Testing the Hypothesis that the Nylonase NylB Protein
Arose de novo via a Frameshift Mutation

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Supplementary Table S1
List of organisms with NylB from uniprot, and conserved domains of NylBs
with sample screen captures from NIH CDD and UNIPROT websites at the bottom

NOTES:

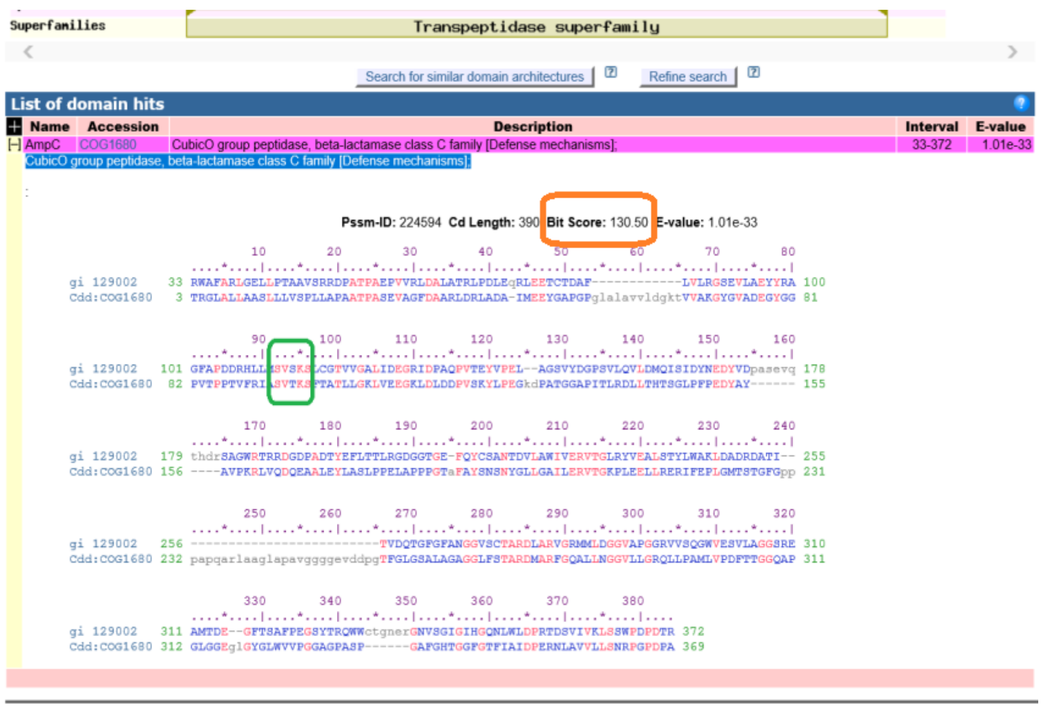
COG1680 = CubicO group peptidase, **beta-lactamase** class C family [Defense mechanisms];
pfam00144 = **Beta-lactamase**; This family appears to be distantly related to pfam00905 and PF00768 ...
n/a = not applicable because the data was embargoed pending publication

no. avail. cdds	173	Average	
count nylbs	201	134.66	

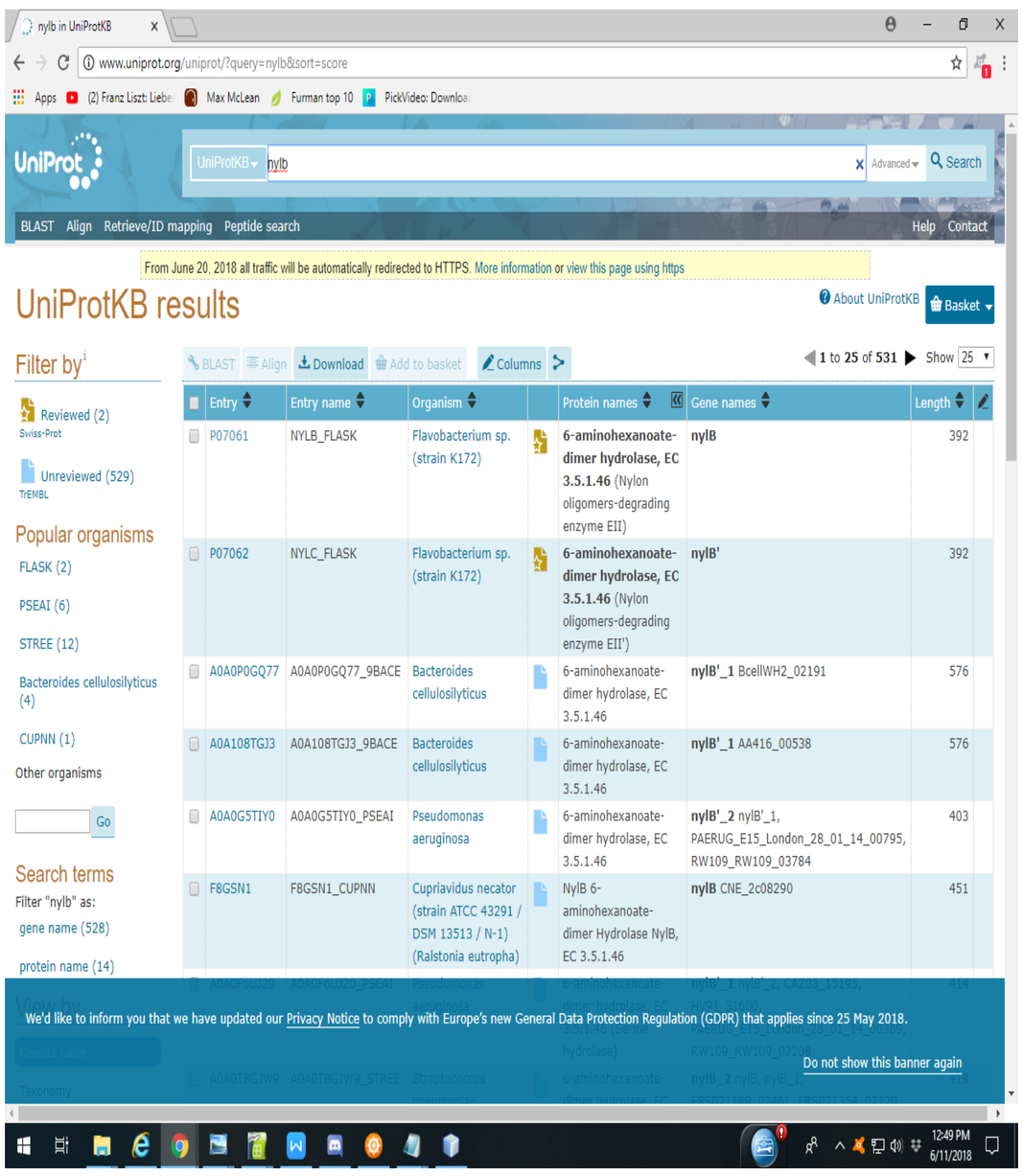
UNIPROT ID	Genbank ID	Conserved Domain Data Available	Primary Conserved Doma ACCESSION ID	Primary Conserved Domai Bit score	Secondary Conserved Domain ACCESSION ID	Secondary Conserved Domain Bit score	ORGANISM
A0A1F2PJC9	OFV71450.1	1	COG1680	153.61			Acetobacterium wieringae
A0A0M7D8K9	CUI49959.1	1	COG1680	154.00			Achromobacter sp.
A0A1G5IJL5	SCY75618.1	1	COG1680	175.18			Acinetobacter baumannii
A0A1V5IP05	removed	0	n/a				Actinobacteria bacterium ADurb.BinA094
Q14TA0	BAE97621.1	1	COG1680	129.73			Agromyces sp. KY5R
A0A164DTT4	KZE94724.1	1	COG1680	129.73			Agromyces sp. NDB4Y10
A0A061QAK6	GAK32671.1	1	COG1680	116.63			alpha proteobacterium Q-1
A0A1V6FWC3	removed	0	n/a				Alphaproteobacteria bacterium ADurb.Bin100
A0A1V5FSP3	removed	0	n/a				Alphaproteobacteria bacterium ADurb.BinA280
A0A0F7KSK3	AKH43388.1	1	COG1680	144.37			Altererythrobacter atlanticus
A0A1B2A9T7	ANY18919.1	1	COG1680	146.68			Altererythrobacter dongtanensis
A0A1C7D5F0	ANU06694.1	1	COG1680	137.43			Altererythrobacter namhicola
A0A0N0XJM8	KPC53432.1	1	COG1680	140.90			Amantichitinum ursilacus
A0A178X0M9	OAP24026.1	1	COG1680	114.71			Amycolatopsis sp. M39
A0A1S1V4U0	OHW61706.1	1	COG1680	138.59			Andreesenia angusta
A0A1B5ZRZ2	GAU57986.1	1	COG1680	143.98			Arenibacter sp. C-21
J7LU22	AFR30965.1	1	COG1680	128.57			Arthrobacter sp. Rue61a
A0A0F7RGC6	BAR75977.1	1	COG1680	137.43			Bacillus anthracis
A0A1Y6B3E8	PDR93506.1	1	COG1680	115.48			Bacillus cereus
A0A0A0WQB8	AIW84412.1	1	COG1680	132.43			Bacillus mycoides
A0A0K6MLC5	CUB53012.1	1	COG1680	136.28			Bacillus subtilis
A0A1B1L838	ANS48888.1	1	COG1680	133.97			Bacillus thuringiensis
A0A1C9BVS0	AOM11896.1	1	COG1680	136.66			Bacillus thuringiensis Bt18247
A0A1V5K7C0	removed	0	n/a				bacterium ADurb.Bin478
A0A0A1P7J7	CEJ11575.1	1	COG1680	154.38			bacterium YEK0313
A0A180EZ91	OAV65418.1	1	COG1680	135.51			Bacteroidales bacterium Barb4
A0A120A2Y7	KWR55989.1	1	COG1680	141.67			Bacteroides stercoris
A0A174H7V0	CUO69517.1	1	COG1680	150.92			Bacteroides uniformis
A0A1V6JEF7	removed	0	n/a				Bacteroidetes bacterium ADurb.Bin008
A0A1V6IDS0	removed	0	n/a				Bacteroidetes bacterium ADurb.Bin035
A0A1V6HGC1	removed	0	n/a				Bacteroidetes bacterium ADurb.Bin041
A0A1V6CTM4	removed	0	n/a				Bacteroidetes bacterium ADurb.Bin123
A0A1V6BDD1	removed	0	n/a				Bacteroidetes bacterium ADurb.Bin141
A0A1V6B290	removed	0	n/a				Bacteroidetes bacterium ADurb.Bin145
A0A1V5JE97	removed	0	n/a				Bacteroidetes bacterium ADurb.BinA012
A0A1V5H839	removed	0	n/a				Bacteroidetes bacterium ADurb.BinA174
A0A1V5QXL4	removed	0	n/a				Betaproteobacteria bacterium ADurb.Bin341
A0A173YDV8	CUN61720.1	1	COG1680	149.38			Blautia obeum
A0A173WUL9	CUN43212.1	1	COG1680	149.76			Blautia wexlerae
G2ZV67	CCA82966.1	1	COG1680	169.79			blood disease bacterium R229
A0A023XFH2	AHY51187.1	1	COG1680	166.71			Bradyrhizobium japonicum SEMIA 5079
A0A095F1I8	KGC11198.1	1	COG1680	149.38			Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata)
A0A221AGB0	ASL47600.1	1	COG1680	119.71			Burkholderia sp. AD24
A0A011PTN3	EXI80185.1	1	COG1680	151.30			Candidatus Accumulibacter sp. BA-92
A0A084Y3U9	KFB69393.1	1	COG1680	63.48	cl05973	36.69	Candidatus Accumulibacter sp. SK-01
A0A080MKD1	KFB77834.1	1	COG1680	60.39			Candidatus Accumulibacter sp. SK-02
A0A1V6B2J0	removed	0	n/a				Candidatus Aminicenantes bacterium ADurb.Bin147
A0A1V6EEM6	removed	0	n/a				Candidatus Hydrogenedentes bacterium ADurb.Bin101
A0A1Q9P628	OLS29815.1	1	COG1680	130.89			Candidatus Thorarchaeota archaeon AB_25
A0A174HD35	CUO70815.1	1	COG1680	150.92			Catenibacterium mitsuokai
K1LUT6	EKB47909.1	1	COG1680	125.88			Cecembia lonarensis LW9
A0A1X6W3T6	SHE12636.1	1	COG1680	123.57			Chlamydia abortus (Chlamydophila abortus)
A0A1V5WGQ7	removed	0	n/a				Chloroflexi bacterium ADurb.Bin222
A0A1V5RV19	removed	0	n/a				Chloroflexi bacterium ADurb.Bin325
A0A1A7KL28	OBW42568.1	1	COG1680	124.72			Chryseobacterium sp. MOF25P
A0A239XLG5	SNV47565.1	1	COG1680	122.03			Chryseobacterium taklimakanense
A0A174Z2S0	CUQ80252.1	1	COG1680	116.25			Clostridium innocuum
A0A1S8TH57	OOM77137.1	1	COG1680	85.43			Clostridium puniceum
A0A1A6B1J1	OBR96138.1	1	COG1680	115.09			Clostridium ragsdalei P11
A0A0U5HF17	CUX46217.1	1	COG1680	130.50			Clostridium sp. C105KSO15
A0A0F0CE38	KJJ70112.1	1	COG1680	128.57			Clostridium sp. FS41
A0A174DWD8	CUO29517.1	1	COG1680	122.41			Coprococcus comes
H8MKX6	AFE09676.1	1	COG1680	122.80			Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)
Q1LCI4	ABF12142.1	1	COG1680	106.23			Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)
F8GSN1	AEI79800.1	1	pfam00144	107.59			Cupriavidus necator (strain ATCC 43291 / DSM 13513 / N-1) (Ralstonia eutropha)
B3RAT4	CAQ72009.1	1	COG1680	177.11			Cupriavidus taiwanensis (strain DSM 17343 / BCRC 17206 / CIP 107171 / LMG 19424 / R1) (Ralstonia taiwanensis (strain LMG 19424))
A0A1Y0N366	ARV17122.1	1	COG1680	167.86			Curvibacter sp. AEP1-3
A0A210W8E3	OWG18506.1	1	COG1680	160.55			Delftia sp. K82
A0A1V6GPD1	removed	0	n/a				Deltaproteobacteria bacterium ADurb.Bin072
A0A1V6AWN4	removed	0	n/a				Deltaproteobacteria bacterium ADurb.Bin151
A0A1V5J9N3	removed	0	n/a				Deltaproteobacteria bacterium ADurb.BinA014
A0A1E3AQH9	ODM10959.1	1	COG1680	138.97			Eisenbergiella tayi
A0A1X7AI28	SMA42681.1	1	COG1680	154.77			Endozoicomonas sp. S-B4-1U
A0A0J0HGF8	KJB99867.1	1	COG1680	157.85			Enterobacter cloacae
G8LI19	AEW74343.1	1	COG1680	153.61			Enterobacter cloacae EcWSU1
A0A181D6J5	SAZ42206.1	1	COG1680	153.23			Enterobacter kobei
A0A1D3U0X1	SCQ13749.1	1	COG1680	146.29			Escherichia coli
A0A174ZK95	CUQ86392.1	1	COG1680	138.97			[Eubacterium] eligens
A0A173ZD16	CUN73366.1	1	COG1680	115.86			Faecalicatena contorta
I0K5V2	CCG99505.1	1	COG1680	143.60			Fibrella aestuarina BUZ 2
A0A1V5Y736	removed	0	n/a				Firmicutes bacterium ADurb.Bin182
A0A1V5U0S1	removed	0	n/a				Firmicutes bacterium ADurb.Bin248
A0A1V5TRM2	removed	0	n/a				Firmicutes bacterium ADurb.Bin262
A0A1J0LMH5	APD06749.1	1	COG1680	137.05			Flavobacteriaceae bacterium UJ101
P07061	CAA24927.1	1	COG1680	130.50			Flavobacterium sp. (strain K172)
A0A174PGN0	CUP57970.1	1	pfam00144	117.60			Fusicatenibacter saccharivorans
A0A174XLK7	CUQ57808.1	1	COG1680	136.28			Fusicatenibacter sp. 2789STDY5834925
W2UH15	ETN93313.1	1	COG1680	142.83			Gammaproteobacteria bacterium MOLA455
A0A161IJZ3	ANC32434.1	1	COG1680	131.27			Isoptericola dokdonensis DS-3
A0A0M6XVQ3	CTQ34802.1	1	COG1680	149.38			Jannaschia rubra
A0A1E7W046	OEZ86618.1	1	COG1680	168.64			Janthinobacterium sp. HH106
A0A0M2WJP3	KKO63049.1	1	COG1680	156.69			Janthinobacterium sp. KBS0711
K6VJY8	GAB96543.1	1	COG1680	133.58			Kineosphaera limosa NBRC 100340
A0A145MIT9	A0A145MIT9	1	COG1680	154.38			Klebsiella aerogenes (Enterobacter aerogenes)
A0A181Y488	A0A181Y488	1	COG1680	151.69			Klebsiella oxytoca
A0A1W1KFI7	SLU24553.1	1	COG1680	150.15			Klebsiella pneumoniae
A0A0M0EIV8	KON65183.1	1	COG1680	131.27			Komagataeibacter europaeus (Gluconacetobacter europaeus)
A0A0M6YQP9	CTQ52194.1	1	pfam00144	88.33			Labrenzia alba
A0A0P0M791	ALK87626.1	1	COG1680	98.14			Limnohabitans sp. 63ED37-2
A0A238KTS8	SMX46098.1	1	COG1680	145.14			Maliponia aquimaris
H8W4J4	CCG96581.1	1	COG1680	162.86			Marinobacter hydrocarbonoclasticus ATCC 49840
A0A1A8T0Y1	SBS25568.1	1	COG1680	170.18			Marinomonas spartinae
A0A068DC64	AID32220.1	1	COG1680	146.68			Mesorhizobium huakuii 7653R
A0A1R3VCN4	SIT57024.1	1	COG1680	156.31			Mesorhizobium prunaredense
M5FIQ6	CCV16028.1	1	COG1680	165.17			Mesorhizobium sp. STM 4661
A0A154NUR2	KZC02620.1	1	COG1680	135.89			Methylobacterium radiotolerans
A0A0F0L6Z7	KJL27296.1	1	COG1680	115.86			Microbacterium azadirachtae
A0A0M2HBF1	KJL43938.1	1	COG1680	78.11			Microbacterium ketosireducens
A0A0F0L4Z2	KJL28208.1	1	COG1680	89.28			Microbacterium oxydans
A0A171DW03	GAT73671.1	1	COG1680	123.95			Microbacterium sp. HM58-2
A0A0F2C737	KJQ53091.1	1	COG1680	92.37			Microbacterium sp. SA39
A0A164BYC9	KZE90582.1	1	COG1680	91.60			Microbacterium sp. TNHR37B
A0A0M2HA45	KJL41039.1	1	COG1680	114.32			Microbacterium trichothecenolyticum
F5XN73	BAK36523.1	1	COG1680	133.20			Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)
A0A1J5STQ6	OIR07397.1	1	COG1680	122.80	pfam13927	50.58	mine drainage metagenome
A0A0X8X008	BAU53359.1	1	COG1680	142.83			Mucilaginibacter gotjawali
A0A1N4P2M1	SII87258.1	1	COG1680	133.20			Mycobacterium abscessus subsp. abscessus
A0A0J6W957	KMO78172.1	1	COG1680	143.98			Mycobacterium chlorophenolicum
A0A0U0QJL1	COU89364.1	1	COG1680	86.59			Mycobacterium tuberculosis
U5EL89	GAD85874.1	1	COG1680	160.16			Nocardia asteroides NBRC 15531
A0A231GU73	OXR40169.1	1	pfam00144	119.14			Nocardia cerradoensis
A0A0B8ND93	APA95039.1	1	COG1680	115.86			Nocardia seriolae
A0A1Y5THU2	SLN62380.1	1	COG1680	153.61			Oceanibacterium hippocampi
A1RBL5	ABM06783.1	1	COG1680	128.96			Paenarthrobacter aurescens (strain TC1)
A0A0B0HYQ6	KHF33049.1	1	COG1680	123.95			Paenibacillus sp. P1XP2
A0A1E3L9K2	ODP29630.1	1	COG1680	125.88			Paenibacillus sp. TI45-13ar
A0A0A8VKA5	CEK30015.1	1	COG1680	146.68			Paeniclostridium sordellii (Clostridium sordellii)
M7NLA9	EMQ99303.1	1	COG1680	67.71			Paeniglutamicibacter gangotriensis Lz1y
A0A1U7CSL2	APW61863.1	1	COG1680	142.83			Paludisphaera borealis
A0A174I3J8	CUN11845.1	1	COG1680	140.52			Parabacteroides distasonis
A0A238KUV0	SMX46579.1	0	querry exception				Pelagimonas varians
A0A0P1H3R0	CUH89508.1	1	COG1680	151.69			Phaeobacter sp. CECT 5382
A0A1C0U4M3	OCQ52869.1	1	COG1680	110.47			Photorhabdus asymbiotica subsp. australis
A0A142WX71	AMV19408.1	1	COG1680	138.20			Planctomyces sp. SH-PL14
A0A142YP87	AMV40750.1	1	COG1680	147.06			Planctomyces sp. SH-PL62
A0A1V6DF56	removed	0	n/a				Planctomycetes bacterium ADurb.Bin126
A0A1L9P0F0	OJI94894.1	1	COG1680	142.83			Planktotalea frisia
A0A0D6IK29	ALV76382.1	1	COG1680	176.34			Pseudomonas aeruginosa
A0A127MZS5	AMO78698.1	1	COG1680	148.22			Pseudomonas citronellolis
A0A0D0SHT7	KIR21553.1	1	pfam00144	104.89			Pseudomonas fluorescens
A0A225DUD8	OWK44613.1	1	COG1680	141.29			Pseudomonas oleovorans subsp. oleovorans
A0A1B2F4H7	ANY86973.1	1	COG1680	87.36			Pseudomonas putida (Arthrobacter siderocapsulatus)
Q59719	BAA01524.1	1	COG1680	143.98			Pseudomonas sp.
A0A1B5F5J3	CRM94056.1	1	COG1680	128.57			Pseudomonas sp. 22 E 5
A0A1B5DZG3	CRM60472.1	1	COG1680	127.03			Pseudomonas sp. 37 R 15
A0A1B5DLW0	CRM45287.1	1	COG1680	128.57			Pseudomonas sp. 44 R 15
A0A105T3Y5	KVV01628.1	1	COG1680	167.48			Pseudomonas sp. TAD18
A0A0S4HPZ6	CRL47957.1	1	COG1680	169.02			Pseudomonas sp. URMO17WK12:I11
A0A1Y5TRM7	SLN66503.1	1	COG1680	142.06			Pseudoruegeria aquimaris

A0A165T3A5	KZL05366.1	1	pfam00144	85.25	Pseudovibrio axinellae
G8PHS5	AEV36518.1	1	COG1680	133.20	Pseudovibrio sp. (strain FO-BEG1)
A0A1U6GQ15	SLJ85613.1	1	COG1680	134.35	Psychrobacter sp. DAB_AL43B
D8NJ41	CBJ43063.1	1	COG1680	180.58	Ralstonia solanacearum CFBP2957
D8NBY7	CBJ37975.1	1	COG1680	186.74	Ralstonia solanacearum CMR15
D8NTL3	CBJ51172.2	1	COG1680	178.65	Ralstonia solanacearum PSI07
F6G7H0	AEG70906.1	1	COG1680	130.12	Ralstonia solanacearum (strain Po82)
G3A899	CCA86522.1	1	COG1680	180.96	Ralstonia syzygii R24
A0A1Y6GHY9	SMQ89731.1	1	COG1680	150.15	Raoultella ornithinolytica (Klebsiella ornithinolytica)
W6S0Z5	CDM60151.1	1	COG1680	126.65	Rhizobium favelukesii
A0A1W6KTY5	ARM90893.1	1	COG1680	150.53	Rhizobium sp. CIAT894
A0A1H8SL49	SEI12907.1	1	COG1680	131.66	Rhizobium tibeticum
D5ANB4	ADE86404.1	1	COG1680	135.89	Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)
X0Q0I2	GAF44337.1	1	COG1680	126.65	Rhodococcus wratislaviensis NBRC 100605
A0A173SRD8	CUM92347.1	1	pfam00144	121.45	Roseburia intestinalis
A0A1X6ZHX4	SLN50150.1	1	COG1680	131.66	Roseivivax jejudonensis
Q161I2	ABG33361.1	1	COG1680	146.29	Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)
A0A1X6ZR95	SLN59152.1	1	pfam00144	106.05	Roseovarius gaetbuli
A0A0P1E3V5	CUH43141.1	1	COG1680	156.69	Ruegeria atlantica
A0A0P1I8K0	CUJ97681.1	1	COG1680	139.36	Ruegeria sp. CECT 5091
A0A174R2F8	CUP79693.1	1	COG1680	147.06	[Ruminococcus] torques
A0A0U6MUP1	CVA82934.1	1	COG1680	155.15	Serratia marcescens
A0A0P1FES5	CUH52959.1	1	COG1680	146.29	Shimia marina
A0A0M9EKA2	KPA23465.1	1	COG1680	132.04	Shimia sp. SK013
A0A173KVC3	ANI78048.1	1	COG1680	124.72	Sphingobium sp. EP60837
A0A245ZHX8	OWK29334.1	1	pfam00144	131.85	Sphingomonas dokdonensis
A0A245ZS72	OWK32584.1	1	COG1680	121.64	Sphingomonas mucosissima
A0A220W924	ASK89323.1	1	COG1680	117.02	Sphingorhabdus flavimaris
A0A1V5WIK4	removed	0	n/a		Spirochaetes bacterium ADurb.Bin215
A0A0T8Y0L9	CKG36687.1	1	COG1680	150.92	Streptococcus pneumoniae
A0A117E7E7	GAQ53093.1	1	pfam00144	138.02	Streptomyces acidiscabies
A0A1D2IE66	ODA72800.1	1	pfam00144	89.10	Streptomyces sp. AVP053U2
A0A1K2FPU2	SFY49811.1	1	COG1680	100.84	Streptomyces sp. F-1
A0A1B9EIG0	OCC07415.1	1	COG1680	124.72	Streptomyces sp. PTY087I2
A0A1D3URL4	SCQ22896.1	1	COG1680	142.44	Tannerella forsythia (Bacteroides forsythus)
A0A0P1FIN3	CUH67776.1	1	COG1680	135.12	Thalassobius gelatinovorus (Ruegeria gelatinovora)
A0A0P1GCY7	CUH73549.1	1	COG1680	124.72	Thalassobius mediterraneus
I3TJC5	AFK52863.1	1	COG1680	156.31	Tistrella mobilis (strain KA081020-065)
A0A1Y5S3B8	SLN31670.1	1	COG1680	145.14	Tropicibacter litoreus R37
A0A1C6JX26	SCJ86692.1	1	COG1680	180.58	uncultured Anaerotruncus sp.
A0A1C6G057	SCJ38643.1	1	COG1680	147.06	uncultured Blautia sp.
A0A1C5PZB2	SCH42505.1	1	COG1680	122.80	uncultured Clostridium sp.
A0A1C5SG29	SCH72758.1	1	COG1680	115.48	uncultured Coprococcus sp.
A0A1C6HH82	SCJ56877.1	1	COG1680	133.97	uncultured Eubacterium sp.
A0A1C5YBZ6	SCI44810.1	1	COG1680	147.06	uncultured Ruminococcus sp.
A0A0H2LTX8	KLN53679.1	1	COG1680	118.17	Variovorax paradoxus
A0A1V6JU22	removed	0	n/a		Verrucomicrobia bacterium ADurb.Bin006
A0A1V6JCM4	removed	0	n/a		Verrucomicrobia bacterium ADurb.Bin018
U3AN41	GAD74717.1	1	COG1680	145.91	Vibrio azureus NBRC 104587
A0A1C3JFB5	SBT13765.1	1	pfam00144	112.59	Vibrio celticus
A0A1B1NP12	ANS85294.1	1	COG1680	132.04	Vibrio scophthalmi
A0A1Y2SKJ5	OTA18532.1	1	COG1680	85.05	Xenorhabdus vietnamensis

SCREEN SAMPLE OF CDD PAGE:



SCREEN SAMPLE OF UNIPROT PAGE FOR NYLB AND NYLB':



Testing the Hypothesis that the Nylonase NylB Protein
Arose *de novo* via a Frameshift Mutation

Salvador Cordova and John Sanford

Supplementary Table S2
List of organisms with NylB' from UNIPROT, and conserved domains of NylB' homologs
with sample screen captures from NIH CDD and UNIPROT websites at the bottom

NOTES:
COG1680 = CubicO group peptidase, **beta-lactamase** class C family [Defense mechanisms];

cd10802 = Thermus thermophiles TTHB029 and similar proteins; This subfamily is represented by an YdjC-family protein TTHB029 from Thermus thermophilus HB8; it is similar to Escherichia coli YdjC, a hypothetical protein encoded by the celG gene. TTHB029 functions as a homodimer. Each of monomer consists of (beta/alpha)-barrel fold. The molecular function of TTHB029 is unclear.

cl21491 = Penicillin binding protein transpeptidase domain; for GenBank A0A011QU85 alignment was was detected with superfamily member COG1680

pfam00144 = **Beta-lactamase**; This family appears to be distantly related to pfam00905 and PF00768 ...

pfam03724 = META domain; Small domain family found in proteins of of unknown function. Some are secreted and implicated in motility in bacteria. Also occurs in Leishmania spp. as an essential gene. Over-expression in L.amazonensis increases virulence. A pair of cysteine residues show correlated conservation, suggesting that they form a disulphide bond.

n/a = not applicable because the data was embargoed pending publication

	no. avail. cdds	121						
	count nylb's	134						Average
								134.83
UNIPROT ID	Genbank ID	Conserved Domain Data Available	Primary Conserved Doma ACCESSION ID	Primary Conserved Domai Bit score	Secondary Conserved Domain ACCESSION ID	Secondary Conserved Domain Bit score	ORGANISM	Beta Lactamase Domain Bit Score
A0A0M7J5X6	CUI87454.1	1	COG1680	126.26			Achromobacter sp.	126.26
A0A1G5L686	SCZ08385.1	1	COG1680	184.04			Acinetobacter baumannii	184.04
A0A1R3U120	SCX34286.1	1	COG1680	132.43			Agrobacterium sp. DSM 25559	132.43
A0A1B3NSJ3	AOG08337.1	1	COG1680	156.69			Agrobacterium sp. RAC06	156.69
Q14T91	BAE97630.1	1	COG1680	130.12			Agromyces sp. KY5R	130.12
A0A0D6I854	CKH88456.1	1	COG1680	113.55			Alcaligenes xylosoxydans xylosoxydans (Achromo	113.55
A0A1B2ADK5	ANY20242.1	1	COG1680	142.44			Altererythrobacter dongtanensis	142.44
A0A0N0GL59	KPC49626.1	1	COG1680	158.23			Amantichitinum ursilacus	158.23

A0A136WJN9	KXL54559.1	1	COG1680	131.66			Anaerotignum neopropionicum	131.66	
A0A222E5F8	ASP21360.1	1	COG1680	137.43			Antarctobacter heliothermus	137.43	
A0A1Y5T7Z2	SLN55856.1	1	COG1680	99.3			Aquimixticola soesokkakensis	99.3	
A0A1Y6AVV0	PEV28669.1	1	COG1680	111.63			Bacillus cereus	111.63	
A0A1V5JGZ1	removed	0	n/a				bacterium ADurb.BinA028		
A0A0A1PJ91	CEJ15450.1	1	COG1680	112.78			bacterium YEK0313	112.78	
A0A180FM12	OAV73346.1	1	COG1680	138.59			Bacteroidales bacterium Barb6	138.59	
A0A180FCF0	OAV69997.1	1	COG1680	136.28			Bacteroidales bacterium Barb6XT	136.28	
A0A0P0GQ77	ALJ59432.1	1	cd10802	265.32	COG1680	121.64	Bacteroides cellulosilyticus	121.64	secondary domain rather than primary domain had the beta lactamase domain
A0A174JUS8	CUP00900.1	1	COG1680	157.46			Bacteroides xylanisolvens	157.46	
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A0A221AGH6	ASL47615.1	1	COG1680	124.34			Burkholderia sp. AD24	124.34	
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A0A084Y3V0	KFB69394.1	1	COG1680	79.65			Candidatus Accumulibacter sp. SK-01	79.65	
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M7NIZ7	EMR01730.1	1	COG1680	150.92			Cesiribacter andamanensis AMV16	150.92	
A0A1X6W741	SHE13305.1	1	COG1680	157.85			Chlamydia abortus (Chlamydophila abortus)	157.85	
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A0A1A7KJK9	OBW41946.1	1	pfam00144	121.45			Chryseobacterium sp. MOF25P	121.45	
A0A1Y3FFF3	OUE17692.1	1	COG1680	96.99			Clavibacter michiganensis subsp. michiganensis	96.99	
A0A143Y291	CVI73461.1	1	pfam00144	128.39			Clostridiales bacterium CHKCI001	128.39	
A0A1R4UEF4	SJT07095.1	1	COG1680	145.14			Clostridioides difficile (Peptoclostridium difficile)	145.14	
A0A174SE58	CUP94651.1	1	COG1680	140.13			[Clostridium] clostridioforme	140.13	
A0A168MLP5	OAA84870.1	1	COG1680	103.15			Clostridium ljungdahlii	103.15	
A0A1V4IZP8	OPJ65244.1	1	COG1680	120.1			Clostridium oryzae	120.1	
A0A1S8TMH4	OOM78792.1	1	COG1680	97.76			Clostridium puniceum	97.76	
A0A0U5PQ27	CUX75402.1	1	COG1680	139.75			Clostridium sp. C105KSO14	139.75	
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A0A132HH88	AVA35740.1	1	COG1680	106.62			Cupriavidus metallidurans	106.62	
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A0A143PQU0	AMY10736.1	1	COG1680	77.54			Luteitalea pratensis	77.54
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D5PH26	EFG74633.1	1	COG1680	137.82			Mycobacterium parascrofulaceum ATCC BAA-614	137.82
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A0A0S4HRC6	CRL48425.1	1	COG1680	147.06			Pseudomonas sp. URMO17WK12:I11	147.06

A0A099SNY9	KUR43944.1	1	COG1680	140.52	Pseudomonas syringae pv. tomato	140.52
A0A1Y5SNP5	SLN44728.1	1	COG1680	133.58	Pseudooctadecabacter jejudonensis	133.58
A0A1Y5RVI3	SLN23768.1	1	COG1680	158.62	Pseudoruegeria aquimaris	158.62
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A0A161XKM1	KZL25998.1	1	COG1680	134.74	Pseudovibrio sp. WM33	134.74
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A0A0P1FIH6	CUH67767.1	1	COG1680	149.76	Thalassobius gelatinovorus (Ruegeria gelatinovora	149.76
A0A0P1FSF4	CUH71927.1	1	COG1680	133.97	Thalassobius mediterraneus	133.97
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A0A1C5Q3J1	SCH43822.1	1	COG1680	154.77	uncultured Dorea sp.	154.77
A0A1C6IY35	SCJ74355.1	1	COG1680	123.95	uncultured Lachnospira sp.	123.95
A0A1C5PT61	SCH40294.1	1	COG1680	133.97	uncultured Ruminococcus sp.	133.97
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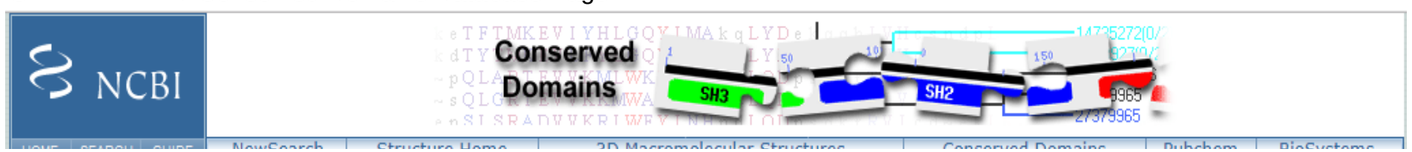
SAMPLE NYLB' Conserved Domains Database Page:



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Conserved domains on [gi|1326315889|gb|PMF19269.1|]

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6-aminohexanoate hydrolase [Vibrio splendidus]

Protein Classification

class C beta-lactamase-related serine hydrolase (domain architecture ID 10004149)
class C beta-lactamase-related serine hydrolase similar to Flavobacterium 6-aminohexanoate-dimer hydrolase, which degrades linear oligomers of 6-aminohexanoate by exo-type cleavage, removing residues sequentially from the N-terminus of nylon-6 oligomers

Graphical summary

Zoom to residue level | show extra options »

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List of domain hits

	Name	Accession	Description	Interval	E-value
[-]	AmpC	COG1680	CubicO group peptidase, beta-lactamase class C family [Defense mechanisms];	63-414	6.98e-24

CubicO group peptidase, beta-lactamase class C family [Defense mechanisms];

:

Pssm-ID: 224594 **Cd Length:** 390 **Bit Score:** 102.00 **E-value:** 6.98e-24

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                      ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1326315889  63 LSRFYPTAQIERDGPVYQFPYQIDQNIGE-ISATVHGESKTLNEHLDsypvdaFLVVKSGEVVFERYNT-MGKTDKHNWF 140
Cdd:COG1680    19 LLAPAATPASEVAGFDAARLDRLADAIMEeYGAPGPGLALAVVLDGK------TVVAKGYGVADEGYGGpVTPPTVFRIA 92

                             90       100       110       120       130       140       150       160
                      ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1326315889 141 SNSKITVGIELAKLVNEGQVNLSDPISKYIPELKGSDWD--TVSVSDTANMATGLNATEhDEPEADsrinPEQPWFKWAV 218
Cdd:COG1680    93 SVTKSFTATLLGKLVEEGKLDLDDPVSKYLPEGKDPATGgaPITLRDLLTHTSGLPFPE-DYAYAV----PKRLVQDQEA 167

                            170       180       190       200       210       220       230       240
                      ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1326315889 219 SigvfegegnqspLEVLAEMKRRAPG--GKTFEYNSINTFVLARLIENVRNLPMNEIVSRDMWQKMGANNDAYTV----- 291
Cdd:COG1680   168 A------------LEYLASLPPELAPppGTAFAYSNSNYGLLGAILERVTGKPLEELLRERIFEPLGMTSTGFGPppapq 235

                            250       260       270       280       290       300       310       320
                      ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1326315889 292 ----------------VSPQGGYPLMFFS-----MNTTIEDMTKFGMLLtpsatkLGNGGVSKEVI---TLIQDSGNP-- 345
Cdd:COG1680   236 arlaaglapavggggeVDDPGTFGLGSALagaggLFSTARDMARFGQAL------LNGGVLLGRQLlpaMLVPDFTTGgq 309

                            330       340       350       360       370       380       390
                      ....*....|....*....|....*....|....*....|....*....|....*....|....*....|...
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SCREEN SAMPLE OF UNIPROT PAGE FOR NYLB AND NYLB':

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STREE (12)

Bacteroides cellulosilyticus (4)

CUPNN (1)

Other organisms

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Search terms

Filter "nylb" as:

gene name (528)

protein name (14)

Entry	Entry name	Organism	Protein names	Gene names	Length
P07061	NYLB_FLASK	Flavobacterium sp. (strain K172)	**6-aminohexanoate-dimer hydrolase, EC 3.5.1.46** (Nylon oligomers-degrading enzyme EII)	**nylB**	392
P07062	NYLC_FLASK	Flavobacterium sp. (strain K172)	**6-aminohexanoate-dimer hydrolase, EC 3.5.1.46** (Nylon oligomers-degrading enzyme EII')	**nylB'**	392
A0A0P0GQ77	A0A0P0GQ77_9BACE	Bacteroides cellulosilyticus	6-aminohexanoate-dimer hydrolase, EC 3.5.1.46	**nylB'_1** BcellWH2_02191	576
A0A108TGJ3	A0A108TGJ3_9BACE	Bacteroides cellulosilyticus	6-aminohexanoate-dimer hydrolase, EC 3.5.1.46	**nylB'_1** AA416_00538	576
A0A0G5TIY0	A0A0G5TIY0_PSEAI	Pseudomonas aeruginosa	6-aminohexanoate-dimer hydrolase, EC 3.5.1.46	**nylB'_2** nylB'_1, PAERUG_E15_London_28_01_14_00795, RW109_RW109_03784	403
F8GSN1	F8GSN1_CUPNN	Cupriavidus necator (strain ATCC 43291 / DSM 13513 / N-1) (Ralstonia eutropha)	NylB 6-aminohexanoate-dimer Hydrolase NylB, EC 3.5.1.46	**nylB** CNE_2c08290	451
A0A0F0UJ20	A0A0F0UJ20_PSEAI	Pseudomonas aeruginosa	6-aminohexanoate-dimer hydrolase, EC 3.5.1.46 (Serine hydrolase)	**nylB'_1** nylB'_2, CAZ03_13195, HV91_31600, PAERUG_E15_London_28_01_14_00369, RW109_RW109_07208	414
A0A0T8GJW9	A0A0T8GJW9_STREE	Streptococcus pneumoniae	6-aminohexanoate-dimer hydrolase, EC	**nylB_2** nylB, nylB_1, ERS021189_02461, ERS021354_03128	410

View by

Results table

Taxonomy

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Testing the Hypothesis that the Nylonase NylB Protein
Arose *de novo* via a Frameshift Mutation

Salvador Cordova and John Sanford

Supplementary Table S3
List of organisms with NylA from uniprot, and conserved domains of NylAs
with sample screen captures from NIH CDD and UNIPROT websites at the bottom

NOTES:

COG0154 = Asp-tRNAAsn/Glu-tRNAGln amidotransferase A subunit or related amidase
[Translation, ribosomal structure and biogenesis];

cl18951 = Amidase;

pfam01425 = Amidase;

PRK07869 = amidase; Provisional

PRK06061 = amidase; Provisional

pfam07501 = G5 domain; This domain is found in a wide range of extracellular proteins. It is found ...

PRK06529 = amidase; Provisional

n/a = not applicable because the data was embargoed pending publication

no. avail. cdds	182
count NylAs	193

UNIPROT ID	Genbank ID	Conserved Domain Data Available	Primary Conserved Doma ACCESSION ID	Primary Conserved Domai Bit score	Secondary Conserved Domain CCESSION I	Secondary Conserved Domain Bit score	ORGANISM
D4XAB8	EFF76383.1	1	COG0154	257.22			Achromobacter piechaudii ATCC 43553
A0A0M7DUQ9	CUI57268.1	1	COG0154	242.2			Achromobacter sp.
A0A066PM46	KDM66920.1	1	COG0154	327.33			Acidiphilium sp. JA12-A1
A0A0D8HH63	KJF16396.1	1	COG0154	303.06			Acidithrix ferrooxidans
A0A239RVT3	SNU14988.1	1	cl18951	361.83			Acinetobacter johnsonii
A0A150I2M3	KXZ73999.1	1	cl18951	364.14			Acinetobacter venetianus
A0A2P4URV2	POM27744.1	1	COG0154	330.41			Actinomadura sp. 5-2
D4YI68	EFG49104.1	1	cl18951	544.03			Aerococcus viridans ATCC 11563 = CCUG 4311
A0A1R3U232	SCX35430.1	1	COG0154	230.26			Agrobacterium sp. DSM 25559
A0A0D6INF8	CKI16847.1	1	COG0154	252.6			Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans)

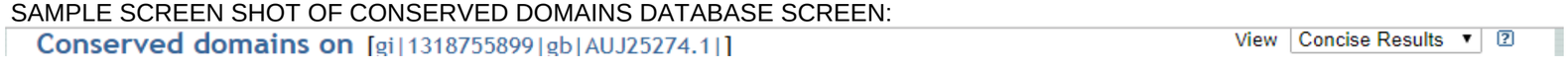
A0A1B2ABP4	ANY19580.1	1	COG0154	266.08	Altererythrobacter dongtanensis
A0A178X0F6	OAP23195.1	1	cl18951	219.86	Amycolatopsis sp. M39
A0A0D6QPK1	GAO05363.1	1	COG0154	299.98	Anaeromyxobacter sp. PSR-1
A0A0U5BA19	BAU27772.1	1	cl18951	278.41	Aneurinibacillus soli
A0A1D7QVD8	AOM82949.1	1	cl18951	377.24	Bacillus beveridgei
A0A1Q9BAH0	OLP65740.1	1	cl18951	501.66	Bacillus pumilus (Bacillus mesentericus)
L8AQW9	BAM53880.1	1	pfam01425	389.35	Bacillus subtilis BEST7613
A0A090IS94	CEE00941.1	1	cl18951	529.78	Bacillus thermoamylovorans
A0A1V5J9J8	removed	0	n/a		bacterium ADurb.BinA028
A0A2H6H4J4	GBE21173.1	1	cl18951	317.7	bacterium BMS3Bbin01
A0A2H5ZNF0	GBD27233.1	1	COG0154	344.28	bacterium HR30
A0A2H6AWV7	GBD42414.1	1	COG0154	309.99	bacterium HR39
A0A2H6AZD7	GBD43293.1	1	cl18951	314.23	bacterium HR40
A0A2H6B6G8	GBD45731.1	1	COG0154	350.06	bacterium HR41
A0A0A1PD21	CEJ11088.1	1	cl18951	307.3	bacterium YEK0313
H6RLD2	CCG02458.1	1	COG0154	311.15	Blastococcus saxobsidens (strain DD2)
A0A157S5C9	SAI65612.1	1	COG0154	276.48	Bordetella ansorpii
A0A0H4WRC0	AKQ57708.1	1	COG0154	278.02	Bordetella hinzii
A0A140KUK9	CZQ35579.1	1	cl18951	98.13	Bordetella pertussis
A0A157SG71	SAI69344.1	1	COG0154	281.88	Bordetella trematum
A0A0H2WG49	AAU48320.1	1	cl18951	321.16	Burkholderia mallei (strain ATCC 23344)
A2S6W5	ABN01555.1	1	cl18951	321.16	Burkholderia mallei (strain NCTC 10229)
A0A1S0SB87	CFL38648.1	1	cl18951	320.78	Burkholderia pseudomallei (Pseudomonas pseudomallei)
Q3JY82	ABA50489.1	1	cl18951	321.55	Burkholderia pseudomallei (strain 1710b)
A0A221AB94	ASL45854.1	1	COG0154	257.22	Burkholderia sp. AD24
V9TR00	AHC73309.1	1	COG0154	313.46	Candidatus Endolissoclinum faulkneri L5
K8EDK6	CCO09833.2	1	cl18951	411.91	Carnobacterium maltaromaticum LMA28
A0A0E9FL18	CRH82220.1	1	cl18951	136.49	Chlamydia trachomatis
F8GPZ8	AEI79351.1	1	cl18951	265.69	Cupriavidus necator (strain ATCC 43291 / DSM 13513 / N-1) (Ralstonia eutropha)
A0A239WBU5	SNV31669.1	1	COG0154	271.09	Cutibacterium granulosum
A0A1V6KGF2	removed	0	n/a		Deltaproteobacteria bacterium ADurb.Bin002
A0A1V6IQ42	removed	0	n/a		Deltaproteobacteria bacterium ADurb.Bin022
A0A1V6G4I0	removed	0	n/a		Deltaproteobacteria bacterium ADurb.Bin072
A0A1V6AWT2	removed	0	n/a		Deltaproteobacteria bacterium ADurb.Bin151
A0A1V5HE73	removed	0	n/a		Deltaproteobacteria bacterium ADurb.BinA179
A0A239V818	SNV18335.1	1	cl18951	368.06	Dermatophilus congolensis
F5SJP9	EGK08499.1	1	cl18951	489.72	Desmospora sp. 8437
C0X1J8	EEI13129.1	1	cl18951	527.47	Enterococcus faecalis TX0104
A0A0D8FVF4	KJE77106.1	1	cl18951	314.84	Ferrimicrobium acidiphilum DSM 19497
P13398	BAA05090.1	1	COG0154	288.42	Flavobacterium sp. (strain K172)
A0A222TFI4	ASR01485.1	1	PRK07869	683.64	Gordonia rubripertincta (Rhodococcus corallinus)
C8NG30	EEW37516.1	1	cl18951	691.18	Granulicatella adiacens ATCC 49175
A0A059NVE7	CDQ23279.1	1	COG0154	316.93	Halobacillus karajensis
A0A2C9D0T4	SON53778.1	0	querry exception		Hartmannibacter diazotrophicus
A0A1E7WAM3	OEZ93467.1	1	COG0154	292.28	Janthinobacterium sp. HH106
A0A0M2WHD7	KKO62249.1	1	COG0154	283.8	Janthinobacterium sp. KBS0711
A0A1S6IQB3	AQS53746.1	1	cl18951	591.41	Jeotgalibaca dankookensis

A0A181C565	SAY46675.1	1 COG0154	311.92	Komagataeibacter rhaeticus
A0A0M6Z8M8	CTQ64276.1	1 cl18951	297.67	Labrenzia alba
C2D288	EEI71107.1	1 cl18951	494.72	Lactobacillus brevis subsp. gravesensis ATCC 27305
C0WQT6	EEI19652.1	1 cl18951	494.72	Lactobacillus buchneri ATCC 11577
J9W3Z9	AFS01208.1	1 cl18951	482.78	Lactobacillus buchneri CD034
A0A2N9KZL5	SPE16009.1	1 cl18951	517.45	Lactobacillus fermentum
C0WXY8	EEI22090.1	1 cl18951	513.6	Lactobacillus fermentum ATCC 14931
C0XGF7	EEI25501.1	1 cl18951	498.19	Lactobacillus hilgardii DSM 20176 = ATCC 8290
C8PAP3	EEW52532.1	1 cl18951	410.75	Lactobacillus iners DSM 13335
C2FBN4	EEI68757.1	1 cl18951	553.27	Lactobacillus paracasei subsp. paracasei ATCC 25302
E7FSC6	EFZ34169.1	1 cl18951	546.73	Lactobacillus ruminis ATCC 25644
A0A1E7X8H4	OFA09389.1	1 cl18951	489.72	Lactobacillus sunkii
C2ESU0	EEJ41066.1	1 cl18951	521.3	Lactobacillus vaginalis DSM 5837 = ATCC 49540
A0A173M330	BAV01662.1	1 cl18951	415.37	Lactococcus garvieae
A0A078KW70	CDZ75999.1	1 COG0154	298.05	Legionella massiliensis
A0A128ZD65	CZI36732.1	1 COG0154	244.51	Legionella pneumophila
A0A110AWJ2	BAU43134.1	1 COG0154	341.97	Leptolyngbya sp. O-77
Q72PS5	AAS70961.1	1 cl18951	398.04	Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130)
A0A2P2D2K7	GBF38899.1	1 cl18951	368.38	Leptospira sp. E8
A0A0N7J8F9	ALK88080.1	1 COG0154	291.51	Limnohabitans sp. 63ED37-2
A0A0Y7J7Z3	CWW90658.1	1 cl18951	527.85	Listeria monocytogenes
A0A238LBI3	SMY06326.1	1 COG0154	299.59	Loktanella marina
A0A238K804	SMX38617.1	1 COG0154	298.44	Maliponia aquimaris
E4PFN8	ADP96787.1	1 PRK07869	677.47	Marinobacter adhaerens (strain DSM 23420 / HP15)
H8WBP3	CCG93690.1	1 COG0154	368.16	Marinobacter hydrocarbonoclasticus ATCC 49840
A0A1W6K3W3	ARM82123.1	1 cl18951	353.36	Marinobacter salarius
A0A1C3JP51	A0A1C3JP51	1 COG0154	316.93	Marinomonas gallaica
A0A1A8T5V6	SBS27780.1	1 COG0154	296.9	Marinomonas spartinae
A0A068DFK2	AID33410.1	1 COG0154	308.45	Mesorhizobium huakuii 7653R
A0A090FKT7	CDX44609.1	1 COG0154	321.55	Mesorhizobium plurifarium
A0A090E4Q5	CDX21843.1	1 COG0154	318.47	Mesorhizobium sp. ORS3359
A0A090ENA9	CDX32438.1	1 COG0154	318.47	Mesorhizobium sp. SOD10
A0A1E3H3I1	ODN70879.1	1 COG0154	179.03	Methylobrevis pamukkalensis
A0A0F0LDS8	KJL31283.1	1 cl18951	255.29	Microbacterium azadirachtae
A0A2P8AY42	PSK65391.1	1 COG0154	318.08	Micromonospora sp. MH33
A0A1J5RNJ1	OIQ97289.1	1 cl18951	295.96	mine drainage metagenome
A0A0U0ZTE6	CPV65311.1	1 COG0154	334.65	Mycobacterium abscessus
A0A1N0DAQ6	SHV30349.1	1 COG0154	330.41	Mycobacterium abscessus subsp. abscessus
A0A1N6AFE1	SIN32756.1	1 COG0154	332.72	Mycobacterium abscessus subsp. bolletii
A0A1T7W6V6	SKM64002.1	1 COG0154	332.72	Mycobacterium abscessus subsp. massiliense
A0A0J6W9F6	KMO78503.1	1 PRK07869	789.57	Mycobacterium chlorophenolicum
A0A0J6W7L7	KMO77627.1	1 PRK06061	769.25	Mycobacterium chubuense
A0A1V3XQ88	OOK80926.1	1 cl18951	46.61	Mycobacterium kansasii
X7Y501	EUA01906.1	1 cl18951	46.61	Mycobacterium kansasii 824
A0A0J6Y9F2	KMO69576.1	1 COG0154	318.85	Mycobacterium obuense
D5P7P7	EFG77891.1	1 PRK06061	789.28	Mycobacterium parascrofulaceum ATCC BAA-614

A0A202FU52	OUZ03240.1	1	COG0154	327.33	Mycobacterium paratuberculosis
A0A0D6IBQ3	CKH95081.1	1	COG0154	251.44	Mycobacterium smegmatis
L8F948	ELQ87854.1	1	PRK06061	786.2	Mycobacterium smegmatis (strain MKD8)
A0A240AD36	SNV81209.1	1	cl18951	321.16	Mycobacterium terrae
A0A0T9S9J6	CNJ51382.1	1	cl18951	79.26	Mycobacterium tuberculosis
X8FKH9	EUA93672.1	1	cl18951	102.27	Mycobacterium ulcerans str. Harvey
X8BHR1	EUA43006.1	0	no entry		Mycobacterium xenopi 3993
Q1CYM7	ABF91800.1	1	COG0154	346.97	Myxococcus xanthus (strain DK 1622)
F9EZJ5	EGQ75050.1	1	COG0154	299.98	Neisseria macacae ATCC 33926
G4CK47	EGY51774.1	1	COG0154	302.29	Neisseria shayeganii 871
A0A2P6L7Y9	PRD34697.1	1	cl18951	357.98	Nephila clavipes (Golden silk orbweaver)
W9V8H0	EXJ12342.1	1	cl18951	115.47	Nitrincola nitratireducens
A0A231GW69	OXR40869.1	1	COG0154	284.19	Nocardia cerradoensis
A0A0H5NGA5	CRY74523.1	1	PRK07869	682.1	Nocardia farcinica
A0A1A9GJH0	ANH38404.1	1	COG0154	263.77	Nocardioides dokdonensis FR1436
A0A1Y5TGA2	SLN63409.1	1	COG0154	326.94	Oceanibacterium hippocampi
A0A0A1MHT8	CEI82653.1	1	cl18951	464.29	Oceanobacillus oncorhynchi
W9AFE3	CDO04193.1	1	cl18951	470.46	Oceanobacillus picturae
R4YTJ3	CCK77043.1	1	COG0154	366.23	Oleispira antarctica RB-8
A0A0E3WGY6	CQR54353.1	1	cl18951	490.49	Paenibacillus riograndensis SBR5
A0A2M9NE97	PJN62497.1	1	cl18951	514.75	Paenibacillus sp. GM1FR
A0A239SAD1	SNU82172.1	1	COG0154	275.33	Pandoraea sputorum
A0A0U1KJ51	CQR46008.1	1	cl18951	479.7	Paraliobacillus sp. PM-2
A0A1X7AFR7	SMA36991.1	1	COG0154	364.69	Parendozoicomonas haliclonae
A0A238KTK6	SMX46135.1	0	querry exception		Pelagimonas varians
A0A0P1GXR8	CUH87486.1	1	cl18951	114.7	Phaeobacter sp. CECT 5382
A0A073CF91	KEI66786.1	1	COG0154	341.97	Planktothrix agardhii NIVA-CYA 126/8
K8WC88	EKT58174.1	1	COG0154	299.98	Providencia burhodogranariea DSM 19968
A0A024H881	CCQ47959.1	1	COG0154	273.02	Pseudarthrobacter siccitolerans
A0A127MTZ1	AMO76736.1	1	COG0154	291.89	Pseudomonas citronellolis
A0A1Q9QYC4	OLS60161.1	1	cl18951	287.65	Pseudomonas putida (Arthrobacter siderocapsulatus)
A0A1C3GU74	SAM33941.1	1	cl18951	319.62	Pseudomonas sp. 1 R 17
A0A1B5ENX2	CRM88048.1	1	cl18951	308.45	Pseudomonas sp. 22 E 5
A0A2H2YM22	CRM80544.1	1	cl18951	308.45	Pseudomonas sp. 31 E 6
A0A1B5DRR8	CRM50573.1	1	cl18951	318.85	Pseudomonas sp. 58 R 3
P13397	AAA25908.1	1	COG0154	285.73	Pseudomonas sp. (strain NK87)
A0A105T8Z6	KVV04240.1	1	cl18951	318.08	Pseudomonas sp. TAD18
A0A099SXA7	KUR41590.1	1	COG0154	305.76	Pseudomonas syringae pv. tomato
A0A1Y2NAK7	OSY43938.1	1	cl18951	612.76	Pseudonocardia autotrophica (Amycolata autotrophica) (Nocardia autotrophica)
A0A165TLS8	KZL06191.1	1	cl18951	211.99	Pseudovibrio sp. Ad26
A0A1R4EGM1	SJM37569.1	1	COG0154	298.05	Psychrobacter pasteurii
A0A1R4GUP9	SJM71966.1	1	COG0154	285.34	Psychrobacter piechaudii
F5SNM6	EGK14717.1	1	COG0154	285.34	Psychrobacter sp. 1501(2011)
A0A1U6GJN2	SLJ83708.1	1	COG0154	284.19	Psychrobacter sp. DAB_AL43B
A0A166H147	KZX19744.1	1	cl18951	130.49	Rathayibacter tanaceti
A0A1W6KTY7	ARM90891.1	1	cl18951	281.88	Rhizobium sp. CIAT894
A0A1H8N0M8	SEI09855.1	1	cl18951	165.54	Rhizobium tibeticum

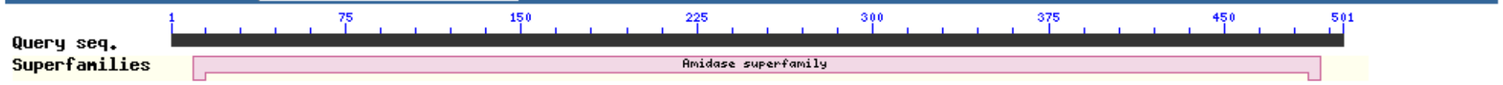
A0A1F2Q4G2	OFV77896.1	1	cl18951	291.12			Rhodococcus erythropolis (Arthrobacter picolinophilus)
A0A165LS60	AMY53540.1	1	COG0154	325.4			Rhodococcus fascians D188
A0A0D8I4R7	KJF25039.1	1	PRK07869	738.72			Rhodococcus sp. AD45
A0A2I9DAU8	GBF16438.1	1	PRK07869	749.12			Rhodococcus sp. Br-6
A0A143Q7E3	AMY18317.1	1	cl18951	315.99			Rhodococcus sp. PBTS 1
A0A143QHT7	AMY22499.1	1	COG0154	326.56			Rhodococcus sp. PBTS 2
A0A1Y5RXJ7	SLN27523.1	1	COG0154	207.92			Roseisalinus antarcticus
A0A1Q2YXL0	GAV35946.1	1	COG0154	271.86			Roseomonas sp. TAS13
A0A0P1E894	CUH44666.1	1	COG0154	209.84			Ruegeria atlantica
Q5LQG3	AAV95777.1	1	COG0154	280.72			Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)
A0A0P1I6U8	CUJ93919.1	1	COG0154	199.06			Ruegeria sp. CECT 5091
A0A0X2PD81	CUW25003.1	1	COG0154	265.31			Serratia
A0A2H1LLX6	SMZ58976.1	1	COG0154	265.31			Serratia grimesii
A0A021XH97	EYR84628.1	1	COG0154	301.91			Shinella sp. DD12
F7XC84	AEH81375.1	1	COG0154	278.41			Sinorhizobium meliloti (strain SM11)
A0A1V5I0C5	removed	0	n/a				Spirochaetes bacterium ADurb.BinA120
A0A239WPY8	SNV36266.1	1	cl18951	339.87	pfam07501	51.38	Streptococcus acidominimus
A0A0G6P5S0	CRV30531.1	1	PRK06529	900.34			Streptococcus equi subsp. equi
A0A239ST89	SNU88701.1	1	cl18951	790.56			Streptococcus merionis
Q8DTV5	AAN58903.1	1	PRK06529	909.2			Streptococcus mutans serotype c (strain ATCC 700610 / UA159)
A0A0Y1XIJ5	CVX74856.1	1	cl18951	112.22			Streptococcus pneumoniae
F8LIY3	CCB93303.1	1	cl18951	813.67			Streptococcus salivarius (strain CCHSS3)
A0A116M201	CYV23554.1	1	cl18951	786.71			Streptococcus suis
A0A2N9B277	SOR77440.1	1	COG0154	290.35			Streptomyces chartreusis NRRL 3882
A0A2K8PAY7	ATZ23280.1	1	COG0154	240.66			Streptomyces lavendulae subsp. lavendulae
A0A1Y2NKS5	OSY48102.1	1	COG0154	282.26			Streptomyces platensis
A0A0U5HFC4	CUW32201.1	1	COG0154	325.4			Streptomyces reticuli
A0A124C331	GAQ60006.1	1	COG0154	338.11			Streptomyces scabiei
A0A2P7ZYE4	PSK53232.1	1	cl18951	253.37			Streptomyces sp. 111WW2
A0A1D2IJJ3	ODA74583.1	1	cl18951	620.08			Streptomyces sp. AVP053U2
A0A1K2FZV5	SFY52671.1	1	COG0154	279.56			Streptomyces sp. F-1
A0A2K8REQ6	AUA15301.1	1	COG0154	264.54			Streptomyces sp. M56
A0A2P9FEF6	SPF06182.1	1	COG0154	339.27			Streptomyces sp. MA5143a
A0A068N7F4	AIE76027.1	1	pfam01425	377.02			Synechocystis sp. (strain PCC 6714) (Aphanocapsa sp. (strain PCC 6714))
A0A1V4XGE4	removed	0	n/a				Syntrophaceae bacterium PtaB.Bin095
A0A238D0E3	SBP86699.1	1	COG0154	340.81			Thiomonas delicata (Thiomonas cuprina)
A0A238DI14	SCC91137.1	1	COG0154	345.82			Thiomonas sp. X19
I3TLI8	AFK53626.1	1	cl18951	304.21			Tistrella mobilis (strain KA081020-065)
A0A0H2LVZ3	KLN54384.1	1	COG0154	262.62			Variovorax paradoxus
A0A1C3JAB8	SBT12094.1	1	COG0154	268.01			Vibrio celticus
A0A1C3II24	SBS61074.1	1	COG0154	266.85			Vibrio splendidus
A0A024QGQ4	CDQ41684.1	1	cl18951	473.15			Virgibacillus massiliensis
A0A2K9J0P4	AUJ25274.1	1	cl18951	460.83			Virgibacillus pantothenticus

SAMPLE SCREEN SHOT OF CONSERVED DOMAINS DATABASE SCREEN:



6-aminohexanoate-cyclic-dimer hydrolase [Virgibacillus pantothenticus]

Graphical summary Zoom to residue level show extra options »



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	Name	Accession	Description	Interval	E-value
[–]	Amidase super family	cl18951	Amidase;	10-491	3.23e-159

Amidase;

The actual alignment was detected with superfamily member PRK06529:

Pssm-ID: 327489 **Cd Length:** 482 **Bit Score:** 460.83 **E-value:** 3.23e-159

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                        10        20        30        40        50        60        70        80
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1318755899  10 DAVDLADLVKKGETTEEELLQASLEQLAQVNPTLHAVISERKEKALQEWKDITY-NRPFRGVPVLLKNTGQQLKGERTTS 88
Cdd:PRK06529    5 DATAMAQAVQQGQVTPLELVTQAIYKAKKLNPTLNAIVSERYEEALEEAKQRDFsGKPFAGVPIFLKDLGQELKGQLSTS 84

                        90       100       110       120       130       140       150       160
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gi 1318755899  89 GSKLLKQYapVAKQDSHFVRAFRDAGFQFIGHTNTPEFGLKNITEPETDGPTRNPWNVAYSPGGSSGGSAAAVAAGIVPL 168
Cdd:PRK06529   85 GSRLFKNY--QATKTDLYVKRLEDLGFIILGRSNTPEFGFKNISDSSLHGPVNLPFDNSRNAGGSSGGAAALVSSGIVAL 162

                       170       180       190       200       210       220       230       240
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1318755899 169 AGASDGGGSIRIPASFTGLFGLKPTRGRTPVGPGAGRQWHGAAIDFVLSRSVRDSAAMLDVLQTSQPEAAFQAPLYLEsy 248
Cdd:PRK06529  163 AAASDGGGSIRIPASFNGLIGLKPSRGRIPVGPGSYRGWQGASVHFALTKSVRDTRRLLYYLQMYQMESPFPLATLSK-- 240

                       250       260       270       280       290       300       310       320
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1318755899 249 lETMKQPPKEELRIAYSVTSPVGTPVSNEAKEAVMKTVQWLERLGYQIEE-NDPPIDGKELMRNYYLMNSGEIATVGMQL 327
Cdd:PRK06529  241 -ESLFQSLQRPLKIAFYQRSPDGSPVSLDAAKALKQAVTFLREQGHEVVEleEFPLDMTEVMRSYYIMNSVETAAMFDDI 319

                       330       340       350       360       370       380       390       400
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1318755899 328 EKMIGRKITSDDVELETWLLHCAGQSVSAAAFSSSIASWDVAAAAMADFHKSYDFYITPATAFTAPKVGELSWDNIEKKR 407
Cdd:PRK06529  320 EDALGRPMTKDDMETMTWAIYQSGQDIPAKRYSQVLQKWDTYSATMASFHETYDLLLTFTTNTPAPKHGQLDPDSKLMAN 399

                       410       420       430       440       450       460       470       480
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 1318755899 408 wITKMENAKANEKQEIIYDMFLPSLTYTPFTQLANLTGQPAMSLPLHVTSENMPLGLQVTANKGEEHRLLQLAYQLEETD 487
Cdd:PRK06529  400 -LAQAEIFSSEEQQNLVETMFEKSLAITPYTALANLTGQPAISLPTYETKEGLPMGVQLIAAKGREDLLLGIAEQFEAAG 478

                ....
gi 1318755899 488 LWQG 491
Cdd:PRK06529  479 LLKI 482
```

SAMPLE SCREEN SHOT OF UNIPROT NYLA SEARCH:

UniProt

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Nylanderia sp. NYLA002 (16)

Nylanderia sp. NYLA003 (17)

Nylanderia sp. NYLA005 (9)

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Entry	Entry name	Organism	Protein names	Gene names	Length
A0A116LMD4	A0A116LMD4_STRSU	Streptococcus suis	Amidase	**nylA** ERS132421_01386	482
A0A0Z8E6P7	A0A0Z8E6P7_STRSU	Streptococcus suis	Amidase	**nylA** ERS132370_01358	482
A0A0Z8L219	A0A0Z8L219_STRSU	Streptococcus suis	Amidase	**nylA** ERS132440_01857	482
A0A0Z8F9P1	A0A0Z8F9P1_STRSU	Streptococcus suis	Amidase	**nylA** ERS132502_00463	482
A0A0Z8SP32	A0A0Z8SP32_STRSU	Streptococcus suis	Amidase	**nylA** ERS132536_01456	482
A0A0Z8S8C1	A0A0Z8S8C1_STRSU	Streptococcus suis	Amidase	**nylA** ERS132551_00941	482
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A0A0Z8GQ06	A0A0Z8GQ06_STRSU	Streptococcus suis	Amidase	**nylA** ERS132393_01944	482
A0A123T3Y1	A0A123T3Y1_STRSU	Streptococcus suis	Amidase	**nylA** ERS132392_02100	482
A0A116LQC9	A0A116LQC9_STRSU	Streptococcus suis	Amidase	**nylA** ERS132410_01796	482
A0A0Z8DJA8	A0A0Z8DJA8_STRSU	Streptococcus suis	Amidase	**nylA** ERS132399_00060	482
A0A0Z8QS84	A0A0Z8QS84_STRSU	Streptococcus suis	Amidase	**nylA** ERS132444_00393	482
A0A123T9P9	A0A123T9P9_STRSU	Streptococcus suis	Amidase	**nylA** ERS13	482

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Testing the Hypothesis that the Nylonase NylB Protein
Arose de novo via a Frameshift Mutation

Salvador Cordova and John Sanford

Supplementary Table S4
List of organisms with NylC from uniprot, and conserved domains of NylCs
with sample screen captures from NIH CDD and UNIPROT websites at the bottom

NOTES:
cd00123 = DmpA/OAT superfamily; composed of L-aminopeptidase D-amidase/D-esterase (DmpA), ornithine acetyltransferase (OAT) and similar proteins. DmpA is an aminopeptidase that releases N-terminal D and L amino acids from peptide substrates. This group represents one of the rare aminopeptidases that are not metalloenzymes. DmpA shows similarity in catalytic mechanism to N-terminal nucleophile (Ntn) hydrolases, which are enzymes that catalyze the cleavage of amide bonds through the nucleophilic attack of the side chain of an N-terminal serine, threonine, or cysteine. OAT catalyzes the first and fifth steps in arginine biosynthesis, coupling acetylation of glutamate with deacetylation of N-acetylornithine, which allows recycling of the acetyl group in the arginine biosynthetic pathway. The superfamily also contains an enzyme, endo-type 6-aminohexanoate-oligomer hydrolase, that have been shown to be involved in nylon degradation. Proteins in this superfamily undergo autocatalytic cleavage of an inactive precursor at the site immediately upstream to the catalytic nucleophile.

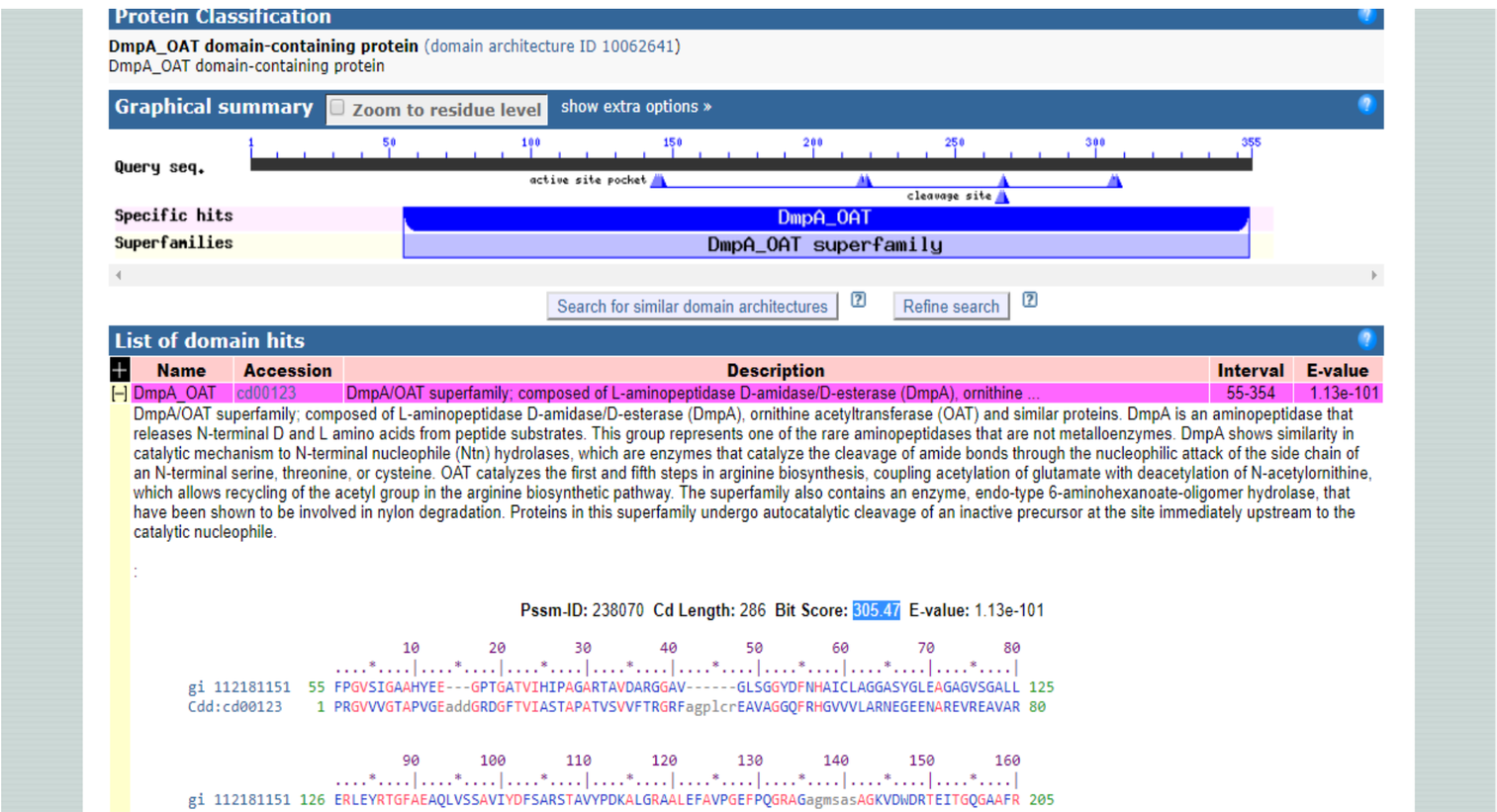
cl00603 = DmpA/OAT superfamily; composed of L-aminopeptidase D-amidase/D-esterase (DmpA), ornithine acetyltransferase (OAT) and similar proteins. DmpA is an aminopeptidase that releases N-terminal D and L amino acids from peptide substrates. This group represents one of the rare aminopeptidases that are not metalloenzymes. DmpA shows similarity in catalytic mechanism to N-terminal nucleophile (Ntn) hydrolases, which are enzymes that catalyze the cleavage of amide bonds through the nucleophilic attack of the side chain of an N-terminal serine, threonine, or cysteine. OAT catalyzes the first and fifth steps in arginine biosynthesis, coupling acetylation of glutamate with deacetylation of N-acetylornithine, which allows recycling of the acetyl group in the arginine biosynthetic pathway. The superfamily also contains an enzyme, endo-type 6-aminohexanoate-oligomer hydrolase, that have been shown to be involved in nylon degradation. Proteins in this superfamily undergo autocatalytic cleavage of an inactive precursor at the site immediately upstream to the catalytic nucleophile.

cd02252 = nylC-like family; composed of proteins with similarity to Flavobacterium endo-type 6-aminohexanoate-oligomer hydrolase (EIII), the product of the nylon oligomer degradation gene, nylC. EIII is an amide hydrolase that catalyzes the degradation of highly-polymerized 6-aminohexanoate oligomers. Together with other nylon degradation enzymes, such as 6-aminohexanoate cyclic dimer hydrolase (EI) and 6-aminohexanoate dimer hydrolase (EII), EIII plays a role in the detoxification and biological removal of the synthetic by-products of nylon manufacture. EIII shows sequence similarity to L-aminopeptidase D-amidase/D-esterase (DmpA), an aminopeptidase that releases N-terminal D and L amino acids from peptide substrates. Like DmpA, EIII undergoes autocatalytic cleavage in front of a nucleophile to form a heterodimer. DmpA shows similarity in catalytic mechanism to N-terminal nucleophile (Ntn) hydrolases, which are enzymes that catalyze the cleavage of amide bonds through the nucleophilic attack of the side chain of an N-terminal serine, threonine, or cysteine.

no. avail. cdds	7
count NylCs	7

UNIPROT ID	Genbank ID	Conserved Domain Data Available	Primary Conserved Doma ACCESSION ID	Primary Conserved Domai Bit score	Secondary Conserved Domain ACCESSION ID	Secondary Conserved Domain Bit score	ORGANISM
Q79F77	BAA01528.1	1	cd00123	313.18			Flavobacterium sp.
Q57326	BAA05088.1	1	cd00123	313.18			Flavobacterium sp. KI723T1
Q1EPR5	BAE95769.2	1	cd00123	305.47			Agromyces sp. KY5R
Q1EPR4	BAE95770.1	1	cd00123	303.16			Kocuria sp. KY2
U2XM45	GAD34180.1	1	cl00603	196.68			Microbacterium sp. TS-1
C0R138	ACN83826.1	1	cd02252	306.46			Brachyspira hyodysenteriae (strain ATCC 49526 / WA1)
G0EJE2	AEM21141.1	1	cd02252	304.15			Brachyspira intermedia (strain ATCC 51140 / PWS/A) (Serpulina intermedia)

SAMPLE CDD WEBSITE SCREEN SHOT:



```
Cdd:cd00123   81 ARGLPRTGFAEEGE*LIASTYDIGRQYTP*ESIRAHLRTALWPAGEGGFDRGRAS------AGAARAI*TTDTGPGEARR 154

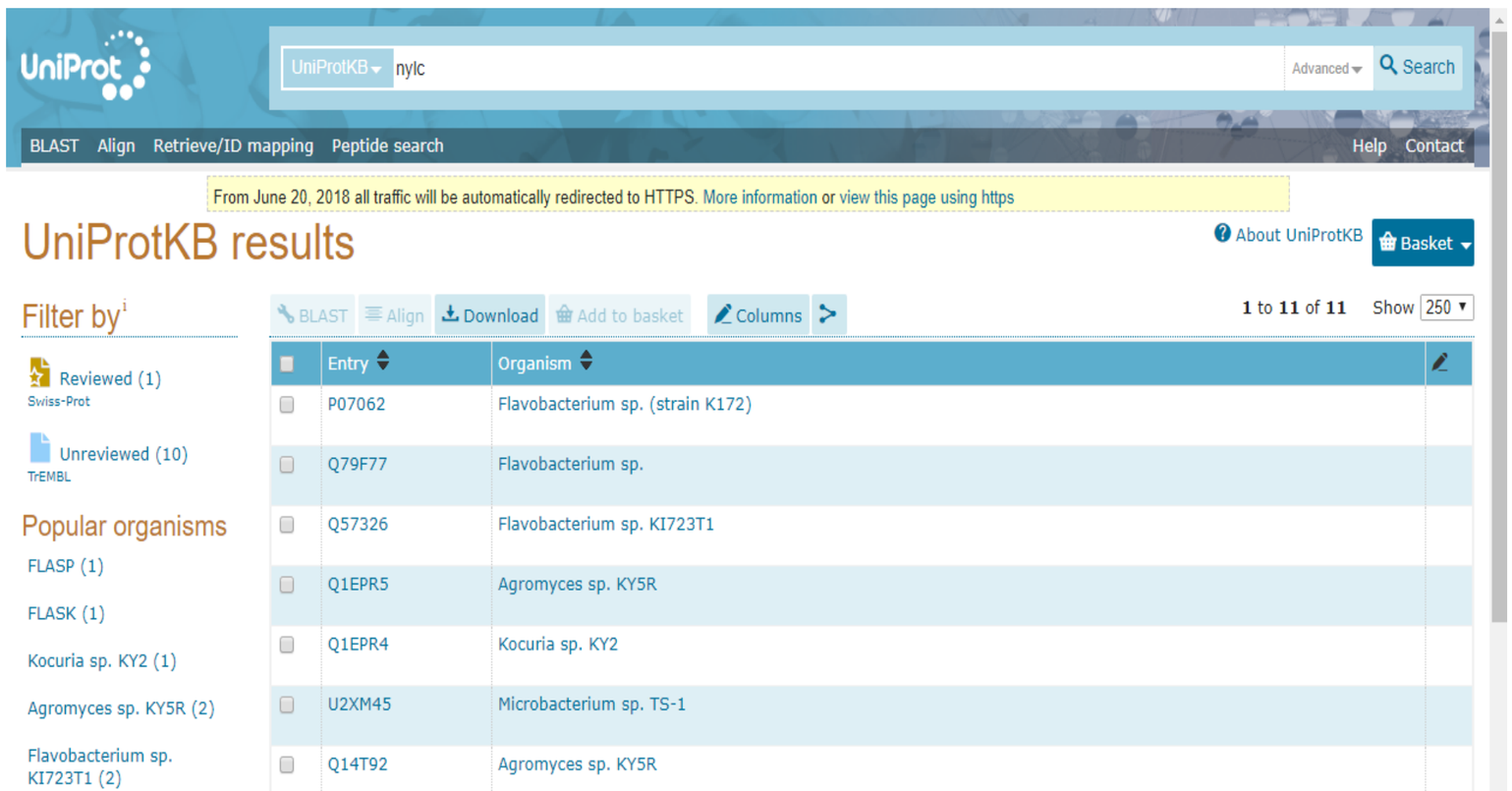
                       170       180       190       200       210       220       230       240
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....|....*....|
gi 112181151 206 RLGDVRILAVVVPNPVGVIMDRAGTVVRGnydaqtgvrrhpvfdyQEAFAEQVPPVTEAGNTTISAIVTNVRMSPVELNQ 285
Cdd:cd00123  155 SVGGATIVAIVKGNG*LEIVDRAGTVVRG---------------QEAFAEQVPPVTPD*ATLITFFATDARLDPAELDR 218

                       250       260       270       280       290       300
                ....*....|....*....|....*....|....*....|....*....|....*....|....*....
gi 112181151 286 FAKQVHSSMHRGIQPfHTDMDGDTLFAVTTDEIDLPTTPGSSRGRLSVNATALGAIASEVMWDAVLEAG 354
Cdd:cd00123  219 LARV*DRTFNRVSID-TDTSTGDTAVAFATGLAGLPTTPGSSRGRLEVDAGEFEEAAHTAALAAVKDAA 286
```

References:

Marchler-Bauer A et al. (2017). "CDD/SPARCLE: functional classification of proteins via subfamily domain architectures." **Nucleic Acids Res 45**(D)200-3.

SAMPLE SCREEN CAPTURE FROM UNIPROT:



Other organisms

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Filter "nylc" as:

gene name (6)

protein name (3)

Q59710	Flavobacterium sp. KI723T1	
C0R138	Brachyspira hyodysenteriae (strain ATCC 49526 / WA1)	
G0EJE2	Brachyspira intermedia (strain ATCC 51140 / PWS/A) (Serpulina intermedia)	
A0A146TFP9	Fundulus heteroclitus (Killifish) (Mummichog)	

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Taxonomy

Testing the Hypothesis that the Nylonase NylB Protein
Arose *de novo* via a Frameshift Mutation

Salvador Cordova and John Sanford

Supplementary Table S5
List of organisms with a 6-aminohexanoate hydrolase from UNIPROT
with sample screen capture from UNIPROT website at the bottom

	UNIPROT ID	ORGANISM
1	A0A1F2PJC9	Acetobacterium wieringae
2	A9NHQ9	Acholeplasma laidlawii (strain PG-8A)
3	A0A1Z3GY09	Achromobacter denitrificans (Alcaligenes denitrificans)
4	A0A225MGN3	Achromobacter marplatensis
5	A0A0L6IER7	Achromobacter piechaudii
6	D4XAB8	Achromobacter piechaudii ATCC 43553
7	A0A1D8IES6	Achromobacter ruhlandii
8	A0A0M7D486	Achromobacter sp.
9	A0A162N388	Achromobacter sp. AR476-2
10	A0A246Q7U7	Achromobacter sp. HZ28
11	A0A0U1QAU6	Achromobacter sp. LC458
12	A0A0Q8K4P9	Achromobacter sp. Root170
13	A0A0Q8BA96	Achromobacter sp. Root565
14	A0A0Q8X5T1	Achromobacter sp. Root83
15	A0A095X3S6	Achromobacter sp. RTa
16	A0A0L0QTC4	Achromobacter spanius
17	A0A066PM46	Acidiphilium sp. JA12-A1
18	F7S2L8	Acidiphilium sp. PM
19	A0A0D8HH63	Acidithrix ferrooxidans
20	A0A165JNH4	Acidovorax sp. GW101-3H11
21	K0HY31	Acidovorax sp. KKS102
22	A0A235EL10	Acidovorax sp. KNDSW-TSA6
23	A0A0S9F8F4	Acidovorax sp. Leaf76
24	A0A0Q4RIF5	Acidovorax sp. Leaf78
25	H0BTY1	Acidovorax sp. NO-1
26	A0A0Q8TAG5	Acidovorax sp. Root217
27	A0A0Q8T7V0	Acidovorax sp. Root219
28	A0A0Q9CUG8	Acidovorax sp. Root275
29	A0A0Q6ZDN0	Acidovorax sp. Root402
30	A0A0Q8LML1	Acidovorax sp. Root70
31	A0A1E3ZU93	Acidovorax sp. SCN 65-28
32	A0A0Q0SWC	Acidovorax sp. SD340
33	A0A1G5L686	Acinetobacter baumannii

34	A0A239RVT3	Acinetobacter johnsonii
35	S7WVF4	Acinetobacter junii MTCC 11364
36	A0A150HSM2	Acinetobacter venetianus
37	A0A1V5IP05	Actinobacteria bacterium ADurb.BinA094
38	W7JEG2	Actinokineospora spheciospongiae
39	A0A1Q9TSC2	Actinomadura sp. CNU-125
40	U5W414	Actinoplanes friuliensis DSM 7358
41	G8SAD2	Actinoplanes sp. (strain ATCC 31044 / CBS 674.73 / SE50/110)
42	A0A0M3DZD5	Afipia massiliensis
43	A0A1M2ZX57	Afipia sp. 62-7
44	A0A1H0JGI6	Afipia sp. GAS231
45	A0A0Q6Z796	Afipia sp. Root123D2
46	A0A1Z9VA19	Afipia sp. TMED4
47	R9PTA2	Agarivorans albus MKT 106
48	K2QYS9	Agrobacterium albertimagni AOL15
49	A0A0D8KR75	Agrobacterium arsenijevicii
50	A0A1S7RI05	Agrobacterium fabrum str. J-07
51	A0A1S7MVW	Agrobacterium genomosp. 1 str. TT111
52	A0A1S7MNB7	Agrobacterium genomosp. 2 str. CFBP 5494
53	B9JH68	Agrobacterium radiobacter (strain K84 / ATCC BAA-868)
54	A0A071I2G0	Agrobacterium rhizogenes
55	A0A1R3U120	Agrobacterium sp. DSM 25559
56	A0A1B3NSJ3	Agrobacterium sp. RAC06
57	A0A1E3Y6R8	Agrobacterium sp. SCN 61-19
58	F0LFF7	Agrobacterium sp. (strain H13-3) (Rhizobium lupini (strain H13-3))
59	H0HHN7	Agrobacterium tumefaciens 5A
60	A0A202F2X2	Agrobacterium vitis (Rhizobium vitis)
61	Q14TA0	Agromyces sp. KY5R
62	A0A164DTT4	Agromyces sp. NDB4Y10
63	A0A0M9GN66	Ahrensia marina
64	A0A1H2T3N9	Albimonas donghaensis
65	A0A1I3JY37	Albimonas pacifica
66	A0A0A2NEC9	Alcaligenes faecalis
67	A0A1B6AXE2	Alcaligenes faecalis subsp. faecalis NBRC 13111
68	Q5YFS2	Alcaligenes xylosoxydans xylosoxydans (Achromobacter xylosoxidans)
69	A0A0P1J495	Alcanivorax dieselolei
70	A0A0B4XK86	Alcanivorax pacificus W11-5
71	A0A154C0V0	Alcanivorax sp. KX64203
72	A0A1V0FQE3	Alcanivorax xenomutans
73	A0A090VEN9	Algibacter lectus
74	B7DSV3	Alicyclobacillus acidocaldarius LAA1
75	A0A0P9CFM4	Alicyclobacillus ferrooxydans
76	A0A2A2G9D6	Aliifodinibius sp. WN023
77	A0A0P7KJ31	Aliiroseovarius crassostreae
78	A0A1B9PJ06	Aliivibrio sp. 1S175

79	A0A259NTY8	Alishewanella sp. 34-51-39
80	A0A011SHZ7	Alkalibacterium sp. AK22
81	A0A225Q6Z4	Alkalimicrobium pacificum
82	A0A1S8CRT6	Alkanindiges sp. H1
83	A0A0N1LKH9	alpha proteobacterium AAP38
84	A0A061QAK6	alpha proteobacterium Q-1
85	A0A1V1PU51	alpha proteobacterium U9-1i
86	A0A2A5BK32	Alphaproteobacteria bacterium
87	A0A258H4W3	Alphaproteobacteria bacterium 32-64-14
88	A0A1Q3JWA2	Alphaproteobacteria bacterium 64-6
89	A0A1Q3IWY5	Alphaproteobacteria bacterium 65-7
90	A0A1V6FWC3	Alphaproteobacteria bacterium ADurb.Bin100
91	A0A1V5FSP3	Alphaproteobacteria bacterium ADurb.BinA280
92	A0A1L9QFD7	Alphaproteobacteria bacterium AO1-B
93	A0A257HQ80	Alphaproteobacteria bacterium PA1
94	A0A257J3M2	Alphaproteobacteria bacterium PA2
95	A0A257JNK2	Alphaproteobacteria bacterium PA3
96	A0A1F3AL54	Alphaproteobacteria bacterium RIFCSPHIGHO2_12_FULL_63_12
97	A0A1Z9D0B1	Alphaproteobacteria bacterium TMED110
98	A0A1Z9WK57	Alphaproteobacteria bacterium TMED89
99	A0A0F7KSK3	Altererythrobacter atlanticus
100	A0A1B2A9T7	Altererythrobacter dongtanensis
101	A0A0M4M6L1	Altererythrobacter epoxidivorans
102	A0A1C7D5F0	Altererythrobacter namhicola
103	A0A0T2QIV8	Altererythrobacter sp. Root672
104	A0A1Z9BMI0	Alteromonadaceae bacterium TMED101
105	A0A0N0XJM8	Amantichitinum ursilacus
106	A0A142M3Y6	Aminobacter aminovorans (Chelatobacter heintzii)
107	A0A0Q6LJV1	Aminobacter sp. Root100
108	A0A178X0M9	Amycolatopsis sp. M39
109	A0A229RJG4	Amycolatopsis thailandensis
110	A0A1B7V2W3	Anabaena sp. LE011-02
111	A0A1B7WVL8	Anabaena sp. MDT14b
112	A0A0D6QPK1	Anaeromyxobacter sp. PSR-1
113	A7HFI3	Anaeromyxobacter sp. (strain Fw109-5)
114	A0A136WJN9	Anaerotignum neopropionicum
115	A0A1S1V4U0	Andreesenia angusta
116	A0A0U5BA19	Aneurinibacillus soli
117	A0A222E5F8	Antarctobacter heliothermus
118	A0A011UTK5	Aquamicrobium defluvii
119	A0A023BRB5	Aquimarina atlantica
120	A0A1Y5T7Z2	Aquimixticola soesokkakensis
121	A0A224VWD9	Aquitalea magnusonii
122	A0A1Q8A510	archaeon 13_1_20CM_2_54_9
123	A0A1Q3HRQ9	Archangium sp. Cb G35

124	A0A1B6A3B9	Arenibacter sp. C-21
125	N1UZN7	Arthrobacter crystallopoietes BAB-32
126	A0A0S7CR24	Arthrobacter sp. Hiyo1
127	A0A0K2QWB	Arthrobacter sp. Hiyo4
128	A0A0K2RNW	Arthrobacter sp. Hiyo8
129	A0A0D4BXM3	Arthrobacter sp. IHBB 11108
130	J7LU22	Arthrobacter sp. Rue61a
131	A0A1E8FMB1	Arthrobacter sp. SW1
132	A2QLY1	Aspergillus niger (strain CBS 513.88 / FGSC A1513)
133	V4MYJ7	Asticcacaulis sp. AC402
134	V4PU99	Asticcacaulis sp. AC460
135	A0A0Q6FA40	Aurantimonas sp. Leaf443
136	A0A0B1Q326	Aureimonas altamirensis
137	A0A0Q5HAK2	Aureimonas sp. Leaf324
138	A0A0Q6CPC6	Aureimonas sp. Leaf427
139	A0A0Q6CP76	Aureimonas sp. Leaf454
140	A0A0Q6DW7	Aureimonas sp. Leaf460
141	A0A175R826	Aureimonas ureilytica
142	A0A087SMR5	Auxenochlorella protothecoides (Green microalga) (Chlorella protothecoides)
143	A0A235H8Q6	Azospirillum brasilense
144	D3P1A2	Azospirillum sp. (strain B510)
145	A0A0F2KK19	Azospirillum thiophilum
146	A0A2C3GRV6	Bacillus anthracis
147	A0A1J6VSB4	Bacillus aquimaris
148	A0A1D7QVD8	Bacillus beveridgei
149	A0A023P794	Bacillus bombysepticus str. Wang
150	A0A2C2HET0	Bacillus cereus
151	C2NZG8	Bacillus cereus 172560W
152	C2TIZ3	Bacillus cereus 95/8201
153	B5ULQ5	Bacillus cereus AH1134
154	C2YSH7	Bacillus cereus AH1271
155	C2Z8T6	Bacillus cereus AH1272
156	C2XV04	Bacillus cereus AH603
157	C2PWE8	Bacillus cereus AH621
158	C2N382	Bacillus cereus ATCC 10876
159	C2QVJ8	Bacillus cereus ATCC 4342
160	R8HVQ8	Bacillus cereus BAG1O-1
161	S3IIV2	Bacillus cereus BAG1O-3
162	R8DWH5	Bacillus cereus BAG1X1-1
163	R8FKZ9	Bacillus cereus BAG1X2-1
164	R8FW19	Bacillus cereus BAG1X2-2
165	R8GEZ8	Bacillus cereus BAG1X2-3
166	R8K6C8	Bacillus cereus BAG2O-1
167	C2T1Y1	Bacillus cereus BDRD-Cer4
168	C2SL82	Bacillus cereus BDRD-ST196

169	C2S4A4	Bacillus cereus BDRD-ST26
170	C2NIK6	Bacillus cereus BGSC 6E1
171	C2XCG9	Bacillus cereus F65185
172	R8D9F4	Bacillus cereus HuA2-9
173	R8D3V5	Bacillus cereus HuA3-9
174	R8M143	Bacillus cereus HuB13-1
175	R8RYL3	Bacillus cereus HuB4-4
176	R8Q0D3	Bacillus cereus ISP2954
177	R8IPR3	Bacillus cereus K-5975c
178	C2MLL8	Bacillus cereus m1293
179	C2RAP0	Bacillus cereus m1550
180	R8K9D9	Bacillus cereus MC118
181	C2PFW9	Bacillus cereus MM3
182	B3Z4G2	Bacillus cereus NVH0597-99
183	C2QCQ2	Bacillus cereus R309803
184	C2UES0	Bacillus cereus Rock1-15
185	C2UWA5	Bacillus cereus Rock3-28
186	C2VCU2	Bacillus cereus Rock3-29
187	C2VUP1	Bacillus cereus Rock3-42
188	C2W8N2	Bacillus cereus Rock3-44
189	C2X0T7	Bacillus cereus Rock4-18
190	C2WPT9	Bacillus cereus Rock4-2
191	R8CAB4	Bacillus cereus str. Schrouff
192	A0A158RQH7	Bacillus cereus (strain 03BB102)
193	B7HXV3	Bacillus cereus (strain AH187)
194	B7JFB1	Bacillus cereus (strain AH820)
195	Q734U4	Bacillus cereus (strain ATCC 10987 / NRS 248)
196	Q81CK3	Bacillus cereus (strain ATCC 14579 / DSM 31 / JCM 2152 / NBRC 15305 / NCIMB 9373 / NRRL B-3711)
197	B7HC46	Bacillus cereus (strain B4264)
198	B7IPG8	Bacillus cereus (strain G9842)
199	B9IRP0	Bacillus cereus (strain Q1)
200	Q63AJ3	Bacillus cereus (strain ZK / E33L)
201	R8Y226	Bacillus cereus TIAC219
202	D8H0A0	Bacillus cereus var. anthracis (strain CI)
203	R8HXD7	Bacillus cereus VD021
204	R8QEP8	Bacillus cereus VD118
205	R8LMS7	Bacillus cereus VD131
206	R8E0R6	Bacillus cereus VD133
207	R8P6H2	Bacillus cereus VD136
208	J7WYF9	Bacillus cereus VD142
209	R8MZI1	Bacillus cereus VD146
210	R8TXJ3	Bacillus cereus VD184
211	R8H2U2	Bacillus cereus VD196
212	R8QBI6	Bacillus cereus VDM006
213	R8ET56	Bacillus cereus VDM019

214	R8TE56	Bacillus cereus VDM021
215	R8P5Z7	Bacillus cereus VDM053
216	A0A0C5CBF9	Bacillus coagulans
217	A0A1D3QXB9	Bacillus cytotoxicus
218	A7GQG2	Bacillus cytotoxicus (strain DSM 22905 / CIP 110041 / 391-98 / NVH 391-98)
219	A0A073JYG4	Bacillus gaemokensis
220	A0A0T6BV65	Bacillus glycinifermentans
221	A0A2C6EZG0	Bacillus halotolerans
222	W4QEL0	Bacillus hemicellulosilyticus JCM 9152
223	A0A1V4FWV8	Bacillus intestinalis
224	A0A1Q8GU13	Bacillus licheniformis
225	A0A073JVJ5	Bacillus manliponensis
226	A0A1C3T9V5	Bacillus mycoides
227	W4EZC5	Bacillus mycoides FSL H7-687
228	C3AUD0	Bacillus mycoides Rock1-4
229	A0A1L8ZGH6	Bacillus obstructivus
230	A0A2C3KNT7	Bacillus pseudomycoides
231	C3BM98	Bacillus pseudomycoides DSM 12442
232	A0A1Q9BAH0	Bacillus pumilus (Bacillus mesentericus)
233	A0A0Q3VNL2	Bacillus solani
234	A0A1K0AIB5	Bacillus sp. 0711P9-1
235	A0A2A8MF21	Bacillus sp. AFS001701
236	A0A2A7X098	Bacillus sp. AFS002410
237	A0A2A8V769	Bacillus sp. AFS015896
238	A0A2A8S7B5	Bacillus sp. AFS018417
239	A0A2C3JV36	Bacillus sp. AFS029533
240	A0A2C3H8D5	Bacillus sp. AFS029637
241	A0A2C2LA07	Bacillus sp. AFS033286
242	A0A2C0YT17	Bacillus sp. AFS041924
243	A0A2C3KYA3	Bacillus sp. AFS051223
244	A0A2B9AS36	Bacillus sp. AFS053548
245	A0A2B8UE39	Bacillus sp. AFS054943
246	A0A2B8TV50	Bacillus sp. AFS055030
247	A0A2B4FNX2	Bacillus sp. AFS059628
248	A0A2B4M774	Bacillus sp. AFS075034
249	A0A2B4NJN4	Bacillus sp. AFS075960
250	A0A2B1GIX3	Bacillus sp. AFS077874
251	A0A2A9S957	Bacillus sp. AFS088145
252	A0A2A7E576	Bacillus sp. AFS094611
253	A0A2A7I6R0	Bacillus sp. AFS096315
254	A0A2A7H3Z5	Bacillus sp. AFS098217
255	A0A1V9W725	Bacillus sp. CDB3
256	A0A0N0E9M0	Bacillus sp. CHD6a
257	A0A1J9ZJK2	Bacillus sp. EB422
258	A0A0M4GRK4	Bacillus sp. FJAT-18017

259	A0A0M0W3R	Bacillus sp. FJAT-18019
260	A0A0M0WY2	Bacillus sp. FJAT-21945
261	A0A1B8W0Y	Bacillus sp. FJAT-26390
262	A0A1B9API9	Bacillus sp. FJAT-27225
263	A0A1B8WPD	Bacillus sp. FJAT-27264
264	A0A0W7Y5B	Bacillus sp. G3(2015)
265	N1LTX0	Bacillus sp. GeD10
266	A0A154AY22	Bacillus sp. GZT
267	W7ZHI9	Bacillus sp. JCM 19045
268	W7ZIP8	Bacillus sp. JCM 19046
269	W7ZMG2	Bacillus sp. JCM 19047
270	A0A135WX0	Bacillus sp. JH7
271	A0A2D0AU11	Bacillus sp. K2I17
272	A0A229M5W	Bacillus sp. KbaB1
273	A0A229MG3	Bacillus sp. KbaL1
274	A0A0J6NW31	Bacillus sp. LK2
275	A0A0J5GSX0	Bacillus sp. LL01
276	A0A226R6S0	Bacillus sp. M13(2017)
277	A0A246US95	Bacillus sp. MB353a
278	A0A1Q9KUV	Bacillus sp. MB366
279	A0A1J9Z069	Bacillus sp. MN5
280	A0A1J9SQX6	Bacillus sp. N35-10-2
281	A0A1J9T6B4	Bacillus sp. N35-10-4
282	A0A1J9VQB7	Bacillus sp. NH24A2
283	Q2B3E8	Bacillus sp. NRRL B-14911
284	A0A0Q9GJS1	Bacillus sp. Root11
285	A0A0Q9GLH	Bacillus sp. Root131
286	A0A1G1UPW	Bacillus sp. RZ2MS9
287	A6CHJ8	Bacillus sp. SG-1
288	A0A1K0A8L5	Bacillus sp. TD41
289	A0A1K0BSB8	Bacillus sp. TD42
290	A0A0F5RJL6	Bacillus sp. UMTAT18
291	A0A150L8N9	Bacillus sporothermodurans
292	A0A0D6Z7E6	Bacillus subterraneus
293	A0A136GAM	Bacillus subtilis
294	L8AQW9	Bacillus subtilis BEST7613
295	A0A0D0G9L6	Bacillus thermoamylovorans
296	A0A2B7CJL1	Bacillus thuringiensis
297	A0A1C9BVD	Bacillus thuringiensis Bt18247
298	J3UJR5	Bacillus thuringiensis HD-771
299	K0FV12	Bacillus thuringiensis MC28
300	C3G580	Bacillus thuringiensis serovar andalousiensis BGSC 4AW1
301	A0A243KDT7	Bacillus thuringiensis serovar argentinensis
302	A0A242Z7T1	Bacillus thuringiensis serovar balearica
303	A0A242WUY	Bacillus thuringiensis serovar cameroun

304	A0A243NER8	Bacillus thuringiensis serovar canadensis
305	A0A242YHW(	Bacillus thuringiensis serovar chanpaisis
306	A0A193CUP1	Bacillus thuringiensis serovar coreanensis
307	A0A243BXK5	Bacillus thuringiensis serovar graciosensis
308	A0A242XVI3	Bacillus thuringiensis serovar guiyangiensis
309	C3H3I2	Bacillus thuringiensis serovar huazhongensis BGSC 4BD1
310	A0A243KKJ1	Bacillus thuringiensis serovar iberica
311	Q3EMT6	Bacillus thuringiensis serovar israelensis ATCC 35646
312	A0A243A015	Bacillus thuringiensis serovar kim
313	A0A242ZE72	Bacillus thuringiensis serovar londrina
314	A0A242X1Z4	Bacillus thuringiensis serovar malayensis
315	A0A242WC7(	Bacillus thuringiensis serovar mexicanensis
316	A0A243A8I4	Bacillus thuringiensis serovar navarrensis
317	A0A242Y6U4	Bacillus thuringiensis serovar novosibirsk
318	A0A243FPY2	Bacillus thuringiensis serovar ostriniae
319	C3E5Q2	Bacillus thuringiensis serovar pakistani str. T13001
320	A0A243AXF7	Bacillus thuringiensis serovar pingluonsis
321	A0A243JFK4	Bacillus thuringiensis serovar pirenaica
322	A0A243BKT3	Bacillus thuringiensis serovar poloniensis
323	C3GJS5	Bacillus thuringiensis serovar pondicheriensis BGSC 4BA1
324	A0A243MNF8	Bacillus thuringiensis serovar sinensis
325	C3DKN7	Bacillus thuringiensis serovar sotto str. T04001
326	A0A243DHS4	Bacillus thuringiensis serovar subtoxicus
327	A0A243HVV7	Bacillus thuringiensis serovar thailandensis
328	M1QNZ9	Bacillus thuringiensis serovar thuringiensis str. IS5056
329	C3C4S0	Bacillus thuringiensis serovar tochigiensis BGSC 4Y1
330	A0A243E9U6	Bacillus thuringiensis serovar toumanoffi
331	A0A243D1M8	Bacillus thuringiensis serovar vazensis
332	A0A243C4A6	Bacillus thuringiensis serovar yosoo
333	A0A2C9Z9R1	Bacillus thuringiensis serovar yunnanensis
334	A0A2C9ZDH8	Bacillus thuringiensis serovar zhaodongensis
335	A0REW9	Bacillus thuringiensis (strain Al Hakam)
336	A0A243I197	Bacillus thuringiensis subsp. aizawai
337	A0A243LK93	Bacillus thuringiensis subsp. dakota
338	A0A243DV89	Bacillus thuringiensis subsp. darmstadiensis
339	A0A243GJ97	Bacillus thuringiensis subsp. finitimus
340	F0PJA2	Bacillus thuringiensis subsp. finitimus (strain YBT-020)
341	A0A243K649	Bacillus thuringiensis subsp. higo
342	A0A0K0SAE3	Bacillus thuringiensis subsp. indiana
343	A0A160LB34	Bacillus thuringiensis subsp. israelensis
344	A0A243MJ97	Bacillus thuringiensis subsp. jegathesan
345	A0A243IJB1	Bacillus thuringiensis subsp. konkukian
346	Q6HHY0	Bacillus thuringiensis subsp. konkukian (strain 97-27)
347	A0A243EUG8	Bacillus thuringiensis subsp. kumamotoensis
348	A0A2C9YWK	Bacillus thuringiensis subsp. kyushuensis

349	A0A243P328	Bacillus thuringiensis subsp. medellin
350	A0A0G4D072	Bacillus thuringiensis subsp. tolworthi
351	A0A0F6J5L2	Bacillus thuringiensis T01-328
352	A0A2B4TBY1	Bacillus toyonensis
353	A9VLT1	Bacillus weihenstephanensis (strain KBAB4)
354	A0A1A9PS17	Bacillus wiedmannii
355	A0A222FPD5	Bacterioplanes sanyensis
356	A0A1V5K7C0	bacterium ADurb.Bin478
357	A0A1V5JGZ1	bacterium ADurb.BinA028
358	A0A0A1P7J7	bacterium YEK0313
359	A0A180EZ91	Bacteroidales bacterium Barb4
360	A0A180FM12	Bacteroidales bacterium Barb6
361	A0A180FCF0	Bacteroidales bacterium Barb6XT
362	A0A0P0GQ77	Bacteroides cellulosilyticus
363	A0A120A2Y7	Bacteroides stercoris
364	A0A174H7V0	Bacteroides uniformis
365	A0A174JUS8	Bacteroides xylanisolvens
366	A0A1V6JEF7	Bacteroidetes bacterium ADurb.Bin008
367	A0A1V6IDS0	Bacteroidetes bacterium ADurb.Bin035
368	A0A1V6HGC1	Bacteroidetes bacterium ADurb.Bin041
369	A0A1V6CTM4	Bacteroidetes bacterium ADurb.Bin123
370	A0A1V6BDD1	Bacteroidetes bacterium ADurb.Bin141
371	A0A1V6BCZ2	Bacteroidetes bacterium ADurb.Bin145
372	A0A1V5P201	Bacteroidetes bacterium ADurb.Bin397
373	A0A1V5JE97	Bacteroidetes bacterium ADurb.BinA012
374	A0A1V5H839	Bacteroidetes bacterium ADurb.BinA174
375	A0A1B6Y5M2	Balneola sp. EhC07
376	A0A0N1B6M2	beta proteobacterium AAP99
377	A0A1V5QXL4	Betaproteobacteria bacterium ADurb.Bin341
378	D2Q8T9	Bifidobacterium dentium (strain ATCC 27534 / DSM 20436 / JCM 1195 / Bd1)
379	A0A173XH31	Bifidobacterium pseudocatenulatum
380	A0A087CCG7	Bifidobacterium pullorum
381	A0A087D044	Bifidobacterium saeculare DSM 6531 = LMG 14934
382	H6RLD2	Blastococcus saxobsidens (strain DD2)
383	A3ZNI7	Blastopirellula marina DSM 3645
384	A0A173YDV8	Blautia obeum
385	A0A173WUL9	Blautia wexlerae
386	A0A1U9VNG4	blood disease bacterium A2-HR MARDI
387	G2ZV67	blood disease bacterium R229
388	A0A146AU06	Bordetella ansorpii
389	A0A0H4WRC	Bordetella hinzii
390	A0A140KUK9	Bordetella pertussis
391	A9IF86	Bordetella petrii (strain ATCC BAA-461 / DSM 12804 / CCUG 43448)
392	A0A1E3ZIY9	Bordetella sp. SCN 67-23
393	A0A157SG71	Bordetella trematum

394	A0A257KPA7	Bradyrhizobiaceae bacterium PARB1
395	F7QJB4	Bradyrhizobiaceae bacterium SG-6C
396	A0A1I7JKF5	Bradyrhizobium arachidis
397	A0A1X3G9T0	Bradyrhizobium canariense
398	A0A2A6N274	Bradyrhizobium diazoefficiens
399	A0A0D1NEM9	Bradyrhizobium elkanii
400	A0A1H4P7Y1	Bradyrhizobium erythrophlei
401	A0A1B1UH73	Bradyrhizobium icense
402	A0A0M9BGF0	Bradyrhizobium japonicum
403	A0A023XFH2	Bradyrhizobium japonicum SEMIA 5079
404	A0A0R3M534	Bradyrhizobium jicamae
405	A0A1M7AIC6	Bradyrhizobium lablabi
406	A0A151G036	Bradyrhizobium liaoningense
407	K5C0A7	Bradyrhizobium lupini HPC(L)
408	A0A0R3DJI8	Bradyrhizobium manausense
409	A0A270RGP4	Bradyrhizobium ottawaense
410	A0A0R3BRG6	Bradyrhizobium pachyrhizi
411	A0A1B9Z1Y9	Bradyrhizobium paxllaeri
412	A0A0R3MQN	Bradyrhizobium retamae
413	A0A265PJ62	Bradyrhizobium sp. 2(2017)
414	A0A265QTQ1	Bradyrhizobium sp. 3(2017)
415	A0A1Q5R6Y1	Bradyrhizobium sp. AS23.2
416	A0A150U3Z1	Bradyrhizobium sp. AT1
417	A0A176YT67	Bradyrhizobium sp. BR 10245
418	A0A109K0E8	Bradyrhizobium sp. BR 10303
419	A0A1V5EMA9	Bradyrhizobium sp. BR10280
420	A0A2A6NSU6	Bradyrhizobium sp. C9
421	A0A0X8CI62	Bradyrhizobium sp. CCGE-LA001
422	A0A1I3SZ38	Bradyrhizobium sp. cf659
423	U1HQ00	Bradyrhizobium sp. DFCI-1
424	A0A0S6UGC6	Bradyrhizobium sp. DOA9
425	A0A1I3NHY1	Bradyrhizobium sp. Gha
426	A0A1I5UD35	Bradyrhizobium sp. Ghvi
427	A0A0Q6AS12	Bradyrhizobium sp. Leaf396
428	A0A1B9Z0V9	Bradyrhizobium sp. LMTR 3
429	A0A0D7PXW	Bradyrhizobium sp. LTSP849
430	A0A0D7PLA1	Bradyrhizobium sp. LTSP885
431	A0A0D7Q971	Bradyrhizobium sp. LTSPM299
432	A0A1Q5RAV8	Bradyrhizobium sp. NAS80.1
433	A0A1Q5RKK5	Bradyrhizobium sp. NAS96.2
434	A0A1H8I081	Bradyrhizobium sp. OK095
435	A0A1Y6KQM9	Bradyrhizobium sp. ORS 285
436	A0A1G7AFE4	Bradyrhizobium sp. R5
437	A0A1G7WSM	Bradyrhizobium sp. Rc2d
438	A0A1I4YQE0	Bradyrhizobium sp. Rc3b

439	I0G9L1	Bradyrhizobium sp. S23321
440	H0TB50	Bradyrhizobium sp. STM 3809
441	H0TIR1	Bradyrhizobium sp. STM 3843
442	A5E828	Bradyrhizobium sp. (strain BTAi1 / ATCC BAA-1182)
443	A4YJA9	Bradyrhizobium sp. (strain ORS 278)
444	H0SSJ3	Bradyrhizobium sp. (strain ORS 375)
445	A0A1C2ESQ5	Bradyrhizobium sp. UASWS1016
446	A0A1R1QGU9	Bradyrhizobium sp. UFLA 03-321
447	A0A2A2VDA7	Bradyrhizobium sp. UFLA03-84
448	A0A2A6PE34	Bradyrhizobium sp. Y36
449	A0A0R3KPP9	Bradyrhizobium valentinum
450	A0A0R3CAP9	Bradyrhizobium yuanmingense
451	A0A0J6BF55	Brevibacillus brevis (Bacillus brevis)
452	A0A0H0SQH3	Brevibacillus formosus
453	A0A0F6XZR3	Brevibacillus laterosporus (Bacillus laterosporus)
454	A0A075QW51	Brevibacillus laterosporus LMG 15441
455	A0A0K9YP49	Brevibacillus reuszeri
456	A0A177XKZ1	Brevibacillus sp. SKDU10
457	A0A0B9A9M9	Brevibacterium linens
458	A0A1S6ER20	Brevundimonas sp. LM2
459	A0A258HLW4	Brevundimonas subvibrioides
460	D7H3I5	Brucella abortus bv. 5 str. B3196
461	C4IUP8	Brucella abortus str. 2308 A
462	Q2YIN0	Brucella abortus (strain 2308)
463	A0A292DRS8	Brucella canis
464	A9MCQ6	Brucella canis (strain ATCC 23365 / NCTC 10854)
465	C0GAV5	Brucella ceti str. Cudo
466	A0A1Z1ZS86	Brucella melitensis
467	Q8YD58	Brucella melitensis biotype 1 (strain 16M / ATCC 23456 / NCTC 10094)
468	C0RMB9	Brucella melitensis biotype 2 (strain ATCC 23457)
469	C7LJ97	Brucella microti (strain CCM 4915)
470	C9V4N3	Brucella neotomae 5K33
471	A0A0E1WUX	Brucella pinnipedialis M292/94/1
472	A0A1P8S6Z0	Brucella sp. 09RB8910
473	A0A1M4LF47	Brucella sp. 10RB9215
474	A0A1G4F5J7	Brucella sp. 141012304
475	D1D0I3	Brucella sp. 83/13
476	E2PLG0	Brucella sp. BO2
477	D6LPC0	Brucella sp. NVSL 07-0026
478	D0P7U4	Brucella suis bv. 5 str. 513
479	A0A0U5MSK5	Brucella vulpis
480	A0A2A7TX17	Burkholderia ambifaria
481	Q0B2Z2	Burkholderia ambifaria (strain ATCC BAA-244 / AMMD) (Burkholderia cepacia (strain AMMD))
482	A0A118PBH1	Burkholderia anthina
483	A0A1V2WW2	Burkholderia cenocepacia

484	B1K5X2	Burkholderia cenocepacia (strain MC0-3)
485	A0A0U3TXS6	Burkholderia cepacia JBK9
486	A0A1Z3YPG9	Burkholderia cepacia (Pseudomonas cepacia)
487	A0A1E3FJI4	Burkholderia contaminans
488	A0A1B4BNP4	Burkholderia diffusa
489	A0A104JVG7	Burkholderia gladioli (Pseudomonas marginata) (Phytomonas marginata)
490	A0A0B6S3A2	Burkholderia glumae PG1
491	A0A0J5YLS6	Burkholderia lata (strain ATCC 17760 / DSM 23089 / LMG 22485 / NCIMB 9086 / R18194 / 383)
492	A0A1B4NNG3	Burkholderia latens
493	C4B1X1	Burkholderia mallei GB8 horse 4
494	A0A153L7U9	Burkholderia mallei (Pseudomonas mallei)
495	A0A0H2WG4	Burkholderia mallei (strain ATCC 23344)
496	A2S6W5	Burkholderia mallei (strain NCTC 10229)
497	A0A1B4HPS8	Burkholderia metallica
498	A0A228DPT2	Burkholderia multivorans
499	A0A0H3KPQ6	Burkholderia multivorans (strain ATCC 17616 / 249)
500	A0A1B4AQ54	Burkholderia oklahomensis C6786
501	A0A1B4AEU8	Burkholderia oklahomensis EO147
502	A0A0P0L247	Burkholderia plantarii
503	A0A1X4K397	Burkholderia pseudomallei (Pseudomonas pseudomallei)
504	A0A0H3HQ04	Burkholderia pseudomallei (strain 1026b)
505	Q3JY82	Burkholderia pseudomallei (strain 1710b)
506	A0A132E8W6	Burkholderia pseudomultivorans
507	A0A1X1PCN6	Burkholderia puraquae
508	A0A104MRE1	Burkholderia pyrrocinia (Pseudomonas pyrrocinia)
509	A0A118FQP0	Burkholderia seminalis
510	A0A103E805	Burkholderia singularis
511	A0A1E4YV47	Burkholderia sp. A2
512	A0A1X0MLR7	Burkholderia sp. A27
513	A0A103B5M3	Burkholderia sp. ABCPW 11
514	A0A132CC19	Burkholderia sp. ABCPW 14
515	A0A221AGH6	Burkholderia sp. AD24
516	A0A228HD74	Burkholderia sp. AU15512
517	A0A228I1E1	Burkholderia sp. AU16741
518	A0A228I2B6	Burkholderia sp. AU17325
519	A0A228KBI4	Burkholderia sp. AU27893
520	A0A228PZY0	Burkholderia sp. AU6039
521	A0A118E0C2	Burkholderia sp. BDU6
522	A0A118E585	Burkholderia sp. BDU8
523	A0A211YXS8	Burkholderia sp. Bk
524	A0A1B4R1K5	Burkholderia sp. Bp7605
525	A0A1J9PLS5	Burkholderia sp. DNA89
526	A0A124QG08	Burkholderia sp. FL-7-2-10-S1-D7
527	A0A1N6KWV	Burkholderia sp. GAS332
528	A0A0M5LLG7	Burkholderia sp. HB1

529	A0A228RJT8	Burkholderia sp. HI2714
530	A0A228QM82	Burkholderia sp. HI2761
531	A0A2A4C586	Burkholderia sp. IDO3
532	A0A132CUT8	Burkholderia sp. LA-2-3-30-S1-D2
533	A0A0Q5NY68	Burkholderia sp. Leaf177
534	A0A0J6M412	Burkholderia sp. LK4
535	A0A084DN29	Burkholderia sp. MSh2
536	A0A1Y9SLT7	Burkholderia sp. MSMB0266
537	A0A1B4M7W	Burkholderia sp. MSMB0856
538	A0A104LGU7	Burkholderia sp. MSMB1552
539	A0A118LL25	Burkholderia sp. MSMB1835
540	A0A1B4S4G4	Burkholderia sp. MSMB617WGS
541	A0A1B4DLK8	Burkholderia sp. NRF60-BP8
542	A0A160FG61	Burkholderia sp. OLGA172
543	A0A0X8L436	Burkholderia sp. PAMC 26561
544	A0A102ET31	Burkholderia sp. RF2-non_BP3
545	A0A1Q8J3Z7	Burkholderia sp. SRS-W-2-2016
546	A0A0N0IFV3	Burkholderia sp. ST111
547	A0A103EHI2	Burkholderia sp. TSV86
548	A0A0D8DX57	Burkholderia sp. USM B20
549	A0A1H5A9M8	Burkholderia sp. WP9
550	A0A1D7ZDR2	Burkholderia stabilis
551	A0A106NXD4	Burkholderia stagnalis
552	A0A105VIA1	Burkholderia territorii
553	A0A1B4K3N0	Burkholderia thailandensis
554	Q2STU4	Burkholderia thailandensis (strain ATCC 700388 / DSM 13276 / CIP 106301 / E264)
555	A0A108CIY8	Burkholderia ubonensis
556	A0A118EHR4	Burkholderia vietnamiensis
557	A0A0F0ESZ6	Burkholderiaceae bacterium 16
558	A0A0F0DFE5	Burkholderiaceae bacterium 26
559	A0A1Q3SCP3	Burkholderiales bacterium 64-34
560	A0A1Q3Y230	Burkholderiales bacterium 67-32
561	A0A257CSA2	Burkholderiales bacterium PBB3
562	A0A257LT33	Burkholderiales bacterium PBB5
563	A0A1F4ES80	Burkholderiales bacterium RIFCSPHIGHO2_01_FULL_64_960
564	A0A1F4IVC3	Burkholderiales bacterium RIFCSPHIGHO2_12_FULL_65_48
565	A0A1F4JN14	Burkholderiales bacterium RIFCSPLOWO2_02_FULL_57_36
566	A0A158CKL0	Caballeronia hypogeia
567	A0A0J1FT51	Caballeronia mineralivorans PML1(12)
568	A0A242M8D8	Caballeronia sordidicola
569	A0A1V5GNM	candidate division BRC1 bacterium ADurb.BinA364
570	A0A011PTN3	Candidatus Accumulibacter sp. BA-92
571	A0A011QU85	Candidatus Accumulibacter sp. BA-94
572	A0A084Y3V0	Candidatus Accumulibacter sp. SK-01
573	A0A080MKD1	Candidatus Accumulibacter sp. SK-02

574	A0A1V6B2J0	Candidatus Aminicenantes bacterium ADurb.Bin147
575	V9TR00	Candidatus Endolissoclinum faulkneri L5
576	A0A2A5EE89	Candidatus Hydrogenedentes bacterium
577	A0A1V6EEM6	Candidatus Hydrogenedentes bacterium ADurb.Bin101
578	X5MEY0	Candidatus Phaeomarinobacter ectocarpi
579	A0A1Z8UQW	Candidatus Puniceispirillum sp. TMED52
580	A0A0J9E550	Candidatus Rhodobacter lobularis
581	A0A1Q9P628	Candidatus Thorarchaeota archaeon AB_25
582	A0A0B7IGW9	Capnocytophaga canimorsus
583	F9YPG4	Capnocytophaga canimorsus (strain 5)
584	A0A0B7INU9	Capnocytophaga canis
585	A0A0B7H2X8	Capnocytophaga cynodegmi
586	A0A0R2JAN1	Carnobacterium maltaromaticum (Carnobacterium piscicola)
587	A0A0R2IS35	Carnobacterium maltaromaticum DSM 20342
588	K8EDK6	Carnobacterium maltaromaticum LMA28
589	A0A0U3MEA8	Carnobacterium sp. CP1
590	A0A0M2NMF	Catabacter hongkongensis
591	A0A174HD35	Catenibacterium mitsuokai
592	Q9A8N0	Caulobacter crescentus (strain ATCC 19089 / CB15)
593	A0A0H3C844	Caulobacter crescentus (strain NA1000 / CB15N)
594	A0A0P0NZJ7	Caulobacter henricii
595	A0A257X495	Caulobacter sp. 12-67-6
596	A0A258IZM8	Caulobacter sp. 32-67-35
597	A0A258KDE6	Caulobacter sp. 35-67-4
598	A0A259ID67	Caulobacter sp. 39-67-4
599	A0A0Q7TB71	Caulobacter sp. Root1455
600	A0A0Q7WNQ	Caulobacter sp. Root1472
601	A0A0Q6TSV5	Caulobacter sp. Root342
602	A0A0Q6UP28	Caulobacter sp. Root343
603	A0A0Q8FWR	Caulobacter sp. Root655
604	A0A0Q8GDX6	Caulobacter sp. Root656
605	A0A290MJ25	Caulobacter vibrioides (Caulobacter crescentus)
606	A0A1B1AF90	Caulobacteraceae bacterium OTSz_A_272
607	A0A258FJV6	Caulobacterales bacterium 32-69-10
608	A0A1Q3JML5	Caulobacterales bacterium 68-7
609	K1LUT6	Cecembia lonarensis LW9
610	A0A291GCN0	Celeribacter ethanolicus
611	A0A1Z9I936	Cellvibrionales bacterium TMED157
612	A0A1Z8MX29	Cellvibrionales bacterium TMED21
613	A0A1Z8RZJ5	Cellvibrionales bacterium TMED47
614	A0A1Z8TWE	Cellvibrionales bacterium TMED48
615	A0A1Z8Z7N2	Cellvibrionales bacterium TMED79
616	M7NIZ7	Cesiribacter andamanensis AMV16
617	A0A0K2DK09	Chelatococcus sp. CO-6
618	C7PKB0	Chitinophaga pinensis (strain ATCC 43595 / DSM 2588 / NCIB 11800 / UQM 2034)

619	A0A1X6W3T6	Chlamydia abortus (Chlamydophila abortus)
620	A0A0E9FL18	Chlamydia trachomatis
621	A0A136K2T4	Chlorobi bacterium OLB4
622	A0A136PFT0	Chlorobi bacterium OLB7
623	A0A1V5WGQ	Chloroflexi bacterium ADurb.Bin222
624	A0A1V5RV19	Chloroflexi bacterium ADurb.Bin325
625	A0A1V5QH62	Chloroflexi bacterium ADurb.Bin344
626	A0A1V5PDI7	Chloroflexi bacterium ADurb.Bin360
627	A0A1Q8TA39	Chromohalobacter japonicus
628	A0A083WRM	Chryseobacterium antarcticum
629	A0A1A7KL28	Chryseobacterium sp. MOF25P
630	A0A077KPP6	Chryseobacterium sp. StRB126
631	A0A239XLG5	Chryseobacterium taklimakanense
632	D0DE53	Citreicella sp. SE45
633	A0A1Y3FFF3	Clavibacter michiganensis subsp. michiganensis
634	A0A143Y291	Clostridiales bacterium CHKCI001
635	A0A1R4UEF4	Clostridioides difficile (Peptoclostridium difficile)
636	A0A0C1U0F9	Clostridium argentinense CDC 2741
637	A0A174SE58	[Clostridium] clostridioforme
638	A0A174Z2S0	Clostridium innocuum
639	A0A168MLP5	Clostridium ljungdahlii
640	A0A2A7ME47	Clostridium neonatale
641	A0A1V4IZP8	Clostridium oryzae
642	A0A1D9N0N6	Clostridium pasteurianum
643	A0A1S8TH57	Clostridium puniceum
644	A0A1A6B1J1	Clostridium ragsdalei P11
645	A0A0U5PQ27	Clostridium sp. C105KSO14
646	A0A0U5HF17	Clostridium sp. C105KSO15
647	A0A0F0CE38	Clostridium sp. FS41
648	A0A1F2CYH6	Clostridium sp. HMSC19B10
649	W6N4Q2	Clostridium tyrobutyricum DIVETGP
650	A0A0J8QLY7	Coccidioides immitis RMSCC 3703
651	A0A0J6IKJ4	Coccidioides posadasii RMSCC 3488
652	E9D435	Coccidioides posadasii (strain RMSCC 757 / Silveira) (Valley fever fungus)
653	G0ACC8	Collimonas fungivorans (strain Ter331)
654	A0A257EI85	Comamonadaceae bacterium PBBC1
655	A0A257G061	Comamonadaceae bacterium PBBC2
656	A0A0M2DUU0	Comamonas sp. E6
657	A0A2A7UQ41	Comamonas terrigena
658	A0A096HCR5	Comamonas testosteroni (Pseudomonas testosteroni)
659	B7WS76	Comamonas testosteroni (strain DSM 14576 / KF-1)
660	A0A076PZE3	Comamonas testosteroni TK102
661	A0A176TST0	Comamonas thiooxydans
662	W7E892	Commensalibacter sp. MX01
663	A0A0N9NR37	Confluentimicrobium sp. EMB200-NS6

664	A0A174DWD	Coprococcus comes
665	H8MKX6	Corallococcus coralloides (strain ATCC 25202 / DSM 2259 / NBRC 100086 / M2) (Myxococcus coralloides)
666	A0A1R3FXV9	Corchorus capsularis (Jute)
667	A0A0B6TVK5	Corynebacterium marinum DSM 44953
668	A0A1Q7LPF6	Crenarchaeota archaeon 13_1_40CM_3_53_5
669	A0A1B1BHD	Cryobacterium arcticum
670	H1SAR3	Cupriavidus basilensis OR16
671	A0A0M4KIS7	Cupriavidus gilardii CR3
672	A0A132HH88	Cupriavidus metallidurans
673	Q1LCI4	Cupriavidus metallidurans (strain ATCC 43123 / DSM 2839 / NBRC 102507 / CH34) (Ralstonia metallidurans)
674	A0A142JSV0	Cupriavidus nantongensis
675	F8GPZ8	Cupriavidus necator (strain ATCC 43291 / DSM 13513 / N-1) (Ralstonia eutropha)
676	Q46SW2	Cupriavidus necator (strain JMP 134 / LMG 1197) (Ralstonia eutropha (strain JMP 134))
677	L2EK81	Cupriavidus sp. HMR-1
678	V2J8V3	Cupriavidus sp. HPC(L)
679	A0A1U9UZA5	Cupriavidus sp. NH9
680	A0A069I7N4	Cupriavidus sp. SK-3
681	A0A022FUI7	Cupriavidus sp. SK-4
682	A0A1D9H6U3	Cupriavidus sp. USMAA2-4
683	B3RAT4	Cupriavidus taiwanensis (strain DSM 17343 / BCRC 17206 / CIP 107171 / LMG 19424 / R1) (Ralstonia taiwanensis (strain LMG 19424))
684	A0A1Y0N366	Curvibacter sp. AEP1-3
685	A0A2C6LKM4	Cutibacterium acnes (Propionibacterium acnes)
686	A0A2B7I057	Cutibacterium acnes subsp. acnes
687	A0A2B7HL54	Cutibacterium acnes subsp. defendens
688	A0A1B3Q1Y9	Cutibacterium avidum
689	G4CUD1	Cutibacterium avidum ATCC 25577
690	A0A239WW2	Cutibacterium granulosum
691	U1GEY5	Cutibacterium granulosum DSM 20700
692	A0A159Z148	Defluviimonas alba
693	A0A059IIY1	Defluviimonas sp. 20V17
694	A0A1U7NW2	Deinococcus marmoris
695	Q9RXS1	Deinococcus radiodurans (strain ATCC 13939 / DSM 20539 / JCM 16871 / LMG 4051 / NBRC 15346 / NCIMB 9279 / R1 / VKM B-1422)
696	A0A291JE33	Delftia acidovorans (Pseudomonas acidovorans) (Comamonas acidovorans)
697	A9BN79	Delftia acidovorans (strain DSM 14801 / SPH-1)
698	A0A081J655	Delftia sp. 670
699	A0A1C7L5Y4	Delftia sp. JD2
700	A0A210W8E3	Delftia sp. K82
701	A0A031IT02	Delftia sp. RIT313
702	F6AL57	Delftia sp. (strain Cs1-4)
703	A0A1D8J8Y0	Delftia tsuruhatensis
704	A0A1V6KGF2	Deltaproteobacteria bacterium ADurb.Bin002
705	A0A1V6IQ42	Deltaproteobacteria bacterium ADurb.Bin022
706	A0A1V6G442	Deltaproteobacteria bacterium ADurb.Bin072
707	A0A1V6AWT2	Deltaproteobacteria bacterium ADurb.Bin151
708	A0A1V5J955	Deltaproteobacteria bacterium ADurb.BinA014

709	A0A1V5HE73	Deltaproteobacteria bacterium ADurb.BinA179
710	A0A0S7YV12	Deltaproteobacteria bacterium SG8_13
711	A0A239V818	Dermatophilus congolensis
712	A0A1K1LEH2	Desulfovibrio piger
713	A0A0F5FSK2	Devosia geojensis
714	A0A0F5LW9C	Devosia limi DSM 17137
715	A0A0F5L6I5	Devosia soli
716	A0A1M3KS5C	Devosia sp. 66-22
717	A0A0Q4P836	Devosia sp. Leaf64
718	A0A178HXF3	Devosia sp. S37
719	A0A177LBJ1	Dietzia cinnamea
720	E6J575	Dietzia cinnamea P4
721	A0A199ATT5	Dietzia sp. 111N12-1
722	A0A1F1K8X7	Dietzia sp. HMSC21D01
723	A0A167H4E9	Dokdonella koreensis DS-123
724	A0A174A4R5	Dorea longicatena
725	A0A1W4UIN8	Drosophila ficusphila (Fruit fly)
726	A0A1E7WFA(	Duganella sp. HH101
727	A0A1E7V5C4	Duganella sp. HH105
728	A0A0Q5D7A2	Duganella sp. Leaf126
729	A0A0Q4P4G1	Duganella sp. Leaf61
730	A0A1E3AQH9	Eisenbergiella tayi
731	A0A0D5BQQ(	Elizabethkingia miricola (Chryseobacterium miricola)
732	A0A1X7AI28	Endozoicomonas sp. S-B4-1U
733	W8IBY1	Ensifer adhaerens OV14
734	A0A0L8BM63	Ensifer adhaerens (Sinorhizobium morelense)
735	A0A178XU98	Ensifer glycinis
736	A0A1C0SKE3	Ensifer sp. LC14
737	A0A1C0SQ09	Ensifer sp. LC54
738	A0A1S1T112	Ensifer sp. LCM 4579
739	A0A0Q7QGS	Ensifer sp. Root142
740	A0A0Q9E8V7	Ensifer sp. Root278
741	A0A1E3V7D0	Ensifer sp. YIC4027
742	A0A0J0HGF8	Enterobacter cloacae
743	G8LI19	Enterobacter cloacae EcWSU1
744	A0A181D6J5	Enterobacter kobei
745	R3L1W8	Enterococcus faecalis ATCC 6055
746	A0A0M2AE38	Enterococcus faecalis EnGen0302
747	A0A0M2AW7	Enterococcus faecalis EnGen0354
748	R3JGQ0	Enterococcus faecalis EnGen0359
749	A0A0M2CLC8	Enterococcus faecalis EnGen0426
750	V7ZSW4	Enterococcus faecalis PF3
751	Q836S5	Enterococcus faecalis (strain ATCC 700802 / V583)
752	A0A246MX18	Enterococcus faecalis (Streptococcus faecalis)
753	C0X1J8	Enterococcus faecalis TX0104

754	A0A1L8TTG8	Enterococcus gallinarum
755	A0A219BFR0	Enterococcus hirae 67-03-C5
756	J0NUD5	Enterococcus sp. C1
757	T0UCQ9	Enterococcus sp. HSIEG1
758	A0A135I9A2	Enterovibrio coralii
759	A0A1C3EPQ9	Enterovibrio pacificus
760	A0A165RC74	Erythrobacter sp. HI0063
761	A0A074M2K7	Erythrobacter sp. JL475
762	A0A0P6X3L4	Erythrobacter sp. SG61-1L
763	A0A1D3U0X1	Escherichia coli
764	A0A174ZK95	[Eubacterium] eligens
765	A0A173ZD16	Faecalicatena contorta
766	A0A0D8FW29	Ferrimicrobium acidiphilum DSM 19497
767	I0K217	Fibrella aestuarina BUZ 2
768	I2GH59	Fibrisoma limi BUZ 3
769	A0A160ILQ3	Fictibacillus phosphorivorans
770	A0A1V6AIT8	Firmicutes bacterium ADurb.Bin146
771	A0A1V5Y736	Firmicutes bacterium ADurb.Bin182
772	A0A1V5U0S1	Firmicutes bacterium ADurb.Bin248
773	A0A1V5TRM2	Firmicutes bacterium ADurb.Bin262
774	R7N860	Firmicutes bacterium CAG:95
775	A3J172	Flavobacteria bacterium BAL38
776	A0A1J0LM14	Flavobacteriaceae bacterium UJ101
777	A0A0D0EX75	Flavobacterium hibernum
778	A0A085ZZ56	Flavobacterium hydatis (Cytophaga aquatilis)
779	A0A226I074	Flavobacterium oncorhynchi
780	A0A226IS47	Flavobacterium plurextorum
781	Q79F77	Flavobacterium sp.
782	A0A1Q3ZT62	Flavobacterium sp. 38-13
783	A0A244D1Q8	Flavobacterium sp. AJR
784	Q57326	Flavobacterium sp. KI723T1
785	A0A0C1DR67	Flavobacterium sp. KMS
786	A0A0Q5V6G0	Flavobacterium sp. Leaf359
787	P13398	Flavobacterium sp. (strain K172)
788	A0A1V2AUB0	[Flexibacter] sp. ATCC 35208
789	A0A0Q9PIG2	Frateuria sp. Soil773
790	A0A0M9EWU	Fusarium langsethiae
791	N4TTL8	Fusarium oxysporum f. sp. cubense (strain race 1) (Panama disease fungus)
792	N1RYA1	Fusarium oxysporum f. sp. cubense (strain race 4) (Panama disease fungus)
793	A0A174KSI3	Fusicatenibacter saccharivorans
794	A0A174XLK7	Fusicatenibacter sp. 2789STDY5834925
795	Q1YU97	gamma proteobacterium HTCC2207
796	W2UH15	Gammaproteobacteria bacterium MOLA455
797	A0A1G0K8X0	Gammaproteobacteria bacterium RIFCSPLOWO2_12_FULL_52_10
798	A0A0S8A877	Gammaproteobacteria bacterium SG8_11

799	A0A0S8DTT8	Gammaproteobacteria bacterium SG8_47
800	A0A1Z9CP29	Gammaproteobacteria bacterium TMED112
801	A0A1Z9NL67	Gammaproteobacteria bacterium TMED219
802	A0A1Z9PFW0	Gammaproteobacteria bacterium TMED225
803	A0A1Z9PCI7	Gammaproteobacteria bacterium TMED226
804	A0A1Z9R0K5	Gammaproteobacteria bacterium TMED242
805	A0A1Z9TMI5	Gammaproteobacteria bacterium TMED278
806	A0A1Z8Q2H1	Gammaproteobacteria bacterium TMED36
807	A0A061NHN0	Geomicrobium sp. JCM 19037
808	A0A061NYJ9	Geomicrobium sp. JCM 19038
809	A0A061PHA8	Geomicrobium sp. JCM 19039
810	A0A061N0V9	Geomicrobium sp. JCM 19055
811	F3S710	Gluconacetobacter sp. SXCC-1
812	G7GNR0	Gordonia amarae NBRC 15530
813	M3VJE8	Gordonia paraffinivorans NBRC 108238
814	A0A222TFI4	Gordonia rubripertincta (Rhodococcus corallinus)
815	C8NIE3	Granulicatella adiacens ATCC 49175
816	A0A128EWV5	Grimontia celer
817	A0A212AFU6	Haematobacter genomosp. 1
818	A0A086Y029	Haematobacter massiliensis
819	A0A212AN47	Haematobacter missouriensis
820	M5E0U2	Halanaerobium saccharolyticum subsp. saccharolyticum DSM 6643
821	A0A2A5WR23	Halieaceae bacterium MED-G27
822	A0A059NVE7	Halobacillus karajensis
823	A0A126V1M6	Halocynthiibacter arcticus
824	A0A1J0VHN5	Halomonas aestuarii
825	A0A265DV80	Halomonas boliviensis LC1
826	A0A246S039	Halomonas campaniensis
827	A0A243T4U5	Halomonas desiderata SP1
828	A0A291JTQ4	Halomonas hydrothermalis
829	A0A098RAP9	Halomonas salina
830	A0A1P8R8J2	Halomonas sp. 1513
831	A0A101D421	Halomonas sp. 54_146
832	T2LAH3	Halomonas sp. A3H3
833	A0A1A9R1G0	Halomonas sp. ALS9
834	A0A1A0FKY5	Halomonas sp. G11
835	A0A2A3XJE5	Halomonas sp. JB37
836	A0A0C3DNU0	Halomonas sp. KHS3
837	A0A2A4HNA3	Halomonas sp. MBT G8648
838	A0A220RGN2	Halomonas sp. N3-2A
839	A0A1J8PCU6	Halomonas sp. QHL1
840	A0A1U9RGR	Halomonas sp. 'Soap Lake #7'
841	A0A2A2EQK1	Halomonas sp. WRN001
842	A0A172YJR4	Halotalea alkalilenta
843	A0A2A2F7D0	Halovibrio sp. YL5-2

844	A0A2C9D0T4	Hartmannibacter diazotrophicus
845	A2RQ43	Herbaspirillum seropedicae
846	D8J0D7	Herbaspirillum seropedicae (strain SmR1)
847	A4G8V7	Herminiimonas arsenicoxydans
848	A9B2R3	Herpetosiphon aurantiacus (strain ATCC 23779 / DSM 785)
849	A0A0P6YIJ7	Herpetosiphon geysericola
850	C6XP16	Hirschia baltica (strain ATCC 49814 / DSM 5838 / IFAM 1418)
851	A0A1C1YZ89	Hoeflea olei
852	F6EJ06	Hoyosella subflava (strain DSM 45089 / JCM 17490 / NBRC 109087 / DQS3-9A1) (Amycolicicoccus subflavus)
853	K1TDC0	human gut metagenome
854	A0A174B3K2	Hungatella hathewayi
855	A0A085WHH	Hyalangium minutum
856	A0A0W8FM0	hydrocarbon metagenome
857	A0A1L1PDA4	Hydrogenophaga intermedia
858	A0A1Q3QEU	Hydrogenophaga sp. 70-12
859	A0A1C9V9S3	Hydrogenophaga sp. PBC
860	Q31IT9	Hydrogenovibrio crunogenus (strain XCL-2) (Thiomicrospira crunogena)
861	A0A1L7SBN4	hydrothermal vent metagenome
862	A0A1E4BXY7	Hyphomicrobium sp. SCN 65-11
863	A0A0F2QIR6	Hyphomonadaceae bacterium BRH_c29
864	A0A069E6Q0	Hyphomonas adhaerens MHS-3
865	A0A059FPN2	Hyphomonas hirschiana VP5
866	A0A059FF25	Hyphomonas jannaschiana VP2
867	A0A059FE75	Hyphomonas johnsonii MHS-2
868	Q0C2K3	Hyphomonas neptunium (strain ATCC 15444)
869	A0A059G865	Hyphomonas oceanitis SCH89
870	A0A062VLC9	Hyphomonas polymorpha PS728
871	A0A259LK04	Hyphomonas sp. 34-62-18
872	A0A0F2RDK4	Hyphomonas sp. BRH_c22
873	A0A1Z9X064	Hyphomonas sp. TMED31
874	A0A0K8NTA2	Ideonella sakaiensis (strain 201-F6)
875	A0A211ZN00	Inquilinus limosus
876	A0A0A0DB64	Inquilinus limosus MP06
877	A0A161IJZ3	Isoptericola dokdonensis DS-3
878	A0A0D1EBH	Jannaschia aquimarina
879	A0A0M6YFF1	Jannaschia donghaensis
880	A0A0M6XQ3	Jannaschia rubra
881	A0A031GX16	Janthinobacterium lividum
882	A0A1I9XVN2	Janthinobacterium sp. 1_2014MBL_MicDiv
883	A0A0S4NRP	Janthinobacterium sp. CG23_2
884	A0A1E7WAM	Janthinobacterium sp. HH106
885	A0A0M2WHD	Janthinobacterium sp. KBS0711
886	A0A1S6F9H1	Janthinobacterium sp. LM6
887	A6T266	Janthinobacterium sp. (strain Marseille) (Minibacterium massiliensis)
888	A0A290WYZ	Janthinobacterium svalbardensis

889	A0A1S6IQB3	Jeotgalibaca dankookensis
890	A0A0M0KXQ4	Jeotgalibacillus marinus
891	A0A1H5TFQ8	Jhaorihella thermophila
892	F9Y4Y6	Ketogulonicigenium vulgare (strain WSH-001)
893	K6VJY8	Kineosphaera limosa NBRC 100340
894	A0A1E7N9G1	Kitasatospora aureofaciens (Streptomyces aureofaciens)
895	A0A145MIT9	Klebsiella aerogenes (Enterobacter aerogenes)
896	A0A181XAP6	Klebsiella oxytoca
897	A0A1W1KFI7	Klebsiella pneumoniae
898	A0A0E1CG09	Klebsiella pneumoniae 30660/NJST258_1
899	W8UHE6	Klebsiella pneumoniae 30684/NJST258_2
900	Q1EPR4	Kocuria sp. KY2
901	A0A0M0EIV8	Komagataeibacter europaeus (Gluconacetobacter europaeus)
902	A0A181C565	Komagataeibacter rhaeticus
903	A0A070A9B3	Komagataeibacter rhaeticus AF1
904	W5Y864	Komagataeibacter xylinus E25
905	D6U8H7	Ktedonobacter racemifer DSM 44963
906	A0A240UKM9	Kushneria marisflavi
907	W7SGA0	Kutzneria sp. 744
908	A0A0M6Y0X3	Labrenzia aggregata
909	A0A0M6Z4Q2	Labrenzia alba
910	A0A174LCT8	Lachnospira pectinoschiza
911	A0A0R1LS40	Lactobacillus acidifarinae DSM 19394
912	A0A0R2KCN4	Lactobacillus acidipiscis
913	M5ADU8	Lactobacillus brevis KB290
914	C2D288	Lactobacillus brevis subsp. gravesensis ATCC 27305
915	C0WQT6	Lactobacillus buchneri ATCC 11577
916	J9W3Z9	Lactobacillus buchneri CD034
917	K6QIN7	Lactobacillus casei 21/1
918	K6QA34	Lactobacillus casei 32G
919	A0A0E2BPL3	Lactobacillus casei A2-362
920	S4ZS02	Lactobacillus casei LOCK919
921	K6QYG7	Lactobacillus casei M36
922	A0A125UAK7	Lactobacillus casei (strain BD-II)
923	K6S6R9	Lactobacillus casei UCD174
924	K6RGF8	Lactobacillus casei UW4
925	K0NAA2	Lactobacillus casei W56
926	A0A0R1SRI6	Lactobacillus diolivorans DSM 14421
927	A0A0R1W698	Lactobacillus farraginis DSM 18382 = JCM 14108
928	A0A158SLK4	Lactobacillus fermentum
929	C0WXY8	Lactobacillus fermentum ATCC 14931
930	D8II88	Lactobacillus fermentum (strain CECT 5716)
931	A0A0R1P1Q9	Lactobacillus frumenti DSM 13145
932	C0XGF7	Lactobacillus hilgardii DSM 20176 = ATCC 8290
933	C8PAP3	Lactobacillus iners DSM 13335

934	A0A0R1P766	Lactobacillus mucosae DSM 13345
935	A0A0R1KMJ0	Lactobacillus nodensis DSM 19682 = JCM 14932 = NBRC 107160
936	A0A0R1RGC9	Lactobacillus oligofermentans DSM 15707 = LMG 22743
937	A0A081BKN6	Lactobacillus oryzae JCM 18671
938	S4PQ60	Lactobacillus otakiensis DSM 19908 = JCM 15040
939	A0A1X1FFM0	Lactobacillus parabuchneri
940	A0A1V0Q8X5	Lactobacillus paracasei
941	C2FBN4	Lactobacillus paracasei subsp. paracasei ATCC 25302
942	S2TJL4	Lactobacillus paracasei subsp. paracasei Lpp49
943	K8QAN6	Lactobacillus rhamnosus LRHMDP2
944	R6S9Q8	Lactobacillus ruminis CAG:367
945	F7R1I8	Lactobacillus ruminis SPM0211
946	A0A0R1R0G7	Lactobacillus spicheri DSM 15429
947	A0A1E7X8H4	Lactobacillus sunkii
948	A0A0R1L4P7	Lactobacillus sunkii DSM 19904
949	A0A0R1IY18	Lactobacillus tucceti DSM 20183
950	C2ESU0	Lactobacillus vaginalis DSM 5837 = ATCC 49540
951	A0A1Y6JZ04	Lactobacillus zymae
952	A0A0R1MN18	Lactobacillus zymae DSM 19395
953	A0A173M330	Lactococcus garvieae
954	K2PPG6	Lactococcus garvieae DCC43
955	G8P4E4	Lactococcus lactis subsp. cremoris A76
956	A0A161TZC1	Lactococcus lactis subsp. cremoris (Streptococcus cremoris)
957	U6ETZ5	Lactococcus lactis subsp. lactis Dephy 1
958	A0A0B8QXB1	Lactococcus lactis subsp. lactis (Streptococcus lactis)
959	A0A1C3SYZ1	Lactococcus piscium
960	A0A0D6DZS4	Lactococcus piscium MKFS47
961	I7JH02	Lactococcus raffinolactis 4877
962	A0A139MG44	Lactococcus sp. DD01
963	A0A1D8B005	Lacunisphaera limnophila
964	A3XGY6	Leeuwenhoekiella blandensis (strain CECT 7118 / CCUG 51940 / MED217) (Flavobacterium sp. (strain MED217))
965	A0A0W0UST3	Legionella gratiana
966	A0A078KW70	Legionella massiliensis
967	A0A128ZD65	Legionella pneumophila
968	G8UUA1	Legionella pneumophila subsp. pneumophila ATCC 43290
969	A0A1S8GMP9	Legionella pneumophila subsp. pneumophila str. Mississauga
970	Q5ZRM8	Legionella pneumophila subsp. pneumophila (strain Philadelphia 1 / ATCC 33152 / DSM 7513)
971	S7X834	Leifsonia rubra CMS 76R
972	A0A1B8RWV3	Leisingera sp. JC1
973	A0A1H3KUN3	Lentibacter algarum
974	A0A1V5UW73	Lentisphaerae bacterium ADurb.Bin242
975	U9VSG3	Leptolyngbya sp. Heron Island J
976	A0A110AWJ2	Leptolyngbya sp. O-77
977	A0A166V5S7	Leptolyngbya valderiana BDU 20041
978	A0A1D7UZC1	Leptospira alstonii

979	Q72PS5	Leptospira interrogans serogroup Icterohaemorrhagiae serovar copenhageni (strain Fiocruz L1-130)
980	A0A1X8WRS	Leptospira interrogans serovar Canicola
981	A0A098MSF5	Leptospira interrogans serovar Lai
982	A0A150FF05	Leptospira sp. ZV016
983	A0A147ENK4	Leucobacter chromiiresistens
984	A0A0D0ILT8	Leucobacter komagatae
985	A0A0M2LXR5	Leucobacter sp. Ag1
986	A0A061LXD1	Leucobacter sp. UCD-THU
987	A6GNC6	Limnobacter sp. MED105
988	A0A0L8AWU0	Limnohabitans planktonicus II-D5
989	A0A0P0M7I9	Limnohabitans sp. 63ED37-2
990	A0A0Y7J7Z3	Listeria monocytogenes
991	A0A1M4V7X3	Loktanella atrilutea
992	A0A238LBI3	Loktanella marina
993	A0A0Q1BAI4	Loktanella sp. 1ANDIMAR09
994	A0A0Q2UI66	Loktanella sp. 3ANDIMAR09
995	A0A0Q3F5K0	Loktanella sp. 5RATIMAR09
996	A0A0F4RI65	Loktanella sp. S4079
997	A0A0F3L255	Luteibacter yeojuensis
998	A0A290XED3	Luteimonas sp. 100111
999	A0A0H1AJ03	Luteimonas sp. FCS-9
1000	A0A1B3W664	Luteimonas sp. JM171
1001	A0A143PQU0	Luteitalea pratensis
1002	V4RKZ2	Lutibaculum baratangense AMV1
1003	A0A2A4D532	Lysinibacillus fusiformis
1004	A0A0A3I369	Lysinibacillus manganicus DSM 26584
1005	A0A0A3HV67	Lysinibacillus sinduriensis BLB-1 = JCM 15800
1006	A0A0M9WVL	Lysinibacillus sp. FJAT-14222
1007	A0A0M0X3A7	Lysinibacillus sp. FJAT-14745
1008	A0A0P7L9V9	Lysinibacillus sp. ZYM-1
1009	A0A0K9FFE7	Lysinibacillus xylanilyticus
1010	A0A120AHI2	Lysobacter capsici AZ78
1011	A0A0A0EL72	Lysobacter concretionis Ko07 = DSM 16239
1012	A0A0A0M5Y1	Lysobacter defluvii IMMIB APB-9 = DSM 18482
1013	W6KA50	Magnetospira sp. QH-2
1014	A0A238KTS8	Maliponia aquimaris
1015	A0A0B3S1J9	Mameliella alba
1016	A0Z923	marine gamma proteobacterium HTCC2080
1017	A0A225NPB5	Marinibacterium profundimaris
1018	A0A1R4JC33	Marinilactibacillus psychrotolerans 42ea
1019	A0A1E3C726	Marinobacter adhaerens
1020	E4PFN8	Marinobacter adhaerens (strain HP15)
1021	A6F4G5	Marinobacter algicola DG893
1022	A0A137SG28	Marinobacter excellens LAMA 842
1023	H8WBP3	Marinobacter hydrocarbonoclasticus ATCC 49840

1024	A0A1M2UY05	Marinobacter hydrocarbonoclasticus (Pseudomonas nautica)
1025	A1U5T4	Marinobacter hydrocarbonoclasticus (strain ATCC 700491 / DSM 11845 / VT8)
1026	G6YQE9	Marinobacter manganoxydans MnI7-9
1027	A0A072MYZ0	Marinobacter nitratireducens
1028	A0A1W6K3W	Marinobacter salarius
1029	A0A1D9GK48	Marinobacter salinus
1030	U7P5N7	Marinobacter sp. C1S70
1031	A0A0K1UDP8	Marinobacter sp. CP1
1032	U7HQ79	Marinobacter sp. EN3
1033	U7NU24	Marinobacter sp. EVN1
1034	A0A142FMH5	Marinobacter sp. LQ44
1035	A0A139DBK7	Marinobacter sp. T13-3
1036	A0A1E7PWU	Marinobacter sp. X15-166B
1037	A0A1C3JR26	Marinomonas gallaica
1038	A6VTQ7	Marinomonas sp. (strain MWYL1)
1039	A0A1A8T0Y1	Marinomonas spartinae
1040	A3V9I8	Maritimibacter alkaliphilus HTCC2654
1041	A0A1X4P2B1	Marivita cryptomonadis
1042	A0A1X4NFB4	Marivita geojedonensis
1043	A0A098UEM2	Massilia sp. JS1662
1044	A0A085FAJ7	Massilia sp. LC238
1045	I6ZPY4	Melioribacter roseus (strain JCM 17771 / P3M-2)
1046	H0I240	Mesorhizobium alhagi CCNWXJ12-2
1047	G6YEM4	Mesorhizobium amorphae CCNWGS0123
1048	A0A143NGF9	Mesorhizobium ciceri
1049	E8TFY8	Mesorhizobium ciceri biovar biserrulae (strain HAMBI 2942 / LMG 23838 / WSM1271)
1050	A0A068DC64	Mesorhizobium huakuii 7653R
1051	A0A271L571	Mesorhizobium mediterraneum
1052	M5F152	Mesorhizobium metallidurans STM 2683
1053	F7YAB6	Mesorhizobium opportunistum (strain LMG 24607 / HAMBI 3007 / WSM2075)
1054	A0A090GTY8	Mesorhizobium plurifarium
1055	A0A1R3V877	Mesorhizobium prunaredense
1056	A0A1Q3M0U5	Mesorhizobium sp. 61-13
1057	A0A1Q4A7E5	Mesorhizobium sp. 65-26
1058	A0A1A5T406	Mesorhizobium sp. AA22
1059	A0A1L3SYH6	Mesorhizobium sp. B7
1060	A0A2A6FLH7	Mesorhizobium sp. BSA136
1061	X6KLJ0	Mesorhizobium sp. L103C105A0
1062	X6K7M6	Mesorhizobium sp. L103C119B0
1063	V7HT44	Mesorhizobium sp. L103C120A0
1064	X6JTW4	Mesorhizobium sp. L103C131B0
1065	X6J3L4	Mesorhizobium sp. L103C565B0
1066	X6J8R5	Mesorhizobium sp. L2C054A000
1067	X6I7N2	Mesorhizobium sp. L2C066B000
1068	X6HJR0	Mesorhizobium sp. L2C067A000

1069	X6H8J8	Mesorhizobium sp. L2C084A000
1070	X6G5S1	Mesorhizobium sp. L2C085B000
1071	V7H9P6	Mesorhizobium sp. L2C089B000
1072	X6FZ61	Mesorhizobium sp. L48C026A00
1073	A0A0H1AES7	Mesorhizobium sp. LC103
1074	A0A1S1SG27	Mesorhizobium sp. LCM 4576
1075	X6FHW4	Mesorhizobium sp. LNHC209A00
1076	X6EHB4	Mesorhizobium sp. LNHC220B00
1077	X6DRB8	Mesorhizobium sp. LNHC221B00
1078	X6EXE1	Mesorhizobium sp. LNHC229A00
1079	X6CV37	Mesorhizobium sp. LNHC232B00
1080	X6CTS0	Mesorhizobium sp. LNHC252B00
1081	X6C982	Mesorhizobium sp. LNJC372A00
1082	X6AVM4	Mesorhizobium sp. LNJC386A00
1083	A0A0E2NY95	Mesorhizobium sp. LNJC391B00
1084	V7G350	Mesorhizobium sp. LNJC394B00
1085	X5ZN91	Mesorhizobium sp. LNJC395A00
1086	X5YTQ4	Mesorhizobium sp. LNJC399B00
1087	X5YED4	Mesorhizobium sp. LNJC405B00
1088	X5XHV3	Mesorhizobium sp. LSHC412B00
1089	A0A0E2NJ11	Mesorhizobium sp. LSHC414A00
1090	V7FFU5	Mesorhizobium sp. LSHC420B00
1091	X5VQD4	Mesorhizobium sp. LSHC422A00
1092	X5UK31	Mesorhizobium sp. LSHC426A00
1093	V7F871	Mesorhizobium sp. LSJC264A00
1094	X5RZX9	Mesorhizobium sp. LSJC265A00
1095	X5R0C6	Mesorhizobium sp. LSJC269B00
1096	X5PEK1	Mesorhizobium sp. LSJC277A00
1097	X5QIX6	Mesorhizobium sp. LSJC280B00
1098	X5QKZ5	Mesorhizobium sp. LSJC285A00
1099	A0A090DDQ8	Mesorhizobium sp. ORS3324
1100	A0A090ETB7	Mesorhizobium sp. ORS3359
1101	A0A1S1TFB8	Mesorhizobium sp. ORS3428
1102	A0A0Q6P2V0	Mesorhizobium sp. Root102
1103	A0A0Q8AKC5	Mesorhizobium sp. Root157
1104	A0A0Q8K469	Mesorhizobium sp. Root172
1105	A0A0Q7W1A4	Mesorhizobium sp. Root552
1106	A0A0Q7WPM	Mesorhizobium sp. Root554
1107	A0A1D2SS43	Mesorhizobium sp. SCN 65-20
1108	A0A1E2SRV1	Mesorhizobium sp. SEMIA 3007
1109	A0A090ENA9	Mesorhizobium sp. SOD10
1110	M5FMD4	Mesorhizobium sp. STM 4661
1111	A0A1C2DE92	Mesorhizobium sp. UASWS1009
1112	A0A1W6X120	Mesorhizobium sp. WSM1497
1113	A0A2A3DTH3	Mesorhizobium sp. WSM3859

1114	A0A2A3DEK6	Mesorhizobium sp. WSM3860
1115	A0A2A3CR40	Mesorhizobium sp. WSM3864
1116	A0A2A3B450	Mesorhizobium sp. WSM3866
1117	A0A1A5S3L8	Mesorhizobium sp. WSM3873
1118	A0A2A3CDF7	Mesorhizobium sp. WSM3876
1119	A0A2A3BZI7	Mesorhizobium sp. WSM4308
1120	A0A2A3AXT4	Mesorhizobium sp. WSM4313
1121	A0A271KQH1	Mesorhizobium sp. WYCCWR 10019
1122	A0A271LNK6	Mesorhizobium temperatum
1123	A0A0E3RYX1	Methanosarcina mazei C16
1124	A0A0E3LW73	Methanosarcina mazei LYC
1125	A0A0F8FYB0	Methanosarcina mazei (Methanosarcina frisia)
1126	A0A0E3RF04	Methanosarcina mazei S-6
1127	A0A0E3RBS4	Methanosarcina mazei SarPi
1128	Q8PSC2	Methanosarcina mazei (strain ATCC BAA-159 / DSM 3647 / Goe1 / Go1 / JCM 11833 / OCM 88) (Methanosarcina frisia)
1129	M1PD91	Methanosarcina mazei Tuc01
1130	A0A0E3PYT3	Methanosarcina mazei WWM610
1131	A0A0F8P197	Methanosarcina sp. 1.H.A.2.2
1132	A0A0F8SR54	Methanosarcina sp. 1.H.T.1A.1
1133	A0A0F8C747	Methanosarcina sp. 2.H.A.1B.4
1134	A0A0F8EQ81	Methanosarcina sp. 2.H.T.1A.15
1135	A0A0F8ESV2	Methanosarcina sp. 2.H.T.1A.3
1136	A0A0F8FHF3	Methanosarcina sp. 2.H.T.1A.6
1137	A0A0F8G5G5	Methanosarcina sp. 2.H.T.1A.8
1138	A0A0E3NWM	Methanosarcina sp. MTP4
1139	A0A154NUR2	Methylobacterium radiotolerans
1140	A0A1E3H3I1	Methylobrevis pamukkalensis
1141	A0A1Z8KTN9	Micavibrio sp. TMED2
1142	A0A0F0LDS8	Microbacterium azadirachtae
1143	A0A0M2HBF1	Microbacterium ketosireducens
1144	A0A0B2A2N2	Microbacterium mangrovi
1145	A0A0F0L4Z2	Microbacterium oxydans
1146	A0A246E6P5	Microbacterium sp. AISO3
1147	A0A171DW03	Microbacterium sp. HM58-2
1148	A0A0Q5L8W0	Microbacterium sp. Leaf159
1149	A0A0Q5FPP4	Microbacterium sp. Leaf320
1150	A0A0Q8LJU1	Microbacterium sp. Root180
1151	A0A0F2C737	Microbacterium sp. SA39
1152	A0A161SK65	Microbacterium sp. TNHR37B
1153	U2XM45	Microbacterium sp. TS-1
1154	A0A0M2HA45	Microbacterium trichothecenolyticum
1155	A0A1C9W5R3	Microbulbifer aggregans
1156	A0A0X3U0N1	Microbulbifer sp. ZGT114
1157	F5XN73	Microlunatus phosphovorus (strain ATCC 700054 / DSM 10555 / JCM 9379 / NBRC 101784 / NCIMB 13414 / VKM Ac-1990 / NM-1)
1158	A0A109IJD6	Micromonospora rifamycinica

1159	A0A1S8Y220	Micromonospora sp. Rc5
1160	A0A246RH91	Micromonospora wenchangensis
1161	A1ZRN3	Microscilla marina ATCC 23134
1162	A0A1B2EJ22	Microvirga ossetica
1163	A0A0H1RG87	Microvirga vignae
1164	E6Q0K6	mine drainage metagenome
1165	A0A066UEG0	Moraxella bovoculi 237
1166	A0A167ZV10	Moraxella ovis
1167	A0A0X8X008	Mucilaginibacter gotjawali
1168	A0A0B2BMY4	Mumia flava
1169	A0A0U1AWE	Mycobacterium abscessus
1170	A0A1N0QLG0	Mycobacterium abscessus subsp. abscessus
1171	A0A1N6AFE1	Mycobacterium abscessus subsp. bolletii
1172	R4URJ3	Mycobacterium abscessus subsp. bolletii 50594
1173	A0A1U4ADK6	Mycobacterium abscessus subsp. massiliense
1174	A0A0H2ZT69	Mycobacterium avium (strain 104)
1175	T2GNH3	Mycobacterium avium subsp. hominissuis (strain TH135)
1176	A0A100VVW2	Mycobacterium brisbanense
1177	A0A220Y6G5	Mycobacterium chimaera
1178	A0A0J6WN57	Mycobacterium chlorophenolicum
1179	A0A0J6ZER6	Mycobacterium chubuense
1180	A0A024LTN1	Mycobacterium farcinogenes
1181	A0A0N9Y2F7	Mycobacterium fortuitum
1182	K0V4A6	Mycobacterium fortuitum subsp. fortuitum DSM 46621 = ATCC 6841
1183	A0A1V3X482	Mycobacterium kansasii
1184	X7XUS9	Mycobacterium kansasii 824
1185	X5L4C9	Mycobacterium mageritense DSM 44476 = CIP 104973
1186	A0A0H5RKE2	Mycobacterium neworleansense
1187	A0A0J6VE36	Mycobacterium obuense
1188	D5PGB3	Mycobacterium parascrofulaceum ATCC BAA-614
1189	A0A202FU52	Mycobacterium paratuberculosis
1190	A0A100IEI0	Mycobacterium pseudoshottsii
1191	A0A0D6GM49	Mycobacterium smegmatis
1192	A0QY21	Mycobacterium smegmatis (strain ATCC 700084 / mc(2)155)
1193	L8FC86	Mycobacterium smegmatis (strain MKD8)
1194	A0A1A2BEH8	Mycobacterium sp. 852002-51759_SCH5129042
1195	A0A1A0X9U3	Mycobacterium sp. 852013-50091_SCH5140682
1196	A0A145SW78	Mycobacterium sp. QIA-37
1197	A0A2C9SVL6	Mycobacterium sp. shizuoka-1
1198	A1UEG1	Mycobacterium sp. (strain KMS)
1199	A0A0A1FQN9	Mycobacterium sp. VKM Ac-1817D
1200	A0A240AD36	Mycobacterium terrae
1201	A0A0U0UQT8	Mycobacterium tuberculosis
1202	L7N542	Mycobacterium tuberculosis (strain CDC 1551 / Oshkosh)
1203	X8FKH9	Mycobacterium ulcerans str. Harvey

1204	K0UTN0	Mycobacterium vaccae ATCC 25954
1205	X5LRH7	Mycobacterium vulneris
1206	X8AXV3	Mycobacterium xenopi 3993
1207	X8BH17	Mycobacterium xenopi 4042
1208	A0A0F7E671	Myxococcus fulvus 124B02
1209	F8CEF7	Myxococcus fulvus (strain ATCC BAA-855 / HW-1)
1210	A0A0H4XJ21	Myxococcus hansupus
1211	L7UL65	Myxococcus stipitatus (strain DSM 14675 / JCM 12634 / Mx s8)
1212	Q1CYM7	Myxococcus xanthus (strain DK 1622)
1213	C8XA27	Nakamurella multipartita (strain ATCC 700099 / DSM 44233 / CIP 104796 / JCM 9543 / NBRC 105858 / Y-104) (Microsphaera multipartita)
1214	A0A0H5D2L7	Nautella italica
1215	A0A0J1C2T6	Neisseria arctica
1216	A0A0B5CIZ5	Neisseria elongata subsp. glycolytica ATCC 29315
1217	A0A154TM64	Neisseria flavescens
1218	C5TNJ7	Neisseria flavescens SK114
1219	F9EZJ5	Neisseria macacae ATCC 33926
1220	E5UL28	Neisseria mucosa C102
1221	G4CK47	Neisseria shayeganii 871
1222	A0A1F1UJC7	Neisseria sp. HMSC03D10
1223	A0A1F1C597	Neisseria sp. HMSC055H02
1224	A0A1F0DW5	Neisseria sp. HMSC056A03
1225	A0A1F0AMB	Neisseria sp. HMSC064E01
1226	A0A1F1FS36	Neisseria sp. HMSC067G11
1227	A0A1E9MTX	Neisseria sp. HMSC068C04
1228	A0A1F1GKP1	Neisseria sp. HMSC069H12
1229	A0A1E9M5I0	Neisseria sp. HMSC070A01
1230	A0A1F1HPY2	Neisseria sp. HMSC073G10
1231	A0A1E9VWU	Neisseria sp. HMSC077D05
1232	A0A1F1SLT0	Neisseria sp. HMSC31F04
1233	A0A1S1G8R	Neisseria sp. HMSC70E02
1234	A0A0T7FTX7	Neorhizobium galegae bv. officinalis
1235	A0A068TGW	Neorhizobium galegae bv. officinalis bv. officinalis str. HAMBI 1141
1236	A0A0T7HMP	Neorhizobium galegae bv. orientalis
1237	A0A068STZ0	Neorhizobium galegae bv. orientalis str. HAMBI 540
1238	A0A0U1NN44	Nereida ignava
1239	A0A1X3PB87	Nesterenkonia sp. PF2B19
1240	A0A084UCB4	Nitratireductor basaltis
1241	W9V8H0	Nitrincola nitratireducens
1242	Q0AH54	Nitrosomonas eutropha (strain C91)
1243	A0A0S8APY1	Nitrospira bacterium SG8_35_4
1244	A0A248K4P8	Nitrospirillum amazonense CBAmc
1245	U5EL89	Nocardia asteroides NBRC 15531
1246	A0A231GYE2	Nocardia cerradoensis
1247	A0A2B4QKU	Nocardia farcinica
1248	A0A0B8ND93	Nocardia seriolae

1249	A0A1A0L1S4	Nocardia sp. 852002-20019_SCH5090214
1250	E9UX93	Nocardioidaceae bacterium Broad-1
1251	A0A1A9GMI1	Nocardioides dokdonensis FR1436
1252	A0A0Q7PV51	Nocardioides sp. Root140
1253	A0A0Q7ZNK7	Nocardioides sp. Root151
1254	A0A0Q8Q364	Nocardioides sp. Root190
1255	A0A0Q8WQC	Nocardioides sp. Root240
1256	A0A0Q8DQG	Nocardioides sp. Root614
1257	A0A0Q8HK2C	Nocardioides sp. Root682
1258	A0A0Q8V1T5	Nocardioides sp. Root79
1259	A0A0Q9RUJ4	Nocardioides sp. Soil796
1260	A0A0Q9SCR8	Nocardioides sp. Soil797
1261	A0A1M4E4Q5	Nonomuraea gerenzanensis
1262	A0A1V0AKQ7	Nonomuraea sp. ATCC 55076
1263	A0A235I1V5	Nostoc sp. 'Peltigera membranacea cyanobiont' 210A
1264	A0A235IRH3	Nostoc sp. 'Peltigera membranacea cyanobiont' 232
1265	Q2G7E0	Novosphingobium aromaticivorans (strain ATCC 700278 / DSM 12444 / CIP 105152 / NBRC 16084 / F199)
1266	A0A117UY79	Novosphingobium fuchskuhlense
1267	A0A1U6HY74	Novosphingobium mathurense
1268	F1Z9M7	Novosphingobium nitrogenifigens DSM 19370
1269	A0A258XNZ9	Novosphingobium sp. 16-62-11
1270	A0A259E054	Novosphingobium sp. 17-62-19
1271	A0A258V6P5	Novosphingobium sp. 28-62-57
1272	A0A0N1AP13	Novosphingobium sp. AAP1
1273	A0A0N1LJI3	Novosphingobium sp. AAP93
1274	A0A102DFP0	Novosphingobium sp. FSW06-99
1275	A0A102DAI9	Novosphingobium sp. Fuku2-ISO-50
1276	A0A257GFJ3	Novosphingobium sp. PASSN1
1277	A0A1E4N4I9	Novosphingobium sp. SCN 63-17
1278	A0A1E4MI48	Novosphingobium sp. SCN 66-18
1279	A0A0B9AG37	Novosphingobium subterraneum
1280	U3A1A2	Novosphingobium tardaugens NBRC 16725
1281	A0A1Y5THU2	Oceanibacterium hippocampi
1282	A0A154W8E6	Oceanibaculum pacificum
1283	A9DQY8	Oceanibulbus indolifex HEL-45
1284	A0A0P7XVY2	Oceanicaulis sp. HLUCCA04
1285	A0A1M7RRW	Oceanicella actignis
1286	A0A1N6GAY5	Oceanicola litoreus
1287	A0A254R1P2	Oceanicola sp. 22II-s10i
1288	A0A235CKE2	Oceanimonas baumannii
1289	A0A233REU1	Oceanimonas doudoroffii
1290	H2FXE8	Oceanimonas sp. (strain GK1)
1291	A0A1Y0D711	Oceanisphaera profunda
1292	A0A1Y0D0L7	Oceanisphaera sp. AMac2203
1293	Q8ESC9	Oceanobacillus iheyensis (strain DSM 14371 / CIP 107618 / JCM 11309 / KCTC 3954 / HTE831)

1294	A0A0A1MHT8	Oceanobacillus oncorhynchi
1295	W9AFE3	Oceanobacillus picturae
1296	A0A137XSC8	Ochrobactrum anthropi
1297	A6WYP4	Ochrobactrum anthropi (strain ATCC 49188 / DSM 6882 / JCM 21032 / NBRC 15819 / NCTC 12168)
1298	A0A1J6HWP2	Ochrobactrum cytisi
1299	U4VF86	Ochrobactrum intermedium 229E
1300	C4WGF5	Ochrobactrum intermedium LMG 3301
1301	M5K1T6	Ochrobactrum intermedium M86
1302	A0A1A9FKX2	Ochrobactrum pseudogrignonense
1303	U1XHP2	Ochrobactrum sp. EGD-AQ16
1304	A0A1V3YKH5	Ochrobactrum sp. P6BS-III
1305	A0A238KNR1	Octadecabacter ascidiaceicola
1306	A0A0K0Y7L4	Octadecabacter temperatus
1307	A0A165SFE7	Oleiphilus sp. HI0065
1308	R4YTJ3	Oleispira antarctica RB-8
1309	A0A1Z8WET7	Opitutae bacterium TMED67
1310	A1RBL5	Paenarthrobacter aurescens (strain TC1)
1311	K5AE03	Paenibacillus alvei DSM 29
1312	A0A168JB90	Paenibacillus antarcticus
1313	A0A1R0XZV7	Paenibacillus borealis
1314	A0A089HPB3	Paenibacillus durus (Paenibacillus azotofixans)
1315	A0A161SCT3	Paenibacillus elgii
1316	A0A0W1AX85	Paenibacillus etheri
1317	A0A1V4HFG4	Paenibacillus ferrarius
1318	A0A168HN33	Paenibacillus glacialis
1319	A0A163LZB8	Paenibacillus glucanolyticus
1320	A0A2A5LKM7	Paenibacillus lautus (Bacillus lautus)
1321	A0A1R1HJD6	Paenibacillus macerans (Bacillus macerans)
1322	A0A168GS77	Paenibacillus macquariensis (Bacillus macquariensis)
1323	A0A167XGX2	Paenibacillus macquariensis subsp. defensor
1324	A0A264EMM6	Paenibacillus odorifer
1325	A0A1T2X1D1	Paenibacillus selenitireducens
1326	A0A0P9DRM9	Paenibacillus sp. A3
1327	A0A0D7KQ86	Paenibacillus sp. E194
1328	A0A0M1P4C6	Paenibacillus sp. FJAT-22460
1329	A0A1R0ZN72	Paenibacillus sp. FSL A5-0031
1330	A0A089I662	Paenibacillus sp. FSL H7-0357
1331	A0A089JUA0	Paenibacillus sp. FSL H7-0737
1332	A0A0D3V785	Paenibacillus sp. IHBB 10380
1333	A0A1B8UWV	Paenibacillus sp. KS1
1334	A0A1S2F3U7	Paenibacillus sp. LC231
1335	A0A0B0I7C6	Paenibacillus sp. P1XP2
1336	A0A1E3L0A7	Paenibacillus sp. TI45-13ar
1337	A0A264E2N8	Paenibacillus sp. VTT E-133280
1338	A0A081PA59	Paenibacillus tyrfis

1339	A0A0A8W0V4	Paeniclostridium sordellii (Clostridium sordellii)
1340	M7NKQ6	Paeniglutamicibacter gangotriensis Lz1y
1341	A0A086XQY2	Paenirhodobacter enshiensis
1342	A0A1U7CSL2	Paludisphaera borealis
1343	A0A0U2XVV8	Pandoraea norimbergensis
1344	R7X1Q8	Pandoraea sp. SD6-2
1345	A0A239SAD1	Pandoraea sputorum
1346	A0A0U3P646	Pannonibacter phragmitetus
1347	A0A0F5XVQ9	Pantoea sp. 3.5.1
1348	A0A174I3J8	Parabacteroides distasonis
1349	A6LC41	Parabacteroides distasonis (strain ATCC 8503 / DSM 20701 / CIP 104284 / JCM 5825 / NCTC 11152)
1350	A0A1H7HJL6	Paraburkholderia caballeronis
1351	A0A142YPP2	Paraburkholderia caribensis
1352	A0A1H0Z455	Paraburkholderia fungorum
1353	A0A1A9NCM4	Paraburkholderia ginsengiterrae
1354	A0A1H6I231	Paraburkholderia hospita
1355	A0A1I3UYM3	Paraburkholderia megapolitana
1356	A0A149PB03	Paraburkholderia monticola
1357	A0A1N7RJA0	Paraburkholderia ribeironis
1358	A0A0A6QGR8	Paraburkholderia sacchari
1359	A0A1H3XWD	Paraburkholderia sartisoli
1360	A0A248VEP8	Paraburkholderia sp. BN5
1361	A0A1L6HS45	Paraburkholderia sp. SOS3
1362	A0A1I9YIB6	Paraburkholderia sprentiae WSM5005
1363	A0A1X7K361	Paraburkholderia susongensis
1364	A0A244DCT3	Paraburkholderia terrae
1365	A0A1M6XT47	Paraburkholderia terricola
1366	A0A1H6ZJ89	Paraburkholderia tropica
1367	A0A1H1DQT9	Paraburkholderia tuberum
1368	Q146S0	Paraburkholderia xenovorans (strain LB400)
1369	S5XML4	Paracoccus aminophilus JCM 7686
1370	A0A099F5D0	Paracoccus halophilus
1371	A0A099GG23	Paracoccus sanguinis
1372	A0A0V0PZU1	Paracoccus sp. MKU1
1373	A0A1L9BQV3	Paracoccus sp. SM22M-07
1374	A0A2A2GLU1	Paracoccus sp. WN007
1375	A0A099F717	Paracoccus versutus (Thiobacillus versutus)
1376	A0A212BJ66	Paracoccus yeei
1377	A0A0U1KJ51	Paraliobacillus sp. PM-2
1378	A0A135HQQ9	Paramesorhizobium deserti
1379	A0A1C7P2K3	Pararhizobium polonicum
1380	H0E165	Patulibacter medicamentivorans
1381	C6XX09	Pedobacter heparinus (strain ATCC 13125 / DSM 2366 / CIP 104194 / JCM 7457 / NBRC 12017 / NCIMB 9290 / NRRL B-14731 / HIM 762-3)
1382	A0A2A2RVW	Pedosphaera sp. Tous-C6FEB
1383	A0A1E4FC10	Pelagibacterium sp. SCN 63-23

1384	A0A1Y5SE37	Pelagicola litorisediminis
1385	A0A238L5C6	Pelagimonas varians
1386	A0A069RH13	Peptoclostridium litorale DSM 5388
1387	A0A1B0ZTM0	Phaeobacter gallaeciensis
1388	A0A135INQ2	Phaeobacter inhibens
1389	A0A0P6RWA	Phaeobacter sp. 11ANDIMAR09
1390	A0A254QXJ5	Phaeobacter sp. 22II1-1F12B
1391	A0A0P1H3R0	Phaeobacter sp. CECT 5382
1392	A0A0P1INL0	Phaeobacter sp. CECT 7735
1393	A0A0C2HNB8	Phaeobacter sp. S26
1394	A0A1G2WBX	Phenylobacterium sp. RIFCSPHIGHO2_01_FULL_69_31
1395	A0A1G2X5F9	Phenylobacterium sp. RIFCSPHIGHO2_01_FULL_70_10
1396	A0A0Q7DHY3	Phenylobacterium sp. Root1277
1397	A0A0Q7FJH9	Phenylobacterium sp. Root1290
1398	A0A0Q8N5J1	Phenylobacterium sp. Root700
1399	A0A0Q8UIE9	Phenylobacterium sp. Root77
1400	A0A1E4GVH1	Phenylobacterium sp. SCN 70-31
1401	A0A227JMM1	Phenylobacterium zucineum
1402	B4RGK0	Phenylobacterium zucineum (strain HLK1)
1403	A0A0B9G044	Photobacterium gaetbulicola
1404	A0A0C5W5H	Photobacterium gaetbulicola Gung47
1405	A0A1B8IG12	Photobacterium phosphoreum
1406	A0A1C0U4M3	Photorhabdus asymbiotica subsp. australis
1407	A0A208YD14	Pigmentiphaga sp. NML030171
1408	A0A177R0P0	Planctomyces sp. SCGC AG-212-M04
1409	A0A142WX71	Planctomyces sp. SH-PL14
1410	A0A142YP87	Planctomyces sp. SH-PL62
1411	A0A1V6DF56	Planctomycetes bacterium ADurb.Bin126
1412	A0A1L9P0F0	Planktotalea frisia
1413	A4C151	Polaribacter irgensii 23-P
1414	A2TYS8	Polaribacter sp. MED152
1415	D3B2W5	Polysphondylium pallidum (strain ATCC 26659 / Pp 5 / PN500)
1416	A0A225PDU6	Ponticoccus lacteus
1417	A0A0W7WL3	Ponticoccus marisrubri
1418	A0A0B2BYW	Porphyrobacter mercurialis
1419	A0A099WYM	Porphyromonas cangingivalis
1420	A0A293NHD9	Porticoccaceae bacterium
1421	A0A167RP12	Powai lake megavirus
1422	W4TMT4	Propionibacterium acnes JCM 18909
1423	W4TS23	Propionibacterium acnes JCM 18916
1424	W4U2X3	Propionibacterium acnes JCM 18918
1425	W4UGU7	Propionibacterium acnes JCM 18920
1426	Q6A7K7	Propionibacterium acnes (strain KPA171202 / DSM 16379)
1427	F3NYU6	[Propionibacterium] humerusii P08
1428	A0A1W9U178	Propionibacterium sp. 4572_24

1429	A0A1J4X7W6	Propionibacterium sp. CG1_02_60_36
1430	A0A1W9I9G9	Proteobacteria bacterium HN_bin10
1431	A0A1W9I5B6	Proteobacteria bacterium SG_bin9
1432	K8WC88	Providencia burhodogranariea DSM 19968
1433	A0A1V8RV42	Pseudaminobacter manganicus
1434	A0A0S2JZG0	Pseudoalteromonas phenolica
1435	A0A0W1LGY	Pseudoalteromonas sp. H105
1436	A0A095VUC7	Pseudohaliea rubra DSM 19751
1437	A0A1G3D8W	Pseudomonadales bacterium GWC2_63_15
1438	A0A2A4EXY0	Pseudomonas acidophila
1439	A0A0G5TIY0	Pseudomonas aeruginosa
1440	A6UYI4	Pseudomonas aeruginosa (strain PA7)
1441	A0A1H6BVG5	Pseudomonas aestusnigri
1442	A0A0P9J0D4	Pseudomonas amygdali
1443	A0A0P9U7U3	Pseudomonas amygdali pv. hibisci
1444	A0A0P9TG04	Pseudomonas amygdali pv. lachrymans (Pseudomonas syringae pv. lachrymans)
1445	F3IMV6	Pseudomonas amygdali pv. lachrymans str. M302278
1446	F3ETR8	Pseudomonas amygdali pv. mori str. 301020
1447	F3E346	Pseudomonas amygdali pv. morsprunorum str. M302280
1448	A0A0Q0BNX2	Pseudomonas amygdali pv. tabaci (Pseudomonas syringae pv. tabaci)
1449	F3K2X6	Pseudomonas amygdali pv. tabaci str. ATCC 11528
1450	K2SL24	Pseudomonas avellanae BPIC 631
1451	A0A031M8M3	Pseudomonas bauzanensis
1452	W8PKE1	Pseudomonas brassicacearum
1453	F2KF85	Pseudomonas brassicacearum (strain NFM421)
1454	A0A0P9MU59	Pseudomonas caricapapayae
1455	V4QC34	Pseudomonas chloritidismutans AW-1
1456	A0A0G3G5P3	Pseudomonas chlororaphis
1457	A0A127MTZ1	Pseudomonas citronellolis
1458	A0A1S2V3L1	Pseudomonas costantinii
1459	A0A0Q0YYC6	Pseudomonas endophytica
1460	A0A0P9TXJ2	Pseudomonas ficuserectae
1461	A0A0B3BZN1	Pseudomonas flexibilis
1462	A0A0F4TBS8	Pseudomonas fluorescens
1463	U1S6N4	Pseudomonas fluorescens EGD-AQ6
1464	G8Q395	Pseudomonas fluorescens F113
1465	E2XQ03	Pseudomonas fluorescens WH6
1466	A0A267AKD6	Pseudomonas fragi
1467	A0A0D0L8A0	Pseudomonas fulva
1468	F6ADS4	Pseudomonas fulva (strain 12-X)
1469	A0A0J6HVH9	Pseudomonas helleri
1470	A0A0F4XW76	Pseudomonas kilonensis
1471	A0A0R2Y5N5	Pseudomonas libanensis
1472	A0A2C8F1D9	Pseudomonas lundensis
1473	A0A098SVW8	Pseudomonas lutea

1474	A0A059KY26	Pseudomonas mandelii PD30
1475	A0A1I7DRP8	Pseudomonas marincola
1476	A0A2A4FBW8	[Pseudomonas] mesoacidophila
1477	A0A225DUD8	Pseudomonas oleovorans subsp. oleovorans
1478	A0A1S8DH43	Pseudomonas pachastrellae
1479	A0A2A4AVP9	Pseudomonas pelagia
1480	S2KU52	Pseudomonas plecoglossicida NB2011
1481	A0A219A3U6	Pseudomonas poae
1482	A0A0J6KLU8	Pseudomonas psychrophila
1483	A0A1B2F4H7	Pseudomonas putida (Arthrobacter siderocapsulatus)
1484	A0A0C5RST4	Pseudomonas putida S13.1.2
1485	B1JA60	Pseudomonas putida (strain W619)
1486	A0A078M5A8	Pseudomonas saudimassiliensis
1487	A0A0P9WZT5	Pseudomonas savastanoi pv. nerii
1488	A0A0P9ZTB9	Pseudomonas savastanoi pv. savastanoi
1489	A0A191YRK0	Pseudomonas silesiensis
1490	A0A1N7U2M7	Pseudomonas simiae
1491	Q59719	Pseudomonas sp.
1492	A0A1S1UYU5	Pseudomonas sp. 06C 126
1493	A0A1C3GPS1	Pseudomonas sp. 1 R 17
1494	A0A0E9ZQP8	Pseudomonas sp. 10-1B
1495	A0A1B5F5J3	Pseudomonas sp. 22 E 5
1496	A0A0F0F9L1	Pseudomonas sp. 2(2015)
1497	A0A1B5DAM2	Pseudomonas sp. 24 E 1
1498	A0A1B5DZG3	Pseudomonas sp. 37 R 15
1499	A0A1B5DJF5	Pseudomonas sp. 44 R 15
1500	A0A1B5EAS6	Pseudomonas sp. 58 R 3
1501	A0A0N0BTR8	Pseudomonas sp. 655
1502	A0A1V3SCY7	Pseudomonas sp. A25(2017)
1503	A0A212BBH3	Pseudomonas sp. A46
1504	J0Y6B6	Pseudomonas sp. Ag1
1505	A0A0I9SH83	Pseudomonas sp. BICA1-14
1506	A0A0F2QHZ9	Pseudomonas sp. BRH_c35
1507	A0A1D9ISN5	Pseudomonas sp. BS-2016
1508	A0A1V3MS54	Pseudomonas sp. C9
1509	S6HMS4	Pseudomonas sp. CF149
1510	A0A1V4FGV7	Pseudomonas sp. Ea RS28
1511	A0A0D9A9M9	Pseudomonas sp. ES3-33
1512	A0A0D6SUR7	Pseudomonas sp. FeS53a
1513	W2DGM3	Pseudomonas sp. FH4
1514	S2FK83	Pseudomonas sp. G5(2012)
1515	W6UZS9	Pseudomonas sp. GM41(2012)
1516	A0A263NQ63	Pseudomonas sp. IB20
1517	A0A0P7MPZ8	Pseudomonas sp. In5
1518	A0A1E5XA91	Pseudomonas sp. J237

1519	A0A246FWX0	Pseudomonas sp. K2I15
1520	A0A1C2K796	Pseudomonas sp. K35
1521	M5QQ88	Pseudomonas sp. Lz4W
1522	A0A1Y0KLY3	Pseudomonas sp. M30-35
1523	A0A1T1HQE8	Pseudomonas sp. MF4836
1524	A0A0A1GEX9	Pseudomonas sp. MT-1
1525	A0A2A3MFH1	Pseudomonas sp. MT5
1526	A0A257E5Z5	Pseudomonas sp. PGPPP1
1527	A0A0N1DC31	Pseudomonas sp. RIT-PI-q
1528	A0A0Q6QAD9	Pseudomonas sp. Root329
1529	A0A0Q8CQ35	Pseudomonas sp. Root569
1530	A0A0Q8IRR4	Pseudomonas sp. Root68
1531	A0A0Q8PJZ1	Pseudomonas sp. Root71
1532	A0A1C1W691	Pseudomonas sp. S1E40
1533	P13397	Pseudomonas sp. (strain NK87)
1534	A0A105T8Z6	Pseudomonas sp. TAD18
1535	A0A0T6VMV0	Pseudomonas sp. TTU2014-105ASC
1536	A0A0S4HRC6	Pseudomonas sp. URMO17WK12:I11
1537	A0A1V4LKD3	Pseudomonas sp. VI4.1
1538	A0A2A2FW13	Pseudomonas sp. WN033
1539	I4CSF9	Pseudomonas stutzeri CCUG 29243
1540	W8R682	Pseudomonas stutzeri (Pseudomonas perfectomarina)
1541	A0A0R2YNI1	Pseudomonas synxantha
1542	A0A085UV41	Pseudomonas syringae
1543	A0A0K8M1N3	Pseudomonas syringae pv. actinidiae
1544	S6SFV9	Pseudomonas syringae pv. actinidiae ICMP 18807
1545	S6SKG4	Pseudomonas syringae pv. actinidiae ICMP 19096
1546	A0A0P9J079	Pseudomonas syringae pv. alisalensis
1547	A0A0P9JNW8	Pseudomonas syringae pv. antirrhini
1548	A0A0P9NE39	Pseudomonas syringae pv. castaneae
1549	A0A0N0X8S9	Pseudomonas syringae pv. cilantro
1550	A0A0P9LJZ6	Pseudomonas syringae pv. coriandricola
1551	A0A0P9PAM0	Pseudomonas syringae pv. daphniphylli
1552	A0A0P9UP84	Pseudomonas syringae pv. delphinii
1553	A0A0P9RAL4	Pseudomonas syringae pv. helianthi
1554	A0A0N0WUZ	Pseudomonas syringae pv. maculicola
1555	A0A0P9XSH6	Pseudomonas syringae pv. primulae
1556	A0A0P9YT75	Pseudomonas syringae pv. ribicola
1557	A0A0Q0CPS7	Pseudomonas syringae pv. solidagae
1558	A0A0P9ZMA8	Pseudomonas syringae pv. spinaceae
1559	S3NNZ0	Pseudomonas syringae pv. syringae SM
1560	A0A0Q0E9B3	Pseudomonas syringae pv. tagetis
1561	A0A099SNY9	Pseudomonas syringae pv. tomato
1562	Q87WM0	Pseudomonas syringae pv. tomato (strain ATCC BAA-871 / DC3000)
1563	A0A0Q0ELZ0	Pseudomonas syringae pv. viburni

1564	A0A0J6GS90	Pseudomonas taetrolens
1565	A0A176NE46	Pseudomonas thivervalensis
1566	A0A0M4R7T3	Pseudomonas versuta
1567	A0A1Y6JJ77	Pseudomonas viridiflava
1568	A0A0J6IH54	Pseudomonas weihenstephanensis
1569	A0A098FMG6	Pseudomonas xanthomarina
1570	A0A1Y2MRT7	Pseudonocardia autotrophica (Amycolata autotrophica) (Nocardia autotrophica)
1571	A0A292YZU5	Pseudonocardia sp. N23
1572	A0A0A0EBG4	Pseudooceanicola atlanticus
1573	A0A1Y5SNP5	Pseudooctadecabacter jejudonensis
1574	A0A081MJ35	Pseudorhizobium pelagicum
1575	A0A257GP62	Pseudorhodobacter sp. PARRP1
1576	A0A0S9KV91	Pseudorhodoferax sp. Leaf265
1577	A0A1Y5RVI3	Pseudoruegeria aquimaris
1578	A0A165T3A5	Pseudovibrio axinellae
1579	A0A165V164	Pseudovibrio sp. Ad26
1580	B6QYG6	Pseudovibrio sp. JE062
1581	G8PHS5	Pseudovibrio sp. (strain FO-BEG1)
1582	A0A165Q4T3	Pseudovibrio sp. W74
1583	A0A161XKM1	Pseudovibrio sp. WM33
1584	A0A144NFV2	Psychrobacter alimentarius
1585	U4T618	Psychrobacter aquaticus CMS 56
1586	Q1Q8U8	Psychrobacter cryohalolentis (strain K5)
1587	A0A1R4EGM	Psychrobacter pasteurii
1588	A0A1R4GUP9	Psychrobacter piechaudii
1589	F5SNM6	Psychrobacter sp. 1501(2011)
1590	A0A229GP87	Psychrobacter sp. DAB_AL32B
1591	A0A1U6GQ15	Psychrobacter sp. DAB_AL43B
1592	S4YWH3	Psychrobacter sp. G
1593	A0A2A2B406	Psychrobacter sp. JB193
1594	A0A1R4I736	Psychrobacter sp. JB385
1595	X0QQK5	Psychrobacter sp. JCM 18900
1596	X0QIF0	Psychrobacter sp. JCM 18901
1597	X0QSL3	Psychrobacter sp. JCM 18902
1598	X0RIH1	Psychrobacter sp. JCM 18903
1599	A0A0Q9ZRI8	Psychrobacter sp. P11F6
1600	A0A0M4U492	Psychrobacter urativorans
1601	D5BRY7	Puniceispirillum marinum (strain IMCC1322)
1602	A0A191ZW16	Ralstonia insidiosa
1603	A0A0D5AQW	Ralstonia mannitolilytica
1604	A0A291ELC1	Ralstonia pickettii (Burkholderia pickettii)
1605	U3QQX9	Ralstonia pickettii DTP0602
1606	C6BID3	Ralstonia pickettii (strain 12D)
1607	B2UC09	Ralstonia pickettii (strain 12J)
1608	A0A223H6L1	Ralstonia pseudosolanacearum

1609	D8NJ41	Ralstonia solanacearum CFBP2957
1610	D8NBY7	Ralstonia solanacearum CMR15
1611	A0A1L3DIY2	Ralstonia solanacearum FJAT-1458
1612	A0A177S2X0	Ralstonia solanacearum (Pseudomonas solanacearum)
1613	D8NTL3	Ralstonia solanacearum PSI07
1614	Q8XYJ3	Ralstonia solanacearum (strain GMI1000) (Pseudomonas solanacearum)
1615	F6G7H0	Ralstonia solanacearum (strain Po82)
1616	A3RX73	Ralstonia solanacearum UW551
1617	A0A0B1YN14	Ralstonia sp. A12
1618	S9S1M4	Ralstonia sp. AU12-08
1619	A0A0J9DWC2	Ralstonia sp. MD27
1620	A0A100HXG4	Ralstonia sp. NT80
1621	G3A899	Ralstonia syzygii R24
1622	A0A127JSC9	Ramlibacter tataouinensis
1623	A0A1Y6GHY9	Raoultella ornithinolytica (Klebsiella ornithinolytica)
1624	A0A166H147	Rathayibacter tanaceti
1625	A0A0Q7AMF9	Rhizobacter sp. Root404
1626	A0A257XGZ6	Rhizobiales bacterium 12-66-7
1627	A0A1Q4BVI8	Rhizobiales bacterium 62-47
1628	A0A1M3AV42	Rhizobiales bacterium 63-7
1629	A0A1M2Z684	Rhizobiales bacterium 65-79
1630	A0A0N0LFA6	Rhizobium acidisoli
1631	A0A120FHW4	Rhizobium altiplani
1632	A0A2A6GKC4	Rhizobium anhuiense
1633	A0A2D0ABR4	Rhizobium esperanzae
1634	F2AAZ5	Rhizobium etli CNPAF512
1635	Q2K6A3	Rhizobium etli (strain CFN 42 / ATCC 51251)
1636	B3PTX9	Rhizobium etli (strain CIAT 652)
1637	W6RDB9	Rhizobium favelukesii
1638	A0A2A6M534	Rhizobium fredii (Sinorhizobium fredii)
1639	G9A8D7	Rhizobium fredii (strain HH103) (Sinorhizobium fredii)
1640	N6V9P4	Rhizobium freirei PRF 81
1641	A0A1S9GKK4	Rhizobium laguerreae
1642	A0A1B1CN08	Rhizobium leguminosarum
1643	A0A1B8R1Q0	Rhizobium leguminosarum bv. trifolii
1644	W0IMH0	Rhizobium leguminosarum bv. trifolii WSM1689
1645	A0A0U3ATX7	Rhizobium leguminosarum bv. viciae
1646	Q1ME15	Rhizobium leguminosarum bv. viciae (strain 3841)
1647	A0A1S9H0G4	Rhizobium leguminosarum bv. viciae USDA 2370
1648	A0A1B4YK92	Rhizobium loti (Mesorhizobium loti)
1649	Q98HG2	Rhizobium loti (strain MAFF303099) (Mesorhizobium loti)
1650	A0A222HER5	Rhizobium meliloti (Ensifer meliloti) (Sinorhizobium meliloti)
1651	Q92UN4	Rhizobium meliloti (strain 1021) (Ensifer meliloti) (Sinorhizobium meliloti)
1652	A0A1Q9B080	Rhizobium oryzae
1653	A0A1Q8ZN64	Rhizobium oryziradicis

1654	A0A2A6H568	Rhizobium phaseoli
1655	A0A0M3GIZ2	Rhizobium phaseoli Ch24-10
1656	A0A1L9CVU4	Rhizobium pusense
1657	A0A0F4G225	Rhizobium radiobacter (Agrobacterium tumefaciens) (Agrobacterium radiobacter)
1658	A0A061MJ24	Rhizobium rhizogenes NBRC 13257
1659	A0A1Q9AM8	Rhizobium rhizosphaerae
1660	A0A2A5KR35	Rhizobium sophoriradicis
1661	A0A248W6S	Rhizobium sp. 10195
1662	A0A1L8PNC4	Rhizobium sp. 58
1663	A0A1M3QF1	Rhizobium sp. 60-20
1664	A0A1M2Z2Z4	Rhizobium sp. 63-7
1665	A0A0N0JP16	Rhizobium sp. AAP116
1666	A0A0N0J5Q8	Rhizobium sp. AAP43
1667	A0A1B9RWR	Rhizobium sp. AC27/96
1668	A0A1B9SHI5	Rhizobium sp. AC44/96
1669	A0A292EBQ9	Rhizobium sp. ACO-34A
1670	A0A2A6JHA7	Rhizobium sp. C5
1671	W6WR90	Rhizobium sp. CF080
1672	A0A1W6KTY	Rhizobium sp. CIAT894
1673	A0A2A6KE93	Rhizobium sp. FH14
1674	A0A2A6R6K9	Rhizobium sp. H4
1675	A0A098RR64	Rhizobium sp. H41
1676	A0A2A6JRW	Rhizobium sp. J15
1677	A0A2A6I3L1	Rhizobium sp. L18
1678	A0A2A6HJS4	Rhizobium sp. L43
1679	A0A2A6L2I5	Rhizobium sp. L9
1680	A0A0M3BF13	Rhizobium sp. LC145
1681	A0A1S1TF47	Rhizobium sp. LCM 4573
1682	A0A0Q5D449	Rhizobium sp. Leaf306
1683	A0A0Q5VUY	Rhizobium sp. Leaf371
1684	A0A0Q5X570	Rhizobium sp. Leaf383
1685	A0A0Q6FS00	Rhizobium sp. Leaf453
1686	A0A2A6LLB4	Rhizobium sp. M10
1687	L0NIB8	Rhizobium sp. NT-26
1688	A0A1V3FBZ9	Rhizobium sp. P44RR-XXIV
1689	A0A246S9G7	Rhizobium sp. R634
1690	A0A2D0B191	Rhizobium sp. R635
1691	A0A246TYN5	Rhizobium sp. R693
1692	A0A246U7E8	Rhizobium sp. R72
1693	A0A0Q6RH8	Rhizobium sp. Root1203
1694	A0A0Q6RIJ7	Rhizobium sp. Root1204
1695	A0A0Q6SC9	Rhizobium sp. Root1212
1696	A0A0Q6VVH	Rhizobium sp. Root1220
1697	A0A0Q6ZP87	Rhizobium sp. Root1240
1698	A0A0Q7Y0T3	Rhizobium sp. Root149

1699	A0A0T1XQP6	Rhizobium sp. Root482
1700	A0A0Q7PNF3	Rhizobium sp. Root483D2
1701	A0A0Q8NV26	Rhizobium sp. Root708
1702	A0A1S1PKL4	Rhizobium sp. RSm-3
1703	A0A0D6SJW8	Rhizobium sp. UR51a
1704	A0A198YT22	Rhizobium sp. WYCCWR10014
1705	A0A1E4YB23	Rhizobium sp. YK2
1706	A0A095VI55	Rhizobium sp. YS-1r
1707	A0A1Q9A3U3	Rhizobium taibaishanense
1708	A0A1H8N0J7	Rhizobium tibeticum
1709	L0LI23	Rhizobium tropici CIAT 899
1710	A0A177QCR3	Rhizomicrobium sp. SCGC AG-212-E05
1711	A0A1V3P819	Rhodanobacter sp. C05
1712	A0A154QJV9	Rhodanobacter thiooxydans
1713	D5ANB4	Rhodobacter capsulatus (strain ATCC BAA-309 / NBRC 16581 / SB1003)
1714	A0A0E2PBB7	Rhodobacter capsulatus Y262
1715	A0A1E3D2B6	Rhodobacter johrii
1716	A0A239D7T4	Rhodobacter megalophilus
1717	A0A1H4KA45	Rhodobacter sp. 24-YEA-8
1718	A0A0R2WMN	Rhodobacter sp. BACL10 MAG-120419-bin15
1719	A0A0R2TNQ8	Rhodobacter sp. BACL10 MAG-120910-bin24
1720	A0A0R2TJK4	Rhodobacter sp. BACL10 MAG-121220-bin24
1721	V7EFI8	Rhodobacter sp. CACIA14H1
1722	A0A1D9MGL3	Rhodobacter sp. LPB0142
1723	Q3J3S2	Rhodobacter sphaeroides (strain ATCC 17023 / 2.4.1 / NCIB 8253 / DSM 158)
1724	A0A1N7JM58	Rhodobacter vinaykumarii
1725	A0A2A4NTN5	Rhodobacteraceae bacterium
1726	A0A1B6YIN3	Rhodobacteraceae bacterium EhC02
1727	A0A1G3FSR3	Rhodobacteraceae bacterium GWE1_64_9
1728	A0A1G3FZY3	Rhodobacteraceae bacterium GWF1_65_7
1729	A0A257EWN6	Rhodobacteraceae bacterium PARR1
1730	A0A257Z7B2	Rhodobacterales bacterium 12-65-15
1731	A0A258F267	Rhodobacterales bacterium 32-66-7
1732	A0A259M970	Rhodobacterales bacterium 34-62-10
1733	A0A1Y5HN86	Rhodobacterales bacterium 56_14_T64
1734	A0A1Q4CU76	Rhodobacterales bacterium 65-51
1735	A0A1G3GE61	Rhodobacterales bacterium RIFCSPHIGHO2_02_FULL_62_130
1736	A0A2A5ETK7	Rhodobiaceae bacterium
1737	A0A1F2Q4G2	Rhodococcus erythropolis (Arthrobacter picolinophilus)
1738	T5IF99	Rhodococcus erythropolis DN1
1739	A0A0U3JJP0	Rhodococcus erythropolis R138
1740	C3JU66	Rhodococcus erythropolis SK121
1741	C0ZQE0	Rhodococcus erythropolis (strain PR4 / NBRC 100887)
1742	A0A165LS60	Rhodococcus fascians D188
1743	I0W6I4	Rhodococcus imtechensis RKJ300 = JCM 13270

1744	Q0SC99	Rhodococcus jostii (strain RHA1)
1745	A0A1B1KET7	Rhodococcus opacus (Nocardia opaca)
1746	W8GQ03	Rhodococcus opacus PD630
1747	A0A069J9P1	Rhodococcus qingshengii
1748	A0A2A3GIH4	Rhodococcus sp. ACPA1
1749	A0A2A3EYS1	Rhodococcus sp. ACS1
1750	A0A0D8HSX4	Rhodococcus sp. AD45
1751	A0A1W7QA5	Rhodococcus sp. Br-6
1752	N1LYT5	Rhodococcus sp. EsD8
1753	J1R5I6	Rhodococcus sp. JVH1
1754	A0A150A6S1	Rhodococcus sp. LB1
1755	U0FDH0	Rhodococcus sp. P27
1756	A0A143Q7E3	Rhodococcus sp. PBTS 1
1757	A0A143QHT7	Rhodococcus sp. PBTS 2
1758	A0A135GTE9	Rhodococcus sp. SC4
1759	L2TBG3	Rhodococcus wratislaviensis IFP 2016
1760	X0PQA1	Rhodococcus wratislaviensis NBRC 100605
1761	A0A037UQ60	Rhodomicrobium udaipurense JA643
1762	A0A255R6Q8	Rhodopirellula sp. MGV
1763	A0A0D7EKS1	Rhodopseudomonas palustris
1764	Q6N5K0	Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)
1765	Q07HP2	Rhodopseudomonas palustris (strain BisA53)
1766	Q13CT2	Rhodopseudomonas palustris (strain BisB5)
1767	E6VER5	Rhodopseudomonas palustris (strain DX-1)
1768	B3QAR9	Rhodopseudomonas palustris (strain TIE-1)
1769	A0A1H8TEL4	Rhodopseudomonas pseudopalustris
1770	A0A0N1C912	Rhodopseudomonas sp. AAP120
1771	A0A095CR32	Rhodovulum sp. NI22
1772	A0A1Z9TEM0	Rickettsiales bacterium TMED269
1773	A0A173SRD8	Roseburia intestinalis
1774	A0A1Y5RXJ7	Roseisalinus antarcticus
1775	W4HPV7	Roseivivax atlanticus
1776	X7EKU0	Roseivivax halodurans JCM 10272
1777	X7F2C3	Roseivivax isoporae LMG 25204
1778	A0A1X6ZHX4	Roseivivax jejudonensis
1779	Q161I2	Roseobacter denitrificans (strain ATCC 33942 / OCh 114) (Erythrobacter sp. (strain OCh 114)) (Roseobacter denitrificans)
1780	A3X3D7	Roseobacter sp. MED193
1781	A0A1J5LNQ1	Roseobacter sp. MedPE-SWchi
1782	A4EWR1	Roseobacter sp. SK209-2-6
1783	A0A1L7AF21	Roseomonas gilardii
1784	A0A1S8D874	Roseomonas mucosa
1785	A0A2C7AGT4	Roseomonas rhizosphaerae
1786	A0A1V2H3V2	Roseomonas sp. M3
1787	A0A1Q2YXL0	Roseomonas sp. TAS13
1788	A0A1X7BXA6	Roseovarius aestuarii

1789	A0A0T5NZX0	Roseovarius atlanticus
1790	A0A1X6ZMI7	Roseovarius gaetbuli
1791	A0A1X6YYU5	Roseovarius halotolerans
1792	A0A0T5P652	Roseovarius indicus
1793	A0A1V0RJX9	Roseovarius mucosus
1794	A0A1V1UE16	Roseovarius sp. A-2
1795	A0A176FG89	Roseovarius sp. HI0049
1796	A6E3Q6	Roseovarius sp. TM1035
1797	A0A0L6CVV1	Roseovarius tolerans
1798	A0A017HPX6	Rubellimicrobium mesophilum DSM 19309
1799	S9QZ20	Rubellimicrobium thermophilum DSM 16684
1800	A0A1H4A5D9	Rubrimonas cliftonensis
1801	F3LLE8	Rubrivivax benzoatilyticus JA2 = ATCC BAA-35
1802	A0A238KXG2	Ruegeria arenilitoris
1803	A0A0P1E894	Ruegeria atlantica
1804	A0A0X3TXF1	Ruegeria marisrubri
1805	A0A1X7A821	Ruegeria meonggei
1806	Q5LV92	Ruegeria pomeroyi (strain ATCC 700808 / DSM 15171 / DSS-3) (Silicibacter pomeroyi)
1807	A0A0X3TSF5	Ruegeria profundi
1808	A0A0C1J220	Ruegeria sp. ANG-R
1809	A0A0C1J930	Ruegeria sp. ANG-S4
1810	A0A0P1IH18	Ruegeria sp. CECT 5091
1811	A0A1E3DEM5	Ruegeria sp. PBVC088
1812	Q1GCS7	Ruegeria sp. (strain TM1040) (Silicibacter sp.)
1813	A0A174R2F8	[Ruminococcus] torques
1814	W7Y3I7	Saccharicrinis fermentans DSM 9555 = JCM 21142
1815	A3K8B3	Sagittula stellata E-37
1816	A0A1Q8SWX	Salinicola socius
1817	A0A1Q8T807	Salinicola sp. MH3R3-1
1818	A0A1S2DGM	Salinicola sp. MIT1003
1819	A0A0S2I4P7	Salinivirga cyanobacteriivorans
1820	A0A2A4XAM4	SAR86 cluster bacterium
1821	A0A0R2W5V4	SAR92 bacterium BACL16 MAG-120619-bin48
1822	A0A0R2TUR9	SAR92 bacterium BACL26 MAG-121220-bin70
1823	A0A139WUT8	Scytonema hofmannii PCC 7110
1824	A0A1I7EDC6	Sedimentitalea nanhaiensis
1825	A0A0X2PD81	Serratia
1826	A0A084YPF9	Serratia grimesii
1827	A0A0X8SJ20	Serratia liquefaciens
1828	A0A069CQX3	Serratia liquefaciens FK01
1829	A0A1Q4P008	Serratia marcescens
1830	Q07YF3	Shewanella frigidimarina (strain NCIMB 400)
1831	B8CPP0	Shewanella piezotolerans (strain WP3 / JCM 13877)
1832	A0A0C3QTN6	Shewanella sp. cp20
1833	A0A0P1FES5	Shimia marina

1834	A0A0M9EEL0	Shimia sp. SK013
1835	A0A021XH97	Shinella sp. DD12
1836	A0A1A9GB88	Shinella sp. HZN7
1837	A0A1L3LNT1	Sinorhizobium americanum
1838	A0A1L3L4T4	Sinorhizobium americanum CCGM7
1839	C3KLK6	Sinorhizobium fredii (strain NBRC 101917 / NGR234)
1840	A0A0T6ZNB2	Sinorhizobium fredii USDA 205
1841	I3X279	Sinorhizobium fredii USDA 257
1842	H0G851	Sinorhizobium meliloti CCNWSX0020
1843	F7XC84	Sinorhizobium meliloti (strain SM11)
1844	A0A178XHH4	Sinorhizobium saheli
1845	A0A1V3R4M6	Sinorhizobium sp. A49
1846	A0A2A6P936	Sinorhizobium sp. BJ1
1847	A0A0T6ZSL8	Sinorhizobium sp. GL28
1848	A0A226CPW4	Sinorhizobium sp. LM21
1849	A0A2A6MJ16	Sinorhizobium sp. NG07B
1850	A0A0T6XVS1	Sinorhizobium sp. Sb3
1851	A0A0D2VRC0	Skermanella aerolata KACC 11604
1852	W9GZH9	Skermanella stibiiresistens SB22
1853	A0A235E3I4	Sphingobacterium cellulitidis
1854	A0A1R4KN13	Sphingobacterium faecium PCAi_F2.5
1855	A0A239XWS0	Sphingobacterium mizutaii
1856	A0A1V3MYC3	Sphingobacterium sp. CZ-UAM
1857	A0A077XW28	Sphingobacterium sp. PM2-P1-29
1858	D4Z350	Sphingobium japonicum (strain NBRC 101211 / UT26S)
1859	A0A013WVX0	Sphingobium sp. Ant17
1860	A0A173KVC3	Sphingobium sp. EP60837
1861	A0A0Q4I429	Sphingobium sp. Leaf26
1862	A0A257DKE9	Sphingomonadaceae bacterium PASS1
1863	A0A259IAD6	Sphingomonadales bacterium 39-62-4
1864	A0A1M3I6E9	Sphingomonadales bacterium 63-6
1865	A0A1G3K345	Sphingomonadales bacterium GWF1_63_6
1866	A0A1G3JW09	Sphingomonadales bacterium RIFCSPLOWO2_12_FULL_63_15
1867	A0A245ZHX8	Sphingomonas dokdonensis
1868	A0A0C5L545	Sphingomonas hengshuiensis
1869	A0A239GD87	Sphingomonas laterariae
1870	A0A245ZS72	Sphingomonas mucosissima
1871	A0A031JEB0	Sphingomonas paucimobilis (Pseudomonas paucimobilis)
1872	A0A147IZK6	Sphingomonas sanguinis
1873	A0A1M2ZJJ3	Sphingomonas sp. 66-10
1874	A0A0M2LVJ2	Sphingomonas sp. Ag1
1875	A0A1X9YCS5	Sphingomonas sp. KC8
1876	A0A0Q4DKY3	Sphingomonas sp. Leaf10
1877	A0A0Q4G6K6	Sphingomonas sp. Leaf20
1878	A0A0Q4EXT7	Sphingomonas sp. Leaf208

1879	A0A0Q4HXJ3	Sphingomonas sp. Leaf22
1880	A0A0S9CIS6	Sphingomonas sp. Leaf231
1881	A0A0Q4L8Y2	Sphingomonas sp. Leaf34
1882	A0A0Q5PA79	Sphingomonas sp. Leaf343
1883	A0A0Q4L2Z1	Sphingomonas sp. Leaf38
1884	A0A0T0PUE0	Sphingomonas sp. Leaf412
1885	A0A0Q4QA40	Sphingomonas sp. Leaf67
1886	A0A196MU22	Sphingomonas sp. TDK1
1887	A0A0W1QLG	Sphingomonas sp. WG
1888	A0A2A4B2I1	Sphingomonas spermidinifaciens
1889	A0A0X8R772	Sphingopyxis granuli
1890	A0A246K3M4	Sphingopyxis witflariensis
1891	A0A220W7L8	Sphingorhabdus flavimaris
1892	A0A1V5WIK4	Spirochaetes bacterium ADurb.Bin215
1893	A0A1V5HU64	Spirochaetes bacterium ADurb.BinA120
1894	A0A0U1KTE0	Sporomusa sp. An4
1895	A0A246HND7	Stenotrophomonas maltophilia (Pseudomonas maltophilia) (Xanthomonas maltophilia)
1896	A0A023Y3E2	Stenotrophomonas rhizophila
1897	A0A1D8YF00	Stenotrophomonas sp. LM091
1898	B8L7U8	Stenotrophomonas sp. SKA14
1899	Q092U4	Stigmatella aurantiaca (strain DW4/3-1)
1900	A0A239X4J1	Streptococcus acidominimus
1901	A0A0H1LVR0	Streptococcus agalactiae
1902	A0A0G6P5S0	Streptococcus equi subsp. equi
1903	B4U3D8	Streptococcus equi subsp. zooepidemicus (strain MGCS10565)
1904	A0A239ST89	Streptococcus merionis
1905	Q8DTV5	Streptococcus mutans serotype c (strain ATCC 700610 / UA159)
1906	A0A2A4KXG5	Streptococcus parauberis
1907	M3IZ37	Streptococcus parauberis KRS-02083
1908	A0A0Y4GBH3	Streptococcus pneumoniae
1909	F8LIY3	Streptococcus salivarius (strain CCHSS3)
1910	F8LQ12	Streptococcus salivarius (strain JIM8777)
1911	A0A139P670	Streptococcus sp. DD11
1912	A0A139NLY0	Streptococcus sp. DD12
1913	A0A139NRA7	Streptococcus sp. DD13
1914	T0UHV3	Streptococcus sp. HSISS1
1915	T0V0E1	Streptococcus sp. HSISS2
1916	T0V5Y5	Streptococcus sp. HSISS3
1917	A0A116LKQ3	Streptococcus suis
1918	R5ZW35	Streptococcus thermophilus CAG:236
1919	A0A117E7E7	Streptomyces acidiscabies
1920	A0A1Z1WPQ4	Streptomyces alboflavus
1921	X0P2D6	Streptomyces albulus PD-1
1922	A0A0X7JDU9	Streptomyces albus subsp. albus
1923	S3ZE18	Streptomyces aurantiacus JA 4570

1924	A0A0K9XKY2	Streptomyces caatingaensis
1925	A0A0C5G7M8	Streptomyces cyaneogriseus subsp. noncyanogenus
1926	N0D5B0	Streptomyces fulvissimus DSM 40593
1927	A0A140DJY8	Streptomyces gandocaensis
1928	A0A1B1B067	Streptomyces griseochromogenes
1929	A0A0L8MPD1	Streptomyces griseoflavus
1930	D9XU43	Streptomyces griseoflavus Tu4000
1931	A0A0X3X681	Streptomyces griseus subsp. griseus
1932	D9WQJ9	Streptomyces himastatinicus ATCC 53653
1933	A0A0F7VM75	Streptomyces leeuwenhoekii
1934	A0A086N889	Streptomyces luteus
1935	A0A1D7VM33	Streptomyces lydicus
1936	A0A1E7M696	Streptomyces nanshensis
1937	V6JFK2	Streptomyces niveus NCIMB 11891
1938	A0A1E7KKR8	Streptomyces oceani
1939	A0A250V3K6	Streptomyces olivochromogenes
1940	A0A191USC4	Streptomyces parvulus
1941	A0A1Y2NKS5	Streptomyces platensis
1942	A0A1E7K6U3	Streptomyces qinglanensis
1943	A0A0A0NFP7	Streptomyces rapamycinicus NRRL 5491
1944	A0A0U5HFC4	Streptomyces reticuli
1945	A0A0M8R3U5	Streptomyces rimosus subsp. pseudoverticillatus
1946	A0A0N0S725	Streptomyces rimosus subsp. rimosus
1947	A0A124C331	Streptomyces scabiei
1948	A0A1P8TQR3	Streptomyces silaceus
1949	A0A0W7WSQ	Streptomyces silvensis
1950	A0A1D2IJJ3	Streptomyces sp. AVP053U2
1951	A0A1Q5DVU3	Streptomyces sp. CB01249
1952	A0A1Q5CL17	Streptomyces sp. CB02414
1953	A0A1Q5LQM3	Streptomyces sp. CB02488
1954	A0A1Q4WE48	Streptomyces sp. CB02923
1955	A0A1Q4YR10	Streptomyces sp. CB03578
1956	A0A151DH83	Streptomyces sp. CC71
1957	A0A0N6ZT93	Streptomyces sp. CCM_MD2014
1958	A0A1K2FMI7	Streptomyces sp. F-1
1959	A0A0S1UGE6	Streptomyces sp. FR-008
1960	A0A0N0SSD8	Streptomyces sp. H036
1961	B4UYT5	Streptomyces sp. Mg1
1962	A0A1V2RPT0	Streptomyces sp. MP131-18
1963	A0A0M8WZ27	Streptomyces sp. NRRL B-3648
1964	A0A0X3V258	Streptomyces sp. NRRL F-4489
1965	A0A0N0SA61	Streptomyces sp. NRRL F-5755
1966	A0A0N0YWV4	Streptomyces sp. NRRL F-6602
1967	A0A0N0B1J8	Streptomyces sp. NRRL F-7442
1968	A0A0X3X4J0	Streptomyces sp. NRRL S-1521

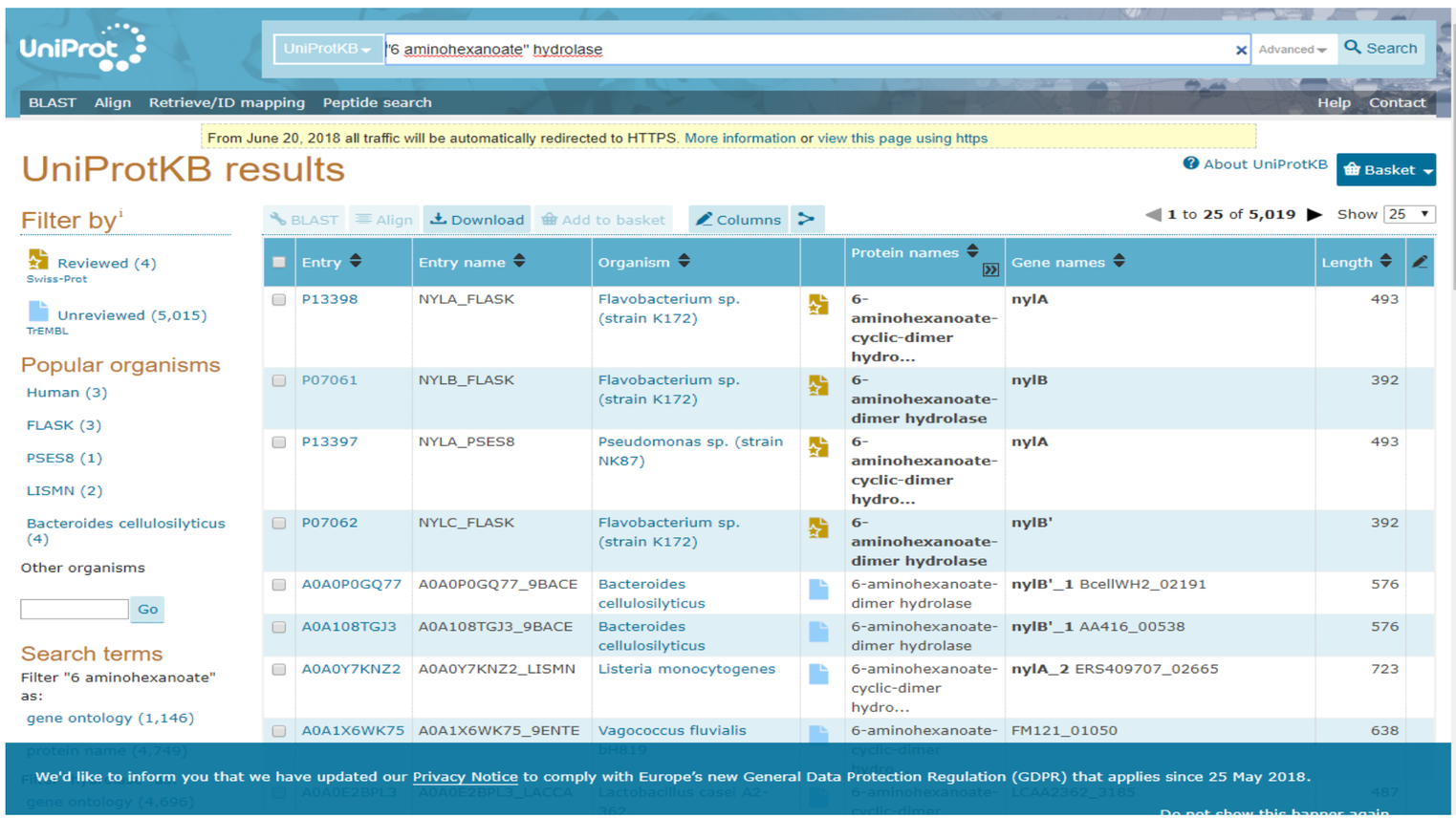
1969	A0A0N1K9U5	Streptomyces sp. NRRL WC-3753
1970	A0A069K0H7	Streptomyces sp. NTK 937
1971	A0A1B9EIG0	Streptomyces sp. PTY087I2
1972	A0A1A9IUG9	Streptomyces sp. SAT1
1973	A0A022MG25	Streptomyces sp. Tu 6176
1974	A0A0M8SV66	Streptomyces sp. WM4235
1975	A0A0M8S759	Streptomyces sp. WM6368
1976	A0A0N0SCU6	Streptomyces sp. WM6372
1977	A0A0L8QS22	Streptomyces varsoviensis
1978	A0A0L8MWR	Streptomyces virginiae
1979	A0A101NPK3	Streptomyces yokosukanensis
1980	A0A073IF04	Sulfitobacter donghicola DSW-25 = KCTC 12864 = JCM 14565
1981	A0A196R0Z5	Sulfitobacter geojensis
1982	A0A061ST62	Sulfitobacter mediterraneus
1983	A0A221K285	Sulfitobacter pseudonitzschiae
1984	A0A1J0WJ09	Sulfitobacter sp. AM1-D1
1985	A0A085BRZ7	Sulfitobacter sp. CB2047
1986	A0A196NMT8	Sulfitobacter sp. EhC04
1987	A0A166T1Z3	Sulfitobacter sp. HI0023
1988	A0A167HP95	Sulfitobacter sp. HI0054
1989	A0A176HXM2	Sulfitobacter sp. HI0076
1990	A0A176IEM4	Sulfitobacter sp. HI0082
1991	A3SVT9	Sulfitobacter sp. (strain NAS-14.1)
1992	A0A0L8V7R6	Sunxiuqinia dokdonensis
1993	A0A1V4XGE4	Syntrophaceae bacterium PtaB.Bin095
1994	A0A1D3URL4	Tannerella forsythia (Bacteroides forsythus)
1995	A0A109ZY28	Tardiphaga robiniae
1996	A0A1H6MY42	Tardiphaga sp. OK245
1997	A0A239JW73	Tardiphaga sp. OK246
1998	A0A1P8MS08	Tateyamaria omphalii
1999	A0A0B4CAC3	Tateyamaria sp. ANG-S1
2000	A0A098GAL2	Tatlockia micdadei (Legionella micdadei)
2001	A0A238UE61	Tenacibaculum jejuense
2002	A0A0J6IW53	Testudinibacter aquarius
2003	W6K428	Tetrasphaera australiensis Ben110
2004	A0A077M3T4	Tetrasphaera japonica T1-X7
2005	A0A0P1FIN3	Thalassobius gelatinovorus (Ruegeria gelatinovora)
2006	A0A0P1FSF4	Thalassobius mediterraneus
2007	A0A154L810	Thalassospira lucentensis
2008	A0A074JQ98	Thalassospira permensis NBRC 106175
2009	A0A199YG65	Thalassospira profundimaris
2010	A0A0D8CM43	Thalassospira sp. HJ
2011	A0A154LCG1	Thalassospira sp. MCCC 1A01148
2012	A0A1X4N4U6	Thalassospira sp. MCCC 1A01428
2013	A0A154VF20	Thalassospira sp. MCCC 1A02898

2014	A0A1X4MZA6	Thalassospira sp. MCCC 1A03138
2015	A0A136HUG4	Thalassospira sp. Nap_22
2016	A0A1Q4UMP9	Thalassospira sp. TSL5-1
2017	A0A199Y2W6	Thalassospira tepidiphila MCCC 1A03514
2018	A0A154KSG4	Thalassospira xiamenensis
2019	R7RUU8	Thermobrachium celere DSM 8682
2020	E8PLX2	Thermus scotoductus (strain ATCC 700910 / SA-01)
2021	A0A0B0SF43	Thermus sp. 2.9
2022	G8N8V5	Thermus sp. CCB_US3_UF1
2023	W2U5E2	Thermus sp. NMX2.A1
2024	Q72KS9	Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039)
2025	B8GT11	Thioalkalivibrio sulfidiphilus (strain HL-EbGR7)
2026	A0A2A4CN89	Thioclava arenosa
2027	A0A1T2AMX5	Thioclava marina
2028	A0A1S6IHX6	Thioclava nitratireducens
2029	A0A074K0M8	Thioclava pacifica DSM 10166
2030	A0A1T2B248	Thioclava sp. DLFJ4-1
2031	A0A1T2BAI7	Thioclava sp. DLFJ5-1
2032	A0A1W9XLR3	Thioclava sp. ElOx9
2033	A0A1T2A5H2	Thioclava sp. F28-4
2034	A0A254UQA8	Thioclava sp. JM3
2035	A0A1T2BXU1	Thioclava sp. L04-15
2036	D6CNE5	Thiomonas arsenitoxydans (strain DSM 22701 / CIP 110005 / 3As)
2037	A0A238D0E3	Thiomonas delicata (Thiomonas cuprina)
2038	A0A078BIV3	Thiomonas sp. CB2
2039	A0A160SPN4	Thiomonas sp. CB3
2040	A0A238DI14	Thiomonas sp. X19
2041	A0A1Z9U3J3	Thiotrichales bacterium TMED285
2042	A0A162KYF5	Tistrella mobilis
2043	I3TJC5	Tistrella mobilis (strain KA081020-065)
2044	F2NW26	Treponema succinifaciens (strain ATCC 33096 / DSM 2489 / 6091)
2045	A0A1Y5RU04	Tropicibacter litoreus R37
2046	A0A0N7M0Q4	Tropicibacter multivorans
2047	A0A238JFC7	Tropicibacter phthalicicus
2048	A0A239K2A8	Tropicimonas sediminicola
2049	A0A1C6JX26	uncultured Anaerotruncus sp.
2050	A0A1C6HKF7	uncultured Bacteroides sp.
2051	A0A1C6G057	uncultured Blautia sp.
2052	A0A1C5WZV3	uncultured Clostridium sp.
2053	A0A1C5SG29	uncultured Coprococcus sp.
2054	A0A1C5Q3J1	uncultured Dorea sp.
2055	A0A1C6HH82	uncultured Eubacterium sp.
2056	A0A1C6IY35	uncultured Lachnospira sp.
2057	A0A075GLM4	uncultured marine group II/III euryarchaeote KM3_177_C07
2058	A0A075GZT7	uncultured marine group II/III euryarchaeote KM3_35_H09

2059	A0A1C5PT61	uncultured Ruminococcus sp.
2060	A0A1Y5PUT5	uncultured Sphingopyxis sp.
2061	A0A1Y5Q6P0	uncultured Stenotrophomonas sp.
2062	A0A1X6WK7!	Vagococcus fluvialis bH819
2063	A0A0S3PSD0	Variibacter gotjawalensis
2064	A0A250DM92	Variovorax boronicumulans
2065	A0A0N8PAS1	Variovorax paradoxus
2066	T1XH04	Variovorax paradoxus B4
2067	C5CP86	Variovorax paradoxus (strain S110)
2068	A0A126ZJR0	Variovorax sp. PAMC 28711
2069	A0A1I5W9H0	Variovorax sp. PDC80
2070	A0A0Q6NAU!	Variovorax sp. Root318D1
2071	A0A0Q7CE9!	Variovorax sp. Root411
2072	A0A0Q7H2W	Variovorax sp. Root434
2073	A0A0Q7LA23	Variovorax sp. Root473
2074	A0A1E4INS6	Variovorax sp. SCN 67-85
2075	A0A109BPV2	Variovorax sp. WDL1
2076	A0A1V6JU22	Verrucomicrobia bacterium ADurb.Bin006
2077	A0A1V6JCM4	Verrucomicrobia bacterium ADurb.Bin018
2078	A0A1V6GRF0	Verrucomicrobia bacterium ADurb.Bin070
2079	A0A1W6VLV!	Vibrio alginolyticus
2080	U3AN41	Vibrio azureus NBRC 104587
2081	A0A193KB01	Vibrio breoganii
2082	A0A1C3JAB8	Vibrio celticus
2083	A0A1E5D9B3	Vibrio cyclitrophicus FF160
2084	A0A066UX83	Vibrio fortis
2085	A0A0B8NQX4	Vibrio ishigakensis
2086	A0A0L1L557	Vibrio lentus
2087	A0A090TR17	Vibrio maritimus
2088	U4KI36	Vibrio nigripulchritudo
2089	A0A090P688	Vibrio ponticus
2090	A0A0C2NV18	Vibrio renipiscarius
2091	A0A1B1NP12	Vibrio scophthalmi
2092	A6CVK8	Vibrio shilonii AK1
2093	A0A1R4K7U3	Vibrio sp. JB196
2094	A0A0B8PKL5	Vibrio sp. JCM 19236
2095	A0A2C6ML20	Vibrio sp. PID17_43
2096	A0A1C3II24	Vibrio splendidus
2097	A0A1E5FVQ4	Vibrio splendidus 12E03
2098	A0A1E5ESR7	Vibrio splendidus 1F-157
2099	A0A1E5AXQ5	Vibrio splendidus ZS-139
2100	A0A109D629	Vibrio toranzoniae
2101	F9T9N2	Vibrio tubiashii ATCC 19109
2102	A0A090SJM3	Vibrio variabilis
2103	A0A1W6MBX	Vibrio vulnificus

2104	A0A024QGQ4	Virgibacillus massiliensis
2105	W4F0I8	Viridibacillus arenosi FSL R5-213
2106	A0A0K1PGS2	Vulgatibacter incomptus
2107	A0A1L6R8U4	Weissella jogaejeotgali
2108	A0A0K0XV16	Wenzhouxiangella marina
2109	A0A2A3LF05	Xanthomonadaceae bacterium NML93-0399
2110	A0A2A3VLL2	Xanthomonadaceae bacterium NML93-0792
2111	A0A222WGX0	Xanthomonas citri pv. mangiferaeindicae (agent of mango bacterial black spot)
2112	A0A0N8HXI0	Xanthomonas sp. Mitacek01
2113	A0A1Y2SKJ5	Xenorhabdus vietnamensis
2114	A0A1B1PSM0	Yangia sp. CCB-MM3
2115	A0A0F4GRK9	Zymoseptoria brevis

SCREEN SAMPLE OF UNIPROT PAGE FOR 6-AMINOHEXANOATE HYDROLASE:



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Testing the Hypothesis that the Nylonase NylB Protein
Arose *de novo* via a Frameshift Mutation

Salvador Cordova and John Sanford

SupplementaryTable S6
List of proteins that were listed as both a beta lactamase and a 6-aminohexanoate hydrolase nylonase in GenBank that were determined by searching for NylB homologs using psi-BLAST

Organism with Nylonase/Beta Lactamase	Accession Number As Beta Lactamase	Accession Number as 6-Aminohexanoate Hydrolase Nylonase	Comment
Bradyrhizobium sp. ORS 375	CCD97170.1	CCD97170.1	listed as both 6AH Nylonase and Beta Lactamase simultaneously
Candidatus Puniceispirillum marinum IMC	ADE39034.1	ADE39034.1	listed as both 6AH Nylonase and Beta Lactamase simultaneously
E. Coli	SCQ13749.1	SCQ13749.1	protein listed as a Beta Lactamase, but gene listed as nylB nylonase
Delftia acidovorans	KFJ13307.1	WP_034393572.1	6AH Nylonse 100% identical with Beta Lactamase
Comamonas thiooxydans	CUA91648.1	WP_034404398.1	6AH Nylonse 100% identical with Beta Lactamase
Comamonas testosteroni	EFI60192.1	WP_034362870.1	6AH Nylonse 100% identical with Beta Lactamase
Sinorhizobium sp. RAC02	AOF94051.1	WP_069063755.1	6AH Nylonase 100% contained inside Beta Lactamase
Burkholderia singularis	SMG00640.1	WP_089340811.1	6AH Nylonase 100% contained inside Beta Lactamase
Burkholderia sp. yr281	SDJ12107.1	WP_091788686.1	6AH Nylonase 100% contained inside Beta Lactamase
Bradyrhizobium arachidis	SFV17448.1	WP_092218251.1	6AH Nylonase 100% contained inside Beta Lactamase

Testing the Hypothesis that the Nylonase NylB Protein
Arose *de novo* via a Frameshift Mutation

Salvador Cordova and John Sanford

Supplementary Table S7
List of proteins that were listed as both an amidase and a 6-aminohexanoate hydrolase nylonase in GenBank that were determined by searching for NylA homologs using psi-BLAST

Organism with Nylonase	Accession Number as Amidase	Accession Number as 6-Aminohexanoate Hydrolase Nylonase	Comment
Rhodococcus erythropolis	WP_031330824.1	EQM35287.1	100% identical
Sphingomonas sp. KC8	WP_010125486.1	ARS27527.1	100% identical
Paenibacillus amylolyticus	WP_100527413.1	PJN62497.1	100% identical
Pseudomonas syringae	WP_020342474.1	EPN22118.1	100% identical
Marinobacter hydrocarbonoclasticus ATCC 49840]	WP_041654449.1	CCG93690.1	Amidase 100% contained inside 6AH Nylonase, covers 99% of 6AH Nylonase
Thiomonas delicata	WP_094159176.1	SBP866 99.1	Amidase 100% contained inside 6AH Nylonase, covers 99% of 6AH Nylonase
Leptospira interrogans	WP_001136113.1	KWV26884.1	Amidase 100% contained inside 6AH Nylonase, covers 99% of 6AH Nylonase

Testing the Hypothesis that the Nylonase NylB Protein
Arose *de novo* via a Frameshift Mutation

Salvador Cordova and John Sanford

Supplementary Table S8
Screen captures of MUSCLE 6.0 alignment of 6 NylB and 4 NylB' proteins.
Proteins 1-8 have experimental support for nylonase activity.
Protein 9 (Paenibacillus sp AD87) had the lowest e-value in psi-Blast search for NylB in Flavobacterium KI72
Protein 10 (E. Coli) is from a well known organism
Highlighted columns have 80% or higher conservation across selected proteins.
Asterisks "*" above a column indicate 100% conservation

Distance Matrix at the bottom

Positions 1-51

