

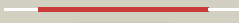


















Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P0ABW3
Date	Thu Jan 5 11:16:31 GMT 2012
Unique Job ID	129080909d600e43

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dliuea_	 Alignment		99.9	36	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
2	dla70a_	 Alignment		99.9	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
3	dlfrfa_	 Alignment		99.9	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
4	dloffa_	 Alignment		99.8	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
5	d2piaa3	 Alignment		99.8	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
6	dlfrda_	 Alignment		99.8	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
7	dlfxia_	 Alignment		99.8	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
8	dlawda_	 Alignment		99.8	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
9	dlpfda_	 Alignment		99.8	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
10	clkrhA_	 Alignment		99.8	28	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray stucture of benzoate dioxygenase reductase
11	dlczpa_	 Alignment		99.8	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related

12	d4fxca_	Alignment		99.8	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
13	c2piaA_	Alignment		99.8	31	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]
14	d1gaqb_	Alignment		99.8	30	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
15	d1jq4a_	Alignment		99.8	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
16	d2cjoa_	Alignment		99.8	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
17	d1wrja_	Alignment		99.8	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
18	d1krha3	Alignment		99.8	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
19	d1doia_	Alignment		99.8	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
20	c3ah7A_	Alignment		99.7	19	PDB header: metal binding protein Chain: A: PDB Molecule: [2fe-2s]ferredoxin; PDBTitle: crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
21	d1i7ha_	Alignment	not modelled	99.7	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
22	d1e0za_	Alignment	not modelled	99.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
23	d1l5pa_	Alignment	not modelled	99.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
24	c2wlbB_	Alignment	not modelled	99.5	20	PDB header: electron transport Chain: B: PDB Molecule: electron transfer protein 1, mitochondrial; PDBTitle: adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
25	c3huiA_	Alignment	not modelled	99.5	17	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: crystal structure of the mutant a105r of [2fe-2s] ferredoxin2 in the class i cyp199a2 system from rhodopseudomonas3 palustris
26	d1xlqa1	Alignment	not modelled	99.4	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
27	d1e9ma_	Alignment	not modelled	99.4	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
28	c3lxfC_	Alignment	not modelled	99.4	19	PDB header: metal binding protein Chain: C: PDB Molecule: ferredoxin; PDBTitle: crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans

29	d1b9ra_	Alignment	not modelled	99.4	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
30	d2bt6a1	Alignment	not modelled	99.3	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
31	d2fug33	Alignment	not modelled	98.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
32	c1l6vA_	Alignment	not modelled	98.9	12	PDB header: electron transport Chain: A: PDB Molecule: adrenodoxin 1; PDBTitle: structure of reduced bovine adrenodoxin
33	d3c8ya2	Alignment	not modelled	98.6	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
34	c1c4cA_	Alignment	not modelled	98.4	23	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
35	c2fugC_	Alignment	not modelled	98.4	22	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	d1vlba2	Alignment	not modelled	98.2	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
37	d1t3qa2	Alignment	not modelled	98.1	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
38	d1dgja2	Alignment	not modelled	98.1	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
39	d1n62a2	Alignment	not modelled	97.9	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
40	d1ffva2	Alignment	not modelled	97.9	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
41	c1t3qD_	Alignment	not modelled	97.8	24	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
42	c3hrdH_	Alignment	not modelled	97.8	27	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
43	d1rm6c2	Alignment	not modelled	97.7	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
44	c1n60D_	Alignment	not modelled	97.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: carbon monoxide dehydrogenase small chain; PDBTitle: crystal structure of the cu,mo-co dehydrogenase (codh); cyanide-2 inactivated form
45	c1rm6F_	Alignment	not modelled	97.6	21	PDB header: oxidoreductase Chain: F: PDB Molecule: 4-hydroxybenzoyl-coa reductase gamma subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
46	c1ffuA_	Alignment	not modelled	97.5	19	PDB header: hydrolase Chain: A: PDB Molecule: cuts, iron-sulfur protein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
47	d1jroa2	Alignment	not modelled	97.4	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
48	c1vlbA_	Alignment	not modelled	97.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
49	c2h89B_	Alignment	not modelled	97.4	27	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
50	d2bs2b2	Alignment	not modelled	97.2	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
51	d1v97a2	Alignment	not modelled	97.2	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
52	c3b9jI_	Alignment	not modelled	97.1	28	PDB header: oxidoreductase Chain: I: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
53	c3eubJ_	Alignment	not modelled	97.0	28	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
						Fold: beta-Grasp (ubiquitin-like)

54	d1kf6b2	Alignment	not modelled	97.0	30	Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
55	c2w3rG	Alignment	not modelled	96.9	24	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
56	c2bs2E	Alignment	not modelled	96.8	21	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
57	d1nekb2	Alignment	not modelled	96.8	28	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
58	c1dgiA	Alignment	not modelled	96.7	27	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
59	c2b76N	Alignment	not modelled	96.6	25	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
60	c1nekB	Alignment	not modelled	96.5	28	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
61	c1wygA	Alignment	not modelled	95.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
62	c1ep3B	Alignment	not modelled	94.7	15	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.
63	d1ep3b2	Alignment	not modelled	92.7	17	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit
64	c1x31A	Alignment	not modelled	91.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
65	c1y56A	Alignment	not modelled	79.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
66	d1tkea1	Alignment	not modelled	32.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
67	d2vv5a2	Alignment	not modelled	26.4	7	Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
68	c2yx5A	Alignment	not modelled	15.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway
69	c3hvvzB	Alignment	not modelled	15.8	4	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the clolep_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
70	c2kmmA	Alignment	not modelled	15.4	15	PDB header: hydrolase Chain: A: PDB Molecule: guanosine-3',5'-bis(diphosphate) 3'- PDBTitle: solution nmr structure of the tgs domain of pg1808 from2 porphyromonas gingivalis. northeast structural genomics3 consortium target pgr122a (418-481)
71	c1feoA	Alignment	not modelled	14.1	63	PDB header: toxin Chain: A: PDB Molecule: omega-conotoxin mvia-gly; PDBTitle: solution structure of omega-conotoxin mvia with c-terminal2 gly
72	d1xn7a	Alignment	not modelled	12.9	42	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Hypothetical protein YhgG
73	d1rubx4	Alignment	not modelled	12.8	54	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
74	d1zud21	Alignment	not modelled	9.0	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
75	c1tygG	Alignment	not modelled	8.9	13	PDB header: biosynthetic protein Chain: G: PDB Molecule: yjbs; PDBTitle: structure of the thiazole synthase/thiS complex
76	d1e0ga	Alignment	not modelled	8.4	17	Fold: LysM domain Superfamily: LysM domain Family: LysM domain
77	c2ixsB	Alignment	not modelled	8.3	15	PDB header: hydrolase Chain: B: PDB Molecule: sdai restriction endonuclease; PDBTitle: structure of sdai restriction endonuclease
78	c3fwaA	Alignment	not modelled	7.3	11	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline PDB header: structural genomics, unknown function

79	c2kl0A_	Alignment	not modelled	7.0	17	Chain: A: PDB Molecule: putative thiamin biosynthesis this; PDBTitle: solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
80	c1tkeA_	Alignment	not modelled	6.9	23	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
81	c3bl5E_	Alignment	not modelled	6.7	21	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
82	d1emoa2	Alignment	not modelled	5.9	38	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: EGF/Laminin Family: EGF-type module
83	d1wt8a1	Alignment	not modelled	5.9	36	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
84	d1vq3a_	Alignment	not modelled	5.8	8	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
85	c3d2hA_	Alignment	not modelled	5.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: berberine bridge-forming enzyme; PDBTitle: structure of berberine bridge enzyme from eschscholzia californica,2 monoclinic crystal form
86	d1tygb_	Alignment	not modelled	5.7	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: ThiS
87	c2i5yS_	Alignment	not modelled	5.4	38	PDB header: virus/viral protein/immune system Chain: S: PDB Molecule: cd4m47, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of cd4m47, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
88	c2i5yM_	Alignment	not modelled	5.4	38	PDB header: virus/viral protein/immune system Chain: M: PDB Molecule: cd4m47, scorpion-toxin mimic of cd4; PDBTitle: crystal structure of cd4m47, a scorpion-toxin mimic of cd4, in complex2 with hiv-1 yu2 gp120 envelope glycoprotein and anti-hiv-1 antibody3 17b
89	c2vv5D_	Alignment	not modelled	5.2	7	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of mscs