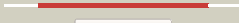

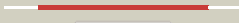















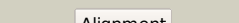


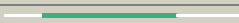

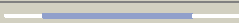



Phyre2

Email nfitzkee@chemistry.msstate.edu
 Description Isomerase
 Date Wed Jun 1 16:30:56 BST 2016
 Unique Job ID 6ef3ff44243acdf6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1jnsa_	Alignment		99.9	49	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
2	d1m5ya3	Alignment		99.9	40	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
3	d2pv2a1	Alignment		99.9	37	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
4	d1eq3a_	Alignment		99.9	41	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
5	c1zk6A_	Alignment		99.9	49	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: nmr solution structure of b. subtilis prsa ppiase
6	c3gpkA_	Alignment		99.9	26	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.
7	c2rqsA_	Alignment		99.9	49	PDB header: isomerase Chain: A: PDB Molecule: parvulin-like peptidyl-prolyl isomerase; PDBTitle: 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
8	d1pina2	Alignment		99.9	52	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
9	c2jzvA_	Alignment		99.9	51	PDB header: isomerase Chain: A: PDB Molecule: foldase protein prsa; PDBTitle: solution structure of s. aureus prsa-ppiase
10	c1f8aB_	Alignment		99.9	48	PDB header: isomerase Chain: B: PDB Molecule: peptidyl-prolyl cis-trans isomerase nima-interacting 1; PDBTitle: structural basis for the phosphoserine-proline recognition by group iv2 ww domains
11	c2kgjA_	Alignment		99.9	32	PDB header: isomerase Chain: A: PDB Molecule: peptidyl-prolyl cis-trans isomerase d; PDBTitle: solution structure of parvulin domain of ppid from e.coli

12	d1j6ya_	 Alignment		99.9	54	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
13	c1yw5A_	 Alignment		99.9	41	PDB header: isomerase Chain: A; PDB Molecule: peptidyl prolyl cis/trans isomerase; PDBTitle: peptidyl-prolyl isomerase ess1 from candida albicans
14	c2lj4A_	 Alignment		99.9	42	PDB header: isomerase Chain: A; PDB Molecule: peptidyl-prolyl cis-trans isomerase/rotamase, putative; PDBTitle: solution structure of the tbpin1
15	c2mntA_	 Alignment		99.9	34	PDB header: isomerase Chain: A; PDB Molecule: tbpar42; PDBTitle: solution structure of the ppiase domain of tbpar42
16	c5htfA_	 Alignment		99.8	40	PDB header: chaperone Chain: A; PDB Molecule: foldase protein prsa 1; PDBTitle: crystal structure of prsa1 from listeria monocytogenes
17	c1m5yB_	 Alignment		99.7	38	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
18	c2pv3B_	 Alignment		99.7	34	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
19	c4wo7A_	 Alignment		99.7	44	PDB header: isomerase Chain: A; PDB Molecule: foldase protein prsa; PDBTitle: crystal structure of prsa from bacillus subtilis
20	c3nrkA_	 Alignment		99.7	13	PDB header: unknown function Chain: A; PDB Molecule: lic12922; PDBTitle: the crystal structure of the leptospiral hypothetical protein lic12922
21	c5ez1B_	 Alignment	not modelled	99.7	42	PDB header: isomerase Chain: B; PDB Molecule: putative peptidyl-prolyl cis-trans isomerase hp_0175; PDBTitle: crystal structure of cell binding factor 2 from helicobacter pylori in2 complex with i2ca
22	c3rfwA_	 Alignment	not modelled	99.7	47	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
23	c3rgcB_	 Alignment	not modelled	99.2	9	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
24	d1vz0a1	 Alignment	not modelled	42.1	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
25	c3prdA_	 Alignment	not modelled	27.9	20	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
26	c1r71B_	 Alignment	not modelled	22.2	18	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
27	d2coba1	 Alignment	not modelled	21.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Psq domain
						Fold: lambda repressor-like DNA-binding domains

28	d1dwka1	Alignment	not modelled	21.5	14	Superfamily: lambda repressor-like DNA-binding domains Family: Cyanase N-terminal domain
29	d1r71a_	Alignment	not modelled	20.1	18	Fold: DNA/RNA-binding 3-helical bundle Superfamily: KorB DNA-binding domain-like Family: KorB DNA-binding domain-like
30	c2iv1j_	Alignment	not modelled	18.0	14	PDB header: lyase Chain: J: PDB Molecule: cyanate hydratase; PDBTitle: site directed mutagenesis of key residues involved in the2 catalytic mechanism of cyanase
31	c2elhA_	Alignment	not modelled	15.3	24	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
32	c3bmbB_	Alignment	not modelled	13.4	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
33	c3mkyP_	Alignment	not modelled	13.3	7	PDB header: dna binding protein/dna Chain: P: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-323)-18mer dna complex, i23 form
34	d1nera_	Alignment	not modelled	13.2	10	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: Phage repressors
35	c3pr9A_	Alignment	not modelled	11.6	20	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
36	c2lgoA_	Alignment	not modelled	10.8	11	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	d1q1ca2	Alignment	not modelled	10.1	14	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
38	c1m98A_	Alignment	not modelled	10.1	23	PDB header: unknown function Chain: A: PDB Molecule: orange carotenoid protein; PDBTitle: crystal structure of orange carotenoid protein
39	d1ix5a_	Alignment	not modelled	9.7	20	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
40	c3vthA_	Alignment	not modelled	9.7	25	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
41	d1fd9a_	Alignment	not modelled	8.9	19	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
42	c2phcB_	Alignment	not modelled	8.8	36	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
43	c4dipD_	Alignment	not modelled	8.7	17	PDB header: isomerase Chain: D: PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp14; PDBTitle: crystal structure of human peptidyl-prolyl cis-trans isomerase fkbp14
44	c1vz0B_	Alignment	not modelled	8.7	15	PDB header: nuclear protein Chain: B: PDB Molecule: chromosome partitioning protein parb; PDBTitle: chromosome segregation protein spo0j from thermus2 thermophilus
45	c3mmlD_	Alignment	not modelled	8.5	36	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
46	c2pn0D_	Alignment	not modelled	8.5	17	PDB header: transcription Chain: D: PDB Molecule: prokaryotic transcription elongation factor PDBTitle: prokaryotic transcription elongation factor grea/greb from2 nitrosomonas europaea
47	c3mkzU_	Alignment	not modelled	8.0	7	PDB header: dna-binding protein/dna Chain: U: PDB Molecule: protein sobp; PDBTitle: structure of sobp(155-272)-18mer complex, p21 form
48	d1kt1a2	Alignment	not modelled	7.7	22	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
49	c1q6uA_	Alignment	not modelled	7.5	12	PDB header: isomerase Chain: A: PDB Molecule: fkbp-type peptidyl-prolyl cis-trans isomerase fkpa; PDBTitle: crystal structure of fkpa from escherichia coli
50	c3hefB_	Alignment	not modelled	7.5	26	PDB header: viral protein Chain: B: PDB Molecule: gene 1 protein; PDBTitle: crystal structure of the bacteriophage sf6 terminase small2 subunit
51	c2zp2B_	Alignment	not modelled	7.2	45	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
52	c2p4vA_	Alignment	not modelled	7.0	28	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
53	d1bw6a_	Alignment	not modelled	6.9	21	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Centromere-binding

54	c2pbcD_	Alignment	not modelled	6.7	23	PDB header: isomerase Chain: D; PDB Molecule: fk506-binding protein 2; PDBTitle: fk506-binding protein 2
55	d2etna2	Alignment	not modelled	6.6	25	Fold: FKBP-like Superfamily: FKBP-like Family: GreA transcript cleavage factor, C-terminal domain
56	c4b1p_	Alignment	not modelled	6.5	35	PDB header: transferase/dna Chain: J; PDB Molecule: rna polymerase subunit 13; PDBTitle: archaeal rnap-dna binary complex at 4.32ang
57	d2ppna1	Alignment	not modelled	6.5	15	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
58	d2phcb1	Alignment	not modelled	6.5	36	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
59	d1yata_	Alignment	not modelled	6.4	23	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
60	d1e0ga_	Alignment	not modelled	6.4	24	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
61	c4aybQ_	Alignment	not modelled	6.4	35	PDB header: transferase Chain: Q; PDB Molecule: dna-directed rna polymerase; PDBTitle: rnap at 3.2ang
62	d1y7ma2	Alignment	not modelled	6.3	15	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
63	d1uhfa_	Alignment	not modelled	6.1	12	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
64	d1kt0a3	Alignment	not modelled	6.1	8	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
65	d1kt1a3	Alignment	not modelled	6.0	8	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
66	c5b8iC_	Alignment	not modelled	6.0	13	PDB header: hydrolase Chain: C; PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: crystal structure of calcineurin a and calcineurin b in complex with2 fkbp12 and fk506 from coccidioides immitis rs
67	c3hkzY_	Alignment	not modelled	5.9	27	PDB header: transferase Chain: Y; PDB Molecule: dna-directed rna polymerase subunit 13; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
68	c2jwxA_	Alignment	not modelled	5.8	6	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)
69	c2k8iA_	Alignment	not modelled	5.7	22	PDB header: isomerase Chain: A; PDB Molecule: peptidyl-prolyl cis-trans isomerase; PDBTitle: solution structure of e.coli slyd
70	c1hxvA_	Alignment	not modelled	5.5	24	PDB header: chaperone Chain: A; PDB Molecule: trigger factor; PDBTitle: ppiase domain of the mycoplasma genitalium trigger factor
71	d1hxva_	Alignment	not modelled	5.5	24	Fold: FKBP-like Superfamily: FKBP-like Family: FKBP immunophilin/proline isomerase
72	c5fcuG_	Alignment	not modelled	5.3	31	PDB header: viral protein/immune system Chain: G; PDB Molecule: clade a/e 93th057 hiv-1 gp120 core; PDBTitle: crystal structure of the inner domain of clade a/e hiv-1 gp120 in2 complex with the adcc-potent rhesus macaque antibody jr4
73	d1e6ha_	Alignment	not modelled	5.3	31	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
74	d2akja1	Alignment	not modelled	5.3	8	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
75	c3o5fA_	Alignment	not modelled	5.2	26	PDB header: isomerase Chain: A; PDB Molecule: peptidyl-prolyl cis-trans isomerase fkbp5; PDBTitle: fk1 domain of fkbp51, crystal form vii
76	d1y0ua_	Alignment	not modelled	5.1	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: ArsR-like transcriptional regulators
77	c4rugA_	Alignment	not modelled	5.1	15	PDB header: protein binding Chain: A; PDB Molecule: slit-robo rho gtpase-activating protein 2; PDBTitle: crystal structure of slit-robo rho gtpase-activating protein 22 fragment