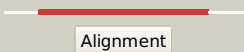

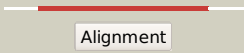


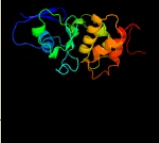
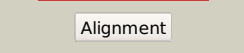



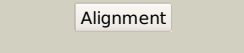

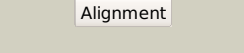
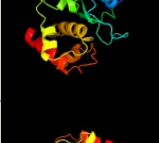
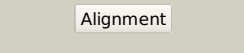

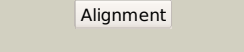
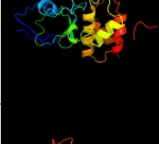
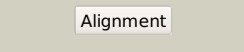

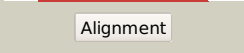












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0374c (-) _451801_452280
Date	Tue Jul 23 14:50:44 BST 2019
Unique Job ID	9faac31061dcce10

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3zyvA_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aox3; <b>PDBTitle:</b> crystal structure of the mouse liver aldehyde oxidase 3 (maox3)
2	<a href="#">c1vlbA_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidoreductase; <b>PDBTitle:</b> structure refinement of the aldehyde oxidoreductase from <i>Desulfovibrio gigas</i> at 1.28 Å
3	<a href="#">c4uhxA_</a>	 Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidase; <b>PDBTitle:</b> human aldehyde oxidase in complex with phthalazine and thioridazine
4	<a href="#">c5y6qA_</a>	 Alignment		100.0	41	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidase small subunit; <b>PDBTitle:</b> crystal structure of an aldehyde oxidase from <i>Methylobacillus</i> sp.2 ky4400
5	<a href="#">c1t3qD_</a>	 Alignment		100.0	48	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> quinoline 2-oxidoreductase small subunit; <b>PDBTitle:</b> crystal structure of quinoline 2-oxidoreductase from <i>Pseudomonas putida</i> 86
6	<a href="#">c1rm6F_</a>	 Alignment		100.0	43	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 4-hydroxybenzoyl-coa reductase gamma subunit; <b>PDBTitle:</b> structure of 4-hydroxybenzoyl-coa reductase from <i>Thauera aromatica</i>
7	<a href="#">c1n60D_</a>	 Alignment		100.0	58	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> carbon monoxide dehydrogenase small chain; <b>PDBTitle:</b> crystal structure of the Cu,Mo-Co dehydrogenase (CODH); cyanide-2 inactivated form
8	<a href="#">c3hrdH_</a>	 Alignment		100.0	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> nicotinate dehydrogenase small subunit; <b>PDBTitle:</b> crystal structure of nicotinate dehydrogenase
9	<a href="#">c1wygA_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xanthine dehydrogenase/oxidase; <b>PDBTitle:</b> crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
10	<a href="#">c1ffuA_</a>	 Alignment		100.0	54	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cuts, iron-sulfur protein of carbon monoxide <b>PDBTitle:</b> carbon monoxide dehydrogenase from <i>Hydrogenophaga pseudoflava</i> which lacks the Mo-pyranopterin moiety of the 3 molybdenum cofactor
11	<a href="#">c1dgiA_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde oxidoreductase; <b>PDBTitle:</b> crystal structure of the aldehyde oxidoreductase from <i>Desulfovibrio desulfuricans</i> ATCC 27774

12	<a href="#">c4zohC_</a>	Alignment		100.0	57	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of glyceraldehyde oxidoreductase
13	<a href="#">c3b9jl_</a>	Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> xanthine oxidase; <b>PDBTitle:</b> structure of xanthine oxidase with 2-hydroxy-6-methylpurine
14	<a href="#">c3eubl_</a>	Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> xanthine dehydrogenase/oxidase; <b>PDBTitle:</b> crystal structure of desulfo-xanthine oxidase with xanthine
15	<a href="#">c2w3rG_</a>	Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> xanthine dehydrogenase; <b>PDBTitle:</b> crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
16	<a href="#">c5g5gA_</a>	Alignment		100.0	42	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative xanthine dehydrogenase yagt iron-sulfur-binding <b>PDBTitle:</b> escherichia coli periplasmic aldehyde oxidase
17	<a href="#">d1n62a1</a>	Alignment		100.0	53	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
18	<a href="#">d1rm6c1</a>	Alignment		100.0	45	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
19	<a href="#">d1ffva1</a>	Alignment		100.0	53	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
20	<a href="#">d1t3qa1</a>	Alignment		100.0	47	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
21	<a href="#">d1zxia1</a>	Alignment	not modelled	100.0	56	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
22	<a href="#">d1vlba1</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
23	<a href="#">d1dgja1</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
24	<a href="#">d1v97a1</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
25	<a href="#">d1jroa1</a>	Alignment	not modelled	100.0	44	<b>Fold:</b> CO dehydrogenase ISP C-domain like <b>Superfamily:</b> CO dehydrogenase ISP C-domain like <b>Family:</b> CO dehydrogenase ISP C-domain like
26	<a href="#">d1t3qa2</a>	Alignment	not modelled	100.0	50	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
27	<a href="#">d1n62a2</a>	Alignment	not modelled	100.0	60	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
28	<a href="#">d1ffva2</a>	Alignment	not modelled	100.0	57	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
29	<a href="#">d1jroa2</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like

						<b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
30	<a href="#">d1rm6c2</a>	Alignment	not modelled	100.0	41	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
31	<a href="#">d1v97a2</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
32	<a href="#">d1vlba2</a>	Alignment	not modelled	99.9	40	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
33	<a href="#">d1dgja2</a>	Alignment	not modelled	99.9	38	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
34	<a href="#">d2bs2b2</a>	Alignment	not modelled	99.6	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
35	<a href="#">d1nekb2</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
36	<a href="#">d1kf6b2</a>	Alignment	not modelled	99.5	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
37	<a href="#">c5xmjl</a>	Alignment	not modelled	99.2	21	<b>PDB header:</b> electron transport <b>Chain:</b> J; <b>PDB Molecule:</b> succinate dehydrogenase iron-sulfur subunit; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
38	<a href="#">c2bs2E</a>	Alignment	not modelled	99.2	22	<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 wolinnella succinogenes
39	<a href="#">c2h89B</a>	Alignment	not modelled	99.2	13	<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
40	<a href="#">c2b76N</a>	Alignment	not modelled	99.2	22	<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
41	<a href="#">c3vrBF</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> F; <b>PDB Molecule:</b> iron-sulfur subunit of succinate dehydrogenase; <b>PDBTitle:</b> mitochondrial rholoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
42	<a href="#">d3c8ya2</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
43	<a href="#">c1nekB</a>	Alignment	not modelled	99.1	18	<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
44	<a href="#">c5xf9F</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F; <b>PDB Molecule:</b> nad-reducing hydrogenase; <b>PDBTitle:</b> crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
45	<a href="#">d2fug33</a>	Alignment	not modelled	98.7	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
46	<a href="#">c1c4cA</a>	Alignment	not modelled	98.6	25	<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
47	<a href="#">c6gcsA</a>	Alignment	not modelled	98.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 75-kda protein (nuam); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
48	<a href="#">c5lnk3</a>	Alignment	not modelled	98.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 3; <b>PDB Molecule:</b> mitochondrial complex i, 75 kda subunit; <b>PDBTitle:</b> entire ovine respiratory complex i
49	<a href="#">c5ldxG</a>	Alignment	not modelled	98.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class3.
50	<a href="#">c5ldwG</a>	Alignment	not modelled	98.3	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class1
51	<a href="#">c5lc5G</a>	Alignment	not modelled	98.2	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> nadh-ubiquinone oxidoreductase 75 kda subunit, <b>PDBTitle:</b> structure of mammalian respiratory complex i, class2
52	<a href="#">d1frfa</a>	Alignment	not modelled	98.1	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
53	<a href="#">d1fxia</a>	Alignment	not modelled	98.0	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
54	<a href="#">d1awda</a>	Alignment	not modelled	97.9	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
						<b>Fold:</b> beta-Grasp (ubiquitin-like)

55	<a href="#">d1wrja_</a>	Alignment	not modelled	97.9	21	<b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
56	<a href="#">d1iuea_</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
57	<a href="#">d1a70a_</a>	Alignment	not modelled	97.9	10	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
58	<a href="#">d1l5pa_</a>	Alignment	not modelled	97.9	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
59	<a href="#">c2fugC_</a>	Alignment	not modelled	97.8	19	<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
60	<a href="#">c4itkA_</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoferrredoxin; <b>PDBTitle:</b> the structure of c.reinhardtii ferredoxin 2
61	<a href="#">c5ogxA_</a>	Alignment	not modelled	97.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 reductase; <b>PDBTitle:</b> crystal structure of amycolatopsis cytochrome p450 reductase gcob.
62	<a href="#">d1czpa_</a>	Alignment	not modelled	97.7	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
63	<a href="#">d2cjoa_</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
64	<a href="#">d1offa_</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
65	<a href="#">c2y5cB_</a>	Alignment	not modelled	97.5	18	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> adrenodoxin-like protein, mitochondrial; <b>PDBTitle:</b> structure of human ferredoxin 2 (fdx2)in complex with 2fe2s2 cluster
66	<a href="#">c1krhA_</a>	Alignment	not modelled	97.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> benzoate 1,2-dioxygenase reductase; <b>PDBTitle:</b> x-ray structure of benzoate dioxygenase reductase
67	<a href="#">d1gaqb_</a>	Alignment	not modelled	97.5	15	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
68	<a href="#">d1jq4a_</a>	Alignment	not modelled	97.5	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
69	<a href="#">c2mjdB_</a>	Alignment	not modelled	97.5	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> adrenodoxin homolog, mitochondrial; <b>PDBTitle:</b> oxidized yeast adrenodoxin homolog 1
70	<a href="#">d1pfda_</a>	Alignment	not modelled	97.4	12	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
71	<a href="#">c5uj5A_</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> adrenodoxin; <b>PDBTitle:</b> solution structure of the oxidized iron-sulfur protein adrenodoxin2 from encephalitozoon cuniculi. seattle structural genomics center for3 infectious disease target encua.00705.a
72	<a href="#">c2wlbB_</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> electron transfer protein 1, mitochondrial; <b>PDBTitle:</b> adrenodoxin-like ferredoxin etp1fd(516-618) of schizosaccharomyces2 pombe mitochondria
73	<a href="#">c2piaA_</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> phthalate dioxygenase reductase; <b>PDBTitle:</b> phthalate dioxygenase reductase: a modular structure for electron2 transfer from pyridine nucleotides to [2fe-2s]
74	<a href="#">d1frda_</a>	Alignment	not modelled	97.3	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
75	<a href="#">d4fxca_</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
76	<a href="#">d2piao3</a>	Alignment	not modelled	97.3	17	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
77	<a href="#">c2mj3A_</a>	Alignment	not modelled	97.3	16	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> iron-sulfur cluster binding protein; <b>PDBTitle:</b> backbone 1h, 13c, and 15n chemical shift assignments and structure of2 iron-sulfur cluster binding protein from ehrlichia chaffeensis
78	<a href="#">d1krha3</a>	Alignment	not modelled	97.3	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
79	<a href="#">c5frc_</a>	Alignment	not modelled	97.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dimeric (2fe-2s) protein; <b>PDBTitle:</b> structure of the fesii (shethna) protein of azotobacter vinelandii
80	<a href="#">c4p6vF_</a>	Alignment	not modelled	97.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit f; <b>PDBTitle:</b> crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene-4-monooxygenase electron

81	<a href="#">c4wqmA_</a>	Alignment	not modelled	97.2	19	transfer component; <b>PDBTitle:</b> structure of the toluene 4-monooxygenase nadh oxidoreductase t4mof,2 k270s k271s variant
82	<a href="#">c3zyyX_</a>	Alignment	not modelled	97.0	24	<b>PDB header:</b> iron-sulfur-binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> iron-sulfur cluster binding protein; <b>PDBTitle:</b> reductive activator for corrinoid,iron-sulfur protein
83	<a href="#">c3lxfC_</a>	Alignment	not modelled	97.0	31	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
84	<a href="#">c3huiA_</a>	Alignment	not modelled	97.0	29	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> crystal structure of the mutant a105r of [2fe-2s] ferredoxin in the2 class i cyp199a2 system from rhodopseudomonas palustris
85	<a href="#">d1e9ma_</a>	Alignment	not modelled	97.0	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
86	<a href="#">d1doia_</a>	Alignment	not modelled	97.0	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
87	<a href="#">c4ltuB_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin; <b>PDBTitle:</b> crystal structure of ferredoxin from rhodopseudomonas palustris haa2
88	<a href="#">c4n58A_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pectocin m2; <b>PDBTitle:</b> crystal structure of pectocin m2 at 1.86 angstroms
89	<a href="#">d1xlqa1</a>	Alignment	not modelled	96.9	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
90	<a href="#">c3ah7A_</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> [2fe-2s]ferredoxin; <b>PDBTitle:</b> crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004
91	<a href="#">c3p1mG_</a>	Alignment	not modelled	96.7	18	<b>PDB header:</b> electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> adrenodoxin, mitochondrial; <b>PDBTitle:</b> crystal structure of human ferredoxin-1 (fdx1) in complex with iron-2 sulfur cluster
92	<a href="#">d2bt6a1</a>	Alignment	not modelled	96.6	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
93	<a href="#">d1b9ra_</a>	Alignment	not modelled	96.6	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
94	<a href="#">d1e0za_</a>	Alignment	not modelled	96.5	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
95	<a href="#">c1x31A_</a>	Alignment	not modelled	96.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit; <b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
96	<a href="#">d1i7ha_</a>	Alignment	not modelled	96.3	16	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
97	<a href="#">c1y56A_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1363; <b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from p.horikoshii
98	<a href="#">c5vj7B_</a>	Alignment	not modelled	93.5	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin-nadp(+) reductase subunit alpha; <b>PDBTitle:</b> ferredoxin nadp oxidoreductase (xfn)
99	<a href="#">c4ylfA_</a>	Alignment	not modelled	92.3	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotate dehydrogenase b (nad(+)), electron transfer <b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
100	<a href="#">c5jcaS_</a>	Alignment	not modelled	91.2	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> S: <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadp oxidoreductase (nfni) <b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
101	<a href="#">c1l6vA_</a>	Alignment	not modelled	91.2	21	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> adrenodoxin 1; <b>PDBTitle:</b> structure of reduced bovine adrenodoxin
102	<a href="#">d1ep3b2</a>	Alignment	not modelled	89.1	15	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Dihydroorotate dehydrogenase B, PyrK subunit
103	<a href="#">c3cwiA_</a>	Alignment	not modelled	85.1	28	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> thiamine-biosynthesis protein this; <b>PDBTitle:</b> crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
104	<a href="#">c2kl0A_</a>	Alignment	not modelled	84.4	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative thiamin biosynthesis this; <b>PDBTitle:</b> solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
105	<a href="#">c1ep3B_</a>	Alignment	not modelled	83.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotate dehydrogenase b (pyrk subunit); <b>PDBTitle:</b> crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions. <b>Fold:</b> beta-Grasp (ubiquitin-like)

106	<a href="#">d1zud21</a>	Alignment	not modelled	81.2	9	<b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
107	<a href="#">d1v86a_</a>	Alignment	not modelled	78.4	11	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
108	<a href="#">c1oqyA_</a>	Alignment	not modelled	76.6	8	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> uv excision repair protein rad23 homolog a; <b>PDBTitle:</b> structure of the dna repair protein hhr23a
109	<a href="#">c2kd0A_</a>	Alignment	not modelled	75.5	12	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> lrr repeats and ubiquitin-like domain-containing <b>PDBTitle:</b> nmr solution structure of o64736 protein from arabidopsis2 thaliana. northeast structural genomics consortium mega3 target ar3445a
110	<a href="#">d1oqya4</a>	Alignment	not modelled	73.0	8	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
111	<a href="#">d1v5oa_</a>	Alignment	not modelled	68.8	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
112	<a href="#">d2znvb1</a>	Alignment	not modelled	68.0	36	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
113	<a href="#">d1bt0a_</a>	Alignment	not modelled	65.9	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
114	<a href="#">d2cu3a1</a>	Alignment	not modelled	65.5	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> MoaD/ThiS <b>Family:</b> ThiS
115	<a href="#">d1uela_</a>	Alignment	not modelled	64.6	19	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
116	<a href="#">c2kk8A_</a>	Alignment	not modelled	64.1	28	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein at4g05270; <b>PDBTitle:</b> nmr solution structure of a putative uncharacterized protein2 obtained from arabidopsis thaliana: northeast structural3 genomics consortium target ar3449a
117	<a href="#">d1ndda_</a>	Alignment	not modelled	62.8	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
118	<a href="#">d1wh3a_</a>	Alignment	not modelled	62.1	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
119	<a href="#">d1sifa_</a>	Alignment	not modelled	61.2	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related
120	<a href="#">d1p1aa_</a>	Alignment	not modelled	61.0	20	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ubiquitin-related