Phyre2

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Description	Q46814
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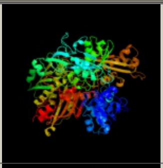
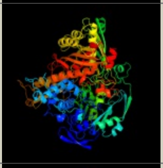
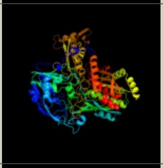
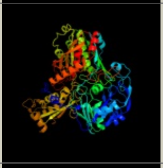
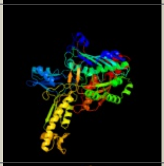
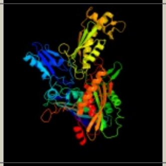
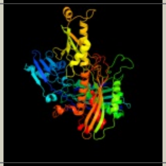
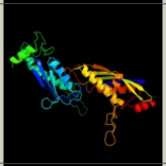
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1wygA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
2	c1vlbA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
3	c1dgjA_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
4	c1sb3D_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**4-hydroxybenzoyl-coa reductase alpha subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
5	c1ffvB_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cutl, molybdoprotein of carbon monoxide **PDBTitle:** carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava
6	c1n62E_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**carbon monoxide dehydrogenase large chain; **PDBTitle:** crystal structure of the mo,cu-co dehydrogenase (codh), n-2 butylisocyanide-bound state
7	c1t3qB_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**quinoline 2-oxidoreductase large subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
8	c2w54F_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**xanthine dehydrogenase; **PDBTitle:** crystal structure of xanthine dehydrogenase from2 rhodobacter capsulatus in complex with bound inhibitor3 pterin-6-aldehyde
9	c3eubL_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
10	d1rm6a2	Alignment		100.0	30	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
11	d1n62b2	Alignment		100.0	24	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain

12	d1ffvb2	Alignment		100.0	25	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
13	d1jrob2	Alignment		100.0	27	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
14	d1t3qb2	Alignment		100.0	27	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
15	d1v97a5	Alignment		100.0	25	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
16	d1vlba4	Alignment		100.0	28	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
17	d1dgja4	Alignment		100.0	27	**Fold:**Molybdenum cofactor-binding domain **Superfamily:**Molybdenum cofactor-binding domain **Family:**Molybdenum cofactor-binding domain
18	c3hrdE_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**nicotinate dehydrogenase large molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
19	c3hrdF_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**nicotinate dehydrogenase medium molybdopterin **PDBTitle:** crystal structure of nicotinate dehydrogenase
20	c2w3rG_	Alignment		100.0	26	**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
21	c1ffuA_	Alignment	not modelled	100.0	22	**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
22	c3b9jI_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
23	c3hrdH_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
24	c1rm6F_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
25	c3eubJ_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
26	c1t3qD_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
27	c1n60D_	Alignment	not modelled	100.0	25	**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
28	d1dgja1	Alignment	not modelled	100.0	23	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
29	d1vlba1	Alignment	not modelled	100.0	25	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
30	d1t3qb1	Alignment	not modelled	100.0	31	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
31	d1v97a1	Alignment	not modelled	100.0	26	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
32	d1zxia1	Alignment	not modelled	100.0	28	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
33	d1n62a1	Alignment	not modelled	100.0	26	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
34	d1rm6c1	Alignment	not modelled	100.0	28	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
35	d1t3qa1	Alignment	not modelled	100.0	18	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
36	d1ffva1	Alignment	not modelled	100.0	21	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
37	d1ffvb1	Alignment	not modelled	100.0	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
38	d1n62b1	Alignment	not modelled	100.0	30	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
39	d1v97a3	Alignment	not modelled	100.0	24	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
40	d1jroa1	Alignment	not modelled	100.0	28	**Fold:**CO dehydrogenase ISP C-domain like **Superfamily:**CO dehydrogenase ISP C-domain like **Family:**CO dehydrogenase ISP C-domain like
41	d3b9jc1	Alignment	not modelled	99.9	27	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
42	d1rm6a1	Alignment	not modelled	99.9	41	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
43	d1v97a2	Alignment	not modelled	99.9	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
44	d1jroa2	Alignment	not modelled	99.9	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
45	d1jrob1	Alignment	not modelled	99.9	26	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
46	d1ffva2	Alignment	not modelled	99.9	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
47	d1rm6c2	Alignment	not modelled	99.9	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
48	d1n62a2	Alignment	not modelled	99.9	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
49	d1t3qa2	Alignment	not modelled	99.9	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
50	d1vlba3	Alignment	not modelled	99.9	29	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
51	d1vlba2	Alignment	not modelled	99.9	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
52	d1dgja3	Alignment	not modelled	99.9	25	**Fold:**alpha/beta-Hammerhead **Superfamily:**CO dehydrogenase molybdoprotein N-domain-like **Family:**CO dehydrogenase molybdoprotein N-domain-like
53	d1dgja2	Alignment	not modelled	99.9	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
54	d2bs2b2	Alignment	not modelled	99.0	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
55	d3c8ya2	Alignment	not modelled	98.9	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

						Family:2Fe-2S ferredoxin domains from multidomain proteins
56	d1nekb2	Alignment	not modelled	98.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
57	d1kf6b2	Alignment	not modelled	98.6	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
58	d2fug33	Alignment	not modelled	98.4	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
59	c2b76N_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
60	c1c4cA_	Alignment	not modelled	98.0	10	**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
61	c2bs2E_	Alignment	not modelled	97.6	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
62	c2h89B_	Alignment	not modelled	97.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
63	c2fugC_	Alignment	not modelled	97.1	11	**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
64	d1frra_	Alignment	not modelled	96.9	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
65	d1fxia_	Alignment	not modelled	96.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
66	d1l5pa_	Alignment	not modelled	96.8	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
67	d1awda_	Alignment	not modelled	96.8	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
68	d1iuea_	Alignment	not modelled	96.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
69	d1czpa_	Alignment	not modelled	96.6	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
70	c1nekB_	Alignment	not modelled	96.6	19	**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
71	d1a70a_	Alignment	not modelled	96.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
72	c3huiA_	Alignment	not modelled	96.4	12	**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
73	d1wria_	Alignment	not modelled	96.3	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
74	c2wlbB_	Alignment	not modelled	96.2	16	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
75	d1e9ma_	Alignment	not modelled	96.0	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
76	d2cjoa_	Alignment	not modelled	95.9	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
77	d2piaa3	Alignment	not modelled	95.8	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
78	d1jq4a_	Alignment	not modelled	95.8	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
79	d4fxca_	Alignment	not modelled	95.7	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
80	d1xlqa1	Alignment	not modelled	95.6	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
81	c3lxfC_	Alignment	not modelled	95.6	18	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from

						novosphingobium2 aromaticivorans
82	d1pfda_	Alignment	not modelled	95.6	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
83	d1offa_	Alignment	not modelled	95.5	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
84	c1krhA_	Alignment	not modelled	95.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
85	c3ah7A_	Alignment	not modelled	95.4	16	**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
86	d1krha3	Alignment	not modelled	95.2	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
87	d1gaqb_	Alignment	not modelled	95.1	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
88	c2piaA_	Alignment	not modelled	95.0	15	**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]
89	d1b9ra_	Alignment	not modelled	95.0	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
90	d1frda_	Alignment	not modelled	94.7	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
91	d1i7ha_	Alignment	not modelled	94.6	15	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
92	d2bt6a1	Alignment	not modelled	94.4	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
93	c1x31A_	Alignment	not modelled	93.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
94	d1doia_	Alignment	not modelled	92.5	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
95	c1l6vA_	Alignment	not modelled	88.3	16	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
96	d1e0za_	Alignment	not modelled	87.4	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
97	c1y56A_	Alignment	not modelled	87.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1363; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
98	d1ep3b2	Alignment	not modelled	76.4	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
99	c2kl0A_	Alignment	not modelled	75.8	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thiamin biosynthesis this; **PDBTitle:** solution nmr structure of rhodopseudomonas palustris rpa3574,2 northeast structural genomics consortium (nesg) target rpr325
100	c3cwiA_	Alignment	not modelled	71.2	26	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**thiamine-biosynthesis protein this; **PDBTitle:** crystal structure of thiamine biosynthesis protein (this)2 from geobacter metallireducens. northeast structural3 genomics consortium target gmr137
101	d2gdga1	Alignment	not modelled	61.9	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
102	d1gd0a_	Alignment	not modelled	61.3	15	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
103	d2cu3a1	Alignment	not modelled	60.8	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
104	d1hfoa_	Alignment	not modelled	58.4	16	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
105	d1zud21	Alignment	not modelled	58.3	19	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
106	c3fwtA_	Alignment	not modelled	57.0	11	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** crystal structure of leishmania major mif2
107	d1uiza_	Alignment	not modelled	56.4	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
						PDB header:cytokine

108	c3gacD_	Alignment	not modelled	55.9	16	**Chain:** D: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** structure of mif with hpp
109	c1ep3B_	Alignment	not modelled	54.4	13	**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.
110	c2os5C_	Alignment	not modelled	53.2	15	**PDB header:**cytokine **Chain:** C: **PDB Molecule:**acemif; **PDBTitle:** macrophage migration inhibitory factor from ancylostoma ceylanicum
111	c3b64A_	Alignment	not modelled	52.3	15	**PDB header:**cytokine **Chain:** A: **PDB Molecule:**macrophage migration inhibitory factor-like **PDBTitle:** macrophage migration inhibitory factor (mif) from2 /leishmania major
112	d1dpta_	Alignment	not modelled	51.9	12	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
113	c2xczA_	Alignment	not modelled	51.9	15	**PDB header:**immune system **Chain:** A: **PDB Molecule:**possible atls1-like light-inducible protein; **PDBTitle:** crystal structure of macrophage migration inhibitory factor2 homologue from prochlorococcus marinus
114	d1fima_	Alignment	not modelled	51.7	14	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**MIF-related
115	d1v86a_	Alignment	not modelled	50.5	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
116	d1v5oa_	Alignment	not modelled	49.9	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
117	d2fug11	Alignment	not modelled	48.0	18	**Fold:**Bromodomain-like **Superfamily:**Nqo1C-terminal domain-like **Family:**Nqo1C-terminal domain-like
118	c2fugA_	Alignment	not modelled	44.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-quinone oxidoreductase chain 1; **PDBTitle:** crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
119	c1tygG_	Alignment	not modelled	44.4	19	**PDB header:**biosynthetic protein **Chain:** G: **PDB Molecule:**yjbs; **PDBTitle:** structure of the thiazole synthase/this complex
120	c2nnzA_	Alignment	not modelled	43.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** solution structure of the hypothetical protein af2241 from2 archaeoglobus fulgidus