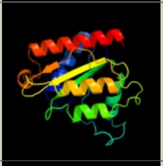
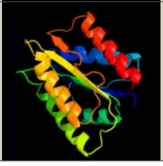
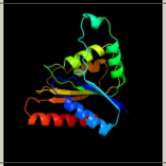
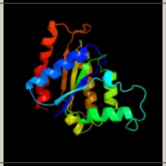
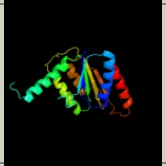
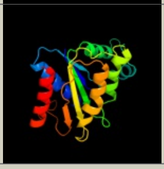
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0A8G6
Date	Thu Jan 5 11:07:47 GMT 2012
Unique Job ID	d1c83e180274347c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b6iB_	Alignment		100.0	100	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
2	c2zkiH_	Alignment		100.0	40	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
3	d1ydga_	Alignment		100.0	38	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
4	d2a5la1	Alignment		100.0	43	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
5	c3d7nA_	Alignment		100.0	31	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
6	d2arka1	Alignment		100.0	32	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
7	d1sqsa_	Alignment		100.0	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
8	c2q62A_	Alignment		100.0	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
9	d1nni1_	Alignment		99.9	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
10	c3lcmB_	Alignment		99.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
11	d1ycga1	Alignment		99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related

12	d1rtta_	Alignment		99.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
13	d1t5ba_	Alignment		99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
14	c2fzvC_	Alignment		99.9	13	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**putative arsenical resistance protein; **PDBTitle:** crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
15	c3k1yE_	Alignment		99.9	18	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
16	d1t0ia_	Alignment		99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
17	d1e5da1	Alignment		99.9	25	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	c3fniA_	Alignment		99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
19	c2hpvA_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
20	c2vzhA_	Alignment		99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
21	c1ychD_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
22	c3fvwA_	Alignment	not modelled	99.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad(p)h-dependent fmn reductase; **PDBTitle:** crystal structure of the q8dwd8_strmu protein from2 streptococcus mutans. northeast structural genomics3 consortium target smr99.
23	c2ohiB_	Alignment	not modelled	99.9	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
24	c2q9uB_	Alignment	not modelled	99.9	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
25	d2fzva1	Alignment	not modelled	99.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
26	d2qwxa1	Alignment	not modelled	99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
27	c3p0rA_	Alignment	not modelled	99.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
						Fold: Flavodoxin-like

28	d2z98a1	Alignment	not modelled	99.9	24	**Superfamily:**Flavoproteins **Family:**Quinone reductase
29	d1qrda_	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
30	c3hlyA_	Alignment	not modelled	99.9	22	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
31	d1d4aa_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
32	d1vmea1	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
33	c2v9cA_	Alignment	not modelled	99.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase 1; **PDBTitle:** x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
34	d1dxqa_	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
35	d1rlia_	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
36	c1e5dA_	Alignment	not modelled	99.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
37	c1vmeB_	Alignment	not modelled	99.9	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
38	c3f2vA_	Alignment	not modelled	99.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
39	c3edoA_	Alignment	not modelled	99.8	21	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
40	c3klbA_	Alignment	not modelled	99.8	21	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
41	c3rpeA_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
42	d2fz5a1	Alignment	not modelled	99.8	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
43	d5nula_	Alignment	not modelled	99.8	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
44	c2amjD_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
45	c3f6sI_	Alignment	not modelled	99.7	24	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
46	c3ha2B_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
47	c3eywA_	Alignment	not modelled	99.7	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
48	c2wc1A_	Alignment	not modelled	99.6	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
49	d1ag9a_	Alignment	not modelled	99.6	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
50	d1oboa_	Alignment	not modelled	99.6	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	c2hnbA_	Alignment	not modelled	99.6	15	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
52	d1czna_	Alignment	not modelled	99.6	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
						Fold: Flavodoxin-like

