






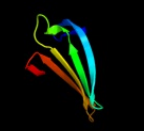





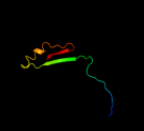



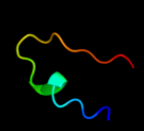




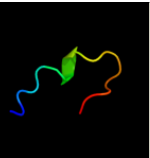
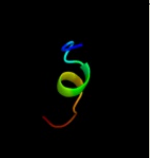
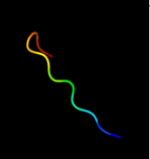
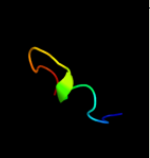

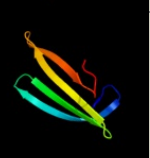
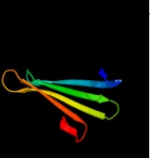
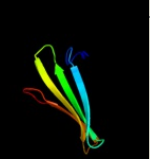
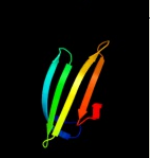


# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P76220
Date	Thu Jan 5 12:20:44 GMT 2012
Unique Job ID	cdcb7f7c543e216f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1sa8a_</a>	 Alignment		29.2	11	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
2	<a href="#">d2cbra_</a>	 Alignment		26.4	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
3	<a href="#">d1hmsa_</a>	 Alignment		26.3	19	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
4	<a href="#">d2fs6a1</a>	 Alignment		21.1	12	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
5	<a href="#">d2r48a1</a>	 Alignment		20.6	55	<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
6	<a href="#">c2gmhA_</a>	 Alignment		19.3	17	<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
7	<a href="#">c1u8cB_</a>	 Alignment		19.1	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> a novel adaptation of the integrin psi domain revealed from its2 crystal structure
8	<a href="#">c3k6sB_</a>	 Alignment		18.3	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-2; <b>PDBTitle:</b> structure of integrin alphaxbeta2 ectodomain
9	<a href="#">d1hfel2</a>	 Alignment		16.5	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
10	<a href="#">c1nijA_</a>	 Alignment		16.4	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein yjia; <b>PDBTitle:</b> yjia protein
11	<a href="#">d1fcaa_</a>	 Alignment		15.5	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins

12	<a href="#">d1blua_</a>	Alignment		15.2	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
13	<a href="#">c2c3yA_</a>	Alignment		15.1	46	<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
14	<a href="#">c2kyrA_</a>	Alignment		15.1	45	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-like phosphotransferase enzyme iib component 1; <b>PDBTitle:</b> solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
15	<a href="#">d1dura_</a>	Alignment		14.8	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
16	<a href="#">d1lfoa_</a>	Alignment		14.6	25	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
17	<a href="#">d1pmpa_</a>	Alignment		14.3	15	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
18	<a href="#">d1yiva1</a>	Alignment		14.2	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
19	<a href="#">d1bwya_</a>	Alignment		13.7	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
20	<a href="#">d2hnxa1</a>	Alignment		13.6	8	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
21	<a href="#">d1gtea5</a>	Alignment	not modelled	13.2	44	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
22	<a href="#">c2jz2A_</a>	Alignment	not modelled	13.1	43	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ssl0352 protein; <b>PDBTitle:</b> solution nmr structure of ssl0352 protein from synechocystis sp. pcc2 6803. northeast structural genomics consortium target sgr42
23	<a href="#">d1lfca_</a>	Alignment	not modelled	12.8	11	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
24	<a href="#">c2lfeA_</a>	Alignment	not modelled	12.5	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase hecw2; <b>PDBTitle:</b> solution nmr structure of n-terminal domain of human e3 ubiquitin-2 protein ligase hecw2, northeast structural genomics consortium (nesg)3 target ht6306a
25	<a href="#">d1kzwa_</a>	Alignment	not modelled	12.4	11	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
26	<a href="#">d1kqwa_</a>	Alignment	not modelled	11.5	20	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
27	<a href="#">c3fcuB_</a>	Alignment	not modelled	11.1	13	<b>PDB header:</b> cell adhesion/blood clotting <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-3; <b>PDBTitle:</b> structure of headpiece of integrin aiiib3 in open conformation
28	<a href="#">d2fdna_</a>	Alignment	not modelled	11.1	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins

29	<a href="#">d1fdqa_</a>	Alignment	not modelled	11.0	13	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
30	<a href="#">d1jb0c_</a>	Alignment	not modelled	10.8	21	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
31	<a href="#">d2gpia1</a>	Alignment	not modelled	10.8	19	<b>Fold:</b> Shew3726-like <b>Superfamily:</b> Shew3726-like <b>Family:</b> Shew3726-like
32	<a href="#">d1b56a_</a>	Alignment	not modelled	10.8	15	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
33	<a href="#">d2r4qa1</a>	Alignment	not modelled	10.6	31	<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
34	<a href="#">d7fd1a_</a>	Alignment	not modelled	10.6	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
35	<a href="#">d1mdca_</a>	Alignment	not modelled	10.4	9	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
36	<a href="#">c2fugG_</a>	Alignment	not modelled	10.1	18	<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
37	<a href="#">d1udxa3</a>	Alignment	not modelled	10.0	25	<b>Fold:</b> Obg GTP-binding protein C-terminal domain <b>Superfamily:</b> Obg GTP-binding protein C-terminal domain <b>Family:</b> Obg GTP-binding protein C-terminal domain
38	<a href="#">d1gsma1</a>	Alignment	not modelled	10.0	26	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Immunoglobulin <b>Family:</b> I set domains
39	<a href="#">d2flna1</a>	Alignment	not modelled	9.9	24	<b>Fold:</b> DNase I-like <b>Superfamily:</b> DNase I-like <b>Family:</b> DNase I-like
40	<a href="#">c3dsoA_</a>	Alignment	not modelled	9.7	28	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein copk; <b>PDBTitle:</b> crystal structure of cu(i) bound copper resistance protein copk
41	<a href="#">d2fug91</a>	Alignment	not modelled	9.6	18	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
42	<a href="#">d1p6pa_</a>	Alignment	not modelled	9.6	18	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
43	<a href="#">c2v4jE_</a>	Alignment	not modelled	9.6	16	<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
44	<a href="#">c2q9sA_</a>	Alignment	not modelled	9.5	9	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein; <b>PDBTitle:</b> linoleic acid bound to fatty acid binding protein 4
45	<a href="#">c2lbaA_</a>	Alignment	not modelled	9.5	24	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> babp protein; <b>PDBTitle:</b> solution structure of chicken ileal babp in complex with2 glycochenodeoxycholic acid
46	<a href="#">d2f73a1</a>	Alignment	not modelled	9.1	26	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
47	<a href="#">d1clfa_</a>	Alignment	not modelled	9.1	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
48	<a href="#">c2zvsB_</a>	Alignment	not modelled	8.6	31	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized ferredoxin-like protein yfhI; <b>PDBTitle:</b> crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
49	<a href="#">d2c42a5</a>	Alignment	not modelled	8.5	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
50	<a href="#">d2i9ua1</a>	Alignment	not modelled	8.5	21	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
51	<a href="#">c1gthD_</a>	Alignment	not modelled	8.5	44	<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
52	<a href="#">d1vyfa_</a>	Alignment	not modelled	8.4	9	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
53	<a href="#">c2vpyB_</a>	Alignment	not modelled	8.4	27	<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)
54	<a href="#">d1vlfn2</a>	Alignment	not modelled	8.1	38	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
55	<a href="#">d1nkb1_</a>	Alignment	not modelled	8.0	20	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin

55	<a href="#">dlfexv1</a>	Alignment	not modelled	8.0	49	<b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain <b>PDB header:</b> oxidoreductase <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
56	<a href="#">c1gx7A</a>	Alignment	not modelled	8.0	31	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
57	<a href="#">d1tw4a</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
58	<a href="#">d1a57a</a>	Alignment	not modelled	7.9	11	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
59	<a href="#">d1g7na</a>	Alignment	not modelled	7.7	13	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
60	<a href="#">d3c7bb1</a>	Alignment	not modelled	7.7	25	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
61	<a href="#">c2kxvA</a>	Alignment	not modelled	7.7	19	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein; <b>PDBTitle:</b> nmr structure and calcium-binding properties of the tellurite2 resistance protein terd from klebsiella pneumoniae
62	<a href="#">c2vdcF</a>	Alignment	not modelled	7.4	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glutamate synthase [nadph] large 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.
63	<a href="#">d1o1va</a>	Alignment	not modelled	7.1	20	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
64	<a href="#">d3c8ya3</a>	Alignment	not modelled	7.0	32	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
65	<a href="#">d1h98a</a>	Alignment	not modelled	6.9	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> 7-Fe ferredoxin
66	<a href="#">c1lm1A</a>	Alignment	not modelled	6.7	47	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-dependent glutamate synthase; <b>PDBTitle:</b> structural studies on the synchronization of catalytic centers in2 glutamate synthase: native enzyme
67	<a href="#">c3pptA</a>	Alignment	not modelled	6.7	17	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium-calcium exchanger; <b>PDBTitle:</b> rep1-nxsq fatty acid transporter
68	<a href="#">c3v4pB</a>	Alignment	not modelled	6.7	15	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-7; <b>PDBTitle:</b> crystal structure of a4b7 headpiece complexed with fab act-1
69	<a href="#">c3ef4A</a>	Alignment	not modelled	6.6	14	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> blue copper protein; <b>PDBTitle:</b> crystal structure of native pseudoazurin from2 hyphomicrobium denitrificans
70	<a href="#">d1h0hb</a>	Alignment	not modelled	6.5	13	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
71	<a href="#">d1iqza</a>	Alignment	not modelled	6.4	11	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Single 4Fe-4S cluster ferredoxin
72	<a href="#">c2bs2E</a>	Alignment	not modelled	6.3	36	<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
73	<a href="#">d1jnrb</a>	Alignment	not modelled	6.1	20	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
74	<a href="#">d2bs2b1</a>	Alignment	not modelled	6.0	36	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
75	<a href="#">c3gyxJ</a>	Alignment	not modelled	6.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> adenylylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
76	<a href="#">c3ibzA</a>	Alignment	not modelled	5.9	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative tellurium resistant like protein terd; <b>PDBTitle:</b> crystal structure of putative tellurium resistant like protein (terd)2 from streptomyces coelicolor a3(2)
77	<a href="#">d2gmha3</a>	Alignment	not modelled	5.9	17	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> ETF-QO domain-like
78	<a href="#">d1eala</a>	Alignment	not modelled	5.8	22	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
79	<a href="#">d1kf6b1</a>	Alignment	not modelled	5.7	29	<b>Fold:</b> Globin-like <b>Superfamily:</b> alpha-helical ferredoxin <b>Family:</b> Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
80	<a href="#">d1p9qc3</a>	Alignment	not modelled	5.7	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
						<b>Fold:</b> Ferredoxin-like

81	<a href="#">d1xera_</a>	Alignment	not modelled	5.6	31	<b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Archaeal ferredoxins
82	<a href="#">c1kqfB_</a>	Alignment	not modelled	5.6	40	<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
83	<a href="#">d1crba_</a>	Alignment	not modelled	5.5	19	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
84	<a href="#">d2fug34</a>	Alignment	not modelled	5.4	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Ferredoxin domains from multidomain proteins
85	<a href="#">c2fgoA_</a>	Alignment	not modelled	5.3	44	<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
86	<a href="#">d1rgva_</a>	Alignment	not modelled	5.3	31	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> 4Fe-4S ferredoxins <b>Family:</b> Short-chain ferredoxins
87	<a href="#">d1t95a3</a>	Alignment	not modelled	5.3	29	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> EF-G C-terminal domain-like <b>Family:</b> Hypothetical protein AF0491, C-terminal domain
88	<a href="#">c1ti2F_</a>	Alignment	not modelled	5.1	42	<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
89	<a href="#">c1dw1A_</a>	Alignment	not modelled	5.1	33	<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