Phyre^2

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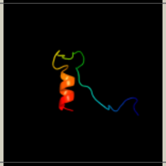
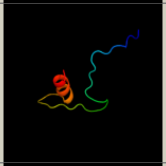
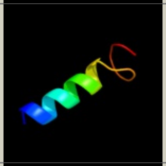
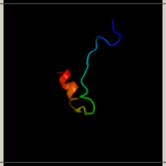
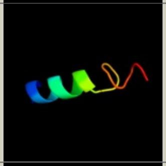
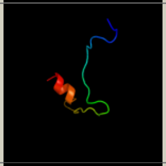
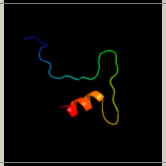
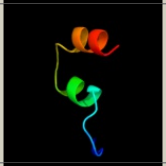
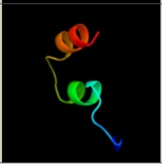
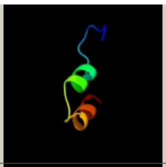
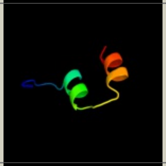
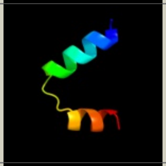
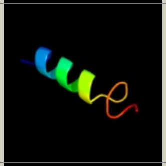
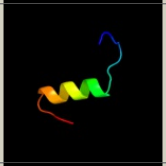
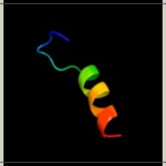
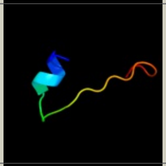
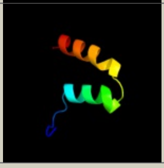
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gk6B_	Alignment		30.6	53	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
2	c2xv5A_	Alignment		28.8	42	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-a/c; **PDBTitle:** human lamin a coil 2b fragment
3	c2p2cD_	Alignment		21.7	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**caspase-2; **PDBTitle:** inhibition of caspase-2 by a designed ankyrin repeat2 protein (darpin)
4	c3sipB_	Alignment		21.4	22	**PDB header:**hydrolase/ligase/hydrolase **Chain:** B: **PDB Molecule:**caspase; **PDBTitle:** crystal structure of drice and diap1-bir1 complex
5	c3movB_	Alignment		21.1	44	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
6	c2qljB_	Alignment		20.1	14	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-7; **PDBTitle:** crystal structure of caspase-7 with inhibitor ac-wehd-cho
7	c1gk4A_	Alignment		16.5	56	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
8	c2c1eB_	Alignment		16.2	17	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-3 subunit p12; **PDBTitle:** crystal structures of caspase-3 in complex with aza-peptide michael2 acceptor inhibitors.
9	c2c2zB_	Alignment		14.3	16	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-8 p10 subunit; **PDBTitle:** crystal structure of caspase-8 in complex with aza-peptide michael2 acceptor inhibitor
10	c2bykB_	Alignment		14.3	26	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**chrac-14; **PDBTitle:** histone fold heterodimer of the chromatin accessibility2 complex
11	d2bykb1	Alignment		14.3	26	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs

12	c1jfiB_	Alignment		14.1	22	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcription regulator nc2 beta chain; **PDBTitle:** crystal structure of the nc2-tbp-dna ternary complex
13	d1jfib_	Alignment		14.1	22	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
14	d1b0na1	Alignment		13.0	24	**Fold:**Dimerisation interlock **Superfamily:**SinR repressor dimerisation domain-like **Family:**SinR repressor dimerisation domain-like
15	d1kx5b_	Alignment		11.2	21	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
16	c1x8yA_	Alignment		9.5	44	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
17	d1id3b_	Alignment		8.6	23	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Nucleosome core histones
18	d1a7wa_	Alignment		8.3	16	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**Archaeal histone
19	c3adyA_	Alignment		8.3	29	**PDB header:**proton transport **Chain:** A: **PDB Molecule:**dotd; **PDBTitle:** crystal structure of dotd from legionella
20	d1n1ja_	Alignment		7.8	14	**Fold:**Histone-fold **Superfamily:**Histone-fold **Family:**TBP-associated factors, TAFs
21	c2h51B_	Alignment	not modelled	7.7	11	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** B: **PDB Molecule:**caspase-1; **PDBTitle:** crystal structure of human caspase-1 (glu390->asp and arg286->lys) in2 complex with 3-[2-(2-benzyloxycarbonylamino-3-methyl-butyrylamino)-3 propionylamino]-4-oxo-pentanoic acid (z-vad-fmk)
22	d1m72a_	Alignment	not modelled	7.7	22	**Fold:**Caspase-like **Superfamily:**Caspase-like **Family:**Caspase catalytic domain
23	c3lyfB_	Alignment	not modelled	7.7	4	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**nucleocapsid protein; **PDBTitle:** crystal structure of the rift valley fever virus nucleocapsid protein
24	d2if1a_	Alignment	not modelled	7.3	58	**Fold:**eIF1-like **Superfamily:**eIF1-like **Family:**eIF1-like
25	c2dtcB_	Alignment	not modelled	7.3	18	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**ral guanine nucleotide exchange factor ralgps1a; **PDBTitle:** crystal structure of ms0666
26	c2l5aA_	Alignment	not modelled	7.2	19	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**histone h3-like centromeric protein cse4, protein scm3, **PDBTitle:** structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
27	d1g4us1	Alignment	not modelled	6.4	10	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
28	d1he1a_	Alignment	not modelled	6.4	25	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain

						Family: Bacterial GAP domain
29	d1kqra_	Alignment	not modelled	5.7	60	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**vp4 sialic acid binding domain
30	c1kriA_	Alignment	not modelled	5.7	60	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vp4; **PDBTitle:** nmr solution structures of the rhesus rotavirus vp4 sialic2 acid binding domain without ligand
31	d2ysca1	Alignment	not modelled	5.5	38	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain