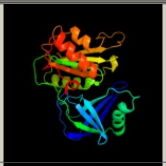
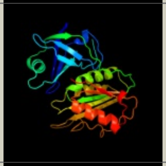
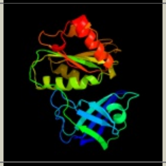
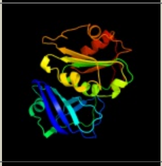
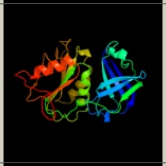
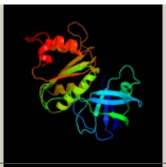
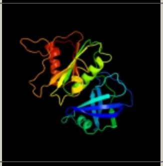
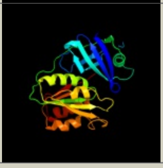
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0AEN1
Date	Thu Jan 5 11:23:45 GMT 2012
Unique Job ID	c8f6a8188fb803e8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qfjD_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (flavin reductase); **PDBTitle:** crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
2	c1krhA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
3	c1gvhA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
4	c2r6hC_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
5	c1tvcA_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
6	c1cqxB_	Alignment		100.0	20	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
7	c2eixA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of physarum polycephalum cytochrome b5 reductase
8	c1a8pA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
9	c2bgjB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
10	c3fpkB_	Alignment		100.0	17	**PDB header:**flavoprotein, oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
11	c2ok8D_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp+ reductase from plasmodium falciparum

12	c1qgyA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase; **PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
13	c1fncA_	Alignment		100.0	20	**PDB header:**oxidoreductase (nadp+(a),ferredoxin(a)) **Chain:** A: **PDB Molecule:**ferredoxin-nadp+ reductase; **PDBTitle:** refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
14	c2b5oA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase
15	c1umkA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of human erythrocyte nadh-cytochrome b52 reductase
16	c2piaA_	Alignment		100.0	16	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
17	c2rc5D_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** refined structure of fnr from leptospira interrogans
18	c1jb9A_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
19	c1cneA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrate reductase; **PDBTitle:** structural studies on corn nitrate reductase: refined2 structure of the cytochrome b reductase fragment at 2.53 angstroms, its adp complex and an active site mutant and4 modeling of the cytochrome b domain
20	c1ep3B_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydroorotate dehydrogenase b (pyrk subunit); **PDBTitle:** crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
21	c2gpjA_	Alignment	not modelled	100.0	13	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
22	d1qfja2	Alignment	not modelled	100.0	100	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
23	c1ddiA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha- **PDBTitle:** crystal structure of sir-fp60
24	c1f20A_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
25	c3qftA_	Alignment	not modelled	99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph--cytochrome p450 reductase; **PDBTitle:** crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
26	c1tllA_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
27	c1j9zB_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
28	d1tvca2	Alignment	not modelled	99.9	27	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like

29	c2qtzA_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine synthase reductase; **PDBTitle:** crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
30	d1gvha3	Alignment	not modelled	99.9	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
31	d1krha2	Alignment	not modelled	99.9	24	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
32	d1cqxa3	Alignment	not modelled	99.9	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
33	d1umka2	Alignment	not modelled	99.9	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
34	d1qx4a2	Alignment	not modelled	99.9	19	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
35	d1a8pa2	Alignment	not modelled	99.9	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
36	c2bpoA_	Alignment	not modelled	99.9	16	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
37	d2bmwa2	Alignment	not modelled	99.9	22	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
38	d2cnda2	Alignment	not modelled	99.9	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
39	d1fnda2	Alignment	not modelled	99.9	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
40	d1fdra2	Alignment	not modelled	99.9	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
41	d1ndha2	Alignment	not modelled	99.8	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
42	d2piaa2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
43	d1gawa2	Alignment	not modelled	99.8	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
44	d1f20a2	Alignment	not modelled	99.8	20	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
45	d1qfza2	Alignment	not modelled	99.8	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
46	d1sm4a2	Alignment	not modelled	99.8	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
47	c3a1fA_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b-245 heavy chain; **PDBTitle:** the crystal structure of nadph binding domain of gp91(phox)
48	d1jb9a2	Alignment	not modelled	99.8	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
49	d1ddga2	Alignment	not modelled	99.8	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
50	d1ja1a3	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
51	c3lrxC_	Alignment	not modelled	99.7	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative hydrogenase; **PDBTitle:** crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
52	d1ep3b2	Alignment	not modelled	99.7	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
53	d1qfja1	Alignment	not modelled	99.7	100	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
54	d1krha1	Alignment	not modelled	99.6	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like

						Family: Ferredoxin reductase FAD-binding domain-like
55	d1fdra1	Alignment	not modelled	99.6	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
56	d1tvca1	Alignment	not modelled	99.5	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
57	d1sm4a1	Alignment	not modelled	99.5	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
58	d1ep3b1	Alignment	not modelled	99.5	13	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
59	d2piaa1	Alignment	not modelled	99.5	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
60	d1a8pa1	Alignment	not modelled	99.5	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
61	d2cnda1	Alignment	not modelled	99.4	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
62	d1qfza1	Alignment	not modelled	99.4	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
63	d1fnda1	Alignment	not modelled	99.4	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
64	d2bmwa1	Alignment	not modelled	99.4	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
65	d1gawa1	Alignment	not modelled	99.4	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
66	d1gvha2	Alignment	not modelled	99.4	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
67	d1qx4a1	Alignment	not modelled	99.4	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
68	d1umka1	Alignment	not modelled	99.3	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
69	d1jb9a1	Alignment	not modelled	99.3	23	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
70	d1ndha1	Alignment	not modelled	99.2	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
71	d1cqxa2	Alignment	not modelled	99.2	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
72	d1ddga1	Alignment	not modelled	97.2	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
73	d1f20a1	Alignment	not modelled	96.5	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
74	d1ja1a1	Alignment	not modelled	87.8	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
75	d1f0ka_	Alignment	not modelled	78.6	18	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
76	d1o5za1	Alignment	not modelled	76.3	11	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
77	d2gc6a1	Alignment	not modelled	58.7	16	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
78	d1v43a2	Alignment	not modelled	51.9	26	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
79	c2pnyA_	Alignment	not modelled	39.4	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 2; **PDBTitle:** structure of human isopentenyl-diphosphate delta-isomerase 2
80	d1g2914	Alignment	not modelled	38.1	18	**Fold:**OB-fold **Superfamily:**MOP-like **Family:**ABC-transporter additional domain
81	c3t5sA_	Alignment	not modelled	33.4	3	**PDB header:**immune system **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor; **PDBTitle:** structure of macrophage migration inhibitory factor from

						giardia2 lamblia
82	d1pn3a_	Alignment	not modelled	32.8	8	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
83	c2ppvA_	Alignment	not modelled	26.9	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
84	c3fwtA_	Alignment	not modelled	26.5	11	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
85	d2hzba1	Alignment	not modelled	25.9	27	**Fold:**CofD-like **Superfamily:**CofD-like **Family:**CofD-like
86	d1fima_	Alignment	not modelled	24.4	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
87	d2gdga1	Alignment	not modelled	23.2	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
88	c1uwvA_	Alignment	not modelled	22.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma; **PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
89	d1iira_	Alignment	not modelled	22.2	13	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Gtf glycosyltransferase
90	d1hfoa_	Alignment	not modelled	21.9	7	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
91	c2i6kA_	Alignment	not modelled	21.7	6	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase 1; **PDBTitle:** crystal structure of human type i ipp isomerase complexed2 with a substrate analog
92	c2q7xA_	Alignment	not modelled	21.3	44	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0052 protein sp_1565; **PDBTitle:** crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
93	c3b64A_	Alignment	not modelled	21.1	21	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
94	c3h75A_	Alignment	not modelled	20.5	10	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**periplasmic sugar-binding domain protein; **PDBTitle:** crystal structure of a periplasmic sugar-binding protein from the2 pseudomonas fluorescens
95	c2p0yA_	Alignment	not modelled	20.0	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein lp_0780; **PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6
96	d1inla_	Alignment	not modelled	19.3	19	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**Spermidine synthase
97	c2iiiA_	Alignment	not modelled	18.8	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**s-adenosylmethionine decarboxylase proenzyme; **PDBTitle:** crystal structure of the adenosylmethionine decarboxylase (aq_254)2 from aquifex aeolicus vf5
98	c3gacD_	Alignment	not modelled	18.5	7	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
99	d1gd0a_	Alignment	not modelled	18.2	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related