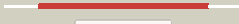



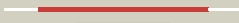




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0753c_(mmsA)_844424_845956
Date	Fri Jul 26 01:50:33 BST 2019
Unique Job ID	30594f073c569280

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fk3B_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure and function of aldehyde dehydrogenase from thermus2 thermophilus: an enzyme with an evolutionarily-distinct c-terminal3 arm (recombinant full-length protein in complex with propanal)
2	c4f9iA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase/delta-1-pyrroline-5-carboxylate PDBTitle: crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
3	c4zz7E_	 Alignment		100.0	55	PDB header: oxidoreductase Chain: E: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate-semialdehyde dehydrogenase (ddd)2 from oceanimonas doudoroffii
4	c5ur2C_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: C: PDB Molecule: bifunctional protein puta; PDBTitle: crystal structure of proline utilization a (puta) from bdellovibrio2 bacteriovorus inactivated by n-propargylglycine
5	c4e4gF_	 Alignment		100.0	66	PDB header: oxidoreductase Chain: F: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
6	c3ed6B_	 Alignment		100.0	28	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	d1a4sa_	 Alignment		100.0	31	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
8	c2jg7G_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
9	c1t90B_	 Alignment		100.0	43	PDB header: oxidoreductase Chain: B: PDB Molecule: probable methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate semialdehyde dehydrogenase from2 bacillus subtilis
10	c3u4jB_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
11	c2d4eB_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: 5-carboxymethyl-2-hydroxyomuconate semialdehyde PDBTitle: crystal structure of the hpcc from thermus thermophilus hb8

12	c4o5hD_	Alignment		100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: phenylacetaldehyde dehydrogenase; PDBTitle: x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
13	c3qanB_	Alignment		100.0	29	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
14	c6mvtA_	Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a bacterial aldH16 complexed with nadh
15	c5izdE_	Alignment		100.0	27	PDB header: oxidoreductase Chain: E: PDB Molecule: d-glyceraldehyde dehydrogenase (nadp(+)); PDBTitle: wild-type glyceraldehyde dehydrogenase from thermoplasma acidophilum2 in complex with nadp
16	d1bxsA_	Alignment		100.0	32	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
17	c3iwkB_	Alignment		100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: aminoaldehyde dehydrogenase; PDBTitle: crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
18	c2o2qA_	Alignment		100.0	30	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
19	d1o9ja_	Alignment		100.0	33	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
20	c3rh9A_	Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase (nad(p)(+)); PDBTitle: the crystal structure of oxidoreductase from marinobacter aquaeolei
21	c4h73E_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: E: PDB Molecule: aldehyde dehydrogenase; PDBTitle: thermostable aldehyde dehydrogenase from pyrobaculum sp. complexed2 with nadp+
22	c4jz6A_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: salicylaldehyde dehydrogenase nahf; PDBTitle: crystal structure of a salicylaldehyde dehydrogenase from pseudomonas2 putida g7 complexed with salicylaldehyde
23	c4pt3C_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase; PDBTitle: nadph complex structure of aldehyde dehydrogenase from bacillus cereus
24	c4go4E_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: E: PDB Molecule: putative gamma-hydroxy-muconic semialdehyde dehydrogenase; PDBTitle: crystal structure of pnpe in complex with nicotinamide adenine2 dinucleotide
25	c5x5uB_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutaric semialdehyde dehydrogenase2 (kgsadh) complexed with nad
26	c3ek1C_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
27	c3k2wD_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: betaine-aldehyde dehydrogenase; PDBTitle: crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
28	c2vo5H_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase;

28	c2ve3H_	Alignment	not modelled	100.0	29	PDBTitle: crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
29	d1uzba_	Alignment	not modelled	100.0	30	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
30	c4pxlB_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: cytosolic aldehyde dehydrogenase rf2c; PDBTitle: structure of zm ald2-3 (rf2c) in complex with nad
31	c4i25B_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-aminomuconate 6-semialdehyde dehydrogenase; PDBTitle: 2.00 angstroms x-ray crystal structure of nad- and substrate-bound 2-2 aminomuconate 6-semialdehyde dehydrogenase from pseudomonas3 fluorescens
32	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
33	c5kf6B_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: bifunctional protein puta; PDBTitle: structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
34	c3r31A_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: A: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
35	c4pxnB_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of zm ald7 in complex with nad
36	d1o04a_	Alignment	not modelled	100.0	32	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
37	c3b4wA_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
38	c5vbfH_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: H: PDB Molecule: nad-dependent succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of succinate semialdehyde dehydrogenase from2 burkholderia vietnamiensis
39	c4yweE_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: E: PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of a putative aldehyde dehydrogenase from2 burkholderia cenocepacia
40	d1wnda_	Alignment	not modelled	100.0	31	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
41	d1euha_	Alignment	not modelled	100.0	31	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
42	c5j6bB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from burkholderia2 thailandensis in covalent complex with nadph
43	d1ag8a_	Alignment	not modelled	100.0	33	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
44	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
45	c4dalB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of putative aldehyde dehydrogenase from2 sinorhizobium meliloti 1021
46	d1ky8a_	Alignment	not modelled	100.0	28	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
47	c2w8qA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase, PDBTitle: the crystal structure of human ssadh in complex with ssa.
48	c3i44A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
49	c5u0mB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: n-succinylglutamate 5-semialdehyde dehydrogenase; PDBTitle: fatty aldehyde dehydrogenase from marinobacter aquaeolei vt8 and2 cofactor complex
50	c2hg2A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase a; PDBTitle: structure of lactaldehyde dehydrogenase
51	c3priD_	Alignment	not modelled	100.0	29	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
52	c6ddbA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: putative aldehyde dehydrogenase family protein; PDBTitle: crystal structure of a putative aldehyde dehydrogenase family protein2 burkholderia cenocepacia j2315 in complex with

						partially reduced nadh
53	c4knaA_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: n-succinylglutamate 5-semialdehyde dehydrogenase; PDBTitle: crystal structure of an n-succinylglutamate 5-semialdehyde2 dehydrogenase from burkholderia thailandensis
54	c5mz5A_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aldh21); PDBTitle: crystal structure of aldehyde dehydrogenase 21 (aldh21) from2 physcomitrella patens in its apoform
55	c4idmA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase; PDBTitle: crystal structure of the delta-pyrroline-5-carboxylate dehydrogenase2 from mycobacterium tuberculosis
56	c4qy1D_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: D: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
57	c3ju8B_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: succinylglutamic semialdehyde dehydrogenase; PDBTitle: crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
58	c4lihG_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: G: PDB Molecule: gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase; PDBTitle: the crystal structure of gamma-glutamyl-gamma-aminobutyraldehyde2 dehydrogenase from burkholderia cenocepacia j2315
59	c4i3wC_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase (nad+); PDBTitle: structure of phosphonoacetaldehyde dehydrogenase in complex with2 glyceraldehyde-3-phosphate and cofactor nad+
60	c3hazA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: proline dehydrogenase; PDBTitle: crystal structure of bifunctional proline utilization a2 (puta) protein
61	d1bi9a_	Alignment	not modelled	100.0	33	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
62	c4ohtB_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of succinic semialdehyde dehydrogenase from2 streptococcus pyogenes in complex with nadp+ as the cofactor
63	c2vroB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
64	c4itaA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase; PDBTitle: structure of bacterial enzyme in complex with cofactor
65	c3vz0B_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad-dependent aldehyde dehydrogenase; PDBTitle: structural insights into cofactor and substrate selection by gox0499
66	c3rosA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
67	c5tjrE_	Alignment	not modelled	100.0	57	PDB header: oxidoreductase Chain: E: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: x-ray crystal structure of a methylmalonate semialdehyde dehydrogenase2 from pseudomonas sp. aac
68	c3efvC_	Alignment	not modelled	100.0	28	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
69	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
70	c4h7nA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: the structure of putative aldehyde dehydrogenase puta from anaebaena2 variabilis.
71	c3pqaA_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: lactaldehyde dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
72	c5fhzF_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: F: PDB Molecule: aldehyde dehydrogenase family 1 member a3; PDBTitle: human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid
73	d1ad3a_	Alignment	not modelled	100.0	23	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
74	c6d97B_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase 12; PDBTitle: structure of aldehyde dehydrogenase 12 (aldh12) from zea mays
75	c4qgkB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty aldehyde dehydrogenase; PDBTitle: structure of the human sjogren larsson syndrome enzyme

