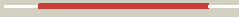
















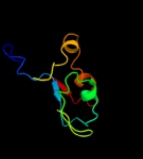

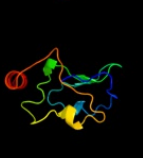


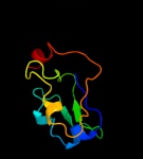



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ivfB_</a>	 Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ethylbenzene dehydrogenase beta-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
2	<a href="#">c1ti2F_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> pyrogallol hydroxytransferase small subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol2 transhydroxylase from pelobacter acidigallici
3	<a href="#">c2vpyB_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nrfc protein; <b>PDBTitle:</b> polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
4	<a href="#">d1kqfb1</a>	 Alignment		100.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
5	<a href="#">c1kqfB_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, iron-sulfur <b>PDBTitle:</b> formate dehydrogenase n from e. coli
6	<a href="#">d1y5ib1</a>	 Alignment		100.0	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
7	<a href="#">d1vlfm2</a>	 Alignment		100.0	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
8	<a href="#">d1h0hb_</a>	 Alignment		100.0	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
9	<a href="#">d2fug91</a>	 Alignment		99.4	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
10	<a href="#">c2fugG_</a>	 Alignment		99.4	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 9; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
11	<a href="#">c2zvsB_</a>	 Alignment		99.4	19	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ferredoxin-like protein yfh1; <b>PDBTitle:</b> crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli

12	<a href="#">dlxera_</a>	Alignment		99.3	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Archaeal ferredoxins
13	<a href="#">c2v2kB_</a>	Alignment		99.3	20	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
14	<a href="#">d1hfel2</a>	Alignment		99.3	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
15	<a href="#">c3gyxl_</a>	Alignment		99.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> adenylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
16	<a href="#">d1blua_</a>	Alignment		99.2	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
17	<a href="#">d7fd1a_</a>	Alignment		99.2	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
18	<a href="#">d1jnrb_</a>	Alignment		99.2	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
19	<a href="#">c2fgoA_</a>	Alignment		99.2	24	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
20	<a href="#">c1gthD_</a>	Alignment		99.2	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
21	<a href="#">d3c8ya3</a>	Alignment	not modelled	99.2	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
22	<a href="#">d1h98a_</a>	Alignment	not modelled	99.1	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
23	<a href="#">d1bc6a_</a>	Alignment	not modelled	99.1	34	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
24	<a href="#">d1jb0c_</a>	Alignment	not modelled	99.1	37	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
25	<a href="#">d1rgva_</a>	Alignment	not modelled	99.1	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
26	<a href="#">d2c42a5</a>	Alignment	not modelled	99.1	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
27	<a href="#">c1hfeL_</a>	Alignment	not modelled	99.1	33	<b>PDB header:</b> hydrogenase <b>Chain:</b> L: <b>PDB Molecule:</b> protein (fe-only hydrogenase (e.c.1.18.99.1) <b>PDBTitle:</b> 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
28	<a href="#">d1gtea5</a>	Alignment	not modelled	99.1	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
						<b>PDB header:</b> oxidoreductase

29	<a href="#">c1gx7A</a>	Alignment	not modelled	99.1	38	<b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic [fe] hydrogenase large subunit; <b>PDBTitle:</b> best model of the electron transfer complex between2 cytochrome c3 and [fe]-hydrogenase
30	<a href="#">d3c7bb1</a>	Alignment	not modelled	99.1	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
31	<a href="#">c2gmhA</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> electron transfer flavoprotein-ubiquinone <b>PDBTitle:</b> structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
32	<a href="#">d2fdna</a>	Alignment	not modelled	99.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
33	<a href="#">d1dura</a>	Alignment	not modelled	99.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
34	<a href="#">d1fcaa</a>	Alignment	not modelled	99.0	30	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
35	<a href="#">c2c3yA</a>	Alignment	not modelled	99.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate-ferredoxin oxidoreductase; <b>PDBTitle:</b> crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
36	<a href="#">d1iqza</a>	Alignment	not modelled	98.9	23	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
37	<a href="#">d2gmha3</a>	Alignment	not modelled	98.9	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> ETF-QO domain-like
38	<a href="#">d1clfa</a>	Alignment	not modelled	98.9	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
39	<a href="#">d2fug34</a>	Alignment	not modelled	98.9	28	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
40	<a href="#">d1vjwa</a>	Alignment	not modelled	98.8	35	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
41	<a href="#">c1c4cA</a>	Alignment	not modelled	98.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fe-only hydrogenase); <b>PDBTitle:</b> binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
42	<a href="#">d1sj1a</a>	Alignment	not modelled	98.7	24	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
43	<a href="#">c1dw1A</a>	Alignment	not modelled	98.7	27	<b>PDB header:</b> electron transfer <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin i; <b>PDBTitle:</b> the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
44	<a href="#">d1fxra</a>	Alignment	not modelled	98.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
45	<a href="#">c3c7bE</a>	Alignment	not modelled	98.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit beta; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
46	<a href="#">c2fugC</a>	Alignment	not modelled	98.4	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 3; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
47	<a href="#">c2v4jE</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
48	<a href="#">c3bk7A</a>	Alignment	not modelled	98.2	32	<b>PDB header:</b> hydrolase/translation <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter atp-binding protein; <b>PDBTitle:</b> structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abyssi
49	<a href="#">c2v4jA</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit <b>PDBTitle:</b> the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
50	<a href="#">c3c7bA</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase, dissimilatory-type subunit alpha; <b>PDBTitle:</b> structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
51	<a href="#">d2bs2b1</a>	Alignment	not modelled	98.0	20	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
52	<a href="#">d1kf6b1</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
53	<a href="#">c2bs2E</a>	Alignment	not modelled	97.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> quinol-fumarate reductase iron-sulfur subunit b;

						<b>PDBTitle:</b> quinol:fumarate reductase from wolinella succinogenes <b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
54	<a href="#">d1nekb1</a>	Alignment	not modelled	97.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase ip subunit; <b>PDBTitle:</b> avian respiratory complex ii with malonate bound
55	<a href="#">c2h89B</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur protein; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
56	<a href="#">c1nekB</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> N: <b>PDB Molecule:</b> fumarate reductase iron-sulfur protein; <b>PDBTitle:</b> e. coli quinol fumarate reductase frda e49q mutation
57	<a href="#">c2b76N</a>	Alignment	not modelled	96.9	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
58	<a href="#">d2v4jb1</a>	Alignment	not modelled	96.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase alpha subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
59	<a href="#">c3cf4A</a>	Alignment	not modelled	95.5	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
60	<a href="#">d2v4ja1</a>	Alignment	not modelled	88.9	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
61	<a href="#">d3c7ba1</a>	Alignment	not modelled	88.4	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
62	<a href="#">c2vdcl</a>	Alignment	not modelled	84.0	22	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Dihydropyrimidine dehydrogenase, N-terminal domain
63	<a href="#">d1fxda</a>	Alignment	not modelled	68.8	28	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
64	<a href="#">d1gtea1</a>	Alignment	not modelled	36.4	39	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
65	<a href="#">d1djqa3</a>	Alignment	not modelled	23.5	33	<b>PDB header:</b> signaling protein,transferase,membrane p <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-2; <b>PDBTitle:</b> crystal structure of erbb2 domains 1-3
66	<a href="#">d1yuza2</a>	Alignment	not modelled	16.0	24	<b>Fold:</b> Rubredoxin-like <b>Superfamily:</b> Rubredoxin-like <b>Family:</b> Rubredoxin
67	<a href="#">c2a91A</a>	Alignment	not modelled	14.9	23	<b>PDB header:</b> hormone receptor/immune system <b>Chain:</b> E: <b>PDB Molecule:</b> insulin receptor; <b>PDBTitle:</b> insulin receptor (ir) ectodomain in complex with fab's
68	<a href="#">d1nnqa2</a>	Alignment	not modelled	14.6	32	<b>Fold:</b> RING/U-box <b>Superfamily:</b> RING/U-box <b>Family:</b> Variant RING domain
69	<a href="#">c2dtgE</a>	Alignment	not modelled	12.6	23	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily <b>PDBTitle:</b> solution structure of the stn_tnfrsf12a_tnfr domain of2 tumor necrosis factor receptor superfamily member 12a3 precursor
70	<a href="#">d2cs3a1</a>	Alignment	not modelled	11.2	27	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
71	<a href="#">c2eqpA</a>	Alignment	not modelled	11.2	36	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> fn14; <b>PDBTitle:</b> solution nmr structure of xenopus fn14
72	<a href="#">d1ncfb3</a>	Alignment	not modelled	11.1	42	<b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> TNF receptor-like
73	<a href="#">c2kn0A</a>	Alignment	not modelled	10.9	36	<b>PDB header:</b> ribosome <b>Chain:</b> T: <b>PDB Molecule:</b> rpl24; <b>PDBTitle:</b> t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
74	<a href="#">d1exta3</a>	Alignment	not modelled	10.7	40	<b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein l24 (l24e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
75	<a href="#">d1lkoa2</a>	Alignment	not modelled	9.4	24	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein;
76	<a href="#">c4a1eT</a>	Alignment	not modelled	9.3	27	
77	<a href="#">c3iz5Z</a>	Alignment	not modelled	8.6	13	
78	<a href="#">c1degD</a>	Alignment	not modelled	8.5	23	
79	<a href="#">c2l7xA</a>	Alignment	not modelled	7.8	33	

					<b>PDBTitle:</b> crimean congo hemorrhagic fever gn zinc finger
80	<a href="#">d1rutx1</a>	Alignment	not modelled	7.8	31 <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
81	<a href="#">c3izcZ</a>	Alignment	not modelled	7.8	7 <b>PDB header:</b> ribosome <b>Chain:</b> Z: <b>PDB Molecule:</b> 60s ribosomal protein rpl24 (l24e); <b>PDBTitle:</b> localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
82	<a href="#">c1g8jC</a>	Alignment	not modelled	7.6	12 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
83	<a href="#">c1s1iS</a>	Alignment	not modelled	7.6	8 <b>PDB header:</b> ribosome <b>Chain:</b> S: <b>PDB Molecule:</b> 60s ribosomal protein l24-a; <b>PDBTitle:</b> structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
84	<a href="#">c2zkru</a>	Alignment	not modelled	7.5	15 <b>PDB header:</b> ribosomal protein/rna <b>Chain:</b> U: <b>PDB Molecule:</b> rna expansion segment es41; <b>PDBTitle:</b> structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
85	<a href="#">d1xu1r</a>	Alignment	not modelled	7.4	28 <b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> BAFF receptor-like
86	<a href="#">d2r4qa1</a>	Alignment	not modelled	6.7	30 <b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
87	<a href="#">c2fugA</a>	Alignment	not modelled	6.0	33 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-quinone oxidoreductase chain 1; <b>PDBTitle:</b> crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
88	<a href="#">d1xuta</a>	Alignment	not modelled	5.5	28 <b>Fold:</b> TNF receptor-like <b>Superfamily:</b> TNF receptor-like <b>Family:</b> BAFF receptor-like
89	<a href="#">d1vqou1</a>	Alignment	not modelled	5.4	33 <b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Ribosomal protein L24e