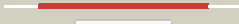



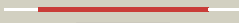



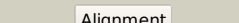













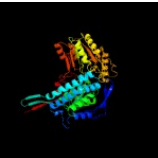






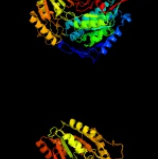
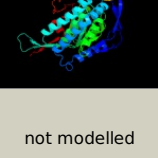


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0223c_(-)_266301_267764
Date	Tue Jul 23 14:50:28 BST 2019
Unique Job ID	1f0be6182f179c23

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3b4wA_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
2	d1a4sa_	 Alignment		100.0	37	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
3	c4o5hD_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: D: PDB Molecule: phenylacetaldehyde dehydrogenase; PDBTitle: x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
4	d1bxsA_	 Alignment		100.0	37	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
5	c3ed6B_	 Alignment		100.0	34	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	c4pxlB_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: B: PDB Molecule: cytosolic aldehyde dehydrogenase rf2c; PDBTitle: structure of zm aldh-2-3 (rf2c) in complex with nad
7	d1o9ja_	 Alignment		100.0	37	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
8	c4f9iA_	 Alignment		100.0	31	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
9	c3u4jB_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
10	c4pt3C_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase; PDBTitle: nadph complex structure of aldehyde dehydrogenase from bacillus cereus
11	c3iwkB_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: B: PDB Molecule: aminoaldehyde dehydrogenase; PDBTitle: crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)

12	c2ve5H_	Alignment		100.0	39	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
13	c5ur2C_	Alignment		100.0	29	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
14	c2o2qA_	Alignment		100.0	35	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
15	c2jg7G_	Alignment		100.0	28	PDB header: oxidoreductase Chain: G: PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of 2 its substrate specificity
16	d1ag8a_	Alignment		100.0	38	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
17	c6fk3B_	Alignment		100.0	34	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)
18	d1o04a_	Alignment		100.0	38	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
19	c3r31A_	Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
20	c3i44A_	Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
21	c4go4E_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: E: PDB Molecule: putative gamma-hydroxymuconic semialdehyde dehydrogenase; PDBTitle: crystal structure of pnpe in complex with nicotinamide adenine2 dinucleotide
22	c2d4eB_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: 5-carboxymethyl-2-hydroxymuconate semialdehyde PDBTitle: crystal structure of the hpcc from thermus thermophilus hb8
23	c6mvtA_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a bacterial ald16 complexed with nadh
24	c3rh9A_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase (nad(p)(+)); PDBTitle: the crystal structure of oxidoreductase from marinobacter aquaeolei
25	c5izdE_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: E: PDB Molecule: d-glyceraldehyde dehydrogenase (nadp(+)); PDBTitle: wild-type glyceraldehyde dehydrogenase from thermoplasma acidophilum2 in complex with nadp
26	c3ifgH_	Alignment	not modelled	100.0	35	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
27	c4yweE_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: E: PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of a putative aldehyde dehydrogenase from2 burkholderia cenocepacia

28	c4i25B_	Alignment	not modelled	100.0	35	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
29	c1t90B_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: probable methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate semialdehyde dehydrogenase from2 bacillus subtilis
30	c5x5uB_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: alpha-ketoglutaric semialdehyde dehydrogenase; PDBTitle: crystal structure of alpha-ketoglutarate-semialdehyde dehydrogenase2 (kgsadh) complexed with nad
31	c4dalB_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of putative aldehyde dehydrogenase from2 sinorhizobium meliloti 1021
32	c4qyjD_	Alignment	not modelled	100.0	36	PDB header: oxidoreductase Chain: D: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
33	c3k2wD_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: betaine-aldehyde dehydrogenase; PDBTitle: crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
34	d1wnda_	Alignment	not modelled	100.0	35	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
35	c3ek1C_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
36	c4zz7E_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: E: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate-semialdehyde dehydrogenase (ddd)2 from oceanimonas doudoroffii
37	d1uzba_	Alignment	not modelled	100.0	31	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
38	c4jz6A_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: salicylaldehyde dehydrogenase nahf; PDBTitle: crystal structure of a salicylaldehyde dehydrogenase from pseudomonas2 putida g7 complexed with salicylaldehyde
39	c3jz4C_	Alignment	not modelled	100.0	35	PDB header: oxidoreductase Chain: C: PDB Molecule: succinate-semialdehyde dehydrogenase [nadp+]; PDBTitle: crystal structure of e. coli nadp dependent enzyme
40	c3qanB_	Alignment	not modelled	100.0	32	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
41	c4e4gF_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: F: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
42	c4lihG_	Alignment	not modelled	100.0	38	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
43	c4h73E_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: E: PDB Molecule: aldehyde dehydrogenase; PDBTitle: thermostable aldehyde dehydrogenase from pyrobaculum sp. complexed2 with nadp+
44	c2w8gA_	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.
45	c5vbfH_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: H: PDB Molecule: nad-dependent succinate-semialdehyde dehydrogenase; PDBTitle: crystal structure of succinate semialdehyde dehydrogenase from2 burkholderia vietnamiensis
46	d1euha_	Alignment	not modelled	100.0	35	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
47	d1ky8a_	Alignment	not modelled	100.0	28	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
48	c4knaA_	Alignment	not modelled	100.0	30	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
49	c5kf6B_	Alignment	not modelled	100.0	27	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
50	c4pxnB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of zm ald7 in complex with nad
						PDB header: oxidoreductase

51	c3priD_	Alignment	not modelled	100.0	34	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	c5j6bB_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from burkholderia2 thailandensis in covalent complex with nadph
53	c5u0mB_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: n-succinylglutamate 5-semialdehyde dehydrogenase; PDBTitle: fatty aldehyde dehydrogenase from marinobacter aquaeolei vt8 and2 cofactor complex
54	c5mz5A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: aldh21); PDBTitle: crystal structure of aldehyde dehydrogenase 21 (aldh21) from2 physcomitrella patens in its apoform
55	d1bi9a_	Alignment	not modelled	100.0	37	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
56	c2hg2A_	Alignment	not modelled	100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase a; PDBTitle: structure of lactaldehyde dehydrogenase
57	c4i3wC_	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: C: PDB Molecule: aldehyde dehydrogenase (nad+); PDBTitle: structure of phosphonoacetaldehyde dehydrogenase in complex with2 glyceraldehyde-3-phosphate and cofactor nad+
58	c6ddbA_	Alignment	not modelled	100.0	23	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
59	c3ju8B_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: succinylglutamic semialdehyde dehydrogenase; PDBTitle: crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
60	c4idmA_	Alignment	not modelled	100.0	24	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
61	c4ohtB_	Alignment	not modelled	100.0	28	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
62	c4itaA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase; PDBTitle: structure of bacterial enzyme in complex with cofactor
63	c3vz0B_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad-dependent aldehyde dehydrogenase; PDBTitle: structural insights into cofactor and substrate selection by gox0499
64	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
65	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
66	c2vroB_	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
67	c3efvC_	Alignment	not modelled	100.0	29	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
68	c5fhzF_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: F: PDB Molecule: aldehyde dehydrogenase family 1 member a3; PDBTitle: human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid
69	c4h7nA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: the structure of putative aldehyde dehydrogenase puta from anaebaena2 variabilis.
70	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
71	c3pqaA_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: lactaldehyde dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
72	c5tjrE_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: E: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: x-ray crystal structure of a methylmalonate semialdehyde dehydrogenase2 from pseudomonas sp. aac
73	c5iuuA_	Alignment	not modelled	100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase family protein; PDBTitle: crystal structure of indole-3-acetaldehyde dehydrogenase in apo form

74	c6d97B	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase 12; PDBTitle: structure of aldehyde dehydrogenase 12 (aldh12) from zea mays
75	c4oe4A	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of yeast ald4a1 complexed with nad+
76	d1ad3a	Alignment	not modelled	100.0	29	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
77	c4qgkB	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: fatty aldehyde dehydrogenase; PDBTitle: structure of the human sjogren larsson syndrome enzyme fatty aldehyde2 dehydrogenase (faldh)
78	c4dngB	Alignment	not modelled	100.0	31	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
79	c5ux5C	Alignment	not modelled	100.0	23	PDB header: oxidoreductase/transferase Chain: C: PDB Molecule: bifunctional protein proline utilization a (puta); PDBTitle: structure of proline utilization a (puta) from corynebacterium2 freiburgense
80	c5nnoA	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of tbalhd3 complexed with nad and an3057 aldehyde
81	c3v9iD	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of human 1-pyrroline-5-carboxylate dehydrogenase2 mutant s352I
82	c3v4cB	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase (nadp+); PDBTitle: crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
83	d1ez0a	Alignment	not modelled	100.0	23	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
84	c3lnsD	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: benzaldehyde dehydrogenase; PDBTitle: benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
85	c5ujuA	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 burkholderia multivorans
86	c4c3sA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a propionaldehyde dehydrogenase from the clostridium2 phytofermentans fucose utilisation bacterial microcompartment
87	c5j78B	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acetylating); PDBTitle: crystal structure of an acetylating aldehyde dehydrogenase from2 geobacillus thermoglucosidasius
88	c3k9dD	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
89	d1o20a	Alignment	not modelled	100.0	19	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
90	c5jfnA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of rhodospseudomonas palustris propionaldehyde2 dehydrogenase with bound coa and acylated cys330
91	c4jbeA	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.
92	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
93	c4ghkB	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: gamma-glutamyl phosphate reductase; PDBTitle: x-ray crystal structure of gamma-glutamyl phosphate reductase from2 burkholderia thailandensis
94	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
95	d1vlua	Alignment	not modelled	100.0	16	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
96	c1vlub	Alignment	not modelled	100.0	17	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
97	d1k75a	Alignment	not modelled	97.9	14	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD

98	c6an0A_	Alignment	not modelled	96.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
99	c4gicB_	Alignment	not modelled	95.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
100	c4g07A_	Alignment	not modelled	94.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
101	c5vldC_	Alignment	not modelled	92.5	15	PDB header: oxidoreductase Chain: C: PDB Molecule: histidinol dehydrogenase, chloroplastic; PDBTitle: crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
102	c2yvqA_	Alignment	not modelled	59.8	13	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
103	c3v42A_	Alignment	not modelled	58.2	20	PDB header: protein binding Chain: A: PDB Molecule: folliculin; PDBTitle: crystal structure of renal tumor suppressor protein, folliculin
104	d1a9xa2	Alignment	not modelled	48.8	22	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
105	c5v2bA_	Alignment	not modelled	29.7	62	PDB header: cell invasion Chain: A: PDB Molecule: thrombospondin-related sporozoite protein; PDBTitle: peptide 38148 modified from fragment 41-60 of plasmodium falciparum2 thrombospondin-related sporozoite protein (trsp)
106	c4oo3A_	Alignment	not modelled	29.4	8	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
107	d1wo8a1	Alignment	not modelled	26.5	16	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
108	c6g4qB_	Alignment	not modelled	26.0	24	PDB header: ligase Chain: B: PDB Molecule: succinate--coa ligase [adp-forming] subunit beta, PDBTitle: structure of human adp-forming succinyl-coa ligase complex suclg1-2 sucla2
109	c5g2rA_	Alignment	not modelled	25.1	15	PDB header: transferase Chain: A: PDB Molecule: molybdopterin biosynthesis protein cnx1; PDBTitle: crystal structure of the mo-insertase domain cnx1e from2 arabidopsis thaliana
110	c5uy2A_	Alignment	not modelled	24.9	62	PDB header: cell invasion Chain: A: PDB Molecule: 20-mer peptide 38146; PDBTitle: peptide 38146 derived from fragment 41-60 of plasmodium falciparum2 thrombospondin-related sporozoite protein (trsp)
111	d1yuaa2	Alignment	not modelled	23.4	25	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment
112	c5vr5A_	Alignment	not modelled	21.2	62	PDB header: cell invasion Chain: A: PDB Molecule: thrombospondin-related sporozoite protein (trsp); PDBTitle: peptide 38142 modified from fragment 41-60 of plasmodium falciparum2 thrombospondin-related sporozoite protein (trsp)