			Acidithiobacillus				
3605	218667529	hypothetical protein AFE 2089	ferrooxidans ATCC 23270	253	0.42	29	4.5
			Burkholderia mallei				
3656	121596846	RNA polymerase sigma factor	SAVP1	231	0.26	51	3.00E-08
3677	299133058	Putative helicase A859L	Afipia sp. 1NLS2	408	0.27	85	2.00E-28
		plasmid maintenance system killer	Rhodopseudomonas				
3742	90424677	protein	palustris BisB18	93	0.31	41	1.4
2=0.6	•••••	hypothetical protein	Shuttleworthia satelles	• • • •	0.4.	4.0	- 0
3786	229828371	GCWU000342_00430	DSM 14600	298	0.15	40	7.9
3786	229828371	hypothetical protein GCWU000342_00430	Shuttleworthia satelles DSM 14600	298	0.15	40	7.7
3780	229828371	GC W 0000342_00430	Methylobacterium nodulans	290	0.13	40	1.1
3891	220922092	NnrS family protein	ORS 2060	392	0.09	68	2.00E-05
3901	221487851	conserved hypothetical protein	Toxoplasma gondii GT1	3229	0.02	39	4.5
		Predicted metal-dependent	800000		****		
		amidohydrolase with the TIM-					
3981	85711049	barrel fold	Idiomarina baltica OS145	558	0.23	26	3.5
3981	89067955	type I secretion target repeat protein		818	0.17	28	4.2
			HTCC2516				
4000	22212722	D	Methylocystis sp. ATCC	204	0.44	61	2.005.25
4000	323136327	Patatin	49242	284	0.44	61	3.00E-37
4020	328541621	hypothetical protein SL003B p0053	Polymorphum gilvum SL003B-26A1	435	0.43	58	2.00E-56
4020	320341021	SE003B_p0033	Myxococcus xanthus DK	733	0.43	30	2.00L-30
4035	108763646	putative lipoprotein	1622	447	0.13	35	7.8
4187	288957870		Azospirillum sp. B510	460	0.09	43	5.9
			Agrobacterium sp. ATCC				
4195	335035794	hypothetical protein AGRO_3125	31749	323	0.09	62	0.55
			Rhodopseudomonas				
4205	90424421	transposase IS3/IS911	palustris BisB18	66	0.38	68	1.6
1205	220020022	hypothetical protein	Dogrihagillus an IICES	604	0.05	0.4	1.00E-10
4305	329928833	HMPREF9412_3689	Paenibacillus sp. HGF5	694		94	
4311	16/6216/5	IS66 Orf2 family protein	Caulobacter sp. K31	117	0.35	59	3.00E-05
4338	209886756	hypothetical protein OCAR 7650	Oligotropha carboxidovorans OM5	362	0.10	64	2.00E-05
1550	207000750	nypotnetical protein ochre_7050	Geodermatophilus obscurus	302	0.10	01	2.00L 03
4381	284989640	hypothetical protein Gobs 1064	DSM 43160	285	0.11	59	2.7
.501	20.5050.0	n, pomenem protein coco_roo	Mesorhizobium loti	200	0.11		,
4492	13475179	hypothetical protein mlr6199	MAFF303099	240	0.18	72	1.00E-09
		5'-nucleotidase domain-containing	Micromonospora sp. ATCC				
4538	238061000	protein	39149	616	0.13	35	7.4
		LOW QUALITY PROTEIN: ABC					
4646	302522431	transporter ATP-binding protein	Streptomyces sp. SPB78	564	0.15	30	4.5
		DNA modification					
4866	299133061	methyltransferase-related protein	Afipia sp. 1NLS2	917	0.14	90	3.00E-58
4903	299741957	endoprotease	Coprinopsis cinerea okayama7#130	613	0.07	44	4.5
1 7U3	477/ 4 173/	hypothetical protein	Methylocystis sp. ATCC	013	0.07	44	4.3
4908	323139523	Met49242DRAFT 3957	49242	482	0.08	97	2.00E-14
-		hypothetical protein	Methylocystis sp. ATCC				
4992	323135620	Met49242DRAFT_0090	49242	153	0.23	91	2.00E-11