

Table 1: DCA query proteins used to identify homologs across the bacterial kingdom										
Name	AccNum	Species	TaxID	Lineage	DomArch:Pfam	DomArch:Mob:DBLite	Length	DUF721 range (aa)	DCA group	Gram stain
BProtoe_Abaumanni_WP_000042456.1	WP_000042456.1	Acinetobacter baumannii	470	Bacteria>Proteobacteria	DcUA	NA	154	27-95	Group 4	-
BSpiroci_Linterrogans_WP_000650726.1	WP_000650726.1	Leptospira interrogans	171	Bacteria>Spirochaetes	DcUA	NA	154	15-103	Group 3	+
BProtoe_Nmeningitidis_WP_002257648.1	WP_002257648.1	Neisseria meningitidis	487	Bacteria>Proteobacteria	DcUA	NA	140	14-79	Group 3	-
BProtoe_Babertus_WP_002963653.1	WP_002963653.1	Brucella abortus	234	Bacteria>Proteobacteria	DcUA	NA	175	12-110	Group 3	-
BProtoe_Paeruginosa_WP_003120896.1	WP_003120896.1	Pseudomonas aeruginosa	286	Bacteria>Proteobacteria	DcUA	NA	131	5-74	Group 3	-
BProtoe_Rgroup_WP_003509079.1	WP_003509079.1	Rhizobium/Agrobacterium group	227290	Bacteria>Proteobacteria	DcUA	NA	173	14-114	Group 3	-
BProtoe_Ngonorrhoea_WP_003688269.1	WP_003688269.1	Neisseria gonorrhoeae	485	Bacteria>Proteobacteria	DcUA	NA	140	3-88	Group 3	-
BActino_Scolecicolar_WP_003975057.1	WP_003975057.1	Streptomyces coelicolor	1883	Bacteria>Actinobacteria	DcUA	disorder region+disorder region+disorder region	190	72-161	Group 4	+
BProtoe_Pmirabilis_WP_004244106.1	WP_004244106.1	Proteus mirabilis	583	Bacteria>Proteobacteria	DcUA	NA	172	8-100	Group 3	-
BProtoe_Rprowazeki_WP_004596839.1	WP_004596839.1	Rickettsia prowazekii	782	Bacteria>Proteobacteria	DcUA	NA	108	4-98	Group 1	-
BProtoe_Vparahemolyticus_WP_005480837.1	WP_005480837.1	Vibrio parahemolyticus	670	Bacteria>Proteobacteria	DcUA	disorder region	151	8-94	Group 3	-
BProtoe_Hinfluenzae_WP_005693258.1	WP_005693258.1	Haemophilus influenzae	727	Bacteria>Proteobacteria	DcUA	NA	104	13-98	Group 1	-
BFusob_Fnecrophorum_WP_005956359.1	WP_005956359.1	Fusobacterium necrophorum	859	Bacteria>Fusobacteria	DcUA	NA	99	4-89	Group 1	-
BChlamy_Pacanthamoebae_WP_006340294.1	WP_006340294.1	Parachlamydia acanthamoebae	83552	Bacteria>Chlamydiae	DcUA	NA	112	21-109	Group 1	variable (NA), counted as -
BActino_Cefficiens_WP_006768689.1	WP_006768689.1	Corynebacterium efficiens	152784	Bacteria>Actinobacteria	DcUA	disorder region+disorder region	193	81-168	Group 2	+
BActino_Blongum_WP_008783054.1	WP_008783054.1	Bifidobacterium longum	216816	Bacteria>Actinobacteria	DcUA	NA	156	54-141	Group 2	+
BActino_Rpost_WP_009476748.1	WP_009476748.1	Rhodococcus jostii	1827	Bacteria>Actinobacteria	DcUA	disorder region+disorder region+disorder region+disorder region	188	76-163	Group 2	+
BChlamy_Ctrachomatis_WP_009871537.1	WP_009871537.1	Chlamydia trachomatis	813	Bacteria>Chlamydiae	DcUA	NA	116	25-113	Group 1	variable (NA), counted as -
BSpiroci_Tpallidum_WP_010881454.1	WP_010881454.1	Treponema pallidum	140	Bacteria>Spirochaetes	DcUA	disorder region+disorder region	145	7-93	Group 3	-
BProtoe_Lpneumophila_WP_010948302.1	WP_010948302.1	Legionella pneumophila	446	Bacteria>Proteobacteria	DcUA	NA	140	3-89	Group 3	-
BProtoe_Ckennetii_WP_010957403.1	WP_010957403.1	Coxiella burnetii	777	Bacteria>Proteobacteria	DcUA	NA	114	25-109	Group 1	-
BActino_Saermitilis_WP_010985745.1	WP_010985745.1	Streptomyces avermectis	1883	Bacteria>Actinobacteria	DcUA	disorder region+disorder region+disorder region	181	66-155	Group 4	+
BCyano_Gviolaceus_WP_01141578.1	WP_01141578.1	Gloeobacter violaceus	33072	Bacteria>Cyanobacteria	DcUA	NA	180	5-93	Group 3	-
BProtoe_Bbacteriovorus_WP_011165754.1	WP_011165754.1	Bdellovibrio bacteriovorus	959	Bacteria>Proteobacteria	DcUA	NA	131	14-102	Group 3	-
BProtoe_Bhenselae_WP_011180388.1	WP_011180388.1	Bartonella henselae	38323	Bacteria>Proteobacteria	DcUA	NA	166	12-110	Group 3	-
BActino_Msmegmatis_WP_011726604.1	WP_011726604.1	Mycobacterium smegmatis	1772	Bacteria>Actinobacteria	DcUA	disorder region+disorder region	194	82-169	Group 2	+
BActino_Mulcerans_WP_011738409.1	WP_011738409.1	Mycobacterium ulcerans	1809	Bacteria>Actinobacteria	DcUA	disorder region+disorder region	187	75-162	Group 2	+
BThermo_Tpetrophila_WP_011942798.1	WP_011942798.1	Thermotoga petrophila	93929	Bacteria>Thermotogae	DcUA	NA	101	3-90	Group 1	-
BActino_Asaccharigenes_WP_012073745.1	WP_012073745.1	Actinobacillus succinogenes	67854	Bacteria>Proteobacteria	DcUA	NA	110	12-97	Group 1	-
BProtoe_Rickettsii_WP_012151389.1	WP_012151389.1	Rickettsia rickettsii	783	Bacteria>Proteobacteria	DcUA	NA	107	4-98	Group 1	-
BElusim_Eminutum_WP_012414187.1	WP_012414187.1	Elusimicrobium minutum	423605	Bacteria>Elusimicrobia	DcUA	NA	98	9-97	Group 1	-
BChloro_Cthalassium_WP_012499396.1	WP_012499396.1	Chloroherpeton thalassium	100716	Bacteria>Chlorobi	DcUA	NA	97	9-96	Group 1	-
BSpiroci_Bcrocidae_WP_012538193.1	WP_012538193.1	Borrelia crocidurae	29520	Bacteria>Spirochaetes	DcUA	NA	99	8-96	Group 1	-
BDictyo_Dthermophilum_WP_012547832.1	WP_012547832.1	Dictyoglomus thermophilum	14	Bacteria>Dictyoglomi	DcUA	NA	160	8-92	Group 3	-
BGemmat_Gaurantica_WP_012682303.1	WP_012682303.1	Gemmatimonas aurantiaca	173480	Bacteria>Gemmatimonadetes	DcUA	NA	103	11-99	Group 1	-
BDefero_Dacriphilus_WP_013009384.1	WP_013009384.1	Dentrobifrio acriphilus	118000	Bacteria>Deferribacteres	DcUA	NA	147	4-84	Group 3	-
BProtoe_Nsalughis_WP_013553388.1	WP_013553388.1	Nitratifactor salughis	269261	Bacteria>Proteobacteria	DcUA	NA	153	6-75	Group 3	-
BProtoe_Mmethanica_WP_013816973.1	WP_013816973.1	Methylomonas methanica	421	Bacteria>Proteobacteria	DcUA	NA	154	14-96	Group 3	-
BProtoe_Ttyctica_WP_013834763.1	WP_013834763.1	Thiomicrospira cyclica	147268	Bacteria>Proteobacteria	DcUA	NA	143	6-89	Group 3	-
BThermo_Tindicus_WP_013908751.1	WP_013908751.1	Thermodesulfator indicus	171695	Bacteria>Thermodesulfobacteria	DcUA	NA	159	3-90	Group 3	-
BProtoe_Maestralicum_WP_015318768.1	WP_015318768.1	Mesorhizobium australicum	68287	Bacteria>Proteobacteria	DcUA	NA	166	12-110	Group 3	-
BSynerg_Ffastidiosum_WP_015556932.1	WP_015556932.1	Ferrobacterium fastidiosum	651822	Bacteria>Synergistetes	DcUA	disorder region+disorder region	176	29-113	Group 4	-
BProtoe_Vcholerae_WP_012481231.1	WP_012481231.1	Vibrio cholerae	666	Bacteria>Proteobacteria	DcUA	NA	157	8-94	Group 3	-
BActino_Catypicum_WP_038603888.1	WP_038603888.1	Corynebacterium atypicum	191610	Bacteria>Actinobacteria	DcUA	disorder region	206	94-181	Group 2	+
BProtoe_Bpseudomallei_WP_038794713.1	WP_038794713.1	Burkholderia pseudomallei	28450	Bacteria>Proteobacteria	DcUA	NA	159	22-105	Group 3	-
BActino_Pmethyhaliphatogenes_WP_041976151.1	WP_041976151.1	Pyrinomonas methyhaliphatogenes	454194	Bacteria>Acidobacteria	DcUA	NA	158	3-90	Group 3	-
BProtoe_Knichiganensis_WP_045781360.1	WP_045781360.1	Klebsiella michiganensis	1134687	Bacteria>Proteobacteria	DcUA	NA	171	8-98	Group 3	-
BProtoe_Smarcescens_WP_049188024.1	WP_049188024.1	Serratia marcescens	615	Bacteria>Proteobacteria	DcUA	NA	171	8-99	Group 3	-
BProtoe_Pluminescens_WP_049582384.1	WP_049582384.1	Photobacillus luminescens	29488	Bacteria>Proteobacteria	DcUA	NA	172	15-100	Group 3	-
BProtoe_Mavis_WP_063513593.1	WP_063513593.1	Moraxella ovis	29433	Bacteria>Proteobacteria	DcUA	NA	172	53-108	Group 4	-
BActino_Cglutamicum_WP_074493017.1	WP_074493017.1	Corynebacterium glutamicum	1718	Bacteria>Actinobacteria	DcUA	disorder region+disorder region	178	66-153	Group 2	+
BActino_Mtuberculosis_WP_077585554.1	WP_077585554.1	Mycobacterium tuberculosis	1773	Bacteria>Actinobacteria	DcUA	disorder region+disorder region+disorder region	187	75-162	Group 2	+
BVerruc_Pdebontii_WP_078816175.1	WP_078816175.1	Prostheco bacter debontii	48467	Bacteria>Verrucomicrobia	DcUA	NA	141	52-138	Group 2	-
BProtoe_Pmulticida_WP_083003370.1	WP_083003370.1	Pasteurella multocida	747	Bacteria>Proteobacteria	DcUA	NA	101	8-93	Group 1	-
BFibro_Fixesternalis_WP_083545550.1	WP_083545550.1	Fibrobacter intestinalis	28122	Bacteria>Fibrobacteres	DcUA	NA	113	25-112	Group 1	-
BPlanct_Ppiforme_WP_092049429.1	WP_092049429.1	Planctomicrobium piforme	1576369	Bacteria>Planctomycetes	DcUA	NA	116	14-102	Group 1	- (but unique)
BProtoe_Cmirabilis_WP_099620986.1	WP_099620986.1	Caulobacter mirabilis	69666	Bacteria>Proteobacteria	DcUA	NA	182	31-122	Group 4	-
BActinob_Belongata_WP_103932439.1	WP_103932439.1	Bryocella elongata	863522	Bacteria>Acidobacteria	DcUA	NA	104	3-89	Group 1	-
BActino_Bindicum_WP_110444323.1	WP_110444323.1	Bifidobacterium indicum	1691	Bacteria>Actinobacteria	DcUA	NA	165	54-140	Group 2	+
BActino_Pdenticola_WP_118866996.1	WP_118866996.1	Prevotella denticola	28129	Bacteria>Bacteroidetes	DcUA	NA	96	8-95	Group 1	-
BActino_Ddubosi_WP_123613775.1	WP_123613775.1	Duncaniella dubosi	2518971	Bacteria>Bacteroidetes	DcUA	NA	96	8-95	Group 1	-
BDefero_Gthophilus_WP_128465527.1	WP_128465527.1	Geovibrio thophilus	139438	Bacteria>Deferribacteres	DcUA	NA	146	2-84	Group 3	-
BProtoe_Mmaenthus_WP_140863302.1	WP_140863302.1	Mycococcus xanthus	34	Bacteria>Proteobacteria	DcUA	NA	101	8-94	Group 1	-
BProtoe_Salpinga_WP_183109841.1	WP_183109841.1	Sphingomonas aljona	653931	Bacteria>Proteobacteria	DcUA	disorder region+disorder region	184	25-118	Group 3	-
BNitros_Nmoscovensis_WP_187299312.1	WP_187299312.1	Nitrospira moscovensis	42253	Bacteria>Nitrospirae	DcUA	disorder region	155	11-96	Group 3	-
BActino_Sseoulensis_WP_217711121.1	WP_217711121.1	Streptomyces seoulensis	73044	Bacteria>Actinobacteria	DcUA+YACr	NA	206	1-75	Group 3	+