Email	l.a.kelley@imperial.ac.uk
Description	P03817
Date	Thu Jan 5 10:58:00 GMT 2012
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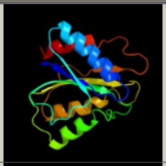
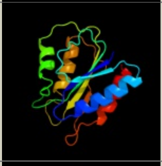
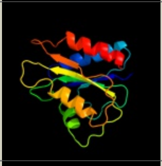
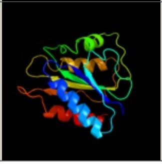
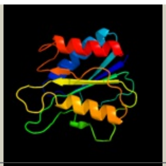
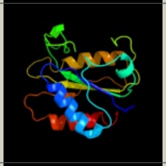
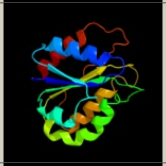
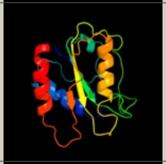
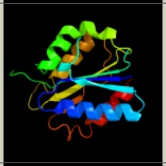
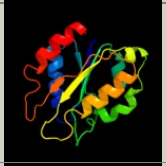
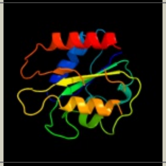
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2hnbA_	Alignment		100.0	100	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
2	d1b1ca_	Alignment		100.0	25	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
3	d1ja1a2	Alignment		100.0	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
4	c3hr4C_	Alignment		100.0	23	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
5	c1j9zB_	Alignment		100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
6	c2bpoA_	Alignment		100.0	24	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
7	c1tllA_	Alignment		100.0	26	**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.
8	d1ykga1	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
9	d1tlla2	Alignment		100.0	25	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
10	c1bvyF_	Alignment		100.0	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)
11	d1bvyf_	Alignment		100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related

12	c3f6sI_	Alignment		100.0	22	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
13	c2wc1A_	Alignment		100.0	22	**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
14	d1oboa_	Alignment		100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
15	d1yoba1	Alignment		100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
16	d1f4pa_	Alignment		100.0	27	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
17	d1czna_	Alignment		99.9	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
18	d2fcra_	Alignment		99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
19	d1ag9a_	Alignment		99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
20	d1fuea_	Alignment		99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
21	c3hlyA_	Alignment	not modelled	99.9	13	**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.
22	c3fniA_	Alignment	not modelled	99.9	13	**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
23	d1e5da1	Alignment	not modelled	99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
24	d1ycga1	Alignment	not modelled	99.9	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
25	c1vmeB_	Alignment	not modelled	99.9	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
26	d2fz5a1	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
27	c1ychD_	Alignment	not modelled	99.9	20	**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
28	d5nula_	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins

						Family: Flavodoxin-related
29	d1vmea1	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
30	c2ohiB_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
31	d1rlja_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
32	c2x2oA_	Alignment	not modelled	99.8	21	**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
33	c3n39D_	Alignment	not modelled	99.8	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
34	c2q9uB_	Alignment	not modelled	99.8	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
35	c1e5dA_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
36	d2arka1	Alignment	not modelled	99.8	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
37	c3d7nA_	Alignment	not modelled	99.7	13	**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
38	d2a5la1	Alignment	not modelled	99.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
39	c3klbA_	Alignment	not modelled	99.6	16	**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
40	d1ydga_	Alignment	not modelled	99.6	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
41	c2zkiH_	Alignment	not modelled	99.6	15	**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)
42	c3b6iB_	Alignment	not modelled	99.6	17	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
43	c3edoA_	Alignment	not modelled	99.3	11	**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
44	d1t5ba_	Alignment	not modelled	98.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
45	c2q62A_	Alignment	not modelled	98.9	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
46	d1rtta_	Alignment	not modelled	98.8	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
47	d1sqsa_	Alignment	not modelled	98.8	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
48	c3rpeA_	Alignment	not modelled	98.8	12	**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.
49	c2hpvA_	Alignment	not modelled	98.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
50	d1t0ia_	Alignment	not modelled	98.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
51	c3lcmB_	Alignment	not modelled	98.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
52	c3k1yE_	Alignment	not modelled	98.7	19	**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
53	c3fvwA_	Alignment	not modelled	98.7	13	**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.
54	c2fzvC_	Alignment	not modelled	98.5	15	**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
55	d1rlia_	Alignment	not modelled	98.5	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
56	d2qwxa1	Alignment	not modelled	98.5	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
57	d1nni1_	Alignment	not modelled	98.5	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
58	c3p0rA_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
59	d2z98a1	Alignment	not modelled	98.4	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
60	d1qrda_	Alignment	not modelled	98.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
61	d2fzva1	Alignment	not modelled	98.4	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
62	c3f2vA_	Alignment	not modelled	98.3	10	**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.
63	c2v9cA_	Alignment	not modelled	98.2	21	**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.
64	c2vzhA_	Alignment	not modelled	98.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
65	d1dxqa_	Alignment	not modelled	98.2	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
66	c2amjD_	Alignment	not modelled	98.2	11	**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
67	d1d4aa_	Alignment	not modelled	98.1	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
68	c3ha2B_	Alignment	not modelled	95.3	11	**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
69	c3czcA_	Alignment	not modelled	93.0	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rmpb; **PDBTitle:** the crystal structure of a putative pts iib(ptxb) from2 streptococcus mutans
70	c1tvmA_	Alignment	not modelled	90.5	16	**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
71	d1ccwa_	Alignment	not modelled	88.6	16	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
72	c2g76A_	Alignment	not modelled	85.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** crystal structure of human 3-phosphoglycerate dehydrogenase
73	c3eywA_	Alignment	not modelled	84.9	14	**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
74	c1vkrA_	Alignment	not modelled	84.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannitol-specific pts system enzyme iiabc components; **PDBTitle:** structure of iib domain of the mannitol-specific permease enzyme ii
75	d1vkra_	Alignment	not modelled	84.1	17	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
76	c3s40C_	Alignment	not modelled	82.9	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
77	c2jjmH_	Alignment	not modelled	82.1	19	**PDB header:**transferase **Chain:** H: **PDB Molecule:**glycosyl transferase, group 1 family protein; **PDBTitle:** crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
78	d1t0ba_	Alignment	not modelled	81.6	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family: ThuA-like
79	d1fmfa_	Alignment	not modelled	81.1	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
80	d2p1ra1	Alignment	not modelled	77.7	17	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
81	c2eklA_	Alignment	not modelled	76.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** structure of st1218 protein from sulfolobus tokodaii
82	d1u0ta_	Alignment	not modelled	74.4	13	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
83	d1t1va_	Alignment	not modelled	74.1	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**SH3BGR (SH3-binding, glutamic acid-rich protein-like)
84	c3ia7A_	Alignment	not modelled	72.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**calg4; **PDBTitle:** crystal structure of calg4, the calicheamicin glycosyltransferase
85	c3qyfA_	Alignment	not modelled	71.3	14	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**crispr-associated protein; **PDBTitle:** crystal structure of the crispr-associated protein sso1393 from2 sulfolobus solfataricus
86	c2r60A_	Alignment	not modelled	70.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glycosyl transferase, group 1; **PDBTitle:** structure of apo sucrose phosphate synthase (sps) of2 halothermothrix orenii
87	d1ydha_	Alignment	not modelled	70.3	24	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
88	c3eeqB_	Alignment	not modelled	69.9	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cobalamin biosynthesis protein g **PDBTitle:** crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
89	d1iloa_	Alignment	not modelled	68.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
90	d1mkza_	Alignment	not modelled	67.8	8	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
91	d1leha1	Alignment	not modelled	66.8	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
92	d3eeqa2	Alignment	not modelled	65.8	15	**Fold:**CbiG N-terminal domain-like **Superfamily:**CbiG N-terminal domain-like **Family:**CbiG N-terminal domain-like
93	c3dhnA_	Alignment	not modelled	65.3	22	**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	c2q4dB_	Alignment	not modelled	62.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**lysine decarboxylase-like protein at5g11950; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
95	d2q4oa1	Alignment	not modelled	62.2	21	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
96	c2q4oA_	Alignment	not modelled	62.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein at2g37210/t2n18.3; **PDBTitle:** ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
97	d1li4a1	Alignment	not modelled	62.1	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
98	c3kxqB_	Alignment	not modelled	61.9	13	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution
99	c3nbmA_	Alignment	not modelled	60.7	8	**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.
100	d1v8ba1	Alignment	not modelled	58.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
101	d1v9la1	Alignment	not modelled	57.3	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
102	c2o4cB_	Alignment	not modelled	56.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**erythronate-4-phosphate dehydrogenase; **PDBTitle:** crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**glycerate dehydrogenase/glyoxylate

103	c2cukC_	Alignment	not modelled	55.0	18	reductase; **PDBTitle:** crystal structure of tt0316 protein from thermus thermophilus hb8
104	d1iiba_	Alignment	not modelled	53.9	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Lactose/Cellobiose specific IIB subunit
105	c3etjB_	Alignment	not modelled	53.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure e. coli purk in complex with mg, adp, and2 pi
106	c3gpiA_	Alignment	not modelled	53.4	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus
107	d1b4ub_	Alignment	not modelled	53.2	11	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
108	c2nm0B_	Alignment	not modelled	53.1	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 3-oxacyl-(acyl-carrier-protein) reductase; **PDBTitle:** crystal structure of sco1815: a beta-ketoacyl-acyl carrier protein2 reductase from streptomyces coelicolor a3(2)
109	d1iowa1	Alignment	not modelled	53.0	21	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
110	c3t66A_	Alignment	not modelled	52.7	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein); **PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans
111	c1d4fD_	Alignment	not modelled	52.3	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
112	c3dhyC_	Alignment	not modelled	50.4	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
113	c2dbqA_	Alignment	not modelled	50.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyoxylate reductase; **PDBTitle:** crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
114	d1hdoa_	Alignment	not modelled	50.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
115	c3gvpB_	Alignment	not modelled	49.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
116	d1y5ea1	Alignment	not modelled	49.6	18	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
117	c3d64A_	Alignment	not modelled	49.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
118	d1vi2a1	Alignment	not modelled	48.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
119	c3m8uA_	Alignment	not modelled	48.5	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**heme-binding protein a; **PDBTitle:** crystal structure of glutathione-binding protein a (gbpa) from2 haemophilus parasuis sh0165 in complex with glutathione disulfide3 (gssg)
120	c2q1wC_	Alignment	not modelled	47.5	29	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+