Phyre2

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Description	P52125
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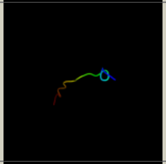
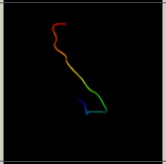
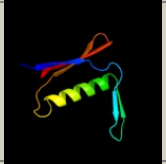
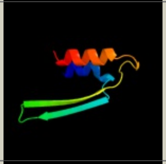
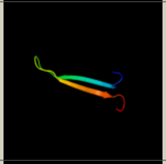
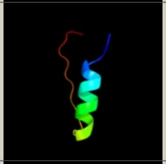
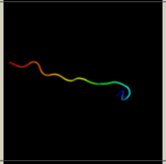
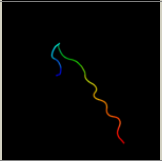
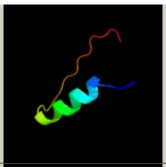
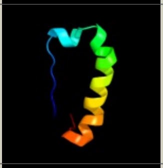
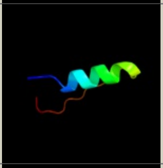
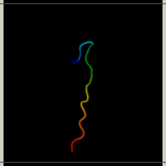
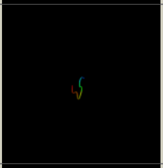
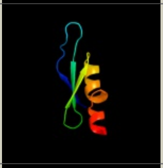
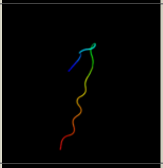
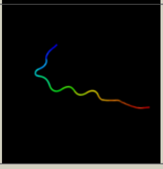
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1l5ia_	Alignment		74.1	16	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**DNA-binding domain of REP protein
2	c3dkxA_	Alignment		69.9	31	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein repb; **PDBTitle:** crystal structure of the replication initiator protein2 encoded on plasmid pmv158 (repb), trigonal form, to 2.7 ang3 resolution
3	c2x3gA_	Alignment		61.1	24	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**sirv1 hypothetical protein orf119; **PDBTitle:** crystal structure of the hypothetical protein orf119 from2 sulfolobus islandicus rod-shaped virus 1
4	c2ns6A_	Alignment		25.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mobilization protein a; **PDBTitle:** crystal structure of the minimal relaxase domain of moba2 from plasmid r1162
5	d2nzca1	Alignment		17.4	17	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**TM1266-like
6	c2hw0A_	Alignment		11.5	9	**PDB header:**hydrolase, replication **Chain:** A: **PDB Molecule:**replicase; **PDBTitle:** nmr solution structure of the nuclease domain from the2 replicator initiator protein from porcine circovirus pcv2
7	c2hwtA_	Alignment		10.2	9	**PDB header:**replication, hydrolase **Chain:** A: **PDB Molecule:**putative replicase-associated protein; **PDBTitle:** nmr solution structure of the master-rep protein nuclease2 domain (2-95) from the faba bean necrotic yellows virus
8	d1m55a_	Alignment		10.2	11	**Fold:**Origin of replication-binding domain, RBD-like **Superfamily:**Origin of replication-binding domain, RBD-like **Family:**Replication protein Rep, nuclease domain
9	c3maxB_	Alignment		9.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histone deacetylase 2; **PDBTitle:** crystal structure of human hdac2 complexed with an n-(2-aminophenyl)2 benzamide
10	c2h1xB_	Alignment		9.9	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**5-hydroxyisourate hydrolase (formerly known as **PDBTitle:** crystal structure of 5-hydroxyisourate hydrolase (formerly2 known as trp, transthyretin related protein)
11	d1f86a_	Alignment		9.8	12	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)

12	c3ew8A_	Alignment		9.6	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histone deacetylase 8; **PDBTitle:** crystal structure analysis of human hdac8 d101l variant
13	c3ugsB_	Alignment		9.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
14	d1t64a_	Alignment		9.0	19	**Fold:**Arginase/deacetylase **Superfamily:**Arginase/deacetylase **Family:**Histone deacetylase, HDAC
15	d1ttaa_	Alignment		9.0	12	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
16	c2elzA_	Alignment		8.9	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 224; **PDBTitle:** solution structure of the 17th zf-c2h2 domain from human2 zinc finger protein 224
17	d2b7ta1	Alignment		8.5	11	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
18	d1tfpa_	Alignment		8.1	18	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
19	c2h0eA_	Alignment		7.9	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transthyretin-like protein pucm; **PDBTitle:** crystal structure of pucm in the absence of substrate
20	c2gpzC_	Alignment		7.8	29	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**transthyretin-like protein; **PDBTitle:** transthyretin-like protein from salmonella dublin
21	d2b7va1	Alignment	not modelled	7.4	9	**Fold:**dsRBD-like **Superfamily:**dsRNA-binding domain-like **Family:**Double-stranded RNA-binding domain (dsRBD)
22	c2jepB_	Alignment	not modelled	6.7	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**xyloglucanase; **PDBTitle:** native family 5 xyloglucanase from paenibacillus pabuli
23	d1oo2a_	Alignment	not modelled	6.6	25	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
24	c2jttD_	Alignment	not modelled	6.1	21	**PDB header:**calcium binding protein/antitumor protei **Chain:** D: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** solution structure of calcium loaded s100a6 bound to c-2 terminal siah-1 interacting protein
25	c2yttA_	Alignment	not modelled	6.0	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 204-2 236) of human zinc finger protein 473
26	c2entA_	Alignment	not modelled	5.9	40	**PDB header:**transcription **Chain:** A: **PDB Molecule:**krueppel-like factor 15; **PDBTitle:** solution structure of the second c2h2-type zinc finger2 domain from human krueppel-like factor 15
27	d1luza_	Alignment	not modelled	5.4	25	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
28	d1kgia_	Alignment	not modelled	5.3	19	**Fold:**Prealbumin-like **Superfamily:**Transthyretin (synonym: prealbumin) **Family:**Transthyretin (synonym: prealbumin)
						Fold:(Phosphotyrosine protein) phosphatases II

29	d1ohea1	Alignment	not modelled	5.1	20	**Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like