

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
Type V secretory pathway, adhesin AidA [Magnetospirillum magneticum AMB-1]	7176	7176	100%	0.0	100%	YP_421364.1
large exoprotein [Magnetospirillum magneticum AMB-1]	2959	13522	46%	0.0	97%	YP_420631.1
Type V secretory pathway [Magnetospirillum magneticum AMB-1]	2061	6654	30%	0.0	96%	YP_420638.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	1976	2249	51%	0.0	86%	WP_009868207.1
COG5295: Autotransporter adhesin [Magnetospirillum magnetotacticum]	1672	3488	63%	0.0	74%	WP_009869454.1
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	1385	2589	46%	0.0	90%	YP_420640.1
Type V secretory pathway, adhesin AidA, partial [Magnetospirillum sp. SO-1]	917	2302	59%	0.0	76%	WP_008619475.1
cell surface glycoprotein precursor [Magnetospirillum magneticum AMB-1]	646	3709	36%	0.0	84%	YP_421357.1
cell surface glycoprotein precursor [Magnetospirillum magneticum AMB-1]	643	3861	50%	0.0	84%	YP_421356.1
hypothetical protein, partial [Magnetospirillum magnetotacticum]	626	1291	39%	0.0	86%	WP_009868028.1
flagellin-like protein [Magnetospirillum magneticum AMB-1]	624	3408	43%	0.0	82%	YP_421362.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	574	1725	51%	1e-164	42%	WP_009868027.1
Autotransporter adhesin [Magnetospirillum gryphiswaldense MSR-1]	579	1060	63%	9e-163	42%	CAM76579.1
hypothetical protein, partial [Magnetospirillum magnetotacticum]	534	2506	43%	3e-162	56%	WP_009868025.1
hypothetical protein RPB_1638 [Rhodopseudomonas palustris HaA2]	562	3550	52%	2e-157	44%	YP_485257.1
hypothetical protein, partial [Vibrio tasmaniensis]	507	3274	45%	1e-143	40%	WP_017102899.1
Type V secretory pathway, partial [Vibrionales bacterium SWAT-3]	446	2207	48%	1e-132	48%	WP_008223511.1
outer membrane adhesin-like protein [Shewanella loihica PV-4]	471	3208	52%	3e-130	37%	YP_001092641.1
hypothetical protein [Achromobacter xylosoxidans]	436	2670	57%	1e-128	43%	WP_006387942.1
hypothetical protein VS_II0512 [Vibrio splendidus LGP32]	454	1648	35%	5e-125	38%	YP_002395108.1
hypothetical protein, partial [Vibrio breoganii]	431	2494	40%	2e-124	43%	WP_017031543.1
hypothetical protein [Vibrio tasmaniensis]	452	3192	49%	5e-124	44%	WP_017109466.1
Large exoprotein [Vibrio furnissii NCTC 11218]	448	1554	37%	7e-123	45%	YP_005048901.1
COG5651: PPE-repeat proteins [Magnetospirillum magnetotacticum]	402	1212	43%	1e-119	60%	WP_009866462.1
hypothetical protein, partial [Variovorax paradoxus]	413	1983	44%	3e-118	37%	WP_018907567.1
hypothetical protein, partial [Vibrio breoganii]	417	2000	49%	4e-118	39%	WP_017029526.1
VCBS repeat-containing protein [Bradyrhizobium sp. WSM471]	424	2024	29%	6e-117	44%	WP_007606711.1
VCBS repeat-containing protein [Desulfomonile tiedjei DSM 6799]	428	2103	41%	1e-116	41%	YP_0064446912.1
outer membrane adhesin like protein, partial [Pseudogulbenkiania ferrooxidans]	402	1967	41%	4e-116	46%	WP_008955916.1
hypothetical protein, partial [Vibrio splendidus]	419	2628	53%	2e-115	37%	WP_017081492.1

FIG. 1A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein amb1998 [Magnetospirillum magneticum AMB-1]	377	2838	28%	2e-114	97%	YP_421361.1
Type V secretory pathway, partial [Vibrionales bacterium SWAT-3]	401	1423	45%	4e-114	44%	WP_008224673.1
outer membrane adhesin-like protein [Calothrix sp. PCC 7507]	417	1307	48%	6e-114	41%	YP_007065062.1
T1SS secreted agglutinin (RTX) [Achromobacter xylosoxidans NH44784-1996]	415	920	51%	2e-113	39%	YP_008030908.1
hypothetical protein, partial [Vibrio tasmaniensis]	394	2338	49%	1e-111	39%	WP_017101375.1
outer membrane adhesin-like protein [Sulfurimonas gotlandica]	404	1294	47%	6e-111	34%	WP_008341635.1
hypothetical protein, partial [Sulfurimonas gotlandica]	404	1325	47%	6e-111	34%	WP_008340241.1
outer membrane adhesin like protein [Variovorax paradoxus S110]	404	2165	41%	6e-110	38%	YP_002947797.1
VCBS repeat protein [Shewanella piezotolerans WP3]	396	3809	64%	7e-107	34%	YP_002313811.1
VCBS [Dechloromonas aromatica RCB]	389	1017	31%	9e-105	41%	YP_286399.1
hypothetical protein Reut_C5971 [Ralstonia eutropha JMP134]	383	1173	56%	5e-104	36%	YP_293166.1
hypothetical protein [Vibrio splendidus]	383	1638	44%	4e-103	34%	WP_017082048.1
VCBS repeat protein [Vibrio splendidus]	382	2732	44%	1e-102	34%	WP_004731498.1
VCBS [Chlorobium ferrooxidans]	380	2923	52%	2e-102	41%	WP_006366861.1
hypothetical protein, partial [Achromobacter piechaudii]	379	915	39%	8e-102	42%	WP_006218690.1
iron-regulated protein FrpC [Vibrio tubiashii]	378	1833	58%	1e-101	40%	WP_004747418.1
toxin [Vibrio sp. MED222]	374	2355	41%	2e-100	39%	WP_009845528.1
type 1 secretion target domain-containing protein, partial [Rhizobium sp. PDO1-076]	370	1692	42%	2e-100	40%	WP_007606142.1
hypothetical protein, partial [Vibrio tasmaniensis]	367	2741	46%	5e-99	38%	WP_017099027.1
hemolysin-type calcium-binding repeat family protein 3, partial [Achromobacter piechaudii]	362	1125	59%	3e-98	37%	WP_006223938.1
hypothetical protein [Vibrio owensii]	365	2665	61%	1e-97	35%	WP_020195639.1
outer membrane adhesin-like protein [Methylobacterium sp. 4-46]	364	1017	52%	2e-97	36%	YP_001770167.1
VCBS repeat-containing protein [Variovorax sp. CF313]	352	1606	65%	5e-96	34%	WP_007828145.1
hypothetical protein, partial [Vibrio splendidus]	343	1802	49%	2e-95	38%	WP_019350838.1
Large exoprotein, partial [Achromobacter piechaudii]	345	1517	47%	5e-95	40%	WP_006228189.1
hypothetical protein, partial [Vibrio splendidus]	353	1655	49%	2e-94	34%	WP_017086433.1
outer membrane adhesin-like protein [Shewanella baltica BA175]	348	950	42%	3e-94	39%	YP_006019007.1
RTX toxin hemolysin-type protein [Rhizobium etli CFN 42]	347	1347	32%	6e-94	36%	YP_470132.1
outer membrane adhesin-like protein [Desulfovibrio aespoensis Aspo-2]	352	1396	62%	1e-93	35%	YP_004120666.1
hypothetical protein, partial [Vibrio splendidus]	335	2564	51%	2e-93	37%	WP_019350792.1
hypothetical protein [Vibrio splendidus]	337	1674	46%	2e-93	37%	WP_020477147.1
RTX toxin exported protein [Ralstonia eutropha H16]	342	1549	65%	4e-92	34%	YP_728854.1

FIG. 1B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein, partial [Vibrio breoganii]	342	4678	65%	2e-90	32%	WP_017243041.1
hypothetical protein AZKH_2157 [Azoarcus sp. KH32C]	341	965	57%	2e-90	33%	YP_007551444.1
hypothetical protein PCA10_42970 [Pseudomonas resinovorans NBRC 106553]	341	2061	66%	2e-90	37%	YP_008104634.1
metalloprotease, hemolysin-type calcium-binding region [Cupriavidus taiwanensis LMG 19424]	336	1092	60%	6e-90	32%	YP_002008092.1
RTX toxin hemolysin-type protein [Sinorhizobium fredii NGR234]	333	1043	53%	9e-90	35%	YP_002827036.1
RTX toxin [Rhizobium leguminosarum]	333	928	37%	9e-90	36%	WP_003580127.1
structural toxin [Chromobacterium violaceum ATCC 12472]	338	1657	62%	3e-89	36%	NP_899981.1
hypothetical protein [Vibrio tubiashii]	335	3285	63%	2e-88	33%	WP_004744158.1
hypothetical protein [Vibrio natriegens]	333	2701	56%	5e-88	33%	WP_020334262.1
hypothetical protein [Vibrionales bacterium SWAT-3]	329	2870	69%	1e-86	38%	WP_008216195.1
hypothetical protein, partial [Vibrio genomsp. F6]	325	2872	57%	2e-86	34%	WP_017054796.1
secreted VCBS domain protein [Shewanella oneidensis MR-1]	328	3931	63%	2e-86	33%	NP_719678.1
VCBS protein [Bilophila wadsworthia]	327	2906	59%	5e-86	34%	WP_016361080.1
VCBS [Chlorobium ferrooxidans]	323	1303	44%	1e-85	38%	WP_006366860.1
Large exoprotein, partial [Achromobacter piechaudii]	307	1303	32%	2e-85	43%	WP_006228258.1
Large exoprotein, partial [Achromobacter piechaudii]	316	1488	40%	3e-85	39%	WP_006228197.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	312	1792	56%	7e-85	46%	WP_009867477.1
hypothetical protein bll3714 [Bradyrhizobium diazoefficiens USDA 110]	320	719	24%	4e-84	36%	NP_770354.1
toxin, partial [Vibrio splendidus]	313	1732	52%	4e-82	36%	WP_017092000.1
RTX toxin exported protein RtxA [Cupriavidus necator N-1]	308	1530	48%	1e-80	37%	YP_004680854.1
hypothetical protein, partial [Enterovibrio calviensis]	304	1484	46%	1e-79	34%	WP_017017027.1
hypothetical protein [Desulfovibrio sp. 6_1_46AFAA]	303	1839	42%	2e-79	32%	WP_009301782.1
hypothetical protein AHA_3491 [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	303	1839	48%	6e-79	41%	YP_857965.1
hypothetical protein [Desulfovibrio sp. 6_1_46AFAA]	298	1945	57%	8e-79	35%	WP_009301784.1
outer membrane adhesin like protein [Pseudogulbenkiania sp. NH8B]	296	1265	43%	2e-78	39%	YP_004848254.1
hypothetical protein, partial [Enterovibrio calviensis]	300	1760	48%	3e-78	33%	WP_017015203.1
iron-regulated protein FrpC [Vibrio rotiferianus]	300	3682	65%	8e-78	34%	WP_010452358.1
large exoprotein [Desulfovibrio sp. 3_1_syn3]	299	2320	58%	1e-77	33%	WP_008684592.1
outer membrane adhesin like protein [Pseudomonas mendocina NK-01]	297	1806	73%	5e-77	33%	YP_004379207.1
iron-regulated protein FrpC, partial [Vibrio nigrilichtrudo]	296	2090	43%	6e-77	33%	WP_004400669.1

FIG. 1C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
iron-regulated protein FrpC [Vibrio fischeri MJ11]	296	2422	55%	8e-77	34%	YP_002156318.1
hypothetical protein, partial [Enterovibrio norvegicus]	290	1683	46%	2e-76	32%	WP_016959134.1
hypothetical protein [Pseudomonas mendocina]	293	1804	64%	1e-75	34%	WP_017361689.1
VCBS repeat protein [Vibrio shilonii]	292	3039	70%	1e-75	33%	WP_006072371.1
hypothetical protein, partial [Desulfovibrio sp. 6_1_46AFAA]	290	1887	56%	3e-75	33%	WP_009301783.1
hypothetical protein, partial [Pseudomonas umsongensis]	286	1822	48%	6e-74	32%	WP_018926333.1
RTX repeat-containing calcium-binding cytotoxin RtxA1 [Vibrio fischeri ES114]	285	2505	57%	3e-73	34%	YP_204889.1
hypothetical protein, partial [Enterovibrio norvegicus]	281	1262	36%	1e-72	32%	WP_017003860.1

FIG. 1D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
RTX toxins and related Ca ²⁺ -binding protein [Magnetospirillum magneticum AMB-1]	3583	3583	100%	0.0	100%	YP_420640.1
COG5295: Autotransporter adhesin [Magnetospirillum magnetotacticum]	2085	3813	99%	0.0	78%	WP_009869454.1
Type V secretory pathway, adhesin AidA [Magnetospirillum magneticum AMB-1]	1390	2215	55%	0.0	90%	YP_421364.1
Type V secretory pathway, adhesin AidA, partial [Magnetospirillum sp. SO-1]	598	846	49%	7e-180	59%	WP_008619475.1
hypothetical protein, partial [Magnetospirillum magnetotacticum]	559	746	27%	3e-179	79%	WP_009868028.1
COG2931: RTX toxins and related Ca ²⁺ -binding proteins [Magnetospirillum magnetotacticum]	539	1231	50%	2e-156	84%	WP_009868027.1
Autotransporter adhesin [Magnetospirillum gryphiswaldense MSR-1]	331	920	64%	3e-88	37%	CAM76579.1
large exoprotein [Magnetospirillum magneticum AMB-1]	291	2139	27%	5e-76	66%	YP_420631.1
Type V secretory pathway [Magnetospirillum magneticum AMB-1]	291	1517	27%	5e-76	66%	YP_420638.1
flagellin-like protein [Magnetospirillum magneticum AMB-1]	244	689	24%	4e-67	71%	YP_421362.1
putative Ca binding RTX toxin [Azospirillum lipoferum 4B]	224	935	96%	1e-55	31%	YP_005040816.1
COG5651: PPE-repeat proteins [Magnetospirillum magnetotacticum]	195	676	36%	3e-49	47%	WP_009866462.1
hemolysin-type calcium-binding region [Azospirillum sp. B510]	191	829	85%	2e-45	30%	YP_003452293.1
VCBS repeat protein [Vibrio shilonii]	189	1538	68%	7e-45	28%	WP_006072371.1
VBCS repeat-containing protein [Colwellia psychrerythraea 34H]	177	1110	52%	4e-41	43%	YP_269146.1
polymer-forming cytoskeletal family protein [Vibrio harveyi]	172	1381	76%	8e-40	31%	WP_017819225.1
hypothetical protein, partial [Enterovibrio calviensis]	169	214	44%	3e-39	27%	WP_017013208.1
hypothetical protein, partial [Vibrio alginolyticus]	170	384	50%	4e-39	31%	WP_017821990.1
hypothetical protein, partial [Vibrio breoganii]	165	581	48%	2e-37	42%	WP_017242742.1
hypothetical protein, partial [Vibrio breoganii]	164	700	36%	2e-37	42%	WP_017029493.1
hypothetical protein, partial [Vibrio breoganii]	165	715	31%	2e-37	42%	WP_017031546.1
hypothetical protein, partial [Vibrio splendidus]	164	518	33%	3e-37	42%	WP_017081491.1
hypothetical protein, partial [Vibrio splendidus]	164	836	58%	3e-37	42%	WP_017077555.1
outer membrane adhesin-like protein, partial [Acetivibrio cellulolyticus]	163	455	55%	5e-37	32%	WP_010245949.1
outer membrane adhesin like protein [Methylobacterium extorquens]	161	878	69%	2e-36	30%	WP_003596515.1
polymer-forming cytoskeletal family protein [Vibrio harveyi]	161	1451	74%	3e-36	27%	WP_005442621.1
hypothetical protein, partial [Vibrio splendidus]	160	438	13%	3e-36	40%	WP_017081492.1
polymer-forming cytoskeletal family protein [Vibrio sp. HENC-03]	160	1270	76%	4e-36	28%	WP_009704723.1
hypothetical protein [Vibrio owensii]	160	1253	59%	4e-36	40%	WP_020195639.1
polymer-forming cytoskeletal family protein [Vibrio alginolyticus]	160	1428	78%	4e-36	27%	WP_005375591.1
hypothetical protein Metbo_1350 [Methanobacterium sp. AL-21]	158	415	29%	1e-35	38%	YP_004290562.1

FIG. 2A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hemolysin-type calcium-binding region, partial [Thalassospira xiamenensis]	157	464	81%	4e-35	27%	WP_007092538.1
hypothetical protein PCA10_42970 [Pseudomonas resinovorans NBRC 106553]	157	797	54%	5e-35	30%	YP_008104634.1
RTX toxins-related Ca2+-binding protein [Methylophaga sp. JAM7]	156	156	18%	8e-35	36%	YP_006294136.1
VCBS repeat-containing protein [Solitalea canadensis DSM 3403]	155	534	50%	1e-34	32%	YP_006254384.1
putative hemolysin [Cellvibrio japonicus Ueda107]	154	521	28%	3e-34	38%	YP_001981885.1
polymer-forming cytoskeletal family protein, partial [Vibrio splendidus]	154	1410	73%	5e-34	27%	WP_017079130.1
type I secretion target GGXGXDXXXX repeat protein domain protein [Methylophaga thiooxydans]	152	152	16%	1e-33	38%	WP_008291998.1
outer membrane adhesin-like protein [Mycobacterium phlei]	150	368	53%	5e-33	32%	WP_003886432.1
polymer-forming cytoskeletal family protein [Vibrio harveyi]	150	1418	74%	6e-33	27%	WP_017188870.1
hypothetical protein, partial [Vibrio splendidus]	148	858	28%	2e-32	38%	WP_017086433.1
putative outer membrane adhesin-like protein [Psychrobacter sp. PRwf-1]	145	536	35%	2e-31	38%	YP_001280066.1
hypothetical protein VS_I10856 [Vibrio splendidus LGP32]	145	1505	76%	2e-31	27%	YP_002395438.1
hypothetical protein [gamma proteobacterium NOR5-3]	144	858	48%	5e-31	31%	WP_009023297.1
polymer-forming cytoskeletal family protein [Vibrio splendidus]	143	1418	75%	8e-31	27%	WP_017082341.1
polymer-forming cytoskeletal family protein, partial [Vibrio splendidus]	142	1555	63%	1e-30	27%	WP_017092649.1
polymer-forming cytoskeletal family protein [Vibrio splendidus]	142	1128	70%	2e-30	27%	WP_019350981.1
polymer-forming cytoskeletal family protein [Vibrio splendidus]	142	1131	70%	2e-30	27%	WP_004730529.1
outer membrane adhesin-like protein [Chitinophaga pinensis DSM 2588]	142	436	24%	2e-30	40%	YP_003125000.1
hypothetical protein, partial [Enterovibrio norvegicus]	140	323	45%	3e-30	27%	WP_017003861.1
hypothetical protein [Paenibacillus sp. HGH0039]	140	311	29%	4e-30	37%	WP_009672533.1
hypothetical protein [Pseudomonas mendocina]	140	620	51%	7e-30	28%	WP_017361689.1
hypothetical protein [Congregibacter litoralis]	140	823	61%	7e-30	30%	WP_008294433.1
outer membrane adhesin like protein [Pseudomonas mendocina NK-01]	139	543	51%	9e-30	28%	YP_004379207.1
polymer-forming cytoskeletal family protein, partial [Vibrio splendidus]	134	1525	77%	3e-28	27%	WP_017081150.1
metalloprotease, hemolysin-type calcium-binding region [Cupriavidus taiwanensis LMG 19424]	134	292	67%	4e-28	27%	YP_002008092.1
hypothetical protein, partial [Vibrio crassostreae]	133	1232	77%	7e-28	26%	WP_017068684.1
polymer-forming cytoskeletal family protein, partial [Vibrio crassostreae]	133	1556	63%	8e-28	26%	WP_017072194.1
polymer-forming cytoskeletal family protein, partial [Vibrio crassostreae]	133	1468	64%	8e-28	26%	WP_017064674.1
VCBS [Chlorobium ferrooxidans]	133	792	45%	9e-28	28%	WP_006366861.1
polymer-forming cytoskeletal family protein, partial [Vibrio tasmaniensis]	133	1497	77%	9e-28	27%	WP_017100400.1
hypothetical protein AM1_E0108 [Acaryochloris marina MBIC11017]	131	436	35%	3e-27	40%	YP_001522191.1

FIG. 2B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
outer membrane adhesin like protein [Cellvibrio sp. BR]	130	408	66%	5e-27	37%	WP_007642508.1
outer membrane adhesin-like protein [Methylobacterium sp. 4-46]	130	446	44%	7e-27	28%	YP_001770167.1
hypothetical protein AZKH_2157 [Azoarcus sp. KH32C]	130	596	38%	8e-27	42%	YP_007551444.1
VCBS repeat protein [Vibrio splendidus]	129	1088	21%	1e-26	39%	WP_004731498.1
hemagglutinin/hemolysin-like protein [Dickeya dadantii 3937]	129	438	30%	2e-26	41%	YP_003881756.1
polymer-forming cytoskeletal family protein, partial [Vibrio splendidus]	129	1389	72%	2e-26	27%	WP_017094008.1
Conserved repeat protein [Bacillus megaterium WSH-002]	127	934	31%	4e-26	37%	YP_005497395.1
RTX toxin [Vibrio sp. EJY3] >refWP_014235121.1 RTX toxin [Vibrio sp. EJY3]	127	835	28%	5e-26	36%	YP_005025033.1
outer membrane adhesin-like protein [Calothrix sp. PCC 7507]	127	372	27%	5e-26	42%	YP_007065062.1
outer membrane adhesin-like protein [Desulfovibrio aespoecensis Aspo-2]	126	757	51%	8e-26	34%	YP_004120666.1
FG-GAP repeat domain protein [Coleofasciculus chthonoplastes]	125	224	44%	2e-25	28%	WP_006103065.1
hypothetical protein, partial [Desulfovibrio sp. 6_1_46AFAA]	125	929	39%	2e-25	36%	WP_009301783.1
hypothetical protein, partial [Pseudomonas nitroreducens TX1]	125	651	71%	2e-25	37%	WP_017519457.1
hypothetical protein [Vibrio natriegens]	125	692	44%	2e-25	32%	WP_020334262.1
VCBS [Roseovarius sp. 217]	125	501	41%	2e-25	33%	WP_009817742.1
outer membrane adhesin-like protein [Chitinophaga pinensis DSM 2588]	124	282	32%	3e-25	38%	YP_003124906.1
putative RTX toxin [Photobacterium damsela]	124	336	36%	4e-25	33%	WP_005301102.1
cadherin prodomain like family protein, partial [Vibrio sp. HENC-01]	122	1053	76%	2e-24	26%	WP_009696193.1
outer membrane adhesin like protein [Variovorax paradoxus S110]	121	798	68%	4e-24	46%	YP_002947797.1
hypothetical protein, partial [Vibrio splendidus]	120	705	35%	6e-24	36%	WP_017094769.1
hypothetical protein, partial [Achromobacter piechaudii]	119	755	19%	1e-23	36%	WP_006218690.1
VCBS [Pelagibaca bermudensis]	118	605	60%	3e-23	36%	WP_009622276.1
hypothetical protein, partial [Variovorax paradoxus]	117	390	29%	3e-23	40%	WP_018907567.1
hypothetical protein AHA_3491 [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	118	489	50%	3e-23	28%	YP_857965.1
secreted VCBS domain protein [Shewanella oneidensis MR-1]	116	1089	38%	1e-22	40%	NP_719678.1
hypothetical protein, partial [Vibrio tasmaniensis]	115	866	23%	1e-22	37%	WP_017102899.1
hemolysin-type calcium-binding repeat family protein 3, partial [Achromobacter piechaudii]	115	785	45%	1e-22	35%	WP_006223938.1
structural toxin [Chromobacterium violaceum ATCC 12472]	115	968	56%	2e-22	26%	NP_899981.1
hemolysin [Achromobacter arsenitoxydans]	115	317	35%	2e-22	55%	WP_008164882.1
hemolysin-type calcium-binding region, partial [Thalassospira profundimaris]	114	244	61%	6e-22	26%	WP_008891487.1
hypothetical protein [Vibrio splendidus]	112	1212	43%	2e-21	39%	WP_017082048.1

FIG. 2C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
outer membrane adhesin-like protein [Variovorax paradoxus S110]	111	406	37%	4e-21	37%	YP_002946474.1
outer membrane adhesin-like protein [Denitrovibrio acetiphilus DSM 12809]	111	484	45%	4e-21	38%	YP_003505219.1
VCBS repeat-containing protein [Desulfomonile tiedjei DSM 6799]	111	1132	36%	4e-21	40%	YP_0064446912.1

FIG. 2D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	2585	2585	100%	0.0	100%	YP_423419.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	910	910	58%	0.0	65%	WP_009869271.1
RTX toxin [Magnetospirillum sp. SO-1]	601	751	63%	0.0	54%	WP_008615895.1
COG4254: Uncharacterized protein conserved in bacteria [Magnetospirillum magnetotacticum]	377	377	15%	1e-116	91%	WP_009869323.1
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	331	569	51%	6e-91	79%	YP_422662.1
RTX toxins and related Ca2+-binding proteins [Magnetospirillum gryphiswaldense MSR-1]	310	602	67%	5e-86	50%	CAM75368.1
proprotein convertase P [Beijerinckia indica subsp. indica ATCC 9039]	163	381	61%	3e-37	32%	YP_001830991.1
calcium binding hemolysin protein [Thalassospira profundimaris]	155	1219	67%	1e-34	30%	WP_008888391.1
hemolysin-type calcium-binding region [Schlesneria paludicola]	143	224	56%	3e-31	30%	WP_010587000.1
hemolysin-type calcium-binding region [Roseibium sp. TrichSKD4]	144	1160	65%	3e-31	32%	WP_009467822.1
HEMAGGLUTININ/HEMOLYSIN-RELATED PROTEIN [Magnetospirillum gryphiswaldense MSR-1]	142	194	32%	9e-31	36%	CAM76811.1
hemolysin-type calcium-binding region [Nostoc punctiforme PCC 73102]	135	135	50%	5e-29	31%	YP_001867978.1
putative rhizobiocin/RTX toxin and hemolysin-type calcium-binding protein [Methylovorus glucosetrophus SIP3-4]	134	271	63%	2e-28	31%	YP_003051754.1
hemolysin-type calcium-binding protein [Pseudovibrio sp. FO-BEG1]	130	371	58%	2e-27	28%	YP_005082876.1
hypothetical protein [Scytonema hofmanni]	127	203	54%	3e-26	29%	WP_017749095.1
hemolysin-type calcium-binding region [Nostoc punctiforme PCC 73102]	125	367	64%	8e-26	29%	YP_001864081.1
Hemolysin-type calcium-binding region [Rhodobacter sp. SW2]	125	641	69%	1e-25	30%	WP_008029683.1
hypothetical protein [Scytonema hofmanni]	124	368	65%	1e-25	31%	WP_017744127.1
hypothetical protein [Rhizobium leguminosarum]	124	810	63%	2e-25	31%	WP_017990332.1
hemolysin-type calcium-binding protein [Paracoccus denitrificans PD1222]	122	568	50%	6e-25	31%	YP_914368.1
rhizobiocin/RTX toxin and hemolysin-type calcium binding protein [Rhizobium etli CIAT 652]	122	680	63%	1e-24	30%	YP_001976973.1
Na-Ca exchanger/integrin-beta4 [Leptothrix cholodnii SP-6]	121	309	65%	1e-24	30%	YP_001789672.1
hypothetical protein AZOL1_p40606 [Azospirillum lipoferum 4B]	122	801	66%	2e-24	31%	YP_004975543.1
hypothetical protein [Novispirillum itersonii]	121	121	20%	2e-24	35%	WP_019646374.1
rhizobiocin/RTX toxin and hemolysin-type calcium binding protein [Azospirillum]	120	298	63%	3e-24	29%	YP_003450680.1

FIG. 3A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
sp. B510]						
hemolysin-type calcium-binding protein [Isosphaera pallida ATCC 43644]	120	700	56%	3e-24	30%	YP_004180362.1
hypothetical protein NGR_c23240 [Sinorhizobium fredii NGR234]	120	409	63%	3e-24	29%	YP_002826836.1
hemolysin-type calcium-binding protein [Rhizobium leguminosarum bv. trifolii WSM2304]	120	445	61%	4e-24	32%	YP_002281223.1
hemolysin-type calcium-binding protein, partial [Thalassospira xiamenensis]	120	823	64%	5e-24	30%	WP_007088891.1
hypothetical protein [Rhizobium sp. BR816]	118	343	55%	8e-24	32%	WP_018236938.1
hemolysin-type calcium-binding protein [Nostoc sp. PCC 7107]	117	272	62%	1e-23	29%	YP_007052011.1
hypothetical protein [Rhizobium sp. BR816]	117	322	50%	2e-23	30%	WP_018236607.1
Hemolysin-type calcium-binding region [Rhodobacter sp. SW2]	117	398	48%	2e-23	33%	WP_008030394.1
type I secretion protein [Pseudovibrio sp. JE062]	117	318	63%	2e-23	29%	WP_008548480.1
Hemolysin-type calcium-binding region [Glaciecola sp. HTCC2999]	118	950	61%	2e-23	26%	WP_010180036.1
Ca2+-binding protein, RTX toxin, partial [Rhizobium leguminosarum]	117	426	63%	3e-23	29%	WP_003545660.1
hypothetical protein, partial [Endozoicomonas elysicola]	117	1493	62%	3e-23	28%	WP_020582427.1
hypothetical protein [Methylovulum miyakonense]	116	241	61%	4e-23	29%	WP_019864974.1
type I secretion protein with C-terminal target domain [Pseudomonas sp. GM74]	115	115	42%	4e-23	29%	WP_008047127.1
type I secretion protein [Vibrio ichthyenteri]	116	346	49%	5e-23	30%	WP_006714325.1
hemolysin D [Sinorhizobium meliloti]	115	399	56%	6e-23	30%	WP_003532128.1
hypothetical protein [Aliivibrio logei]	115	301	48%	8e-23	30%	WP_017023581.1
hypothetical protein AZKH_2325 [Azoarcus sp. KH32C]	115	499	63%	8e-23	28%	YP_007551607.1
Collagen alpha-2(I) chain Alpha-2 type I collagen [Sinorhizobium fredii HH103]	115	160	63%	8e-23	28%	YP_005189185.1
Ca2+-binding protein, RTX toxin [Herbaspirillum sp. YR522]	115	852	71%	1e-22	28%	WP_008110911.1
hemolysin-type calcium-binding protein [Methylovorus glucosetrophus SIP3-4]	114	158	52%	2e-22	29%	YP_003050467.1
type I secretion protein [Vibrio sp. N418]	114	456	49%	3e-22	31%	WP_009385092.1
hypothetical protein [Magnetospirillum sp. SO-1]	114	672	78%	4e-22	43%	WP_008614612.1
hypothetical protein SFHH103_02192 [Sinorhizobium fredii HH103]	112	471	64%	8e-22	30%	YP_005189512.1
hypothetical protein [Methylovulum miyakonense]	112	645	61%	1e-21	31%	WP_019867288.1
Hemolysin-type calcium-binding domain-containing protein [Candidatus Accumulibacter phosphatis clade IIA str. UW-1]	112	653	64%	2e-21	28%	YP_003168877.1
type I secretion protein [Vibrio scophthalmi]	111	273	51%	2e-21	30%	WP_005594452.1
hypothetical protein [Pseudomonas alcaliphila]	111	508	63%	2e-21	28%	WP_017677435.1
type I secretion protein [Photobacterium profundum]	110	417	62%	3e-21	28%	WP_006231502.1
rhizobiocin Rzca [Asticcacaulis biprosthecium]	110	778	57%	4e-21	29%	WP_006274635.1

FIG. 3B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hemolysin-type calcium-binding protein [Chlorobium limicola DSM 245]	110	678	68%	4e-21	29%	YP_001944163.1
rhizobiocin RzcA [Asticcacaulis biprosthecium]	110	863	67%	5e-21	29%	WP_006274634.1
hemolysin-type calcium-binding region [Bradyrhizobium oligotrophicum S58]	110	1221	76%	6e-21	28%	YP_007511038.1
FecR protein [Desulfovibrio aespoecensis Asp-2]	109	371	84%	7e-21	27%	YP_004120097.1
hemolysin-adenylate cyclase [Sinorhizobium meliloti 1021]	108	445	50%	7e-21	29%	NP_436619.1
hemolysin [Rhizobium sp. BR816]	108	516	64%	8e-21	29%	WP_018240167.1
hemolysin-type calcium-binding protein [Sinorhizobium meliloti AK83]	108	444	50%	1e-20	29%	YP_004556664.1
rhizobiocin/RTX toxin and hemolysin-type calcium binding protein [Rhizobium etli CFN 42]	108	639	66%	1e-20	28%	YP_468266.1
hemolysin D [Sinorhizobium meliloti]	108	300	50%	1e-20	29%	WP_017265529.1
hypothetical protein, partial [Magnetospirillum sp. SO-1]	108	319	70%	1e-20	31%	WP_008622436.1
probable type I secretion target repeat protein [Sinorhizobium meliloti SM11]	108	442	50%	1e-20	29%	YP_005723848.1
hypothetical protein PCA10_43500 [Pseudomonas resinovorans NBRC 106553]	108	212	51%	1e-20	29%	YP_008104687.1
hypothetical protein, partial [Acinetobacter beijerinckii]	108	382	61%	1e-20	28%	WP_005052115.1
hypothetical protein [Oscillatoria sp. PCC 10802]	107	485	50%	1e-20	30%	WP_017717249.1
hypothetical protein [Sphingobium yanoikuyae]	108	303	63%	2e-20	29%	WP_004210915.1
hemolysin-type calcium-binding region, partial [Thalassospira xiamenensis]	108	597	65%	2e-20	29%	WP_007091705.1
putative calcium binding hemolysin protein [Bradyrhizobium oligotrophicum S58]	107	472	66%	3e-20	29%	YP_007515571.1
hemolysin D, partial [Sinorhizobium meliloti]	106	383	47%	4e-20	29%	WP_017274029.1
hypothetical protein [Methylobacterium sp. 88A]	106	246	61%	4e-20	27%	WP_018043892.1
putative calcium-binding protein, partial [Rhizobium leguminosarum]	105	303	52%	5e-20	29%	WP_003545662.1
RTX toxins and related Ca2+-binding protein [alpha proteobacterium BAL199]	106	106	51%	5e-20	30%	WP_007675223.1
hemolysin-type calcium-binding protein [Sinorhizobium meliloti BL225C]	106	358	54%	5e-20	30%	YP_005716684.1
hemolysin D [Sinorhizobium meliloti]	106	254	54%	6e-20	30%	WP_017263229.1
hypothetical protein, partial [Acinetobacter tjernbergiae]	106	465	75%	7e-20	28%	WP_018679436.1
calcium binding hemolysin protein, putative [Erythrobacter sp. SD-21]	106	648	59%	8e-20	28%	WP_006833885.1
rhizobiocin/RTX toxin and hemolysin-type calcium binding protein, partial [Rhizobium etli]	105	316	52%	9e-20	27%	WP_010060462.1
Hemolysin-type calcium-binding region [Shewanella piezotolerans WP3]	105	744	64%	1e-19	29%	YP_002310757.1
type I secretion target GGXGDXDXXX repeat protein domain protein [Coleofasciculus chthonoplastes]	103	437	48%	4e-19	28%	WP_006102484.1
hemolysin D [Sinorhizobium meliloti]	103	381	56%	4e-19	27%	WP_018095958.1
rhizobiocin [Rhizobium leguminosarum bv. viciae 3841]	103	536	63%	5e-19	29%	YP_766400.1

FIG. 3C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hemolysin-type calcium-binding protein [Desulfomicrobium baculatum DSM 4028]	103	250	61%	7e-19	28%	YP_003158921.1
hemolysin [Sinorhizobium fredii NGR234]	102	452	63%	7e-19	27%	YP_002826449.1
hemolysin-type calcium-binding repeat protein [Leptolyngbya sp. PCC 7375]	103	511	63%	7e-19	28%	WP_006519062.1
calcium-binding protein [Acaryochloris sp. CCMEE 5410]	102	540	62%	9e-19	29%	WP_010480511.1
hemolysin-type calcium-binding region [Rhodobacteraceae bacterium KKLH11]	102	519	61%	2e-18	30%	WP_008758430.1
hypothetical protein, partial [Nodularia spumigena]	101	244	48%	2e-18	27%	WP_017804098.1
Collagen alpha-1(XXVII) chain [Sinorhizobium fredii HH103]	101	364	63%	2e-18	27%	YP_005189186.1

FIG. 3D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
large exoprotein [Magnetospirillum magneticum AMB-1]	10086	10086	100%	0.0	100%	YP_420631.1
Type V secretory pathway [Magnetospirillum magneticum AMB-1]	5598	31637	95%	0.0	94%	YP_420638.1
Type V secretory pathway, adhesin AidA [Magnetospirillum magneticum AMB-1]	2958	12311	90%	0.0	97%	YP_421364.1
VCBS repeat-containing protein [Desulfomonile tiedjei DSM 6799]	2012	14277	86%	0.0	46%	YP_006446912.1
hypothetical protein, partial [Achromobacter piechaudii]	1758	9327	77%	0.0	45%	WP_006218690.1
large exoprotein [Desulfovibrio sp. 3_1_syn3]	1706	7674	90%	0.0	34%	WP_008684592.1
VCBS protein [Bilophila wadsworthia]	1519	8397	87%	0.0	35%	WP_016361080.1
RTX toxin [Shewanella violacea DSS12]	1445	4982	92%	0.0	36%	YP_003558595.1
VCBS [Dechloromonas aromatica RCB]	1434	4571	67%	0.0	39%	YP_286399.1
outer membrane adhesin-like protein [Methylobacterium sp. 4-46]	1360	5020	80%	0.0	38%	YP_001770167.1
VCBS repeat protein [Vibrio splendidus]	1303	7811	89%	0.0	34%	WP_004731498.1
structural toxin [Chromobacterium violaceum ATCC 12472]	1280	6732	95%	0.0	37%	NP_899981.1
iron-regulated protein FrpC [Vibrio rotiferianus]	1248	4663	92%	0.0	34%	WP_010452358.1
hypothetical protein AHA_3491 [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	1240	2434	65%	0.0	40%	YP_857965.1
MadA [Mesorhizobium sp. R88B]	1238	3594	85%	0.0	39%	ABM65821.1
secreted VCBS domain protein [Shewanella oneidensis MR-1]	1201	15090	90%	0.0	35%	NP_719678.1
iron-regulated protein FrpC [Vibrio fischeri MJ11]	1185	6646	90%	0.0	34%	YP_002156318.1
RTX repeat-containing calcium-binding cytotoxin RtxA1 [Vibrio fischeri ES114]	1172	6610	89%	0.0	34%	YP_204889.1
Large exoprotein [Vibrio furnissii NC7C 11218]	1158	6670	94%	0.0	43%	YP_005048901.1
hypothetical protein RPB_1638 [Rhodopseudomonas palustris HaA2]	1149	9056	93%	0.0	46%	YP_485257.1
RTX toxin [Aliivibrio fischeri]	1144	4512	87%	0.0	33%	WP_005419658.1
cell surface glycoprotein precursor [Magnetospirillum magneticum AMB-1]	1111	15837	88%	0.0	99%	YP_421356.1
iron-regulated protein FrpC [Vibrio tubiashii]	1110	4979	84%	0.0	35%	WP_004747418.1
VCBS repeat-containing protein [Pseudomonas sp. GIM21]	1087	11274	87%	0.0	33%	WP_007942972.1
iron-regulated protein FrpC [Vibrio shilonii]	1060	3937	87%	0.0	32%	WP_006070242.1
T1SS secreted agglutinin (RTX) [Achromobacter xylosoxidans NH44784-1996]	1011	4297	87%	0.0	44%	YP_008030908.1
hypothetical protein Sden_0384 [Shewanella denitrificans OS217]	1016	2508	59%	0.0	36%	YP_561402.1
hypothetical protein [Vibrio natriegens]	1005	5432	89%	0.0	32%	WP_020334262.1
hypothetical protein, partial [Pseudomonas sp. 35MFCvi1.1]	998	2395	85%	0.0	32%	WP_020621311.1
hypothetical protein [Vibrio splendidus]	992	9722	90%	0.0	34%	WP_017082048.1
hypothetical protein, partial [Oxalobacteraceae bacterium JGI 0001004-K23]	965	6950	86%	0.0	36%	WP_018058402.1
outer membrane adhesin like protein [Variovorax paradoxus S110]	888	5136	79%	0.0	38%	YP_002947797.1

FIG. 4A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein, partial [Aliivibrio logei]	895	6776	92%	0.0	32%	WP_017021259.1
hypothetical protein Plut 0676 [Chlorobium luteolum DSM 273]	905	3584	82%	0.0	32%	YP_374597.1
hypothetical protein, partial [Aliivibrio fischeri]	885	4569	86%	0.0	32%	WP_017019291.1
hypothetical protein, partial [Enterovibrio calviensis]	861	5168	85%	0.0	34%	WP_017011038.1
iron-regulated protein FrpC, partial [Vibrio nigrripulchritudo]	865	7506	85%	0.0	34%	WP_004400669.1
hypothetical protein, partial [Desulfovibrio sp. 6_1_46AFAA]	838	7019	89%	0.0	35%	WP_009301783.1
hypothetical protein [Vibrio tasmaniensis]	838	5072	87%	0.0	35%	WP_017109466.1
hypothetical protein, partial [Pseudomonas umsongensis]	808	2556	84%	0.0	33%	WP_018926333.1
VCBS [Chlorobium ferrooxidans]	796	6644	88%	0.0	39%	WP_006366861.1
outer membrane adhesin-like protein [Shewanella loihica PV-4]	789	5554	88%	0.0	40%	YP_001092641.1
VCBS repeat protein [Shewanella piezotolerans WP3]	790	7524	91%	0.0	36%	YP_002313811.1
hypothetical protein, partial [Vibrio tasmaniensis]	748	7602	87%	0.0	35%	WP_017099027.1
hypothetical protein [Vibrio owensii]	768	5374	69%	0.0	31%	WP_020195639.1
hypothetical protein VS_II0512 [Vibrio splendidus LGP32]	754	4627	83%	0.0	34%	YP_002395108.1
cell surface glycoprotein precursor [Magnetospirillum magneticum AMB-1]	665	16303	87%	0.0	91%	YP_421357.1
toxin [Vibrio sp. MED222]	737	4790	78%	0.0	32%	WP_009845528.1
hypothetical protein, partial [Enterovibrio calviensis]	707	2841	83%	0.0	33%	WP_017017027.1
hypothetical protein, partial [Enterovibrio norvegicus]	707	4934	88%	0.0	35%	WP_017003860.1
hypothetical protein, partial [Vibrio tasmaniensis]	694	5353	88%	0.0	36%	WP_017102899.1
COG5295: Autotransporter adhesin [Magnetospirillum magnetotacticum]	709	3950	70%	0.0	52%	WP_009869454.1
flagellin-like protein [Magnetospirillum magneticum AMB-1]	635	24960	85%	0.0	83%	YP_421362.1
hypothetical protein, partial [Vibrio genomosp. F6]	689	3809	62%	0.0	33%	WP_017053340.1
hypothetical protein PCA10_42970 [Pseudomonas resinovorans NBRC 106553]	703	1746	90%	0.0	29%	YP_008104634.1
type 1 secretion target domain-containing protein, partial [Rhizobium sp. PDO1-076]	673	5887	84%	0.0	40%	WP_007606142.1
iron-regulated protein FrpC, partial [Vibrio tubiashii]	682	6239	84%	0.0	32%	WP_004749162.1
hypothetical protein, partial [Vibrio breoganii]	690	5398	90%	0.0	29%	WP_017243041.1
hypothetical protein, partial [Magnetospirillum magnetotacticum]	631	9349	85%	0.0	57%	WP_009868025.1
hypothetical protein, partial [Enterovibrio calviensis]	668	2259	85%	0.0	33%	WP_017015203.1
RTX toxin [Vibrio sp. EJY3]	667	5392	86%	0.0	32%	YP_005025033.1
hypothetical protein [Vibrio tubiashii]	667	4513	87%	0.0	31%	WP_004744158.1
hypothetical protein [Vibrio breoganii]	653	8014	89%	0.0	31%	WP_017029498.1
VCBS repeat protein [Vibrio shilonii]	643	4858	87%	0.0	29%	WP_006072371.1
hypothetical protein, partial [Sulfurimonas gotlandica]	624	6822	90%	0.0	36%	WP_008340241.1

FIG. 4B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
biofilm-associated surface protein [Vibrio parahaemolyticus RIMD 2210633]	632	4064	79%	0.0	35%	NP_800463.1
RTX toxin exported protein RtxA [Cupriavidus necator N-1]	630	2948	58%	3e-180	39%	YP_004680854.1
toxin, partial [Vibrio splendidus]	631	5002	88%	3e-179	31%	WP_017092000.1
outer membrane adhesin-like protein [Shewanella woodyi ATCC 51908]	632	1130	43%	5e-179	33%	YP_001758872.1
outer membrane adhesin-like protein [Calothrix sp. PCC 7507]	625	4740	76%	1e-178	41%	YP_007065062.1
hypothetical protein, partial [Vibrio splendidus]	609	5290	89%	7e-177	34%	WP_017081492.1
hypothetical protein [Vibrionales bacterium SWAT-3]	613	4587	88%	1e-172	31%	WP_008216195.1
outer membrane adhesin-like protein [Sulfurimonas gotlandica]	592	5281	90%	1e-171	36%	WP_008341635.1
VBCS repeat-containing protein [Colwellia psychrerythraea 34H]	609	3630	90%	2e-171	28%	YP_269146.1
hypothetical protein, partial [Variovorax paradoxus]	563	8220	83%	2e-169	41%	WP_018907567.1
hypothetical protein [Desulfovibrio sp. 6_1_46AFAA]	586	4127	88%	1e-168	32%	WP_009301782.1
VBCS repeat-containing protein [Vibrio scophthalmi]	592	5438	89%	2e-166	29%	WP_005594382.1
outer membrane adhesin-like protein [Desulfovibrio aespoensis Aspo-2]	585	2905	69%	3e-164	34%	YP_004120666.1
hypothetical protein [Vibrio splendidus]	575	4781	83%	2e-161	29%	WP_019825879.1
outer membrane adhesin-like protein [Shewanella baltica BA175]	544	2992	86%	1e-158	39%	YP_006019007.1
Large exoprotein, partial [Achromobacter piechaudii]	531	4718	87%	1e-157	45%	WP_006228189.1
hypothetical protein AZKH_2157 [Azoarcus sp. KH32C]	559	2386	87%	5e-157	32%	YP_007551444.1
hypothetical protein, partial [Vibrio breoganii]	520	8003	83%	2e-154	44%	WP_017031543.1
outer membrane adhesin-like protein [Shewanella loihica PV-4]	550	789	73%	4e-153	29%	YP_001092444.1
outer membrane adhesin-like protein [Shewanella woodyi ATCC 51908]	548	2148	69%	4e-153	31%	YP_001758871.1
RTX toxin [Shewanella violacea DSS12]	540	2178	75%	1e-150	31%	YP_003558594.1
COG2931: RTX toxins and related Ca ²⁺ -binding proteins [Magnetospirillum magnetotacticum]	531	2545	50%	2e-150	49%	WP_009868027.1
VBCS repeat-containing protein [Bradyrhizobium sp. WSM471]	530	4756	81%	2e-150	44%	WP_007606711.1
Type V secretory pathway, partial [Vibrionales bacterium SWAT-3]	500	7321	87%	2e-147	42%	WP_008224673.1
hypothetical protein [Kordiimonas gwangyangensis]	524	2060	61%	1e-146	43%	WP_020398403.1
Large exoprotein, partial [Achromobacter piechaudii]	494	4610	85%	9e-145	45%	WP_006228197.1
RTX toxin hemolysin-type protein [Rhizobium etli CFN 42]	503	5109	87%	1e-144	37%	YP_470132.1
hypothetical protein Reut_C5971 [Ralstonia eutropha JMP134]	508	5154	90%	4e-143	38%	YP_293166.1
hypothetical protein [Achromobacter xylosoxidans]	474	6194	87%	3e-141	45%	WP_006387942.1
VBCS [Chlorobium ferrooxidans] >gb EAT58497.1 VCBS [Chlorobium ferrooxidans DSM 13031]	498	2074	53%	8e-141	40%	WP_006366860.1
hypothetical protein, partial [Vibrio splendidus]	506	2630	82%	3e-140	28%	WP_017077555.1

FIG. 4C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein, partial [Vibrio breoganii]	482	5025	85%	1e-139	38%	WP_017029526.1
hypothetical protein [Vibrio coralliilyticus]	496	3596	85%	4e-137	29%	WP_006962234.1
Type V secretory pathway, partial [Vibrionales bacterium SWAT-3]	458	7873	88%	1e-136	51%	WP_008223511.1
hypothetical protein bll3714 [Bradyrhizobium diazoefficiens USDA 110]	482	2856	41%	8e-133	38%	NP_770354.1

FIG. 4D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
Type V secretory pathway [Magnetospirillum magneticum AMB-1]	6895	6895	100%	0.0	100%	YP_420638.1
large exoprotein [Magnetospirillum magneticum AMB-1]	5612	31712	92%	0.0	94%	YP_420631.1
Type V secretory pathway, adhesin AidA [Magnetospirillum magneticum AMB-1]	2065	9344	87%	0.0	96%	YP_421364.1
VCBS repeat-containing protein [Desulfomonile tiedjei DSM 6799]	1810	6831	83%	0.0	45%	YP_006446912.1
hypothetical protein, partial [Achromobacter piechaudii]	1673	3568	89%	0.0	43%	WP_006218690.1
VCBS [Dechloromonas aromatica RCB] >ref WP_011288925.1 VCBS [Dechloromonas aromatica]	1451	4700	84%	0.0	39%	YP_286399.1
cell surface glycoprotein precursor [Magnetospirillum magneticum AMB-1]	1398	11419	87%	0.0	100%	YP_421356.1
outer membrane adhesin-like protein [Methylobacterium sp. 4-46]	1347	3611	80%	0.0	38%	YP_001770167.1
structural toxin [Chromobacterium violaceum ATCC 12472]	1293	3871	88%	0.0	38%	NP_899981.1
VCBS repeat protein [Vibrio splendidus]	1199	4321	81%	0.0	35%	WP_004731498.1
large exoprotein [Desulfovibrio sp. 3 1 syn3]	1168	5537	82%	0.0	34%	WP_008684592.1
hypothetical protein AHA_3491 [Aeromonas hydrophila subsp. hydrophila ATCC 7966]	1164	3229	85%	0.0	40%	YP_857965.1
Large exoprotein [Vibrio furnissii NCTC 11218]	1137	4348	87%	0.0	47%	YP_005048901.1
VCBS protein [Bilophila wadsworthia] >gb EPC05682.1	1118	9652	87%	0.0	34%	WP_016361080.1
secreted VCBS domain protein [Shewanella oneidensis MR-1]	1111	7756	85%	0.0	35%	NP_719678.1
iron-regulated protein FrpC [Vibrio tubiashii]	1092	3731	80%	0.0	35%	WP_004747418.1
RTX toxin [Shewanella violacea DSS12]	1069	5469	85%	0.0	35%	YP_003558595.1
TISS secreted agglutinin (RTX) [Achromobacter xylosoxidans NH44784-1996]	1016	3734	88%	0.0	44%	YP_008030908.1
hypothetical protein RPB_1638 [Rhodopseudomonas palustris HaA2]	1041	2369	82%	0.0	41%	YP_485257.1
hypothetical protein Sden_0384 [Shewanella denitrificans OS217]	1013	3119	82%	0.0	36%	YP_561402.1
RTX repeat-containing calcium-binding cytotoxin RtxA1 [Vibrio fischeri ES114]	1004	1986	84%	0.0	33%	YP_204889.1
iron-regulated protein FrpC [Vibrio fischeri MJ11]	991	6052	89%	0.0	32%	YP_002156318.1
hypothetical protein, partial [Oxalobacteraceae bacterium JGI 0001004-K23]	976	2447	86%	0.0	36%	WP_018058402.1
RTX toxin [Aliivibrio fischeri]	981	2915	89%	0.0	33%	WP_005419658.1
VCBS repeat-containing protein [Pseudomonas sp. GM21]	974	5340	83%	0.0	33%	WP_007942972.1
iron-regulated protein FrpC [Vibrio rotiferianus]	978	2883	88%	0.0	34%	WP_010452358.1
hypothetical protein [Vibrio splendidus]	978	5373	82%	0.0	34%	WP_017082048.1
MadA [Mesorhizobium sp. R88B]	966	2463	86%	0.0	39%	ABM65821.1
outer membrane adhesin like protein [Variovorax paradoxus S110]	885	4564	80%	0.0	38%	YP_002947797.1
hypothetical protein [Vibrio natriegens]	896	2536	84%	0.0	32%	WP_020334262.1
iron-regulated protein FrpC [Vibrio shilonii]	893	2962	87%	0.0	31%	WP_006070242.1

FIG. 5A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein, partial [Aliivibrio fischeri]	879	2558	86%	0.0	32%	WP_017019291.1
iron-regulated protein FrpC, partial [Vibrio nigrripulchritudo]	862	4903	80%	0.0	34%	WP_004400669.1
hypothetical protein, partial [Enterovibrio calviensis]	847	3923	84%	0.0	34%	WP_017011038.1
hypothetical protein, partial [Aliivibrio logei]	860	2391	89%	0.0	31%	WP_017021259.1
hypothetical protein, partial [Desulfovibrio sp. 6_1_46AFAA]	835	7361	82%	0.0	35%	WP_009301783.1
hypothetical protein, partial [Pseudomonas sp. 35MFCvi1.1]	855	2870	83%	0.0	32%	WP_020621311.1
COG5295: Autotransporter adhesin [Magnetospirillum magnetotacticum]	847	2549	87%	0.0	50%	WP_009869454.1
hypothetical protein [Vibrio tasmaniensis]	835	4468	81%	0.0	35%	WP_017109466.1
hypothetical protein, partial [Pseudomonas umsongensis]	800	2758	80%	0.0	33%	WP_018926333.1
hypothetical protein Plut_0676 [Chlorobium luteolum DSM 273]	810	3074	75%	0.0	34%	YP_374597.1
outer membrane adhesin-like protein [Shewanella loihica PV-4]	783	3547	85%	0.0	40%	YP_001092641.1
VCBS [Chlorobium ferrooxidans]	784	5024	81%	0.0	38%	WP_006366861.1
VCBS repeat protein [Shewanella piezotolerans WP3]	783	5217	89%	0.0	36%	YP_002313811.1
COG2931: RTX toxins and related Ca ²⁺ -binding proteins [Magnetospirillum magnetotacticum]	746	3446	60%	0.0	55%	WP_009868027.1
hypothetical protein VS_I0512 [Vibrio splendidus LGP32] >	762	3064	82%	0.0	33%	YP_002395108.1
hypothetical protein, partial [Vibrio tasmaniensis]	744	5366	84%	0.0	35%	WP_017099027.1
hypothetical protein, partial [Vibrio tasmaniensis]	734	4232	85%	0.0	36%	WP_017102899.1
hypothetical protein [Vibrio owensii]	754	2886	80%	0.0	31%	WP_020195639.1
cell surface glycoprotein precursor [Magnetospirillum magneticum AMB-1]	669	10927	82%	0.0	94%	YP_421357.1
toxin [Vibrio sp. MED222]	735	2929	83%	0.0	33%	WP_009845528.1
hypothetical protein, partial [Enterovibrio norvegicus]	710	4623	81%	0.0	35%	WP_017003860.1
hypothetical protein PCA10_42970 [Pseudomonas resinovorans NBRC 106553]	728	877	83%	0.0	31%	YP_008104634.1
RTX toxin exported protein RtxA [Cupriavidus necator N-1]	710	2660	90%	0.0	36%	YP_004680854.1
hypothetical protein [Vibrio breoganii]	717	3466	83%	0.0	29%	WP_017029498.1
flagellin-like protein [Magnetospirillum magneticum AMB-1]	636	15101	79%	0.0	83%	YP_421362.1
type 1 secretion target domain-containing protein, partial [Rhizobium sp. PDO1-076]	672	4527	73%	0.0	40%	WP_007606142.1
hypothetical protein, partial [Vibrio genomosp. F6]	681	6195	81%	0.0	32%	WP_017053340.1
hypothetical protein, partial [Enterovibrio calviensis]	671	6495	77%	0.0	33%	WP_017015203.1
hypothetical protein, partial [Magnetospirillum magnetotacticum]	634	8403	80%	0.0	58%	WP_009868025.1
hypothetical protein, partial [Vibrio breoganii]	686	3666	85%	0.0	29%	WP_017243041.1
iron-regulated protein FrpC, partial [Vibrio tubiashii]	668	3859	79%	0.0	32%	WP_004749162.1
RTX toxin [Vibrio sp. EJY3]	674	3458	84%	0.0	33%	YP_005025033.1

FIG. 5B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein [Vibrio tubiashii]	661	3112	83%	0.0	30%	WP_004744158.1
hypothetical protein, partial [Enterovibrio calviensis]	639	1195	78%	0.0	32%	WP_017017027.1
outer membrane adhesin-like protein [Shewanella woodyi ATCC 51908]	648	1694	62%	0.0	33%	YP_001758872.1
outer membrane adhesin-like protein [Calothrix sp. PCC 7507]	628	4317	84%	3e-180	42%	YP_007065062.1
biofilm-associated surface protein [Vibrio parahaemolyticus RIMD 2210633]	626	2237	83%	2e-179	35%	NP_800463.1
toxin, partial [Vibrio splendidus]	623	4290	83%	3e-177	31%	WP_017092000.1
VCBS repeat protein [Vibrio shilonii]	620	3907	84%	3e-175	28%	WP_006072371.1
hypothetical protein, partial [Sulfurimonas gotlandica]	601	2983	52%	1e-174	40%	WP_008340241.1
hypothetical protein [Vibrionales bacterium SWAT-3]	617	3055	80%	2e-174	31%	WP_008216195.1
hypothetical protein, partial [Vibrio splendidus]	598	2563	80%	1e-173	34%	WP_017081492.1
VCBS repeat-containing protein [Colwellia psychrerythraea 34H]	607	2638	82%	2e-171	28%	YP_269146.1
hypothetical protein, partial [Variovorax paradoxus]	560	3541	77%	8e-169	40%	WP_018907567.1
outer membrane adhesin-like protein [Desulfovibrio aespoensis Aspo-2]	592	2175	86%	6e-167	34%	YP_004120666.1
hypothetical protein [Desulfovibrio sp. 6_1_46FAFA]	576	1697	78%	7e-166	33%	WP_009301782.1
outer membrane adhesin-like protein [Sulfurimonas gotlandica]	572	1212	53%	2e-165	39%	WP_008341635.1
VCBS repeat-containing protein [Vibrio scophthalmi]	578	3121	80%	9e-163	29%	WP_005594382.1
hypothetical protein [Vibrio splendidus]	571	3250	85%	1e-160	29%	WP_019825879.1
outer membrane adhesin-like protein [Shewanella baltica BA175]	546	1960	80%	7e-160	39%	YP_006019007.1
Large exoprotein, partial [Achromobacter piechaudii]	530	4054	81%	2e-157	45%	WP_006228189.1
hypothetical protein, partial [Vibrio breoganii]	523	6044	76%	5e-156	44%	WP_017031543.1
RTX toxin [Shewanella violacea DSS12]	555	2108	77%	1e-155	31%	YP_003558594.1
outer membrane adhesin-like protein [Shewanella woodyi ATCC 51908]]	540	2704	81%	6e-151	30%	YP_001758871.1
hypothetical protein AZKH_2157 [Azoarcus sp. KH32C]	537	2180	90%	1e-150	33%	YP_007551444.1
outer membrane adhesin-like protein [Shewanella loihica PV-4]	537	674	89%	6e-150	30%	YP_001092444.1
VCBS repeat-containing protein [Bradyrhizobium sp. WSM471]	527	1903	72%	1e-149	44%	WP_007606711.1
Type V secretory pathway, partial [Vibrionales bacterium SWAT-3]	505	4894	85%	1e-149	45%	WP_008224673.1
hypothetical protein [Kordiimonas gwangyangensis]	529	1823	77%	1e-148	44%	WP_020398403.1
Large exoprotein, partial [Achromobacter piechaudii]	495	3024	79%	1e-145	45%	WP_006228197.1
RTX toxin hemolysin-type protein [Rhizobium etli CFN 42]	500	2327	68%	2e-144	38%	YP_470132.1
hypothetical protein Reut_C5971 [Ralstonia eutropha JMP134]	501	1866	85%	6e-141	38%	YP_293166.1
hypothetical protein [Achromobacter xylosoxidans]	472	3451	83%	6e-141	44%	WP_006387942.1
Type V secretory pathway, partial [Vibrionales bacterium SWAT-3]	466	4572	83%	1e-139	51%	WP_008223511.1
hypothetical protein, partial [Vibrio tasmaniensis]	475	5374	79%	4e-139	40%	WP_017101375.1

FIG. 5C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
VCBS [Chlorobium ferrooxidans]	491	1870	80%	4e-139	39%	WP_006366860.1
hypothetical protein, partial [Vibrio breoganii]	476	3784	82%	6e-138	38%	WP_017029526.1
hypothetical protein, partial [Vibrio splendidus]	490	2879	83%	1e-135	28%	WP_017077555.1
hypothetical protein [Vibrio coralliilyticus]	489	2158	71%	2e-135	29%	WP_006962234.1

FIG. 5D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	2448	2448	100%	0.0	100%	YP_4222662.1
RTX toxin [Magnetospirillum sp. SO-1] >gb EME70692.1 RTX toxin [Magnetospirillum sp. SO-1]	437	754	55%	3e-126	57%	WP_008615895.1
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	407	407	32%	8e-117	63%	YP_423419.1
COG4254: Uncharacterized protein conserved in bacteria [Magnetospirillum magnetotacticum]	332	332	16%	1e-100	80%	WP_009869323.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	232	408	55%	7e-59	38%	WP_009869271.1
protein conserved in bacteria [Magnetospirillum gryphiswaldense MSR-1]	170	170	9%	5e-45	66%	CAM74103.1
proprotein convertase P [Beijerinckia indica subsp. indica ATCC 9039]	131	402	29%	1e-27	34%	YP_001830991.1
protein conserved in bacteria [Magnetospirillum gryphiswaldense MSR-1]	124	124	11%	2e-26	47%	CAM76248.1
RTX toxins and related Ca2+-binding proteins [Magnetospirillum gryphiswaldense MSR-1]	124	224	19%	9e-26	53%	CAM75368.1
hypothetical protein [Novispirillum itersonii]	123	123	21%	4e-25	36%	WP_019646374.1
rhizobiocin RzcA [Ahrensia sp. R2A130]	114	504	42%	3e-22	32%	WP_009758714.1
hypothetical protein [Magnetospirillum sp. SO-1]	110	415	59%	4e-21	43%	WP_008614612.1
calcium binding hemolysin protein [Thalassospira profundimaris]	110	1342	37%	5e-21	31%	WP_008888391.1
hypothetical protein [Oscillatoria sp. PCC 10802]	109	291	36%	9e-21	31%	WP_017719322.1
hemolysin-type calcium-binding repeat family protein [Micavibrio aeruginosavorus ARL-13]	104	152	31%	2e-19	32%	YP_004866759.1
Hemolysin-type calcium-binding region [Micavibrio aeruginosavorus EPB]	103	278	37%	5e-19	30%	YP_007642128.1
calcium binding hemolysin protein, putative [Oceanicola granulosus]	102	434	54%	1e-18	31%	WP_007254292.1
Hemolysin-type calcium-binding region [Methylosinus trichosporium]	99.0	99.0	30%	3e-18	31%	WP_003615611.1
hemolysin-type calcium-binding protein [Sinorhizobium meliloti AK83]	99.4	541	34%	7e-18	29%	YP_004556664.1
hypothetical protein [Rhodobacter sp. AKP1]	99.8	316	31%	8e-18	31%	WP_009564177.1
regulatory P domain of subtilisin-like proprotein convertases [Nostoc sp. PCC 7524]	99.0	368	33%	1e-17	30%	YP_007076420.1
hemolysin-adenylate cyclase [Sinorhizobium meliloti 1021]	98.6	501	34%	1e-17	29%	NP_436619.1
putative calcium-binding protein [Nostoc sp. PCC 7524]	97.4	190	32%	1e-17	31%	YP_007076007.1
probable type I secretion target repeat protein [Sinorhizobium meliloti SM11]	98.2	543	34%	1e-17	29%	YP_005723848.1
Hemolysin-type calcium-binding region [Glaciecola sp. HTCC2999]	98.6	1034	40%	2e-17	32%	WP_010180036.1
Hemolysin-type calcium-binding region, RTX [Rhodobacter sphaeroides KD131]	97.8	246	36%	2e-17	31%	YP_002520640.1

FIG. 6A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein [Methylovulum miyakonense]	97.4	591	29%	3e-17	32%	WP_019867288.1
hemolysin D [Sinorhizobium meliloti]	97.1	517	34%	4e-17	28%	WP_018095958.1
hemolysin-type calcium-binding protein [Paracoccus denitrificans PD1222]	96.7	143	30%	5e-17	29%	YP_914368.1
hypothetical protein, partial [Endozoicomonas elysicola]	96.3	1326	35%	9e-17	34%	WP_020582427.1
Hemolysin-type calcium-binding protein [Sinorhizobium medicae WSM419]	94.7	407	32%	2e-16	37%	YP_001312798.1
outer membrane adhesin-like protein [Rhodobacter sphaeroides ATCC 17029]	94.7	151	30%	2e-16	29%	YP_001045054.1
adhesin [Rhodobacter sphaeroides]	94.4	94.4	30%	3e-16	29%	WP_002724414.1
adhesin [Rhodobacter sphaeroides]	94.0	152	30%	5e-16	30%	WP_017140389.1
hemolysin D [Sinorhizobium meliloti]	92.8	408	32%	7e-16	28%	WP_003532128.1
hemolysin-type calcium-binding region [Rhodobacteraceae bacterium KLH11]	92.8	549	34%	9e-16	29%	WP_008758430.1
proprotein convertase P [Cyanotheca sp. PCC 7822]	92.0	244	30%	9e-16	30%	YP_003886691.1
hemolysin-type calcium-binding region [Roseibium sp. TrichSKD4]	91.3	1162	45%	3e-15	31%	WP_009467822.1
hemolysin D [Sinorhizobium meliloti]	90.9	596	34%	3e-15	31%	WP_017265529.1
calcium-binding protein [Caulobacter crescentus CB15]	90.1	320	37%	3e-15	31%	NP_421411.1
iron-regulated protein FrpC [Caulobacter crescentus NA1000]	90.1	257	37%	3e-15	31%	YP_002518066.1
Hemolysin-type calcium-binding repeat (2 copies) [Sinorhizobium meliloti GR4]	90.5	417	32%	4e-15	28%	YP_007195216.1
hemolysin D, partial [Sinorhizobium meliloti]	89.7	658	31%	6e-15	31%	WP_017274029.1
hypothetical protein [Methylobacterium sp. 77]	89.4	89.4	31%	8e-15	29%	WP_019906466.1
hypothetical protein [Oscillatoria sp. PCC 10802]	88.6	333	35%	8e-15	32%	WP_017718625.1
calcium binding hemolysin protein [Azospirillum sp. B510]	89.4	894	30%	1e-14	30%	YP_003450312.1
hemolysin D [Sinorhizobium medicae]	87.8	377	32%	2e-14	28%	WP_018207839.1
hemolysin-type calcium-binding protein, partial [Thalassospira xiamenensis]	88.2	822	31%	3e-14	36%	WP_007088891.1
proprotein convertase P [Methylobacterium nodulans ORS 2060]	86.7	210	29%	4e-14	31%	YP_002495897.1
hemolysin-type calcium-binding protein [Sinorhizobium meliloti BL225C]	87.0	326	32%	4e-14	28%	YP_005716684.1
hypothetical protein AZOLI_p40606 [Azospirillum lipoferum 4B]	87.4	812	37%	5e-14	34%	YP_004975543.1
hemolysin-type calcium-binding region [Polaromonas sp. JS666]	86.7	531	29%	6e-14	31%	YP_551701.1
hypothetical protein RLDS_09615 [Sphingobium lactosutens DS20]	86.3	86.3	33%	6e-14	30%	EQB15964.1
rhizobiocin/RTX toxin and hemolysin-type calcium binding protein [Tistrella mobilis KA081020-065]	84.7	160	30%	1e-13	32%	YP_006370736.1
hemolysin D [Sinorhizobium medicae]	85.5	421	32%	1e-13	28%	WP_018009580.1
Ca2+-binding protein, RTX toxin [Microvirga sp. WSM3557]	85.1	316	34%	2e-13	29%	WP_009490921.1
hemolysin D [Sinorhizobium meliloti]	84.0	322	32%	3e-13	28%	WP_017263229.1
type I secretion target repeat-containing protein [Roseobacter denitrificans OCh 114]	83.2	83.2	28%	4e-13	29%	YP_681508.1

FIG. 6B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
protein of unknown function [Azospirillum brasilense Sp245]	84.0	84.0	31%	4e-13	29%	YP_005030312.1
hemolysin-type calcium-binding region [Desulfovibrio salexigens DSM 2638]	84.0	191	37%	4e-13	29%	YP_002992972.1
hypothetical protein [Sphingobium yanokuyae]	83.2	277	35%	7e-13	30%	WP_004210915.1
hypothetical protein [Brachymonas chironomi]	82.4	150	34%	7e-13	28%	WP_018716239.1
Hemolysin-type calcium-binding region [Shewanella piezotolerans WP3]	82.8	506	34%	1e-12	33%	YP_002310757.1
Hemolysin-type calcium-binding region [Rhodobacter sp. SW2]	82.4	406	33%	1e-12	31%	WP_008029683.1
hemolysin-type calcium-binding region [Aeromonas media]	81.6	239	30%	1e-12	31%	WP_005332196.1
Alkaline phosphatase [Micavibrio aeruginosavorus EPB]	81.6	81.6	15%	2e-12	37%	YP_007643803.1
RTX toxins/related Ca2+-binding protein [Rubellimicrobium thermophilum DSM 16684]	79.7	250	33%	5e-12	32%	EPX86685.1
type I secretion target GGXGXDXXX repeat protein [uncultured marine bacterium 582]	80.5	420	36%	5e-12	33%	AAR38409.1
hemolysin-type calcium-binding repeat family protein, partial [uncultured bacterium]	79.3	204	33%	7e-12	30%	EKD61936.1
hypothetical protein [Methylovulum miyakonense]	79.3	120	30%	8e-12	30%	WP_019867241.1
hemolysin-type calcium-binding region, RTX, partial [Rhodobacter sphaeroides 2.4.1]	78.6	172	31%	1e-11	30%	YP_355041.1
hypothetical protein [Massilia niastensis]	79.0	314	37%	1e-11	29%	WP_020655477.1
hypothetical protein, partial [Magnetospirillum sp. SO-1]	79.0	175	42%	1e-11	28%	WP_008622436.1
hypothetical protein [Methylovulum miyakonense]	78.6	78.6	30%	1e-11	32%	WP_019867066.1
hypothetical protein [Methylobacterium sp. 77]	78.2	142	29%	2e-11	37%	WP_019903186.1
calcium binding hemolysin protein [Tistrella mobilis KA081020-065]	78.6	271	31%	2e-11	37%	YP_006370737.1
Alkaline phosphatase [Thalassobacter arenae DSM 19593]	77.4	132	29%	3e-11	27%	EPX78170.1
RTX toxin exported protein RtxA [Cupriavidus necator N-1]	77.8	126	15%	4e-11	34%	YP_004680854.1
hypothetical protein [Oscillatoria sp. PCC 10802]	77.4	139	33%	4e-11	30%	WP_020480612.1
proprotein convertase P [Tistrella mobilis KA081020-065]	77.0	143	30%	4e-11	29%	YP_006370739.1
hemolysin-type calcium-binding repeat protein [Leptolyngbya sp. PCC 7375]	77.4	261	29%	5e-11	33%	WP_006519062.1
Hemolysin-type calcium-binding region [Rhodobacter sp. SW2]	76.6	307	33%	5e-11	31%	WP_008030394.1
hypothetical protein [Sphingobium yanokuyae]	77.0	238	36%	5e-11	29%	WP_004207719.1
hemolysin-type calcium-binding protein [Starkeya novella DSM 506]	76.6	251	34%	6e-11	30%	YP_003693926.1
hypothetical protein [Oscillatoria sp. PCC 10802]	76.3	260	31%	6e-11	31%	WP_017717249.1
5'-nucleotidase domain-containing protein [Rhodopseudomonas palustris DX-1]	77.0	120	32%	6e-11	29%	YP_004110428.1
calcium binding hemolysin protein [Tistrella mobilis KA081020-065]	75.9	302	33%	8e-11	30%	YP_006370049.1
hypothetical protein [Alivibrio logei]	76.3	185	28%	8e-11	32%	WP_017023581.1

FIG. 6C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hemolysin-type calcium-binding region [Nitrosomonas sp. AL212]	75.5	230	32%	8e-11	28%	YP_004295065.1
calcium binding hemolysin protein, putative [Bradyrhizobium oligotrophicum S58]	76.3	343	39%	1e-10	28%	YP_007512736.1
Hemolysin-type calcium-binding protein [Agrobacterium vitis S4]	75.9	242	28%	1e-10	29%	YP_002548098.1
hemolysin-adenylate cyclase [Phaeospirillum fulvum MGU-K5]	75.9	172	37%	1e-10	29%	EPY02797.1
hemolysin-type calcium-binding protein [Desulfomicrobium baculatum DSM 4028]	75.9	306	34%	1e-10	30%	YP_003158921.1
hypothetical protein [Pseudomonas alcaliphila]	75.5	363	33%	2e-10	30%	WP_017677435.1
type I secretion protein [Vibrio sp. N418]	75.1	261	28%	2e-10	30%	WP_009385092.1
hypothetical protein, partial [Endozoicomonas elysicola]	75.1	249	29%	2e-10	30%	WP_020583217.1
hypothetical protein [Oscillatoria sp. PCC 10802]	73.9	283	35%	4e-10	28%	WP_017721018.1
hemolysin-type calcium-binding protein [Desulfomicrobium baculatum DSM 4028]	72.8	734	36%	1e-09	27%	YP_003158384.1
hypothetical protein [Methylobacterium sp. 77]	72.4	292	37%	1e-09	28%	WP_019903589.1
hypothetical protein BJ6T_06520 [Bradyrhizobium japonicum USDA 6]	71.2	71.2	29%	2e-09	32%	YP_005605535.1

FIG. 6D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
hypothetical protein amb3422 [Magnetospirillum magneticum AMB-1]	1830	1925	100%	0.0	100%	YP_422785.1
hypothetical protein [Magnetospirillum sp. SO-1] >	1082	1211	100%	0.0	64%	WP_008614612.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	688	1045	98%	0.0	58%	WP_009870351.1
hypothetical protein K678_05578 [Phaeospirillum fulvum MGUK5]	272	272	48%	1e-75	41%	EPY02541.1
HEMAGGLUTININ/HEMOLYSIN-RELATED PROTEIN [Magnetospirillum gryphiswaldense MSR-1]	126	249	74%	3e-26	30%	CAM76811.1
outer membrane adhesin like protein, partial [Achromobacter piechaudii]	88.2	880	34%	2e-14	32%	WP_006216951.1
VCBS repeat-containing protein [Solitalea canadensis DSM 3403]	87.0	806	33%	3e-14	34%	YP_006254384.1
hypothetical protein, partial [Pedobacter agri]	85.9	125	34%	8e-14	29%	WP_010602925.1
hypothetical protein AM1_E0108 [Acaryochloris marina MBIC11017]	82.8	82.8	28%	7e-13	34%	YP_001522191.1
putative hemolysin [Cellvibrio japonicus Ueda107]	82.0	505	34%	1e-12	31%	YP_001981885.1
outer membrane adhesin-like protein [Pseudomonas denitrificans ATCC 13867]	75.5	321	36%	1e-10	30%	YP_007656731.1
hypothetical protein Plut_0379 [Chlorobium luteolum DSM 273]	75.5	134	28%	1e-10	30%	YP_374310.1
hypothetical protein [Rhizobium sp. 2MFC03.1]	72.8	1046	40%	9e-10	32%	WP_018896697.1
hemagglutinin/hemolysin-like protein [Dickeya dadantii 3937]	67.0	450	27%	4e-08	31%	YP_003881756.1
hypothetical protein [Novispirillum itersonii]	67.0	122	35%	5e-08	28%	WP_019646374.1
rhizobiocin RzcA [Asticcacaulis biprosthecium]	66.6	66.6	11%	7e-08	40%	WP_006274635.1
outer membrane adhesin-like protein [Chitinophaga pinensis DSM 2588]	66.2	458	31%	7e-08	29%	YP_003125000.1
uncharacterized protein [uncultured bacterium]	60.8	107	28%	4e-06	31%	CAX84233.1
outer membrane adhesin-like protein [Cyanotheca sp. PCC 7822]	59.3	117	24%	1e-05	30%	YP_003890797.1
hypothetical protein [Methyloversatilis universalis]	57.8	103	37%	3e-05	29%	WP_018230537.1
Large exoprotein [Roseovarius sp. TM1035]	53.5	140	25%	6e-04	28%	WP_008281368.1
outer membrane autotransporter barrel domain protein [Methylobacterium sp. GXF4]	50.4	50.4	33%	0.005	27%	WP_007560973.1
cadherin [Rhodopirellula baltica]	50.1	50.1	14%	0.007	32%	WP_007329466.1
outer membrane transport barrel [Sphingomonas sp. MM-1]	49.3	49.3	29%	0.012	28%	YP_007614514.1
hypothetical protein [Methyloversatilis universalis]	46.2	46.2	37%	0.099	30%	WP_008064234.1
hypothetical protein AZL_f01290 [Azospirillum sp. B510]	45.8	45.8	9%	0.13	39%	YP_003453433.1
outer membrane autotransporter [Burkholderia ambifaria MC40-6]]	44.3	44.3	35%	0.36	29%	YP_001816158.1
hemolysin-type calcium-binding region [Nostoc punctiforme PCC 73102]	41.6	41.6	23%	2.5	27%	YP_001867978.1
transporter [Pseudomonas chlororaphis]	41.2	41.2	12%	3.2	35%	WP_009043135.1
hypothetical protein [Bradyrhizobium sp. WSM471]	40.0	40.0	16%	6.8	29%	WP_007605159.1

FIG. 7

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
ABC-type protease/lipase transport system, ATPase and permease components [Magnetospirillum magneticum AMB-1]	1220	1220	100%	0.0	100%	YP_422838.1
COG2274: ABC-type bacteriocin/lantibiotic exporters, contain an N-terminal double-glycine peptidase domain [Magnetospirillum magnetotacticum]	1090	1090	93%	0.0	95%	WP_009870208.1
ABC-type protease/lipase transport system, ATPase and permease component protein [Magnetospirillum sp. SO-1]	1076	1076	98%	0.0	91%	WP_008619118.1
ABC-type protease/lipase transport system, ATPase and permease component [Phaeospirillum fulvum MGU-K5]	896	896	93%	0.0	79%	EPY00949.1
hypothetical protein [Novispirillum itersonii]	611	611	91%	0.0	56%	WP_019643622.1
ABC-type protease/lipase transporter [Caenispirillum salinarum]	592	592	94%	0.0	54%	WP_009539978.1
ABC-type protease/lipase transport system, ATPase and permease components [Rhodospirillum photometricum DSM 122]	581	581	92%	0.0	55%	YP_005416034.1
protein containing ABC transporter domain [Magnetospirillum gryphiswaldense MSR-1]	525	525	59%	9e-180	70%	CAM77380.1
ABC-type protease/lipase transport system, ATPase and permease components [Glaciecola sp. HTCC2999]	449	449	91%	1e-146	39%	WP_010180038.1
ABC-type protease/lipase transport system, ATPase and permease components [Limnobacter sp. MED105]	448	448	95%	7e-146	39%	WP_008248572.1
ABC-type protease/lipase transport system [Pseudomonas stutzeri]	439	439	93%	4e-143	42%	WP_003293555.1
ABC transporter related protein [Oscidax symbiont Rs1]	351	351	90%	6e-108	36%	WP_019813773.1
ABC transporter ATP-binding/permease protein [Thauera sp. 28]	350	350	92%	4e-107	37%	WP_002931922.1
ABC transporter ATP-binding/permease protein [Thauera sp. 27]	350	350	92%	5e-107	37%	WP_002944457.1
hypothetical protein [Thioalkalivibrio sp. ALgr5]	345	345	92%	8e-107	35%	WP_019592978.1
hypothetical protein [Thioalkalivibrio sp. ALE27]	343	343	92%	3e-106	35%	WP_018882170.1
ABC transporter [Thioalkalivibrio sp. ALE25]	345	345	92%	4e-106	35%	WP_018867039.1
ABC transporter [Thioalkalivibrio sp. AKL3]	346	346	92%	6e-106	35%	WP_018937733.1
ABC transporter [Azoarcus toluclasticus]	346	346	92%	9e-106	37%	WP_018987943.1
type I secretion system ATPase [Desulfomicrobium baculatum DSM 4028]	346	346	94%	1e-105	35%	YP_003158388.1
ABC transporter [Thioalkalivibrio sp. ALMg2]	345	345	92%	1e-105	35%	WP_019563530.1
toxin secretion ABC transporter permease and ATP-binding protein [Azoarcus sp. KH32C]	345	345	92%	1e-105	38%	YP_007553126.1
ABC transporter [Thioalkalivibrio sp. ALE28]	343	343	92%	2e-105	35%	WP_018877499.1
ABC-type bacteriocin/lantibiotic exporter [Vibrio fluvialis]	344	344	91%	3e-105	32%	WP_020331854.1

FIG. 8A

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
ABC transporter [Thioalkalivibrio sp. ALM2T]	344	344	92%	5e-105	35%	WP_019594102.1
ABC transporter [Thioalkalivibrio sp. ALMg13-2]	344	344	92%	5e-105	35%	WP_019568356.1
ABC transporter [Thioalkalivibrio sp. AKL12]	344	344	92%	5e-105	35%	WP_018951739.1
ABC transporter related protein [Osedax symbiont Rs2]	343	343	93%	6e-105	34%	WP_020286188.1
ABC transporter [Thioalkalivibrio sp. AKL10]	343	343	92%	6e-105	35%	WP_019628234.1
ABC transporter [Thioalkalivibrio sp. ALJ3]	343	343	92%	7e-105	36%	WP_018861453.1
ABC transporter [Thioalkalivibrio sp. ALJ16]	343	343	92%	9e-105	36%	WP_018873589.1
ABC transporter [Neptuniibacter caesiensis]	342	342	91%	3e-104	35%	WP_007022486.1
ATPase [Halomonas sp. GFJAJ-1]	342	342	93%	3e-104	35%	WP_009100771.1
ABC transporter, transmembrane region:ABC transporter:Peptidase C39, bacteriocin processing [Methylophaga sp. JAM7] >	342	342	91%	4e-104	34%	YP_006292562.1
ABC transporter [Thioalkalivibrio sp. ALJ10]	342	342	92%	4e-104	35%	WP_018868670.1
ABC transporter [Thioalkalivibrio sp. ALJT]	340	340	92%	8e-104	36%	WP_019626728.1
ABC transporter [Thioalkalivibrio sp. AKL11]	341	341	92%	1e-103	35%	WP_018939823.1
type I secretion system ATPase [Sulfurospirillum deleyianum DSM 6946]	340	340	93%	2e-103	34%	YP_003303859.1
ABC transporter [Methylophaga sp. JAM1]	340	340	91%	2e-103	35%	YP_006295629.1
ABC transporter [Thioalkalivibrio sp. ARh5]	338	338	92%	7e-103	35%	WP_019624185.1
ABC transporter [Thioalkalivibrio sp. ALJ20]	338	338	92%	9e-103	35%	WP_019024347.1
ABC transporter [Campylobacter rectus]	338	338	92%	9e-103	34%	WP_004318584.1
ABC transporter [Comamonas testosteroni]	338	338	93%	1e-102	34%	WP_003069985.1
ABC transporter [Thioalkalivibrio sp. ALE20]	337	337	92%	2e-102	35%	WP_019592005.1
ABC transporter [Thioalkalivibrio sp. ARh3]	338	338	92%	2e-102	35%	WP_018863861.1
peptidase C39 [Rheinheimera nanhaiensis]	337	337	91%	3e-102	33%	WP_008220329.1
ABC transporter [Thioalkalivibrio sp. HL-Eb18]	336	336	92%	5e-102	35%	WP_017926137.1
ABC transporter [Comamonas testosteroni]	337	337	93%	5e-102	34%	WP_003075146.1
ABC transporter ATP-binding protein [Marinobacter hydrocarbonoclasticus ATCC 49840]	336	336	91%	5e-102	35%	YP_005431238.1
ABC transporter [Thioalkalivibrio sp. ALE10]	335	335	92%	7e-102	35%	WP_019590480.1
ATPase [Halomonas sp. TD01]	335	335	90%	7e-102	35%	WP_009724196.1
ABC transporter [Variovorax paradoxus EPS]	332	332	92%	9e-102	36%	YP_004157431.1
ABC transporter [Thioalkalivibrio sp. ALJ11]	335	335	92%	1e-101	35%	WP_018139367.1
ATPase [Halomonas stevensii]	335	335	90%	1e-101	35%	WP_016915006.1
type I secretion system ATPase [Thioalkalivibrio sp. K90mix]	335	335	92%	2e-101	35%	YP_003460560.1

FIG. 8B

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
ABC transporter [Thioalkalivibrio sp. ALRh]	335	335	92%	2e-101	35%	WP_019592545.1
toxin secretion ATP-binding protein [Comamonas testosteroni CNB-2]	335	335	93%	2e-101	34%	YP_003279062.1
ABC transporter [Thioalkalivibrio thiocyanodinitrificans]	335	335	92%	2e-101	35%	WP_018233111.1
hypothetical protein [Catenovulum agarivorans]	333	333	90%	4e-101	36%	WP_016954151.1
ABC transporter [Thioalkalivibrio sp. ALgr1]	333	333	92%	6e-101	35%	WP_018993876.1
ABC transporter ATP-binding component [Arcobacter sp. L]	333	333	90%	8e-101	34%	YP_005552492.1
ABC transporter [Pseudalteromonas arctica]	332	332	91%	1e-100	34%	WP_010553238.1
ABC transporter [Pseudalteromonas sp. BSi20429]	331	331	91%	4e-100	34%	WP_007583161.1
ABC transporter [Campylobacter curvus]	331	331	92%	4e-100	33%	WP_018136203.1
ABC transporter [Campylobacter sp. FOBRC14]	331	331	92%	5e-100	33%	WP_009650523.1
ABC transporter [Comamonas testosteroni]	330	330	93%	5e-100	34%	WP_003053581.1
ABC transporter [Campylobacter sp. 10_1_50]	330	330	91%	6e-100	34%	WP_009294535.1
ABC transporter [gamma proteobacterium IMCC1989]	332	332	92%	6e-100	34%	WP_009670226.1
hypothetical protein CCC13826_0891 [Campylobacter concisus 13826]	330	330	91%	7e-100	34%	YP_001466532.1
bacteriocin/lantibiotic ABC transporter [Hahella chejuensis KCTC 2396]	331	331	91%	9e-100	33%	YP_437190.1
toxin secretion ATP-binding protein [Campylobacter curvus 525.92]	330	330	92%	1e-99	33%	YP_001408654.1
ABC transporter [Comamonas testosteroni]	331	331	93%	1e-99	34%	WP_019043539.1
ABC transporter [Variovorax sp. CF313]	326	326	90%	2e-99	37%	WP_007838295.1
hypothetical protein [Succinispira mobilis]	330	330	91%	2e-99	34%	WP_019878733.1
ABC transporter [Pseudalteromonas haloplanktis]	329	329	91%	2e-99	33%	WP_002961326.1
ABC transporter permease/ATP-binding protein [Xanthomonas fragariae]	329	329	95%	2e-99	35%	WP_002804835.1
ABC transporter permease/ATP-binding protein [Xanthomonas axonopodis]	328	328	95%	3e-99	35%	WP_005913568.1
peptidase C39 [Methylophaga aminisulfidivorans]	329	329	89%	3e-99	34%	WP_007145632.1
ABC transporter [Achromobacter arsenitoxydans]	328	328	91%	4e-99	33%	WP_008164875.1
peptidase C39 [Xanthomonas arboricola]	328	328	95%	4e-99	35%	WP_016902305.1
peptidase C39 [Xanthomonas fuscans]	328	328	95%	4e-99	35%	WP_007972241.1
peptidase C39 [Xanthomonas gardneri]	328	328	95%	4e-99	34%	WP_006449299.1
toxin secretion ABC transporter permease and ATP-binding protein [Thauera linaloolentis]	328	328	91%	7e-99	36%	WP_004332497.1
ABC transporter [Variovorax paradoxus S110]	325	325	91%	8e-99	35%	YP_002946334.1
ABC transporter [Alcaligenes faecalis]	327	327	91%	8e-99	34%	WP_003802991.1
ABC transporter [Vibrio alginolyticus]	327	327	92%	9e-99	34%	WP_005374556.1
ABC transporter [Burkholderia ubonensis]	328	328	91%	9e-99	34%	WP_010089615.1

FIG. 8C

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
ABC transporter permease/ATP-binding protein [Xanthomonas axonopodis pv. citrumelo F1]	327	327	95%	1e-98	35%	YP_004852936.1
ABC transporter [Vibrio sp. 712i1]	327	327	92%	1e-98	34%	WP_017634537.1
ABC transporter [Vibrio alginolyticus]	327	327	92%	2e-98	34%	WP_005383569.1
type I secretion system ATPase [Leptothrix cholodnii SP-6]	327	327	91%	2e-98	35%	YP_001791124.1
ABC transporter [Variovorax paradoxus]	323	323	91%	2e-98	35%	WP_018906841.1
ABC transporter [Vibrio sinoensis]	326	326	92%	2e-98	34%	WP_008074445.1
ABC transporter [Halomonas sp. KM-1]	327	327	91%	2e-98	36%	WP_010628832.1
type I secretion system AtPase HlyB [Candidatus Nitrospira defluvi]	326	326	91%	3e-98	33%	YP_003799068.1
ABC transporter [Marinobacterium stanieri]	326	326	91%	3e-98	35%	WP_010325122.1
peptidase C39 [Arhodomonas aquaeolei]	325	325	90%	3e-98	34%	WP_018719059.1
ABC transporter ATP-binding/permease [Aromatoleum aromaticum EbN1]	327	327	92%	3e-98	37%	YP_158002.1
ABC transporter [Pectobacterium wasabiae]	327	327	90%	3e-98	35%	WP_005973599.1
type I secretion system ATPase, partial [Candidatus Nitrosopumilus salaria]	322	322	92%	3e-98	33%	WP_008297682.1

FIG. 8D

Description	Max score	Total score	Query cover	E value	Ident	Accession No.
Autotransporter adhesin [Magnetospirillum gryphiswaldense MSR-1]	46.6	78.6	19%	1e-05	40%	CAM74531.1
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	45.1	105	13%	4e-05	45%	YP_420640.1
COG5295: Autotransporter adhesin [Magnetospirillum magnetotacticum]	44.7	105	15%	7e-05	46%	WP_009869454.1
hypothetical protein, partial [Magnetospirillum sp. SO-1] >	43.9	132	19%	1e-04	37%	WP_008622436.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	43.9	174	32%	1e-04	42%	WP_009869271.1
hypothetical protein amb3422 [Magnetospirillum magneticum AMB-1]	43.5	192	46%	1e-04	39%	YP_422785.1
Type V secretory pathway, adhesin AidA [Magnetospirillum magneticum AMB-1]	41.6	183	15%	6e-04	36%	YP_421364.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	41.6	288	13%	6e-04	44%	WP_009868027.1
large exoprotein [Magnetospirillum magneticum AMB-1]	40.8	115	11%	0.001	44%	YP_420631.1
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	39.7	107	15%	0.003	47%	YP_423419.1
RTX toxin [Magnetospirillum sp. SO-1]	37.7	133	19%	0.008	29%	WP_008615895.1
Hemolysin-type calcium-binding region [Magnetospirillum gryphiswaldense MSR-1]	37.0	196	42%	0.014	30%	CAM77170.1
hypothetical protein [Magnetospirillum sp. SO-1]	37.0	404	23%	0.019	36%	WP_008614612.1
Type V secretory pathway [Magnetospirillum magneticum AMB-1]	36.6	36.6	6%	0.019	52%	YP_420638.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	36.2	70.5	16%	0.026	33%	WP_009868207.1
VBCS repeat-containing protein, partial [Magnetospirillum sp. SO-1]	35.4	35.4	11%	0.042	40%	WP_008621158.1
RTX toxins and related Ca2+-binding protein [Magnetospirillum magneticum AMB-1]	35.4	63.1	10%	0.045	45%	YP_422662.1
outer membrane adhesin-like protein, partial [Magnetospirillum sp. SO-1]	35.4	35.4	13%	0.049	35%	WP_008622382.1
hemolysin-type calcium-binding repeat-containing protein, partial [Magnetospirillum sp. SO-1]	35.4	125	22%	0.051	33%	WP_008617421.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	34.3	34.3	9%	0.054	38%	WP_009865035.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	33.9	33.9	14%	0.064	32%	WP_009864918.1
Autotransporter adhesin [Magnetospirillum gryphiswaldense MSR-1]	34.3	324	16%	0.12	47%	CAM76579.1
COG2931: RTX toxins and related Ca2+-binding proteins, partial [Magnetospirillum]	33.1	97.4	13%	0.15	43%	WP_009865796.1

FIG. 9A

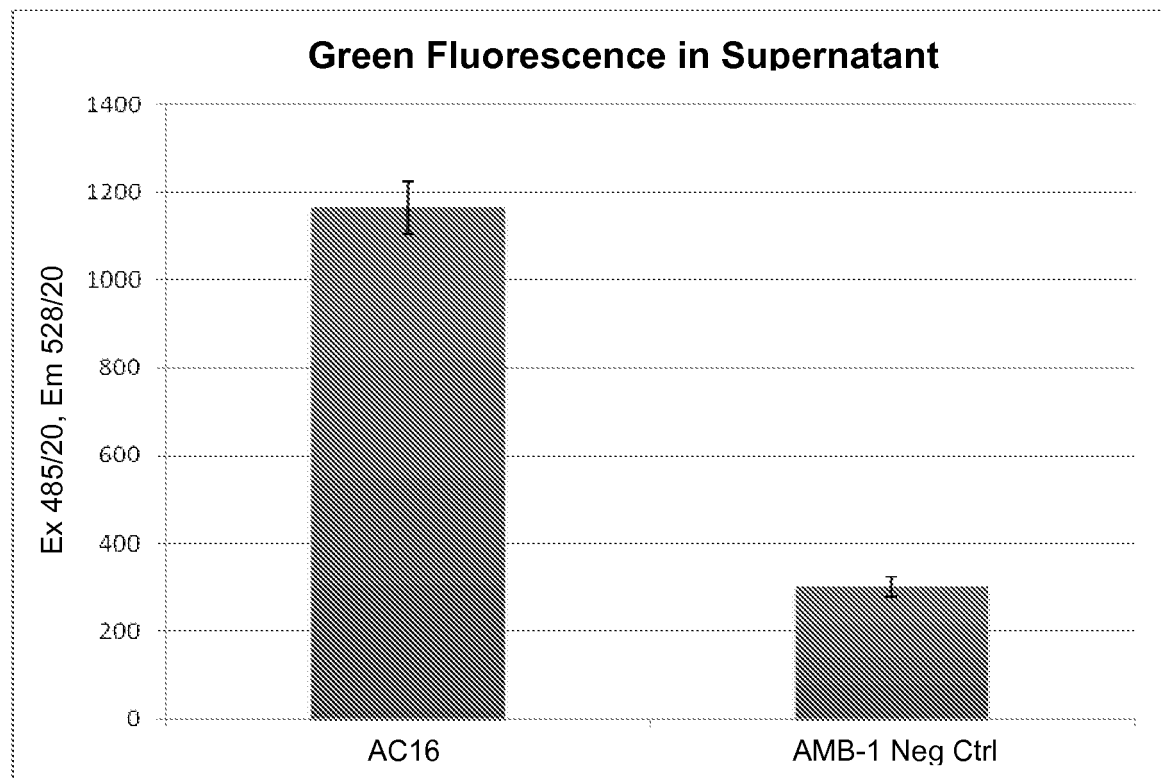
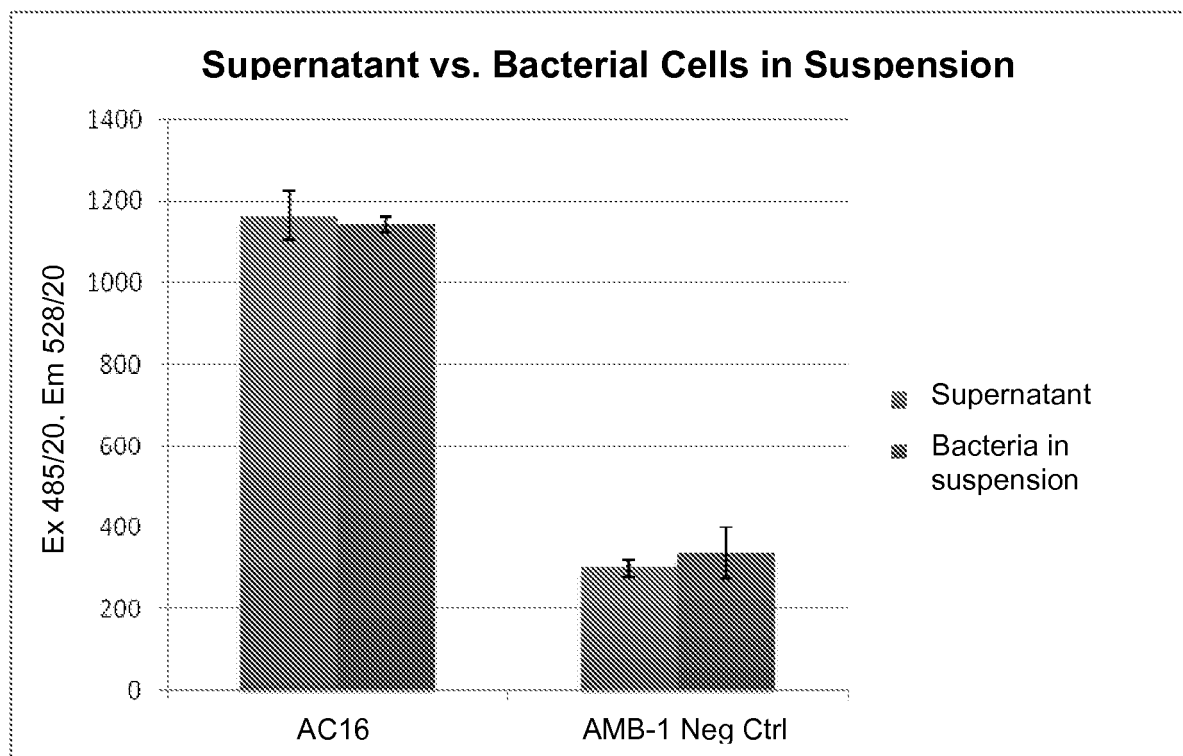
Description	Max score	Total score	Query cover	E value	Ident	Accession No.
magnetotacticum]						
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	33.9	158	13%	0.16	32%	WP_009870351.1
Type V secretory pathway, adhesin AidA, partial [Magnetospirillum sp. SO-1]	33.1	33.1	11%	0.22	35%	WP_008619475.1
hypothetical protein, partial [Magnetospirillum sp. SO-1]	32.0	90.5	14%	0.36	32%	WP_008622842.1
Holliday junction DNA helicase RuvB [Magnetospirillum magnetotacticum AMB-1]	31.6	31.6	7%	0.61	47%	YP_422579.1
COG2931: RTX toxins and related Ca2+-binding proteins, partial [Magnetospirillum magnetotacticum]	31.6	119	13%	0.62	49%	WP_009865379.1
Holliday junction DNA helicase RuvB [Magnetospirillum sp. SO-1]	31.2	31.2	7%	0.66	47%	WP_008621034.1
COG2931: RTX toxins and related Ca2+-binding proteins, partial [Magnetospirillum magnetotacticum]	31.2	60.1	22%	0.70	26%	WP_009863686.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	31.2	60.4	24%	0.81	31%	WP_009865975.1
COG2931: RTX toxins and related Ca2+-binding proteins [Magnetospirillum magnetotacticum]	31.2	150	18%	0.83	45%	WP_009865835.1
hypothetical protein, partial [Magnetospirillum sp. SO-1]	30.4	57.8	18%	0.90	39%	WP_008622434.1
COG4953: Membrane carboxypeptidase/penicillin-binding protein PbpC, partial [Magnetospirillum magnetotacticum]	30.8	30.8	16%	1.0	31%	WP_009868232.1
COG2931: RTX toxins and related Ca2+-binding proteins, partial [Magnetospirillum magnetotacticum]	30.4	59.7	21%	1.1	28%	WP_009862535.1
RTX toxins and related Ca2+-binding proteins [Magnetospirillum gryphiswaldense MSR-1]	30.8	30.8	8%	1.3	34%	CAM75368.1
calcium binding hemolysin protein, partial [Magnetospirillum sp. SO-1]	29.3	85.9	11%	2.2	31%	WP_008615635.1
COG2931: RTX toxins and related Ca2+-binding proteins, partial [Magnetospirillum magnetotacticum]	28.5	28.5	8%	3.2	35%	WP_009861891.1
COG2931: RTX toxins and related Ca2+-binding proteins, partial [Magnetospirillum magnetotacticum]	29.3	57.4	13%	3.3	40%	WP_009865727.1
lipoprotein releasing system ATP-binding protein [Magnetospirillum gryphiswaldense MSR-1]	28.1	28.1	7%	5.5	37%	CAM74983.1
hypothetical protein MGR_1109 [Magnetospirillum gryphiswaldense MSR-1]	28.5	28.5	19%	6.1	31%	CAM76862.1
COG0265: Trypsin-like serine proteases, typically periplasmic, contain C-terminal PDZ domain, partial [Magnetospirillum magnetotacticum]	28.1	28.1	6%	6.3	37%	WP_009865351.1
COG1680: Beta-lactamase class C and other penicillin binding proteins	28.1	28.1	7%	6.9	42%	WP_009870006.1

FIG. 9B

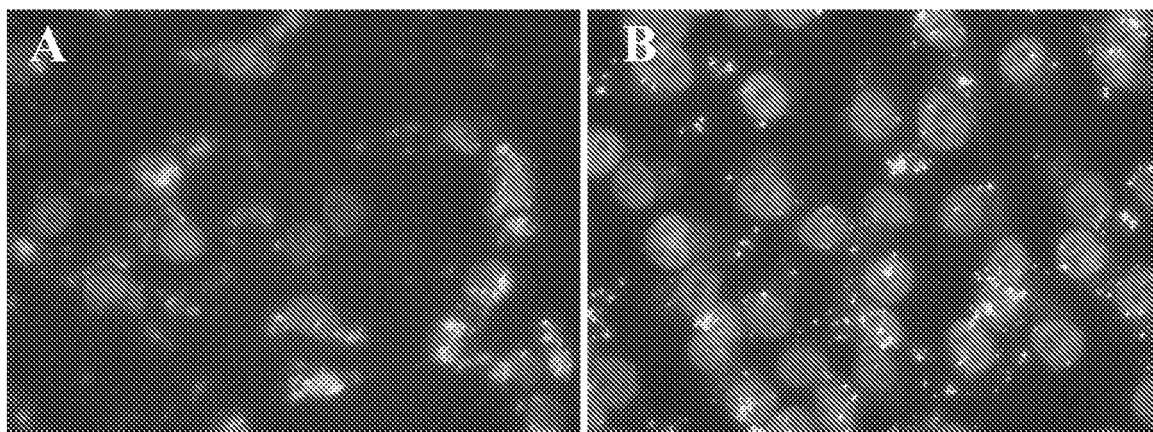
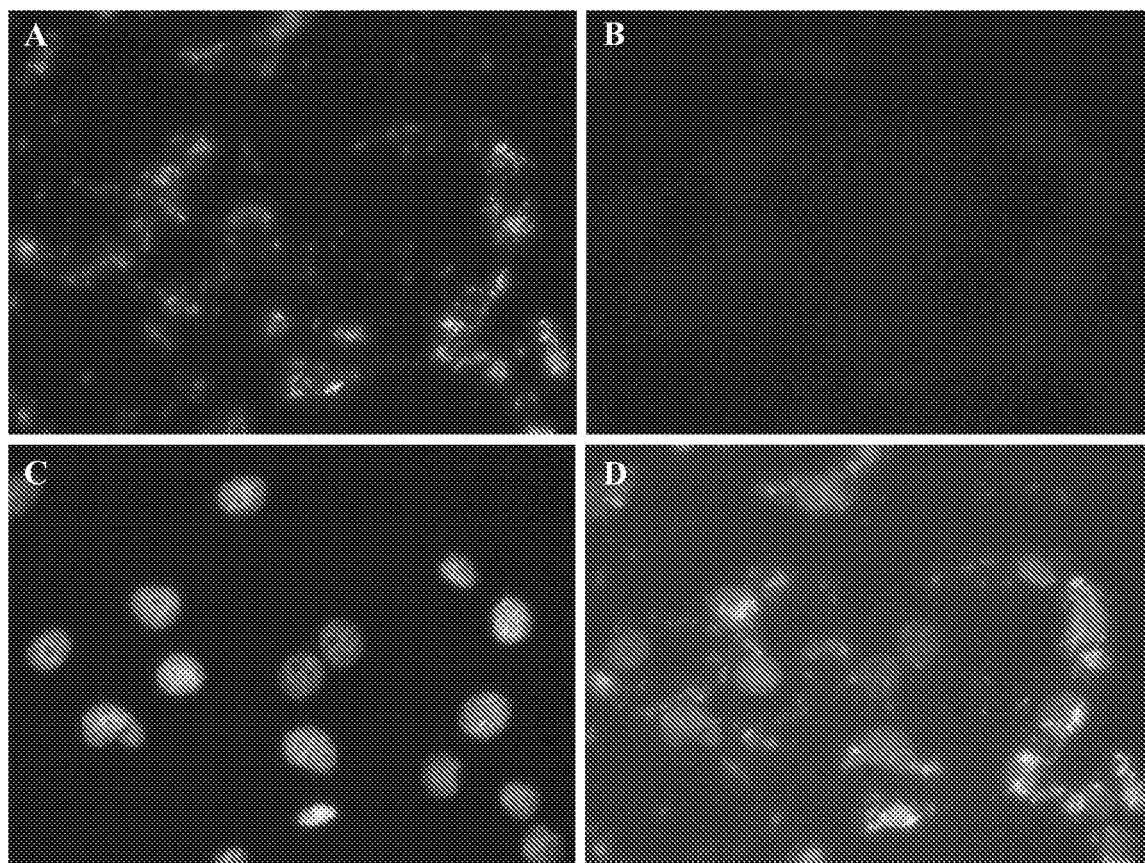
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[Magnetospirillum magnetotacticum]						
COG2931: RTX toxins and related Ca ²⁺ -binding proteins [Magnetospirillum magnetotacticum]	26.2	26.2	5%	6.9	50%	WP_009862419.1
asparagine synthase [Magnetospirillum sp. SO-1] >gb EME69335.1 asparagine synthase [Magnetospirillum sp. SO-1]	28.1	28.1	14%	7.8	28%	WP_008618626.1

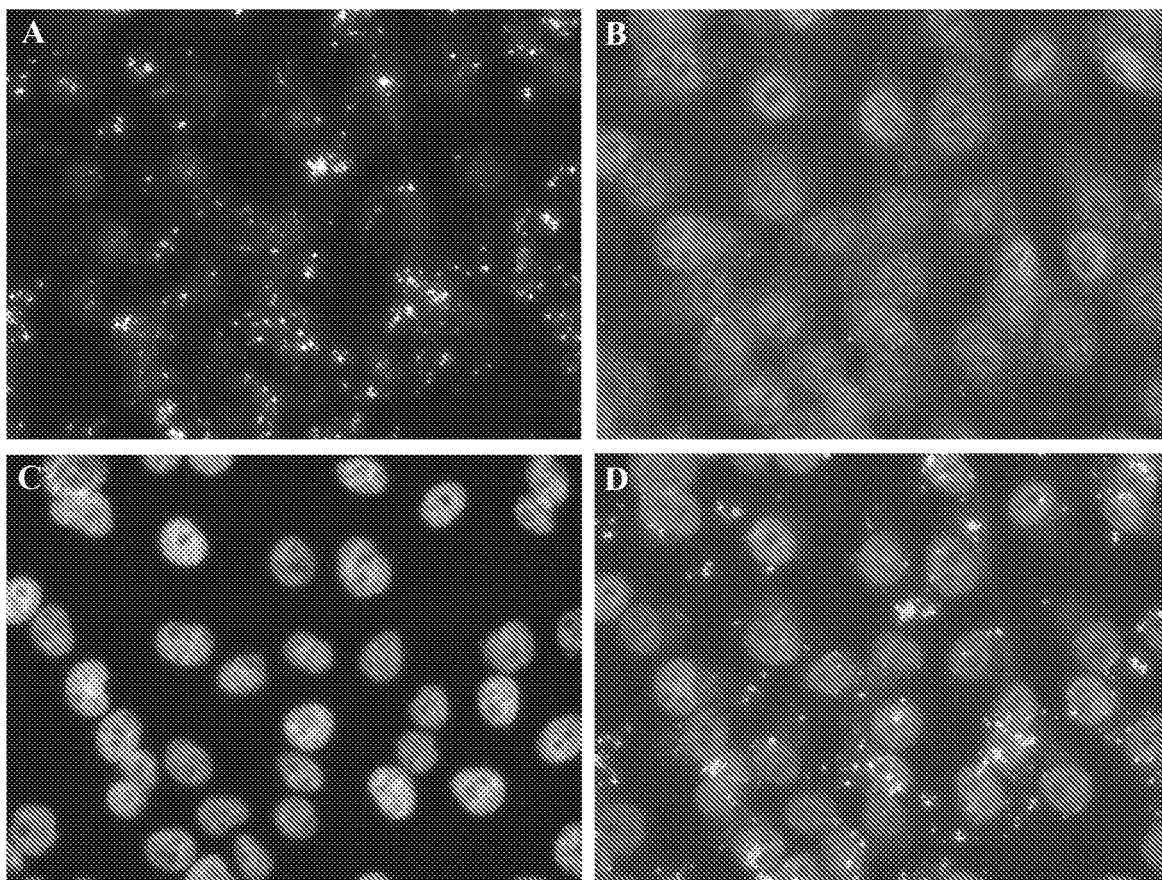
FIG. 9C

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**FIG. 10****FIG. 11**

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**FIG. 12****FIG. 13**

**FIG. 14**