Phyre2

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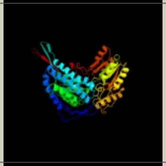
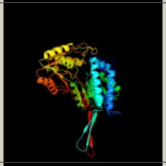
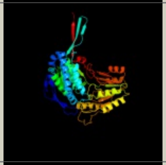
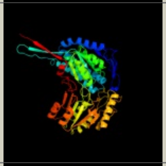
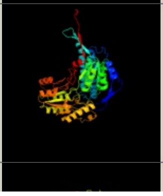
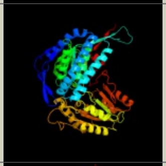
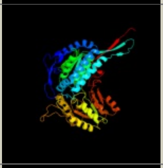
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2ve5H_	Alignment		100.0	77	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
2	d1bxsa_	Alignment		100.0	39	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
3	d1a4sa_	Alignment		100.0	51	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
4	c3ed6B_	Alignment		100.0	40	**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
5	d1o9ja_	Alignment		100.0	39	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
6	d1o04a_	Alignment		100.0	42	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
7	d1ag8a_	Alignment		100.0	43	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
8	c2o2qA_	Alignment		100.0	39	**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
9	c2d4eB_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
10	c3r31A_	Alignment		100.0	54	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
11	c3iwkB_	Alignment		100.0	41	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)

12	c3rh9A_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
13	c3i44A_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
14	c3k2wD_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
15	c2jg7G_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
16	c3b4wA_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
17	d1wnda_	Alignment		100.0	38	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
18	c3ifgH_	Alignment		100.0	37	**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
19	c3ek1C_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
20	c3qanB_	Alignment		100.0	30	**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
21	d1uzba_	Alignment	not modelled	100.0	32	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
22	c1t90B_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
23	c3jz4C_	Alignment	not modelled	100.0	37	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
24	c2w8qA_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
25	d1euha_	Alignment	not modelled	100.0	33	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
26	c3prlD_	Alignment	not modelled	100.0	33	**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
27	c2hg2A_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
28	d1ky8a_	Alignment	not modelled	100.0	31	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
		Alignment				**Fold:**ALDH-like

29	d1bi9a_	Alignment	not modelled	100.0	40	**Superfamily:**ALDH-like **Family:**ALDH-like
30	c3ju8B_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
31	c3hazA_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
32	c3rosA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
33	c2vroB_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
34	c3efvC_	Alignment	not modelled	100.0	32	**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
35	c3r64A_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
36	c3pqaA_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**lactaldehyde dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
37	d1ad3a_	Alignment	not modelled	100.0	27	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
38	c3v4cB_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase (nadp+); **PDBTitle:** crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
39	d1ez0a_	Alignment	not modelled	100.0	25	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
40	c3lnsD_	Alignment	not modelled	100.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**benzaldehyde dehydrogenase; **PDBTitle:** benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
41	c3k9dD_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
42	d1o20a_	Alignment	not modelled	100.0	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
43	c3my7A_	Alignment	not modelled	100.0	20	**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
44	c2h5gA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta 1-pyrroline-5-carboxylate synthetase; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate synthetase
45	d1vlua_	Alignment	not modelled	100.0	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
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	98.5	17	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
48	c2yvqA_	Alignment	not modelled	42.9	11	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
49	d1a9xa2	Alignment	not modelled	40.4	15	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
50	d1uz5a3	Alignment	not modelled	33.2	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
51	d1y5ea1	Alignment	not modelled	30.9	21	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
52	c2yukA_	Alignment	not modelled	30.7	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
53	d1xxaa_	Alignment	not modelled	28.1	18	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor

54	c1uz5A_	Alignment	not modelled	27.9	15	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
55	c3jtpB_	Alignment	not modelled	26.7	14	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
56	d2bona1	Alignment	not modelled	26.6	18	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
57	d2g2ca1	Alignment	not modelled	26.6	14	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
58	d1k99a_	Alignment	not modelled	26.1	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
59	d1e3ha5	Alignment	not modelled	25.7	34	**Fold:**Ribonuclease PH domain 2-like **Superfamily:**Ribonuclease PH domain 2-like **Family:**Ribonuclease PH domain 2-like
60	c2crjA_	Alignment	not modelled	24.0	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
61	d1yuaa2	Alignment	not modelled	23.8	18	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Prokaryotic DNA topoisomerase I, a C-terminal fragment
62	c2is8A_	Alignment	not modelled	23.1	16	**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
63	d1o66a_	Alignment	not modelled	22.4	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Ketopantoate hydroxymethyltransferase PanB
64	c2ec4A_	Alignment	not modelled	22.1	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
65	d1mkza_	Alignment	not modelled	21.2	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
66	d1j3xa_	Alignment	not modelled	21.0	19	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
67	c1j3xA_	Alignment	not modelled	21.0	19	**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
68	d2ioja1	Alignment	not modelled	20.6	19	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
69	c3fghA_	Alignment	not modelled	20.0	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
70	c3q3hA_	Alignment	not modelled	19.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hmw1c-like glycosyltransferase; **PDBTitle:** crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
71	c2eqzA_	Alignment	not modelled	19.6	16	**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
72	c1eakA_	Alignment	not modelled	19.5	20	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**72 kda type iv collagenase; **PDBTitle:** catalytic domain of prommp-2 e404q mutant
73	c1v9nA_	Alignment	not modelled	19.2	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structure of malate dehydrogenase from pyrococcus horikoshii ot3
74	c2co9A_	Alignment	not modelled	18.5	10	**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
75	d1xrha_	Alignment	not modelled	18.2	18	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
76	c2pjkA_	Alignment	not modelled	17.8	13	**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
77	d1j46a_	Alignment	not modelled	16.7	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
78	c1l6jA_	Alignment	not modelled	16.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**matrix metalloproteinase-9; **PDBTitle:** crystal structure of human matrix metalloproteinase mmp92 (gelatinase b).
79	c3i0pA_	Alignment	not modelled	16.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** crystal structure of malate dehydrogenase from entamoeba histolytica

80	d2lefa_	Alignment	not modelled	15.9	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
81	d1rfma_	Alignment	not modelled	15.8	19	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
82	c2cs1A_	Alignment	not modelled	15.8	16	**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
83	c3uoeB_	Alignment	not modelled	15.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from sinorhizobium meliloti
84	d1v64a_	Alignment	not modelled	15.5	11	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
85	d1s7ia_	Alignment	not modelled	15.4	8	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
86	c1vbiA_	Alignment	not modelled	15.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
87	d1hsma_	Alignment	not modelled	14.9	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
88	c2nqqA_	Alignment	not modelled	14.7	13	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
89	d1u0ta_	Alignment	not modelled	14.7	13	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
90	d2ftsa3	Alignment	not modelled	14.4	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
91	d1nxua_	Alignment	not modelled	14.4	25	**Fold:**L-sulfolactate dehydrogenase-like **Superfamily:**L-sulfolactate dehydrogenase-like **Family:**L-sulfolactate dehydrogenase-like
92	d1s99a_	Alignment	not modelled	14.4	12	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**Putative thiamin/HMP-binding protein YkoF
93	d1lwma_	Alignment	not modelled	14.0	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
94	c2l69A_	Alignment	not modelled	13.8	13	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
95	d2fiua1	Alignment	not modelled	13.6	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Atu0297-like
96	c3lo3E_	Alignment	not modelled	13.4	15	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
97	d1wu2a3	Alignment	not modelled	13.2	20	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
98	c1wtjB_	Alignment	not modelled	13.2	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ureidoglycolate dehydrogenase; **PDBTitle:** crystal structure of delta1-piperideine-2-carboxylate2 reductase from pseudomonas syringae pvar.tomato
99	c1b4aA_	Alignment	not modelled	13.1	14	**PDB header:**repressor **Chain:** A: **PDB Molecule:**arginine repressor; **PDBTitle:** structure of the arginine repressor from bacillus stearothermophilus