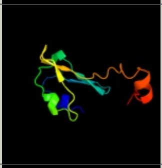
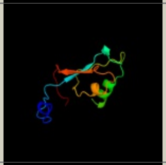
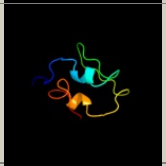
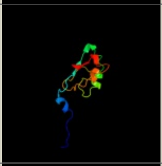
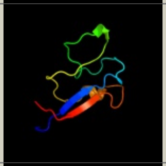
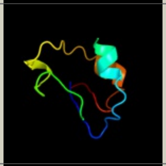
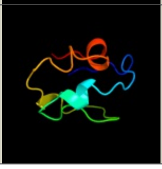
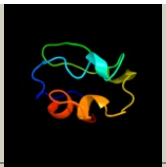
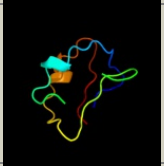
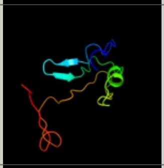
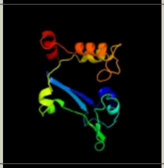
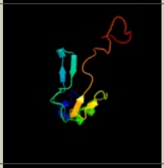
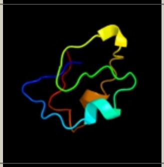
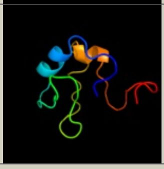
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P52636
Date	Thu Jan 5 12:05:55 GMT 2012
Unique Job ID	1e88f44bd382c1da

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gx7A_	Alignment		98.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**periplasmic [fe] hydrogenase large subunit; **PDBTitle:** best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
2	c1kqfB_	Alignment		98.8	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
3	d1gtea5	Alignment		98.8	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
4	c1hfeL_	Alignment		98.8	22	**PDB header:**hydrogenase **Chain:** L: **PDB Molecule:**protein (fe-only hydrogenase (e.c.1.18.99.1) **PDBTitle:** 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
5	c2fugG_	Alignment		98.8	32	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**nadh-quinone oxidoreductase chain 9; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
6	d2fug91	Alignment		98.8	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
7	c2c3yA_	Alignment		98.7	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
8	d1kqfb1	Alignment		98.7	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
9	c1gthD_	Alignment		98.7	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
10	c1c4cA_	Alignment		98.7	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (fe-only hydrogenase); **PDBTitle:** binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
11	d1xera_	Alignment		98.6	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins

12	d1dura_	Alignment		98.6	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
13	d2fdna_	Alignment		98.6	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
14	c2vpyB_	Alignment		98.6	31	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)
15	d1vjwa_	Alignment		98.6	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
16	d1y5ib1	Alignment		98.6	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
17	c1ti2F_	Alignment		98.6	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
18	d1iqza_	Alignment		98.6	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
19	d1hfel2	Alignment		98.6	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	d7fd1a_	Alignment		98.6	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
21	d1h0hb_	Alignment	not modelled	98.6	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
22	c2ivfB_	Alignment	not modelled	98.6	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
23	c3gyxJ_	Alignment	not modelled	98.5	25	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
24	d1jnrb_	Alignment	not modelled	98.5	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
25	d1jb0c_	Alignment	not modelled	98.5	31	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
26	d1bc6a_	Alignment	not modelled	98.5	27	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
27	d1fcaa_	Alignment	not modelled	98.5	29	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
28	d3c8ya3	Alignment	not modelled	98.4	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
						Fold: Ferredoxin-like

29	d1h98a_	Alignment	not modelled	98.4	30	**Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
30	c2gmhA_	Alignment	not modelled	98.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone **PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
31	d2fug34	Alignment	not modelled	98.4	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
32	d1sj1a_	Alignment	not modelled	98.4	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
33	c2zvsB_	Alignment	not modelled	98.4	25	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**uncharacterized ferredoxin-like protein yfhl; **PDBTitle:** crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
34	d1clfa_	Alignment	not modelled	98.3	33	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
35	c2fugC_	Alignment	not modelled	98.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh-quinone oxidoreductase chain 3; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
36	d1rgva_	Alignment	not modelled	98.3	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
37	d1blua_	Alignment	not modelled	98.3	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
38	d2c42a5	Alignment	not modelled	98.3	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
39	c2v2kB_	Alignment	not modelled	98.2	24	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
40	d1vlfn2	Alignment	not modelled	98.2	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
41	c1dwlA_	Alignment	not modelled	98.2	21	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
42	c2fgoA_	Alignment	not modelled	98.2	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
43	d1fxra_	Alignment	not modelled	98.1	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
44	c3c7bE_	Alignment	not modelled	98.0	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
45	d2gmha3	Alignment	not modelled	98.0	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
46	c2v4jE_	Alignment	not modelled	98.0	24	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
47	c3c7bA_	Alignment	not modelled	97.7	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
48	c2v4jA_	Alignment	not modelled	97.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit **PDBTitle:** the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
49	d3c7bb1	Alignment	not modelled	97.6	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
50	d1nekb1	Alignment	not modelled	97.5	31	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
51	d1kf6b1	Alignment	not modelled	97.5	31	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
52	d2bs2b1	Alignment	not modelled	97.5	24	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
53	c1nekB_	Alignment	not modelled	97.4	32	**PDB header:**oxidoreductase/electron transport **Chain:** B: **PDB Molecule:**succinate dehydrogenase iron-sulfur protein; **PDBTitle:** complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound

54	c2h89B_	Alignment	not modelled	97.4	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
55	c2b76N_	Alignment	not modelled	97.4	29	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
56	c2bs2E_	Alignment	not modelled	97.4	28	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
57	c3cf4A_	Alignment	not modelled	97.3	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetyl-coa decarboxylase/synthase alpha subunit; **PDBTitle:** structure of the codh component of the m. barkeri acds complex
58	c3bk7A_	Alignment	not modelled	97.3	22	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
59	c2vdcI_	Alignment	not modelled	95.7	36	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
60	d2v4ja1	Alignment	not modelled	93.7	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
61	d3c7ba1	Alignment	not modelled	93.3	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
62	d2v4jb1	Alignment	not modelled	88.8	32	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
63	d1gtea1	Alignment	not modelled	67.9	32	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
64	c2dtgE_	Alignment	not modelled	66.5	24	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
65	d1fxda_	Alignment	not modelled	44.9	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
66	c1g8jC_	Alignment	not modelled	34.1	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
67	c1igrA_	Alignment	not modelled	33.9	26	**PDB header:**hormone receptor **Chain:** A: **PDB Molecule:**insulin-like growth factor receptor 1; **PDBTitle:** type 1 insulin-like growth factor receptor (domains 1-3)
68	c2hr7B_	Alignment	not modelled	33.8	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (domains 1-3)
69	d3cx5c2	Alignment	not modelled	31.3	25	**Fold:**Heme-binding four-helical bundle **Superfamily:**Transmembrane di-heme cytochromes **Family:**Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
70	c2fugA_	Alignment	not modelled	25.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
71	c2eoyA_	Alignment	not modelled	24.9	46	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 473; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 557-2 589) of human zinc finger protein 473
72	d1ofda2	Alignment	not modelled	20.7	37	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
73	c2l3kA_	Alignment	not modelled	19.0	21	**PDB header:**oncoprotein **Chain:** A: **PDB Molecule:**rhombotin-2, linker, lim domain-binding protein 1; **PDBTitle:** solution structure of lmo2(lim2)-ldb1(lid)
74	d1ea0a2	Alignment	not modelled	17.1	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
75	c1x4lA_	Alignment	not modelled	16.1	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 3; **PDBTitle:** solution structure of lim domain in four and a half lim2 domains protein 2
76	c1moxB_	Alignment	not modelled	15.5	24	**PDB header:**transferase/growth factor **Chain:** B: **PDB Molecule:**epidermal growth factor receptor; **PDBTitle:** crystal structure of human epidermal growth factor receptor (residues2 1-501) in complex with tgf-alpha
77	c2l6yB_	Alignment	not modelled	15.4	23	**PDB header:**transcription regulation/oncoprotein **Chain:** B: **PDB Molecule:**lim domain only 2, linker, lim domain-binding protein 1; **PDBTitle:** haddock model of gata1nf:lmo2lim2-ldb1lid
78	d2dkta2	Alignment	not modelled	15.2	30	**Fold:**Zinc hairpin stack **Superfamily:**Zinc hairpin stack **Family:**Zinc hairpin stack
79	c1x64A_	Alignment	not modelled	14.0	27	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**alpha-actinin-2 associated lim protein; **PDBTitle:** solution structure of the lim domain of alpha-actinin-22 associated lim protein
						PDB header:metal binding protein

