Phyre2

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Description	P0ABX5
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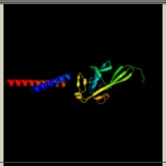
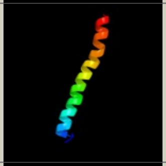
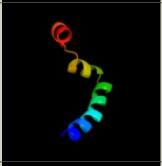
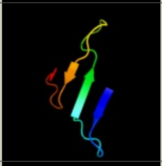
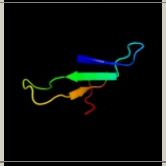
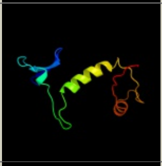
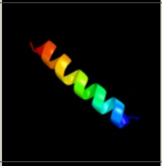
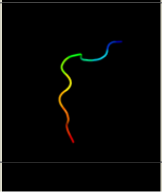
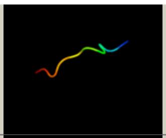
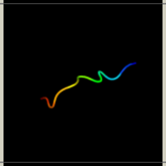
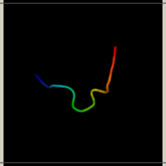
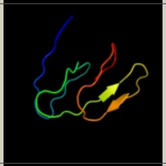
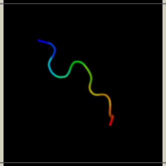
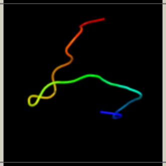
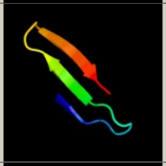
Unique Job ID	fbc72de219bf138c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a69A_	Alignment		100.0	51	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar hook protein flge; **PDBTitle:** atomic model of the bacterial flagellar hook based on2 docking an x-ray derived structure and terminal two alpha-3 helices into an 7.1 angstrom resolution cryoem map
2	d1wlga_	Alignment		100.0	46	**Fold:**Flagellar hook protein flgE **Superfamily:**Flagellar hook protein flgE **Family:**Flagellar hook protein flgE
3	d1ucua_	Alignment		85.1	21	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
4	c1jzdA_	Alignment		49.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** dsbc-dsbdalpha complex
5	c1oryB_	Alignment		35.5	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**flagellin; **PDBTitle:** flagellar export chaperone in complex with its cognate binding partner
6	c1zxuA_	Alignment		28.2	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g01750 protein; **PDBTitle:** x-ray structure of protein from arabidopsis thaliana2 at5g01750
7	d2q4ma1	Alignment		28.2	17	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**At5g01750-like
8	c1t3bA_	Alignment		28.1	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbc; **PDBTitle:** x-ray structure of dsbc from haemophilus influenzae
9	c3k8vB_	Alignment		27.6	18	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c20
10	d1niga_	Alignment		17.9	24	**Fold:**Ferritin-like **Superfamily:**Cobalamin adenosyltransferase-like **Family:**Hypothetical protein Ta1238
11	d1lvoa_	Alignment		15.8	36	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold

12	c2q6fB_	Alignment		15.2	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**infectious bronchitis virus (ibv) main protease; **PDBTitle:** crystal structure of infectious bronchitis virus (ibv) main2 protease in complex with a michael acceptor inhibitor n3
13	c3d23A_	Alignment		12.6	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like proteinase; **PDBTitle:** main protease of hcov-hku1
14	d2duca1	Alignment		12.6	27	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
15	c3kglB_	Alignment		10.6	20	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**cruciferin; **PDBTitle:** crystal structure of procruciferin, 11s globulin from2 brassica napus
16	d1t3ba2	Alignment		10.1	15	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
17	d1p9sa_	Alignment		10.1	18	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
18	d2v4jc1	Alignment		9.8	42	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
19	c2oqkA_	Alignment		9.3	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
20	d1eeja2	Alignment		8.3	23	**Fold:**Cystatin-like **Superfamily:**DsbC/DsbG N-terminal domain-like **Family:**DsbC/DsbG N-terminal domain-like
21	d1ji8a_	Alignment	not modelled	7.9	21	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase
22	d1b2pa_	Alignment	not modelled	7.8	12	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
23	c2iyjA_	Alignment	not modelled	7.8	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**thiol disulfide interchange protein dsbc; **PDBTitle:** crystal structure of the n-terminal dimer domain of e.coli2 dsbc
24	c2dgyA_	Alignment	not modelled	7.8	14	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
25	d2czra1	Alignment	not modelled	7.4	32	**Fold:**Restriction endonuclease-like **Superfamily:**TBP-interacting protein-like **Family:**TBP-interacting protein-like
26	c3bk2A_	Alignment	not modelled	7.2	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**metal dependent hydrolase; **PDBTitle:** crystal structure analysis of the rnase j/ump complex
27	c2cazF_	Alignment	not modelled	6.2	9	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**protein srn2; **PDBTitle:** escrt-i core
28	c1fxzC_	Alignment	not modelled	6.0	18	**PDB header:**plant protein **Chain:** C: **PDB Molecule:**glycinin g1; **PDBTitle:** crystal structure of soybean proglycinin a1ab1b homotrimer
29	c2a5wC_	Alignment	not modelled	6.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfite reductase, desulfoviridin-type subunit gamma

						PDBTitle: crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
30	c3kscD_	Alignment	not modelled	5.9	20	**PDB header:**plant protein **Chain:** D: **PDB Molecule:**lega class; **PDBTitle:** crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
31	d2enga_	Alignment	not modelled	5.9	35	**Fold:**Double psi beta-barrel **Superfamily:**Barwin-like endoglucanases **Family:**Eng V-like
32	d2c5ra1	Alignment	not modelled	5.5	33	**Fold:**Phage replication organizer domain **Superfamily:**Phage replication organizer domain **Family:**Phage replication organizer domain
33	d1fxza2	Alignment	not modelled	5.5	19	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
34	c1yx3A_	Alignment	not modelled	5.3	36	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
35	c2kjzA_	Alignment	not modelled	5.2	29	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**atc0852; **PDBTitle:** solution nmr structure of protein atc0852 from agrobacterium2 tumefaciens. northeast structural genomics consortium (nesg) target3 att2.