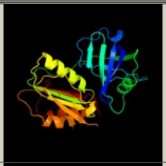
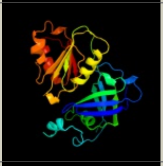
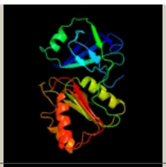
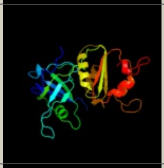
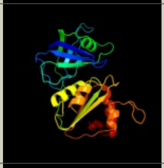
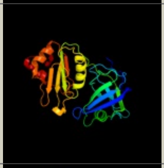
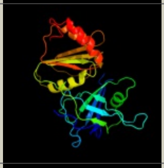
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	Q46871
Date	Thu Jan 5 12:35:28 GMT 2012
Unique Job ID	e4f02d9869b86823

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gpjA_	Alignment		100.0	29	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
2	c1krhA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
3	c1gvhA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
4	c2bgjB_	Alignment		100.0	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
5	c2r6hC_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
6	c3fpkB_	Alignment		100.0	16	**PDB header:**flavoprotein, oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
7	c1cqxB_	Alignment		100.0	15	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
8	c2eixA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of physarum polycephalum cytochrome b5 reductase
9	c2piaA_	Alignment		100.0	14	**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]
10	c1a8pA_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
11	c1umkA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of human erythrocyte nadh-cytochrome b52 reductase

12	c1tvcA_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
13	c1qgyA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase; **PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
14	c2ok8D_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp+ reductase from plasmodium falciparum
15	c1fncA_	Alignment		100.0	16	**PDB header:**oxidoreductase (nadp+(a),ferredoxin(a)) **Chain:** A: **PDB Molecule:**ferredoxin-nadp+ reductase; **PDBTitle:** refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
16	c1qfjD_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (flavin reductase); **PDBTitle:** crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
17	c1jb9A_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
18	c2b5oA_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase
19	c1ep3B_	Alignment		100.0	17	**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.
20	c2rc5D_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** refined structure of fnr from leptospira interrogans
21	c1cneA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrate reductase; **PDBTitle:** structural studies on corn nitrate reductase: refined2 structure of the cytochrome b reductase fragment at 2.53 angstroms, its adp complex and an active site mutant and4 modeling of the cytochrome b domain
22	c1tllA_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
23	c1f20A_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
24	c1ddiA_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha- **PDBTitle:** crystal structure of sir-fp60
25	c1j9zB_	Alignment	not modelled	99.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
26	c3qftA_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph--cytochrome p450 reductase; **PDBTitle:** crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
27	c2qtzA_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine synthase reductase; **PDBTitle:** crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
28	c2bpoA_	Alignment	not modelled	99.8	18	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2

						y75f, k78a.
29	d1qfja2	Alignment	not modelled	99.8	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
30	d1tvca2	Alignment	not modelled	99.8	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
31	d2piaa2	Alignment	not modelled	99.8	9	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
32	d1gvha3	Alignment	not modelled	99.8	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
33	d1gvha2	Alignment	not modelled	99.8	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
34	d1krha2	Alignment	not modelled	99.8	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
35	d1a8pa2	Alignment	not modelled	99.8	9	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
36	d1qx4a1	Alignment	not modelled	99.8	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
37	d1umka2	Alignment	not modelled	99.8	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
38	d1cqxa3	Alignment	not modelled	99.8	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
39	d1fdra1	Alignment	not modelled	99.8	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
40	d1qx4a2	Alignment	not modelled	99.8	11	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
41	d1a8pa1	Alignment	not modelled	99.8	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
42	d2cnda2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
43	d1cqxa2	Alignment	not modelled	99.7	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
44	d1fdra2	Alignment	not modelled	99.7	10	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
45	d1umka1	Alignment	not modelled	99.7	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
46	d1krha1	Alignment	not modelled	99.7	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
47	d2bmwa1	Alignment	not modelled	99.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
48	d1ndha1	Alignment	not modelled	99.7	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
49	d1ep3b1	Alignment	not modelled	99.7	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
50	d2cnda1	Alignment	not modelled	99.7	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
51	d1sm4a1	Alignment	not modelled	99.7	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
52	d1ndha2	Alignment	not modelled	99.7	10	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
53	d2piaa1	Alignment	not modelled	99.7	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
54	d1gawa1	Alignment	not modelled	99.7	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
55	d1fnda1	Alignment	not modelled	99.7	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like

						Family: Ferredoxin reductase FAD-binding domain-like
56	c3lrxC_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative hydrogenase; **PDBTitle:** crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
57	c3a1fA_	Alignment	not modelled	99.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b-245 heavy chain; **PDBTitle:** the crystal structure of nadph binding domain of gp91(phox)
58	d1qfza1	Alignment	not modelled	99.6	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
59	d1tvca1	Alignment	not modelled	99.6	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
60	d1ddga2	Alignment	not modelled	99.6	9	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
61	d2bmwa2	Alignment	not modelled	99.6	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
62	d1qfza2	Alignment	not modelled	99.6	15	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
63	d1gawa2	Alignment	not modelled	99.6	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
64	d1jb9a2	Alignment	not modelled	99.6	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
65	d1fnda2	Alignment	not modelled	99.6	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
66	d1ep3b2	Alignment	not modelled	99.6	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
67	d1f20a2	Alignment	not modelled	99.6	12	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
68	d1qfja1	Alignment	not modelled	99.5	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
69	d1sm4a2	Alignment	not modelled	99.5	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
70	d1jb9a1	Alignment	not modelled	99.5	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
71	d1ja1a3	Alignment	not modelled	99.5	13	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
72	d1f20a1	Alignment	not modelled	97.2	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
73	d1ddga1	Alignment	not modelled	97.2	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
74	d1ja1a1	Alignment	not modelled	96.3	22	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
75	c2l26A_	Alignment	not modelled	69.3	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**uncharacterized protein rv0899/mt0922; **PDBTitle:** rv0899 from mycobacterium tuberculosis contains two separated domains
76	c2zf8A_	Alignment	not modelled	59.4	10	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**component of sodium-driven polar flagellar motor; **PDBTitle:** crystal structure of moty
77	c1uwvA_	Alignment	not modelled	57.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**23s rrna (uracil-5-)-methyltransferase ruma; **PDBTitle:** crystal structure of ruma, the iron-sulfur cluster2 containing e. coli 23s ribosomal rna 5-methyluridine3 methyltransferase
78	c1r1mA_	Alignment	not modelled	53.8	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein class 4; **PDBTitle:** structure of the ompa-like domain of rmpm from neisseria2 meningitidis
79	d1r1ma_	Alignment	not modelled	53.8	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
80	d2aizp1	Alignment	not modelled	53.5	9	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like

81	c3khnB_	Alignment	not modelled	50.3	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**motb protein, putative; **PDBTitle:** crystal structure of putative motb like protein dvu_22282 from desulfovibrio vulgaris.
82	d2hqsc1	Alignment	not modelled	43.6	4	**Fold:**Bacillus chorismate mutase-like **Superfamily:**OmpA-like **Family:**OmpA-like
83	d1f0ka_	Alignment	not modelled	37.1	9	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**Peptidoglycan biosynthesis glycosyltransferase MurG
84	c2k1sA_	Alignment	not modelled	36.7	12	**PDB header:**lipoprotein **Chain:** A: **PDB Molecule:**inner membrane lipoprotein yiad; **PDBTitle:** solution nmr structure of the folded c-terminal fragment of yiad from2 escherichia coli. northeast structural genomics consortium target3 er553.
85	c3ougA_	Alignment	not modelled	36.4	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
86	c2pssC_	Alignment	not modelled	34.1	8	**PDB header:**transferase **Chain:** C: **PDB Molecule:**spermidine synthase; **PDBTitle:** the structure of plasmodium falciparum spermidine synthase in its apo-2 form
87	c3cyqM_	Alignment	not modelled	33.9	9	**PDB header:**membrane protein **Chain:** M: **PDB Molecule:**chemotaxis protein motb; **PDBTitle:** the crystal structure of the complex of the c-terminal domain of2 helicobacter pylori motb (residues 125-256) with n-acetylmuramic acid
88	c2kgwA_	Alignment	not modelled	33.3	9	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein a; **PDBTitle:** solution structure of the carboxy-terminal domain of ompatb, a pore2 forming protein from mycobacterium tuberculosis
89	c2ep5B_	Alignment	not modelled	27.0	8	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**350aa long hypothetical aspartate-semialdehyde **PDBTitle:** structural study of project id st1242 from sulfolobus tokodaii strain7
90	c3pe3D_	Alignment	not modelled	25.8	4	**PDB header:**transferase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine--peptide n- **PDBTitle:** structure of human o-glcnac transferase and its complex with a peptide2 substrate
91	d1t8ha_	Alignment	not modelled	23.4	4	**Fold:**CNF1/YfiH-like putative cysteine hydrolases **Superfamily:**CNF1/YfiH-like putative cysteine hydrolases **Family:**YfiH-like
92	d2gc6a1	Alignment	not modelled	20.5	12	**Fold:**MurD-like peptide ligases, peptide-binding domain **Superfamily:**MurD-like peptide ligases, peptide-binding domain **Family:**Folylpolyglutamate synthetase, C-terminal domain
93	d1ppya_	Alignment	not modelled	17.9	15	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
94	c2fsxA_	Alignment	not modelled	17.1	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cog0607: rhodanese-related sulfurtransferase; **PDBTitle:** crystal structure of rv0390 from m. tuberculosis
95	d2nvma1	Alignment	not modelled	16.1	0	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
96	c2p0yA_	Alignment	not modelled	15.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein lp_0780; **PDBTitle:** crystal structure of q88yi3_lacpl from lactobacillus2 plantarum. northeast structural genomics consortium target3 lpr6
97	d2nlva1	Alignment	not modelled	14.9	0	**Fold:**XisI-like **Superfamily:**XisI-like **Family:**XisI-like
98	c2oghA_	Alignment	not modelled	14.6	0	**PDB header:**translation **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor eif-1; **PDBTitle:** solution structure of yeast eif1
99	c2q7xA_	Alignment	not modelled	14.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0052 protein sp_1565; **PDBTitle:** crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution