Phyre^2

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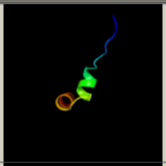
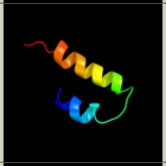
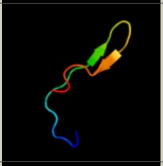
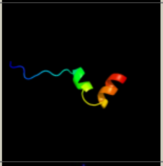
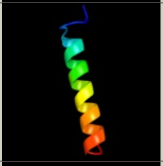
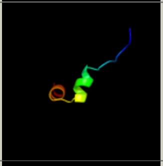
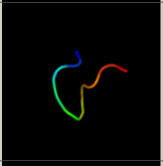
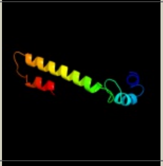
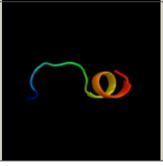
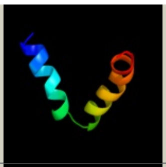
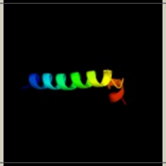
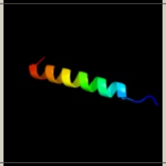
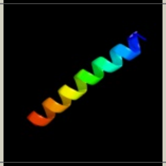
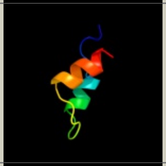
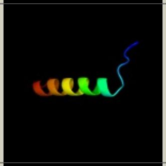
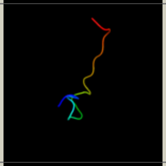
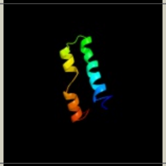
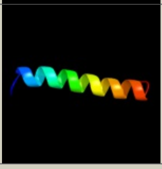
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a6ca1	Alignment		69.0	22	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Comoviridae-like VP
2	d1wiia_	Alignment		20.5	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Putative zinc binding domain
3	c2p7vA_	Alignment		17.5	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**regulator of sigma d; **PDBTitle:** crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
4	c2gk9D_	Alignment		16.1	45	**PDB header:**transferase **Chain:** D: **PDB Molecule:**phosphatidylinositol-4-phosphate 5-kinase, type **PDBTitle:** human phosphatidylinositol-4-phosphate 5-kinase, type ii,2 gamma
5	c1a6cA_	Alignment		16.0	22	**PDB header:**virus **Chain:** A: **PDB Molecule:**tobacco ringspot virus capsid protein; **PDBTitle:** structure of tobacco ringspot virus
6	c2q9lA_	Alignment		16.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of imazg from vibrio dat 722: ctag-imazg (p43212)
7	c3dl8D_	Alignment		14.0	44	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**sece; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
8	c2y7uM_	Alignment		13.5	15	**PDB header:**virus **Chain:** M: **PDB Molecule:**coat protein; **PDBTitle:** x-ray structure of the grapevine fanleaf virus
9	d1dxqa_	Alignment		11.3	50	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
10	c3aq0G_	Alignment		11.3	11	**PDB header:**transferase **Chain:** G: **PDB Molecule:**geranyl diphosphate synthase; **PDBTitle:** ligand-bound form of arabidopsis medium/long-chain length prenyl2 pyrophosphate synthase (surface polar residue mutant)
11	d1cmca_	Alignment		11.2	43	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Met repressor, MetJ (MetR)

12	d2id6a2	Alignment		11.2	18	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
13	c3obcB_	Alignment		10.2	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**pyrophosphatase; **PDBTitle:** crystal structure of a pyrophosphatase (af1178) from archaeoglobus2 fulgidus at 1.80 a resolution
14	d2gtaa1	Alignment		9.8	8	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
15	d2oiea1	Alignment		9.6	23	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
16	c3a9fA_	Alignment		9.5	10	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**cytochrome c; **PDBTitle:** crystal structure of the c-terminal domain of cytochrome cz2 from chlorobium tepidum
17	d2gtad1	Alignment		9.4	8	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
18	c2f3iA_	Alignment		9.2	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 17.1 **PDBTitle:** solution structure of a subunit of rna polymerase ii
19	d1np3a1	Alignment		8.7	21	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Acetohydroxy acid isomeroreductase (ketol-acid reductoisomerase, KARI)
20	d1vmga_	Alignment		8.5	19	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
21	d1ebfa1	Alignment	not modelled	8.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
22	c2khsB_	Alignment	not modelled	7.9	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nuclease; **PDBTitle:** solution structure of snase121:snase(111-143) complex
23	c2l5fA_	Alignment	not modelled	7.6	10	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**pre-mrna-processing factor 40 homolog a; **PDBTitle:** solution structure of the tandem ww domains from hypa/fbp11
24	c2q4pA_	Alignment	not modelled	7.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein rs21-c6; **PDBTitle:** ensemble refinement of the crystal structure of protein from mus2 musculus mm.29898
25	d2a3qa1	Alignment	not modelled	7.2	18	**Fold:**all-alpha NTP pyrophosphatases **Superfamily:**all-alpha NTP pyrophosphatases **Family:**MazG-like
26	c3lj4i_	Alignment	not modelled	7.0	10	**PDB header:**viral protein **Chain:** I: **PDB Molecule:**portal protein; **PDBTitle:** bacteriophage p22 portal protein bound to middle tail factor gp4. this2 file contain the first biological assembly
27	c3iz5W_	Alignment	not modelled	6.1	39	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**60s ribosomal protein l22 (l22e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
28	c3p7jA_	Alignment	not modelled	6.0	16	**PDB header:**transcription **Chain:** A: **PDB Molecule:**heterochromatin protein 1; **PDBTitle:** drosophila hp1a chromo shadow domain

29	d1pn2a1	Alignment	not modelled	6.0	33	**Fold:**Thioesterase/thiol ester dehydrase-isomerase **Superfamily:**Thioesterase/thiol ester dehydrase-isomerase **Family:**MaoC-like
30	d1d8ca_	Alignment	not modelled	6.0	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Malate synthase G **Family:**Malate synthase G
31	d1pcfa_	Alignment	not modelled	5.9	13	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
32	d2rm0w1	Alignment	not modelled	5.8	20	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
33	d1unda_	Alignment	not modelled	5.8	6	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
34	d2hanb1	Alignment	not modelled	5.8	25	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
35	c3oyrA_	Alignment	not modelled	5.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trans-isoprenyl diphosphate synthase; **PDBTitle:** crystal structure of polyprenyl synthase from caulobacter crescentus2 cb15 complexed with calcium and isoprenyl diphosphate
36	d1gpca_	Alignment	not modelled	5.6	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Phage ssDNA-binding proteins
37	c2dzjA_	Alignment	not modelled	5.5	33	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**synaptic glycoprotein sc2; **PDBTitle:** 2dzj/solution structure of the n-terminal ubiquitin-like2 domain in human synaptic glycoprotein sc2
38	d1qzpa_	Alignment	not modelled	5.4	12	**Fold:**VHP, Villin headpiece domain **Superfamily:**VHP, Villin headpiece domain **Family:**VHP, Villin headpiece domain
39	c3efyB_	Alignment	not modelled	5.4	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
40	c3gp2B_	Alignment	not modelled	5.4	71	**PDB header:**metal binding protein/transferase **Chain:** B: **PDB Molecule:**calcium/calmodulin-dependent protein kinase type **PDBTitle:** calmodulin bound to peptide from calmodulin kinase ii2 (camkii)
41	c1cm4B_	Alignment	not modelled	5.4	71	**PDB header:**complex (calcium-binding/transferase) **Chain:** B: **PDB Molecule:**calmodulin-dependent protein kinase ii-alpha; **PDBTitle:** motions of calmodulin-four-conformer refinement
42	c1cdmB_	Alignment	not modelled	5.4	71	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**calmodulin; **PDBTitle:** modulation of calmodulin plasticity in molecular2 recognition on the basis of x-ray structures
43	c1cm1B_	Alignment	not modelled	5.4	71	**PDB header:**complex (calcium-binding/transferase) **Chain:** B: **PDB Molecule:**calmodulin-dependent protein kinase ii-alpha; **PDBTitle:** motions of calmodulin-single-conformer refinement
44	d2fmma1	Alignment	not modelled	5.2	23	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo domain
45	d1thta_	Alignment	not modelled	5.1	55	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Thioesterases
46	d2o3bb1	Alignment	not modelled	5.1	40	**Fold:**Nuclease A inhibitor (NuiA) **Superfamily:**Nuclease A inhibitor (NuiA) **Family:**Nuclease A inhibitor (NuiA)
47	c3cbbA_	Alignment	not modelled	5.0	31	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 4-alpha, dna binding **PDBTitle:** crystal structure of hepatocyte nuclear factor 4alpha in2 complex with dna: diabetes gene product