Phyre^2

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Description	P77163
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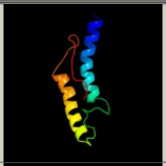
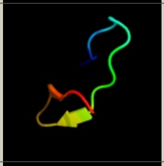
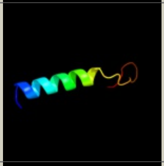
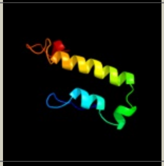
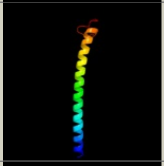
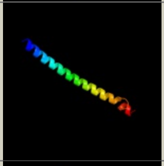
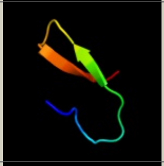
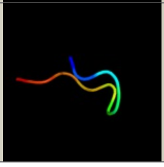
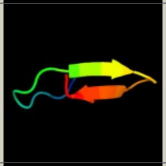
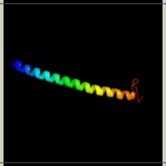
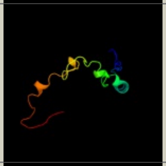
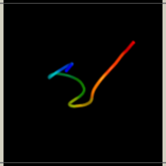
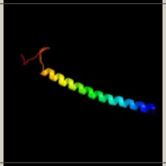
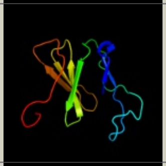
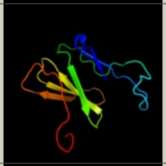
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kz6A_	Alignment		97.5	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
2	c2jxwA_	Alignment		41.8	21	**PDB header:**formin binding protein **Chain:** A: **PDB Molecule:**ww domain-binding protein 4; **PDBTitle:** solution structure of the tandem ww domains of fbp21
3	d1jofa_	Alignment		33.2	16	**Fold:**7-bladed beta-propeller **Superfamily:**3-carboxy-cis,cis-mucoante lactonizing enzyme **Family:**3-carboxy-cis,cis-mucoante lactonizing enzyme
4	c1rfoC_	Alignment		32.4	30	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**whisker antigen control protein; **PDBTitle:** trimeric foldon of the t4 phagehead fibritin
5	c3o0rC_	Alignment		30.5	28	**PDB header:**immune system/oxidoreductase **Chain:** C: **PDB Molecule:**nitric oxide reductase subunit c; **PDBTitle:** crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
6	c2kt9A_	Alignment		29.7	22	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**probable 30s ribosomal protein psrp-3; **PDBTitle:** solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
7	c1gk6B_	Alignment		28.0	20	**PDB header:**vimentin **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment linked to gcn4 leucine2 zipper (z2b)
8	c2xv5A_	Alignment		26.8	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin-a/c; **PDBTitle:** human lamin a coil 2b fragment
9	c1v1hB_	Alignment		24.4	30	**PDB header:**adenovirus **Chain:** B: **PDB Molecule:**fibritin, fiber protein; **PDBTitle:** adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibritin foldon trimerisation motif with3 a short linker
10	c1ox3A_	Alignment		21.7	30	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** crystal structure of mini-fibritin
11	c2ov2O_	Alignment		19.6	20	**PDB header:**protein binding/transferase **Chain:** O: **PDB Molecule:**serine/threonine-protein kinase pak 4; **PDBTitle:** the crystal structure of the human rac3 in complex with the crib2 domain of human p21-activated kinase 4 (pak4)

12	d1x4ta1	Alignment		18.8	24	**Fold:**Long alpha-hairpin **Superfamily:**ISY1 domain-like **Family:**ISY1 N-terminal domain-like
13	c1avyA_	Alignment		18.6	30	**PDB header:**coiled coil **Chain:** A: **PDB Molecule:**fibritin; **PDBTitle:** fibritin deletion mutant m (bacteriophage t4)
14	c1x8yA_	Alignment		18.1	24	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**lamin a/c; **PDBTitle:** human lamin coil 2b
15	c1w18A_	Alignment		17.2	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**levansucrase; **PDBTitle:** crystal structure of levansucrase from gluconacetobacter2 diazotrophicus
16	c2odbB_	Alignment		17.2	20	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak 6; **PDBTitle:** the crystal structure of human cdc42 in complex with the crib domain2 of human p21-activated kinase 6 (pak6)
17	c1gk4A_	Alignment		15.9	26	**PDB header:**vimentin **Chain:** A: **PDB Molecule:**vimentin; **PDBTitle:** human vimentin coil 2b fragment (cys2)
18	d2ghsa1	Alignment		15.5	11	**Fold:**6-bladed beta-propeller **Superfamily:**Calcium-dependent phosphotriesterase **Family:**SGL-like
19	c2ghsA_	Alignment		15.5	11	**PDB header:**calcium-binding protein **Chain:** A: **PDB Molecule:**agr_c_1268p; **PDBTitle:** crystal structure of a calcium-binding protein, regucalcin2 (agr_c_1268) from agrobacterium tumefaciens str. c58 at 1.55 a3 resolution
20	c3movB_	Alignment		13.6	21	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**lamin-b1; **PDBTitle:** crystal structure of human lamin-b1 coil 2 segment
21	d1ln1a_	Alignment	not modelled	13.0	17	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**STAR domain
22	c1e0aB_	Alignment	not modelled	11.0	50	**PDB header:**signalling protein **Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** cdc42 complexed with the gtpase binding domain of p212 activated kinase
23	d2oa5a1	Alignment	not modelled	10.8	22	**Fold:**BLRF2-like **Superfamily:**BLRF2-like **Family:**BLRF2-like
24	d2diia1	Alignment	not modelled	9.6	23	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
25	c3nmbA_	Alignment	not modelled	9.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sugar hydrolase; **PDBTitle:** crystal structure of a putative sugar hydrolase (bacova_03189) from2 bacteroides ovatus at 2.40 a resolution
26	d2dk1a1	Alignment	not modelled	9.1	30	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
27	d1o6wa1	Alignment	not modelled	9.0	26	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
28	d1ll7a2	Alignment	not modelled	9.0	17	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
						PDB header:transferase

29	c1f3mB_	Alignment	not modelled	8.7	50	**Chain:** B: **PDB Molecule:**serine/threonine-protein kinase pak-alpha; **PDBTitle:** crystal structure of human serine/threonine kinase pak1
30	c2c7hA_	Alignment	not modelled	8.6	39	**PDB header:**ubiquitin-like protein **Chain:** A: **PDB Molecule:**retinoblastoma-binding protein 6, isoform 3; **PDBTitle:** solution nmr structure of the dwnn domain from human rbbp6
31	c2jz8A_	Alignment	not modelled	8.1	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bh09830; **PDBTitle:** solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
32	d1w9pa2	Alignment	not modelled	7.8	25	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
33	d1rzhh1	Alignment	not modelled	7.8	13	**Fold:**PRC-barrel domain **Superfamily:**PRC-barrel domain **Family:**Photosynthetic reaction centre, H-chain, cytoplasmic domain
34	c1zr7A_	Alignment	not modelled	7.7	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**huntingtin-interacting protein hypa/fbp11; **PDBTitle:** solution structure of the first ww domain of fbp11
35	c1tk7A_	Alignment	not modelled	7.3	11	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**cg4244-pb; **PDBTitle:** nmr structure of ww domains (ww3-4) from suppressor of2 deltex
36	c1k6nH_	Alignment	not modelled	7.1	13	**PDB header:**photosynthesis **Chain:** H: **PDB Molecule:**photosynthetic reaction center h subunit; **PDBTitle:** e(l212)a,d(l213)a double mutant structure of photosynthetic reaction2 center from rhodobacter sphaeroides
37	c2v43A_	Alignment	not modelled	7.0	18	**PDB header:**regulator **Chain:** A: **PDB Molecule:**sigma-e factor regulatory protein rseb; **PDBTitle:** crystal structure of rseb: a sensor for periplasmic stress2 response in e. coli
38	d1pcna1	Alignment	not modelled	7.0	33	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Colipase-like **Family:**Colipase-like
39	c2diiA_	Alignment	not modelled	6.5	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
40	d1g4us1	Alignment	not modelled	6.3	17	**Fold:**Four-helical up-and-down bundle **Superfamily:**Bacterial GAP domain **Family:**Bacterial GAP domain
41	c2dk7A_	Alignment	not modelled	6.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation regulator 1; **PDBTitle:** solution structure of ww domain in transcription elongation2 regulator 1
42	c3ok8A_	Alignment	not modelled	6.1	6	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**brain-specific angiogenesis inhibitor 1-associated protein **PDBTitle:** i-bar of pinkbar
43	c1gq1B_	Alignment	not modelled	6.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytochrome cd1 nitrite reductase; **PDBTitle:** cytochrome cd1 nitrite reductase, y25s mutant, oxidised2 form
44	d2rm0w1	Alignment	not modelled	5.7	29	**Fold:**WW domain-like **Superfamily:**WW domain **Family:**WW domain
45	c2h47F_	Alignment	not modelled	5.4	17	**PDB header:**oxidoreductase/electron transport **Chain:** F: **PDB Molecule:**aromatic amine dehydrogenase; **PDBTitle:** crystal structure of an electron transfer complex between2 aromatic amine dephydrogenase and azurin from alcaligenes3 faecalis (form 1)