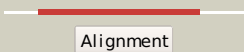

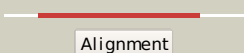



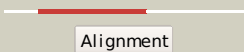

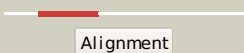







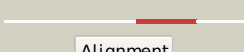


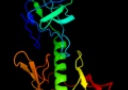
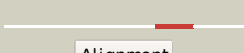












#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2zzfA_	 Alignment		100.0	31	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of alanyl-trna synthetase without2 oligomerization domain
2	c2ztgA_	 Alignment		100.0	31	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase lacking the c-terminal dimerization domain in3 complex with ala-sa
3	c3hxxA_	 Alignment		100.0	99	PDB header: ligase Chain: A: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of catalytic fragment of e. coli alars in complex2 with amppcp
4	c1yfsB_	 Alignment		100.0	55	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: the crystal structure of alanyl-trna synthetase in complex2 with l-alanine
5	d1riqa2	 Alignment		100.0	64	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
6	d1j5wa_	 Alignment		100.0	23	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
7	c3rf1B_	 Alignment		100.0	23	PDB header: ligase Chain: B: PDB Molecule: glycyl-trna synthetase alpha subunit; PDBTitle: the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
8	d1riqa1	 Alignment		100.0	41	Fold: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Superfamily: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS) Family: Putative anticodon-binding domain of alanyl-tRNA synthetase (AlaRS)
9	c3kewA_	 Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: dhha1 domain protein; PDBTitle: crystal structure of probable alanyl-trna-synthase from clostridium2 perfringens
10	c2e1bA_	 Alignment		100.0	30	PDB header: ligase, hydrolase Chain: A: PDB Molecule: 216aa long hypothetical alanyl-trna synthetase; PDBTitle: crystal structure of the alax-m trans-editing enzyme from2 pyrococcus horikoshii
11	d2e1ba2	 Alignment		100.0	25	Fold: RRF/tRNA synthetase additional domain-like Superfamily: ThrRS/AlaRS common domain Family: AlaX-like

12	d1v4pa_	Alignment		100.0	25	Fold: RRF/tRNA synthetase additional domain-like Superfamily: ThrRS/AlaRS common domain Family: AlaX-like
13	c2zvfG_	Alignment		99.9	23	PDB header: ligase Chain: G: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus alanyl-trna2 synthetase c-terminal dimerization domain
14	d1nyra3	Alignment		99.9	24	Fold: RRF/tRNA synthetase additional domain-like Superfamily: ThrRS/AlaRS common domain Family: Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
15	c1nyqA_	Alignment		99.9	22	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase 1; PDBTitle: structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
16	d1tkea2	Alignment		99.9	20	Fold: RRF/tRNA synthetase additional domain-like Superfamily: ThrRS/AlaRS common domain Family: Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
17	c1tkeA_	Alignment		99.9	15	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
18	c1qf6A_	Alignment		99.9	15	PDB header: ligase/rna Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
19	c3g98B_	Alignment		99.8	33	PDB header: ligase Chain: B: PDB Molecule: alanyl-trna synthetase; PDBTitle: crystal structure of the c-ala domain from aquifex aeolicus2 alanyl-trna synthetase
20	d2e1ba1	Alignment		99.5	33	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: AlaX-M N-terminal domain-like
21	c1ir6A_	Alignment	not modelled	95.4	18	PDB header: hydrolase Chain: A: PDB Molecule: exonuclease recj; PDBTitle: crystal structure of exonuclease recj bound to manganese
22	d1ir6a_	Alignment	not modelled	95.4	18	Fold: DHH phosphoesterases Superfamily: DHH phosphoesterases Family: Exonuclease Recj
23	d1h4vb2	Alignment	not modelled	90.4	15	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
24	c2rhqA_	Alignment	not modelled	86.1	17	PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: phers from staphylococcus haemolyticus- rational protein2 engineering and inhibitor studies
25	c3devB_	Alignment	not modelled	85.3	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: sh1221; PDBTitle: crystal structure of sh1221 protein from staphylococcus haemolyticus,2 northeast structural genomics consortium target shr87
26	c2znjB_	Alignment	not modelled	84.8	19	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pyrrolysyl-trna synthetase from2 desulfitobacterium hafniense
27	c2zxrA_	Alignment	not modelled	83.2	20	PDB header: hydrolase Chain: A: PDB Molecule: single-stranded dna specific exonuclease recj; PDBTitle: crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8
						PDB header: ligase Chain: C: PDB Molecule: phenylalanyl-trna synthetase, alpha

28	c3pcoC_	Alignment	not modelled	78.0	18	subunit; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase regulatory subunit; PDBTitle: atp phosphoribosyl transferase (hiszg atp-prtase) from2 lactococcus lactis with bound prpp substrate PDB header: ligase Chain: A: PDB Molecule: phenylalanyl-trna synthetase; PDBTitle: phenylalanyl trna synthetase complexed with phenylalanine Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
29	c1z7nB_	Alignment	not modelled	75.0	18	PDB header: ligase Chain: I: PDB Molecule: phenylalanyl-trna synthetase alpha chain; PDBTitle: crystal structure of homo sapiens cytoplasmic phenylalanyl-trna2 synthetase Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
30	c1b70A_	Alignment	not modelled	74.7	29	PDB header: ligase Chain: A: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-ppp Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
31	d1jjca_	Alignment	not modelled	73.6	29	PDB header: immune system Chain: A: PDB Molecule: macrophage migration inhibitory factor; PDBTitle: structure of macrophage migration inhibitory factor from giardia2 lamblia Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
32	c3l4gl_	Alignment	not modelled	72.9	22	PDB header: ligase/rna Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved domain protein; PDBTitle: solution nmr structure of the n-terminal domain of protein pg_03612 from p.gingivalis, northeast structural genomics consortium target3 pgr37a
33	d1c0aa3	Alignment	not modelled	72.8	26	PDB header: ligase Chain: C: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of methanococcus jannacshii o-phosphoseryl-trna2 synthetase PDB header: ligase Chain: B: PDB Molecule: putative lysyl-trna synthetase; PDBTitle: structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
34	c1e22A_	Alignment	not modelled	72.4	30	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
35	d1eova2	Alignment	not modelled	71.9	30	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
36	c3t5sA_	Alignment	not modelled	71.5	21	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
37	d1l0wa3	Alignment	not modelled	70.5	27	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
38	c1efwA_	Alignment	not modelled	69.5	26	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
39	c2kw7A_	Alignment	not modelled	69.4	13	PDB header: ligase Chain: B: PDB Molecule: putative lysyl-trna synthetase; PDBTitle: structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
40	c2du7C_	Alignment	not modelled	69.1	29	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
41	c3g1zB_	Alignment	not modelled	67.4	18	PDB header: ligase Chain: B: PDB Molecule: putative lysyl-trna synthetase; PDBTitle: structure of idp01693/yjea, a potential t-rna synthetase from2 salmonella typhimurium
42	c3bjuB_	Alignment	not modelled	67.1	39	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
43	c1n9wA_	Alignment	not modelled	66.5	22	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
44	d1nj8a3	Alignment	not modelled	66.3	20	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
45	c1eqrC_	Alignment	not modelled	65.6	26	PDB header: ligase Chain: C: PDB Molecule: aspartyl-trna synthetase; PDBTitle: crystal structure of free aspartyl-trna synthetase from2 escherichia coli Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
46	d1qf6a4	Alignment	not modelled	64.6	18	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna2 synthetase PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of subunit i,2 homolog of subunit a, of v-atpase PDB header: complex (aminoacyl-trna synthase/trna) Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
47	c3rrkA_	Alignment	not modelled	63.7	15	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
48	c1asyA_	Alignment	not modelled	63.0	30	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
49	d1b8aa2	Alignment	not modelled	63.0	15	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
50	c1wydB_	Alignment	not modelled	62.9	39	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
51	c3e9hB_	Alignment	not modelled	62.8	33	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate
52	c2zimA_	Alignment	not modelled	62.8	21	PDB header: ligase Chain: A: PDB Molecule: pyrrolysyl-trna synthetase; PDBTitle: pyrrolysyl-trna synthetase bound to adenylated pyrrolysine and2 pyrophosphate

53	c1b8aB_	Alignment	not modelled	62.7	27	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
54	c3fwta_	Alignment	not modelled	62.3	24	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: crystal structure of leishmania major mif2
55	c3dmaA_	Alignment	not modelled	61.6	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: exopolyphosphatase-related protein; PDBTitle: crystal structure of an exopolyphosphatase-related protein2 from bacteroides fragilis. northeast structural genomics3 target bfr192
56	c2xcza_	Alignment	not modelled	61.2	10	PDB header: immune system Chain: A: PDB Molecule: possible atls1-like light-inducible protein; PDBTitle: crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
57	c3m4qA_	Alignment	not modelled	60.8	26	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnrs)
58	d1dpta_	Alignment	not modelled	60.6	24	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
59	d1nnha_	Alignment	not modelled	60.4	27	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
60	c1x55A_	Alignment	not modelled	60.3	30	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase; PDBTitle: crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
61	d1hfoa_	Alignment	not modelled	60.3	15	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
62	d1n9wa2	Alignment	not modelled	60.1	21	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
63	c3b64A_	Alignment	not modelled	59.9	14	PDB header: cytokine Chain: A: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: macrophage migration inhibitory factor (mif) from2 /leishmania major
64	d1uiza_	Alignment	not modelled	59.9	21	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
65	c2os5C_	Alignment	not modelled	57.7	17	PDB header: cytokine Chain: C: PDB Molecule: acemif; PDBTitle: macrophage migration inhibitory factor from ancylostoma ceylanicum
66	c3i7fa_	Alignment	not modelled	57.0	32	PDB header: ligase Chain: A: PDB Molecule: aspartyl-trna synthetase; PDBTitle: aspartyl trna synthetase from entamoeba histolytica
67	c2xgtB_	Alignment	not modelled	56.8	36	PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
68	c2du4B_	Alignment	not modelled	56.2	38	PDB header: ligase/rna Chain: B: PDB Molecule: o-phosphoseryl-trna synthetase; PDBTitle: crystal structure of archaeoglobus fulgidus o-phosphoseryl-2 trna synthetase complexed with trnacys
69	d2gdga1	Alignment	not modelled	55.8	15	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
70	d1gd0a_	Alignment	not modelled	55.5	12	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related
71	c3gacD_	Alignment	not modelled	52.6	10	PDB header: cytokine Chain: D: PDB Molecule: macrophage migration inhibitory factor-like PDBTitle: structure of mif with hpp
72	d1bbua2	Alignment	not modelled	52.1	23	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
73	d1e2wa2	Alignment	not modelled	51.6	20	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
74	c2i7uA_	Alignment	not modelled	50.8	24	PDB header: de novo protein/ligand binding protein Chain: A: PDB Molecule: four-alpha-helix bundle; PDBTitle: structural and dynamical analysis of a four-alpha-helix2 bundle with designed anesthetic binding pockets
75	d2di4a1	Alignment	not modelled	49.6	19	Fold: FtsH protease domain-like Superfamily: FtsH protease domain-like Family: FtsH protease domain-like
76	d1wu7a2	Alignment	not modelled	49.5	13	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
77	d1fima_	Alignment	not modelled	48.8	17	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: MIF-related

78	d1hnja2	Alignment	not modelled	46.4	16	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
79	d1u6ea2	Alignment	not modelled	44.8	9	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
80	d1jt6a1	Alignment	not modelled	44.2	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Tetracycline repressor-like, N-terminal domain
81	c2di4B_	Alignment	not modelled	43.7	18	PDB header: hydrolase Chain: B: PDB Molecule: cell division protein ftsH homolog; PDBTitle: crystal structure of the ftsH protease domain
82	d1ub7a2	Alignment	not modelled	42.1	19	Fold: Thiolase-like Superfamily: Thiolase-like Family: Chalcone synthase-like
83	d1e1oa2	Alignment	not modelled	41.7	25	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
84	d1u9pa1	Alignment	not modelled	39.8	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
85	cli5pA_	Alignment	not modelled	39.0	12	PDB header: toxin Chain: A: PDB Molecule: pesticidal crystal protein cry2aa; PDBTitle: insecticidal crystal protein cry2aa
86	c3mf2B_	Alignment	not modelled	38.3	13	PDB header: ligase Chain: B: PDB Molecule: blI0957 protein; PDBTitle: crystal structure of class ii aars homologue (blI0957) complexed with2 amp
87	d1tvca2	Alignment	not modelled	38.2	29	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Aromatic dioxygenase reductase-like
88	c1rb6C_	Alignment	not modelled	37.0	37	PDB header: dna binding protein Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: antiparallel trimer of gcn4-leucine zipper core mutant as2 n16a tetragonal form
89	c1swiA_	Alignment	not modelled	37.0	37	PDB header: leucine zipper Chain: A: PDB Molecule: gcn4p1; PDBTitle: gcn4-leucine zipper core mutant as n16a complexed with2 benzene
90	c3gwaA_	Alignment	not modelled	36.7	19	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-(acyl-carrier-protein) synthase iii; PDBTitle: 1.6 angstrom crystal structure of 3-oxoacyl-(acyl-carrier-protein)2 synthase iii
91	c1ij3B_	Alignment	not modelled	36.7	37	PDB header: transcription Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
92	c1ij2C_	Alignment	not modelled	36.3	38	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
93	c1rb1A_	Alignment	not modelled	36.2	34	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
94	c3k7zB_	Alignment	not modelled	36.2	34	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
95	c1rb1B_	Alignment	not modelled	36.2	34	PDB header: dna binding protein Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
96	c3k7zA_	Alignment	not modelled	36.2	34	PDB header: dna binding protein Chain: A: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-leucine zipper core mutant as n16a trigonal automatic2 solution
97	c2o7hF_	Alignment	not modelled	35.9	30	PDB header: transcription Chain: F: PDB Molecule: general control protein gcn4; PDBTitle: crystal structure of trimeric coiled coil gcn4 leucine zipper
98	c1ij3C_	Alignment	not modelled	35.8	34	PDB header: transcription Chain: C: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvsl coiled-coil trimer with serine at the a(16)2 position
99	d1myka_	Alignment	not modelled	35.3	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
100	d1baza_	Alignment	not modelled	34.5	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
101	c3izbO_	Alignment	not modelled	34.2	8	PDB header: ribosome Chain: O: PDB Molecule: 40s ribosomal protein rps13 (s15p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
102	d1vp7a_	Alignment	not modelled	34.0	26	Fold: Spectrin repeat-like Superfamily: XseB-like Family: XseB-like
103	d1j98a_	Alignment	not modelled	34.0	13	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
						PDB header: transcription

104	c1ij2B_	Alignment	not modelled	33.7	38	Chain: B: PDB Molecule: general control protein gcn4; PDBTitle: gcn4-pvtl coiled-coil trimer with threonine at the a(16)2 position
105	d2oa5a1	Alignment	not modelled	33.7	9	Fold: BLRF2-like Superfamily: BLRF2-like Family: BLRF2-like
106	c2zc2A_	Alignment	not modelled	33.4	22	PDB header: replication Chain: A: PDB Molecule: dnad-like replication protein; PDBTitle: crystal structure of dnad-like replication protein from2 streptococcus mutans ua159, gi 24377835, residues 127-199
107	d2i09a2	Alignment	not modelled	33.2	25	Fold: DeoB insert domain-like Superfamily: DeoB insert domain-like Family: DeoB insert domain-like
108	d1bdta_	Alignment	not modelled	33.1	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
109	d1z7ma1	Alignment	not modelled	32.2	14	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
110	d1ljma_	Alignment	not modelled	32.2	41	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
111	d1eaqa_	Alignment	not modelled	31.8	41	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: p53-like transcription factors Family: RUNT domain
112	d1wlza1	Alignment	not modelled	31.4	13	Fold: EF Hand-like Superfamily: EF-hand Family: EF-hand modules in multidomain proteins
113	d1mylb_	Alignment	not modelled	31.3	28	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
114	d1zunb1	Alignment	not modelled	31.2	26	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
115	d1myla_	Alignment	not modelled	30.0	25	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
116	c1emzA_	Alignment	not modelled	29.7	44	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein e1; PDBTitle: solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1
117	c1wlzD_	Alignment	not modelled	29.6	12	PDB header: unknown function Chain: D: PDB Molecule: cap-binding protein complex interacting protein PDBTitle: crystal structure of djbp fragment which was obtained by2 limited proteolysis
118	c2qnxA_	Alignment	not modelled	29.5	13	PDB header: transferase Chain: A: PDB Molecule: 3-oxoacyl-[acyl-carrier-protein] synthase 3; PDBTitle: crystal structure of the complex between the mycobacterium beta-2 ketoacyl-acyl carrier protein synthase iii (fabh) and 11-3 [(decyloxy carbonyl)dithio]-undecanoic acid
119	c3couA_	Alignment	not modelled	28.8	18	PDB header: hydrolase Chain: A: PDB Molecule: nucleoside diphosphate-linked moiety x motif 16; PDBTitle: crystal structure of human nudix motif 16 (nudt16)
120	c2w83C_	Alignment	not modelled	28.1	21	PDB header: protein transport Chain: C: PDB Molecule: c-jun-amino-terminal kinase-interacting protein PDBTitle: crystal structure of the arf6 gtpase in complex with a2 specific effector, jip4