Phyre2

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Description	RVBD3312A_(-)_3700876_3701187
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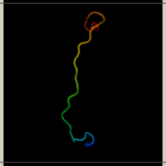
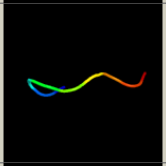
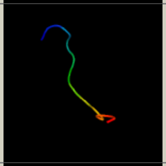
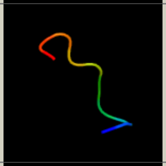
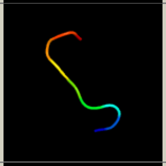
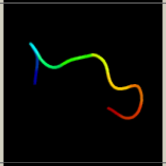
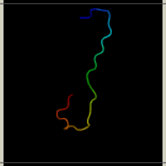
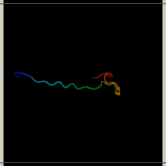
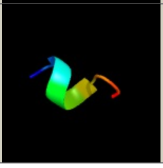
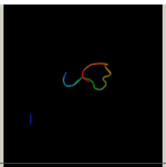
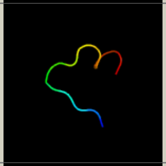
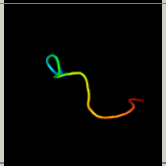
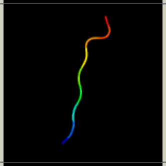
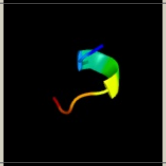
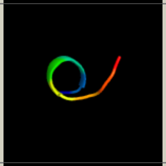
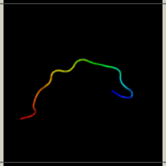
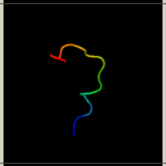
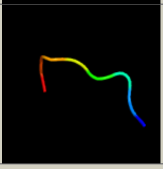
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1pgsA_	Alignment		48.3	44	**PDB header:**endoglycosidase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-d-glucosaminyl) **PDBTitle:** the three-dimensional structure of pngase f, a2 glycosylasparaginase from flavobacterium meningosepticum
2	d1pgsa2	Alignment		34.3	63	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**PHM/PNGase F **Family:**Glycosyl-asparaginase
3	c6mizC_	Alignment		27.4	23	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**transient receptor potential cation channel subfamily m **PDBTitle:** human trpm2 ion channel in an adpr-bound state
4	c3ks7D_	Alignment		25.0	56	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative putative pngase f; **PDBTitle:** crystal structure of putative peptide:n-glycosidase f (pngase f)2 (yp_210507.1) from bacteroides fragilis nctc 9343 at 2.30 a3 resolution
5	c4m1xB_	Alignment		15.9	54	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein 201phi2-1p060; **PDBTitle:** tetrameric ring structure of 201phi2-1p060 from pseudomonas phage2 201phi2-1
6	d1dkga1	Alignment		15.0	30	**Fold:**Head domain of nucleotide exchange factor GrpE **Superfamily:**Head domain of nucleotide exchange factor GrpE **Family:**Head domain of nucleotide exchange factor GrpE
7	c3lnoA_	Alignment		13.2	22	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of domain of unknown function duf59 from2 bacillus anthracis
8	c1dkgB_	Alignment		13.2	30	**PDB header:**complex (hsp24/hsp70) **Chain:** B: **PDB Molecule:**nucleotide exchange factor grpe; **PDBTitle:** crystal structure of the nucleotide exchange factor grpe2 bound to the atpase domain of the molecular chaperone dnak
9	c3oruA_	Alignment		12.5	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**duf1989 family protein; **PDBTitle:** crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution
10	d1q33a_	Alignment		12.2	31	**Fold:**Nudix **Superfamily:**Nudix **Family:**MutT-like
11	d2ccya_	Alignment		10.9	44	**Fold:**Four-helical up-and-down bundle **Superfamily:**Cytochromes **Family:**Cytochrome c'-like

12	c1iyjC_	Alignment		10.0	44	**PDB header:**gene regulation/antitumor protein **Chain:** C: **PDB Molecule:**deleted in split hand/split foot protein 1; **PDBTitle:** structure of a brca2-dss1 complex
13	d1g7ea_	Alignment		9.3	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**ERP29 N domain-like
14	c6gvwJ_	Alignment		8.6	67	**PDB header:**signaling protein **Chain:** J: **PDB Molecule:**brca1-a complex subunit rap80; **PDBTitle:** crystal structure of the brca1-a complex
15	c2jobA_	Alignment		8.5	44	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**antilipopolysaccharide factor; **PDBTitle:** solution structure of an antilipopolysaccharide factor from2 shrimp and its possible lipid a binding site
16	c4ulvB_	Alignment		8.0	50	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**cytochrome c, class ii; **PDBTitle:** cytochrome c prime from shewanella frigidimarina
17	c6a3kA_	Alignment		7.5	50	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of cytochrome c' from shewanella benthica db6705
18	c2nasA_	Alignment		6.8	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of a pwwp doamin from trypanosoma brucei
19	c3t5xB_	Alignment		6.8	50	**PDB header:**transcription **Chain:** B: **PDB Molecule:**26s proteasome complex subunit dss1; **PDBTitle:** pcid2:dss1 structure
20	c4aniA_	Alignment		6.1	63	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**protein grpe; **PDBTitle:** structural basis for the intermolecular communication between2 dnak and grpe in the dnak chaperone system from3 geobacillus kaustophilus hta426
21	c1dmlD_	Alignment	not modelled	5.9	37	**PDB header:**dna binding protein/transferase **Chain:** D: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
22	c1dmlB_	Alignment	not modelled	5.9	37	**PDB header:**dna binding protein/transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
23	c1dmlF_	Alignment	not modelled	5.8	37	**PDB header:**dna binding protein/transferase **Chain:** F: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
24	c1dmlH_	Alignment	not modelled	5.8	37	**PDB header:**dna binding protein/transferase **Chain:** H: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of herpes simplex ul42 bound to the c-terminus of2 hsv pol
25	d1lcsa_	Alignment	not modelled	5.6	50	**Fold:**ENV polyprotein, receptor-binding domain **Superfamily:**ENV polyprotein, receptor-binding domain **Family:**ENV polyprotein, receptor-binding domain
26	d1qmga2	Alignment	not modelled	5.3	36	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
27	c3t5vC_	Alignment	not modelled	5.2	50	**PDB header:**transcription **Chain:** C: **PDB Molecule:**26s proteasome complex subunit sem1; **PDBTitle:** sac3:thp1:sem1 complex