Phyre^2

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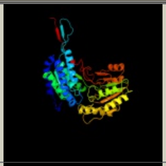
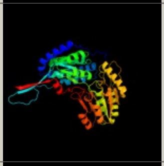
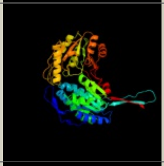
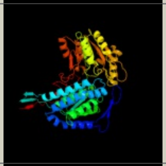
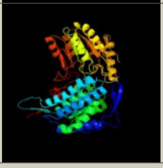
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hazA_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
2	c2jg7G_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
3	c3qanB_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-pyrroline-5-carboxylate dehydrogenase 1; **PDBTitle:** crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
4	d1uzba_	Alignment		100.0	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
5	d1a4sa_	Alignment		100.0	14	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
6	c3ed6B_	Alignment		100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
7	c3prlD_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125
8	d1bxsa_	Alignment		100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
9	c2o2qA_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**formyltetrahydrofolate dehydrogenase; **PDBTitle:** crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
10	c2ve5H_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
11	d1euha_	Alignment		100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like

12	d1o9ja_	Alignment		100.0	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
13	c3iwkB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
14	d1o04a_	Alignment		100.0	14	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
15	c2d4eB_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
16	c3rh9A_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
17	d1ky8a_	Alignment		100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
18	d1ag8a_	Alignment		100.0	15	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
19	c3ek1C_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
20	d1wnda_	Alignment		100.0	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
21	c3ifgH_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
22	c2w8qA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
23	c1t90B_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
24	c3r31A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
25	c3b4wA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
26	c3pqaA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactaldehyde dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
27	c3i44A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
28	c3k2wD_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase;

						PDBTitle: crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
29	c3jz4C_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
30	c3efvC_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative succinate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
31	c3rosA_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
32	c2hg2A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
33	c3ju8B_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
34	d1bi9a_	Alignment	not modelled	100.0	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
35	d1ez0a_	Alignment	not modelled	100.0	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
36	d1ad3a_	Alignment	not modelled	100.0	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
37	c3k9dD_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
38	c3v4cB_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
39	c3r64A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
40	c2vroB_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
41	d1o20a_	Alignment	not modelled	100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
42	c3my7A_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alcohol dehydrogenase/acetaldehyde dehydrogenase; **PDBTitle:** the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
43	c3lnsD_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**benzaldehyde dehydrogenase; **PDBTitle:** benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
44	d1vlua_	Alignment	not modelled	100.0	21	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
45	c2h5gA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta 1-pyrroline-5-carboxylate synthetase; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate synthetase
46	c1vluB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gamma-glutamyl phosphate reductase; **PDBTitle:** crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
47	d1k75a_	Alignment	not modelled	97.4	15	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
48	d1y5ea1	Alignment	not modelled	42.3	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
49	c2yvqA_	Alignment	not modelled	26.5	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
50	c3iv4A_	Alignment	not modelled	24.8	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** a putative oxidoreductase with a thioredoxin fold
51	d1np7a2	Alignment	not modelled	22.1	10	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
52	c3jtpB_	Alignment	not modelled	19.2	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
53	d1a9xa2	Alignment	not modelled	19.0	15	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric,

						C-terminal domain
54	d2g2ca1	Alignment	not modelled	18.7	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
55	d1wo8a1	Alignment	not modelled	18.4	10	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
56	d1s7ia_	Alignment	not modelled	17.1	15	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
57	c2is8A_	Alignment	not modelled	15.5	12	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
58	d2j07a2	Alignment	not modelled	14.0	13	**Fold:**Cryptochrome/photolyase, N-terminal domain **Superfamily:**Cryptochrome/photolyase, N-terminal domain **Family:**Cryptochrome/photolyase, N-terminal domain
59	d1oy0a_	Alignment	not modelled	13.7	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
60	c3labA_	Alignment	not modelled	12.5	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative kdpg (2-keto-3-deoxy-6-phosphogluconate) **PDBTitle:** crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
61	d1o66a_	Alignment	not modelled	11.6	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
62	c3q3hA_	Alignment	not modelled	10.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
63	d1uz5a3	Alignment	not modelled	9.5	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
64	d1g99a2	Alignment	not modelled	8.6	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
65	c3ibpA_	Alignment	not modelled	8.5	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**chromosome partition protein mukb; **PDBTitle:** the crystal structure of the dimerization domain of escherichia coli2 structural maintenance of chromosomes protein mukb
66	d1mkza_	Alignment	not modelled	8.5	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
67	c2pjkA_	Alignment	not modelled	8.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
68	c2xigA_	Alignment	not modelled	8.0	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**ferric uptake regulation protein; **PDBTitle:** the structure of the helicobacter pylori ferric uptake2 regulator fur reveals three functional metal binding sites
69	d2e1za2	Alignment	not modelled	7.7	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Acetokinase-like
70	c2g4rB_	Alignment	not modelled	7.3	12	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis mog protein; **PDBTitle:** anomalous substructure of moga
71	c2ec4A_	Alignment	not modelled	7.3	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** solution structure of the uas domain from human fas-2 associated factor 1
72	c1uz5A_	Alignment	not modelled	7.2	18	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
73	d1ydua1	Alignment	not modelled	7.1	13	**Fold:**At5g01610-like **Superfamily:**At5g01610-like **Family:**At5g01610-like
74	d1hkya_	Alignment	not modelled	7.1	21	**Fold:**Hairpin loop containing domain-like **Superfamily:**Hairpin loop containing domain-like **Family:**Pan module (APPLE domain)
75	c2vpiA_	Alignment	not modelled	6.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
76	d1xxaa_	Alignment	not modelled	6.5	29	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
77	c2hw2A_	Alignment	not modelled	6.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rifampin adp-ribosyl transferase; **PDBTitle:** crystal structure of rifampin adp-ribosyl transferase in2 complex with rifampin
78	d2f7wa1	Alignment	not modelled	6.4	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
79	c1gr0A_	Alignment	not modelled	6.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**inositol-3-phosphate synthase; **PDBTitle:** myo-inositol 1-phosphate synthase from mycobacterium2

						tuberculosis in complex with nad and zinc.
80	c3jtoE_	Alignment	not modelled	6.0	13	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**adapter protein meca 2; **PDBTitle:** crystal structure of the c-terminal domain of ypbh
81	d1v8da_	Alignment	not modelled	5.9	14	**Fold:**TTHA0583/YokD-like **Superfamily:**TTHA0583/YokD-like **Family:**Hypothetical protein TT1679
82	c2iirJ_	Alignment	not modelled	5.9	19	**PDB header:**transferase **Chain:** J: **PDB Molecule:**acetate kinase; **PDBTitle:** acetate kinase from a hypothermophile thermotoga maritima
83	d2ey4c1	Alignment	not modelled	5.7	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Gar1-like SnoRNP
84	c2hvyB_	Alignment	not modelled	5.5	33	**PDB header:**isomerase/biosynthetic protein/rna **Chain:** B: **PDB Molecule:**small nucleolar rnp similar to gar1; **PDBTitle:** crystal structure of an h/aca box rnp from pyrococcus furiosus
85	d2ftsa3	Alignment	not modelled	5.5	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
86	c3v4gA_	Alignment	not modelled	5.4	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
87	d1ovma2	Alignment	not modelled	5.3	9	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
88	c3rfqC_	Alignment	not modelled	5.2	23	**PDB header:**biosynthetic protein **Chain:** C: **PDB Molecule:**pterin-4-alpha-carbinolamine dehydratase moab2; **PDBTitle:** crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
89	d1jx6a_	Alignment	not modelled	5.2	12	**Fold:**Periplasmic binding protein-like I **Superfamily:**Periplasmic binding protein-like I **Family:**L-arabinose binding protein-like