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BLAST® >> blastp suite >> results for RID-UWT1SRV1013

Your search parameters were adjusted to search for a short input sequence.

Job Title	Protein Sequence ...
RID	UWT1SRV1013 Search expires on 01-23 19:48 pm
Program	BLASTP
Database	nr
Query ID	Icl Query_7865240
Description	unnamed protein product ...
Molecule type	amino acid
Query Length	17

**Descriptions**

Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
threonine/serine exporter family protein [Shewanella sp. NIFS-20-20]	Shewanella sp. NIFS-20-20	36.7	36.7	88%	1.4	66.67%	253	MBV7315808.1
peptidylprolyl isomerase [Bacteroidales bacterium]	Bacteroidales bacterium	34.6	34.6	100%	8.1	58.82%	455	MDO4496460.1
hypothetical protein ADK66_22520 [Micromonospora sp. NRRL B-16802]	Micromonospora sp. NRRL B-16802	33.7	33.7	76%	16	76.92%	167	KOX06643.1
DUF1097 domain-containing protein [Micromonospora sp. NRRL B-16802]	Micromonospora sp. NRRL B-16802	33.7	33.7	76%	16	76.92%	172	WP_157552811.1
DUF1097 domain-containing protein [Micromonospora profundi]	Micromonospora profundi	33.7	33.7	76%	16	76.92%	172	WP_167944661.1
glutamine synthetase, type I [Ignisphaera aggregans DSM 17230]	Ignisphaera aggregans DSM 17230	33.7	33.7	94%	16	50.00%	463	ADM27753.1
unnamed protein product [Owenia fusiformis]	Owenia fusiformis	33.7	33.7	70%	16	73.33%	558	CAH1775346.1
efflux RND transporter permease subunit [Flavobacterium sp.]	Flavobacterium sp.	33.7	33.7	70%	16	76.92%	677	WP_325261504.1
cation:proton antiporter [Leptospirales bacterium]	Leptospirales bacterium	33.7	33.7	70%	16	75.00%	707	MBX7085483.1
unnamed protein product [Owenia fusiformis]	Owenia fusiformis	33.7	33.7	70%	16	73.33%	709	CAH1775345.1
efflux RND transporter permease subunit [unclassified Flavobacterium]	unclassified Flavobacterium	33.7	33.7	70%	16	76.92%	1056	WP_116797931.1
efflux RND transporter permease subunit [Flavobacterium sp. 5]	Flavobacterium sp. 5	33.7	33.7	70%	16	76.92%	1056	WP_100844170.1
efflux RND transporter permease subunit [Flavobacterium sp.]	Flavobacterium sp.	33.7	33.7	70%	16	76.92%	1056	WP_326400544.1
efflux RND transporter permease subunit [uncultured Flavobacterium sp.]	uncultured Flavobacterium sp.	33.7	33.7	70%	16	76.92%	1056	WP_315153806.1
efflux RND transporter permease subunit [uncultured Flavobacterium sp.]	uncultured Flavobacterium sp.	33.7	33.7	70%	16	76.92%	1056	WP_315257618.1
efflux RND transporter permease subunit [Flavobacterium sp.]	Flavobacterium sp.	33.7	33.7	70%	16	76.92%	1056	WP_310559616.1
efflux RND transporter permease subunit [Flavobacterium aquicola]	Flavobacterium aquicola	33.7	33.7	70%	16	76.92%	1056	WP_115810187.1
efflux RND transporter permease subunit [Flavobacterium aquariorum]	Flavobacterium aquariorum	33.7	33.7	70%	16	76.92%	1056	WP_111408624.1
efflux RND transporter permease subunit [Flavobacterium]	Flavobacterium	33.7	33.7	70%	16	76.92%	1056	WP_194640962.1
efflux RND transporter permease subunit [uncultured Flavobacterium sp.]	uncultured Flavobacterium sp.	33.7	33.7	70%	16	76.92%	1056	WP_3152002
efflux RND transporter permease subunit [Flavobacterium franklandianum]	Flavobacterium franklandianum	33.7	33.7	70%	16	76.92%	1056	WP_144071274.1



Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
efflux RND transporter permease subunit [Flavobacterium sp. 1]	Flavobacterium sp. 1	33.7	33.7	70%	16	76.92%	1056	WP_100430275.1
ubiquitin conjugation factor E4 A-like [Acanthaster planci]	Acanthaster planci	33.7	33.7	58%	16	90.00%	1067	XP_022107418.1
hypothetical protein [Bacillota bacterium]	Bacillota bacterium	33.7	33.7	88%	16	64.71%	2449	MBR3785194.1
ABC transporter permease [Gammaproteobacteria bacterium]	Gammaproteobacteria bacterium	33.3	33.3	88%	23	68.75%	302	MDX1514413.1
MFS transporter [Candidatus Melainabacteria bacterium]	Candidatus Melainabacteria bacterium	33.3	33.3	88%	23	64.71%	452	MDZ4833912.1
domain S-box protein [Frankiales bacterium]	Frankiales bacterium	33.3	33.3	52%	23	100.00%	511	MCU1601538.1
diguanylate cyclase [Anaeromyxobacter sp. Fw109-5]	Anaeromyxobacter sp. Fw109-5	33.3	33.3	88%	23	60.00%	739	WP_234945290.1
diguanylate cyclase [Anaeromyxobacter sp. Fw109-5]	Anaeromyxobacter sp. Fw109-5	33.3	33.3	88%	23	60.00%	758	ABS26442.1
probable ubiquitin conjugation factor E4 [Selaginella moellendorffii]	Selaginella moellendorffii	33.3	33.3	64%	23	81.82%	1015	XP_002992051.1
probable ubiquitin conjugation factor E4 [Selaginella moellendorffii]	Selaginella moellendorffii	33.3	33.3	64%	23	81.82%	1015	XP_002964116.1
energy coupling factor transporter S component ThiW [Candidatus Culexarchaeum yellowstonense]	Candidatus Culexarchaeum yellowstonense	32.9	32.9	76%	32	69.23%	169	MCR6623897.1
LptF/LptG family permease [Spirochaetales bacterium]	Spirochaetales bacterium	32.9	32.9	76%	32	68.75%	358	MBN2651385.1
MFS transporter [Defluviateaceae bacterium]	Defluviateaceae bacterium	32.9	32.9	70%	32	83.33%	421	MCL2421141.1
MFS transporter [Candidatus Melainabacteria bacterium]	Candidatus Melainabacteria bacterium	32.9	32.9	76%	32	71.43%	455	MCC6979192.1
MFS transporter [Cyanobacteria bacterium PR.3.49]	Cyanobacteria bacterium PR.3.49	32.9	32.9	76%	32	71.43%	455	MBA3856889.1
hypothetical protein SELMODRAFT_130016 [Selaginella moellendorffii]	Selaginella moellendorffii	32.9	32.9	58%	32	90.00%	463	EFJ09410.1
efflux RND transporter permease subunit [Chitinophagaceae bacterium]	Chitinophagaceae bacterium	32.9	32.9	82%	32	64.71%	467	MBO9658993.1
hypothetical protein SELMODRAFT_81029 [Selaginella moellendorffii]	Selaginella moellendorffii	32.9	32.9	58%	32	90.00%	469	EFJ34608.1
vacuolar protein sorting-associated protein 9A [Selaginella moellendorffii]	Selaginella moellendorffii	32.9	32.9	58%	32	90.00%	486	XP_0029895...
vacuolar protein sorting-associated protein 9A [Selaginella moellendorffii]	Selaginella moellendorffii	32.9	32.9	58%	32	90.00%	492	XP_0029642...
efflux RND transporter permease subunit [Terrimonas ginsenosidimutans]	Terrimonas ginsenosidimutans	32.9	32.9	82%	32	64.71%	1055	WP_237869499.1



Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
efflux RND transporter permease subunit [Chitinophaga hortii]	Chitinophaga hortii	32.9	32.9	82%	32	64.71%	1055	WP_264280605.1
site-2 protease family protein [Deltaproteobacteriabacterium]	Deltaproteobacteriabacterium	32.5	32.5	82%	45	71.43%	98	MCX7959575.1
TPA: MFS transporter [Candidatus Bathyarchaeota archaeon]	Candidatus Bathyarchaeota archaeon	32.5	32.5	100%	46	70.59%	437	HIIH88784.1
elongation factor G [Deltaproteobacteriabacterium]	Deltaproteobacteriabacterium	32.5	32.5	70%	46	83.33%	690	MBW2434215.1
elongation factor G [Deltaproteobacteriabacterium]	Deltaproteobacteriabacterium	32.5	32.5	70%	46	83.33%	690	MBW2487061.1
hypothetical protein CBR_g12533 [Chara braunii]	Chara braunii	32.5	32.5	70%	46	75.00%	857	GBG60795.1
DUF2892 domain-containing protein [Thermoflexaceae bacterium]	Thermoflexaceae bacterium	32.0	32.0	76%	64	76.92%	69	MBK6663876.1
monovalent cation/H(+) antiporter subunit G [Phascolarctobacterium sp.]	Phascolarctobacterium sp.	32.0	32.0	82%	64	64.29%	118	MBQ8417459.1
unnamed protein product [Caenorhabditis angaria]	Caenorhabditis angaria	32.0	32.0	94%	64	55.56%	210	CAI5437402.1
hypothetical protein HPB51_020388 [Rhipicephalus microplus]	Rhipicephalus microplus	32.0	32.0	76%	64	69.23%	247	KAH8026404.1
carbohydrate ABC transporter permease [Anaerolineae bacterium]	Anaerolineae bacterium	32.0	32.0	82%	64	50.00%	296	MCL6432292.1
site-2 protease family protein [Deltaproteobacteriabacterium]	Deltaproteobacteriabacterium	32.0	32.0	70%	64	75.00%	312	MCX7944202.1
dynamin family protein [Synergistaceae bacterium]	Synergistaceae bacterium	32.0	32.0	100%	64	66.67%	323	MDR1580934.1
cation:proton antiporter [Gammaproteobacteria bacterium]	Gammaproteobacteria bacterium	32.0	32.0	82%	64	70.59%	389	MDH5710653.1
cation:proton antiporter [Gammaproteobacteria bacterium]	Gammaproteobacteria bacterium	32.0	32.0	82%	64	70.59%	389	MDH3342175.1
hypothetical protein HID58_061832 [Brassica napus]	Brassica napus	32.0	32.0	88%	65	60.00%	454	KAH0885736.1
ABC transporter ATP-binding protein [Oscillospiraceae bacterium]	Oscillospiraceae bacterium	32.0	32.0	58%	65	80.00%	578	MBE6939758.1
Sodium/hydrogen exchanger family-domain-containing protein [Parasitella parasitica]	Parasitella parasitica	32.0	32.0	82%	65	64.29%	715	KAI8636592.1
hypothetical protein F2Q68_00027025 [Brassica cretica]	Brassica cretica	32.0	32.0	88%	65	60.00%	764	KAF2567097
cation/H(+) antiporter 20-like [Mercurialis annua]	Mercurialis annua	32.0	32.0	88%	65	60.00%	780	XP_0502144
Sodium/hydrogen exchanger family-domain-containing protein [Cokeromyces recurvatus]	Cokeromyces recurvatus	32.0	32.0	82%	65	64.29%	781	XP_051381614.1



Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
hypothetical protein Bca52824_046414 [Brassica carinata]	Brassica carinata	32.0	32.0	88%	65	60.00%	783	KAG2286810.1
BnaCnng11150D [Brassica napus]	Brassica napus	32.0	32.0	88%	65	60.00%	790	CDY44462.1
Cation/H(+) antiporter 18 [Hirschfeldia incana]	Hirschfeldia incana	32.0	32.0	88%	65	60.00%	799	KAJ0260632.1
PREDICTED: cation/H(+) antiporter 18 [Brassica oleracea var. oleracea]	Brassica oleracea var. oleracea	32.0	32.0	88%	65	60.00%	800	XP_013631329.1
cation/H(+) antiporter 18 [Beta vulgaris subsp. vulgaris]	Beta vulgaris subsp. vulgaris	32.0	32.0	88%	65	60.00%	800	XP_010676379.2
hypothetical protein DY000_02033837 [Brassica cretica]	Brassica cretica	32.0	32.0	88%	65	60.00%	800	KAF3582271.1
unnamed protein product [Brassica napus]	Brassica napus	32.0	32.0	88%	65	60.00%	800	CAF1859574.1
cation/H(+) antiporter 18-like [Amaranthus tricolor]	Amaranthus tricolor	32.0	32.0	88%	65	60.00%	800	XP_057521570.1
hypothetical protein BVRB_5g099630 [Beta vulgaris subsp. vulgaris]	Beta vulgaris subsp. vulgaris	32.0	32.0	88%	65	60.00%	800	KMT12001.1
cation/H(+) antiporter 18-like [Spinacia oleracea]	Spinacia oleracea	32.0	32.0	88%	65	60.00%	800	XP_021838496.1
cation/H(+) antiporter 18-like [Chenopodium quinoa]	Chenopodium quinoa	32.0	32.0	88%	65	60.00%	801	XP_021757592.1
cation/H(+) antiporter 19-like [Lotus japonicus]	Lotus japonicus	32.0	32.0	88%	65	60.00%	813	XP_057456846.1
Sodium/hydrogen exchanger family-domain-containing protein [Blakeslea trispora]	Blakeslea trispora	32.0	32.0	88%	65	60.00%	819	KAI8389338.1
hypothetical protein AXG93_4278s1050 [Marchantia polymorpha subsp. ruderaleis]	Marchantia polymorpha subsp. ruderaleis	32.0	32.0	88%	65	60.00%	837	OAE27086.1
cation/H(+) antiporter 20 [Lotus japonicus]	Lotus japonicus	32.0	32.0	88%	65	60.00%	847	XP_057438443.1
importin-7-like [Rhipicephalus microplus]	Rhipicephalus microplus	32.0	32.0	76%	65	69.23%	1055	XP_037276134.1
hypothetical protein [Bdellovibrionales bacterium]	Bdellovibrionales bacterium	31.6	31.6	82%	90	68.75%	95	MCB0406421.1
hypothetical protein [Bdellovibrionales bacterium]	Bdellovibrionales bacterium	31.6	31.6	82%	90	68.75%	99	MCB0416933.1
hypothetical protein [Paenibacillus arenosi]	Paenibacillus arenosi	31.6	31.6	88%	91	68.75%	202	WP_192024018.1
hypothetical protein [Paenibacillus assamensis]	Paenibacillus assamensis	31.6	31.6	88%	91	68.75%	202	WP_028593546.1
hypothetical protein [Paenibacillus sp. SC116]	Paenibacillus sp. SC116	31.6	31.6	88%	91	68.75%	202	WP_258276798.1
hypothetical protein [Deltaproteobacteria bacterium]	Deltaproteobacteria bacterium	31.6	31.6	76%	91	76.92%	206	MBN2255574
hypothetical protein [Clostridium sp. WB02_MRS01]	Clostridium sp. WB02_MRS01	31.6	31.6	76%	91	71.43%	262	WP_1545213
MFS transporter [Microbacterium sp. HD4P20]	Microbacterium sp. HD4P20	31.6	31.6	94%	91	66.67%	401	WP_219983032.1



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hypothetical protein [Verrucomicrobiales bacterium]	Verrucomicrobiales bacterium	31.6	31.6	88%	91	60.00%	445	MBO35604.1
efflux RND transporter permease subunit [Pedobacter sp.]	Pedobacter sp.	31.6	31.6	76%	91	68.75%	468	RZK62004.1
hypothetical protein [Desulfovibrio sp.]	Desulfovibrio sp.	31.6	31.6	88%	91	70.59%	490	MBQ9452250.1
efflux RND transporter permease subunit [Pedobacter sp.]	Pedobacter sp.	31.6	31.6	76%	91	68.75%	582	RZK90562.1
efflux RND transporter permease subunit [Pedobacter sp.]	Pedobacter sp.	31.6	31.6	76%	91	68.75%	611	MBC7419007.1
efflux RND transporter permease subunit [Sphingobacteriales bacterium]	Sphingobacteriales bacterium	31.6	31.6	76%	91	68.75%	615	RYE53020.1
hydrophobe/amphiphile efflux-1 family RND transporter [Pedobacter sp.]	Pedobacter sp.	31.6	31.6	76%	91	68.75%	627	RZK67390.1
hydrophobe/amphiphile efflux-1 family RND transporter [Flavobacterium sp.]	Flavobacterium sp.	31.6	31.6	76%	91	68.75%	627	RZJ74129.1
hypothetical protein [candidate division KSB1 bacterium]	candidate division KSB1 bacterium	31.6	31.6	100%	91	64.71%	747	MBN1466682.1
hypothetical protein Leryth_018725 [Lithospermum erythrorhizon]	Lithospermum erythrorhizon	31.6	31.6	88%	91	60.00%	814	KAG9153462.1
multidrug transporter AcrB [Pedobacter mendelii]	Pedobacter mendelii	31.6	31.6	76%	91	68.75%	1032	GGI27221.1
efflux RND transporter permease subunit [Pedobacter aquatilis]	Pedobacter aquatilis	31.6	31.6	76%	91	68.75%	1056	WP_316829634.1
efflux RND transporter permease subunit [Pedobacter aquatilis]	Pedobacter aquatilis	31.6	31.6	76%	91	68.75%	1056	WP_316758238.1

Graphic Summary



Distribution of the top 100 Blast Hits on 100 subject sequences



Alignments

Alignment view CDS feature

threonine-serine exporter family protein [Shewanella sp. NIFS-20-20]

Sequence ID: **MBV7315808.1** Length: 253 Number of Matches: 1

Range 1: 139 to 153

Score	Expect	Identities	Positives	Gaps	Frame
36.7 bits(79)	1.4()	10/15(67%)	12/15(80%)	0/15(0%)	
Query 3	MAFIVTFMSSPIGMA	17			
Sbjct 139	MAF+ TF+ S IGMA				
	MAFVMTFLASSIGMA	153			

peptidylprolyl isomerase [Bacteroidales bacterium]

Sequence ID: **MDO4496460.1** Length: 455 Number of Matches: 1

Range 1: 7 to 23

Score	Expect	Identities	Positives	Gaps	Frame

Feedback

34.6 bits(74)	8.1()	10/17(59%)	12/17(70%)	0/17(0%)
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Query  1  RAMAFIVTFMSSPIGMA  17
      RAMAF+ T M   +GMA
Sbjct  7  RAMAFVATLMTAVVGMA  23
```

hypothetical protein ADK66_22520 [Micromonospora sp. NRRL B-16802]

Sequence ID: **KOX06643.1** Length: 167 Number of Matches: 1

Range 1: 82 to 94

Score	Expect	Identities	Positives	Gaps	Frame
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33.7 bits(72)	16()	10/13(77%)	11/13(84%)	0/13(0%)	
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```
Query  5  FIVTFMSSPIGMA  17
      FIV F+SS IGMA
Sbjct 82  FIVAFLSSHIGMA  94
```

DUF1097 domain-containing protein [Micromonospora sp. NRRL B-16802]

Sequence ID: **WP_157552811.1** Length: 172 Number of Matches: 1

Range 1: 87 to 99

Score	Expect	Identities	Positives	Gaps	Frame
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33.7 bits(72)	16()	10/13(77%)	11/13(84%)	0/13(0%)	
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```
Query  5  FIVTFMSSPIGMA  17
      FIV F+SS IGMA
Sbjct 87  FIVAFLSSHIGMA  99
```

DUF1097 domain-containing protein [Micromonospora profundi]

Sequence ID: **WP_167944661.1** Length: 172 Number of Matches: 1

Range 1: 87 to 99

Score	Expect	Identities	Positives	Gaps	Frame
-------	--------	------------	-----------	------	-------

33.7 bits(72)	16()	10/13(77%)	11/13(84%)	0/13(0%)	
---------------	------	------------	------------	----------	--

```
Query  5  FIVTFMSSPIGMA  17
      FIV F+SS IGMA
Sbjct 87  FIVAFLSSHIGMA  99
```

Taxonomy

Reports

Lineage

Organism	Blast Name	Score	Number of Hits	Description
cellular organisms		131		
.Bacteria	bacteria	80		
..Gammaproteobacteria	g-proteobacteria	4		
...Shewanella sp. NIFS-20-20	g-proteobacteria	36.7	1	Shewanella sp. NIFS-20-20 hits
...Gammaproteobacteria bacterium	g-proteobacteria	33.3	3	Gammaproteobacteria bacterium hits
..Bacteroidales bacterium	CFB group bacteria	34.6	1	Bacteroidales bacterium hits
..Micromonospora sp. NRRL B-16802	high G+C Gram-positive bacteria	33.7	2	Micromonospora sp. NRRL B-16802 hits
..Micromonospora profundi	high G+C Gram-positive bacteria	33.7	3	Micromonospora profundi hits
..Flavobacterium sp.	CFB group bacteria	33.7	4	Flavobacterium sp. hits
..Leptospirales bacterium	bacteria	33.7	1	Leptospirales bacterium hits
..unclassified Flavobacterium	CFB group bacteria	33.7	1	unclassified Flavobacterium hits
..Flavobacterium sp. 103	CFB group bacteria	33.7	1	Flavobacterium sp. 103 hits
..Flavobacterium sp. M31R6	CFB group bacteria	33.7	1	Flavobacterium sp. M31R6 hits
..Flavobacterium sp. 5	CFB group bacteria	33.7	2	Flavobacterium sp. 5 hits
..uncultured Flavobacterium sp.	CFB group bacteria	33.7	3	uncultured Flavobacterium sp. hits
..Flavobacterium aquicola	CFB group bacteria	33.7	2	Flavobacterium aquicola hits
..Flavobacterium aquariorum	CFB group bacteria	33.7	2	Flavobacterium aquariorum hits
..Flavobacterium	CFB group bacteria	33.7	1	Flavobacterium hits
..Flavobacterium sp. HJJ	CFB group bacteria	33.7	1	Flavobacterium sp. HJJ hits



..Flavobacterium franklandianum	CFB group bacteria	33.7	2	Flavobacterium franklandianum hits
..Flavobacterium sp. 1	CFB group bacteria	33.7	2	Flavobacterium sp. 1 hits
..Bacillota bacterium	firmicutes	33.7	1	Bacillota bacterium hits
..Candidatus Melainabacteria bacterium	bacteria	33.3	2	Candidatus Melainabacteria bacterium hits
..Frankiales bacterium	high G+C Gram-positive bacteria	33.3	1	Frankiales bacterium hits
..Anaeromyxobacter sp. Fw109-5	bacteria	33.3	2	Anaeromyxobacter sp. Fw109-5 hits
..Spirochaetales bacterium	spirochetes	32.9	1	Spirochaetales bacterium hits
..Defluvitaleaceae bacterium	firmicutes	32.9	1	Defluvitaleaceae bacterium hits
..Cyanobacteria bacterium PR.3.49	cyanobacteria	32.9	1	Cyanobacteria bacterium PR.3.49 hits
..Chitinophagaceae bacterium	CFB group bacteria	32.9	1	Chitinophagaceae bacterium hits
..Terrimonas ginsenosidimutans	CFB group bacteria	32.9	2	Terrimonas ginsenosidimutans hits
..Chitinophaga horti	CFB group bacteria	32.9	2	Chitinophaga horti hits
..Deltaproteobacteria bacterium	bacteria	32.5	5	Deltaproteobacteria bacterium hits
..Thermoflexaceae bacterium	GNS bacteria	32.0	1	Thermoflexaceae bacterium hits
..Phascolarctobacterium sp.	firmicutes	32.0	1	Phascolarctobacterium sp. hits
..Anaerolineae bacterium	GNS bacteria	32.0	1	Anaerolineae bacterium hits
..Synergistaceae bacterium	bacteria	32.0	1	Synergistaceae bacterium hits
..Oscillospiraceae bacterium	firmicutes	32.0	1	Oscillospiraceae bacterium hits
..Bdellovibrionales bacterium	bacteria	31.6	2	Bdellovibrionales bacterium hits
..Pseudobdellovibrionaceae bacterium	bacteria	31.6	1	Pseudobdellovibrionaceae bacterium hits
..Paenibacillus arenosi	firmicutes	31.6	2	Paenibacillus arenosi hits
..Paenibacillus assamensis	firmicutes	31.6	1	Paenibacillus assamensis hits
..Paenibacillus sp. SC116	firmicutes	31.6	2	Paenibacillus sp. SC116 hits
..Clostridium sp. WB02_MRS01	firmicutes	31.6	2	Clostridium sp. WB02_MRS01 hits
..Microbacterium sp. HD4P20	high G+C Gram-positive bacteria	31.6	2	Microbacterium sp. HD4P20 hits
..Verrucomicrobiales bacterium	verrucomicrobia	31.6	1	Verrucomicrobiales bacterium hits
..Pedobacter sp.	CFB group bacteria	31.6	4	Pedobacter sp. hits
..Desulfovibrio sp.	bacteria	31.6	1	Desulfovibrio sp. hits
..Sphingobacteriales bacterium	CFB group bacteria	31.6	1	Sphingobacteriales bacterium hits
..candidate division KSB1 bacterium	bacteria	31.6	1	candidate division KSB1 bacterium hits
..Pedobacter mendelii	CFB group bacteria	31.6	1	Pedobacter mendelii hits
..Pedobacter aquatilis	CFB group bacteria	31.6	2	Pedobacter aquatilis hits
..Ignisphaera aggregans DSM 17230	crenarchaeotes	33.7	1	Ignisphaera aggregans DSM 17230 hits
..Owenia fusiformis	segmented worms	33.7	2	Owenia fusiformis hits
..Acanthaster planci	starfish	33.7	2	Acanthaster planci hits
..Selaginella moellendorffii	club-mosses	33.3	8	Selaginella moellendorffii hits
..Candidatus Culexarchaeum yellowstonense	archaea	32.9	1	Candidatus Culexarchaeum yellowstonense hits
..Candidatus Bathyarchaeota archaeon	archaea	32.5	1	Candidatus Bathyarchaeota archaeon hits
..Chara braunii	green plants	32.5	1	Chara braunii hits
..Caenorhabditis angaria	nematodes	32.0	1	Caenorhabditis angaria hits
..Rhipicephalus microplus	mites & ticks	32.0	2	Rhipicephalus microplus hits
..Brassica napus	eudicots	32.0	3	Brassica napus hits
..Parasitella parasitica	mucoromycotan fungi	32.0	1	Parasitella parasitica hits
..Brassica cretica	eudicots	32.0	2	Brassica cretica hits
..Mercurialis annua	eudicots	32.0	1	Mercurialis annua hits
..Cokeromyces recurvatus	mucoromycotan fungi	32.0	2	Cokeromyces recurvatus hits
..Brassica carinata	eudicots	32.0	1	Brassica carinata hits
..Hirschfeldia incana	eudicots	32.0	1	Hirschfeldia incana hits
..Brassica oleracea var. oleracea	eudicots	32.0	2	Brassica oleracea var. oleracea hits
..Beta vulgaris subsp. vulgaris	eudicots	32.0	3	Beta vulgaris subsp. vulgaris hits
..Brassica oleracea	eudicots	32.0	1	Brassica oleracea hits
..Amaranthus tricolor	eudicots	32.0	2	Amaranthus tricolor hits
..Spinacia oleracea	eudicots	32.0	5	Spinacia oleracea hits



.Chenopodium quinoa	eudicots	32.0	1	Chenopodium quinoa hits
.Lotus japonicus	eudicots	32.0	2	Lotus japonicus hits
.Blakeslea trispora	mucoromycotan fungi	32.0	1	Blakeslea trispora hits
.Marchantia polymorpha subsp. ruderale	liverworts	32.0	2	Marchantia polymorpha subsp. ruderale hits
.Marchantia polymorpha	liverworts	32.0	1	Marchantia polymorpha hits
.Lithospermum erythrorhizon	eudicots	31.6	1	Lithospermum erythrorhizon hits

Organism

Description		Score	E value	Accession
Shewanella sp. NIFS-20-20 [g-proteobacteria]				
threonine-serine exporter family protein [Shewanella sp. NIFS-20-20]		36.7	1.4	MBV7315808
Bacteroidales bacterium [CFB group bacteria]				
peptidylprolyl isomerase [Bacteroidales bacterium]		34.6	8.1	MDO4496460
Micromonospora sp. NRRL B-16802 [high G+C Gram-positive bacteria]				
hypothetical protein ADK66_22520 [Micromonospora sp. NRRL B-16802]		33.7	16	KOX06643
DUF1097 domain-containing protein [Micromonospora sp. NRRL B-16802]		33.7	16	WP_157552811
Micromonospora profundi [high G+C Gram-positive bacteria]				
DUF1097 domain-containing protein [Micromonospora profundi]		33.7	16	WP_167944661
hypothetical protein [Micromonospora profundi]		33.7	16	NJC13083
DUF1097 domain-containing protein [Micromonospora profundi]		33.7	16	WLS44821
Ignisphaera aggregans DSM 17230 [crenarchaeotes]				
glutamine synthetase, type I [Ignisphaera aggregans DSM 17230]		33.7	16	ADM27753
Owenia fusiformis [segmented worms]				
unnamed protein product [Owenia fusiformis]		33.7	16	CAH1775346
unnamed protein product [Owenia fusiformis]		33.7	16	CAH1775345
Flavobacterium sp. [CFB group bacteria]				
efflux RND transporter permease subunit, partial [Flavobacterium sp.]		33.7	16	WP_325261504
efflux RND transporter permease subunit [Flavobacterium sp.]		33.7	16	WP_326400544
efflux RND transporter permease subunit [Flavobacterium sp.]		33.7	16	WP_310559616
MAG: hydrophobe/amphiphile efflux-1 family RND transporter, partial [Flavobacterium sp.]		31.6	91	RZJ74129
Leptospirales bacterium [bacteria]				
cation:proton antiporter [Leptospirales bacterium]		33.7	16	MBX7085483
unclassified Flavobacterium [CFB group bacteria]				
MULTISPECIES: efflux RND transporter permease subunit [unclassified Flavobacterium]		33.7	16	WP_116797931
Flavobacterium sp. 103 [CFB group bacteria]				
HAE1 family hydrophobic/amphiphilic exporter-1 [Flavobacterium sp. 103]		33.7	16	PVX47400
Flavobacterium sp. M31R6 [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium sp. M31R6]		33.7	16	QKJ63988
Flavobacterium sp. 5 [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium sp. 5]		33.7	16	WP_100844170
HAE1 family hydrophobic/amphiphilic exporter-1 [Flavobacterium sp. 5]		33.7	16	PKB18245
uncultured Flavobacterium sp. [CFB group bacteria]				
efflux RND transporter permease subunit [uncultured Flavobacterium sp.]		33.7	16	WP_315153806
efflux RND transporter permease subunit [uncultured Flavobacterium sp.]		33.7	16	WP_315257618
efflux RND transporter permease subunit [uncultured Flavobacterium sp.]		33.7	16	WP_315200286
Flavobacterium aquicola [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium aquicola]		33.7	16	WP_1158101
HAE1 family hydrophobic/amphiphilic exporter-1 [Flavobacterium aquicola]		33.7	16	REH00794
Flavobacterium aquariorum [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium aquariorum]		33.7	16	WP_1114086
hydrophobe/amphiphile efflux-1 family RND transporter [Flavobacterium aquariorum]		33.7	16	PZX94524
Flavobacterium [CFB group bacteria]				
MULTISPECIES: efflux RND transporter permease subunit [Flavobacterium]		33.7	16	WP_194640962



Description		Score	E value	Accession
Flavobacterium sp. HJJ [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium sp. HJJ]		33.7	16	MBF4471253
Flavobacterium franklandianum [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium franklandianum]		33.7	16	WP_144071274
efflux RND transporter permease subunit [Flavobacterium franklandianum]		33.7	16	TRX21648
Flavobacterium sp. 1 [CFB group bacteria]				
efflux RND transporter permease subunit [Flavobacterium sp. 1]		33.7	16	WP_100430275
HAE1 family hydrophobic/amphiphilic exporter-1 [Flavobacterium sp. 1]		33.7	16	PJJ07499
Acanthaster planci (crown-of-thorns starfish) [starfish]				
ubiquitin conjugation factor E4 A-like [Acanthaster planci]		33.7	16	XP_022107418
ubiquitin conjugation factor E4 A-like [Acanthaster planci]		33.7	16	XP_022107419
Bacillota bacterium [firmicutes]				
hypothetical protein [Bacillota bacterium]		33.7	16	MBR3785194
Gammaproteobacteria bacterium [g-proteobacteria]				
ABC transporter permease [Gammaproteobacteria bacterium]		33.3	23	MDX1514413
cation:proton antiporter [Gammaproteobacteria bacterium]		32.0	64	MDH5710653
cation:proton antiporter [Gammaproteobacteria bacterium]		32.0	64	MDH3342175
Candidatus Melainabacteria bacterium [bacteria]				
MFS transporter [Candidatus Melainabacteria bacterium]		33.3	23	MDZ4833912
MFS transporter [Candidatus Melainabacteria bacterium]		32.9	32	MCC6979192
Frankiales bacterium [high G+C Gram-positive bacteria]				
domain S-box protein [Frankiales bacterium]		33.3	23	MCU1601538
Anaeromyxobacter sp. Fw109-5 [bacteria]				
diguanylate cyclase [Anaeromyxobacter sp. Fw109-5]		33.3	23	WP_234945290
diguanylate cyclase [Anaeromyxobacter sp. Fw109-5]		33.3	23	ABS26442
Selaginella moellendorffii [club-mosses]				
probable ubiquitin conjugation factor E4 [Selaginella moellendorffii]		33.3	23	XP_002992051
ubiquitin-protein ligase, UFD2 [Selaginella moellendorffii]		33.3	23	EFJ06900
probable ubiquitin conjugation factor E4 [Selaginella moellendorffii]		33.3	23	XP_002964116
ubiquitin-protein ligase, UFD2 [Selaginella moellendorffii]		33.3	23	EFJ34449
hypothetical protein SELMODRAFT_130016 [Selaginella moellendorffii]		32.9	32	EFJ09410
hypothetical protein SELMODRAFT_81029 [Selaginella moellendorffii]		32.9	32	EFJ34608
vacuolar protein sorting-associated protein 9A [Selaginella moellendorffii]		32.9	32	XP_002989534
vacuolar protein sorting-associated protein 9A [Selaginella moellendorffii]		32.9	32	XP_002964275
Candidatus Culexarchaeum yellowstonense [archaea]				
energy coupling factor transporter S component ThiW [Candidatus Culexarchaeum yellowstonense]		32.9	32	MCR6623897
Spirochaetales bacterium [spirochetes]				
LptF/LptG family permease [Spirochaetales bacterium]		32.9	32	MBN2651385
Defluvitaleaceae bacterium [firmicutes]				
MFS transporter [Defluvitaleaceae bacterium]		32.9	32	MCL2421141
Cyanobacteria bacterium PR.3.49 [cyanobacteria]				
MFS transporter [Cyanobacteria bacterium PR.3.49]		32.9	32	MBA3856889
Chitinophagaceae bacterium [CFB group bacteria]				
efflux RND transporter permease subunit [Chitinophagaceae bacterium]		32.9	32	MBO9658993
Terrimonas ginsenosidimutans [CFB group bacteria]				
efflux RND transporter permease subunit [Terrimonas ginsenosidimutans]		32.9	32	WP_237869499
efflux RND transporter permease subunit [Terrimonas ginsenosidimutans]		32.9	32	MCG2613766
Chitinophaga horti [CFB group bacteria]				
efflux RND transporter permease subunit [Chitinophaga horti]		32.9	32	WP_2642806
efflux RND transporter permease subunit [Chitinophaga horti]		32.9	32	UYQ92326
Deltaproteobacteria bacterium [bacteria]				
site-2 protease family protein [Deltaproteobacteria bacterium]		32.5	45	MCX7959575
elongation factor G [Deltaproteobacteria bacterium]		32.5	46	MBW2434215



Description	Score	E value	Accession
elongation factor G [Deltaproteobacteria bacterium]	32.5	46	MBW2487061
site-2 protease family protein [Deltaproteobacteria bacterium]	32.0	64	MCX7944202
hypothetical protein [Deltaproteobacteria bacterium]	31.6	91	MBN2255574
Candidatus Bathyarchaeota archaeon [archaea]			
MFS transporter [Candidatus Bathyarchaeota archaeon]	32.5	46	HIH88784
Chara braunii [green plants]			
hypothetical protein CBR_g12533 [Chara braunii]	32.5	46	GBG60795
Thermoflexaceae bacterium [GNS bacteria]			
DUF2892 domain-containing protein [Thermoflexaceae bacterium]	32.0	64	MBK6663876
Phascolarctobacterium sp. [firmicutes]			
monovalent cation/H(+) antiporter subunit G [Phascolarctobacterium sp.]	32.0	64	MBQ8417459
Caenorhabditis angaria [nematodes]			
unnamed protein product [Caenorhabditis angaria]	32.0	64	CAI5437402
Rhipicephalus microplus (southern cattle tick) [mites & ticks]			
hypothetical protein HPB51_020388 [Rhipicephalus microplus]	32.0	64	KAH8026404
importin-7-like [Rhipicephalus microplus]	32.0	65	XP_037276134
Anaerolineae bacterium [GNS bacteria]			
carbohydrate ABC transporter permease [Anaerolineae bacterium]	32.0	64	MCL6432292
Synergistaceae bacterium [bacteria]			
dynamin family protein [Synergistaceae bacterium]	32.0	64	MDR1580934
Brassica napus (rape) [eudicots]			
hypothetical protein HID58_061832 [Brassica napus]	32.0	65	KAH0885736
BnaCnng11150D [Brassica napus]			
unnamed protein product [Brassica napus]	32.0	65	CAF1859574
Oscillospiraceae bacterium [firmicutes]			
ABC transporter ATP-binding protein [Oscillospiraceae bacterium]	32.0	65	MBE6939758
Parasitella parasitica [mucoromycotan fungi]			
Sodium/hydrogen exchanger family-domain-containing protein [Parasitella parasitica]	32.0	65	KAI8636592
Brassica cretica [eudicots]			
hypothetical protein F2Q68_00027025 [Brassica cretica]	32.0	65	KAF2567097
hypothetical protein DY000_02033837 [Brassica cretica]	32.0	65	KAF3582271
Mercurialis annua (annual mercury) [eudicots]			
cation/H(+) antiporter 20-like [Mercurialis annua]	32.0	65	XP_050214466
Cokeromyces recurvatus [mucoromycotan fungi]			
Sodium/hydrogen exchanger family-domain-containing protein [Cokeromyces recurvatus]	32.0	65	XP_051381614
Sodium/hydrogen exchanger family-domain-containing protein [Cokeromyces recurvatus]	32.0	65	KAI7901629
Brassica carinata [eudicots]			
hypothetical protein Bca52824_046414 [Brassica carinata]	32.0	65	KAG2286810
Hirschfeldia incana [eudicots]			
Cation/H(+) antiporter 18 [Hirschfeldia incana]	32.0	65	KAJ0260632
Brassica oleracea var. oleracea [eudicots]			
PREDICTED: cation/H(+) antiporter 18 [Brassica oleracea var. oleracea]	32.0	65	XP_013631329
PREDICTED: cation/H(+) antiporter 18 [Brassica oleracea var. oleracea]	32.0	65	XP_013631330
Beta vulgaris subsp. vulgaris [eudicots]			
cation/H(+) antiporter 18 [Beta vulgaris subsp. vulgaris]	32.0	65	XP_010676379
cation/H(+) antiporter 18 [Beta vulgaris subsp. vulgaris]	32.0	65	XP_010676380
hypothetical protein BVRB_5g099630 [Beta vulgaris subsp. vulgaris]	32.0	65	KMT12001
Brassica oleracea (wild cabbage) [eudicots]			
unnamed protein product [Brassica oleracea]	32.0	65	VDD12050
Amaranthus tricolor [eudicots]			
cation/H(+) antiporter 18-like [Amaranthus tricolor]	32.0	65	XP_05752157
cation/H(+) antiporter 18-like [Amaranthus tricolor]	32.0	65	XP_057521571
Spinacia oleracea (spinach) [eudicots]			

Feedback

Description	Score	E value	Accession
cation/H(+) antiporter 18-like [Spinacia oleracea]	32.0	65	XP_021838496
cation/H(+) antiporter 18-like [Spinacia oleracea]	32.0	65	XP_021838503
cation/H(+) antiporter 18-like [Spinacia oleracea]	32.0	65	XP_021838508
cation/H(+) antiporter 18-like [Spinacia oleracea]	32.0	65	XP_056687683
hypothetical protein SOVF_189560 [Spinacia oleracea]	32.0	65	KNA05519
Chenopodium quinoa (quinoa) [eudicots]			
cation/H(+) antiporter 18-like [Chenopodium quinoa]	32.0	65	XP_021757592
Lotus japonicus [eudicots]			
cation/H(+) antiporter 19-like [Lotus japonicus]	32.0	65	XP_057456846
cation/H(+) antiporter 20 [Lotus japonicus]	32.0	65	XP_057438443
Blakeslea trispora [mucoromycotan fungi]			
Sodium/hydrogen exchanger family-domain-containing protein [Blakeslea trispora]	32.0	65	KAI8389338
Marchantia polymorpha subsp. ruderale [liverworts]			
hypothetical protein AXG93_4278s1050 [Marchantia polymorpha subsp. ruderale]	32.0	65	OAE27086
hypothetical protein Mp_4g10470 [Marchantia polymorpha subsp. ruderale]	32.0	65	BBN08301
Marchantia polymorpha (liverwort) [liverworts]			
hypothetical protein MARPO_0011s0034 [Marchantia polymorpha]	32.0	65	PTQ46337
Bdellovibrionales bacterium [bacteria]			
hypothetical protein [Bdellovibrionales bacterium]	31.6	90	MCB0406421
hypothetical protein [Bdellovibrionales bacterium]	31.6	90	MCB0416933
Pseudobdellovibrionaceae bacterium [bacteria]			
hypothetical protein [Pseudobdellovibrionaceae bacterium]	31.6	90	MCB9254511
Paenibacillus arenosi [firmicutes]			
hypothetical protein [Paenibacillus arenosi]	31.6	91	WP_192024018
hypothetical protein [Paenibacillus arenosi]	31.6	91	MBD8497606
Paenibacillus assamensis [firmicutes]			
hypothetical protein [Paenibacillus assamensis]	31.6	91	WP_028593546
Paenibacillus sp. SC116 [firmicutes]			
hypothetical protein [Paenibacillus sp. SC116]	31.6	91	WP_258276798
hypothetical protein [Paenibacillus sp. SC116]	31.6	91	MCR8842948
Clostridium sp. WB02_MRS01 [firmicutes]			
hypothetical protein [Clostridium sp. WB02_MRS01]	31.6	91	WP_154521384
hypothetical protein [Clostridium sp. WB02_MRS01]	31.6	91	MSS08184
Microbacterium sp. HD4P20 [high G+C Gram-positive bacteria]			
MFS transporter [Microbacterium sp. HD4P20]	31.6	91	WP_219983032
MFS transporter [Microbacterium sp. HD4P20]	31.6	91	MCP2638428
Verrucomicrobiales bacterium [verrucomicrobia]			
hypothetical protein [Verrucomicrobiales bacterium]	31.6	91	MBO35604
Pedobacter sp. [CFB group bacteria]			
MAG: efflux RND transporter permease subunit, partial [Pedobacter sp.]	31.6	91	RZK62004
MAG: efflux RND transporter permease subunit, partial [Pedobacter sp.]	31.6	91	RZK90562
efflux RND transporter permease subunit [Pedobacter sp.]	31.6	91	MBC7419007
MAG: hydrophobe/amphiphile efflux-1 family RND transporter, partial [Pedobacter sp.]	31.6	91	RZK67390
Desulfovibrio sp. [bacteria]			
hypothetical protein [Desulfovibrio sp.]	31.6	91	MBQ9452250
Sphingobacteriales bacterium [CFB group bacteria]			
MAG: efflux RND transporter permease subunit, partial [Sphingobacteriales bacterium]	31.6	91	RYE53020
candidate division KSB1 bacterium [bacteria]			
hypothetical protein [candidate division KSB1 bacterium]	31.6	91	MBN1466682
Lithospermum erythrorhizon [eudicots]			
hypothetical protein Leryth_018725 [Lithospermum erythrorhizon]	31.6	91	KAG9153462
Pedobacter mendelii [CFB group bacteria]			
multidrug transporter AcrB [Pedobacter mendelii]	31.6	91	GGI27221



Description	Score	E value	Accession
Pedobacter aquatilis [CFB group bacteria]			
efflux RND transporter permease subunit [Pedobacter aquatilis]	31.6	91	WP_316829634
efflux RND transporter permease subunit [Pedobacter aquatilis]	31.6	91	WP_316758238

Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
cellular organisms	131	75	
.. Bacteria	80	48	
... Gammaproteobacteria	4	2	
... Shewanella sp. NIFS-20-20	1	1	Shewanella sp. NIFS-20-20 hits
... Gammaproteobacteria bacterium	3	1	Gammaproteobacteria bacterium hits
.. Bacteroidota	36	20	
... Bacteroidales bacterium	1	1	Bacteroidales bacterium hits
... Flavobacteriaceae	22	12	
.... Flavobacterium	1	12	Flavobacterium hits
.... unclassified Flavobacterium	1	7	unclassified Flavobacterium hits
..... Flavobacterium sp.	4	1	Flavobacterium sp. hits
..... Flavobacterium sp. 103	1	1	Flavobacterium sp. 103 hits
..... Flavobacterium sp. M31R6	1	1	Flavobacterium sp. M31R6 hits
..... Flavobacterium sp. 5	2	1	Flavobacterium sp. 5 hits
..... Flavobacterium sp. HJJ	1	1	Flavobacterium sp. HJJ hits
..... Flavobacterium sp. 1	2	1	Flavobacterium sp. 1 hits
.... uncultured Flavobacterium sp.	3	1	uncultured Flavobacterium sp. hits
.... Flavobacterium aquicola	2	1	Flavobacterium aquicola hits
.... Flavobacterium aquariorum	2	1	Flavobacterium aquariorum hits
