Phyre2

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Description	P06627
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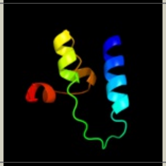
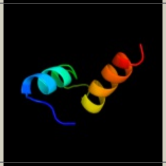
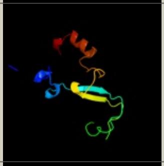
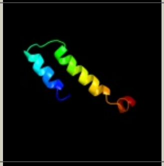
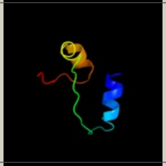
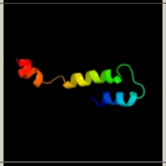
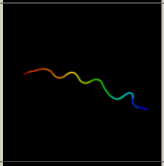
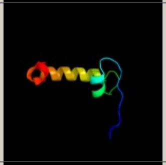
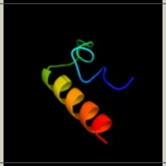
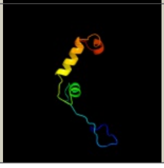
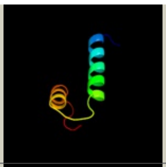
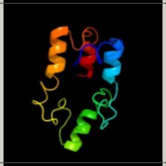
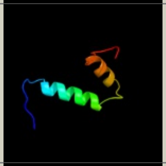
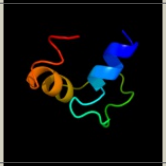
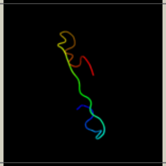
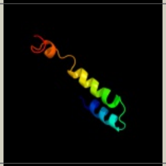
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1u9pA_	Alignment		68.0	25	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**parc; **PDBTitle:** permuted single-chain arc
2	c2vl7A_	Alignment		39.4	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**xpd; **PDBTitle:** structure of s. tokodaii xpd4
3	d1mnta_	Alignment		32.8	25	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**Arc/Mnt-like phage repressors
4	c2ehoL_	Alignment		18.5	16	**PDB header:**replication **Chain:** L: **PDB Molecule:**gins complex subunit 3; **PDBTitle:** crystal structure of human gins complex
5	c1ezyA_	Alignment		17.1	20	**PDB header:**signaling protein inhibitor **Chain:** A: **PDB Molecule:**regulator of g-protein signaling 4; **PDBTitle:** high-resolution solution structure of free rgs4 by nmr
6	c3crw1_	Alignment		16.9	19	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
7	d2jm5a1	Alignment		15.6	22	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
8	d3d85d1	Alignment		15.0	42	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**I set domains
9	c3pt2A_	Alignment		14.3	4	**PDB header:**hydrolase/protein binding **Chain:** A: **PDB Molecule:**rna polymerase; **PDBTitle:** structure of a viral otu domain protease bound to ubiquitin
10	d1kxpd3	Alignment		12.6	26	**Fold:**Serum albumin-like **Superfamily:**Serum albumin-like **Family:**Serum albumin-like
11	c3c0rC_	Alignment		12.2	16	**PDB header:**cell cycle, hydrolase **Chain:** C: **PDB Molecule:**ubiquitin thioesterase otu1; **PDBTitle:** structure of ovarian tumor (otu) domain in complex with ubiquitin

12	d1ufaa1	Alignment		10.7	21	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**AmyC C-terminal domain-like
13	c1ygmA_	Alignment		10.4	29	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**hypothetical protein bsu31320; **PDBTitle:** nmr structure of mistic
14	d2b5dx1	Alignment		10.4	21	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Families 57/38 glycoside transferase middle domain **Family:**AmyC C-terminal domain-like
15	c3dtfB_	Alignment		10.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**branched-chain amino acid aminotransferase; **PDBTitle:** structural analysis of mycobacterial branched chain aminotransferase-2 implications for inhibitor design
16	d1y6ia2	Alignment		10.0	16	**Fold:**GUN4-like **Superfamily:**GUN4-like **Family:**GUN4-like
17	c3cxbA_	Alignment		9.8	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein sifa; **PDBTitle:** crystal structure of sifa and skip
18	d1914a2	Alignment		9.1	17	**Fold:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Superfamily:**Signal recognition particle alu RNA binding heterodimer, SRP9/14 **Family:**Signal recognition particle alu RNA binding heterodimer, SRP9/14
19	d2ik8b1	Alignment		8.3	24	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
20	c2jpiA_	Alignment		7.7	50	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** chemical shift assignments of pa4090 from pseudomonas2 aeruginosa
21	c2abjG_	Alignment	not modelled	7.5	10	**PDB header:**transferase **Chain:** G: **PDB Molecule:**branched-chain-amino-acid aminotransferase, cytosolic; **PDBTitle:** crystal structure of human branched chain amino acid transaminase in a2 complex with an inhibitor, c16h10n2o4f3scl, and pyridoxal 5'3 phosphate.
22	d2a1ha1	Alignment	not modelled	7.4	10	**Fold:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Superfamily:**D-aminoacid aminotransferase-like PLP-dependent enzymes **Family:**D-aminoacid aminotransferase-like PLP-dependent enzymes
23	d1ljma_	Alignment	not modelled	7.4	44	**Fold:**Common fold of diphtheria toxin/transcription factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**RUNT domain
24	d1z3xa2	Alignment	not modelled	6.9	13	**Fold:**GUN4-like **Superfamily:**GUN4-like **Family:**GUN4-like
25	c3enpA_	Alignment	not modelled	6.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tp53rk-binding protein; **PDBTitle:** crystal structure of human cgi121
26	c3qqmD_	Alignment	not modelled	6.8	25	**PDB header:**transferase **Chain:** D: **PDB Molecule:**mlr3007 protein; **PDBTitle:** crystal structure of a putative amino-acid aminotransferase2 (np_104211.1) from mesorhizobium loti at 2.30 a resolution
27	c3j0gO_	Alignment	not modelled	6.3	30	**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
						Fold: Common fold of diphtheria toxin/transcription

28	d1eaqa_	Alignment	not modelled	5.9	50	factors/cytochrome f **Superfamily:**p53-like transcription factors **Family:**RUNT domain
29	d1y9ba1	Alignment	not modelled	5.7	26	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**VCA0319-like
30	d1c4oa2	Alignment	not modelled	5.7	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
31	c2konA_	Alignment	not modelled	5.3	42	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr solution structure of cv_2116 from chromobacterium2 violaceum. northeast structural genomics consortium target3 cvt4(1-82)
32	c2elxA_	Alignment	not modelled	5.2	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 406; **PDBTitle:** solution structure of the 8th c2h2 zinc finger of mouse2 zinc finger protein 406