Phyre^2

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Description	P0A9R4
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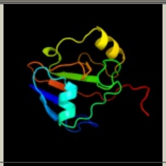
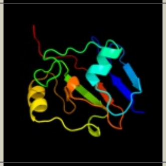
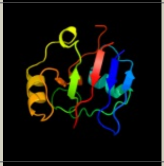
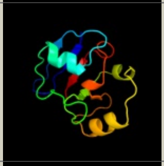
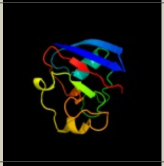
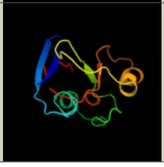
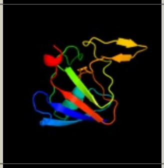
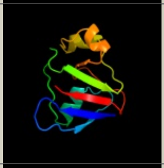
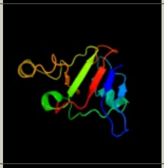
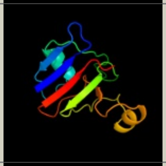
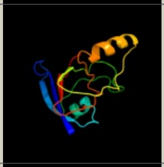
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1i7ha_	Alignment		100.0	100	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
2	c3ah7A_	Alignment		100.0	58	**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
3	c3huiA_	Alignment		99.9	38	**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
4	c2wlbB_	Alignment		99.9	45	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
5	c3lxfC_	Alignment		99.9	36	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
6	d2bt6a1	Alignment		99.9	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
7	d1b9ra_	Alignment		99.9	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
8	d1xlqa1	Alignment		99.9	36	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
9	d1e9ma_	Alignment		99.9	37	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
10	c1l6vA_	Alignment		99.8	33	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
11	d1l5pa_	Alignment		99.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related

12	d1krha3	Alignment		99.8	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
13	d1iuea_	Alignment		99.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
14	c1krhA_	Alignment		99.8	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
15	d1fxia_	Alignment		99.8	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
16	d1jq4a_	Alignment		99.8	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
17	d1pfda_	Alignment		99.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
18	d1frra_	Alignment		99.7	31	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
19	d4fxca_	Alignment		99.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
20	d1czpa_	Alignment		99.7	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
21	d1offa_	Alignment	not modelled	99.7	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
22	d1frda_	Alignment	not modelled	99.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
23	d1awda_	Alignment	not modelled	99.7	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
24	d1a70a_	Alignment	not modelled	99.7	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
25	d2cjoa_	Alignment	not modelled	99.7	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
26	d1gaqb_	Alignment	not modelled	99.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
27	d1wria_	Alignment	not modelled	99.7	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
28	d2piaa3	Alignment	not modelled	99.6	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
29	d1doia_	Alignment	not modelled	99.6	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

						Family:2Fe-2S ferredoxin-related
30	d1e0za_	Alignment	not modelled	99.5	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
31	c2piaA_	Alignment	not modelled	99.4	20	**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]
32	d2fug33	Alignment	not modelled	99.1	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
33	d3c8ya2	Alignment	not modelled	99.0	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
34	c1c4cA_	Alignment	not modelled	98.8	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	98.7	24	**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	98.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
37	d1dgja2	Alignment	not modelled	98.0	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
38	d1t3qa2	Alignment	not modelled	97.8	14	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
39	d1n62a2	Alignment	not modelled	97.5	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
40	c1t3qD_	Alignment	not modelled	97.5	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
41	c3hrdH_	Alignment	not modelled	97.3	21	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
42	c1n60D_	Alignment	not modelled	97.2	10	**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
43	d1ffva2	Alignment	not modelled	97.2	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
44	d1rm6c2	Alignment	not modelled	97.2	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
45	c1rm6F_	Alignment	not modelled	97.1	16	**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	96.9	8	**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	c2h89B_	Alignment	not modelled	96.6	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
48	d1jroa2	Alignment	not modelled	96.5	12	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
49	d1v97a2	Alignment	not modelled	96.4	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
50	c2w3rG_	Alignment	not modelled	96.3	12	**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
51	d2bs2b2	Alignment	not modelled	96.3	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
52	c3eubJ_	Alignment	not modelled	96.2	18	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
53	d1kf6b2	Alignment	not modelled	96.2	23	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
54	c3b9jI_	Alignment	not modelled	96.2	18	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine

55	c2bs2E_	Alignment	not modelled	96.1	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
56	c2b76N_	Alignment	not modelled	96.1	19	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
57	c1dgjA_	Alignment	not modelled	96.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
58	c1vlbA_	Alignment	not modelled	96.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
59	c1nekB_	Alignment	not modelled	94.5	23	**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
60	d1nekb2	Alignment	not modelled	94.0	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
61	c1wygA_	Alignment	not modelled	91.9	18	**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	c1x31A_	Alignment	not modelled	91.6	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
63	c1y56A_	Alignment	not modelled	91.3	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1363; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
64	d1tkea1	Alignment	not modelled	89.9	42	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
65	c1tkeA_	Alignment	not modelled	84.9	42	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** crystal structure of the editing domain of threonyl-trna2 synthetase complexed with serine
66	c1ep3B_	Alignment	not modelled	80.4	24	**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.
67	d1ep3b2	Alignment	not modelled	80.4	24	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
68	c2kmmA_	Alignment	not modelled	57.1	26	**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)
69	c3hvzB_	Alignment	not modelled	52.6	32	**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	c3na0C_	Alignment	not modelled	45.9	60	**PDB header:**oxidoreductase, electron transport **Chain:** C: **PDB Molecule:**adrenodoxin, mitochondrial; **PDBTitle:** crystal structure of human cyp11a1 in complex with 20,22-2 dihydroxycholesterol
71	c1rrbA_	Alignment	not modelled	41.3	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**raf proto-oncogene serine/threonine-protein **PDBTitle:** the ras-binding domain of raf-1 from rat, nmr, 1 structure
72	c1qf6A_	Alignment	not modelled	38.6	40	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**threonyl-trna synthetase; **PDBTitle:** structure of e. coli threonyl-trna synthetase complexed with its2 cognate trna
73	c2l05A_	Alignment	not modelled	38.0	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**serine/threonine-protein kinase b-raf; **PDBTitle:** solution nmr structure of the ras-binding domain of serine/threonine-2 protein kinase b-raf from homo sapiens, northeast structural genomics3 consortium target hr4694f
74	d1c1yb_	Alignment	not modelled	35.7	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
75	d1nyra2	Alignment	not modelled	32.8	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**TGS-like **Family:**TGS domain
76	d1e0ga_	Alignment	not modelled	29.8	25	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
77	c1wwtA_	Alignment	not modelled	26.1	30	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase, cytoplasmic; **PDBTitle:** solution structure of the tgs domain from human threonyl-2 trna synthetase
78	d1zud21	Alignment	not modelled	24.5	11	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
79	d1wxma1	Alignment	not modelled	23.9	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD

80	c1nyqA_	Alignment	not modelled	21.2	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**threonyl-trna synthetase 1; **PDBTitle:** structure of staphylococcus aureus threonyl-trna synthetase2 complexed with an analogue of threonyl adenylate
81	c2hj1A_	Alignment	not modelled	19.8	25	**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
82	d2hj1a1	Alignment	not modelled	19.8	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**HI0395-like
83	c3c75L_	Alignment	not modelled	18.7	28	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**methylamine dehydrogenase light chain; **PDBTitle:** paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
84	d2bbkl_	Alignment	not modelled	18.5	28	**Fold:**Methylamine dehydrogenase, L chain **Superfamily:**Methylamine dehydrogenase, L chain **Family:**Methylamine dehydrogenase, L chain
85	d1mdal_	Alignment	not modelled	18.3	28	**Fold:**Methylamine dehydrogenase, L chain **Superfamily:**Methylamine dehydrogenase, L chain **Family:**Methylamine dehydrogenase, L chain
86	d1rwsa_	Alignment	not modelled	18.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**MoaD/ThiS **Family:**ThiS
87	d1y7ma2	Alignment	not modelled	17.2	19	**Fold:**LysM domain **Superfamily:**LysM domain **Family:**LysM domain
88	c2iurD_	Alignment	not modelled	13.8	28	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aromatic amine dehydrogenase beta subunit; **PDBTitle:** crystal structure of n-quinol form of aromatic amine2 dehydrogenase (aadh) from alcaligenes faecalis, form a3 cocrystal
89	c3bw7A_	Alignment	not modelled	13.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytokinin dehydrogenase 1; **PDBTitle:** maize cytokinin oxidase/dehydrogenase complexed with the allenic2 cytokinin analog ha-1
90	c2g1eA_	Alignment	not modelled	11.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein ta0895; **PDBTitle:** solution structure of ta0895
91	c2po8A_	Alignment	not modelled	11.4	22	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**mcoti-ii; **PDBTitle:** the structure of a two-disulfide intermediate of mcoti-ii
92	c2c1dB_	Alignment	not modelled	11.2	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**soxx; **PDBTitle:** crystal structure of soxxa from p. pantotrophus
93	d1rutx4	Alignment	not modelled	11.1	33	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
94	c1y7mB_	Alignment	not modelled	10.8	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein bsu14040; **PDBTitle:** crystal structure of the b. subtilis ykud protein at 2 a2 resolution
95	d1iqca1	Alignment	not modelled	10.0	30	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase
96	c2it8A_	Alignment	not modelled	9.9	25	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**trypsin inhibitor 2; **PDBTitle:** solution structure of a linear analog of the cyclic squash2 trypsin inhibitor mcoti-ii
97	d2it8a1	Alignment	not modelled	9.9	25	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Plant inhibitors of proteinases and amylases **Family:**Plant inhibitors of proteinases and amylases
98	d2al3a1	Alignment	not modelled	9.7	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**UBX domain
99	d1eb7a1	Alignment	not modelled	9.2	44	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Di-heme cytochrome c peroxidase