```
Species/Abbrv
1. NylB_Flavobacterium_KI72                ------MNARSTGQHPARYPGAAAGEPTLDSWQEAPHNRWAFARLGELLP
2. NylB_Prime_Flavobacterium_KI72          ------MNTPTTGSHPARYPSAAAGEPTLDSWQEPPHNRWAFAHLGEMVP
3. NylB_Agromyces_KY5R                     ------MNARSTGQHPARYPGAAAGEPTLDSWQEAPHNRWAFARLGELLP
4. NylB_Prime_Agromyces_KY5R               ------MNARSTGQHPARYPGAAAGEPTLDSWQEAPHNRWAFARLGELLP
5. NylB_Bacillus_cereus                    ------MN-----------------------------------FKQ------
6. NylB_Prime_Bacillus_cereus              ------MD-----------------------------------FKQ------
7. NylB_Pseudomonas_aeruginosa_PAO1        ------MLGLPLDRREG--PPMPA-LPLSRRALAALALVFALPALAEDWP
8. NylB_Pseudomonas_NK87                   ------MNTVPPFRDPT-VPGNSH-IPRQD-WDRAPWNRWTFQHVRELLP
9. NylB_Prime_Paenibacillus_sp._AD87       ------MN-----------------------------------PSSIPSMLH
10. NylB/beta-lactamase_E._coli            MIRKPLALALILAALPAAAMAQHCGSLTLD-VCPTPYDQ-TLPAAKDMLS
```

Positions 52-131

```
Spe                                                                                  *
1. ------------------TAAVSR-RDPATPAEPVVR-LDALA----TRLPDLEQRLEETCTDAFLVLRGSEVLAEYYRAGF
2. ------------------SAAVSR-RPVNAPGHALAR-LGAIA----AQLPDLEQRLEQTYTDAFLVLRGTEVVAEYYRAGF
3. ------------------TAAVSR-RDPATPAEPVVR-LDALA----TRLPDLEQRLEETCTDAFLVLRGSEVLAEYYRAGF
4. ------------------TAAVSR-RDPATPAEPVVR-LDALA----TRLPDLEQRLEETCTDAFLVLRGTEVVAEYYRAGF
```

```
5. ----------------------------------------------------LENKFEKKKVNTFLVYQKGKLTTEYYKTPE
6. ----------------------------------------------------LENKFEKKKVNTFLVYQKGELTTEYYKTPE
7. -----------------DTDWPRAQQPAGPA------LEAFERYAFGRRDDV--RRKGIRTDAVVVIRDGRLVYERYAGPS
8. -----------------TTKVWRGTGPASPLPVDLRDIDAVSFAAEGQSHTIAGFLETSYADGFLVLHGGKIVAERYLNGM
9. ---------------------------------------------QIIPPLDLR---SC----LVSMRGEIIYEHYRNQE
10.WDQTSRVIGFRNDYRNYAGDVFR-HGASTPLERAEKQLTDARYTLNGHTWNLQDYLKRENVSGMLVLKDGKVAWKYLAEGN
```

Positions 132-212

