122	25.1521	24.8303	25.319	25.1165	24.7405
	Q9I7A7	PA0020	12	52.2	37.586	151.99	5.94E+09	69	341	27.6214	27.6424	27.8749	27.4849	26.9802	26.863	27.0621	27.3852
de deform	Q9I7A8	def	10	86.9	19.365	135.45	9.46E+09	121	168	27.9725	28.0161	27.7762	28.0861	27.5284	27.5928	27.6581	27.4052
	Q9I7B0	trkA	13	45.7	49.926	64.181	1.45E+09	56	457	25.6637	25.6492	25.9374	25.0927	25.4329	25.5473	25.7747	25.7818
4A ligase al	Q9I7B7	glyQ	9	47.3	36.14	104.53	8.94E+09	81	315	28.6488	28.4745	28.0671	28.8089	29.009	28.7784	28.2638	28.178
NA ligase b	Q9I7B8	glyS	31	50	73.973	314.82	9.54E+09	206	684	26.9537	26.9435	27.0282	26.7406	26.891	27.0431	27.0938	27.3102
ptose-1,7-i	Q9I7C0	gmhB	6	54.5	19.115	58.057	3.74E+09	52	178	28.1234	28.2345	27.4334	28.337	28.122	28.3798	27.8591	28.285
γrase subr	Q9I7C2	gyrB	36	61.9	90.188	255.39	8.55E+09	197	806	27.1171	27.4305	26.8451	27.2076	27.6822	27.5334	27.2535	28.087
erage III su	Q9I7C4	dnaN	17	54	40.694	323.01	4.15E+10	188	367	29.9261	30.0943	30.3271	29.8024	29.8841	29.9323	30.1214	29.861
ication init	Q9I7C5	dnaA	21	59.1	57.754	152.48	3.33E+09	100	514	25.9654	26.1182	26.054	25.9588	26.1603	26.186	26.1044	26.3383
5-phosphat	Q9KGU6	dxr	15	54.8	42.508	149.97	2.17E+09	68	396	26.1922	26.0069	26.0723	26.0411	26.4133	26.4887	26.4005	26.3649
ose-5-phor	Q9KGU7	dxs	17	33.3	68.049	88.225	1.64E+09	72	627	25.7329	25.8707	25.5501	25.5206	25.871	26.1685	25.936	26.3196
nslocase su	Q9LCT3	secA	41	57	103.85	323.31	2.28E+10	356	916	28.3758	28.5279	28.5871	28.41	28.8102	28.8357	28.8671	29.0657
l-D-alanin	Q9LCT6	ddlB	14	61.4	34.363	109.23	5.04E+09	104	319	26.9503	27.0276	27.0785	27.016	26.988	27.2589	27.3297	27.2903
colate phc	Q95586	gph1	5	32.4	29.812	12.379	3.74E+08	17	272	24.3106	23.9755	24.1717	24.176	24.7531	24.8347	24.3834	24.8992
ogluconol	Q9K2N2	pgl	9	48.3	25.571	80.76	1.25E+09	44	238	25.3603	25.1244	24.9394	25.2435	25.3502	25.4189	25.5306	25.32
lthioredoxi	Q9K2T1	trxA	8	74.1	11.87	82.25	1.03E+11	174	108	32.5341	31.5223	30.8505	32.7362	31.5396	32.3863	31.5319	32.1547
P-N-acetyl	Q9X6P4	lpxA	10	52.3	28.009	52.269	3.51E+09	60	258	27.1533	27.2629	27.2575	26.9702	27.3176	27.3113	27.2687	27.0865
ninopropyl	Q9X6R0	speE1	16	64.7	32.238	106.89	6.78E+09	101	286	27.4346	27.7155	27.535	27.2248	27.5844	27.6482	27.7621	28.0246
3D protein i	Q9X6V8	PA3998	6	82.8	10.338	101.17	5.19E+09	56	93	27.7737	27.2087	27.1685	27.6667	27.6378	27.4569	27.5957	27.6542
noyltransfr	Q9X6V9	lipB	8	73.3	23.856	33.215	9.58E+08	34	217	25.3359	25.0525	25.4787	23.1592	25.5247	25.2813	25.7854	25.7687
nate-tRNA	Q9XCL6	glxX	27	70.6	56.749	197.49	1.29E+10	218	494	27.5661	27.7968	27.2295	28.0505	28.2287	28.0898	27.8949	28.1813
GTPase Era	Q9XCX8	era	17	64.3	34.549	95.359	7.8E+09	92	305	28.1332	28.2931	28.3282	28.1819	27.8055	28.0692	27.9389	27.9833
bonuclease	Q9XCX9	rnc	10	43.7	25.506	39.538	2.42E+09	60	229	26.1629	26.1391	26.4527	26.2062	26.2334	26.135	26.1119	25.8564
rotein] rec	Q9ZFE4	fabl	12	63	28.006	71.88	2.03E+09	56	265	25.5828	25.8858	25.9854	25.4195	26.2178	26.0101	25.9326	25.454
gphospho	Q9ZFK4	kdsA	19	75.1	31.143	97.321	1.45E+10	151	281	28.1427	28.2784	28.3899	28.0465	28.1441	28.3256	28.1825	28.1627