Phyre^2

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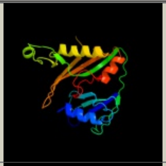
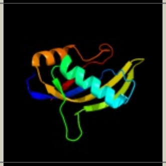
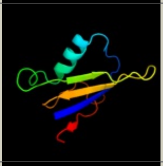
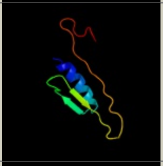
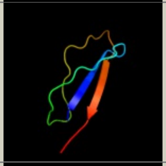
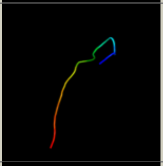
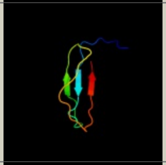
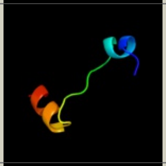
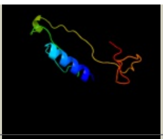
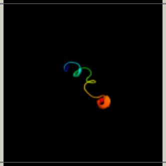
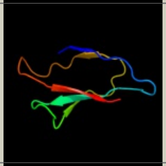
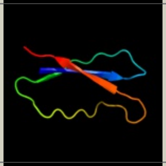
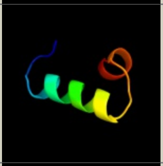
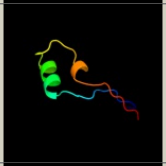
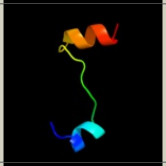
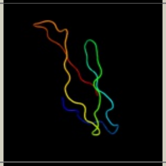
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qrqA_	Alignment		100.0	34	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**putative uncharacterized protein tthb192; **PDBTitle:** structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
2	c1wj9A_	Alignment		100.0	34	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**crispr-associated protein; **PDBTitle:** crystal structure of a crispr-associated protein from2 thermus thermophilus
3	d1wj9a2	Alignment		100.0	40	**Fold:**Ferredoxin-like **Superfamily:**CRISPR-associated protein **Family:**CRISPR-associated protein
4	d1wj9a1	Alignment		99.9	25	**Fold:**Ferredoxin-like **Superfamily:**CRISPR-associated protein **Family:**CRISPR-associated protein
5	c3i4hX_	Alignment		92.6	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**endoribonuclease; **PDBTitle:** crystal structure of cas6 in pyrococcus furiosus
6	c3ramC_	Alignment		46.7	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**hmra protein; **PDBTitle:** crystal structure of hmra
7	d1axib2	Alignment		46.6	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
8	d1iarb2	Alignment		32.4	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
9	c2db8A_	Alignment		27.4	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 9, isoform 2; **PDBTitle:** solution structures of the fn3 domain of human tripartite2 motif protein 9
10	c3uoeB_	Alignment		25.9	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti
11	c1wtjB_	Alignment		24.6	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato

12	c2q43A_	Alignment		23.3	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**iaa-amino acid hydrolase ilr1-like 2; **PDBTitle:** ensemble refinement of the protein crystal structure of iaa-aminoacid2 hydrolase from arabidopsis thaliana gene at5g56660
13	d1nxua_	Alignment		22.1	12	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
14	c3mpcB_	Alignment		22.0	15	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fn3-like protein; **PDBTitle:** the crystal structure of a fn3-like protein from clostridium2 thermocellum
15	d1uc6a_	Alignment		20.1	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
16	c2h5xA_	Alignment		19.6	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction atp-dependent dna helicase ruva; **PDBTitle:** ruva from mycobacterium tuberculosis
17	d2h1qa1	Alignment		18.5	5	**Fold:**PLP-dependent transferase-like **Superfamily:**Dhaf3308-like **Family:**Dhaf3308-like
18	d1rfma_	Alignment		17.1	20	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
19	c1zlgA_	Alignment		16.1	13	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**anosmin 1; **PDBTitle:** solution structure of the extracellular matrix protein2 anosmin-1
20	c1d8lA_	Alignment		14.7	19	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**protein (holliday junction dna helicase ruva); **PDBTitle:** e. coli holliday junction binding protein ruva nh2 region2 lacking domain iii
21	c2b5iC_	Alignment	not modelled	14.5	13	**PDB header:**cytokine/cytokine receptor **Chain:** C: **PDB Molecule:**cytokine receptor common gamma chain; **PDBTitle:** cytokine receptor complex
22	d1cd9b2	Alignment	not modelled	13.7	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
23	c3bpoB_	Alignment	not modelled	13.4	28	**PDB header:**cytokine/cytokine receptor **Chain:** B: **PDB Molecule:**interleukin-4 receptor alpha chain; **PDBTitle:** crystal structure of the il13-il4r-il13ra ternary complex
24	c3q3wB_	Alignment	not modelled	13.1	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** isopropylmalate isomerase small subunit from campylobacter jejuni.
25	d1wfua_	Alignment	not modelled	12.8	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
26	d1f6fb2	Alignment	not modelled	12.6	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
27	c1hjpA_	Alignment	not modelled	12.6	21	**PDB header:**dna recombination **Chain:** A: **PDB Molecule:**ruva; **PDBTitle:** holliday junction binding protein ruva from e. coli
28	d2gysa4	Alignment	not modelled	12.6	20	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
29	c3h5jA_	Alignment	not modelled	12.3	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit;

						PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
30	d2ic2a1	Alignment	not modelled	12.1	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
31	c1ysjB_	Alignment	not modelled	11.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein yxep; **PDBTitle:** crystal structure of bacillus subtilis yxep protein (apc1829), a2 dinuclear metal binding peptidase from m20 family
32	d1x5ya1	Alignment	not modelled	11.6	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
33	d1qgpa_	Alignment	not modelled	11.4	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Z-DNA binding domain
34	d2crza1	Alignment	not modelled	10.5	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
35	c2hcuA_	Alignment	not modelled	10.4	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-isopropylmalate dehydratase small subunit; **PDBTitle:** crystal structure of smu.1381 (or leud) from streptococcus2 mutans
36	d2d9qb2	Alignment	not modelled	10.3	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
37	d3d48r2	Alignment	not modelled	10.3	9	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
38	d1bvsa2	Alignment	not modelled	10.2	26	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
39	d1v7la_	Alignment	not modelled	10.0	43	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
40	d1x4xa1	Alignment	not modelled	9.9	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
41	c3npgD_	Alignment	not modelled	9.9	6	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**uncharacterized duf364 family protein; **PDBTitle:** crystal structure of a protein with unknown function from duf3642 family (ph1506) from pyrococcus horikoshii at 2.70 a resolution
42	d1cuka2	Alignment	not modelled	9.9	19	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
43	d1ltza_	Alignment	not modelled	9.8	24	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
44	d1x5ia1	Alignment	not modelled	9.8	10	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
45	c3siiA_	Alignment	not modelled	9.3	60	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**poly(adp-ribose) glycohydrolase; **PDBTitle:** the x-ray crystal structure of poly(adp-ribose) glycohydrolase bound2 to the inhibitor adp-hpd from thermomonospora curvata
46	d1v5ja_	Alignment	not modelled	9.1	46	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
47	c1acyP_	Alignment	not modelled	9.1	43	**PDB header:**complex(antibody/hiv-1 fragment) **Chain:** P: **PDB Molecule:**hiv-1 gp120 (mn isolate); **PDBTitle:** crystal structure of the principal neutralizing site of hiv-2 1
48	d2b5ic1	Alignment	not modelled	9.1	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
49	d1phza2	Alignment	not modelled	9.0	35	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
50	d2haza1	Alignment	not modelled	9.0	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
51	d2oo3a1	Alignment	not modelled	9.0	50	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**LPG1296-like
52	c2pkpA_	Alignment	not modelled	8.9	43	**PDB header:**lyase **Chain:** A: **PDB Molecule:**homoaconitase small subunit; **PDBTitle:** crystal structure of 3-isopropylmalate dehydratase (leud)2 from methhanocaldococcus jannaschii dsm2661 (mj1271)
53	c3e2tA_	Alignment	not modelled	8.7	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tryptophan 5-hydroxylase 1; **PDBTitle:** the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
						Fold: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains

54	d1mlwa_	Alignment	not modelled	8.6	35	**Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
55	c2eddA_	Alignment	not modelled	8.5	14	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**netrin receptor dcc; **PDBTitle:** solution structure of the fifth fibronectin type iii domain2 of human netrin receptor dcc
56	d1j8ua_	Alignment	not modelled	8.4	35	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
57	c3ujiP_	Alignment	not modelled	8.4	43	**PDB header:**immune system **Chain:** P: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 2558 in complex with mn peptide
58	c3mlwQ_	Alignment	not modelled	8.4	43	**PDB header:**immune system **Chain:** Q: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 1006-15d in complex with an mn2 v3 peptide
59	c3mlwP_	Alignment	not modelled	8.4	43	**PDB header:**immune system **Chain:** P: **PDB Molecule:**hiv-1 gp120 third variable region (v3) crown; **PDBTitle:** crystal structure of anti-hiv-1 v3 fab 1006-15d in complex with an mn2 v3 peptide
60	c2yuxA_	Alignment	not modelled	8.4	38	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**myosin-binding protein c, slow-type; **PDBTitle:** solution structure of 3rd fibronectin type three domain of2 slow type myosin-binding protein c
61	d1n7va_	Alignment	not modelled	8.1	55	**Fold:**Adsorption protein p2 **Superfamily:**Adsorption protein p2 **Family:**Adsorption protein p2
62	d1ryqa_	Alignment	not modelled	8.0	10	**Fold:**Rubredoxin-like **Superfamily:**RNA polymerase subunits **Family:**RpoE2-like
63	d1toha_	Alignment	not modelled	7.9	41	**Fold:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Superfamily:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains **Family:**Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
64	d1ixra1	Alignment	not modelled	7.8	21	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**DNA helicase RuvA subunit, middle domain
65	d1wfta_	Alignment	not modelled	7.8	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
66	c3lpeF_	Alignment	not modelled	7.7	13	**PDB header:**transferase **Chain:** F: **PDB Molecule:**dna-directed rna polymerase subunit e''; **PDBTitle:** crystal structure of spt4/5ngn heterodimer complex from methanococcus2 jannaschii
67	c2v27A_	Alignment	not modelled	7.5	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**phenylalanine hydroxylase; **PDBTitle:** structure of the cold active phenylalanine hydroxylase from2 colwellia psychrerythraea 34h
68	d1sisa_	Alignment	not modelled	7.5	19	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
69	c1ixrA_	Alignment	not modelled	7.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruva; **PDBTitle:** ruva-ruvb complex
70	c2phmA_	Alignment	not modelled	7.4	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (phenylalanine-4-hydroxylase); **PDBTitle:** structure of phenylalanine hydroxylase dephosphorylated
71	c1kf9C_	Alignment	not modelled	7.2	12	**PDB header:**hormone/growth factor **Chain:** C: **PDB Molecule:**extracellular domain human growth hormone **PDBTitle:** phage display derived variant of human growth hormone2 complexed with two copies of the extracellular domain of3 its receptor
72	c3hhrC_	Alignment	not modelled	7.0	12	**PDB header:**hormone/receptor **Chain:** C: **PDB Molecule:**human growth hormone receptor (hghbp); **PDBTitle:** human growth hormone and extracellular domain of its2 receptor: crystal structure of the complex
73	d1chla_	Alignment	not modelled	7.0	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
74	d1p9ma3	Alignment	not modelled	6.9	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
75	d1wisa1	Alignment	not modelled	6.8	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
76	c3h7hA_	Alignment	not modelled	6.6	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt4; **PDBTitle:** crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
77	d1vlpa1	Alignment	not modelled	6.6	19	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like

78	d1x5xa1	Alignment	not modelled	6.6	6	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
79	c3dclC_	Alignment	not modelled	6.6	50	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**tm1086; **PDBTitle:** crystal structure of tm1086
80	c2erjF_	Alignment	not modelled	6.4	27	**PDB header:**immune system/cytokine **Chain:** F: **PDB Molecule:**interleukin-2 receptor beta chain; **PDBTitle:** crystal structure of the heterotrimeric interleukin-2 receptor in2 complex with interleukin-2
81	d2b5ib2	Alignment	not modelled	6.4	27	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
82	c2wgnB_	Alignment	not modelled	6.4	38	**PDB header:**hydrolase inhibitor **Chain:** B: **PDB Molecule:**inhibitor of cysteine peptidase compnd 3; **PDBTitle:** pseudomonas aeruginosa icp
83	c2yuwA_	Alignment	not modelled	6.4	21	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**myosin binding protein c, slow type; **PDBTitle:** solution structure of 2nd fibronectin domain of slow type2 myosin-binding protein c
84	d1j9ia_	Alignment	not modelled	6.4	10	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**Terminase gpNU1 subunit domain
85	d1ybea2	Alignment	not modelled	6.3	31	**Fold:**alpha/beta-Hammerhead **Superfamily:**Nicotinate/Quinolinate PRTase N-terminal domain-like **Family:**Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
86	d1x5aa1	Alignment	not modelled	6.3	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
87	c2g8yB_	Alignment	not modelled	6.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**malate/l-lactate dehydrogenases; **PDBTitle:** the structure of a putative malate/lactate dehydrogenase from e. coli.
88	d1cfba1	Alignment	not modelled	6.2	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
89	d1qg3a2	Alignment	not modelled	6.1	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
90	d2gysa2	Alignment	not modelled	6.0	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
91	d3d4ub1	Alignment	not modelled	5.9	50	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Tick carboxypeptidase inhibitor-like
92	c2yrzA_	Alignment	not modelled	5.9	38	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**integrin beta-4; **PDBTitle:** solution structure of the fibronectin type iii domain of2 human integrin beta-4
93	d2b3ya1	Alignment	not modelled	5.9	43	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**LeuD-like
94	d2ixta1	Alignment	not modelled	5.8	27	**Fold:**Subtilisin-like **Superfamily:**Subtilisin-like **Family:**Subtilases
95	d1u5tb1	Alignment	not modelled	5.8	36	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Vacuolar sorting protein domain
96	c2e7hA_	Alignment	not modelled	5.7	31	**PDB header:**transferase, signaling protein **Chain:** A: **PDB Molecule:**ephrin type-b receptor 4; **PDBTitle:** solution structure of the second fn3 domain from human2 ephrin type-b receptor 4
97	d1uema_	Alignment	not modelled	5.5	31	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III
98	d2k49a1	Alignment	not modelled	5.5	29	**Fold:**YegP-like **Superfamily:**YegP-like **Family:**YegP-like
99	d2crma1	Alignment	not modelled	5.4	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Fibronectin type III **Family:**Fibronectin type III