

SUPPLEMENTARY INFORMATION

A Fosmid Cloning Strategy for Detecting the Widest Possible Spectrum of Microbes from the International Space Station Drinking Water System

**Sangdun Choi^{1,2*}, Mi Sook Chang², Tara Stuecker³, Christine Chung²,
David A. Newcombe³, Kasthuri Venkateswaran^{3**}**

¹Department of Molecular Science and Technology, Ajou University, Suwon 443-749, Korea,

²Division of Biology, California Institute of Technology, Pasadena, CA 91125, USA,

³Jet Propulsion Laboratory, California Institute of Technology, Pasadena, CA 91109, USA

Supplementary Table 1. Representative BLAST search results from GenBank for the Prebiocide, Tank A, and control sample clones

Clone ID	Input length (nt)	Nearest species	Protein	Identity (%)	Amino acid length	Protein accession no.
Prebio_2_E20	456	<i>Burkholderia fungorum</i> LB400	Thiamine pyrophosphate-requiring enzymes	99	117	gi 48784310 ref ZP_00280676.1
Prebio_1_H17	398	<i>Bradyrhizobium</i> sp. BTAi1	Putative recombinase	98	131	gi 78699807 ref ZP_00864293.1
Prebio_2_F7	455	<i>Burkholderia fungorum</i> LB400	Transaldolase	98	95	gi 48784330 ref ZP_00280696.1
Prebio_2_F12	352	<i>Burkholderia fungorum</i> LB400	NADH : flavin oxidoreductases, Old Yellow Enzyme family	97	117	gi 48786168 ref ZP_00282377.1
Prebio_2_E6	447	<i>Burkholderia fungorum</i> LB400	Site-specific recombinase XerD	97	136	gi 48784965 ref ZP_00281270.1
Prebio_1_H15	498	<i>Burkholderia fungorum</i> LB400	Membrane carboxypeptidase	96	144	gi 48781092 ref ZP_00277746.1
Prebio_2_D2	449	<i>Burkholderia fungorum</i> LB400	Rieske Fe-S protein	96	107	gi 48781642 ref ZP_00278233.1
Prebio_2_I1	502	<i>Burkholderia fungorum</i> LB400	Flagellar motor switch protein	95	166	gi 48782453 ref ZP_00278982.1
Prebio_1_D6	448	<i>Burkholderia fungorum</i> LB400	Permeases of the major facilitator superfamily	95	135	gi 48784831 ref ZP_00281136.1
Prebio_2_M9	400	<i>Burkholderia fungorum</i> LB400	Uncharacterized conserved protein	95	129	gi 48783618 ref ZP_00280070.1
Prebio_2_D3	453	<i>Burkholderia fungorum</i> LB400	Cation/multidrug efflux pump	94	150	gi 48783521 ref ZP_00279973.1
Prebio_2_I21	400	<i>Burkholderia fungorum</i> LB400	Cobalamin biosynthesis protein CobN and related Mg-chelataes	93	133	gi 48781993 ref ZP_00278566.1
Prebio_1_D24	400	<i>Burkholderia</i> sp. 383	ABC nitrate/sulfonate/bicarbonate family transporter	93	133	gi 78063456 ref YP_373364.1
Prebio_2_E16	452	<i>Erythrobacter</i> sp. NAP1	Hypothetical protein NAP1_09092	91	123	gi 85710554 ref ZP_01041618.1
Prebio_2_C13	454	<i>Ralstonia solanacearum</i>	ISRSO6-TRANSPOSASE ORFB PROTEIN	90	113	gi 17431425 emb CAD18104.1
Prebio_11_I24	399	<i>Burkholderia fungorum</i> LB400	Flagellar hook-associated protein	89	128	gi 48782466 ref ZP_00278995.1
Prebio_11_G7	397	<i>Burkholderia</i> sp. 383	Two component heavy metal response transcriptional regulator	89	89	gi 77971162 gb ABB12541.1
Prebio_11_I16	298	<i>Bradyrhizobium</i> sp. BTAi1	Low-affinity inorganic phosphate transporter	87	99	gi 27351280 dbj BAC48287.1
Prebio_2_C10	403	<i>Burkholderia ambifaria</i> AMMD	Cation efflux protein	87	120	gi 74015476 ref ZP_00686104.1
Prebio_2_E13	452	<i>Burkholderia fungorum</i> LB400	Cobalamin biosynthesis protein CobN and related Mg-chelataes	86	150	gi 48781993 ref ZP_00278566.1
Prebio_2_F3	517	<i>Burkholderia vietnamiensis</i> G4	Integrase, catalytic region	85	107	gi 67546049 ref ZP_00423966.1
Prebio_1_H21	350	<i>Mesorhizobium loti</i> MAFF303099	Hypothetical protein mll1065	85	116	gi 14021912 dbj BAB48523.1
Prebio_2_I10	251	<i>Pseudomonas putida</i> KT2440	Hypothetical protein PP2485	85	82	gi 26989208 ref NP_744633.1
Prebio_2_M8	450	<i>Burkholderia</i> sp. 383	TonB-dependent receptor	83	149	gi 77971332 gb ABB12711.1
Prebio_11_G11	298	<i>Burkholderia cenocepacia</i> PC184	Transcriptional regulator	82	92	gi 84353630 ref ZP_00978556.1

Supplementary Table 1. Continued

Clone ID	Input length (nt)	Nearest species	Protein	Identity (%)	Amino acid length	Protein accession no.
Prebio_2_D9	447	<i>Xanthomonas campestris</i> pv. <i>campestris</i> str.	Fumarate hydratase	80	142	gi 66574381 gb AA49791.1
TankA_2_B14	455	<i>Burkholderia fungorum</i> LB400	Predicted permeases	100	96	gi 48786728 ref ZP_00282862.1
TankA_2_E20	503	<i>Ralstonia metallidurans</i> CH34	Transposase Tn3	100	86	gi 68559260 ref ZP_00598594.1
TankA_2_G17	353	<i>Propionibacterium acnes</i> KPA171202	NADH pyrophosphatase	99	101	gi 50840400 gb AAT83067.1
TankA_2_H8	502	<i>Burkholderia fungorum</i> LB400	COG1048: aconitase A	98	130	gi 48787197 ref ZP_00283279.1
TankA_2_P6	406	<i>Burkholderia fungorum</i> LB400	ABC-type proline/glycine betaine transport systems	97	134	gi 48782632 ref ZP_00279138.1
TankA_2_H20	402	<i>Burkholderia fungorum</i> LB400	ABC-type sugar transport system, periplasmic component	96	133	gi 48783705 ref ZP_00280157.1
TankA_2_G9	455	<i>Burkholderia fungorum</i> LB400	DNA-directed RNA polymerase specialized sigma subunit	96	143	gi 48786500 ref ZP_00282634.1
TankA_6_M19	349	<i>Burkholderia fungorum</i> LB400	Hypothetical protein Bcep02005255	95	116	gi 48783492 ref ZP_00279944.1
TankA_2_B16	506	<i>Burkholderia fungorum</i> LB400	Predicted amino acid aldolase or racemase	95	168	gi 48786561 ref ZP_00282695.1
TankA_2_A21	500	<i>Burkholderia fungorum</i> LB400	Response regulator	95	138	gi 48787830 ref ZP_00283809.1
TankA_1_L7	499	<i>Burkholderia fungorum</i> LB400	Transcriptional regulator containing an amidase domain	94	137	gi 48782642 ref ZP_00279148.1
TankA_1_F2	500	<i>Burkholderia fungorum</i> LB400	Cytochrome c553	93	107	gi 48784325 ref ZP_00280691.1
TankA_1_E17	259	<i>Burkholderia fungorum</i> LB400	Predicted membrane protein	92	85	gi 48786764 ref ZP_00282898.1
TankA_2_P8	503	<i>Burkholderia fungorum</i> LB400	ATP-dependent Zn proteases	91	145	gi 48787183 ref ZP_00283265.1
TankA_2_P10	504	<i>Burkholderia fungorum</i> LB400	Uncharacterized protein SCO1/SenC/PrrC	91	167	gi 48788110 ref ZP_00284089.1
TankA_2_G7	505	<i>Burkholderia fungorum</i> LB400	ABC-type Fe3+ transport system, periplasmic component	90	168	gi 48786422 ref ZP_00282556.1
TankA_2_L3	456	<i>Burkholderia fungorum</i> LB400	Predicted dehydrogenases and related proteins	90	152	gi 48788026 ref ZP_00284005.1
TankA_2_E10	502	<i>Burkholderia fungorum</i> LB400	Rad3-related DNA helicases	90	141	gi 48785794 ref ZP_00282003.1
TankA_1_L11	249	<i>Ralstonia eutropha</i> JMP134	Regulatory protein GntR, HTH : GntR, C-terminal	90	82	gi 72119546 gb AAZ61809.1
TankA_2_F20	556	<i>Burkholderia fungorum</i> LB400	ABC-type phosphate transport system, periplasmic component	88	184	gi 48788085 ref ZP_00284064.1
TankA_6_H10	300	<i>Burkholderia fungorum</i> LB400	Glycine cleavage system protein P	87	100	gi 48781419 ref ZP_00278041.1
TankA_1_F10	297	<i>Burkholderia fungorum</i> LB400	Cyclopropane fatty acid synthase and related methyltransferases	86	98	gi 48784437 ref ZP_00280803.1
TankA_2_H6	503	<i>Burkholderia fungorum</i> LB400	Hypothetical protein Bcep02004041	85	113	gi 48784957 ref ZP_00281262.1

Supplementary Table 1. Continued

Clone ID	Input length (nt)	Nearest species	Protein	Identity (%)	Amino acid length	Protein accession no.
TankA_2_I15	502	<i>Brucella suis</i> 16M	Transcriptional regulatory protein OmpR, putative	83	123	gi 23502389 ref NP_698516.1
TankA_2_O20	451	<i>Burkholderia fungorum</i> LB400	ABC-type phosphate transport system, periplasmic component	82	82	gi 48788085 ref ZP_00284064.1
TankA_2_C11	517	<i>Agrobacterium tumefaciens</i> str. C58	ABC transporter, nucleotide binding/ATPase protein [sugar]	80	169	gi 17743360 gb AAL45637.1
TankA_2_A17	457	<i>Mycobacterium avium</i> subsp.	EchA10	80	89	gi 41408495 ref NP_961331.1
Control_9_P23	448	<i>Halomonas</i> sp. C6	Transposase	100	149	gi 14532243 gb AAK66553.1
Control_2_D10	299	<i>Propionibacterium acnes</i> KPA171202	ABC transporter, nucleotide binding/ATPase protein	100	89	gi 50839747 gb AAT82414.1
Control_9_P13	500	<i>Burkholderia fungorum</i> LB400	Thiamine pyrophosphate-requiring enzymes	98	166	gi 48781448 ref ZP_00278056.1
Control_1_C22	298	<i>Burkholderia vietnamiensis</i> G4	Transposase IS66	98	99	gi 67549058 ref ZP_00426933.1
Control_9_N2	448	<i>Burkholderia fungorum</i> LB400	Molecular chaperone	97	148	gi 48786660 ref ZP_00282794.1
Control_2_B12	353	<i>Burkholderia fungorum</i> LB400	Trypsin-like serine proteases, typically periplasmic	97	117	gi 48781640 ref ZP_00278231.1
Control_9_P3	352	<i>Burkholderia fungorum</i> LB400	Thioredoxin reductase	94	115	gi 48787275 ref ZP_00283357.1
Control_9_N6	398	<i>Burkholderia fungorum</i> LB	Permeases of the major facilitator superfamily	93	132	gi 48787160 ref ZP_00283242.1
Control_2_H4	455	<i>Burkholderia fungorum</i> LB400	Glycosyltransferases involved in cell wall biogenesis	92	132	gi 48782690 ref ZP_00279196.1
Control_2_G17	452	<i>Ralstonia eutropha</i> JMP134	Protein of unknown function DUF796	92	116	gi 72122421 gb AAZ64607.1
Control_2_G21	450	<i>Burkholderia fungorum</i> LB400	ABC-type Mn/Zn transport systems, ATPase component	91	131	gi 48784999 ref ZP_00281304.1
Control_1_O9	448	<i>Burkholderia fungorum</i> LB400	Transposase and inactivated derivatives, IS30 family	91	148	gi 48782710 ref ZP_00279216.1
Control_2_C9	505	<i>Ralstonia metallidurans</i> CH34	Phage integrase : Phage integrase, N-terminal SAM-like	91	167	gi 68555939 ref ZP_00595283.1
Control_2_G23	304	<i>Burkholderia fungorum</i> LB400	ABC-type sugar transport systems, permease components	86	100	gi 48782725 ref ZP_00279231.1
Control_2_G5	404	<i>Burkholderia fungorum</i> LB400	Predicted esterase	85	128	gi 48782042 ref ZP_00278615.1
Control_9_N16	349	<i>Burkholderia</i> sp. 383	Heavy metal sensor signal transduction histidine kinase	84	115	gi 78063616 ref YP_373524.1
Control_1_A1	399	<i>Burkholderia fungorum</i> LB400	AraC-type DNA-binding domain-containing proteins	83	132	gi 48786277 ref ZP_00282411.1
Control_1_O13	399	<i>Burkholderia dolosa</i> AUO	3-Isopropylmalate dehydratase large subunit	82	129	gi 84359323 ref ZP_00984071.1
Control_2_A19	454	<i>Mycobacterium avium</i> subsp.	GltD	82	150	gi 41406271 ref NP_959107.1
Control_2_E13	447	<i>Burkholderia pseudomallei</i> 1106a	Multidrug resistance efflux pump	81	94	gi 82530542 ref ZP_00889772.1
Control_1_O23	448	<i>Bacillus subtilis</i> subsp. <i>subtilis</i> str. 168	2-Methylcitrate dehydratase	80	147	gi 16079469 ref NP_390293.1