```
Spe          *   **                  *                                                  *
1. APDDRHLLMSVSKSLCGTVVGALIDEGRI-DPAQPVTEYVPEL---AGSVYDGPSVLQVLDMQISIDYNEDY--VDPASEV
2. APDDRHLLMSVSKSLCGTVVGALVDEGRI-DPAQPVTEYVPEL---AGSVYDGPSVLQVLDMQISIDYNEDY--VDPASEV
3. APDDRHLLMSVSKSLCGTVVGALIDEGRI-DPAQPVTEYVPEL---AGSVYDGPSVLQVLDMQISIDYNEDY--VDPASEV
4. APDDRHLLMSVSKSLCGTVVGALVDEGRI-DPAQPVTEYVPEL---AGSVYDGPSVLQVLDMQISIDYNEDY--VDPASEV
5. CTNNLYKINSITKSIVSLLIGIAIDKGYINDIHTPITEWIENV---PEGKHD-LTLYHLLTMTTGEEWKE-F--GNGVVFP
6. CANNLYKINSITKSIVSLLIGIAIDKGYINDIHTSITEWIENV---PGEKHD-LTLYHLLTMTTGEDWKE-F--GNGVVFP
7. RAETPHLTWSVSKSLLATLLGVAEGEGRF-QLDDPVARYYP-----PFARHPEVTLRHLLNWSSGLDWQEDYEFAPLKSSV
8. APHTQHLSQSVAKSVVGTVAGILIDRGVV-NPAALLTHYLPEL---EATAYRGATVQHVLDMTSGVVFDETY--TALDSHM
9. AGTHIAKINSCTKSVLSALICIAMDHGWLPEASTPISTFFPQLVSDPDPRKSEITLEQLLTMTAGFNWDE-F--GGQNSFP
10.TDTTLWTSRSVGKSVVSTLVGIAIQQGKIHSLDDLITVYEPEL---KGTAWDGVTLKQLIQHTSGVEWNEDY--TDPQSHF
```

Positions 213-293

```
Spe                                                                  *  *     *                                                  *
1. QTHDRSAGWRTRRDGD-PADTYEFLTTLRG-DGGTG-EFQYCSANTDVLAWIVERVTGLRYVEALSTYLWAKLDADRDATI
2. QTHGRSAGWRTRATGD-PADTYEFLTTLRG-DGSTG-EFQYCSANTDVLAWIVERVTGLRYVEALSTYLWAKLDADRDATI
3. QTHDRSAGWRTRRDGD-PADTYEFLTTLRG-DGGTG-EFQYCSANTDVLAWIVERVTGLRYVEALSTYLWANVDADRDATI
4. QTHGRSAGWRTRRHGD-PADTYEFLTTLRG-DGSTG-EFQYCSANTDVLAWIVERVTGLRYVEALSTYLWAKLDADRDATI
5. NDFVESANW------------VQYILEKPIIEEPAT-KMNYNSGSSHLLSYIIQKATGMPTEQFAKRYLFNPLEI-TEYEW
```

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6.  NDFVESENW-------------VQYILEKPIIEEPAT-KMNYNSGSSHLLSYIIQEATGMSTERFAKKYLFDPLKI-NEYEW
7.  VAMLYTRG---------RDDMAGFVAETPQ-ARPPGRRFRYSSGDSNVLAAALHGMLGADYAEYPWRALFEPLGI-RSAVW
8.  AQLDVASGWKDSPNPDWPTHVWDLILSLKDLECPHGASFRYRSIETDVLAFVLQRAAAAPLAELVSRELWAPMGAEEDAYF
9.  R-MTRTDHW-------------VNFALEQRLSHVPGT-YMEYNSGVSQILSAILMQSTGISVAEFAERYLFGPLGI-QQYEW
10. ARLTQCEA-----HPGVYACVRKIVTGLAR-QHPAGEQWSYSSGGAWLLGDILERATGMSLAAWLEQALWQPAGMAHDGVW
```

Positions 294-374

```
Spe                 *                   *                   *                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
1.  TVDQTGFG-FANGGVSCTARDLARVGRMMLDGGVA-PGGRVVSQGWVESVLAGGSREAMTDEGFTSAFPE-GSYTRQWW--
2.  TVDTTGFG-FAHGGVSCTARDLARVGRMMLDGGVA-PGGRVVSEDWVRRVLAGGSHEAMTDKGFTNTFPD-GSYTRQWW--
3.  TVDQTGFG-FANGGVSCTARDLARVGRMMLDGGVA-PGGRVVSQGWVESVLAGGSREAMTDEGFTSAFPE-GSYTRQWW--
4.  TVDTTGFG-FAHGGVSCTARDLARVGRMMLDGGVA-PGGRVVSEDWVRRVLAGGSHEAMTDKGFTNTFPD-GSYTRQWW--
5.  QQDSQGIY-VGGFGMKMKSKDLLKLGILCLQNGIW-QGNEIVSSKWLEESS---------TPLFETYEHV-GAYGYHWW--
6.  QQDPQGIY-VGGFGMKMKSTDLLKLGKLCLQNGYW-NEKEIVSAKWLEESS---------RAQFETYEHV-GAYGYHWW--
7.  ERDAAGTF-VGSSYVYMSARDLARVGLLMQRHGRW-RERQLLPLAWVEFNLTPFARYRPSAEEEGEAVPG-GQ----WW--
8.  TVDTAGYA-LGDGGFNATLRDYARFALLHLRGGEI-DGRRIVSPGWIAATR-FGADPALFGDIYREALPA-GAYHNQFW--
9.  ESDPQGVH-TGGFGLKLLPEDLLKFGQLFLQQGMW-NGQSMISSDHVSRST---------KPAITVTPPNHGSYAWHWW--
10. HAYQQGKHDVGAHGFNATLEDWGRFGEFVARDGRLSNGKQLVPAGWFDQAA----SWTKALNSVSAAHPE-GIYGYQWWNN
```

Positions 375-455

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Spe                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                
1.  -C------TGNERG-----------NVSGIGIHGQNLWLDPRTDSVIVKLSSWPD--PDTRHWHGLQSGILLDVSRALDAV
2.  -C------TGNERG-----------NVSGIGIHGQNLWLDPLTDSVIVKLSSWPD--PDTEHWHRLQNGILLDVSRALDAV
3.  -C------TGNERG-----------NVSGIGIHGQNLWLDPRTDSVIVKLSSWPD--PDTRHWHGLQSGILLDVSRALDAV
4.  -C------TGNERG-----------NVSGIGIHGQNLWLDPLTDSVIVKLSSWPD--PDTEHWHRLQNGILLDVSRALDAV
5.  -V------LNNERF------HIPYCMYFAMGYGGQYIVVIPQLEVVAVISSHMPK-----RGLVPLKLFI-EHVQENYKFV
6.  -V------LHNERF------HIPYCIYFAMGYGGQYIVIIPQLEVVSIISSHMPK-----RGLVPLNLFI-EHVQGNSNYI
```

```
7. -L------NRAVKGAPAPWPDVAETAFAALGHWGQALYVLPEEKLVIVRYADDRDGRFRHNEFLRLAQAAFAGEARP----
8. -I------EDTARG-----------AYMARGVFGQLIYIDPEADFAAVILSSWPE--FVSTTRLRTALAAVRAVREALSA-
9. -VGAYTNETAEAKF--TEQPTSILHYYYARGFGGQFVYIVPALELVVVLTNDKRK-----KEKPPLDVFPKQIAPQLAKLL
10. AI------PANAQNVQPTPQEGLKGSLWALGIYGQVIMVNRAEHLVIVQWSTWPQAEPSFNAQPLEAALMYSAIARELR--
```

MUSCLE Parameters:
Gap Open -2.9, Gap Extend 0, Hydrophobicity Multiplier 1.2, Max Memory in MB 487, Max Iterations, 8,
Clustering Method (Iteration 1,2) UPGMB, Clustering Method (Other Iterations) UPGMB, Min Diag Length (lambda).

MUSCLE Citation: Edgar, Robert C. (2004), MUSCLE: multiple sequence alignment with high accuracy and hight throughput, Nucleic Acids Research 32(5), 1792-1797.

M6: Pairwise Distances (D:\muscle\supplementary_s9.meg)

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	1	2	3	4	5	6	7	8	9	10
1. NylB CAA24927.1 Flavobacterium KI72										
2. NylB Prime CAA26616.1 Flavobacterium KI72	21.000									
3. BAE97621.1 NylB Agromyces KY5R	2.000	23.000								
4. BAE97630.1 NylB Prime Agromyces KY5R	19.000	2.000	21.000							
5. NylB SME41718.1 Bacillus cereus	209.000	212.000	210.000	212.000						
6. SME45458.1 NylB Prime Bacillus cereus	211.000	214.000	212.000	214.000	33.000					
7. NylB-like AAG07735.1 Pseudomonas aeruginosa PAO1	197.000	198.000	198.000	198.000	211.000	212.000				
8. NylB BAA01524.1 Pseudomonas NK87	175.000	174.000	175.000	176.000	206.000	213.000	196.000			
9. OAX47860.1 NylB Paenibacillus sp. AD87 7e-5	215.000	213.000	216.000	212.000	165.000	167.000	199.000	213.000		
10. SCQ13749.1 nylb gene/beta-lactamase protein Escherichia coli	203.000	208.000	203.000	208.000	207.000	206.000	194.000	190.000	208.000	

Table. Estimates of Evolutionary Divergence between Sequences
The number of amino acid differences per sequence from between sequences are shown. The analysis involved 10 amino acid sequences. All positions with less than 95% site coverage were eliminated. That is, fewer than 5% alignment gaps, missing data, and ambiguous bases were allowed at any position. There were a total of 277 positions in the final dataset. Evolutionary analyses were conducted in MEGA6 [1].

1. Tamura K., Stecher G., Peterson D., Filipski A., and Kumar S. (2013). MEGA6: Molecular Evolutionary Genetics Analysis version 6.0. Molecular Biology and Evolution30: 2725-2729.

>Testing the Hypothesis that the Nylonase NylB Protein
>Arose de novo via a Frameshift Mutation
>Salvador Cordova and John Sanford
>Supplementary Table S9

>NylB CAA24927.1 Flavobacterium KI72
MNARSTGQHPARYPGAAAGEPTLDSWQEAPHNRWAFARLGELLPTAAVSRRDPATPAEPV
VRLDALATRLPDLEQRLEETCTDAFLVLRGSEVLAEYYRAGFAPDDRHLLMSVSKSLCGT
VVGALIDEGRIDPAQPVTEYVPELAGSVYDGPSVLQVLDMQISIDYNEDYVDPASEVQTH
DRSAGWRTRRDGDPADTYEFLTTLRGDGGTGEFQYCSANTDVLAWIVERVTGLRYVEALS
TYLWAKLDADRDATITVDQTGFGFANGGVSCTARDLARVGRMMLDGGVAPGGRVVSQGWV
ESVLAGGSREAMTDEGFTSAFPEGSYTRQWWCTGNERGNVSGIGIHGQNLWLDPRTDSVI
VKLSSWPDPDTRHWHGLQSGILLDVSRALDAV

>NylB Prime CAA26616.1 Flavobacterium KI72
MNTPTTGSHPARYPSAAAGEPTLDSWQEPPHNRWAFAHLGEMVPSAAVSRRPVNAPGHAL
ARLGAIAAQLPDLEQRLEQTYTDAFLVLRGTEVVAEYYRAGFAPDDRHLLMSVSKSLCGT
VVGALVDEGRIDPAQPVTEYVPELAGSVYDGPSVLQVLDMQISIDYNEDYVDPASEVQTH
GRSAGWRTRATGDPADTYEFLTTLRGDGSTGEFQYCSANTDVLAWIVERVTGLRYVEALS
TYLWAKLDADRDATITVDTTGFGFAHGGVSCTARDLARVGRMMLDGGVAPGGRVVSEDWV
RRVLAGGSHEAMTDKGFTNTFPDGSYTRQWWCTGNERGNVSGIGIHGQNLWLDPLTDSVI
VKLSSWPDPDTEHWHRLQNGILLDVSRALDAV

>BAE97621.1 NylB Agromyces KY5R
MNARSTGQHPARYPGAAAGEPTLDSWQEAPHNRWAFARLGELLPTAAVSRRDPATPAEPVVRLDALATRL
PDLEQRLEETCTDAFLVLRGSEVLAEYYRAGFAPDDRHLLMSVSKSLCGTVVGALIDEGRIDPAQPVTEY
VPELAGSVYDGPSVLQVLDMQISIDYNEDYVDPASEVQTHDRSAGWRTRRDGDPADTYEFLTTLRGDGGT
GEFQYCSANTDVLAWIVERVTGLRYVEALSTYLWANVDADRDATITVDQTGFGFANGGVSCTARDLARVG
RMMLDGGVAPGGRVVSQGWVESVLAGGSREAMTDEGFTSAFPEGSYTRQWWCTGNERGNVSGIGIHGQNL
WLDPRTDSVIVKLSSWPDPDTRHWHGLQSGILLDVSRALDAV

>BAE97630.1 NylB Prime Agromyces KY5R
MNARSTGQHPARYPGAAAGEPTLDSWQEAPHNRWAFARLGELLPTAAVSRRDPATPAEPVVRLDALATRL
PDLEQRLEETCTDAFLVLRGTEVVAEYYRAGFAPDDRHLLMSVSKSLCGTVVGALVDEGRIDPAQPVTEY
VPELAGSVYDGPSVLQVLDMQISIDYNEDYVDPASEVQTHGRSAGWRTRRHGDPADTYEFLTTLRGDGST
GEFQYCSANTDVLAWIVERVTGLRYVEALSTYLWAKLDADRDATITVDTTGFGFAHGGVSCTARDLARVG
RMMLDGGVAPGGRVVSEDWVRRVLAGGSHEAMTDKGFTNTFPDGSYTRQWWCTGNERGNVSGIGIHGQNL
WLDPLTDSVIVKLSSWPDPDTEHWHRLQNGILLDVSRALDAV

>NylB SME41718.1 Bacillus cereus
MNFKQLENKFEKKKVNTFLVYQKGKLTTEYYKTPECTNNLYKINSITKSIVSLLIGIAIDKGYINDIHTP
ITEWIENVPEGKHDLTLYHLLTMTTGEEWKEFGNGVVFPNDFVESANWVQYILEKPIIEEPATKMNYNSG
SSHLLSYIIQKATGMPTEQFAKRYLFNPLEITEYEWQQDSQGIYVGGFGMKMKSKDLLKLGILCLQNGIW
QGNEIVSSKWLEESSTPLFETYEHVGAYGYHWWVLNNERFHIPYCMYFAMGYGGQYIVVIPQLEVVAVIS
SHMPKRGLVPLKLFIEHVQENYKFV

>SME45458.1 NylB Prime Bacillus cereus
MDFKQLENKFEKKKVNTFLVYQKGELTTEYYKTPECANNLYKINSITKSIVSLLIGIAIDKGYINDIHTS
ITEWIENVPGEKHDLTLYHLLTMTTGEDWKEFGNGVVFPNDFVESENWVQYILEKPIIEEPATKMNYNSG
SSHLLSYIIQEATGMSTERFAKKYLFDPLKINEYEWQQDPQGIYVGGFGMKMKSTDLLKLGKLCLQNGYW
NEKEIVSAKWLEESSRAQFETYEHVGAYGYHWWVLHNERFHIPYCIYFAMGYGGQYIVIIPQLEVVSIIS
SHMPKRGLVPLNLFIEHVQGNSNYI

>NylB-like AAG07735.1 Pseudomonas aeruginosa PAO1
MLGLPLDRREGPPMPALPLSRRALAALALVFALPALAEDWPDTDWPRAQQPAGPALEAFE
RYAFGRRDDVRRKGIRTDAVVVIRDGRLVYERYAGPSRAETPHLTWSVSKSLLATLLGVA
EGEGRFQLDDPVARYYPPFARHPEVTLRHLLNWSSGLDWQEDYEFAPLKSSVVAMLYTRG
RDDMAGFVAETPQARPPGRRFRYSSGDSNVLAAALHGMLGADYAEYPWRALFEPLGIRSA
VWERDAAGTFVGSSYVYMSARDLARVGLLMQRHGRWRERQLLPLAWVEFNLTPFARYRPS
AEEEGEAVPGGQWWLNRAVKGAPAPWPDVAETAFAALGHWGQALYVLPEEKLVIVRYADD
RDGRFRHNEFLRLAQAAFAGEARP

>NylB BAA01524.1 Pseudomonas NK87
MNTVPPFRDPTVPGNSHIPRQDWDRAPWNRWTFQHVRELLPTTKVWRGTGPASPLPVDLRDIDAVSFAAE
GQSHTIAGFLETSYADGFLVLHGGKIVAERYLNGMAPHTQHLSQSVAKSVVGTVAGILIDRGVVNPAALL
THYLPELEATAYRGATVQHVLDMTSGVVFDETYTALDSHMAQLDVASGWKDSPNPDWPTHVWDLILSLKD
LECPHGASFRYRSIETDVLAFVLQRAAAAPLAELVSRELWAPMGAEEDAYFTVDTAGYALGDGGFNATLR
DYARFALLHLRGGEIDGRRIVSPGWIAATRFGADPALFGDIYREALPAGAYHNQFWIEDTARGAYMARGV
FGQLIYIDPEADFAAVILSSWPEFVSTTRLRTALAAVRAVREALSA

>OAX47860.1 NylB' Paenibacillus sp. AD87 7e^-5
MNPSSIPSMLHQIIPPLDLRSCLVSMRGEIIYEHYRNQEAGTHIAKINSCTKSVLSALICIAMDHGWLPE
ASTPISTFFPQLVSDPDPRKSEITLEQLLTMTAGFNWDEFGGQNSFPRMTRTDHWVNFALEQRLSHVPGT
YMEYNSGVSQILSAILMQSTGISVAEFAERYLFGPLGIQQYEWESDPQGVHTGGFGLKLLPEDLLKFGQL
FLQQGMWNGQSMISSDHVSRSTKPAITVTPPNHGSYAWHWWVGAYTNETAEAKFTEQPTSILHYYYARGF

GGQFVYIVPALELVVVLTNDKRKKEKPPLDVFPKQIAPQLAKLL

>SCQ13749.1 nylb gene/beta-lactamase protein Escherichia coli
MIRKPLALALILAALPAAAMAQHCGSLTLDVCPTPYDQTLPAAKDMLSWDQTSRVIGFRNDYRNYAGDVF
RHGASTPLERAEKQLTDARYTLNGHTWNLQDYLKRENVSGMLVLKDGKVAWKYLAEGNTDTTLWTSRSVG
KSVVSTLVGIAIQQGKIHSLDDLITVYEPELKGTAWDGVTLKQLIQHTSGVEWNEDYTDPQSHFARLTQC
EAHPGVYACVRKIVTGLARQHPAGEQWSYSSGGAWLLGDILERATGMSLAAWLEQALWQPAGMAHDGVWH
AYQQGKHDVGAHGFNATLEDWGRFGEFVARDGRLSNGKQLVPAGWFDQAASWTKALNSVSAAHPEGIYGY
QWWNNAIPANAQNVQPTPQEGLKGSLWALGIYGQVIMVNRAEHLVIVQWSTWPQAEPSFNAQPLEAALMY
SAIARELR