Phyre^2

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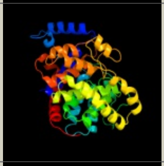
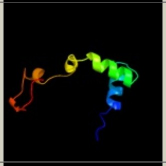
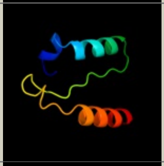
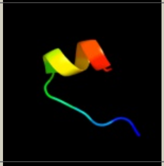
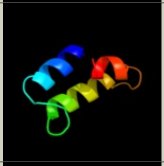
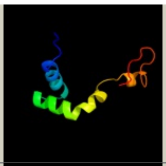
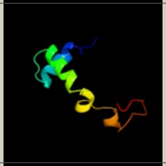
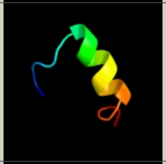
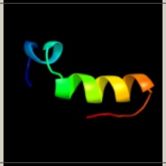
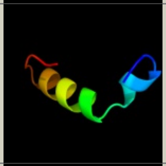
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3g9dB_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dinitrogenase reductase activacting **PDBTitle:** crystal structure glycohydrolase
2	c2wocA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosyl-[dinitrogen reductase] glycohydrolase; **PDBTitle:** crystal structure of the dinitrogenase reductase-activating2 glycohydrolase (drag) from rhodospirillum rubrum
3	d1t5ja_	Alignment		100.0	29	**Fold:**ADP-ribosylglycohydrolase **Superfamily:**ADP-ribosylglycohydrolase **Family:**ADP-ribosylglycohydrolase
4	c3hfwA_	Alignment		100.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein adp-ribosylarginine hydrolase; **PDBTitle:** crystal structure of human adp-ribosylhydrolase 1 (harh1)
5	c2qtyB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(adp-ribose) glycohydrolase arh3; **PDBTitle:** crystal structure of mouse adp-ribosylhydrolase 3 (marh3)
6	c2yzwA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adp-ribosylglycohydrolase; **PDBTitle:** adp-ribosylglycohydrolase-related protein complex
7	d2i7na2	Alignment		19.1	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
8	d1j9ja_	Alignment		16.8	24	**Fold:**SurE-like **Superfamily:**SurE-like **Family:**SurE-like
9	c2odbB_	Alignment		15.8	29	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
10	d1mw7a_	Alignment		14.3	25	**Fold:**YebC-like **Superfamily:**YebC-like **Family:**YebC-like
11	c1e0aB_	Alignment		13.1	17	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase

12	c3smpA_	Alignment		11.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 1; **PDBTitle:** monoclinic crystal structure of human pantothenate kinase 1 alpha
13	d2i7pa1	Alignment		11.4	12	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Fumble-like
14	c1f3mB_	Alignment		10.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
15	c1ceeB_	Alignment		9.5	30	**PDB header:**structural protein regulation **Chain:** B: **PDB Molecule:**wiskott-aldrich syndrome protein wasp; **PDBTitle:** solution structure of cdc42 in complex with the gtpase2 binding domain of wasp
16	c2phjA_	Alignment		9.2	35	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of sure protein from aquifex aeolicus
17	c2i7pA_	Alignment		8.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pantothenate kinase 3; **PDBTitle:** crystal structure of human pank3 in complex with accoa
18	c2j0wA_	Alignment		8.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lysine-sensitive aspartokinase 3; **PDBTitle:** crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
19	c2e6gI_	Alignment		8.3	38	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**5'-nucleotidase sure; **PDBTitle:** crystal structure of the stationary phase survival protein sure from2 thermus thermophilus hb8 in complex with phosphate
20	c3c9pA_	Alignment		8.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
21	c1ir6A_	Alignment	not modelled	8.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease recj; **PDBTitle:** crystal structure of exonuclease recj bound to manganese
22	d1ir6a_	Alignment	not modelled	8.0	13	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Exonuclease RecJ
23	c3bowC_	Alignment	not modelled	7.8	25	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** C: **PDB Molecule:**calpastatin; **PDBTitle:** structure of m-calpain in complex with calpastatin
24	d2j0wa1	Alignment	not modelled	7.7	25	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
25	c3devB_	Alignment	not modelled	7.5	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**sh1221; **PDBTitle:** crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
26	c1w6kA_	Alignment	not modelled	6.8	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**lanosterol synthase; **PDBTitle:** structure of human osc in complex with lanosterol
27	c2ogxB_	Alignment	not modelled	6.7	18	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**molybdenum storage protein subunit beta; **PDBTitle:** the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
28	d1ykwa1	Alignment	not modelled	6.6	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain

29	c2k42A_	Alignment	not modelled	5.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**wiskott-aldrich syndrome protein; **PDBTitle:** solution structure of the gtpase binding domain of wasp in2 complex with espfu, an ehec effector
30	c3ab4K_	Alignment	not modelled	5.7	31	**PDB header:**transferase **Chain:** K: **PDB Molecule:**aspartokinase; **PDBTitle:** crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
31	c2ap7A_	Alignment	not modelled	5.6	43	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**bombinin h2; **PDBTitle:** solution structure of bombinin h2 in dpc micelles
32	d2cdqa1	Alignment	not modelled	5.6	19	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
33	c2v4oB_	Alignment	not modelled	5.6	38	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**multifunctional protein sur e; **PDBTitle:** crystal structure of salmonella typhimurium sure at 2.752 angstrom resolution in monoclinic form
34	d1w6ka1	Alignment	not modelled	5.5	10	**Fold:**alpha/alpha toroid **Superfamily:**Terpenoid cyclases/Protein prenyltransferases **Family:**Terpene synthases
35	d2gpia1	Alignment	not modelled	5.4	10	**Fold:**Shew3726-like **Superfamily:**Shew3726-like **Family:**Shew3726-like
36	d2hmfa1	Alignment	not modelled	5.3	25	**Fold:**Carbamate kinase-like **Superfamily:**Carbamate kinase-like **Family:**PyrH-like
37	d1ekqa_	Alignment	not modelled	5.3	19	**Fold:**Ribokinase-like **Superfamily:**Ribokinase-like **Family:**Thiamin biosynthesis kinases
38	c3ll9A_	Alignment	not modelled	5.0	6	**PDB header:**transferase **Chain:** A: **PDB Molecule:**isopentenyl phosphate kinase; **PDBTitle:** x-ray structures of isopentenyl phosphate kinase