Phyre^2

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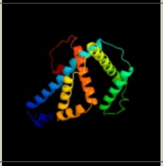
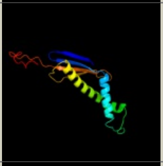
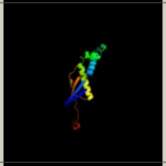
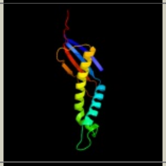
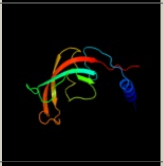
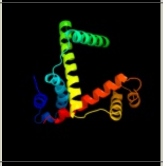
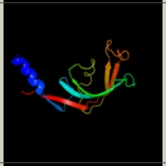
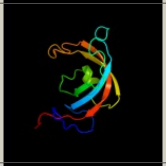
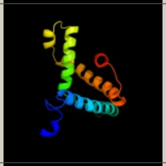
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w26B_	Alignment		100.0	97	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor in complex with the ribosome forms a2 molecular cradle for nascent proteins
2	c1t11A_	Alignment		100.0	71	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** trigger factor
3	c3gtyX_	Alignment		100.0	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
4	d1w26a1	Alignment		100.0	97	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**TF C-terminus
5	d1t11a2	Alignment		100.0	64	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
6	d1w26a2	Alignment		100.0	98	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
7	d1p9ya_	Alignment		99.9	99	**Fold:**Ribosome binding domain-like **Superfamily:**Trigger factor ribosome-binding domain **Family:**Trigger factor ribosome-binding domain
8	d1w26a3	Alignment		99.9	97	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
9	c2nsaA_	Alignment		99.9	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritim
10	d1t11a3	Alignment		99.9	74	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
11	c2nscA_	Alignment		99.8	23	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** structures of and interactions between domains of trigger factor from2 themotoga maritima

12	c2d3o1_	Alignment		99.8	23	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**trigger factor; **PDBTitle:** structure of ribosome binding domain of the trigger factor2 on the 50s ribosomal subunit from d. radiodurans
13	d1l1pa_	Alignment		99.8	99	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
14	d1t11a1	Alignment		99.8	75	**Fold:**Triger factor/SurA peptide-binding domain-like **Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**TF C-terminus
15	d1hxva_	Alignment		99.7	33	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
16	c1hxvA_	Alignment		99.7	33	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**trigger factor; **PDBTitle:** ppiase domain of the mycoplasma genitalium trigger factor
17	c3prdA_	Alignment		99.3	25	**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
18	c3pr9A_	Alignment		98.9	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
19	c3cgnA_	Alignment		98.9	35	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** crystal structure of thermophilic slyd
20	c2kfwA_	Alignment		98.8	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase **PDBTitle:** solution structure of full-length slyd from e.coli
21	c2k8iA_	Alignment	not modelled	98.8	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of e.coli slyd
22	c2pbcD_	Alignment	not modelled	98.7	28	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**fk506-binding protein 2; **PDBTitle:** fk506-binding protein 2
23	d1ix5a_	Alignment	not modelled	98.5	29	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
24	c2kr7A_	Alignment	not modelled	98.5	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase slyd; **PDBTitle:** solution structure of helicobacter pylori slyd
25	d1c9ha_	Alignment	not modelled	98.3	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
26	c1q6uA_	Alignment	not modelled	98.3	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; **PDBTitle:** crystal structure of fkpa from escherichia coli
27	c2vcdA_	Alignment	not modelled	98.3	25	**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
28	d1fd9a_	Alignment	not modelled	98.3	25	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
						Fold:FKBP-like

29	d1q6ha_	Alignment	not modelled	98.3	23	**Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
30	d1kt0a2	Alignment	not modelled	98.2	24	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
31	c2d9fA_	Alignment	not modelled	98.2	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 8 variant; **PDBTitle:** solution structure of ruh-047, an fkbp domain from human2 cdna
32	d1jvwa_	Alignment	not modelled	98.2	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
33	d2ppna1	Alignment	not modelled	98.2	22	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
34	c2vn1A_	Alignment	not modelled	98.2	20	**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
35	d1yata_	Alignment	not modelled	98.2	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
36	c2lgoA_	Alignment	not modelled	98.1	23	**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
37	c3jxvA_	Alignment	not modelled	98.1	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**70 kda peptidyl-prolyl isomerase; **PDBTitle:** crystal structure of the 3 fkbp domains of wheat fkbp73
38	c2ke0A_	Alignment	not modelled	98.1	28	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase; **PDBTitle:** solution structure of peptidyl-prolyl cis-trans isomerase from2 burkholderia pseudomallei
39	d1q1ca1	Alignment	not modelled	98.1	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
40	c1q1cA_	Alignment	not modelled	98.1	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 4; **PDBTitle:** crystal structure of n(1-260) of human fkbp52
41	c1rouA_	Alignment	not modelled	98.1	23	**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
42	c2jwxA_	Alignment	not modelled	98.1	17	**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)
43	d1kt0a3	Alignment	not modelled	98.1	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
44	c3o5dB_	Alignment	not modelled	98.0	14	**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
45	d1kt1a3	Alignment	not modelled	98.0	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
46	c3o5fA_	Alignment	not modelled	98.0	23	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase fkbp5; **PDBTitle:** fk1 domain of fkbp51, crystal form vii
47	d1kt1a2	Alignment	not modelled	98.0	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
48	d1r9ha_	Alignment	not modelled	97.9	18	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
49	d1q1ca2	Alignment	not modelled	97.9	14	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
50	d1pbka_	Alignment	not modelled	97.9	23	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
51	c3oe2A_	Alignment	not modelled	97.9	21	**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)
52	c1zxjB_	Alignment	not modelled	97.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein mg377 homolog; **PDBTitle:** crystal structure of the hypthetical mycoplasma protein,2 mpn555
53	c1qz2B_	Alignment	not modelled	97.7	9	**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
54	c1kt0A_	Alignment	not modelled	97.7	24	**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
						Fold: Triger factor/SurA peptide-binding domain-like

55	d1m5ya1	Alignment	not modelled	97.7	12	**Superfamily:**Triger factor/SurA peptide-binding domain-like **Family:**Porin chaperone SurA, peptide-binding domain
56	c3b7xA_	Alignment	not modelled	97.6	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**fk506-binding protein 6; **PDBTitle:** crystal structure of human fk506-binding protein 6
57	c2f4eB_	Alignment	not modelled	97.5	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**atfkbp42; **PDBTitle:** n-terminal domain of fkbp42 from arabidopsis thaliana
58	d1u79a_	Alignment	not modelled	96.9	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
59	c1m5yB_	Alignment	not modelled	96.9	10	**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
60	c2if4A_	Alignment	not modelled	96.3	12	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**atfkbp42; **PDBTitle:** crystal structure of a multi-domain immunophilin from2 arabidopsis thaliana
61	c2pv3B_	Alignment	not modelled	93.5	14	**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
62	c3nrkA_	Alignment	not modelled	91.0	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**lic12922; **PDBTitle:** the crystal structure of the leptospiral hypothetical protein lic12922
63	c2p4vA_	Alignment	not modelled	90.8	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor greb; **PDBTitle:** crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
64	c3htxA_	Alignment	not modelled	89.4	17	**PDB header:**transferase/rna **Chain:** A: **PDB Molecule:**hen1; **PDBTitle:** crystal structure of small rna methyltransferase hen1
65	c3rgcB_	Alignment	not modelled	88.7	7	**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
66	c1grjA_	Alignment	not modelled	84.0	14	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**grea protein; **PDBTitle:** grea transcript cleavage factor from escherichia coli
67	c3bmbB_	Alignment	not modelled	79.7	17	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
68	c2etnA_	Alignment	not modelled	74.3	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-cleavage anti-grea transcription factor **PDBTitle:** crystal structure of thermus aquaticus gfh1
69	d2f23a2	Alignment	not modelled	72.2	19	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
70	c3s6bA_	Alignment	not modelled	66.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** crystal structure of methionine aminopeptidase 1b from plasmodium2 falciparum, pf10_0150
71	d1jmxa1	Alignment	not modelled	66.1	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
72	d2etna2	Alignment	not modelled	65.6	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
73	c3rfwA_	Alignment	not modelled	65.3	24	**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
74	d1pbya1	Alignment	not modelled	63.3	5	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
75	c2pn0D_	Alignment	not modelled	55.4	18	**PDB header:**transcription **Chain:** D: **PDB Molecule:**prokaryotic transcription elongation factor **PDBTitle:** prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
76	c2wwbA_	Alignment	not modelled	51.2	11	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**protein transport protein sec61 subunit alpha isoform 1; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
77	c3j01A_	Alignment	not modelled	48.9	17	**PDB header:**ribosome/ribosomal protein **Chain:** A: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** structure of the ribosome-secye complex in the membrane environment
78	c3dinF_	Alignment	not modelled	43.6	19	**PDB header:**membrane protein, protein transport **Chain:** F: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
79	d1grja2	Alignment	not modelled	43.3	15	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**GreA transcript cleavage factor, C-terminal domain
						PDB header:ribosome

80	c2wwaA_	Alignment	not modelled	42.8	13	**Chain:** A: **PDB Molecule:**sec sixty-one protein homolog; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
81	c3dl8H_	Alignment	not modelled	42.6	24	**PDB header:**protein transport **Chain:** H: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
82	d1b8za_	Alignment	not modelled	41.9	32	**Fold:**IHF-like DNA-binding proteins **Superfamily:**IHF-like DNA-binding proteins **Family:**Prokaryotic DNA-bending protein
83	c2akiY_	Alignment	not modelled	41.0	25	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** normal mode-based flexible fitted coordinates of a2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
84	c3mp7A_	Alignment	not modelled	35.8	38	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase subunit secy; **PDBTitle:** lateral opening of a translocon upon entry of protein suggests the2 mechanism of insertion into membranes
85	c2zqpY_	Alignment	not modelled	33.8	17	**PDB header:**protein transport **Chain:** Y: **PDB Molecule:**preprotein translocase secy subunit; **PDBTitle:** crystal structure of secye translocon from thermus2 thermophilus
86	c2rhfA_	Alignment	not modelled	31.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna helicase recq; **PDBTitle:** d. radiodurans recq hrdc domain 3
87	c1yw7A_	Alignment	not modelled	30.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 2; **PDBTitle:** h-metap2 complexed with a444148
88	c2q8kA_	Alignment	not modelled	30.2	26	**PDB header:**transcription **Chain:** A: **PDB Molecule:**proliferation-associated protein 2g4; **PDBTitle:** the crystal structure of ebp1
89	c3i18A_	Alignment	not modelled	28.9	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo2051 protein; **PDBTitle:** crystal structure of the pdz domain of the sdrc-like protein2 (lmo2051) from listeria monocytogenes, northeast structural3 genomics consortium target lmr166b
90	c1b6aA_	Alignment	not modelled	28.4	19	**PDB header:**angiogenesis inhibitor **Chain:** A: **PDB Molecule:**methionine aminopeptidase; **PDBTitle:** human methionine aminopeptidase 2 complexed with tnp-470
91	c2bpbB_	Alignment	not modelled	27.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**sulfite\:cytochrome c oxidoreductase subunit b; **PDBTitle:** sulfite dehydrogenase from starkeya novella
92	c1yx3A_	Alignment	not modelled	26.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dsrc; **PDBTitle:** nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
93	c2g6pA_	Alignment	not modelled	25.9	19	**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
94	c2gz5A_	Alignment	not modelled	25.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**methionine aminopeptidase 1; **PDBTitle:** human type 1 methionine aminopeptidase in complex with ovalicin at 1.12 ang
95	d1hmja_	Alignment	not modelled	25.8	16	**Fold:**RPB5-like RNA polymerase subunit **Superfamily:**RPB5-like RNA polymerase subunit **Family:**RPB5
96	d1wuda1	Alignment	not modelled	24.6	17	**Fold:**SAM domain-like **Superfamily:**HRDC-like **Family:**HRDC domain from helicases
97	d1qxya_	Alignment	not modelled	23.6	19	**Fold:**Creatinase/aminopeptidase **Superfamily:**Creatinase/aminopeptidase **Family:**Creatinase/aminopeptidase
98	c2xzmO_	Alignment	not modelled	23.0	11	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rps13e; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
99	c2vcbA_	Alignment	not modelled	22.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylglucosaminidase; **PDBTitle:** family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac