Phyre2

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Description	RVBD2517c_(-)_2833520_2833771
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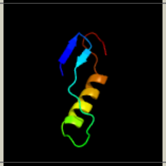
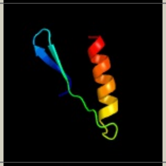
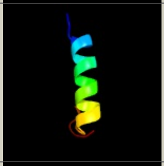
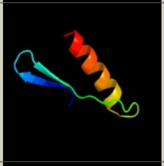
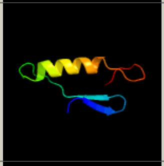
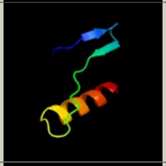
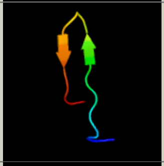
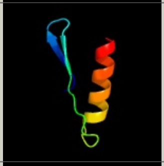
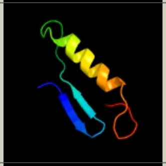
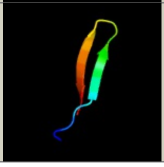
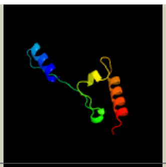
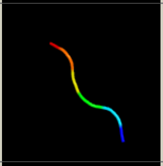
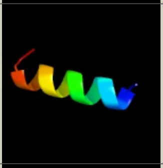
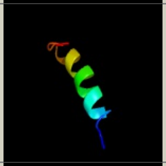
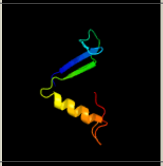
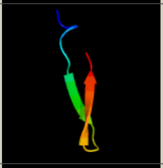
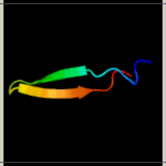
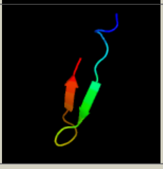
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ewoa1	Alignment		38.7	14	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
2	d1vkpa_	Alignment		37.4	16	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
3	d2cmua1	Alignment		33.8	14	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
4	c2l6pA_	Alignment		29.3	24	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**phac1, phac2 and phad genes; **PDBTitle:** nmr solution structure of the protein np_253742.1
5	c2jerG_	Alignment		23.9	22	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**agmatine deiminase; **PDBTitle:** agmatine deiminase of enterococcus faecalis catalyzing its2 reaction.
6	d1zbra1	Alignment		22.7	15	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
7	d1xkna_	Alignment		22.3	27	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
8	d1ylxa1	Alignment		21.9	33	**Fold:**N domain of copper amine oxidase-like **Superfamily:**GK1464-like **Family:**GK1464-like
9	d2jera1	Alignment		21.2	22	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
10	c4ytgA_	Alignment		21.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidylarginine deiminase; **PDBTitle:** crystal structure of porphyromonas gingivalis peptidylarginine2 deiminase (ppad) mutant c351a in complex with dipeptide met-arg.
11	d1upsa2	Alignment		20.1	53	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**GlcNAc-alpha-1,4-Gal-releasing endo-beta-galactosidase, GngC, C-terminal domain

12	c3tquD_	Alignment		17.9	22	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** structure of a ham1 protein from coxiella burnetii
13	c2qvtA_	Alignment		17.8	100	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**avrl567-d; **PDBTitle:** structure of melampsora lini avirulence protein, avrl567-d
14	c2pr7A_	Alignment		17.3	53	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**haloacid dehalogenase/epoxide hydrolase family; **PDBTitle:** crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
15	c2l6nA_	Alignment		17.1	26	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yp_001092504.1; **PDBTitle:** nmr solution structure of the protein yp_001092504.1
16	c3dntB_	Alignment		16.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**protein hipa; **PDBTitle:** structures of mdt proteins
17	c2vsaA_	Alignment		15.5	35	**PDB header:**toxin **Chain:** A: **PDB Molecule:**mosquitocidal toxin; **PDBTitle:** structure and mode of action of a mosquitocidal holotoxin
18	c6eujC_	Alignment		14.6	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**beta-glucanase; **PDBTitle:** the gh43, beta 1,3 galactosidase, bt0265
19	d2hg6a1	Alignment		14.2	40	**Fold:**PA1123-like **Superfamily:**PA1123-like **Family:**PA1123-like
20	c3phzA_	Alignment		13.9	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**ricin b-related lectin; **PDBTitle:** crystal structure analysis of polyporus squamosus lectin bound to2 human-type influenza-binding epitope neu5aca2-6galb1-4glcnac
21	c1yr2A_	Alignment	not modelled	13.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**prolyl oligopeptidase; **PDBTitle:** structural and mechanistic analysis of two prolyl endopeptidases: role2 of inter-domain dynamics in catalysis and specificity
22	c2k8vA_	Alignment	not modelled	12.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 12; **PDBTitle:** solution structure of oxidised erp18
23	d2f2fa1	Alignment	not modelled	11.7	15	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
24	c6b2wB_	Alignment	not modelled	11.4	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative peptidyl-arginine deiminase family protein; **PDBTitle:** c. jejuni c315s agmatine deiminase with substrate bound
25	d2qrda1	Alignment	not modelled	11.2	20	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
26	c3bc9A_	Alignment	not modelled	10.5	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha amylase, catalytic region; **PDBTitle:** alpha-amylase b in complex with acarbose
27	d1zcaa1	Alignment	not modelled	10.5	24	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
28	d1z0xa2	Alignment	not modelled	10.3	29	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
						PDB header:hormone receptor

29	c3qrzC_	Alignment	not modelled	9.8	44	**Chain:** C: **PDB Molecule:**abscisic acid receptor pyl5; **PDBTitle:** crystal structure of native abscisic acid receptor pyl5 at 2.62 angstrom
30	d1k7ka_	Alignment	not modelled	9.6	17	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
31	d1dvpa1	Alignment	not modelled	9.5	28	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
32	c5uqyB_	Alignment	not modelled	9.2	30	**PDB header:**viral protein/immune system **Chain:** B: **PDB Molecule:**envelope glycoprotein gp2; **PDBTitle:** crystal structure of marburg virus gp in complex with the human2 survivor antibody mr78
33	d2v8qa1	Alignment	not modelled	9.1	20	**Fold:**TBP-like **Superfamily:**KA1-like **Family:**Ssp2 C-terminal domain-like
34	d2bcjq1	Alignment	not modelled	9.1	14	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
35	c2jwlB_	Alignment	not modelled	8.5	23	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
36	c5ld1D_	Alignment	not modelled	8.4	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**polyphosphate:amp phosphotransferase; **PDBTitle:** crystal structure of polyphosphate kinase from meiothermus ruber bound2 to atp
37	d2f99a1	Alignment	not modelled	8.2	19	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**SnoaL-like polyketide cyclase
38	c1x5bA_	Alignment	not modelled	8.1	27	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
39	c1ybiA_	Alignment	not modelled	8.1	12	**PDB header:**toxin **Chain:** A: **PDB Molecule:**non-toxin haemagglutinin ha34; **PDBTitle:** crystal structure of ha33a, a neurotoxin-associated protein2 from clostridium botulinum type a
40	c4bz0A_	Alignment	not modelled	8.0	29	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**putative type iv pilus biosynthesis protein; **PDBTitle:** structural characterization using sulfur-sad of the cytoplasmic2 domain of burkholderia pseudomallei pilo2bp, an actin-like3 protein component of a type ivb r64-derivative pilus machinery.
41	c3plwA_	Alignment	not modelled	7.8	56	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**recombination enhancement function protein; **PDBTitle:** ref protein from p1 bacteriophage
42	c2dxcG_	Alignment	not modelled	7.3	14	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**thiocyanate hydrolase subunit alpha; **PDBTitle:** recombinant thiocyanate hydrolase, fully-matured form
43	c3gjxE_	Alignment	not modelled	7.3	35	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
44	d1o9ja_	Alignment	not modelled	7.1	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
45	c4owlA_	Alignment	not modelled	7.0	17	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cytolysin; **PDBTitle:** crystal structure of the vibrio vulnificus hemolysin/cytolysin beta-2 trefoil lectin with n-acetyl-d-lactosamine bound
46	c6jx3B_	Alignment	not modelled	6.9	21	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**tfub1; **PDBTitle:** lasso peptide synthetase b1 complexed with the leader peptide
47	c5xg5A_	Alignment	not modelled	6.9	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**mitsuba-1; **PDBTitle:** crystal structure of mitsuba-1 with bound nacgal
48	d1juqa_	Alignment	not modelled	6.9	29	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
49	c2cpmA_	Alignment	not modelled	6.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sperm-associated antigen 7; **PDBTitle:** solution structure of the r3h domain of human sperm-2 associated antigen 7
50	c1sr4A_	Alignment	not modelled	6.8	14	**PDB header:**toxin **Chain:** A: **PDB Molecule:**cytolethal distending toxin subunit a; **PDBTitle:** crystal structure of the haemophilus ducreyi cytolethal2 distending toxin
51	d1sr4a_	Alignment	not modelled	6.8	14	**Fold:**beta-Trefoil **Superfamily:**Ricin B-like lectins **Family:**Ricin B-like
52	c1ij2C_	Alignment	not modelled	6.8	45	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
53	c1ij3C_	Alignment	not modelled	6.8	45	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
54	c1rb1B_	Alignment	not modelled	6.8	45	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
						PDB header:dna binding protein

55	c1rb1A_	Alignment	not modelled	6.8	45	**Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
56	c3k7zB_	Alignment	not modelled	6.8	45	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
57	c3k7zA_	Alignment	not modelled	6.8	45	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
58	c6au0A_	Alignment	not modelled	6.7	24	**PDB header:**transferase/transferase inhibitor **Chain:** A: **PDB Molecule:**polyphosphate:amp phosphotransferase; **PDBTitle:** crystal structure of ppk2 (class iii) in complex with bisphosphonate2 inhibitor (2-((3,5-dichlorophenyl)amino)ethane-1,1-diyl)diphosphonic3 acid
59	c1dvpA_	Alignment	not modelled	6.7	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
60	c1ij2B_	Alignment	not modelled	6.6	45	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
61	c3gb8B_	Alignment	not modelled	6.5	33	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of crm1/snurportin-1 complex
62	c4eagA_	Alignment	not modelled	6.5	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**eg:132e8.2 protein; **PDBTitle:** co-crystal structure of an chimeric ampk core with atp
63	c6dbbA_	Alignment	not modelled	6.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative aldehyde dehydrogenase family protein; **PDBTitle:** crystal structure of a putative aldehyde dehydrogenase family protein2 burkholderia cenocepacia j2315 in complex with partially reduced nadh
64	d1zcba1	Alignment	not modelled	6.5	25	**Fold:**Transducin (alpha subunit), insertion domain **Superfamily:**Transducin (alpha subunit), insertion domain **Family:**Transducin (alpha subunit), insertion domain
65	d1q3ma_	Alignment	not modelled	6.4	71	**Fold:**GLA-domain **Superfamily:**GLA-domain **Family:**GLA-domain
66	c1rb6C_	Alignment	not modelled	6.4	45	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel trimer of gcn4-leucine zipper core mutant as n16a2 tetragonal form
67	c4as2D_	Alignment	not modelled	6.1	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**phosphorylcholine phosphatase; **PDBTitle:** pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
68	c4eajA_	Alignment	not modelled	5.9	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5'-amp-activated protein kinase catalytic subunit alpha-1; **PDBTitle:** co-crystal of ampk core with amp soaked with atp
69	c5lnk2_	Alignment	not modelled	5.8	29	**PDB header:**oxidoreductase **Chain:** 2: **PDB Molecule:**mitochondrial complex i, 24 kda subunit; **PDBTitle:** entire ovine respiratory complex i
70	c1ij3B_	Alignment	not modelled	5.6	45	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
71	c1mszA_	Alignment	not modelled	5.6	30	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-binding protein smubp-2; **PDBTitle:** solution structure of the r3h domain from human smubp-2
72	d1msza_	Alignment	not modelled	5.6	30	**Fold:**IF3-like **Superfamily:**R3H domain **Family:**R3H domain
73	c2q83A_	Alignment	not modelled	5.6	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ytaa protein; **PDBTitle:** crystal structure of ytaa (2635576) from bacillus subtilis at 2.50 a2 resolution
74	d1mxga1	Alignment	not modelled	5.6	21	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
75	c2cceB_	Alignment	not modelled	5.5	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
76	c3auoB_	Alignment	not modelled	5.5	30	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase beta family (x family); **PDBTitle:** dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
77	d1rj9a1	Alignment	not modelled	5.5	70	**Fold:**Four-helical up-and-down bundle **Superfamily:**Domain of the SRP/SRP receptor G-proteins **Family:**Domain of the SRP/SRP receptor G-proteins
78	c5by4A_	Alignment	not modelled	5.5	29	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein tolr; **PDBTitle:** structure and function of the escherichia coli tol-pal stator protein2 tolr
79	c6g1cV_	Alignment	not modelled	5.4	21	**PDB header:**antitoxin **Chain:** V: **PDB Molecule:**antitoxin hicb; **PDBTitle:** crystal structure of the n-terminal domain of burkholderia2 pseudomallei antitoxin hicb
						Fold:4-helical cytokines

80	d1v7mv_	Alignment	not modelled	5.4	35	**Superfamily:**4-helical cytokines **Family:**Short-chain cytokines
81	c4bnqA_	Alignment	not modelled	5.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-canonical purine ntp pyrophosphatase; **PDBTitle:** the structure of the staphylococcus aureus ham1 protein
82	d1lvaa3	Alignment	not modelled	5.4	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
83	c1ce0B_	Alignment	not modelled	5.3	55	**PDB header:**hiv-1 envelope protein **Chain:** B: **PDB Molecule:**protein (leucine zipper model h38-p1); **PDBTitle:** trimerization specificity in hiv-1 gp41: analysis with a2 gcn4 leucine zipper model
84	d1v29b_	Alignment	not modelled	5.2	36	**Fold:**SH3-like barrel **Superfamily:**Electron transport accessory proteins **Family:**Nitrile hydratase beta chain
85	c3j21M_	Alignment	not modelled	5.1	31	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**50s ribosomal protein l15e; **PDBTitle:** promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)