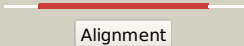

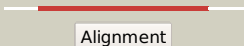

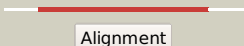







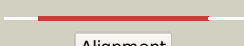




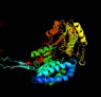






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0147 (-)_173236_174756
Date	Tue Jul 23 14:50:19 BST 2019
Unique Job ID	ac94643a6140f00e

Detailed template information









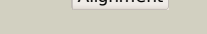
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4f9iA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase/delta-1-pyrroline-5-carboxylate <b>PDBTitle:</b> crystal structure of proline utilization a (puta) from geobacter2 sulfurreducens pca
2	<a href="#">c5ur2C_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> crystal structure of proline utilization a (puta) from bdellovibrio2 bacteriovorus inactivated by n-propargylglycine
3	<a href="#">c4qgkB_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty aldehyde dehydrogenase; <b>PDBTitle:</b> structure of the human sjogren larsson syndrome enzyme fatty aldehyde2 dehydrogenase (faldh)
4	<a href="#">c6mvtA_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> structure of a bacterial ald16 complexed with nadh
5	<a href="#">c5nnoA_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> structure of tbalhd3 complexed with nad and an3057 aldehyde
6	<a href="#">d1a4sa_</a>	 Alignment		100.0	23	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
7	<a href="#">c3ed6B_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
8	<a href="#">d1uzba_</a>	 Alignment		100.0	24	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
9	<a href="#">c6fk3B_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> 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)
10	<a href="#">c3iwkB_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
11	<a href="#">c2jg7G_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> antiquitin; <b>PDBTitle:</b> crystal structure of seabream antiquitin and elucidation of2 its substrate specificity

12	<a href="#">c5kf6B_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein puta; <b>PDBTitle:</b> structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
13	<a href="#">c4o5hD_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> phenylacetaldehyde dehydrogenase; <b>PDBTitle:</b> x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
14	<a href="#">d1ad3a_</a>	Alignment		100.0	44	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
15	<a href="#">c3qanB_</a>	Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-pyrroline-5-carboxylate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
16	<a href="#">c2o2qA_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
17	<a href="#">c3u4jB_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
18	<a href="#">d1bxsa_</a>	Alignment		100.0	29	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
19	<a href="#">c3hazA_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of bifunctional proline utilization a2 (puta) protein
20	<a href="#">c5izdE_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> d-glyceraldehyde dehydrogenase (nadp(+)); <b>PDBTitle:</b> wild-type glyceraldehyde dehydrogenase from thermoplasma acidophilum2 in complex with nadp
21	<a href="#">d1wnda_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
22	<a href="#">c4dalB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of putative aldehyde dehydrogenase from2 sinorhizobium meliloti 1021
23	<a href="#">c4i25B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-aminomuconate 6-semialdehyde dehydrogenase; <b>PDBTitle:</b> 2.00 angstroms x-ray crystal structure of nad- and substrate-bound 2-2 aminomuconate 6-semialdehyde dehydrogenase from pseudomonas3 fluorescens
24	<a href="#">c4pt3C_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> nadph complex structure of aldehyde dehydrogenase from bacillus cereus
25	<a href="#">c4pxlB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytosolic aldehyde dehydrogenase rf2c; <b>PDBTitle:</b> structure of zm ald2-3 (rf2c) in complex with nad
26	<a href="#">c2d4eB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-carboxymethyl-2-hydroxyuconate semialdehyde <b>PDBTitle:</b> crystal structure of the hpcc from thermus thermophilus hb8
27	<a href="#">d1o9ja_</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
28	<a href="#">c5x5uB_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-ketoglutaric semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of alpha-ketoglutarate-semialdehyde

					dehydrogenase2 (kgsadh) complexed with nad <b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
29	<a href="#">c2ve5H_</a>	Alignment	not modelled	100.0	26
30	<a href="#">c3rh9A_</a>	Alignment	not modelled	100.0	24
31	<a href="#">c4jz6A_</a>	Alignment	not modelled	100.0	24
32	<a href="#">c4knaA_</a>	Alignment	not modelled	100.0	22
33	<a href="#">c3ifgH_</a>	Alignment	not modelled	100.0	27
34	<a href="#">c5u0mB_</a>	Alignment	not modelled	100.0	23
35	<a href="#">c3b4wA_</a>	Alignment	not modelled	100.0	27
36	<a href="#">c3ek1C_</a>	Alignment	not modelled	100.0	23
37	<a href="#">c4zz7E_</a>	Alignment	not modelled	100.0	23
38	<a href="#">d1ag8a_</a>	Alignment	not modelled	100.0	25
39	<a href="#">d1o04a_</a>	Alignment	not modelled	100.0	27
40	<a href="#">c4go4E_</a>	Alignment	not modelled	100.0	25
41	<a href="#">d1ky8a_</a>	Alignment	not modelled	100.0	27
42	<a href="#">c3r31A_</a>	Alignment	not modelled	100.0	26
43	<a href="#">c4yweE_</a>	Alignment	not modelled	100.0	29
44	<a href="#">c4h73E_</a>	Alignment	not modelled	100.0	24
45	<a href="#">c3prlD_</a>	Alignment	not modelled	100.0	25
46	<a href="#">d1euha_</a>	Alignment	not modelled	100.0	26
47	<a href="#">c1t90B_</a>	Alignment	not modelled	100.0	22
48	<a href="#">c2w8qA_</a>	Alignment	not modelled	100.0	25
49	<a href="#">c3i44A_</a>	Alignment	not modelled	100.0	26
50	<a href="#">c5j6bB_</a>	Alignment	not modelled	100.0	23
51	<a href="#">c5vbfH_</a>	Alignment	not modelled	100.0	28
52	<a href="#">c3iz4C_</a>	Alignment	not modelled	100.0	25

