Your results are filtered to match records with query coverage between 90 and 100.

Job Title	**pdb|6KFS|A**
RID	0BHTFJ0U016 *Search expires on 01-20 00:36 am* Download All
Program	PSI-BLAST Iteration 3 Citation
Database	refseq_protein See details
Query ID	6KFS_A
Description	None
Molecule type	amino acid
Query Length	267
Other reports	Distance tree of results Multiple alignment MSA viewer ?

Filter Results

Organism *only top 20 will appear* ☐ exclude

Type common name, binomial, taxid or group name

+ Add organism

Percent Identity [ ] to [ ] **E value** [ ] to [ ] **Query Coverage** [90] to [100]

PSI-BLAST incl. threshold [1e-40]

Filter | Reset

Run PSI-Blast iteration 4

Number of sequences [500] Run

Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments

Download | New Select columns | Show 500 | ?

115 sequences selected | sequences newly added this iteration ? | GenPept | Graphics | Distance tree of results | Multiple alignment | New MSA Viewer

Sequences with E-value BETTER than threshold

☑ select all *115 sequences selected* Skip to the first new sequence **PSI-BLAST iteration 3**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession	Select for PSI blast	Used to build PSSM	Newly added
predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	Phaeodactylum tricornut…	412	412	95%	1e-139	100.00%	517	XP_002177507.1	☑	✓	
predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	Phaeodactylum tricornut…	388	702	93%	2e-129	59.51%	568	XP_002177506.1	☑	✓	
predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	Phaeodactylum tricornut…	384	695	92%	2e-128	59.51%	545	XP_002177505.1	☑	✓	
predicted protein [Thalassiosira pseudonana CCMP1335]	Thalassiosira pseudonan…	371	371	90%	6e-127	44.86%	297	XP_002297283.1	☑	✓	
predicted protein [Thalassiosira pseudonana CCMP1335]	Thalassiosira pseudonan…	366	366	90%	1e-124	44.44%	310	XP_002297285.1	☑	✓	
predicted protein [Phaeodactylum tricornutum CCAP 1055/1]	Phaeodactylum tricornut…	344	344	90%	1e-116	49.02%	267	XP_002177508.1	☑	✓	
hypothetical protein [Pedobacter cryoconitis]	Pedobacter cryoconitis	322	322	92%	4e-108	31.85%	248	WP_184628527.1	☑	✓	
hypothetical protein [Pedobacter caeni]	Pedobacter caeni	287	287	92%	2e-94	32.26%	248	WP_073235363.1	☑		✓
hypothetical protein [Pedobacter steynii]	Pedobacter steynii	286	286	92%	5e-94	33.47%	248	WP_069380885.1	☑		✓
hypothetical protein [Pedobacter steynii]	Pedobacter steynii	282	282	92%	2e-92	31.05%	248	WP_074610199.1	☑		✓
hypothetical protein [Pedobacter sp. KBW06]	Pedobacter sp. KBW06	278	278	92%	1e-90	31.45%	248	WP_124576869.1	☑		✓
hypothetical protein [Pedobacter sp. Hv1]	Pedobacter sp. Hv1	273	273	91%	1e-88	30.89%	248	WP_055131730.1	☑		✓
hypothetical protein [Pedobacter sp. PACM 27299]	Pedobacter sp. PACM 27…	271	271	92%	4e-88	29.44%	254	WP_062549423.1	☑		✓
hypothetical protein [Pedobacter sp. LMG 31462]	Pedobacter sp. LMG 31462	271	271	92%	4e-88	29.44%	248	WP_182959330.1	☑		✓
hypothetical protein [Runella sp. CRIBMP]	Runella sp. CRIBMP	265	265	91%	1e-85	31.71%	248	WP_166559794.1	☑		✓
hypothetical protein [Runella sp. HYN0085]	Runella sp. HYN0085	265	265	91%	1e-85	31.30%	248	WP_114067546.1	☑		✓
hypothetical protein [Runella sp. YX9]	Runella sp. YX9	264	264	91%	3e-85	31.30%	248	WP_114460255.1	☑		✓
hypothetical protein [Emticicia aquatilis]	Emticicia aquatilis	263	263	91%	7e-85	30.20%	251	WP_188764399.1	☑		✓
hypothetical protein [Spirosoma sp. 209]	Spirosoma sp. 209	263	263	91%	7e-85	31.71%	255	WP_077921918.1	☑		✓
hypothetical protein [Spirosoma sordidisoli]	Spirosoma sordidisoli	263	263	91%	9e-85	32.11%	255	WP_129601184.1	☑		✓
hypothetical protein [Haliscomenobacter hydrossis]	Haliscomenobacter hydr…	261	261	92%	4e-84	33.06%	249	WP_044234271.1	☑		✓
hypothetical protein [Flavobacterium chilense]	Flavobacterium chilense	261	261	91%	5e-84	30.49%	250	WP_068842713.1	☑		✓
hypothetical protein [Flavobacterium sp. ASV13]	Flavobacterium sp. ASV13	261	261	91%	6e-84	30.49%	250	WP_198999553.1	☑		✓
hypothetical protein [Pedobacter sp. LMG 31464]	Pedobacter sp. LMG 31464	260	260	91%	8e-84	30.20%	249	WP_182921498.1	☑		✓
hypothetical protein [Fibrella aestuarina]	Fibrella aestuarina	259	259	91%	2e-83	29.27%	247	WP_015332822.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	258	258	91%	5e-83	29.27%	247	WP_121360601.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	258	258	91%	5e-83	28.46%	249	WP_071634644.1	☑		✓
hypothetical protein [Dyadobacter jejuensis]	Dyadobacter jejuensis	258	258	91%	7e-83	31.71%	247	WP_109673212.1	☑		✓
hypothetical protein [Spirosoma sp. HMF4905]	Spirosoma sp. HMF4905	258	258	92%	8e-83	29.72%	249	WP_157588272.1	☑		✓
hypothetical protein [Flavobacterium sp. CSZ]	Flavobacterium sp. CSZ	257	257	91%	1e-82	29.27%	248	WP_194618990.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	257	257	91%	1e-82	29.27%	247	WP_012026570.1	☑		✓
hypothetical protein [Flavobacterium sp. JRR 20_7]	Flavobacterium sp. JRR …	257	257	91%	1e-82	29.67%	248	WP_121319619.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	256	256	91%	2e-82	29.27%	247	WP_073408386.1	☑		✓
hypothetical protein [Lacibacter sp. S13-6-6]	Lacibacter sp. S13-6-6	256	256	91%	2e-82	30.08%	243	WP_182804567.1	☑		✓
hypothetical protein [Flavobacterium sp. KBS0721]	Flavobacterium sp. KBS0…	256	256	91%	3e-82	29.27%	247	WP_078005321.1	☑		✓
hypothetical protein [Flavobacterium piscis]	Flavobacterium piscis	256	256	91%	4e-82	29.27%	255	WP_065450348.1	☑		✓
hypothetical protein [Flavobacterium hibernum]	Flavobacterium hibernum	254	254	91%	1e-81	30.89%	250	WP_041518387.1	☑		✓
hypothetical protein [Flavobacterium bizetiae]	Flavobacterium bizetiae	254	254	91%	2e-81	30.08%	248	WP_173970031.1	☑		✓
hypothetical protein [Flavobacterium sp. 2]	Flavobacterium sp. 2	254	254	91%	2e-81	28.86%	249	WP_099719401.1	☑		✓
hypothetical protein [Flavobacterium sp. GA093]	Flavobacterium sp. GA093	254	254	91%	2e-81	31.71%	248	WP_160376098.1	☑		✓
hypothetical protein [Flavobacterium plurextorum]	Flavobacterium plurextor…	254	254	91%	2e-81	28.46%	249	WP_089058649.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	253	253	91%	7e-81	30.49%	247	WP_121360438.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	252	252	91%	9e-81	30.49%	247	WP_073408637.1	☑		✓
hypothetical protein [Flavobacterium sp. 245]	Flavobacterium sp. 245	253	253	91%	9e-81	29.27%	249	WP_133527124.1	☑		✓
hypothetical protein [Flavobacterium sp. YO64]	Flavobacterium sp. YO64	252	252	91%	1e-80	28.05%	249	WP_129052752.1	☑		✓
hypothetical protein [Runella defluvii]	Runella defluvii	252	252	91%	1e-80	29.96%	248	WP_183971264.1	☑		✓
hypothetical protein [Chryseobacterium sp. 16F]	Chryseobacterium sp. 16F	252	252	92%	2e-80	29.84%	245	WP_173779818.1	☑		✓
hypothetical protein [Flavobacterium oncorhynchi]	Flavobacterium oncorhyn…	252	252	91%	2e-80	28.05%	249	WP_089053068.1	☑		✓
hypothetical protein [Pedobacter sp. RP-1-13]	Pedobacter sp. RP-1-13	252	252	91%	2e-80	30.61%	248	WP_131554884.1	☑		✓
hypothetical protein [Cellulophaga sp. BC115SP]	Cellulophaga sp. BC115SP	251	251	91%	2e-80	30.36%	247	WP_166549273.1	☑		✓
hypothetical protein [Fluviicola sp. SGL-29]	Fluviicola sp. SGL-29	251	251	91%	2e-80	30.08%	248	WP_163490139.1	☑		✓
hypothetical protein [Flavobacterium johnsoniae]	Flavobacterium johnsoniae	251	251	91%	2e-80	30.49%	247	WP_012026804.1	☑		✓
hypothetical protein [Runella limosa]	Runella limosa	251	251	91%	2e-80	29.96%	248	WP_028521775.1	☑		✓
hypothetical protein [Runella sp. SP2]	Runella sp. SP2	249	249	91%	1e-79	29.96%	248	WP_122929104.1	☑		✓
hypothetical protein [Flavobacterium sp. YO12]	Flavobacterium sp. YO12	249	249	91%	2e-79	27.64%	249	WP_129022758.1	☑		✓
hypothetical protein [Sphingobacterium endophyticum]	Sphingobacterium endop…	248	248	90%	7e-79	30.20%	249	WP_156309406.1	☑		✓
hypothetical protein [Pedobacter sp. LMG 31463]	Pedobacter sp. LMG 31463	247	247	91%	9e-79	28.46%	248	WP_173087507.1	☑		✓
hypothetical protein [Rudanella paleaurantiibacter]	Rudanella paleaurantiiba…	247	247	92%	2e-78	30.52%	255	WP_152124200.1	☑		✓
hypothetical protein [Chryseobacterium sp. 1_F178]	Chryseobacterium sp. 1_…	246	246	91%	2e-78	29.96%	248	WP_115970805.1	☑		✓
hypothetical protein [Sphingobacterium endophyticum]	Sphingobacterium endop…	246	246	90%	3e-78	30.20%	250	WP_197091696.1	☑		✓
hypothetical protein [Sphingobacterium sp. JUb56]	Sphingobacterium sp. JU…	246	246	91%	3e-78	29.96%	248	WP_183916567.1	☑		✓
hypothetical protein [Chitinophaga sp. SYP-B3965]	Chitinophaga sp. SYP-B…	243	243	92%	3e-77	29.44%	248	WP_153657706.1	☑		✓
hypothetical protein [Flavobacterium caeni]	Flavobacterium caeni	243	243	91%	5e-77	27.35%	249	WP_091140989.1	☑		✓
hypothetical protein [Arsenicibacter rosenii]	Arsenicibacter rosenii	241	241	91%	2e-76	29.15%	247	WP_071505270.1	☑		✓
hypothetical protein [Emticicia sp. CRIBPO]	Emticicia sp. CRIBPO	233	233	91%	3e-73	32.65%	249	WP_166563382.1	☑		✓
hypothetical protein [Chitinophaga polysaccharea]	Chitinophaga polysaccha…	233	233	92%	4e-73	29.32%	245	WP_142686817.1	☑		✓
hypothetical protein [Chryseobacterium sp. OV705]	Chryseobacterium sp. O…	228	228	92%	2e-71	28.51%	244	WP_047493470.1	☑		✓
hypothetical protein [Chryseobacterium shigense]	Chryseobacterium shige…	228	228	92%	4e-71	27.71%	247	WP_184160290.1	☑		✓
hypothetical protein [Chryseobacterium sp. YR221]	Chryseobacterium sp. Y…	228	228	92%	5e-71	28.11%	244	WP_084085857.1	☑		✓
hypothetical protein [Elizabethkingia anophelis]	Elizabethkingia anophelis	228	228	92%	6e-71	28.11%	244	WP_106011341.1	☑		✓
hypothetical protein [Chryseobacterium sp. BLS98]	Chryseobacterium sp. BL…	227	227	92%	6e-71	28.11%	244	WP_048503838.1	☑		✓
hypothetical protein [Sphingobacterium sp. DR205]	Sphingobacterium sp. D…	227	227	92%	9e-71	27.71%	246	WP_165307541.1	☑		✓
hypothetical protein [Chryseobacterium rhizosphaerae]	Chryseobacterium rhizos…	227	227	92%	9e-71	28.92%	244	WP_115919248.1	☑		✓
hypothetical protein [Sphingobacterium sp. DR205]	Sphingobacterium sp. D…	226	226	92%	1e-70	28.51%	244	WP_165308671.1	☑		✓
hypothetical protein [Chryseobacterium sp. G0201]	Chryseobacterium sp. G…	226	226	92%	3e-70	29.44%	245	WP_123983592.1	☑		✓
hypothetical protein [Chryseobacterium defluvii]	Chryseobacterium defluvii	225	225	92%	5e-70	27.31%	248	WP_184184064.1	☑		✓
hypothetical protein [Vaginella massiliensis]	Vaginella massiliensis	225	225	91%	6e-70	27.64%	247	WP_068598662.1	☑		✓
hypothetical protein [Chryseobacterium phosphatilyticum]	Chryseobacterium phosp…	225	225	92%	6e-70	26.91%	247	WP_103248721.1	☑		✓
MULTISPECIES: hypothetical protein [Elizabethkingia]	Elizabethkingia	224	224	92%	1e-69	28.11%	245	WP_078674445.1	☑		✓
hypothetical protein [Flavobacterium croceum]	Flavobacterium croceum	223	223	91%	3e-69	28.16%	247	WP_103727191.1	☑		✓
hypothetical protein [Chryseobacterium sp. FH2]	Chryseobacterium sp. FH2	222	222	92%	5e-69	27.71%	244	WP_048510624.1	☑		✓
hypothetical protein [Chryseobacterium elymi]	Chryseobacterium elymi	222	222	92%	5e-69	27.82%	245	WP_116012095.1	☑		✓
hypothetical protein [Sphingobacterium composti Ten et al. 2007 non Yoo et al. 2…	Sphingobacterium comp…	222	222	92%	7e-69	28.51%	245	WP_159635845.1	☑		✓
hypothetical protein [Maribacter sp. T28]	Maribacter sp. T28	221	221	91%	3e-68	29.27%	244	WP_068484510.1	☑		✓
hypothetical protein [Chryseobacterium echinoideorum]	Chryseobacterium echin…	221	221	92%	3e-68	28.23%	246	WP_144282205.1	☑		✓
hypothetical protein [Chryseobacterium hungaricum]	Chryseobacterium hunga…	220	220	92%	4e-68	27.71%	244	WP_089871418.1	☑		✓
hypothetical protein [Chryseobacterium sp. CBTAP 102]	Chryseobacterium sp. C…	219	219	91%	9e-68	28.34%	245	WP_110366918.1	☑		✓
hypothetical protein [Chryseobacterium candidae]	Chryseobacterium candi…	219	219	91%	9e-68	28.34%	245	WP_136523142.1	☑		✓
hypothetical protein [Chitinophaga ginsengisegetis]	Chitinophaga ginsengise…	219	219	92%	1e-67	28.63%	247	WP_079467908.1	☑		✓
hypothetical protein [Chryseobacterium caeni]	Chryseobacterium caeni	218	218	92%	2e-67	27.71%	244	WP_027384690.1	☑		✓
hypothetical protein [Chryseobacterium geocarposphaerae]	Chryseobacterium geoca…	217	217	92%	4e-67	26.61%	245	WP_100375240.1	☑		✓
hypothetical protein [Dyadobacter jiangsuensis]	Dyadobacter jiangsuensis	217	217	92%	6e-67	26.61%	249	WP_106599283.1	☑		✓
hypothetical protein [Chryseobacterium sp. YR460]	Chryseobacterium sp. Y…	217	217	92%	1e-66	27.31%	244	WP_047400736.1	☑		✓
hypothetical protein [Sphingobacterium sp. DR205]	Sphingobacterium sp. D…	213	213	91%	3e-65	27.53%	245	WP_165308567.1	☑		✓
hypothetical protein [Sphingobacterium puteale]	Sphingobacterium puteale	212	212	91%	5e-65	27.94%	245	WP_121122592.1	☑		✓
hypothetical protein [Sphingobacterium athyrii]	Sphingobacterium athyrii	212	212	91%	6e-65	27.13%	245	WP_108635588.1	☑		✓
hypothetical protein [Terrimonas sp. NS-102]	Terrimonas sp. NS-102	211	211	91%	2e-64	28.57%	248	WP_116873322.1	☑		✓
hypothetical protein [Siphonobacter sp. BAB-5404]	Siphonobacter sp. BAB-5…	210	210	92%	3e-64	28.00%	245	WP_106635994.1	☑		✓
hypothetical protein [Nonlabens dokdonensis]	Nonlabens dokdonensis	209	209	91%	7e-64	28.98%	248	WP_015361113.1	☑		✓
hypothetical protein [Chitinophaga parva]	Chitinophaga parva	209	209	91%	1e-63	28.46%	252	WP_108686810.1	☑		✓
hypothetical protein [Leadbetterella byssophila]	Leadbetterella byssophila	208	208	94%	2e-63	28.46%	245	WP_013407705.1	☑		✓
hypothetical protein [Siphonobacter aquaeclarae]	Siphonobacter aquaeclarae	207	207	92%	4e-63	29.44%	245	WP_093196548.1	☑		✓
hypothetical protein [Pseudoflavitalea rhizosphaerae]	Pseudoflavitalea rhizosp…	207	207	90%	4e-63	27.16%	247	WP_127125117.1	☑		✓
hypothetical protein [Pedobacter nyackensis]	Pedobacter nyackensis	206	206	92%	1e-62	26.61%	245	WP_084289446.1	☑		✓
hypothetical protein [Pedobacter antarcticus]	Pedobacter antarcticus	183	183	92%	2e-53	27.49%	254	WP_074591362.1	☑		✓
hypothetical protein [Pedobacter antarcticus]	Pedobacter antarcticus	183	183	92%	2e-53	27.49%	254	WP_037437692.1	☑		✓
hypothetical protein [Cecembia rubra]	Cecembia rubra	179	179	92%	5e-52	33.47%	255	WP_106567585.1	☑		✓
hypothetical protein [Cecembia calidifontis]	Cecembia calidifontis	179	179	92%	8e-52	33.07%	255	WP_130277659.1	☑		✓
hypothetical protein [Methylobacter tundripaludum]	Methylobacter tundripalu…	176	176	91%	9e-51	26.94%	253	WP_104422403.1	☑		✓
hypothetical protein [Methylobacter tundripaludum]	Methylobacter tundripalu…	174	174	91%	8e-50	26.32%	253	WP_036244726.1	☑		✓
hypothetical protein [Methylobacter tundripaludum]	Methylobacter tundripalu…	174	174	91%	8e-50	26.32%	253	WP_036305061.1	☑		✓
hypothetical protein [Methylobacter tundripaludum]	Methylobacter tundripalu…	173	173	91%	1e-49	26.32%	253	WP_006893469.1	☑		✓
hypothetical protein [Methylobacter tundripaludum]	Methylobacter tundripalu…	173	173	91%	2e-49	26.02%	253	WP_104428652.1	☑		✓
hypothetical protein [Algoriphagus resistens]	Algoriphagus resistens	170	170	91%	2e-48	26.53%	248	WP_057937867.1	☑		✓
hypothetical protein [Arcticibacter pallidicorallinus]	Arcticibacter pallidicoralli…	169	169	90%	6e-48	30.45%	254	WP_106290784.1	☑		✓

Run PSI-BLAST Iteration 4 with max number of sequences [500] Run