Phyre^2

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Description	P0AEM0
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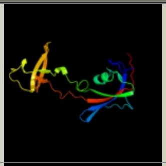
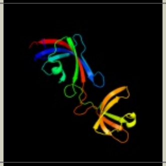
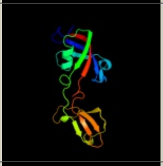
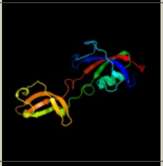
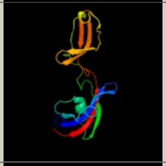
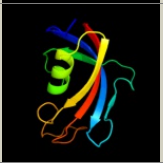
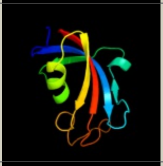
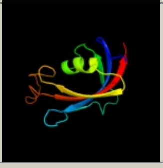
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kfwA_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
2	c2k8iA_	Alignment		100.0	31	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
3	c2kr7A_	Alignment		100.0	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
4	c3cgnA_	Alignment		100.0	30	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
5	c3pr9A_	Alignment		100.0	30	**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
6	c3prdA_	Alignment		100.0	29	**PDB header:**chaperone, isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** structural analysis of protein folding by the methanococcus jannaschii2 chaperone fkbp26
7	d1ix5a_	Alignment		100.0	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
8	c1q6uA_	Alignment		99.8	32	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; **PDBTitle:** crystal structure of fkpa from escherichia coli
9	d1q6ha_	Alignment		99.8	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
10	c2pbcD_	Alignment		99.8	34	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**fk506-binding protein 2; **PDBTitle:** fk506-binding protein 2
11	d1c9ha_	Alignment		99.8	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase

12	d1fd9a_	Alignment		99.8	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
13	d2ppna1	Alignment		99.8	33	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	d1yata_	Alignment		99.8	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
15	c3jxvA_	Alignment		99.8	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidyl-prolyl isomerase; **PDBTitle:** crystal structure of the 3 fkbp domains of wheat fkbp73
16	c2vcdA_	Alignment		99.8	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**outer membrane protein mip; **PDBTitle:** solution structure of the fkbp-domain of legionella2 pneumophila mip in complex with rapamycin
17	c1rouA_	Alignment		99.7	31	**PDB header:**rotamase (isomerase) **Chain:** A: **PDB Molecule:**fkbp59-i; **PDBTitle:** structure of fkbp59-i, the n-terminal domain of a 59 kda2 fk506-binding protein, nmr, 22 structures
18	c2lgoA_	Alignment		99.7	32	**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
19	c2vn1A_	Alignment		99.7	25	**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
20	d1q1ca1	Alignment		99.7	31	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
21	d1r9ha_	Alignment	not modelled	99.7	30	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
22	c2jwxA_	Alignment	not modelled	99.7	19	**PDB header:**apoptosis, isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant; **PDBTitle:** solution structure of the n-terminal domain of human fkbp382 (fkbp38ntd)
23	c3o5fA_	Alignment	not modelled	99.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** fk1 domain of fkbp51, crystal form vii
24	d1pbka_	Alignment	not modelled	99.7	27	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
25	c2f4eB_	Alignment	not modelled	99.7	21	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**atfkbp42; **PDBTitle:** n-terminal domain of fkbp42 from arabidopsis thaliana
26	d1jvwa_	Alignment	not modelled	99.7	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
27	c2ke0A_	Alignment	not modelled	99.7	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
28	c3o5dB_	Alignment	not modelled	99.7	21	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** crystal structure of a fragment of fkbp51 comprising the fk1 and fk22 domains

29	c2d9fA_	Alignment	not modelled	99.7	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant; **PDBTitle:** solution structure of ruh-047, an fkbp domain from human2 cdna
30	c3oe2A_	Alignment	not modelled	99.7	24	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** 1.6 a crystal structure of peptidyl-prolyl cis-trans isomerase ppiase2 from pseudomonas syringae pv. tomato str. dc3000 (pspto dc3000)
31	c1q1cA_	Alignment	not modelled	99.7	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of n(1-260) of human fkbp52
32	d1u79a_	Alignment	not modelled	99.6	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
33	d1kt0a2	Alignment	not modelled	99.6	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
34	d1l1pa_	Alignment	not modelled	99.6	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
35	d1kt0a3	Alignment	not modelled	99.6	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
36	d1hxva_	Alignment	not modelled	99.6	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
37	c1hxvA_	Alignment	not modelled	99.6	25	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor
38	c1kt0A_	Alignment	not modelled	99.6	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**51 kda fk506-binding protein; **PDBTitle:** structure of the large fkbp-like protein, fkbp51, involved in steroid2 receptor complexes
39	d1q1ca2	Alignment	not modelled	99.6	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
40	d1kt1a3	Alignment	not modelled	99.5	18	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
41	c3b7xA_	Alignment	not modelled	99.5	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 6; **PDBTitle:** crystal structure of human fk506-binding protein 6
42	d1t11a3	Alignment	not modelled	99.5	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
43	d1w26a3	Alignment	not modelled	99.4	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
44	d1kt1a2	Alignment	not modelled	99.4	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
45	c2if4A_	Alignment	not modelled	99.4	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
46	c1qz2B_	Alignment	not modelled	99.2	22	**PDB header:**isomerase/chaperone **Chain:** B: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of fkbp52 c-terminal domain complex with2 the c-terminal peptide meevd of hsp90
47	c1w26B_	Alignment	not modelled	99.1	24	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
48	c1t11A_	Alignment	not modelled	99.1	22	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
49	c3gtyX_	Alignment	not modelled	98.6	20	**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
50	c3htxA_	Alignment	not modelled	96.9	23	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1
51	c2e6zA_	Alignment	not modelled	77.9	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
52	d1vhka1	Alignment	not modelled	58.3	15	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
53	d1nxza1	Alignment	not modelled	56.2	16	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
54	d1qfha1	Alignment	not modelled	47.2	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Filamin repeat (rod domain)
55	d2g50a1	Alignment	not modelled	45.8	13	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain

56	d1pkma1	Alignment	not modelled	44.4	15	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
57	c3fm3B_	Alignment	not modelled	39.2	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** crystal structure of an encephalitozoon cuniculi methionine2 aminopeptidase type 2
58	c1b6aA_	Alignment	not modelled	36.1	6	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
59	c2jvvA_	Alignment	not modelled	31.2	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
60	c2kvqG_	Alignment	not modelled	31.2	12	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
61	c2khjA_	Alignment	not modelled	30.1	12	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**30s ribosomal protein s1; **PDBTitle:** nmr structure of the domain 6 of the e. coli ribosomal2 protein s1
62	c2v6cA_	Alignment	not modelled	29.8	24	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** crystal structure of erbb3 binding protein 1 (ebp1)
63	c1qfhB_	Alignment	not modelled	29.7	18	**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
64	c1yw7A_	Alignment	not modelled	29.7	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
65	d1liua1	Alignment	not modelled	29.5	13	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
66	c3s6bA_	Alignment	not modelled	26.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
67	c2p4vA_	Alignment	not modelled	25.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
68	c2ds4A_	Alignment	not modelled	24.7	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**tripartite motif protein 45; **PDBTitle:** solution structure of the filamin domain from human2 tripartite motif protein 45
69	d1nz9a_	Alignment	not modelled	24.4	14	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
70	d2etna2	Alignment	not modelled	23.8	32	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
71	d2f23a2	Alignment	not modelled	22.8	32	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
72	c3besR_	Alignment	not modelled	21.1	22	**PDB header:**immune system **Chain:** R: **PDB Molecule:**interferon-gamma binding protein c4r; **PDBTitle:** structure of a poxvirus ifngbp/ifng complex
73	c2q8kA_	Alignment	not modelled	20.8	22	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** the crystal structure of ebp1
74	c3pxpA_	Alignment	not modelled	20.4	18	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**helix-turn-helix domain protein; **PDBTitle:** crystal structure of a pas and dna binding domain containing protein2 (caur_2278) from chloroflexus aurantiacus j-10-fl at 2.30 a3 resolution
75	d1fw8a_	Alignment	not modelled	18.8	53	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
76	c2etnA_	Alignment	not modelled	18.7	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
77	d2hi6a1	Alignment	not modelled	18.3	21	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**LeuD/IlvD-like **Family:**AF0055-like
78	c2equA_	Alignment	not modelled	18.1	25	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
79	d1kk1a2	Alignment	not modelled	17.5	16	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
80	c1vhkA_	Alignment	not modelled	16.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
81	c3qiiA_	Alignment	not modelled	16.7	29	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20

82	d1s0ua2	Alignment	not modelled	16.4	18	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
83	d1pkla1	Alignment	not modelled	16.3	11	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
84	c2g6pA_	Alignment	not modelled	16.3	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** crystal structure of truncated (delta 1-89) human methionine2 aminopeptidase type 1 in complex with pyridyl pyrimidine derivative
85	c2gz5A_	Alignment	not modelled	16.3	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
86	d1oz2a3	Alignment	not modelled	15.7	5	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
87	d1f00i1	Alignment	not modelled	15.7	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Invasin/intimin cell-adhesion fragments **Family:**Invasin/intimin cell-adhesion fragments
88	c1xezA_	Alignment	not modelled	15.4	24	**PDB header:**toxin **Chain:** A: **PDB Molecule:**hemolysin; **PDBTitle:** crystal structure of the vibrio cholerae cytolysin (hlya)2 pro-toxin with octylglucoside bound
89	c3k2yD_	Alignment	not modelled	14.7	10	**PDB header:**nucleotide binding protein **Chain:** D: **PDB Molecule:**uncharacterized protein lp_0118; **PDBTitle:** crystal structure of protein lp_0118 from lactobacillus2 plantarum,northeast structural genomics consortium target3 lpr91b
90	c2jz2A_	Alignment	not modelled	14.6	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ssl0352 protein; **PDBTitle:** solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
91	d1c8za_	Alignment	not modelled	14.6	18	**Fold:**Tubby C-terminal domain-like **Superfamily:**Tubby C-terminal domain-like **Family:**Transcriptional factor tubby, C-terminal domain
92	d1wjsa_	Alignment	not modelled	14.5	13	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
93	d1jnsa_	Alignment	not modelled	14.1	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
94	d2qn6a2	Alignment	not modelled	13.9	18	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain **Family:**EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
95	c1xgnB_	Alignment	not modelled	13.7	16	**PDB header:**aminopeptidase **Chain:** B: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** methionine aminopeptidase from hyperthermophile pyrococcus2 furiosus
96	c3bmbB_	Alignment	not modelled	13.4	11	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
97	d1ea9c2	Alignment	not modelled	13.4	31	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
98	d2do3a1	Alignment	not modelled	13.4	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
99	d1je3a_	Alignment	not modelled	13.4	20	**Fold:**IF3-like **Superfamily:**SirA-like **Family:**SirA-like