

## Supporting Information

### The Hunt for 8-Oxoguanine Deaminase

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*Purification of Pa0142.* Pa0142 was cloned into a pET-30b(+) expression vector from Novagen through the use of *NdeI* and *EcoRI* restriction sites. Gene sequences were verified by the Gene Technologies Lab at Texas A&M University. The expression plasmids were inserted into BL21 (DE3) cells by electroporation. The transformation solution was then transferred into LB growth medium for incubation at 37 °C for 30 minutes, which was followed by plating onto LB agar containing 50 µg/mL kanamycin. Single colonies were selected for growth in liquid LB medium. Typically, prior to induction with 0.1 - 1.0 mM IPTG at an  $A_{600\text{ nm}}$  of ~ 0.6, 50 - 100 µM bipyridyl and 1.0 mM ZnCl<sub>2</sub> were added to supplement the growth medium. The cells grew overnight after which they were collected by centrifugation. The cells were then re-suspended and disrupted by sonication in 50 mM Hepes buffer, pH 8.0 and 100 µg/mL of the protease inhibitor phenylmethanesulfonyl fluoride. Insoluble cell debris was removed by centrifugation, after which ~1% w/v protamine sulfate was used to precipitate the nucleic acids. The precipitate was removed by centrifugation and the protein fractionated with ammonium sulfate to 50% of saturation. The precipitated protein was isolated by centrifugation. The protein was then re-suspended in a minimal amount of 20 mM Hepes buffer, pH 8.0, and then passed through a 0.2 µm pore filter prior to loading onto a pre-equilibrated Amersham HiLoad 26/60 Superdex 200 prep grade gel filtration column. The pooled fractions containing enzyme were loaded onto an Amersham 6 mL Resource Q anion exchange column. The column was washed with several column volumes of the same buffer and the protein eluted with a linear gradient buffer containing 1 M NaCl. The appropriate fractions were pooled after analysis with SDS PAGE.

Protein concentrations were determined by absorbance at 280 nm using the sequence based extinction coefficients calculated at [www.scripps.edu/~cdputnam/protcalc.html](http://www.scripps.edu/~cdputnam/protcalc.html). The purified protein migrated as a single band on SDS-PAGE. Amino acid analysis of the first five residues of the enzyme matched those expected from the DNA sequence of the target gene for Pa0142. The protein contained an average of 0.25 and 0.05 equivalents of  $\text{Zn}^{2+}$  and  $\text{Fe}^{2+}$ , respectively, per subunit. Pa0134 and b2883 were purified using the same protocol as the purification of Pa0142.

*Crystallization and Data Collection.* The crystals of the SeMet Pa0142 homologue complexed with  $\text{Zn}^{2+}$  were grown by vapor diffusion at room temperature. The following crystallization conditions were used: the protein solution contained the selenomethionine – substituted Pa0142 homologue (6.2 mg/mL) in 10 mM HEPES, pH 7.5, 150 mM NaCl, 10 mM methionine, and 10% glycerol; the precipitant contained 2.8 M sodium acetate, and 0.05 mM  $\text{ZnCl}_2$ . Crystals appeared in 6 days and exhibited diffraction consistent with the space group  $\text{P3}_221$ , with two molecules of the protein per asymmetric unit.

Prior to data collection, the crystals were transferred to cryoprotectant solutions composed of their mother liquors and 20% glycerol. After incubation for ~15 s, the crystals were flash-cooled in a nitrogen stream. A single-wavelength anomalous dispersion (SAD) data set for a crystal of the SeMet Pa0142 homologue with Zn was collected to 2.2 Å resolution at the NSLS X4A beamline (Brookhaven National Laboratory) on an ADSC CCD detector. Intensities were integrated and scaled with DENZO and SCALEPACK (1). Data collection statistics are given in **Table S1**.

*Structure Determination and Refinement.* The structure of the SeMet-substituted Pa0142 homologue complexed with  $\text{Zn}^{2+}$  was determined by SAD with PHENIX (2). Iterative cycles of automatic model rebuilding with PHENIX, ARP (3), manual rebuilding with TOM (4), and refinement with CNS (5) were performed. The model was refined at 2.2 Å with an  $R_{\text{cryst}}$  of 0.232 and an  $R_{\text{free}}$  of

0.276. The final structure (PDB ID 3HPA) contained two protein molecules, 129 water molecules and two well-defined Zn<sup>2+</sup> ions. Final crystallographic refinement statistics are provided in **Table S1**.

*Docking calculations.* Calculations were performed with DOCK3.5.54 (6-9). The pose of the substrate was calculated based on the docking spheres. These are anchor points for the heavy atoms of the substrate and are generated so that they will fill the protein binding site (6). Spheres are usually derived off of the atom positions of a ligand in the binding site. Since there is no such ligand present in the original structure, default settings for the sphere generation were used and modified manually to achieve more homogenous coverage. After matching each molecule on all possible sphere quartets, each pose is subjected to 25 steps of minimization with the simplex method. The binding affinity is estimated by adding the electrostatic and van der Waals interaction energies and correcting for the desolvation penalty incurred when the ligand is transferred from water into the low-dielectric environment of the protein (10). For efficiency reasons, these energy terms are precalculated and stored on grids.

*High-energy intermediates.* Docking of potential substrates can benefit from the representation of the molecules in their transition state (or high-energy intermediate [HEI]) geometry (11-14). In the case of the reactions catalyzed by the amidohydrolase superfamily, this is the tetrahedral state immediately after the attack of the catalytic water. For every potential substrate, all enantiomers of the tetrahedral intermediate as well as all protonation states of the leaving group are generated, resulting in four HEI variants for every reactable group.

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**Table S1:** Data Collection and Refinement Statistics

	SeMet Pa0142 homolog
<b><i>Data collection</i></b>	
Beamline	NLSL X4A
wavelength (Å)	0.97915
space group	P3 <sub>2</sub> 21
# of molecules in a.u.	2
<b>Unit cell parameters</b>	
a (Å)	83.30
c (Å)	229.12
resolution (Å) <sup>a</sup>	25-2.2 (2.28-2.2)
unique reflections <sup>a</sup>	47567 (4288)
completeness (%) <sup>a</sup>	99.7 ( 97.0)
R <sub>merge</sub> <sup>a</sup>	0.079 (0.246)
Average I/σ <sup>a</sup>	22.5 (4.1)
<b><i>Refinement</i></b>	
resolution	25.0-2.2
R <sub>cryst</sub>	0.232
R <sub>free</sub>	0.276
rmsd for bonds (Å)	0.006
rmsd for angles (°)	1.3
# of protein atoms	6494
# of waters	129
# of ions	2 Zn <sup>2+</sup>
PDB entry	3HPA

<sup>a</sup> Numbers in parentheses indicate values for the highest resolution shell.

**Table S2:** List of proteins predicted to possess 8-oxoguanine deaminase activity.

	Locus tag	GI	Organism
1	PA0142	879447	<i>Pseudomonas aeruginosa</i> PA01
2	PaerPA_01000142	107099133	<i>Pseudomonas aeruginosa</i> PACS2
3	PA2G_04056	6715071	<i>Pseudomonas aeruginosa</i> 2192
4	PACG_03701	6720155	<i>Pseudomonas aeruginosa</i> C3719
5	PA14_01750	4383541	<i>Pseudomonas aeruginosa</i> UCBPP-PA14
6	PSPA7_0219	5356948	<i>Pseudomonas aeruginosa</i> PA7
7	Pmen_3705	5105700	<i>Pseudomonas mendocina</i> ymp
8	PSEEN0675	4088425	<i>Pseudomonas entomophila</i> L48
9	Pf101_0675	3713960	<i>Pseudomonas fluorescens</i> PfO-1
10	PFL_0724	3481313	<i>Pseudomonas fluorescens</i> Pf-5
11	PFLU0669	7819150	<i>Pseudomonas fluorescens</i> SBW25
12	PSPTOT1_3659	213969358	<i>Pseudomonas syringae</i> pv. tomato T1
13	atzB	1182385	<i>Pseudomonas syringae</i> pv. tomato str. DC3000
14	Psyr_0669	3366147	<i>Pseudomonas syringae</i> pv. <i>Syringae</i> B728a
15	Psyrpo1_010100001930	237797581	<i>Pseudomonas syringae</i> pv. <i>oryzae</i> str. 1_6
16	PSPPH_4628	3555934	<i>Pseudomonas syringae</i> pv. <i>phaseolicola</i> 1448A
17	atzB	5096040	<i>Pseudomonas stutzeri</i> A1501
18	Arth_3425	4444155	<i>Arthrobacter</i> sp. FB24

19	AAur_3399	4639368	<i>Arthrobacter aurescens</i> TC1
20	Achl_3205	7294686	<i>Arthrobacter chloophenolicus</i> A6
21	ACIAD0761	2879221	<i>Acinetobacter sp.</i> ADP1
22	BlinB01003114	62423337	<i>Brevibacterium linens</i> BL2
23	VSAK1_24940	149188732	<i>Vibrio shilonii</i> AK1
24	V12B01_19391	84386830	<i>Vibrio splendid</i> 12B01
25	VSWAT3_19088	148978109	<i>Vibrionales bacterium</i> SWAT-3
26	P3TCK_01255	90413684	<i>Photobacterium profundum</i> 3TCK
27	PBPRA2267	3122820	<i>Photobacterium profundum</i> SS9
28	KT99_04812	163751045	<i>Shewanella benthica</i> KT99
29	PE36_19015	149908977	<i>Moritella sp.</i> PE36
30	SI859A1_03023	90420336	<i>Aurantimonas manganoxydans</i> SI85-9A1
31	Pcryo_1786	4033973	<i>Psychrobacter cryohalolentis</i> K5
32	Mnod_1111	7304423	<i>Methylobacterium nodulans</i> ORS 2060
33	MELB17_16823	126666105	<i>Marinobacter sp.</i> ELB17
34	Mext_1697	5832952	<i>Methylobacterium extorquens</i> PA1
35	Mchl_2016	7118716	<i>Methylobacterium chloromethanicum</i> CM4
36	BRADO1738	5118449	<i>Bradyrhizobium sp.</i> ORS278
37	Mchl_3248	7117587	<i>Methylobacterium chloromethanicum</i> CM4
38	Mpop_1121	6313798	<i>Methylobacterium populi</i> BJ001
39	M446_2144	6130066	<i>Methylobacterium sp.</i> 4-46
40	FP2506_15334	114705851	<i>Fulvimarina pelagi</i> HTCC2506
41	B116159	1048904	<i>Bradyrhizobium japonicum</i> USDA 110



42	MED121_14459	87118237	<i>Marinomonas sp.</i> MED121
43	MDG893_15717	149375925	<i>Marinobacter algicola</i> DG893
44	BBta 2050	5153053	<i>Brandyrhizobium sp.</i> BTAi1
45	Mrad2831_4071	6140129	<i>Methylobacterium radiotolerans</i> JCM 2831
46	HCH_01106	3841406	<i>Hahella chejuensis</i> KCTC 2396
47	Mext_3024	5835455	<i>Methylobacterium extorquens</i> PA1
48	CJA_0540	6415371	<i>Cellvibrio japonicus</i> Uedal07
49	Patl_2224	4172376	<i>Pseudoalteromonas atlantica</i> T6c
50	StermDRAFT_06890	229881741	<i>Sebaldella termitidis</i> ATCC 33386
51	Francci3_0845	3904327	<i>Frankia sp.</i> Cc13
52	Bphy_1293	6242785	<i>Burkholderia phymatum</i> STM815
53	Bxe_A1936	4003154	<i>Burkholderia xenovorans</i> LB400
54	Bphyt_2323	6281242	<i>Burkholderia phytofirmans</i> PsJN
55	BgramDRAFT_5200	170695243	<i>Burkholderia graminis</i> C4D1M
56	SADFL11_1395	7514273	<i>Labrenzia alexandrii</i> DFL-11
57	NOR53_2032	7635455	<i>Gamma proteobacterium</i> NOR5-3
58	Bcep18194_A5267	3750479	<i>Burkholderia sp.</i> 383
59	BuboB_010100016293	167586903	<i>Burkholderia ubonensis</i> Bu
60	BTH_I2073	3848116	<i>Burkholderia thailandensis</i> E264
61*	NYSGXRC-9236e	44264246	Env. Samp. of Sargasso sea
62	BDAG_01340	6703425	<i>Burkholderia dolosa</i> AUO158
63	BthaT_010100025531	167581531	<i>Burkholderia thailandensis</i> TXDOH
64	Bpse38_010100010869	167836982	<i>Burkholderia thailandensis</i> MSMB43

65	BH160DRAFT_3765	209518669	<i>Burkholderia</i> sp. H160
66	BCPG_02756	6709226	<i>Burkholderia cenocepacia</i> PC184
67	BCAL2029	6932197	<i>Burkholderia cenocepacia</i> J2315
68	Bcenmc03 1980	6123644	<i>Burkholderia cenocepacia</i> MC0-3
69	Bglu_1g13210	7908425	<i>Burkholderia glumae</i> BGR1
70	KoleDRAFT_1086	213014337	<i>Thermotogales bacterium</i> TBF 19.5.1
71	Bcen_6122	4097155	<i>Burkholderia cenocepacia</i> AU 1054
72	KT71_15846	88703340	<i>Congregibacter litoralis</i> KT71
73	atzB	3688614	<i>Burkholderia pseudomallei</i> 1710b
74	Bpse112_010100013174	167911441	<i>Burkholderia pseudomallei</i> 112
75	GBP346_A2491	7888169	<i>Burkholderia pseudomallei</i> MSHR346
76	Bpse17_030300030822	161374040	<i>Burkholderia pseudomallei</i> 1710a
78	BPSL2112	3092957	<i>Burkholderia pseudomallei</i> K96243
79	BURPS1106A_2422	4901051	<i>Burkholderia pseudomallei</i> 1106a
80	PputW619_3055	6112005	<i>Pseudomonas putida</i> W619
81	Bpse7_010100013763	167894812	<i>Burkholderia pseudomallei</i> 7894
82	BpseN_010100013161	167903203	<i>Burkholderia pseudomallei</i> NCTC 13177
83	Bamb_1943	4310181	<i>Burkholderia ambifaria</i> AMMD
84	Bpse110_020300007234	161355267	<i>Burkholderia pseudomallei</i> 1106b
85	pC2C203U28_p100	7636495	<i>Clostridium botulinum</i>
86	BamIOP4010DRAFT_5246	170702284	<i>Burkholderia ambifaria</i> IOP40-10
87	BamMEX5DRAFT_6744	171322619	<i>Burkholderia ambifaria</i> MEX-5
88	CSBG_01722	7864561	<i>Clostridium</i> sp. 7_2_43FAA

89	BamMC406_1870	6178204	<i>Burkholderia ambifaria</i> MC40-6
90	BURMUCGD1_1300	221215518	<i>Burkholderia multivorans</i> CGD1
91	Bcep1808_1882	4953605	<i>Burkholderia vietnamiensis</i> G4
92	PputGB1_3262	5871047	<i>Pseudomonas putida</i> GB-1
93	PP_2584	1045965	<i>Pseudomonas putida</i> KT2440
94	NT01EI_2443	7959175	<i>Edwardsiella ictaluri</i> 93-146
95	Pput_3132	5195102	<i>Pseudomonas putida</i> F1
96	Daci_1591	5747148	<i>Delftia acidovorans</i> SPH-1
97	PB2503_11584	84704671	<i>Parvularcula bermudensis</i> HTCC2503
98	BURMUCGD2M_1761	221198260	<i>Burkholderia multivorans</i> CGD2M
99	Noca_1626	4600005	<i>Nocardioides</i> sp. JS614
100	Bmul_1313	5764920	<i>Burkholderia multivorans</i> ATCC 17616
101	mma_0509	5352721	<i>Janthinobacterium</i> Sp. Marseille
102	Mpop_1247	6313306	<i>Methylobacterium populi</i> BJ001
103	CLL_A0628	6293100	<i>Clostridium botulinum</i> B str. Eklund 17B
104	Mchl_2080	7115864	<i>Methylobacterium chloromethanicum</i> CM4
105	BoklC_010100010767	167570319	<i>Burkholderia oklahomensis</i> C6786
106	Pden_3916	4582467	<i>Paracoccus denitrificans</i> PD1222
107	Xaut_2741	5424708	<i>Xanthobactor autotrophicus</i> Py2
108	CLH_0589	6317741	<i>Clostridium botulinum</i> E3 str. Alaska E43
109	Rxyl_2838	4117689	<i>Rubrobacter xylanophilus</i> DSM 9941
110	Franean1_5674	5674001	<i>Frankia</i> sp. EAN1pec
111	Mrad2831_6206	6142345	<i>Methylobacterium radiotolerans</i> JCM2831

112	BACCAP_04381	154500708	<i>Bacteroides capillosus</i> ATCC 29799
113	Tmel_1728	5296651	<i>Thermosipho melanesiensis</i> BI429
114	Cbei_2067	5293279	<i>Clostridium beijerinckii</i> NCIMB 8052
115	FRAAL1474	4235777	<i>Frankia alni</i> ACN14a
116	h16_A1363	4249475	<i>Ralstonia eutropha</i> H16
117	Pmob_1736	5757974	<i>Petrotoga mobilis</i> SJ95
118	RALTA_A1283	6453012	<i>Cupriavidus taiwanensis</i>
119	RCCS2_14544	126735104	<i>Roseobacter</i> sp. CCS2
120	Mpe_A0782	4784170	<i>Methylibium petroleiphilum</i> PM1
121	CtesDRAFT_PD0564	221065227	<i>Comamonas testosteroni</i> KF-1
122	Lcho_1140	6163813	<i>Leptothrix cholodnii</i> SP-6
123	RB2150_16594	126727973	<i>Rhodobacterales bacterium</i> HTCC2150
124	Cbac1_010100016929	224388129	<i>Clostridiales bacterium</i> 1_7_47_FAA
125	R2601_20986	114762995	<i>Roseovarius</i> sp. HTCC2601
126	THA_25	7070815	<i>Thermosipho africanus</i> TCF52B
127	S7335_3628	7570418	<i>Synechococcus</i> sp. PCC 7335
128	HneapDRAFT_0499	225303291	<i>Halothiobacillus neapolitanus</i> c2
129	VDG1235_1698	7583649	<i>Verrucomicrobiae bacterium</i> DG1235
130	ANACOL_00024	167768708	<i>Anaerotruncus colihominis</i> DSM 17241
131	CLOSTASPAR_03878	225390128	<i>Clostridium asparagiforme</i> DSM 15981
132	CLOBOL_06600	160941704	<i>Clostridium bolteae</i> ATCC BAA-613
133	Reut_A1294	3611928	<i>Ralstonia eutropha</i> JMP134
134	Rpic_2259	6289356	<i>Ralstonia pickettii</i> 12J

135	VspiD_010100021095	171913717	<i>Verrucomicrobi spinosum</i> DSM 4136
136	OIH45_10143	163745939	<i>Oceanibulbus indolifex</i> HEL-45
137	MAB_2927c	5965434	<i>Mycobacterium abscessus</i>
138	Rpic12DDRAFT_0675	153888567	<i>Ralstonia picketti</i> 12D
139	Jann_1234	3933679	<i>Jannaschia sp.</i> CCS1
140	GobsDRAFT_06540	227405252	<i>Geodermatophilus obscurus</i> DSM 43160
141	atzB	7593298	<i>Roseobacter sp.</i> GAI101
142	SIAM614_20905	118591899	<i>Stappia aggregata</i> IAM 12614
143	TM1040_1906	4077403	<i>Silicibacter sp.</i> TM1040
144	BHWA1_02619	7667707	<i>Brachyspira hyodysenteriae</i> WA1
145	RB2654_08457	84686221	<i>Rhodobacterales bacterium</i> HTCC2654
146	BmurDRAFT_00390	227999304	<i>Brachyspira murdochii</i> DSM 12563
147	RR11_659	7624076	<i>Ruegeria sp.</i> R11
148	MSMEG_1297	4531257	<i>Mycobacterium smegmatis str.</i> MC2 155
149	OG2516_00245	89069700	<i>Oceanicola granulosus</i> HTCC2516
150	RRSL_01271	83748887	<i>Ralstonia solanacearum</i> UW551
151	RSMK01192	6954169	<i>Ralstonia solanacearum</i> Molk2
152	RB2083_1302	7579673	<i>Rhodobacterales bacterium</i> HTCC2083
153	SSCG_02005	6838461	<i>Streptomyces clavuligerus</i>
154	Magn03006515	46203056	<i>Magnetospirillum magnetotacticum</i> MS-1
155	RSK20926_22599	126739238	<i>Roseobacter sp.</i> SK209-2-6
156	RKLH11_2317	7627427	<i>Rhodobacteraceae bacterium</i> KLH11
157	atzB	4941115	<i>Saccharopolyspora erythraea</i> NRRL 2338

158	Dshi_2773	5713672	<i>Dinoroseobacter shibae</i> DFL 12
159	SnasDRAFT_44920	229865225	<i>Stackebrandtia nassauensis</i> DSM 44728
160	Bpse9_010100014316	167816318	<i>Burkholderia pseudomallei</i> 91
161	Gdia_3513	6976965	<i>Gluconacetobacter diazotrophicus</i> PA1 5
162	guaD	5789984	<i>Gluconacetobacter diazotrophicus</i> PA1 5
163	RGBS107_18053	163737460	<i>Phaeobacter gallaeciensis</i> BS107
164	OA238_3529	7523411	<i>Octadecabacter antarcticus</i> 238
165	RG210_13486	163740856	<i>Phaeobacter gallaeciensis</i> 2.10
166	RHOER0001_4250	229489548	<i>Rhodococcus erythropolis</i> SK121
167	EE36_11673	83944527	<i>Sulfitobacter</i> sp. EE-36
168	OA307_342	7603653	<i>Octadecabacter antarcticus</i> 307
169	SPO2957	3194390	<i>Silicibacter pomeroyi</i> DSS-3
170	RER_21130	7714318	<i>Rhodococcus erythropolis</i> PR4
171	atzB	1220960	<i>Ralstonia solanacearum</i> GMI1000
172	CaciDRAFT_38210	229248212	<i>Catenulispora acidiphila</i> DSM 44928
173	MED193_21601	86140035	<i>Roseobacter</i> sp. MED193
174	NAS141_16899	83955348	<i>Sulfitobacter</i> sp. NAS-14.1
175	SGR_1307	6209440	<i>Streptomyces griseus</i> subsp. <i>Griseus</i> NBRC 13350
176	atzB	4222059	<i>Rhodococcus</i> sp. RHA1
177	atzB	4196714	<i>Roseobacter denitrificans</i> OCh 114
178	RLO149_17318	163733433	<i>Roseobacter litoralis</i> Och 149
179	NamuDRAFT_10270	229222217	<i>Nakamurella multipartita</i> DSM 44233

180	Rmet_1186	4037987	<i>Ralstonia metallidurans</i> CH34
181	ROP_44280	7742160	<i>Rhodococcus opacus</i> B4
182	SSDG_03874	6842290	<i>Streptomyces pristinaespiralis</i> ATCC 25486
183	SCO6213	1101654	<i>Streptomyces coelicolor</i> A3 (2)
184	SAV_2017	1213459	<i>Streptomyces avermitilis</i> MA-4680
185	GbroDRAFT_06290	227400018	<i>Gordonia bronchialis</i> DSM 43247
186	SSEG_02091	6852719	<i>Streptomyces sviveus</i> ATCC 29083
187	Bpse14_010100013624	167739105	<i>Burkholderia pseudomallei</i> 14
188	RB4I_2538	7619385	<i>Rhodobacterales bacterium</i> Y4I
189	SSBG_04646	6861992	<i>Streptomyces</i> sp. SPB74
190	OB2597_10014	84500269	<i>Oceanicola batsensis</i> HTCC2597
191	SrosDRAFT_80950	229857618	<i>Streptosporangium roseum</i> DSM 43021
192	Nfa52410	3110729	<i>Nocardia farcinica</i> IFM 10152
193	SSAG_01926	6859830	<i>Streptomyces</i> sp. Mg1
194	OM2255_10461	114769985	<i>Rhodobacterales bacterium</i> HTCC2255
195	MCAG_05318	238064352	<i>Micromonospora</i> sp. ATCC 39149
196	MMAR_2844	6227111	<i>Mycobacterium marinum</i> M
197	NdasDRAFT_4742	229209177	<i>Nocardiopsis dassonvillei</i> subsp. <i>dassonvillei</i> DSM 43111
198	MUL_2914	4553343	<i>Mycobacterium ulcerans</i> Agy99
199			
200	Krad_4281	5335917	<i>Kineococcus radiotolerans</i> SRA30216
201	BpseD_010100013846	167720093	<i>Burkholderia pseudomallei</i> DM98
202	Noca_0677	4599542	<i>Nocardioides</i> sp. JS614

203	BokIE_010100011296	167563133	<i>Burkholderia oklahomensis</i> EO147
204	R2601_07911	114767058	<i>Roseovarius</i> sp. HTCC2601
205	RHE_PC00089	3895310	<i>Rhizobium etli</i> CFN 42
206	pRL100336	116254776	<i>Rhizobium leguminosarum</i> bv. <i>viciae</i> 3841
207	HPDFL43_14672	163758676	<i>Hoeflea phototrophica</i> DFL-43
208	smzB	111183223	<i>Herbaspirillum</i> sp. B601
209	atzB	55416015	<i>beta proteobacterium</i> CDB21
210	Rleg2_4464	6977558	<i>Rhizobium leguminosarum</i> bv. <i>Trifolii</i> WSM2304
211	Magn03006970	23012454	<i>Magnetospirillum magnetotacticum</i> MS-1
212	Cbac1_010100004932	224385745	<i>Clostridiales bacterium</i> 1_7_47_FAA
213	CLOBOL_05339	160940449	<i>Clostridium bolteae</i> ATCC BAA-613
214	trzN	156257442	<i>Arthrobacter</i> sp. AD26
215	trzN	17432321	<i>Nocardioides</i> sp. C190
216	AtzB	117583158	<i>Arthrobacter</i> sp. AD25
217	AAur_pTC10087	119952514	<i>Arthrobacter aurescens</i> TC1