Phyre^2

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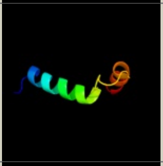
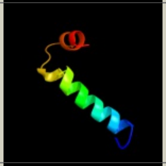
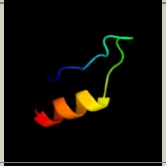
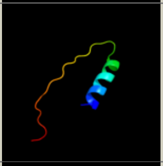
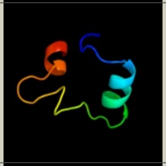
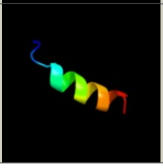
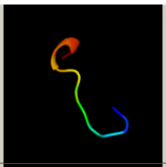
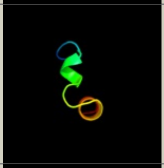
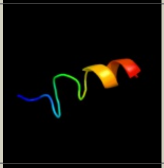
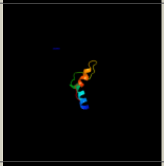
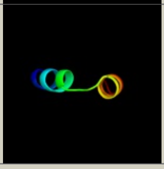
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c4rC_	Alignment		100.0	36	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharacterized protein encoded by2 cryptic prophage
2	c2qxvB_	Alignment		21.3	75	**PDB header:**gene regulation **Chain:** B: **PDB Molecule:**enhancer of zeste homolog 2; **PDBTitle:** structural basis of ezh2 recognition by eed
3	d1y7qa1	Alignment		19.9	12	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**SCAN domain
4	d2fi2a1	Alignment		19.7	15	**Fold:**Acyl carrier protein-like **Superfamily:**Retrovirus capsid dimerization domain-like **Family:**SCAN domain
5	c3lhrA_	Alignment		15.7	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**zinc finger protein 24; **PDBTitle:** crystal structure of the scan domain from human znf24
6	c3l6aA_	Alignment		15.6	17	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 4 gamma 2; **PDBTitle:** crystal structure of the c-terminal region of human p97
7	c3e96B_	Alignment		13.9	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
8	c2ek0B_	Alignment		12.5	12	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**stage v sporulation protein s (spovs) related protein; **PDBTitle:** stage v sporolation protein s (spovs) from thermus thermophilus zinc2 form
9	c2l53B_	Alignment		11.5	40	**PDB header:**ca-binding protein/proton transport **Chain:** B: **PDB Molecule:**voltage-gated sodium channel type v alpha isoform b **PDBTitle:** solution nmr structure of apo-calmodulin in complex with the iq motif2 of human cardiac sodium channel nav1.5
10	c3bd1B_	Alignment		10.3	27	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
11	d1pu1a_	Alignment		9.4	12	**Fold:**Hypothetical protein MTH677 **Superfamily:**Hypothetical protein MTH677 **Family:**Hypothetical protein MTH677

12	c3fggA_	Alignment		8.7	45	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bce2196; **PDBTitle:** crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
13	d2a2ja1	Alignment		8.5	24	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
14	d1tp6a_	Alignment		8.1	30	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**PA1314-like
15	c2kxwB_	Alignment		8.0	33	**PDB header:**calcium-binding protein/metal transport **Chain:** B: **PDB Molecule:**sodium channel protein type 2 subunit alpha; **PDBTitle:** structure of the c-domain fragment of apo calmodulin bound to the iq2 motif of nav1.2
16	c1xdtT_	Alignment		7.4	26	**PDB header:**complex (toxin/growth factor) **Chain:** T: **PDB Molecule:**diphtheria toxin; **PDBTitle:** complex of diphtheria toxin and heparin-binding epidermal growth2 factor
17	d1ijwc_	Alignment		7.0	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
18	d2nr5a1	Alignment		7.0	20	**Fold:**Ferritin-like **Superfamily:**SO2669-like **Family:**SO2669-like
19	d1ug3a2	Alignment		6.7	24	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
20	c2ow7A_	Alignment		6.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-mannosidase 2; **PDBTitle:** golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
21	d1hcra_	Alignment	not modelled	6.4	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
22	c2gqcA_	Alignment	not modelled	5.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rhomboid intramembrane protease; **PDBTitle:** solution structure of the n-terminal domain of rhomboid intramembrane2 protease from p. aeruginosa
23	d1i74a_	Alignment	not modelled	5.5	38	**Fold:**DHH phosphoesterases **Superfamily:**DHH phosphoesterases **Family:**Manganese-dependent inorganic pyrophosphatase (family II)