						fatty aldehyde2 dehydrogenase (faldh) PDB header: oxidoreductase/transferase Chain: C: PDB Molecule: bifunctional protein proline utilization a (puta); PDBTitle: structure of proline utilization a (puta) from corynebacterium2 freiburgense
76	c5ux5C_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of yeast ald4a1 complexed with nad+
77	c4oe4A_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized aldehyde dehydrogenase aldy; PDBTitle: crystal structure of putative aldehyde dehydrogenase from bacillus2 subtilis subsp. subtilis str. 168
78	c5nnoA_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of tbalhd3 complexed with nad and an3057 aldehyde
79	c4dngB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase (nadp+); PDBTitle: crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
80	c3v4cB_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase family protein; PDBTitle: crystal structure of indole-3-acetaldehyde dehydrogenase in apo form
81	c5iuuA_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: D: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of human 1-pyrroline-5-carboxylate dehydrogenase2 mutant s352l
82	c3v9iD_	Alignment	not modelled	100.0	23	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
83	d1ez0a_	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 burkholderia multivorans
84	c5ujuA_	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
85	c3lnsD_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acetylating); PDBTitle: crystal structure of an acetylating aldehyde dehydrogenase from2 geobacillus thermoglucosidasius
86	c5j78B_	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
87	c3k9dD_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a propionaldehyde dehydrogenase from the clostridium2 phytofermentans fucose utilisation bacterial microcompartment
88	c4c3sA_	Alignment	not modelled	100.0	21	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
89	d1o20a_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: 1.95 angstrom crystal structure of gamma-glutamyl phosphate reductase2 from saccharomonospora viridis.
90	c4jbeA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of rhodospseudomonas palustris propionaldehyde2 dehydrogenase with bound coa and acylated cys330
91	c5jfnA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: x-ray crystal structure of gamma-glutamyl phosphate reductase from2 burkholderia thailandensis
92	c4ghkB_	Alignment	not modelled	100.0	23	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
93	c3my7A_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: delta 1-pyrroline-5-carboxylate synthetase; PDBTitle: crystal structure of human pyrroline-5-carboxylate synthetase
94	c2h5gA_	Alignment	not modelled	100.0	20	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
95	d1vlua_	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
96	c1vlub_	Alignment	not modelled	100.0	17	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD
97	d1k75a_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
98	c4g07A_	Alignment	not modelled	98.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase;
99	c6an0A_	Alignment	not modelled	98.3	11	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase;

99	c6n1vA	Alignment	not modelled	98.3	11	PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis PDB header: oxidoreductase
100	c5vldC	Alignment	not modelled	97.8	15	Chain: C; PDB Molecule: histidinol dehydrogenase, chloroplastic; PDBTitle: crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
101	c4gicB	Alignment	not modelled	97.3	18	PDB header: oxidoreductase Chain: B; PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
102	c3e5bB	Alignment	not modelled	85.7	19	PDB header: lyase Chain: B; PDB Molecule: isocitrate lyase; PDBTitle: 2.4 a crystal structure of isocitrate lyase from brucella melitensis
103	c3fa4D	Alignment	not modelled	76.2	15	PDB header: lyase Chain: D; PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
104	c3lyeA	Alignment	not modelled	74.2	16	PDB header: hydrolase Chain: A; PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
105	c2yvqA	Alignment	not modelled	73.4	11	PDB header: ligase Chain: A; PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
106	d1s7ia	Alignment	not modelled	65.9	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
107	d1a9xa2	Alignment	not modelled	62.0	15	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
108	c3v42A	Alignment	not modelled	57.9	21	PDB header: protein binding Chain: A; PDB Molecule: folliculin; PDBTitle: crystal structure of renal tumor suppressor protein, folliculin
109	c2jgqB	Alignment	not modelled	41.2	12	PDB header: isomerase Chain: B; PDB Molecule: triosephosphate isomerase; PDBTitle: kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
110	c2yukA	Alignment	not modelled	33.4	19	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
111	c3jtpB	Alignment	not modelled	30.5	17	PDB header: protein binding Chain: B; PDB Molecule: adapter protein meca 1; PDBTitle: crystal structure of the c-terminal domain of meca
112	d1k99a	Alignment	not modelled	29.2	8	Fold: HMG-box Superfamily: HMG-box Family: HMG-box
113	c5vveA	Alignment	not modelled	26.7	11	PDB header: transcription Chain: A; PDB Molecule: fact complex subunit ssrp1; PDBTitle: solution nmr structure of the hmg domain of human fact complex subunit2 ssrp1
114	c2criA	Alignment	not modelled	25.9	15	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
115	c2eqzA	Alignment	not modelled	25.9	5	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
116	c4oo3A	Alignment	not modelled	25.1	10	PDB header: oxidoreductase Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
117	c2ixaA	Alignment	not modelled	24.7	14	PDB header: hydrolase Chain: A; PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
118	c3fghA	Alignment	not modelled	24.6	8	PDB header: transcription Chain: A; PDB Molecule: transcription factor a, mitochondrial; PDBTitle: human mitochondrial transcription factor a box b
119	d2zdra2	Alignment	not modelled	24.4	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
120	c3ereD	Alignment	not modelled	24.1	25	PDB header: dna binding protein/dna Chain: D; PDB Molecule: arginine repressor; PDBTitle: crystal structure of the arginine repressor protein from mycobacterium2 tuberculosis in complex with the dna operator