Phyre^2

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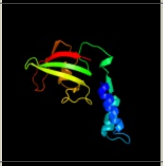
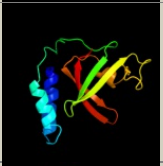
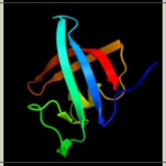
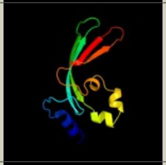
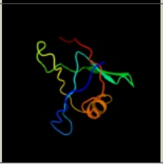
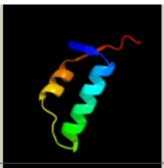
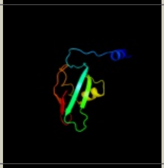
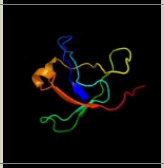
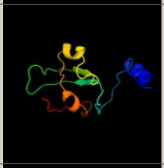
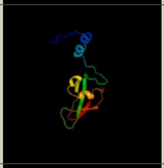
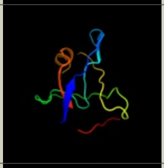
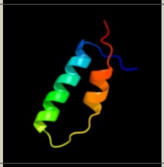
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bmbB_	Alignment		100.0	100	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
2	c2pn0D_	Alignment		100.0	48	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
3	c2p4vA_	Alignment		100.0	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
4	c1grjA_	Alignment		100.0	23	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
5	c2etnA_	Alignment		99.9	27	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
6	d2f23a2	Alignment		99.9	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
7	d2etna2	Alignment		99.9	30	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
8	d1grja2	Alignment		99.9	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
9	c3gtyX_	Alignment		92.1	16	**PDB header:**chaperone/ribosomal protein **Chain:** X: **PDB Molecule:**trigger factor; **PDBTitle:** promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
10	d1krha1	Alignment		91.0	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
11	d1fdra1	Alignment		84.7	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like

12	d1grja1	Alignment		83.4	27	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
13	d2cnda1	Alignment		78.8	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
14	d1t11a3	Alignment		78.8	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
15	d1gvha2	Alignment		78.5	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
16	d1w26a3	Alignment		75.6	11	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
17	c1w26B_	Alignment		75.5	15	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
18	d1a8pa1	Alignment		72.6	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
19	d2f23a1	Alignment		72.5	27	**Fold:**Long alpha-hairpin **Superfamily:**GreA transcript cleavage protein, N-terminal domain **Family:**GreA transcript cleavage protein, N-terminal domain
20	c2l55A_	Alignment		70.1	19	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**silb,silver efflux protein, mfp component of the three **PDBTitle:** solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
21	d2j3sa2	Alignment	not modelled	69.8	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
22	d1qx4a1	Alignment	not modelled	67.3	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
23	c2gpjA_	Alignment	not modelled	65.3	15	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
24	d1ndha1	Alignment	not modelled	65.0	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
25	c1krhA_	Alignment	not modelled	58.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
26	d1ep3b1	Alignment	not modelled	58.0	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
27	c1t11A_	Alignment	not modelled	55.8	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
28	d1tvca1	Alignment	not modelled	54.8	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
						Fold: Reductase/isomerase/elongation factor common domain

29	d1qfja1	Alignment	not modelled	53.4	13	**Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
30	d2piaa1	Alignment	not modelled	51.4	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
31	d1l1pa_	Alignment	not modelled	49.7	16	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
32	c2kr7A_	Alignment	not modelled	49.7	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
33	c2kfwA_	Alignment	not modelled	48.3	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
34	d1umka1	Alignment	not modelled	47.0	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
35	c1a8pA_	Alignment	not modelled	46.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
36	c2k7pA_	Alignment	not modelled	39.4	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 16-17
37	c2jf1A_	Alignment	not modelled	37.9	26	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the filamin a repeat 21 complexed with2 the integrin beta2 cytoplasmic tail peptide
38	c2k7qA_	Alignment	not modelled	37.6	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-a; **PDBTitle:** filamin a ig-like domains 18-19
39	d1fnda1	Alignment	not modelled	36.6	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
40	c1hxvA_	Alignment	not modelled	35.8	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor
41	d1hxva_	Alignment	not modelled	35.8	15	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
42	d1gawa1	Alignment	not modelled	35.1	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
43	c2k8iA_	Alignment	not modelled	31.9	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
44	d2d7na1	Alignment	not modelled	30.5	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
45	d2d7ma1	Alignment	not modelled	29.9	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
46	c3pr9A_	Alignment	not modelled	29.7	29	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
47	c3cgnA_	Alignment	not modelled	27.6	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
48	d2dmca1	Alignment	not modelled	26.7	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
49	c2bgjB_	Alignment	not modelled	26.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
50	d2bmwa1	Alignment	not modelled	25.0	14	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
51	c3h0gE_	Alignment	not modelled	23.5	22	**PDB header:**transcription **Chain:** E: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
52	d2e9ia1	Alignment	not modelled	23.4	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
53	c2l27B_	Alignment	not modelled	23.4	26	**PDB header:**membrane protein, peptide binding protei **Chain:** B: **PDB Molecule:**peptide agonist; **PDBTitle:** nmr structure of the ecd1 of crf-r1 in complex with a peptide agonist
54	d1cqxa2	Alignment	not modelled	23.1	11	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
55	c2pbcD_	Alignment	not modelled	22.2	18	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**fk506-binding protein 2; **PDBTitle:** fk506-binding protein 2
						PDB header:chaperone, isomerase

56	c3prdA_	Alignment	not modelled	22.1	29	**Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
57	d1eika_	Alignment	not modelled	21.8	13	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
58	c2rmfA_	Alignment	not modelled	21.5	22	**PDB header:**hormone **Chain:** A: **PDB Molecule:**urocortin; **PDBTitle:** human urocortin 1
59	d2diaa1	Alignment	not modelled	21.4	23	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
60	c1zeqX_	Alignment	not modelled	21.3	7	**PDB header:**metal binding protein **Chain:** X: **PDB Molecule:**cation efflux system protein cusf; **PDBTitle:** 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
61	d2iv2x1	Alignment	not modelled	21.1	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
62	d1ix5a_	Alignment	not modelled	21.0	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
63	c2h8rA_	Alignment	not modelled	20.7	14	**PDB header:**transcription activator/dna **Chain:** A: **PDB Molecule:**hepatocyte nuclear factor 1-beta; **PDBTitle:** hepatocyte nuclear factor 1b bound to dna: mody5 gene2 product
64	d1t9fa_	Alignment	not modelled	20.1	47	**Fold:**beta-Trefoil **Superfamily:**MIR domain **Family:**MIR domain
65	c2vn1A_	Alignment	not modelled	20.1	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidylprolyl isomerase; **PDBTitle:** crystal structure of the fk506-binding domain of plasmodium2 falciparum fkbp35 in complex with fk506
66	c2piaA_	Alignment	not modelled	20.0	16	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
67	d2dj4a1	Alignment	not modelled	19.5	26	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
68	c2e9jA_	Alignment	not modelled	19.1	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**filamin-b; **PDBTitle:** solution structure of the 14th filamin domain from human2 filamin-b
69	c2lgoA_	Alignment	not modelled	19.1	10	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp; **PDBTitle:** solution nmr structure of a fkbp-type peptidyl-prolyl cis-trans2 isomerase from giardia lamblia, seattle structural genomics center3 for infectious disease target gilaa.00840.a
70	c3entB_	Alignment	not modelled	18.7	25	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of nitrollin, a betagamma-crystallin from2 nitrosospira multiformis-in alternate space group (p65)
71	d1rl2a1	Alignment	not modelled	18.4	20	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
72	d1kt0a2	Alignment	not modelled	18.1	8	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
73	d1h0ha1	Alignment	not modelled	17.8	26	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
74	d2jioa1	Alignment	not modelled	17.4	29	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
75	d1vqoa1	Alignment	not modelled	17.4	17	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**C-terminal domain of ribosomal protein L2
76	d1q1ca1	Alignment	not modelled	17.2	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
77	c2ka3C_	Alignment	not modelled	17.2	33	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**emilin-1; **PDBTitle:** structure of emilin-1 c1q-like domain
78	d1qfha1	Alignment	not modelled	17.2	19	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
79	c1wlfA_	Alignment	not modelled	17.0	26	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisome biogenesis factor 1; **PDBTitle:** structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
80	d1dzfa2	Alignment	not modelled	16.9	23	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
81	c2opgB_	Alignment	not modelled	16.4	19	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**multiple pdz domain protein; **PDBTitle:** the crystal structure of the 10th pdz domain of mpdz
82	c3o5fA_	Alignment	not modelled	15.6	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase

82	[illegible]	Alignment	not modelled	15.6	14	fkbp5; **PDBTitle:** fk1 domain of fkbp51, crystal form vii
83	d1c9ha_	Alignment	not modelled	15.6	7	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
84	c2xvsA_	Alignment	not modelled	14.9	14	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**tetratricopeptide repeat protein 5; **PDBTitle:** crystal structure of human ttc5 (strap) c-terminal ob2 domain
85	c3shwA_	Alignment	not modelled	14.9	19	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**tight junction protein zo-1; **PDBTitle:** crystal structure of zo-1 pdz3-sh3-guk supramodule complex with2 connexin-45 peptide
86	c1qfhB_	Alignment	not modelled	14.4	19	**PDB header:**actin binding protein **Chain:** B: **PDB Molecule:**protein (gelation factor); **PDBTitle:** dimerization of gelation factor from dictyostelium2 discoideum: crystal structure of rod domains 5 and 6
87	c2pmzV_	Alignment	not modelled	14.2	17	**PDB header:**translation, transferase **Chain:** V: **PDB Molecule:**dna-directed rna polymerase subunit h; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
88	d2d7pa1	Alignment	not modelled	14.0	16	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
89	c3cnkB_	Alignment	not modelled	13.9	23	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**filamin-a; **PDBTitle:** crystal structure of the dimerization domain of human2 filamin a
90	d1ogya1	Alignment	not modelled	13.8	23	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
91	c3pr3B_	Alignment	not modelled	13.8	33	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of plasmodium falciparum glucose-6-phosphate2 isomerase (pf14_0341) in complex with fructose-6-phosphate
92	d1r5pa_	Alignment	not modelled	13.8	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
93	d2diba1	Alignment	not modelled	13.6	29	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
94	d1cm3a_	Alignment	not modelled	13.3	20	**Fold:**HPr-like **Superfamily:**HPr-like **Family:**HPr-like
95	d1gr3a_	Alignment	not modelled	13.1	28	**Fold:**TNF-like **Superfamily:**TNF-like **Family:**TNF-like
96	c1gr3A_	Alignment	not modelled	13.1	28	**PDB header:**collagen **Chain:** A: **PDB Molecule:**collagen x; **PDBTitle:** structure of the human collagen x nc1 trimer
97	d1vlfm1	Alignment	not modelled	12.8	22	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Formate dehydrogenase/DMSO reductase, C-terminal domain
98	c3ujhB_	Alignment	not modelled	12.7	47	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glucose-6-phosphate isomerase; **PDBTitle:** crystal structure of substrate-bound glucose-6-phosphate isomerase2 from toxoplasma gondii
99	c3fpkB_	Alignment	not modelled	12.6	16	**PDB header:**flavoprotein, oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium