Phyre^2

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Description	P26608
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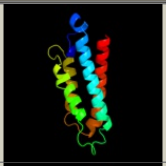
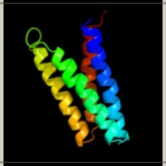
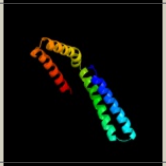
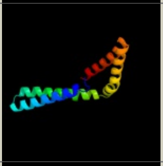
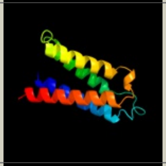
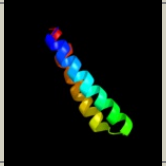
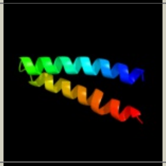
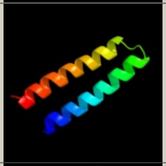
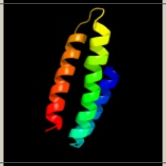
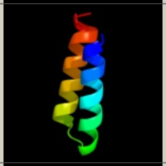
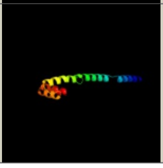
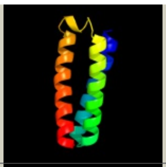
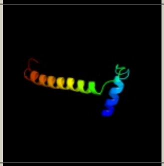
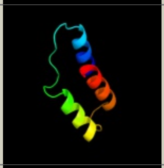
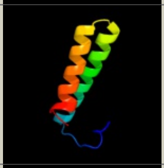
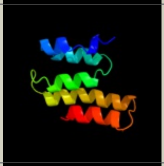
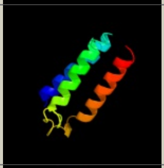
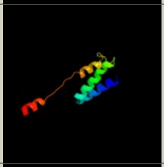
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1orja_	Alignment		100.0	23	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
2	c3k1iA_	Alignment		100.0	27	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**flagellar protein; **PDBTitle:** crystal strcture of flis-hp1076 complex in h. pylori
3	c1vh6A_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**flagellar protein flis; **PDBTitle:** crystal structure of a flagellar protein
4	d1vh6a_	Alignment		100.0	34	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
5	d1orjb_	Alignment		100.0	22	**Fold:**Four-helical up-and-down bundle **Superfamily:**Flagellar export chaperone FliS **Family:**Flagellar export chaperone FliS
6	d2nw8a1	Alignment		46.8	12	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Bacterial tryptophan 2,3-dioxygenase
7	c2noxP_	Alignment		45.9	16	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**tryptophan 2,3-dioxygenase; **PDBTitle:** crystal structure of tryptophan 2,3-dioxygenase from ralstonia2 metallidurans
8	c2nw7C_	Alignment		42.6	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**tryptophan 2,3-dioxygenase; **PDBTitle:** crystal structure of tryptophan 2,3-dioxygenase (tdo) from2 xanthomonas campestris in complex with ferric heme.3 northeast structural genomics target xcr13
9	d1x91a_	Alignment		25.7	11	**Fold:**Bromodomain-like **Superfamily:**Plant invertase/pectin methylesterase inhibitor **Family:**Plant invertase/pectin methylesterase inhibitor
10	c3mhvA_	Alignment		24.6	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein vta1; **PDBTitle:** crystal structure of vps4 and vta1
11	c3opcB_	Alignment		18.7	17	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of flgn chaperone from bordetella pertussis

12	c3rauB_	Alignment		16.9	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**tyrosine-protein phosphatase non-receptor type 23; **PDBTitle:** crystal structure of the hd-ptp bro1 domain
13	c3o3nB_	Alignment		16.4	4	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
14	d2e9xb1	Alignment		15.5	20	**Fold:**GINS helical bundle-like **Superfamily:**GINS helical bundle-like **Family:**PSF2 C-terminal domain-like
15	d2pmra1	Alignment		13.1	9	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**AF1782-like **Family:**AF1782-like
16	c2wpvG_	Alignment		11.3	22	**PDB header:**protein binding **Chain:** G: **PDB Molecule:**upf0363 protein yor164c; **PDBTitle:** crystal structure of s. cerevisiae get4-get5 complex
17	c1zb1A_	Alignment		10.9	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**bro1 protein; **PDBTitle:** structure basis for endosomal targeting by the bro1 domain
18	c2rklB_	Alignment		10.7	11	**PDB header:**lipid transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein vta1; **PDBTitle:** crystal structure of s.cerevisiae vta1 c-terminal domain
19	c3n71A_	Alignment		10.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**histone lysine methyltransferase smyd1; **PDBTitle:** crystal structure of cardiac specific histone methyltransferase smyd1
20	c1nvpB_	Alignment		9.6	13	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription initiation factor iia alpha chain; **PDBTitle:** human tfiia/tbp/dna complex
21	d1nvpb_	Alignment	not modelled	9.6	13	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
22	c2xzeA_	Alignment	not modelled	9.0	12	**PDB header:**hydrolase/protein transport **Chain:** A: **PDB Molecule:**stam-binding protein; **PDBTitle:** structural basis for amsh-escrt-iii chmp3 interaction
23	c2dl1A_	Alignment	not modelled	9.0	9	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**spartin; **PDBTitle:** solution structure of the mit domain from human spartin
24	c2v6yA_	Alignment	not modelled	8.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aaa family atpase, p60 katanin; **PDBTitle:** structure of the mit domain from a s. solfataricus vps4-2 like atpase
25	d1z6om1	Alignment	not modelled	8.1	15	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
26	c2e9xF_	Alignment	not modelled	7.8	19	**PDB header:**replication **Chain:** F: **PDB Molecule:**dna replication complex gins protein psf2; **PDBTitle:** the crystal structure of human gins core complex
27	c2v6xA_	Alignment	not modelled	7.5	5	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** stractural insight into the interaction between escrt-iii2 and vps4
28	c2nuxB_	Alignment	not modelled	7.3	7	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate **PDBTitle:** 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution

29	c2yruA_	Alignment	not modelled	7.3	5	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**steroid receptor rna activator 1; **PDBTitle:** solution structure of mouse steroid receptor rna activator2 1 (sra1) protein
30	c3kh1B_	Alignment	not modelled	6.2	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**predicted metal-dependent phosphohydrolase; **PDBTitle:** crystal structure of predicted metal-dependent2 phosphohydrolase (zp_00055740.2) from magnetospirillum3 magnetotacticum ms-1 at 1.37 a resolution
31	d2ijqa1	Alignment	not modelled	6.2	9	**Fold:**Hyaluronidase domain-like **Superfamily:**TTHA0068-like **Family:**TTHA0068-like
32	c1rm1C_	Alignment	not modelled	5.6	12	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription initiation factor iia large chain; **PDBTitle:** structure of a yeast tfiia/tbp/tata-box dna complex
33	d2za7a1	Alignment	not modelled	5.5	21	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Ferritin
34	d2g5ca1	Alignment	not modelled	5.4	11	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**TyrA dimerization domain-like
35	c3e6sD_	Alignment	not modelled	5.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ferritin; **PDBTitle:** crystal structure of ferritin soaked with iron from pseudo-2 nitzschia multiseries