.... Flavobacterium franklandianum	2	1	Flavobacterium franklandianum hits
... Chitinophagaceae	5	3	
.... Chitinophagaceae bacterium	1	1	Chitinophagaceae bacterium hits
.... Terrimonas ginsenosidimutans	2	1	Terrimonas ginsenosidimutans hits
... Chitinophaga horti	2	1	Chitinophaga horti hits
... Sphingobacteriales	8	4	
... Pedobacter	7	3	
... Pedobacter sp.	4	1	Pedobacter sp. hits
... Pedobacter mendelii	1	1	Pedobacter mendelii hits
... Pedobacter aquatilis	2	1	Pedobacter aquatilis hits
... Sphingobacteriales bacterium	1	1	Sphingobacteriales bacterium hits
.. Terrabacteria group	24	16	
... Actinomycetes	8	4	
... Micromonospora	5	2	
.... Micromonospora sp. NRRL B-16802	2	1	Micromonospora sp. NRRL B-16802 hits
.... Micromonospora profundi	3	1	Micromonospora profundi hits
... Frankiales bacterium	1	1	Frankiales bacterium hits
... Microbacterium sp. HD4P20	2	1	Microbacterium sp. HD4P20 hits
... Bacillota	11	8	
... Bacillota bacterium	1	1	Bacillota bacterium hits
... Eubacteriales	4	3	
... Defluviitaleaceae bacterium	1	1	Defluviitaleaceae bacterium hits
... Oscillospiraceae bacterium	1	1	Oscillospiraceae bacterium hits
... Clostridium sp. WB02_MRS01	2	1	Clostridium sp. WB02_MRS01 hits
... Phascolarctobacterium sp.	1	1	Phascolarctobacterium sp. hits
... Paenibacillus	5	3	

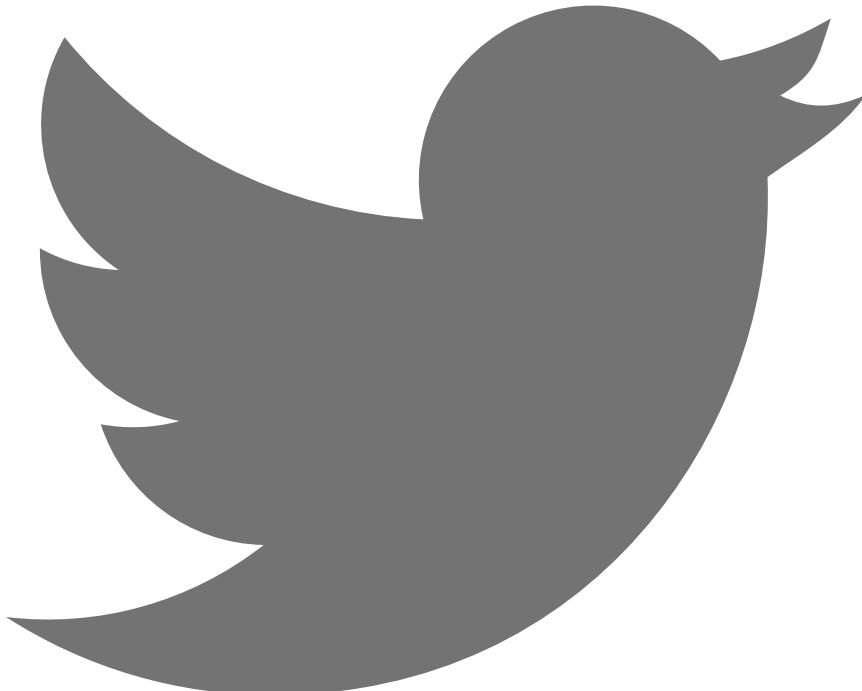


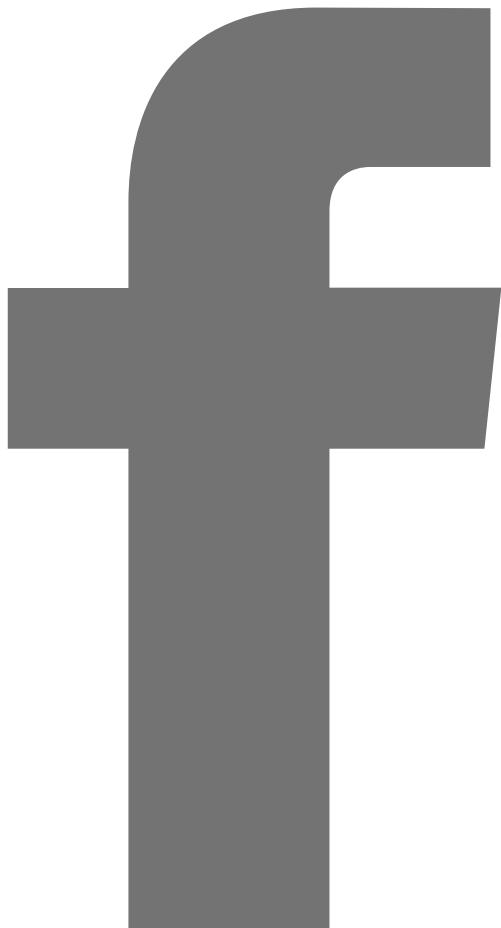
.... Paenibacillus arenosi	<u>2</u>	1	Paenibacillus arenosi hits
.... Paenibacillus assamensis	<u>1</u>	1	Paenibacillus assamensis hits
.... Paenibacillus sp. SC116	<u>2</u>	1	Paenibacillus sp. SC116 hits
... Cyanobacteriota/Melanabacteria group	<u>3</u>	2	
... Candidatus Melainabacteria bacterium	<u>2</u>	1	Candidatus Melainabacteria bacterium hits
... Cyanobacteria bacterium PR.3.49	<u>1</u>	1	Cyanobacteria bacterium PR.3.49 hits
... Chloroflexota	<u>2</u>	2	
... Thermoflexaceae bacterium	<u>1</u>	1	Thermoflexaceae bacterium hits
... Anaerolineae bacterium	<u>1</u>	1	Anaerolineae bacterium hits
.. Spirochaetia	<u>2</u>	2	
... Leptospirales bacterium	<u>1</u>	1	Leptospirales bacterium hits
... Spirochaetales bacterium	<u>1</u>	1	Spirochaetales bacterium hits
.. Myxococcia	<u>7</u>	2	
... Anaeromyxobacter sp. Fw109-5	<u>2</u>	1	Anaeromyxobacter sp. Fw109-5 hits
... Deltaproteobacteria bacterium	<u>5</u>	1	Deltaproteobacteria bacterium hits
.. Synergistaceae bacterium	<u>1</u>	1	Synergistaceae bacterium hits
.. Bdellovibrionales	<u>3</u>	2	
... Bdellovibrionales bacterium	<u>2</u>	1	Bdellovibrionales bacterium hits
... Pseudobdellovibrionaceae bacterium	<u>1</u>	1	Pseudobdellovibrionaceae bacterium hits
.. Verrucomicrobiales bacterium	<u>1</u>	1	Verrucomicrobiales bacterium hits
.. Desulfovibrio sp.	<u>1</u>	1	Desulfovibrio sp. hits
.. candidate division KSB1 bacterium	<u>1</u>	1	candidate division KSB1 bacterium hits
. TACK group	<u>3</u>	3	
.. Ignisphaera aggregans DSM 17230	<u>1</u>	1	Ignisphaera aggregans DSM 17230 hits
.. Candidatus Culexarchaeum yellowstonense	<u>1</u>	1	Candidatus Culexarchaeum yellowstonense hits
.. Candidatus Bathyarchaeota archaeon	<u>1</u>	1	Candidatus Bathyarchaeota archaeon hits
. Eukaryota	<u>48</u>	24	
.. Opisthokonta	<u>11</u>	7	
... Bilateria	<u>7</u>	4	
... Protostomia	<u>5</u>	3	
.... Owenia fusiformis	<u>2</u>	1	Owenia fusiformis hits
.... Ecdysozoa	<u>3</u>	2	
.... Caenorhabditis angaria	<u>1</u>	1	Caenorhabditis angaria hits
.... Rhipicephalus microplus	<u>2</u>	1	Rhipicephalus microplus hits
.... Acanthaster planci	<u>2</u>	1	Acanthaster planci hits
... Mucorineae	<u>4</u>	3	
... Mucoraceae	<u>3</u>	2	
.... Parasitella parasitica	<u>1</u>	1	Parasitella parasitica hits
.... Cokeromyces recurvatus	<u>2</u>	1	Cokeromyces recurvatus hits
... Blakeslea trispora	<u>1</u>	1	Blakeslea trispora hits
.. Streptophytina	<u>37</u>	17	
... Embryophyta	<u>36</u>	16	
... Tracheophyta	<u>33</u>	14	
... Selaginella moellendorffii	<u>8</u>	1	Selaginella moellendorffii hits
... Pentapetalae	<u>25</u>	13	
.... rosids	<u>13</u>	8	
.... Brassicaceae	<u>10</u>	6	
..... Brassica	<u>9</u>	5	
..... Brassica napus	<u>3</u>	1	Brassica napus hits
..... Brassica cretica	<u>2</u>	1	Brassica cretica hits
..... Brassica carinata	<u>1</u>	1	Brassica carinata hits
..... Brassica oleracea	<u>1</u>	2	Brassica oleracea hits
..... Brassica oleracea var. oleracea	<u>2</u>	1	Brassica oleracea var. oleracea hits



..... Hirschfeldia incana	<u>1</u>	1	Hirschfeldia incana hits
..... fabids	<u>3</u>	2	
..... Mercurialis annua	<u>1</u>	1	Mercurialis annua hits
..... Lotus japonicus	<u>2</u>	1	Lotus japonicus hits
..... Caryophyllales	<u>11</u>	4	
..... Chenopodiaceae	<u>9</u>	3	
..... Beta vulgaris subsp. vulgaris	<u>3</u>	1	Beta vulgaris subsp. vulgaris hits
..... Chenopodioideae	<u>6</u>	2	
..... Spinacia oleracea	<u>5</u>	1	Spinacia oleracea hits
..... Chenopodium quinoa	<u>1</u>	1	Chenopodium quinoa hits
..... Amaranthus tricolor	<u>2</u>	1	Amaranthus tricolor hits
.... Lithospermum erythrorhizon	<u>1</u>	1	Lithospermum erythrorhizon hits
... Marchantia	<u>3</u>	2	
.... Marchantia polymorpha	<u>1</u>	2	Marchantia polymorpha hits
.... Marchantia polymorpha subsp. ruderalis	<u>2</u>	1	Marchantia polymorpha subsp. ruderalis hits
... Chara braunii	<u>1</u>	1	Chara braunii hits

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