80	c2co8A_	Alignment	not modelled	13.8	18	**Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** solution structures of the lim domain of human nedd92 interacting protein with calponin homology and lim domains
81	c3mjhD_	Alignment	not modelled	13.6	33	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**early endosome antigen 1; **PDBTitle:** crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
82	c2pmzS_	Alignment	not modelled	13.5	24	**PDB header:**translation, transferase **Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
83	c2b5lC_	Alignment	not modelled	13.3	33	**PDB header:**protein binding/viral protein **Chain:** C: **PDB Molecule:**nonstructural protein v; **PDBTitle:** crystal structure of ddb1 in complex with simian virus 5 v2 protein
84	c2crcA_	Alignment	not modelled	12.5	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ubiquitin conjugating enzyme 7 interacting **PDBTitle:** solution structure of the zf-ranbp domain of the protein2 hbv associated factor
85	c1w1nA_	Alignment	not modelled	11.8	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase tor1; **PDBTitle:** the solution structure of the fatc domain of the protein2 kinase tor1 from yeast
86	c1x62A_	Alignment	not modelled	11.7	30	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**c-terminal lim domain protein 1; **PDBTitle:** solution structure of the lim domain of carboxyl terminal2 lim domain protein 1
87	d1wt8a1	Alignment	not modelled	11.6	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
88	c1zlgA_	Alignment	not modelled	11.4	24	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**anosmin 1; **PDBTitle:** solution structure of the extracellular matrix protein2 anosmin-1
89	d1kbsa_	Alignment	not modelled	11.4	45	**Fold:**Snake toxin-like **Superfamily:**Snake toxin-like **Family:**Snake venom toxins
90	c1x68A_	Alignment	not modelled	11.3	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**fhl5 protein; **PDBTitle:** solution structures of the c-terminal lim domain of human2 fhl5 protein
91	c1v06A_	Alignment	not modelled	10.7	22	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** axh domain of the transcription factor hbp1 from m.musculus
92	c3qntA_	Alignment	not modelled	10.6	45	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**niemann-pick c1-like protein 1; **PDBTitle:** npc1l1 (ntd) structure
93	c1m6bA_	Alignment	not modelled	10.1	26	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**receptor protein-tyrosine kinase erbb-3; **PDBTitle:** structure of the her3 (erbb3) extracellular domain
94	c1x63A_	Alignment	not modelled	9.6	22	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**skeletal muscle lim-protein 1; **PDBTitle:** solution structure of the second lim domain of skeletal2 muscle lim protein 1
95	c2a91A_	Alignment	not modelled	9.6	23	**PDB header:**signaling protein,transferase,membrane p **Chain:** A: **PDB Molecule:**receptor tyrosine-protein kinase erbb-2; **PDBTitle:** crystal structure of erbb2 domains 1-3
96	c2x9qA_	Alignment	not modelled	9.3	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**cyclodipeptide synthetase; **PDBTitle:** structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
97	d1djqa3	Alignment	not modelled	9.0	36	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
98	c3gczA_	Alignment	not modelled	8.8	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** yokose virus methyltransferase in complex with adomet
99	c3u5ga_	Alignment	not modelled	8.7	22	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution