Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AGE6
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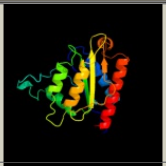
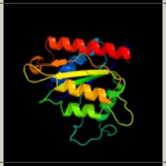
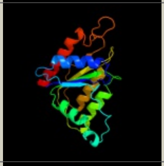
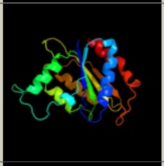
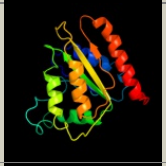
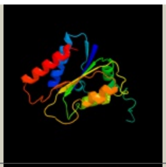
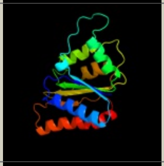
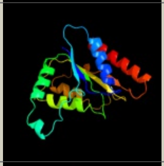
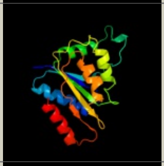
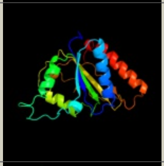
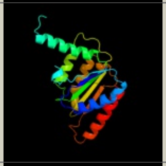
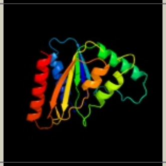
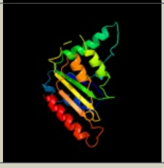
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2q62A_	Alignment		100.0	19	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
2	c2fzvC_	Alignment		100.0	18	**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
3	d2fzva1	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
4	d1rtta_	Alignment		100.0	47	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
5	d1nni1_	Alignment		100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
6	c3fvwA_	Alignment		100.0	28	**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.
7	c2vzhA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-dependent fmn reductase; **PDBTitle:** structures of nadh:fmn oxidoreductase (emob)-fmn complex
8	d1t0ia_	Alignment		100.0	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
9	c3k1yE_	Alignment		100.0	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
10	d1sqsa_	Alignment		100.0	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein SP1951
11	d1ydga_	Alignment		100.0	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like

12	c3lcmB_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of smu.1420 from streptococcus mutans ua159
13	d2qwxa1	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
14	d1t5ba_	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
15	c2zkiH_	Alignment		100.0	19	**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)
16	d1d4aa_	Alignment		99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
17	d1dxqa_	Alignment		99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
18	c2hpvA_	Alignment		99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fmn-dependent nadh-azoreductase; **PDBTitle:** crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
19	d2z98a1	Alignment		99.9	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
20	c3p0rA_	Alignment		99.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**azoreductase; **PDBTitle:** crystal structure of azoreductase from bacillus anthracis str. sterne
21	c3b6iB_	Alignment	not modelled	99.9	12	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
22	d1qrda_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
23	c2v9cA_	Alignment	not modelled	99.9	25	**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.
24	d2a5la1	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
25	d1rlia_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Hypothetical protein YwqN
26	c3f2vA_	Alignment	not modelled	99.9	13	**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.
27	c3rpeA_	Alignment	not modelled	99.9	14	**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.
28	c3d7nA_	Alignment	not modelled	99.9	16	**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

29	d2arka1	Alignment	not modelled	99.8	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
30	c2amjD_	Alignment	not modelled	99.8	14	**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
31	c3eywA_	Alignment	not modelled	99.8	18	**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
32	c3ha2B_	Alignment	not modelled	99.8	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
33	d1e5da1	Alignment	not modelled	99.8	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
34	d1ycga1	Alignment	not modelled	99.7	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
35	c1ychD_	Alignment	not modelled	99.7	17	**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
36	c2ohiB_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
37	d1vmea1	Alignment	not modelled	99.6	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
38	c2q9uB_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
39	c3klbA_	Alignment	not modelled	99.6	15	**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	c3fniA_	Alignment	not modelled	99.5	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
41	c1e5dA_	Alignment	not modelled	99.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
42	c3edoA_	Alignment	not modelled	99.5	13	**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
43	c3hlyA_	Alignment	not modelled	99.4	15	**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.
44	c1vmeB_	Alignment	not modelled	99.4	15	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
45	d2fz5a1	Alignment	not modelled	99.2	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
46	c3f6sI_	Alignment	not modelled	99.2	15	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
47	d5nula_	Alignment	not modelled	99.1	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
48	d1oboa_	Alignment	not modelled	99.0	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
49	d1czna_	Alignment	not modelled	99.0	15	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
50	d1ag9a_	Alignment	not modelled	99.0	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	d2fcra_	Alignment	not modelled	98.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
52	d1yoba1	Alignment	not modelled	98.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
53	d1tlla2	Alignment	not modelled	98.9	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like

54	d1fuea_	Alignment	not modelled	98.8	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
55	d1ykga1	Alignment	not modelled	98.8	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
56	c2wc1A_	Alignment	not modelled	98.8	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
57	d1bvyf_	Alignment	not modelled	98.7	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
58	c1bvyF_	Alignment	not modelled	98.7	19	**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	d1f4pa_	Alignment	not modelled	98.7	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
60	d1b1ca_	Alignment	not modelled	98.7	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
61	c2hnbA_	Alignment	not modelled	98.6	12	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
62	c3hr4C_	Alignment	not modelled	98.5	13	**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	98.3	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
64	c1tllA_	Alignment	not modelled	98.2	17	**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	97.6	14	**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	c1j9zB_	Alignment	not modelled	97.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
67	c2x2oA_	Alignment	not modelled	95.9	18	**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
68	d1rlja_	Alignment	not modelled	95.3	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
69	c3orsD_	Alignment	not modelled	94.3	11	**PDB header:**isomerase,biosynthetic protein **Chain:** D: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
70	c3lp6D_	Alignment	not modelled	93.3	10	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase catalytic subunit; **PDBTitle:** crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
71	c3n39D_	Alignment	not modelled	93.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
72	c3lwzC_	Alignment	not modelled	91.8	13	**PDB header:**lyase **Chain:** C: **PDB Molecule:**3-dehydroquinate dehydratase; **PDBTitle:** 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
73	c2ys6A_	Alignment	not modelled	91.7	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
74	d1qcza_	Alignment	not modelled	91.3	16	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
75	c3ic5A_	Alignment	not modelled	91.2	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
76	c2kyrA_	Alignment	not modelled	91.1	15	**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
77	c3qvjB_	Alignment	not modelled	88.4	12	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative hydantoin racemase; **PDBTitle:** allantoin racemase from klebsiella pneumoniae
78	c3nbmA_	Alignment	not modelled	87.1	16	**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.
79	d2a9va1	Alignment	not modelled	87.0	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
80	d1u7za_	Alignment	not modelled	86.8	12	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
81	d1xmpa_	Alignment	not modelled	86.0	15	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
82	c3rggD_	Alignment	not modelled	85.6	12	**PDB header:**lyase **Chain:** D: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, pure protein; **PDBTitle:** crystal structure of treponema denticola pure bound to air
83	c1tvmA_	Alignment	not modelled	84.6	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
84	d2r4qa1	Alignment	not modelled	84.5	13	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
85	d1o4va_	Alignment	not modelled	83.9	10	**Fold:**Flavodoxin-like **Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
86	c3k5iB_	Alignment	not modelled	81.9	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosyl-aminoimidazole carboxylase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimadazole ribonucleotide
87	c1rcuB_	Alignment	not modelled	81.8	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved hypothetical protein vt76; **PDBTitle:** x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
88	d1rcua_	Alignment	not modelled	81.8	17	**Fold:**MCP/YpsA-like **Superfamily:**MCP/YpsA-like **Family:**MoCo carrier protein-like
89	c3se7A_	Alignment	not modelled	81.8	9	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
90	c3c4vB_	Alignment	not modelled	80.9	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**predicted glycosyltransferases; **PDBTitle:** structure of the retaining glycosyltransferase msha:the2 first step in mycothiol biosynthesis. organism:3 corynebacterium glutamicum : complex with udp and 1l-ins-1-4 p.
91	d2r48a1	Alignment	not modelled	80.2	19	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
92	d1iowa1	Alignment	not modelled	80.0	7	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**D-Alanine ligase N-terminal domain
93	c3lwbA_	Alignment	not modelled	78.6	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
94	d1mkza_	Alignment	not modelled	78.1	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
95	c2khzB_	Alignment	not modelled	78.1	21	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**c-myc-responsive protein rcl; **PDBTitle:** solution structure of rcl
96	c2l2qA_	Alignment	not modelled	76.5	20	**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
97	c3e5nA_	Alignment	not modelled	75.5	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
98	c3oy2A_	Alignment	not modelled	75.4	12	**PDB header:**viral protein,transferase **Chain:** A: **PDB Molecule:**glycosyltransferase b736l; **PDBTitle:** crystal structure of a putative glycosyltransferase from paramecium2 bursaria chlorella virus ny2a
99	c2fw9A_	Alignment	not modelled	75.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide mutase; **PDBTitle:** structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
100	c2z2vA_	Alignment	not modelled	75.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
101	c3c7cB_	Alignment	not modelled	74.7	18	**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)
						Fold: Flavodoxin-like

102	d1u11a_	Alignment	not modelled	74.3	12	**Superfamily:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) **Family:**N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
103	c3tqtB_	Alignment	not modelled	73.6	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
104	c3l6dB_	Alignment	not modelled	73.5	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
105	c3lp8A_	Alignment	not modelled	71.6	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
106	c2gk4A_	Alignment	not modelled	71.5	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
107	c3kklA_	Alignment	not modelled	71.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
108	c3ot5D_	Alignment	not modelled	70.9	14	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-n-acetylglucosamine 2-epimerase; **PDBTitle:** 2.2 angstrom resolution crystal structure of putative udp-n-2 acetylglucosamine 2-epimerase from listeria monocytogenes
109	d1txga2	Alignment	not modelled	70.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	c1e4eB_	Alignment	not modelled	69.2	12	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
111	d1qzua_	Alignment	not modelled	69.0	21	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
112	c1e5lA_	Alignment	not modelled	68.7	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
113	c3i12A_	Alignment	not modelled	68.1	12	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
114	c2pvpB_	Alignment	not modelled	68.0	9	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
115	c3ktdC_	Alignment	not modelled	67.6	10	**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
116	d1sc6a2	Alignment	not modelled	66.8	21	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
117	d1gtza_	Alignment	not modelled	66.3	19	**Fold:**Flavodoxin-like **Superfamily:**Type II 3-dehydroquinate dehydratase **Family:**Type II 3-dehydroquinate dehydratase
118	d2hy5a1	Alignment	not modelled	66.1	8	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
119	c1jr2A_	Alignment	not modelled	65.4	9	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
120	d1jr2a_	Alignment	not modelled	65.4	9	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like