Phyre2

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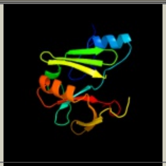
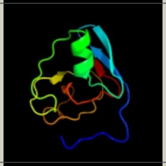
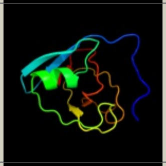
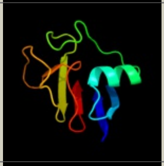
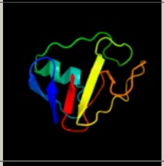
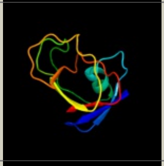
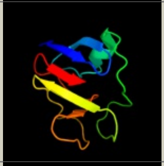
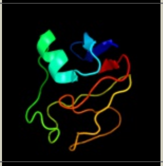
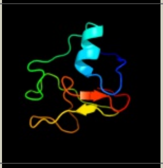
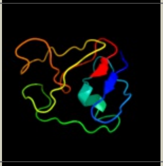
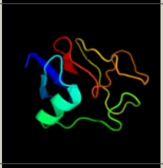
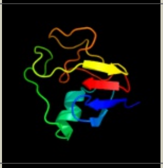
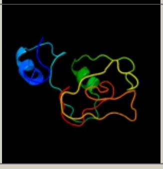
Description	P75863
Date	Thu Jan 5 12:15:13 GMT 2012
Unique Job ID	986b362cc329d8ca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2exna1	Alignment		100.0	13	**Fold:**MOSC N-terminal domain-like **Superfamily:**MOSC N-terminal domain-like **Family:**MOSC N-terminal domain-like
2	c2piaA_	Alignment		99.8	29	**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]
3	d2piaa3	Alignment		99.7	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
4	d1orua_	Alignment		99.7	21	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**MOSC (MOCO sulphurase C-terminal) domain
5	d1a70a_	Alignment		99.7	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
6	d1fxia_	Alignment		99.7	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
7	d1frra_	Alignment		99.7	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
8	d1offa_	Alignment		99.7	28	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
9	d1iuea_	Alignment		99.7	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
10	d1pfda_	Alignment		99.7	34	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
11	d1czpa_	Alignment		99.7	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related

12	c1krhA_	Alignment		99.7	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
13	d1frda_	Alignment		99.7	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
14	d1awda_	Alignment		99.7	30	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
15	d1doia_	Alignment		99.7	32	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
16	d1gaqb_	Alignment		99.7	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
17	d4fxca_	Alignment		99.7	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
18	d2cjoa_	Alignment		99.6	34	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
19	d1wria_	Alignment		99.6	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
20	d1e0za_	Alignment		99.6	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
21	d1jq4a_	Alignment	not modelled	99.6	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
22	d1krha3	Alignment	not modelled	99.6	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
23	c3ah7A_	Alignment	not modelled	99.2	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
24	d1i7ha_	Alignment	not modelled	99.2	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
25	d1l5pa_	Alignment	not modelled	99.1	17	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
26	c2wlbB_	Alignment	not modelled	99.0	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**electron transfer protein 1, mitochondrial; **PDBTitle:** adrenodoxin-like ferredoxin etp1fd(516-618) of2 schizosaccharomyces pombe mitochondria
27	d1xlqa1	Alignment	not modelled	98.9	16	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
28	d1e9ma_	Alignment	not modelled	98.8	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
						Fold:PK beta-barrel domain-like

29	d1o65a_	Alignment	not modelled	98.7	15	**Superfamily:**PK beta-barrel domain-like **Family:**MOSC (MOCO sulphurase C-terminal) domain
30	d2bt6a1	Alignment	not modelled	98.7	21	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
31	c3huiA_	Alignment	not modelled	98.7	18	**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
32	c3lxfC_	Alignment	not modelled	98.7	22	**PDB header:**metal binding protein **Chain:** C: **PDB Molecule:**ferredoxin; **PDBTitle:** crystal structure of [2fe-2s] ferredoxin arx from novosphingobium2 aromaticivorans
33	d1b9ra_	Alignment	not modelled	98.6	26	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin-related
34	d2fug33	Alignment	not modelled	98.5	13	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
35	d3c8ya2	Alignment	not modelled	98.0	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
36	c1l6vA_	Alignment	not modelled	97.9	17	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**adrenodoxin 1; **PDBTitle:** structure of reduced bovine adrenodoxin
37	c1c4cA_	Alignment	not modelled	97.8	22	**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
38	d1dgja2	Alignment	not modelled	97.4	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
39	d1t3qa2	Alignment	not modelled	97.4	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
40	d1vlba2	Alignment	not modelled	97.4	25	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
41	d1ffva2	Alignment	not modelled	97.3	20	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
42	d1n62a2	Alignment	not modelled	97.3	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
43	d1rm6c2	Alignment	not modelled	97.2	22	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
44	c1t3qD_	Alignment	not modelled	97.2	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**quinoline 2-oxidoreductase small subunit; **PDBTitle:** crystal structure of quinoline 2-oxidoreductase from pseudomonas2 putida 86
45	c2fugC_	Alignment	not modelled	97.1	18	**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
46	c1rm6F_	Alignment	not modelled	96.9	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**4-hydroxybenzoyl-coa reductase gamma subunit; **PDBTitle:** structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
47	c3hrdH_	Alignment	not modelled	96.9	24	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**nicotinate dehydrogenase small fes subunit; **PDBTitle:** crystal structure of nicotinate dehydrogenase
48	d1kf6b2	Alignment	not modelled	96.8	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
49	d2bs2b2	Alignment	not modelled	96.8	27	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
50	c1n60D_	Alignment	not modelled	96.7	22	**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
51	c1ffuA_	Alignment	not modelled	96.7	20	**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
52	d1nekb2	Alignment	not modelled	96.5	29	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
53	c2h89B_	Alignment	not modelled	96.4	37	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinate dehydrogenase ip subunit; **PDBTitle:** avian respiratory complex ii with malonate bound
54	d1jroa2	Alignment	not modelled	96.0	33	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like

						Family:2Fe-2S ferredoxin domains from multidomain proteins
55	c2b76N_	Alignment	not modelled	95.9	27	**PDB header:**oxidoreductase **Chain:** N: **PDB Molecule:**fumarate reductase iron-sulfur protein; **PDBTitle:** e. coli quinol fumarate reductase frda e49q mutation
56	c2bs2E_	Alignment	not modelled	95.9	27	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**quinol-fumarate reductase iron-sulfur subunit b; **PDBTitle:** quinol:fumarate reductase from wolinella succinogenes
57	c1nekB_	Alignment	not modelled	95.8	29	**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
58	c1vlbA_	Alignment	not modelled	95.6	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** structure refinement of the aldehyde oxidoreductase from2 desulfovibrio gigas at 1.28 a
59	c2w3rG_	Alignment	not modelled	95.5	30	**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
60	d1v97a2	Alignment	not modelled	95.1	24	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**2Fe-2S ferredoxin-like **Family:**2Fe-2S ferredoxin domains from multidomain proteins
61	c1dgjA_	Alignment	not modelled	95.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde oxidoreductase; **PDBTitle:** crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
62	c3eubJ_	Alignment	not modelled	95.0	28	**PDB header:**oxidoreductase **Chain:** J: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of desulfo-xanthine oxidase with xanthine
63	c3b9jI_	Alignment	not modelled	94.9	29	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**xanthine oxidase; **PDBTitle:** structure of xanthine oxidase with 2-hydroxy-6-methylpurine
64	c1ep3B_	Alignment	not modelled	94.4	23	**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.
65	d1ep3b2	Alignment	not modelled	92.9	23	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
66	c1wygA_	Alignment	not modelled	92.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**xanthine dehydrogenase/oxidase; **PDBTitle:** crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
67	c1x31A_	Alignment	not modelled	89.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
68	c1y56A_	Alignment	not modelled	86.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1363; **PDBTitle:** crystal structure of l-proline dehydrogenase from p.horikoshii
69	c3esgA_	Alignment	not modelled	56.2	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of hutd from pseudomonas fluorescens sbw25
70	d1ylla1	Alignment	not modelled	44.6	26	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**PA5104-like
71	c2k5hA_	Alignment	not modelled	29.4	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
72	d1kk1a1	Alignment	not modelled	27.8	58	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
73	d1g7sa2	Alignment	not modelled	27.0	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
74	d1s0ua1	Alignment	not modelled	26.8	53	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
75	d2qn6a1	Alignment	not modelled	26.2	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
76	d2gy9q1	Alignment	not modelled	25.5	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
77	c3bbnQ_	Alignment	not modelled	24.5	22	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17; **PDBTitle:** homology model for the spinach chloroplast 30s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome.
78	d1i94q_	Alignment	not modelled	22.6	35	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
79	d2uubq1	Alignment	not modelled	21.7	30	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
						PDB header:ribosome **Chain:** Q: **PDB Molecule:**40s ribosomal protein s11;

80	c1s1hQ_	Alignment	not modelled	20.7	22	**PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
81	d2c78a1	Alignment	not modelled	17.7	57	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
82	d2exda1	Alignment	not modelled	16.2	24	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
83	c2zkqq_	Alignment	not modelled	16.2	31	**PDB header:**ribosomal protein/rna **Chain:** Q: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
84	d2o3aa1	Alignment	not modelled	15.8	25	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF0751-like
85	c2xznQ_	Alignment	not modelled	15.3	13	**PDB header:**ribosome **Chain:** Q: **PDB Molecule:**ribosomal protein s17 containing protein; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
86	c2zkrt_	Alignment	not modelled	15.2	50	**PDB header:**ribosomal protein/rna **Chain:** T: **PDB Molecule:**rna expansion segment es39 part iii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
87	c3cxgA_	Alignment	not modelled	14.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
88	d1xn7a_	Alignment	not modelled	14.2	50	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Hypothetical protein YhgG
89	d1zunb1	Alignment	not modelled	13.8	36	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
90	d2nqra1	Alignment	not modelled	13.7	29	**Fold:**beta-clip **Superfamily:**MoeA C-terminal domain-like **Family:**MoeA C-terminal domain-like
91	d1vfsa1	Alignment	not modelled	13.5	27	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
92	d1qvpa_	Alignment	not modelled	12.9	33	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**FeoA-like
93	d1f60a1	Alignment	not modelled	12.8	36	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
94	d2zjru1	Alignment	not modelled	12.5	43	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L28
95	c1ssfA_	Alignment	not modelled	12.4	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**transformation related protein 53 binding **PDBTitle:** solution structure of the mouse 53bp1 fragment (residues2 1463-1617)
96	d1efca1	Alignment	not modelled	12.2	57	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
97	c4a1cS_	Alignment	not modelled	12.1	50	**PDB header:**ribosome **Chain:** S: **PDB Molecule:**rpl26; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
98	d1wt8a1	Alignment	not modelled	12.1	50	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
99	d1vqot1	Alignment	not modelled	10.8	50	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e