Phyre2

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Description	P76217
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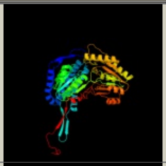
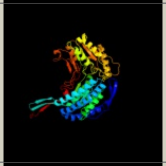
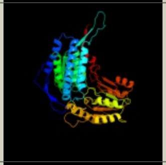
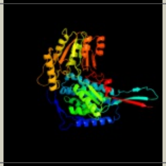
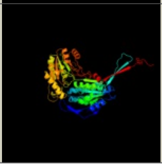
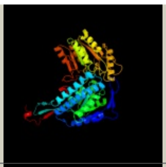
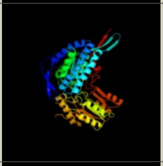
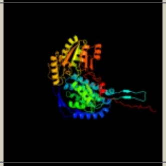
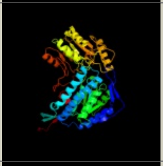
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ju8B_	Alignment		100.0	62	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
2	c2jg7G_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**antiquitin; **PDBTitle:** crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
3	d1a4sa_	Alignment		100.0	27	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
4	d1bxsa_	Alignment		100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
5	c3ed6B_	Alignment		100.0	26	**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
6	c3qanB_	Alignment		100.0	26	**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
7	c2d4eB_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
8	d1uzba_	Alignment		100.0	31	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
9	c2o2qA_	Alignment		100.0	26	**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	d1o9ja_	Alignment		100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
11	c3iwkB_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)

12	d1o04a_	Alignment		100.0	27	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
13	c2ve5H_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
14	d1ag8a_	Alignment		100.0	27	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
15	c1t90B_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde **PDBTitle:** crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
16	c2w8qA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
17	d1ky8a_	Alignment		100.0	23	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
18	c3b4wA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
19	c3r31A_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
20	d1wnda_	Alignment		100.0	27	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
21	c3rh9A_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
22	d1euha_	Alignment	not modelled	100.0	27	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
23	c3ifgH_	Alignment	not modelled	100.0	31	**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
24	c3i44A_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
25	c3prlD_	Alignment	not modelled	100.0	25	**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
26	c3ek1C_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
27	c3jz4C_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
						PDB header:oxidoreductase

28	c2hg2A_	Alignment	not modelled	100.0	28	**Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
29	c3k2wD_	Alignment	not modelled	100.0	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
30	c3hazA_	Alignment	not modelled	100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**proline dehydrogenase; **PDBTitle:** crystal structure of bifunctional proline utilization a2 (puta) protein
31	c3rosA_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
32	c3efvC_	Alignment	not modelled	100.0	24	**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
33	c2vroB_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
34	d1bi9a_	Alignment	not modelled	100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
35	c3r64A_	Alignment	not modelled	100.0	28	**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	27	**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	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
38	c3v4cB_	Alignment	not modelled	100.0	27	**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	22	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
40	c3lnsD_	Alignment	not modelled	100.0	24	**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	18	**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	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
43	c3my7A_	Alignment	not modelled	100.0	18	**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	18	**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	15	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
46	c1vluB_	Alignment	not modelled	100.0	16	**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	97.8	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
48	c2crjA_	Alignment	not modelled	33.7	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
49	d1a9xa2	Alignment	not modelled	31.9	21	**Fold:**Methylglyoxal synthase-like **Superfamily:**Methylglyoxal synthase-like **Family:**Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
50	d1k99a_	Alignment	not modelled	31.7	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
51	c1j3xA_	Alignment	not modelled	31.4	14	**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
52	d1j3xa_	Alignment	not modelled	31.4	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
						PDB header:transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage

53	c2yukA_	Alignment	not modelled	30.8	19	leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
54	c2eqzA_	Alignment	not modelled	30.3	18	**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
55	d1u0ta_	Alignment	not modelled	29.9	15	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
56	c3jtpB_	Alignment	not modelled	29.0	27	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
57	c3fghA_	Alignment	not modelled	28.6	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
58	d2lefa_	Alignment	not modelled	26.6	17	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
59	d2bona1	Alignment	not modelled	25.0	14	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
60	d1j46a_	Alignment	not modelled	24.9	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
61	c2cs1A_	Alignment	not modelled	22.6	21	**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
62	d1hsma_	Alignment	not modelled	22.4	16	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
63	d1lwma_	Alignment	not modelled	21.7	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
64	c2yvqA_	Alignment	not modelled	21.3	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**carbamoyl-phosphate synthase; **PDBTitle:** crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
65	c3u2bC_	Alignment	not modelled	20.9	14	**PDB header:**transcription/dna **Chain:** C: **PDB Molecule:**transcription factor sox-4; **PDBTitle:** structure of the sox4 hmg domain bound to dna
66	c3nrlB_	Alignment	not modelled	20.9	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein rumgna_01417; **PDBTitle:** crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
67	d1gt0d_	Alignment	not modelled	20.2	17	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
68	d1ckta_	Alignment	not modelled	19.5	17	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
69	d1u2ca2	Alignment	not modelled	19.5	14	**Fold:**Dystroglycan, domain 2 **Superfamily:**Dystroglycan, domain 2 **Family:**Dystroglycan, domain 2
70	d1v64a_	Alignment	not modelled	19.4	18	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
71	d1s7ia_	Alignment	not modelled	19.2	11	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
72	d1v63a_	Alignment	not modelled	19.1	16	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
73	c2co9A_	Alignment	not modelled	18.5	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
74	c1hmfA_	Alignment	not modelled	18.3	14	**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
75	d1hmfa_	Alignment	not modelled	18.3	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
76	c2yulA_	Alignment	not modelled	18.2	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sox-17; **PDBTitle:** solution structure of the hmg box of human transcription2 factor sox-17
77	d1j3da_	Alignment	not modelled	18.0	18	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
78	c3g5oC_	Alignment	not modelled	17.7	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
79	d1s99a_	Alignment	not modelled	17.1	11	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**Putative thiamin/HMP-binding protein YkoF

80	d1t0tv_	Alignment	not modelled	16.7	28	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
81	d1vdha_	Alignment	not modelled	16.5	21	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Chlorite dismutase-like
82	c3labA_	Alignment	not modelled	16.4	22	**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
83	c2lhjA_	Alignment	not modelled	15.7	13	**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)
84	c3v4gA_	Alignment	not modelled	15.1	13	**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
85	c3gyyC_	Alignment	not modelled	14.9	11	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**periplasmic substrate binding protein; **PDBTitle:** the ectoine binding protein of the teaabc trap transporter teaa in the2 apo-state
86	d2jgra1	Alignment	not modelled	14.5	14	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**Diacylglycerol kinase-like
87	d2tpta3	Alignment	not modelled	14.5	23	**Fold:**alpha/beta-Hammerhead **Superfamily:**Pyrimidine nucleoside phosphorylase C-terminal domain **Family:**Pyrimidine nucleoside phosphorylase C-terminal domain
88	d2gzka2	Alignment	not modelled	14.4	14	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
89	c1hrzA_	Alignment	not modelled	14.4	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**human sry; **PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multi-dimensional heteronuclear-edited and-filtered nmr
90	c1hryA_	Alignment	not modelled	14.4	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**human sry; **PDBTitle:** the 3d structure of the human sry-dna complex solved by2 multid-dimensional heteronuclear-edited and-filtered nmr
91	c2e6oA_	Alignment	not modelled	13.6	23	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1
92	c3e7hA_	Alignment	not modelled	13.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna-directed rna polymerase subunit beta; **PDBTitle:** the crystal structure of the beta subunit of the dna-2 directed rna polymerase from vibrio cholerae o1 biovar3 eltor
93	d1xxaa_	Alignment	not modelled	13.2	19	**Fold:**DCoH-like **Superfamily:**C-terminal domain of arginine repressor **Family:**C-terminal domain of arginine repressor
94	d1wu2a3	Alignment	not modelled	13.2	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
95	c2bonB_	Alignment	not modelled	13.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**lipid kinase; **PDBTitle:** structure of an escherichia coli lipid kinase (yegs)
96	c3qwuA_	Alignment	not modelled	13.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** putative atp-dependent dna ligase from aquifex aeolicus.
97	d1y5ea1	Alignment	not modelled	12.6	26	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
98	c1usdA_	Alignment	not modelled	12.5	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**vasodilator-stimulated phosphoprotein; **PDBTitle:** human vasp tetramerisation domain l352m
99	c2ec4A_	Alignment	not modelled	12.1	16	**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