Phyre^2

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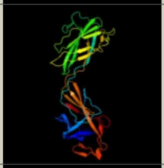
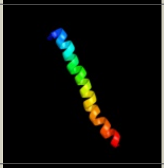
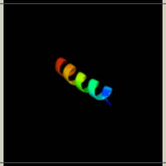
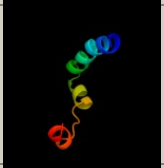
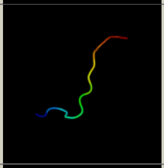
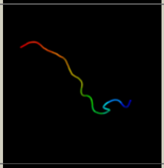
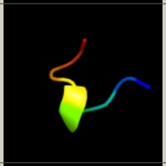
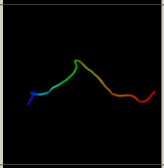
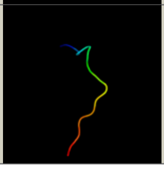
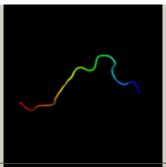
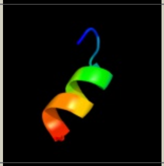
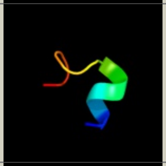
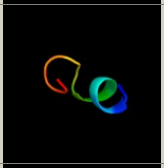
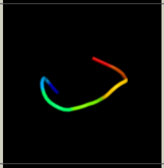
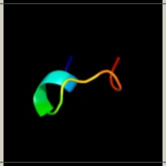
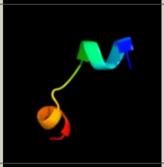
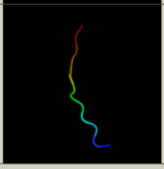
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3a69A_	Alignment		100.0	85	**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		99.9	84	**Fold:**Flagellar hook protein flgE **Superfamily:**Flagellar hook protein flgE **Family:**Flagellar hook protein flgE
3	c2d4yA_	Alignment		97.0	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**flagellar hook-associated protein 1; **PDBTitle:** crystal structure of a 49k fragment of hap1 (flgk)
4	d1ucua_	Alignment		92.7	24	**Fold:**Phase 1 flagellin **Superfamily:**Phase 1 flagellin **Family:**Phase 1 flagellin
5	c3k8vB_	Alignment		53.8	30	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**flagellin homolog; **PDBTitle:** crysatl structure of a bacterial cell-surface flagellin n20c20
6	c1oryB_	Alignment		29.7	22	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**flagellin; **PDBTitle:** flagellar export chaperone in complex with its cognate binding partner
7	d1lvoa_	Alignment		13.3	27	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
8	c2q6fB_	Alignment		12.9	33	**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
9	d1nrja_	Alignment		12.6	56	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**SRP alpha N-terminal domain-like
10	d1p9sa_	Alignment		11.4	20	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
11	c3d23A_	Alignment		9.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3c-like proteinase; **PDBTitle:** main protease of hcov-hku1

12	d2duca1	Alignment		9.4	20	**Fold:**Trypsin-like serine proteases **Superfamily:**Trypsin-like serine proteases **Family:**Viral cysteine protease of trypsin fold
13	d2npta1	Alignment		8.9	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
14	d2goma1	Alignment		6.6	17	**Fold:**Spectrin repeat-like **Superfamily:**Efb C-domain-like **Family:**Efb C-domain-like
15	c1q8hA_	Alignment		6.4	38	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**osteocalcin; **PDBTitle:** crystal structure of porcine osteocalcin
16	d1q8ha_	Alignment		6.4	38	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
17	c3j0gO_	Alignment		6.3	29	**PDB header:**virus **Chain:** O: **PDB Molecule:**e3 protein; **PDBTitle:** homology model of e3 protein of venezuelan equine encephalitis virus2 tc-83 strain fitted with a cryo-em map
18	d1q3ma_	Alignment		6.2	38	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
19	c3ikmD_	Alignment		6.1	35	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
20	d2dlda2	Alignment		6.0	0	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
21	d2g3qa1	Alignment	not modelled	5.9	27	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**UBA domain
22	c3m9hB_	Alignment	not modelled	5.8	26	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain of the2 mycobacterium tuberculosis proteasomal atpase mpa