53	d1f4pa_	Alignment	not modelled	99.5	23	**Superfamily:**Flavoproteins **Family:**Flavodoxin-related
54	d1yoba1	Alignment	not modelled	99.5	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
55	d2fcra_	Alignment	not modelled	99.5	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
56	d1ykga1	Alignment	not modelled	99.5	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
57	d1fuea_	Alignment	not modelled	99.4	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
58	c1bvyF_	Alignment	not modelled	99.4	22	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
59	d1bvyf_	Alignment	not modelled	99.4	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
60	d1b1ca_	Alignment	not modelled	99.4	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
61	d1tlla2	Alignment	not modelled	99.4	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
62	c3hr4C_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
63	d1ja1a2	Alignment	not modelled	99.2	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
64	c1tllA_	Alignment	not modelled	98.9	18	**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.
65	c2bpoA_	Alignment	not modelled	98.8	21	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
66	c2x2oA_	Alignment	not modelled	98.7	22	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
67	c1j9zB_	Alignment	not modelled	98.6	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
68	d1rlja_	Alignment	not modelled	98.3	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
69	c3n39D_	Alignment	not modelled	98.1	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
70	c2kyrA_	Alignment	not modelled	95.1	31	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
71	c3czcA_	Alignment	not modelled	95.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
72	d2r4qa1	Alignment	not modelled	94.7	33	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
73	c3a9rA_	Alignment	not modelled	94.3	20	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-arabinose isomerase; **PDBTitle:** x-ray structures of bacillus pallidus d-arabinose2 isomerasecomplex with (4r)-2-methylpentane-2,4-diol
74	d1n1ea2	Alignment	not modelled	92.1	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
75	d2a9va1	Alignment	not modelled	91.9	12	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
76	d1uqra_	Alignment	not modelled	91.8	25	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
77	c3kklA_	Alignment	not modelled	91.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
78	c1tvmA_	Alignment	not modelled	91.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, galactitol-specific iib component; **PDBTitle:** nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system

79	d2r48a1	Alignment	not modelled	90.7	27	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
80	c3ghyA_	Alignment	not modelled	90.7	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
81	c3c7cB_	Alignment	not modelled	90.5	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
82	c3u80A_	Alignment	not modelled	90.5	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase, type ii; **PDBTitle:** 1.60 angstrom resolution crystal structure of a 3-dehydroquinate2 dehydratase-like protein from bifidobacterium longum
83	d1jvna2	Alignment	not modelled	90.5	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
84	c3d54D_	Alignment	not modelled	90.2	21	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
85	c2gcgB_	Alignment	not modelled	90.2	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyoxylate reductase/hydroxypyruvate reductase; **PDBTitle:** ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
86	c2vpiA_	Alignment	not modelled	90.1	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
87	c1jvnB_	Alignment	not modelled	90.0	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional histidine biosynthesis protein hishf; **PDBTitle:** crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
88	c3qvjB_	Alignment	not modelled	89.9	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
89	c3dojA_	Alignment	not modelled	89.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
90	c2ho3D_	Alignment	not modelled	89.5	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
91	d1txga2	Alignment	not modelled	89.3	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
92	c3ic5A_	Alignment	not modelled	88.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
93	c3dhnA_	Alignment	not modelled	88.7	16	**PDB header:**isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
94	c3nbmA_	Alignment	not modelled	87.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, lactose-specific iibc components; **PDBTitle:** the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
95	c2l2qA_	Alignment	not modelled	87.2	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pts system, cellobiose-specific iib component (cela); **PDBTitle:** solution structure of cellobiose-specific phosphotransferase iib2 component protein from borrelia burgdorferi
96	c3s40C_	Alignment	not modelled	86.6	23	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
97	c3euwB_	Alignment	not modelled	86.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
98	d2p1ra1	Alignment	not modelled	85.5	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
99	c2axqA_	Alignment	not modelled	84.8	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
100	d2ab0a1	Alignment	not modelled	84.7	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
101	c3upsA_	Alignment	not modelled	84.5	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**iojap-like protein; **PDBTitle:** crystal structure of iojap-like protein from zymomonas mobilis
102	c3f5dA_	Alignment	not modelled	84.3	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis

103	d1u7za_	Alignment	not modelled	84.2	14	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
104	c3plnA_	Alignment	not modelled	83.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
105	d2nv0a1	Alignment	not modelled	83.9	32	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
106	c3d8tB_	Alignment	not modelled	83.9	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
107	d1iiba_	Alignment	not modelled	83.8	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
108	d1ka9h_	Alignment	not modelled	83.7	26	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
109	d1ks9a2	Alignment	not modelled	83.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	c3l6dB_	Alignment	not modelled	83.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
111	d1u9ca_	Alignment	not modelled	82.6	16	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
112	d1mv8a3	Alignment	not modelled	82.6	20	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain **Family:**UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
113	c2f1kD_	Alignment	not modelled	82.5	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
114	c3ktdC_	Alignment	not modelled	81.6	8	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
115	c3fd8A_	Alignment	not modelled	81.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
116	d1vjta1	Alignment	not modelled	81.4	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
117	c2z2vA_	Alignment	not modelled	81.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
118	d1i36a2	Alignment	not modelled	81.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
119	c3ia7A_	Alignment	not modelled	80.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
120	c2eklA_	Alignment	not modelled	80.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii