Phyre^2

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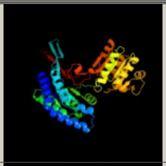
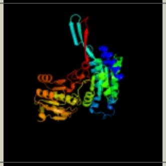
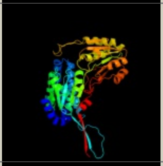
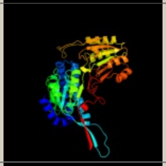
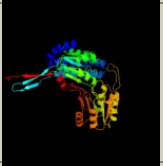
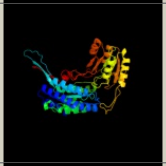
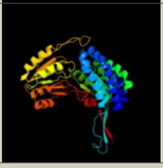
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1o20a_	Alignment		100.0	46	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
2	c2h5gA_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta 1-pyrroline-5-carboxylate synthetase; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate synthetase
3	c3hazA_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
4	d1uzba_	Alignment		100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
5	d1a4sa_	Alignment		100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
6	d1vlua_	Alignment		100.0	36	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
7	c3qanB_	Alignment		100.0	17	**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
8	c2jg7G_	Alignment		100.0	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
9	c3ed6B_	Alignment		100.0	18	**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
10	d1ad3a_	Alignment		100.0	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
11	d1bxsa_	Alignment		100.0	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like

12	d1o9ja_	Alignment		100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
13	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
14	c2d4eB_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
15	d1ag8a_	Alignment		100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
16	c2o2qA_	Alignment		100.0	16	**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
17	d1euha_	Alignment		100.0	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
18	c3rh9A_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
19	c3prlD_	Alignment		100.0	19	**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
20	d1wnda_	Alignment		100.0	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
21	c2w8qA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
22	d1o04a_	Alignment	not modelled	100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
23	c3iwkB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
24	d1ky8a_	Alignment	not modelled	100.0	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
25	c3ifgH_	Alignment	not modelled	100.0	16	**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
26	c3ek1C_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
27	c1t90B_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
28	c3rosA_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus

29	c3r31A_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
30	c3k2wD_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
31	c3jz4C_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
32	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+
33	c3i44A_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
34	c1vluB_	Alignment		100.0	38	**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
35	c3k9dD_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
36	c2hg2A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
37	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
38	c3v4cB_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
39	c3efvC_	Alignment	not modelled	100.0	17	**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
40	d1ez0a_	Alignment	not modelled	100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
41	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.
42	d1bi9a_	Alignment	not modelled	100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
43	c2vroB_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
44	c3lnsD_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**benzaldehyde dehydrogenase; **PDBTitle:** benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
45	c3r64A_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
46	c3my7A_	Alignment	not modelled	100.0	19	**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
47	d1k75a_	Alignment	not modelled	98.5	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
48	c3jtpB_	Alignment	not modelled	50.5	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
49	c2yukA_	Alignment	not modelled	47.6	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
50	d1k99a_	Alignment	not modelled	36.6	17	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
51	d1s7ia_	Alignment	not modelled	35.7	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
52	d1g62a_	Alignment	not modelled	32.9	17	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Ribosome anti-association factor eIF6 (aIF6)

53	c2crjA_	Alignment	not modelled	31.2	18	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
54	c3fghA_	Alignment	not modelled	30.2	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
55	c2ec4A_	Alignment	not modelled	29.1	8	**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
56	c2qguA_	Alignment	not modelled	27.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
57	c3c8eB_	Alignment	not modelled	26.3	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**yghu, glutathione s-transferase homologue; **PDBTitle:** crystal structure analysis of yghu from e. coli
58	c2eqzA_	Alignment	not modelled	26.3	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group protein b3; **PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3
59	d1acoa2	Alignment	not modelled	25.8	7	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
60	d1j3xa_	Alignment	not modelled	25.6	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
61	c1j3xA_	Alignment	not modelled	25.6	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**high mobility group protein 2; **PDBTitle:** solution structure of the n-terminal domain of the hmgb2
62	d1wo8a1	Alignment	not modelled	24.4	10	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Methylglyoxal synthase, MgsA
63	c3e5bB_	Alignment	not modelled	24.3	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**isocitrate lyase; **PDBTitle:** 2.4 a crystal structure of isocitrate lyase from brucella2 melitensis
64	c2cs1A_	Alignment	not modelled	23.8	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pms1 protein homolog 1; **PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein
65	d1y5ea1	Alignment	not modelled	23.6	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
66	d1hsma_	Alignment	not modelled	21.1	19	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
67	d2ftsa3	Alignment	not modelled	21.0	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
68	c5acnA_	Alignment	not modelled	20.8	7	**PDB header:**lyase(carbon-oxygen) **Chain:** A: **PDB Molecule:**aconitase; **PDBTitle:** structure of activated aconitase. formation of the (4fe-4s)2 cluster in the crystal
69	d1j46a_	Alignment	not modelled	20.5	20	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
70	c2co9A_	Alignment	not modelled	20.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
71	d1lwma_	Alignment	not modelled	20.4	16	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
72	d1vdha_	Alignment	not modelled	20.3	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
73	c3g5oC_	Alignment	not modelled	20.2	24	**PDB header:**toxin/antitoxin **Chain:** C: **PDB Molecule:**uncharacterized protein rv2866; **PDBTitle:** the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
74	d1eucb2	Alignment	not modelled	20.0	4	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
75	d1v64a_	Alignment	not modelled	19.4	18	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
76	d1v63a_	Alignment	not modelled	19.2	5	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
77	d1j3da_	Alignment	not modelled	19.0	21	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
78	d1u2ca2	Alignment	not modelled	18.9	14	**Fold:**Dystroglycan, domain 2 **Superfamily:**Dystroglycan, domain 2 **Family:**Dystroglycan, domain 2
						PDB header:ligase

79	c2yvqA_	Alignment	not modelled	18.7	23	**Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
80	d1hmfa_	Alignment	not modelled	18.5	19	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
81	c1hmfA_	Alignment	not modelled	18.5	19	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein fragment-b; **PDBTitle:** structure of the hmg box motif in the b-domain of hmg1
82	d2lefa_	Alignment	not modelled	18.1	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
83	d1t0tv_	Alignment	not modelled	17.9	7	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
84	d2b3ya2	Alignment	not modelled	17.5	14	**Fold:**Aconitase iron-sulfur domain **Superfamily:**Aconitase iron-sulfur domain **Family:**Aconitase iron-sulfur domain
85	d1ckta_	Alignment	not modelled	16.5	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
86	c3labA_	Alignment	not modelled	16.0	13	**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
87	c2b3yB_	Alignment	not modelled	15.4	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**iron-responsive element binding protein 1; **PDBTitle:** structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
88	d1gt0d_	Alignment	not modelled	15.2	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
89	c1wx2A_	Alignment	not modelled	15.1	16	**PDB header:**oxidoreductase/metal transport **Chain:** A: **PDB Molecule:**tyrosinase; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of hydrogenperoxide
90	d1wmia1	Alignment	not modelled	14.9	25	**Fold:**RelE-like **Superfamily:**RelE-like **Family:**RelE-like
91	c2vxhF_	Alignment	not modelled	14.5	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**chlorite dismutase; **PDBTitle:** the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
92	c1v8dC_	Alignment	not modelled	14.2	21	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein (tt1679); **PDBTitle:** crystal structure of the conserved hypothetical protein2 tt1679 from thermus thermophilus
93	d2dlxa1	Alignment	not modelled	14.0	8	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
94	c1aabA_	Alignment	not modelled	13.5	15	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein; **PDBTitle:** nmr structure of rat hmg1 hmga fragment
95	d1aaba_	Alignment	not modelled	13.5	15	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
96	c1usdA_	Alignment	not modelled	13.5	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
97	d2nu7b2	Alignment	not modelled	13.2	9	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
98	c2lhjA_	Alignment	not modelled	12.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**high mobility group protein homolog nhp1; **PDBTitle:** nmr structure of the high mobility group protein-like protein nhp12 from babesia bovis t2bo (baboa.00841.a)
99	c3bpqD_	Alignment	not modelled	12.7	14	**PDB header:**toxin **Chain:** D: **PDB Molecule:**toxin rele3; **PDBTitle:** crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii