Phyre^2

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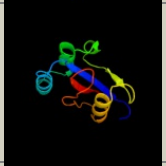
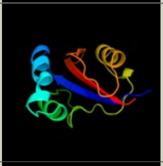
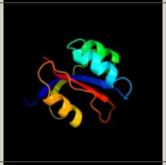
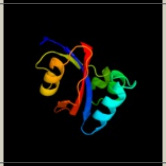
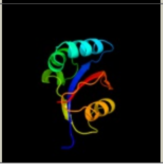
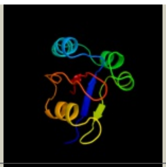
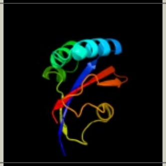
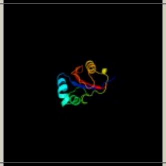
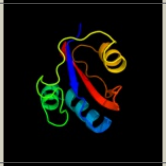
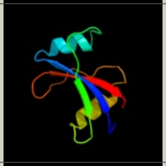
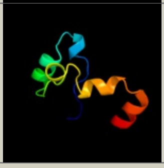
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jnsa_	Alignment		100.0	100	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
2	c2rqsA_	Alignment		99.9	47	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
3	d1eq3a_	Alignment		99.9	35	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
4	c1zk6A_	Alignment		99.9	42	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** nmr solution structure of b. subtilis prsa ppiase
5	c3gpkA_	Alignment		99.9	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ppic-type peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of ppic-type peptidyl-prolyl cis-trans isomerase2 domain at 1.55a resolution.
6	d1pina2	Alignment		99.9	41	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
7	d2pv2a1	Alignment		99.9	34	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
8	d1m5ya3	Alignment		99.9	33	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
9	c2jzvA_	Alignment		99.9	33	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**foldase protein prsa; **PDBTitle:** solution structure of s. aureus prsa-ppiase
10	c1f8aB_	Alignment		99.9	36	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
11	c1yw5A_	Alignment		99.9	36	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans

12	d1j6ya_	Alignment		99.9	39	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
13	c2kgjA_	Alignment		99.9	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase d; **PDBTitle:** solution structure of parvulin domain of ppid from e.coli
14	c1m5yB_	Alignment		99.8	31	**PDB header:**isomerase, cell cycle **Chain:** B: **PDB Molecule:**survival protein sura; **PDBTitle:** crystallographic structure of sura, a molecular chaperone2 that facilitates outer membrane porin folding
15	c2pv3B_	Alignment		99.7	26	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**chaperone sura; **PDBTitle:** crystallographic structure of sura fragment lacking the second2 peptidyl-prolyl isomerase domain complexed with peptide nftlkfwdifrk
16	c3nrkA_	Alignment		99.7	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**lic12922; **PDBTitle:** the crystal structure of the leptospiral hypothetical protein lic12922
17	c3rfwA_	Alignment		99.7	40	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cell-binding factor 2; **PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally-related sura-like chaperones in the human pathogen3 campylobacter jejuni
18	c3rgcB_	Alignment		99.2	12	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**possible periplasmic protein; **PDBTitle:** the virulence factor peb4 and the periplasmic protein cj1289 are two2 structurally related sura-like chaperones in the human pathogen3 campylobacter jejuni
19	c3prdA_	Alignment		31.8	30	**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
20	d1vz0a1	Alignment		30.7	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
21	d1zata2	Alignment	not modelled	27.2	13	**Fold:**L,D-transpeptidase pre-catalytic domain-like **Superfamily:**L,D-transpeptidase pre-catalytic domain-like **Family:**L,D-transpeptidase pre-catalytic domain-like
22	c2elhA_	Alignment	not modelled	22.0	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**cg11849-pa; **PDBTitle:** solution structure of the cenp-b n-terminal dna-binding2 domain of fruit fly distal antenna cg11849-pa
23	d2coba1	Alignment	not modelled	17.9	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Psq domain
24	c1r71B_	Alignment	not modelled	16.2	13	**PDB header:**transcription/dna **Chain:** B: **PDB Molecule:**transcriptional repressor protein korb; **PDBTitle:** crystal structure of the dna binding domain of korb in2 complex with the operator dna
25	d1dwka1	Alignment	not modelled	15.7	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Cyanase N-terminal domain
26	d1q1ca2	Alignment	not modelled	15.3	11	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
27	d1r71a_	Alignment	not modelled	14.3	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**KorB DNA-binding domain-like **Family:**KorB DNA-binding domain-like
28	c2iv1J_	Alignment	not modelled	13.7	14	**PDB header:**lyase **Chain:** J: **PDB Molecule:**cyanate hydratase; **PDBTitle:** site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
						Fold:DNA/RNA-binding 3-helical bundle

29	d1y0ua_	Alignment	not modelled	12.4	14	**Superfamily:**"Winged helix" DNA-binding domain **Family:**ArsR-like transcriptional regulators
30	c1q6uA_	Alignment	not modelled	12.3	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; **PDBTitle:** crystal structure of fkpa from escherichia coli
31	d1q6ha_	Alignment	not modelled	11.9	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
32	c1m98A_	Alignment	not modelled	11.5	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
33	c2phcB_	Alignment	not modelled	11.5	27	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein ph0987; **PDBTitle:** crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
34	d1kt1a3	Alignment	not modelled	11.4	20	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
35	d2ppna1	Alignment	not modelled	11.3	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
36	c3mmlD_	Alignment	not modelled	11.2	27	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**allophanate hydrolase subunit 1; **PDBTitle:** allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
37	d1kt0a3	Alignment	not modelled	10.7	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
38	c2vcdA_	Alignment	not modelled	10.6	17	**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
39	d1ix5a_	Alignment	not modelled	10.2	18	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
40	c2lgoA_	Alignment	not modelled	9.9	13	**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
41	c2zp2B_	Alignment	not modelled	9.8	36	**PDB header:**transferase inhibitor **Chain:** B: **PDB Molecule:**kinase a inhibitor; **PDBTitle:** c-terminal domain of kipi from bacillus subtilis
42	d1jvwa_	Alignment	not modelled	9.6	12	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
43	d1yata_	Alignment	not modelled	9.2	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
44	c3pr9A_	Alignment	not modelled	9.2	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
45	d1fd9a_	Alignment	not modelled	9.1	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
46	c3bmbB_	Alignment	not modelled	9.0	12	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
47	c3o5fA_	Alignment	not modelled	8.8	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** fk1 domain of fkbp51, crystal form vii
48	c3dnlB_	Alignment	not modelled	8.8	23	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the b12-2 bound state
49	d2phcb1	Alignment	not modelled	8.5	27	**Fold:**Cyclophilin-like **Superfamily:**Cyclophilin-like **Family:**PH0987 C-terminal domain-like
50	c3oe2A_	Alignment	not modelled	8.4	13	**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)
51	d1nera_	Alignment	not modelled	8.2	14	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
52	c3hefB_	Alignment	not modelled	7.9	22	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**gene 1 protein; **PDBTitle:** crystal structure of the bacteriophage sf6 terminase small2 subunit
53	c2pbcD_	Alignment	not modelled	7.9	19	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**fk506-binding protein 2; **PDBTitle:** fk506-binding protein 2
54	d1kt0a2	Alignment	not modelled	7.9	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
						Fold:FKBP-like

55	d1c9ha_	Alignment	not modelled	7.9	6	**Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
56	c3bd1B_	Alignment	not modelled	7.6	10	**PDB header:**transcription **Chain:** B: **PDB Molecule:**cro protein; **PDBTitle:** structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
57	d1y7ma2	Alignment	not modelled	7.4	20	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
58	d1q1ca1	Alignment	not modelled	7.1	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
59	d1e0ga_	Alignment	not modelled	7.1	24	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
60	d1wfwa_	Alignment	not modelled	7.0	11	**Fold:**SH3-like barrel **Superfamily:**SH3-domain **Family:**SH3-domain
61	c2kfwA_	Alignment	not modelled	7.0	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
62	d2akja1	Alignment	not modelled	6.9	3	**Fold:**Ferredoxin-like **Superfamily:**Nitrite/Sulfite reductase N-terminal domain-like **Family:**Duplicated SiR/NiR-like domains 1 and 3
63	c2pn0D_	Alignment	not modelled	6.4	6	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
64	d2nxya1	Alignment	not modelled	6.4	23	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
65	d1yymg1	Alignment	not modelled	5.9	23	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
66	d1r9ha_	Alignment	not modelled	5.8	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
67	d2b4cg1	Alignment	not modelled	5.5	23	**Fold:**gp120 core **Superfamily:**gp120 core **Family:**gp120 core
68	d1bw6a_	Alignment	not modelled	5.5	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
69	d1pbka_	Alignment	not modelled	5.3	13	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
70	d1w5sa1	Alignment	not modelled	5.3	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
71	c2jwxA_	Alignment	not modelled	5.2	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)