


Phyre2

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Description	FER_CAPAN_1-144
Date	Wed Jan 4 12:02:18 GMT 2017
Unique Job ID	56da5616b4559c93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4n58A_	 Alignment		100.0	54	PDB header: hydrolase Chain: A: PDB Molecule: pectocin m2; PDBTitle: crystal structure of pectocin m2 at 1.86 angstroms
2	d1a70a_	 Alignment		100.0	71	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
3	d1offa_	 Alignment		100.0	73	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
4	d1frfa_	 Alignment		99.9	62	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
5	d1pfda_	 Alignment		99.9	70	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
6	d1frda_	 Alignment		99.9	50	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
7	d1fxia_	 Alignment		99.9	62	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
8	d1gaqb_	 Alignment		99.9	71	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
9	d1iuea_	 Alignment		99.9	48	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
10	d1awda_	 Alignment		99.9	68	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
11	d1wria_	 Alignment		99.9	59	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related

12	d1czpa_	Alignment		99.9	64	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
13	d2cjoa_	Alignment		99.9	63	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
14	d4fxca_	Alignment		99.9	64	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
15	c4itkA_	Alignment		99.9	57	PDB header: electron transport Chain: A: PDB Molecule: apoferredoxin; PDBTitle: the structure of c.reinhardtii ferredoxin 2
16	c1krhA_	Alignment		99.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: benzoate 1,2-dioxygenase reductase; PDBTitle: x-ray stucture of benzoate dioxygenase reductase
17	d1krha3	Alignment		99.9	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
18	d1jq4a_	Alignment		99.9	29	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
19	c4wqmA_	Alignment		99.9	28	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene-4-monooxygenase electron transfer component; PDBTitle: structure of the toluene 4-monooxygenase nadh oxidoreductase t4mof,2 k270s k271s variant
20	c2piaA_	Alignment		99.9	22	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]
21	d2piaa3	Alignment	not modelled	99.9	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
22	d1doia_	Alignment	not modelled	99.9	34	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
23	d1e0za_	Alignment	not modelled	99.8	34	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
24	c4p6vF_	Alignment	not modelled	99.8	22	PDB header: oxidoreductase Chain: F: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit f; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
25	c3zzyX_	Alignment	not modelled	99.8	29	PDB header: iron-sulfur-binding protein Chain: X: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: reductive activator for corrinoid,iron-sulfur protein
26	c5frtC_	Alignment	not modelled	99.8	26	PDB header: oxidoreductase Chain: C: PDB Molecule: dimeric (2fe-2s) protein; PDBTitle: structure of the fesii (shethna) protein of azotobacter vinelandii
27	c3ah7A_	Alignment	not modelled	99.7	22	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
28	c2y5cB_	Alignment	not modelled	99.7	20	PDB header: electron transport Chain: B: PDB Molecule: adrenodoxin-like protein, mitochondrial; PDBTitle: structure of human ferredoxin 2 (fdx2)in complex with 2fe2s2 cluster

29	c2mjdB	Alignment	not modelled	99.7	25	PDB header: metal binding protein Chain: A: PDB Molecule: adrenodoxin homolog, mitochondrial; PDBTitle: oxidized yeast adrenodoxin homolog 1
30	c2wlbB	Alignment	not modelled	99.7	28	PDB header: electron transport Chain: B: PDB Molecule: electron transfer protein 1, mitochondrial; PDBTitle: adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
31	d1i7ha	Alignment	not modelled	99.6	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
32	d1e9ma	Alignment	not modelled	99.6	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
33	c3lxfC	Alignment	not modelled	99.6	24	PDB header: metal binding protein Chain: C: PDB Molecule: ferredoxin; PDBTitle: crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
34	c2mj3A	Alignment	not modelled	99.6	21	PDB header: metal binding protein Chain: A: PDB Molecule: iron-sulfur cluster binding protein; PDBTitle: backbone 1h, 13c, and 15n chemical shift assignments and structure of2 iron-sulfur cluster binding protein from ehrlichia chaffeensis
35	d1xlqa1	Alignment	not modelled	99.6	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
36	c4ltuB	Alignment	not modelled	99.6	19	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: crystal structure of ferredoxin from rhodopseudomonas palustris haa2
37	d2bt6a1	Alignment	not modelled	99.6	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
38	d1l5pa	Alignment	not modelled	99.6	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
39	c3huiA	Alignment	not modelled	99.6	14	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: crystal structure of the mutant a105r of [2fe-2s] ferredoxin in the2 class i cyp199a2 system from rhodopseudomonas palustris
40	c3p1mG	Alignment	not modelled	99.5	20	PDB header: electron transport Chain: G: PDB Molecule: adrenodoxin, mitochondrial; PDBTitle: crystal structure of human ferredoxin-1 (fdx1) in complex with iron-2 sulfur cluster
41	d1b9ra	Alignment	not modelled	99.5	22	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
42	c1l6vA	Alignment	not modelled	99.2	19	PDB header: electron transport Chain: A: PDB Molecule: adrenodoxin 1; PDBTitle: structure of reduced bovine adrenodoxin
43	d2fug33	Alignment	not modelled	98.9	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
44	d3c8ya2	Alignment	not modelled	98.7	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
45	c1c4cA	Alignment	not modelled	98.6	26	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 (cpl) from clostridium3 pasteurianum
46	c2fugC	Alignment	not modelled	98.3	25	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
47	d1t3qa2	Alignment	not modelled	98.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
48	d1n62a2	Alignment	not modelled	98.2	14	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
49	d1vlba2	Alignment	not modelled	98.2	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
50	d1ffva2	Alignment	not modelled	98.1	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
51	d1dgja2	Alignment	not modelled	98.1	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
52	c3hrdH	Alignment	not modelled	98.0	21	PDB header: oxidoreductase Chain: H: PDB Molecule: nicotinate dehydrogenase small fes subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
53	c1t3qD	Alignment	not modelled	98.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: quinoline 2-oxidoreductase small subunit; PDBTitle: crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
54	d1rm6c2	Alignment	not modelled	98.0	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
						PDB header: oxidoreductase

55	c1rm6F_	Alignment	not modelled	97.9	27	Chain: F: PDB Molecule: 4-hydroxybenzoyl-coa reductase gamma subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
56	c4zohC_	Alignment	not modelled	97.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase iron-sulfur subunit; PDBTitle: crystal structure of glyceraldehyde oxidoreductase
57	c1n60D_	Alignment	not modelled	97.9	14	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
58	d2bs2b2	Alignment	not modelled	97.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
59	c1ffuA_	Alignment	not modelled	97.8	13	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
60	d1kf6b2	Alignment	not modelled	97.7	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
61	c2bs2E_	Alignment	not modelled	97.7	26	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
62	c2h89B_	Alignment	not modelled	97.5	33	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
63	c2b76N_	Alignment	not modelled	97.5	28	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
64	d1jroa2	Alignment	not modelled	97.4	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
65	c2w3rG_	Alignment	not modelled	97.3	15	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
66	c3vrBF_	Alignment	not modelled	97.3	31	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: F: PDB Molecule: iron-sulfur subunit of succinate dehydrogenase; PDBTitle: mitochondrial rhoquoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
67	d1v97a2	Alignment	not modelled	97.3	13	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
68	d1nekb2	Alignment	not modelled	97.3	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
69	c1nekB_	Alignment	not modelled	97.1	26	PDB header: oxidoreductase/electron transport protein; Chain: B: PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
70	c3b9jI_	Alignment	not modelled	97.1	13	PDB header: oxidoreductase Chain: I: PDB Molecule: xanthine oxidase; PDBTitle: structure of xanthine oxidase with 2-hydroxy-6-methylpurine
71	c1vlbA_	Alignment	not modelled	97.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
72	c3eubJ_	Alignment	not modelled	97.0	13	PDB header: oxidoreductase Chain: J: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of desulfo-xanthine oxidase with xanthine
73	c1dgiA_	Alignment	not modelled	96.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
74	c3zyvA_	Alignment	not modelled	96.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aox3; PDBTitle: crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
75	c4uhxA_	Alignment	not modelled	96.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
76	c1wygA_	Alignment	not modelled	95.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
77	c1ep3B_	Alignment	not modelled	95.4	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.
78	d1ep3b2	Alignment	not modelled	93.8	15	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Dihydroorotate dehydrogenase B, PyrK subunit PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase b (nad(+)),

79	c4yifA_	Alignment	not modelled	93.3	26	electron transfer PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
80	c1x31A_	Alignment	not modelled	53.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
81	d2hj1a1	Alignment	not modelled	50.0	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: MoaD/ThiS Family: HI0395-like
82	c2hj1A_	Alignment	not modelled	50.0	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a 3d domain-swapped dimer of protein hi0395 from2 haemophilus influenzae
83	c2kmmA_	Alignment	not modelled	44.8	31	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)
84	d1wx8a1	Alignment	not modelled	36.2	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
85	c3hvvB_	Alignment	not modelled	35.4	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the tgs domain of the cleop_03100 protein from2 clostridium leptum, northeast structural genomics consortium target3 qlr13a
86	d1tkea1	Alignment	not modelled	29.8	26	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
87	d1j8ca_	Alignment	not modelled	24.2	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
88	d1wxma1	Alignment	not modelled	22.5	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
89	d2a13a1	Alignment	not modelled	22.3	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: UBX domain
90	d2bwfa1	Alignment	not modelled	18.7	12	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
91	c1feoA_	Alignment	not modelled	17.4	63	PDB header: toxin Chain: A: PDB Molecule: omega-conotoxin mviiia-gly; PDBTitle: solution structure of omega-conotoxin mviiia with c-terminal2 gly
92	c1wwtA_	Alignment	not modelled	16.6	17	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
93	d1nyra2	Alignment	not modelled	15.6	18	Fold: beta-Grasp (ubiquitin-like) Superfamily: TGS-like Family: TGS domain
94	d2vv5a2	Alignment	not modelled	15.3	36	Fold: Ferredoxin-like Superfamily: Mechanosensitive channel protein MscS (YggB), C-terminal domain Family: Mechanosensitive channel protein MscS (YggB), C-terminal domain
95	c2kanA_	Alignment	not modelled	14.2	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ar3433a; PDBTitle: solution nmr structure of ubiquitin-like domain of f2 arabidopsis thaliana protein at2g32350. northeast3 structural genomics consortium target ar3433a
96	c3j60I_	Alignment	not modelled	14.0	26	PDB header: ribosome Chain: I: PDB Molecule: 40s ribosomal protein s8e; PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
97	d2znbv1	Alignment	not modelled	13.9	17	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ubiquitin-related
98	d1rutx4	Alignment	not modelled	13.8	31	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
99	c3bl5E_	Alignment	not modelled	13.5	29	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