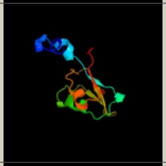
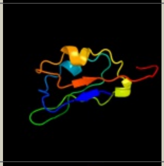
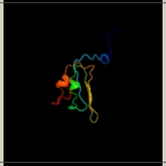
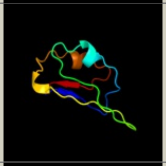
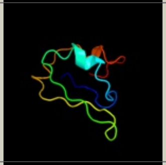
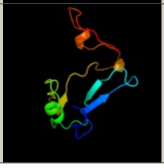
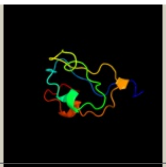
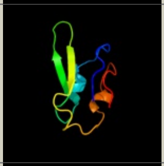
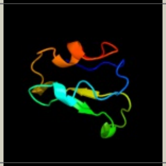
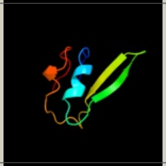
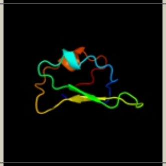
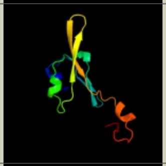
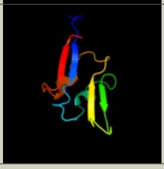
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P33934
Date	Thu Jan 5 11:52:55 GMT 2012
Unique Job ID	e1f2c1dc3566528b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2fug91	Alignment		99.1	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
2	c2fugG_	Alignment		99.1	20	**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
3	d1gtea5	Alignment		99.1	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
4	d1jb0c_	Alignment		99.0	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
5	c1kqfB_	Alignment		99.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**formate dehydrogenase, nitrate-inducible, iron-sulfur **PDBTitle:** formate dehydrogenase n from e. coli
6	c2c3yA_	Alignment		99.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyruvate-ferredoxin oxidoreductase; **PDBTitle:** crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
7	d1xera_	Alignment		99.0	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Archaeal ferredoxins
8	c1hfeL_	Alignment		99.0	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
9	c1gx7A_	Alignment		99.0	23	**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
10	d1jnrb_	Alignment		99.0	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
11	c2vpyB_	Alignment		98.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nrfc protein; **PDBTitle:** polysulfide reductase with bound quinone inhibitor,2 pentachlorophenol (pcp)

12	d1hfel2	Alignment		98.9	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
13	c3gyxJ_	Alignment		98.9	22	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**adenylylsulfate reductase; **PDBTitle:** crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
14	d1dura_	Alignment		98.9	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
15	d1h0hb_	Alignment		98.9	14	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
16	d7fd1a_	Alignment		98.9	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
17	d2fdna_	Alignment		98.9	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
18	c2gmhA_	Alignment		98.9	12	**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
19	d1kqfb1	Alignment		98.8	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
20	c1gthD_	Alignment		98.8	25	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
21	d2c42a5	Alignment	not modelled	98.8	28	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
22	d1fcaa_	Alignment	not modelled	98.8	25	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
23	c1ti2F_	Alignment	not modelled	98.8	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**pyrogallol hydroxytransferase small subunit; **PDBTitle:** crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
24	d1h98a_	Alignment	not modelled	98.8	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
25	d1bc6a_	Alignment	not modelled	98.8	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**7-Fe ferredoxin
26	d1iqza_	Alignment	not modelled	98.8	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
27	d3c8ya3	Alignment	not modelled	98.8	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
28	d1y5ib1	Alignment	not modelled	98.7	18	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
						Fold: Ferredoxin-like

29	d2fug34	Alignment	not modelled	98.7	15	**Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
30	d1blua_	Alignment	not modelled	98.7	21	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
31	c1c4cA_	Alignment	not modelled	98.7	22	**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
32	d1vjwa_	Alignment	not modelled	98.7	22	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
33	c2zvsB_	Alignment	not modelled	98.7	23	**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	d1rgva_	Alignment	not modelled	98.7	17	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
35	c2ivfB_	Alignment	not modelled	98.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ethylbenzene dehydrogenase beta-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
36	d2gmha3	Alignment	not modelled	98.7	14	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**ETF-QO domain-like
37	d1clfa_	Alignment	not modelled	98.6	24	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Short-chain ferredoxins
38	c2fgoA_	Alignment	not modelled	98.6	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**ferredoxin; **PDBTitle:** structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
39	d1sj1a_	Alignment	not modelled	98.6	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
40	c2v2kB_	Alignment	not modelled	98.5	17	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**ferredoxin; **PDBTitle:** the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
41	c3c7bE_	Alignment	not modelled	98.5	19	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit beta; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
42	c2fugC_	Alignment	not modelled	98.5	18	**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
43	c2v4jE_	Alignment	not modelled	98.5	16	**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
44	d1vlfn2	Alignment	not modelled	98.4	19	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
45	c1dwlA_	Alignment	not modelled	98.3	18	**PDB header:**electron transfer **Chain:** A: **PDB Molecule:**ferredoxin i; **PDBTitle:** the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
46	d3c7bb1	Alignment	not modelled	98.3	20	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
47	c3c7bA_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase, dissimilatory-type subunit alpha; **PDBTitle:** structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
48	c3bk7A_	Alignment	not modelled	98.2	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
49	d1fxra_	Alignment	not modelled	98.2	13	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
50	c2v4jA_	Alignment	not modelled	98.2	16	**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
51	c1nekB_	Alignment	not modelled	97.9	19	**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
52	d1nekb1	Alignment	not modelled	97.8	25	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
						Fold: Globin-like

53	d2bs2b1	Alignment	not modelled	97.8	29	**Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
54	c2bs2E_	Alignment	not modelled	97.8	28	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
55	c2b76N_	Alignment	not modelled	97.8	23	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
56	d1kf6b1	Alignment	not modelled	97.8	25	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Fumarate reductase/Succinate dehydogenase iron-sulfur protein, C-terminal domain
57	c2h89B_	Alignment	not modelled	97.8	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
58	c3cf4A_	Alignment	not modelled	97.5	27	**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
59	c2vdcI_	Alignment	not modelled	96.0	20	**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	d2v4jb1	Alignment	not modelled	95.9	23	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
61	d2v4ja1	Alignment	not modelled	95.5	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
62	d3c7ba1	Alignment	not modelled	95.5	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Ferredoxin domains from multidomain proteins
63	d1fxda_	Alignment	not modelled	87.0	16	**Fold:**Ferredoxin-like **Superfamily:**4Fe-4S ferredoxins **Family:**Single 4Fe-4S cluster ferredoxin
64	d1gtea1	Alignment	not modelled	72.6	15	**Fold:**Globin-like **Superfamily:**alpha-helical ferredoxin **Family:**Dihydropyrimidine dehydrogenase, N-terminal domain
65	c2dtgE_	Alignment	not modelled	57.8	30	**PDB header:**hormone receptor/immune system **Chain:** E: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (ir) ectodomain in complex with fab's
66	c2hr7B_	Alignment	not modelled	52.0	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**insulin receptor; **PDBTitle:** insulin receptor (domains 1-3)
67	c1moxB_	Alignment	not modelled	32.3	16	**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
68	c2eoyA_	Alignment	not modelled	30.8	31	**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
69	c1igrA_	Alignment	not modelled	30.6	23	**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)
70	c2pmzS_	Alignment	not modelled	30.5	24	**PDB header:**translation, transferase **Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
71	c1g8jC_	Alignment	not modelled	30.4	8	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**arsenite oxidase; **PDBTitle:** crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
72	c2a91A_	Alignment	not modelled	27.9	19	**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
73	d1ofda2	Alignment	not modelled	26.8	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
74	c2fugA_	Alignment	not modelled	23.7	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
75	c3u5ga_	Alignment	not modelled	18.4	12	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**40s ribosomal protein s0-a; **PDBTitle:** the structure of the eukaryotic ribosome at 3.0 a resolution
76	d1ea0a2	Alignment	not modelled	18.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
77	c1zlgA_	Alignment	not modelled	18.0	27	**PDB header:**hormone/growth factor **Chain:** A: **PDB Molecule:**anosmin 1; **PDBTitle:** solution structure of the extracellular matrix protein2 anosmin-1
78	c2xzn5_	Alignment	not modelled	17.2	24	**PDB header:**ribosome **Chain:** 5: **PDB Molecule:**ribosomal protein s26e containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2

79	c2vdcF_	Alignment	not modelled	15.6	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glutamate synthase [nadph] large chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
80	d2dlqa2	Alignment	not modelled	15.4	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
81	c1skzA_	Alignment	not modelled	14.7	27	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**antistasin; **PDBTitle:** protease inhibitor
82	d1djqa3	Alignment	not modelled	14.6	27	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
83	c1lm1A_	Alignment	not modelled	13.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-dependent glutamate synthase; **PDBTitle:** structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
84	c3plcA_	Alignment	not modelled	13.3	25	**PDB header:**toxin **Chain:** A: **PDB Molecule:**beta-cardiotoxin oh-27; **PDBTitle:** crystal structure of beta-cardiotoxin, a novel three-finger2 cardiotoxin from the venom of ophiophagus hannah
85	c2e4wA_	Alignment	not modelled	12.7	25	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**metabotropic glutamate receptor 3; **PDBTitle:** crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
86	d1mn3a_	Alignment	not modelled	12.4	43	**Fold:**RuvA C-terminal domain-like **Superfamily:**UBA-like **Family:**CUE domain
87	d1ce3a_	Alignment	not modelled	12.3	16	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
88	c2crcA_	Alignment	not modelled	12.2	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
89	d1dl6a_	Alignment	not modelled	12.2	20	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
90	c3qntA_	Alignment	not modelled	12.1	30	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**niemann-pick c1-like protein 1; **PDBTitle:** npc1l1 (ntd) structure
91	d1rp4a_	Alignment	not modelled	11.6	33	**Fold:**ERO1-like **Superfamily:**ERO1-like **Family:**ERO1-like
92	d1mr1c_	Alignment	not modelled	11.6	36	**Fold:**SAND domain-like **Superfamily:**SAND domain-like **Family:**SMAD4-binding domain of oncoprotein Ski
93	c2eqpA_	Alignment	not modelled	11.5	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tumor necrosis factor receptor superfamily **PDBTitle:** solution structure of the stn_tnfrsf12a_tnfr domain of2 tumor necrosis factor receptor superfamily member 12a3 precursor
94	c1ovxB_	Alignment	not modelled	11.0	63	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** nmr structure of the e. coli clpx chaperone zinc binding domain dimer
95	d2ds5a1	Alignment	not modelled	11.0	63	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**ClpX chaperone zinc binding domain
96	c3b08H_	Alignment	not modelled	10.8	50	**PDB header:**signaling protein/metal binding protein **Chain:** H: **PDB Molecule:**ranbp-type and c3hc4-type zinc finger-containing protein 1; **PDBTitle:** crystal structure of the mouse hoil1-l-nzf in complex with linear di-2 ubiquitin
97	d1wt8a1	Alignment	not modelled	10.0	67	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
98	c3lmfA_	Alignment	not modelled	9.5	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of nmul_a1745 protein from nitrosospira2 multiformis, northeast structural genomics consortium3 target nmr72
99	c3ahrA_	Alignment	not modelled	9.4	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ero1-like protein alpha; **PDBTitle:** inactive human ero1