			DSM 43021				
1074	222120155	mentionation manation C	Methylocystis sp. ATCC	4.4.4	0.60	<i>(</i> 0	1 005 04
1074	323139155	replication protein C hypothetical protein	49242 Labrenzia alexandrii DFL-	444	0.60	68	1.00E-94
1083	254502301	SADFL11_2339	11	993	0.12	83	3.00E-43
1097	85708226	putative DNA methylase	Erythrobacter sp. NAP1	909	0.66	76	0
1120	323139416	protein of unknown function DUF188	Methylocystis sp. ATCC 49242	152	0.34	0.5	9.00E-17
1128	323139410	protein of unknown function	Methylocystis sp. ATCC	132	0.34	85	9.00E-1/
1128	323139416	DUF188	49242	152	0.50	87	8.00E-18
1171	323139522	hypothetical protein Met49242DRAFT 3956	Methylocystis sp. ATCC 49242	444	0.60	91	2.00E-138
1200	299133058	Putative helicase A859L	Afipia sp. 1NLS2	408	0.48	81	1.00E-89
		PREDICTED: hypothetical protein,					
1250	224107413	partial	Taeniopygia guttata Opitutaceae bacterium	369	0.22	33	4.6
1259	225156592	conserved hypothetical protein	TAV2	275	0.17	35	3.5
		succinate dehydrogenase,					
1290	298293273	hydrophobic membrane anchor protein	Starkeya novella DSM 506	136	0.84	54	1.00E-24
1292	194761572	*	Drosophila ananassae	514	0.14	37	4.5
			Rhodopseudomonas				
1302	316934586	hypothetical protein Rpdx1_3258 hypothetical protein	palustris DX-1 Bacteroides capillosus	253	0.27	72	1.00E-18
1310	154495963	BACCAP 00246	ATCC 29799	166	0.23	49	4.5
		_	Methylocystis sp. ATCC				
1324	323137236	DNA gyrase, B subunit	49242	810	0.07	81	1.00E-15
1352	195442410	GK17748	Drosophila willistoni Methylocystis sp. ATCC	421	0.10	45	5.9
1357	323137126	glycosyl transferase group 1	49242	408	0.14	70	2.00E-14
		major facilitator superfamily	Methylocystis sp. ATCC				
1369	323136028	MFS_1	49242	528	0.15	65	1.00E-20
1374	90420316	phosphomethylpyrimidine kinase	Aurantimonas manganoxydans SI85-9A1	317	0.06	75	5.9
1436		hypothetical protein bglu 2p0290	Burkholderia glumae BGR1	476	0.29	36	5.00E-13
1.50	250025510	njpomenom protein ogta_po_so	Pseudomonas syringae pv.	.,,	0.2		0.002 10
1498	330966470	hypothetical protein PSYAC_17830	actinidiae str. M302091	437	0.10	47	0.0009
1615	338820076	hypothetical protein Agau P200245	Agrobacterium tumefaciens	783	0.11	47	6.00E-14
1013	338820070	nypometicai protein Agau_i 200243	Rhodobacter sphaeroides	763	0.11	47	0.00E-14
1691	332560244	Mg chelatase-related protein	WS8N	512	0.11	38	4.5
1734	323137126	glycosyl transferase group 1	Methylocystis sp. ATCC 49242	408	0.24	77	9.00E-39
1/34	323137120	Pseudomurein-binding repeat	47242	400	0.24	//	9.00E-39
1787	299133059	protein	Afipia sp. 1NLS2	686	0.13	99	9.00E-39
1787	299133059	Pseudomurein-binding repeat	Afipia sp. 1NLS2	686	0.09	98	9.00E-25
1/0/	299133039	protein	Methylocystis sp. ATCC	080	0.09	98	9.00E-23
1793	323137126	glycosyl transferase group 1	49242	408	0.08	88	6.00E-08
1793	323137126	glycosyl transferase group 1	Methylocystis sp. ATCC 49242	408	0.08	88	6.00E-08
1/93	323137120	tyrosine-protein phosphatase non-	47242	400	0.08	00	0.00E-08
1836	150378510	receptor type 22	Danio rerio	887	0.05	34	7.6
1856	17232905	hypothetical protein alr8532	Nostoc sp. PCC 7120	304	0.25	48	4.00E-11
			Roseomonas cervicalis				