52	<a href="#">c3z4C_</a>	Alignment	not modelled	100.0	20	[nadp+]; <b>PDBTitle:</b> crystal structure of e. coli nadp dependent enzyme
53	<a href="#">c4e4gF_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> methylmalonate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
54	<a href="#">c4qyID_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
55	<a href="#">c4pxnB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> structure of zm aldH7 in complex with nad
56	<a href="#">c6dbbA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative aldehyde dehydrogenase family protein; <b>PDBTitle:</b> crystal structure of a putative aldehyde dehydrogenase family protein2 burkholderia cenocepacia j2315 in complex with partially reduced nadh
57	<a href="#">c3k2wD_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> betaine-aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
58	<a href="#">c4ohtB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of succinic semialdehyde dehydrogenase from2 streptococcus pyogenes in complex with nadp+ as the cofactor
59	<a href="#">c4h7nA_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> the structure of putative aldehyde dehydrogenase puta from anaebaena2 variabilis.
60	<a href="#">c4idmA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta-1-pyrroline-5-carboxylate dehydrogenase; <b>PDBTitle:</b> crystal structure of the delta-pyrroline-5-carboxylate dehydrogenase2 from mycobacterium tuberculosis
61	<a href="#">c5mz5A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldh21); <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase 21 (aldh21) from2 physcomitrella patens in its apoform
62	<a href="#">c3efvC_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative succinate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
63	<a href="#">c4itaA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase; <b>PDBTitle:</b> structure of bacterial enzyme in complex with cofactor
64	<a href="#">c4lihG_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> gamma-glutamyl-gamma-aminobutyraldehyde dehydrogenase; <b>PDBTitle:</b> the crystal structure of gamma-glutamyl-gamma-aminobutyraldehyde2 dehydrogenase from burkholderia cenocepacia j2315
65	<a href="#">c2hg2A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase a; <b>PDBTitle:</b> structure of lactaldehyde dehydrogenase
66	<a href="#">c3ju8B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> succinylglutamic semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
67	<a href="#">c3vz0B_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> structural insights into cofactor and substrate selection by gox0499
68	<a href="#">c3rosA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
69	<a href="#">c4i3wC_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> aldehyde dehydrogenase (nad+); <b>PDBTitle:</b> structure of phosphonoacetaldehyde dehydrogenase in complex with2 glycerlaldehyde-3-phosphate and cofactor nad+
70	<a href="#">c2vroB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
71	<a href="#">d1bi9a_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
72	<a href="#">c5ux5C_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> bifunctional protein proline utilization a (puta); <b>PDBTitle:</b> structure of proline utilization a (puta) from corynebacterium2 freiburgense
73	<a href="#">c3pqaA_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
74	<a href="#">c5tjrE_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> methylmalonate-semialdehyde dehydrogenase; <b>PDBTitle:</b> x-ray crystal structure of a methylmalonate semialdehyde dehydrogenase2 from pseudomonas sp. aac
						<b>PDB header:</b> oxidoreductase

75	<a href="#">c3lnsD_</a>	Alignment	not modelled	100.0	36	<b>Chain:</b> D: <b>PDB Molecule:</b> benzaldehyde dehydrogenase; <b>PDBTitle:</b> benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
76	<a href="#">c3r64A_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad dependent benzaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
77	<a href="#">c5fhzF_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> aldehyde dehydrogenase family 1 member a3; <b>PDBTitle:</b> human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid
78	<a href="#">c3v4cB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
79	<a href="#">c6d97B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase 12; <b>PDBTitle:</b> structure of aldehyde dehydrogenase 12 (aldh12) from zea mays
80	<a href="#">d1ez0a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
81	<a href="#">c4oe4A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta-1-pyrroline-5-carboxylate dehydrogenase, <b>PDBTitle:</b> crystal structure of yeast aldh4a1 complexed with nad+
82	<a href="#">c5iuuA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase family protein; <b>PDBTitle:</b> crystal structure of indole-3-acetaldehyde dehydrogenase in apo form
83	<a href="#">c3v9iD_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> delta-1-pyrroline-5-carboxylate dehydrogenase, <b>PDBTitle:</b> crystal structure of human 1-pyrroline-5-carboxylate dehydrogenase2 mutant s352l
84	<a href="#">c5ujuA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent aldehyde dehydrogenase from2 burkholderia multivorans
85	<a href="#">c4dngB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized aldehyde dehydrogenase aldy; <b>PDBTitle:</b> crystal structure of putative aldehyde dehydrogenase from bacillus2 subtilis subsp. subtilis str. 168
86	<a href="#">c5j78B_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase (acetylating); <b>PDBTitle:</b> crystal structure of an acetylating aldehyde dehydrogenase from2 geobacillus thermoglucosidasius
87	<a href="#">c4c3sA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> structure of a propionaldehyde dehydrogenase from the clostridium2 phytofermentans fucose utilisation bacterial microcompartment
88	<a href="#">d1o20a_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
89	<a href="#">c3k9dD_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e
90	<a href="#">c4jbeA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gamma-glutamyl phosphate reductase; <b>PDBTitle:</b> 1.95 angstrom crystal structure of gamma-glutamyl phosphate reductase2 from saccharomonospora viridis.
91	<a href="#">c5jfnA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of rhodospseudomonas palustris propionaldehyde2 dehydrogenase with bound coa and acylated cys330
92	<a href="#">c4ghkB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyl phosphate reductase; <b>PDBTitle:</b> x-ray crystal structure of gamma-glutamyl phosphate reductase from2 burkholderia thailandensis
93	<a href="#">c3my7A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase/acetaldehyde dehydrogenase; <b>PDBTitle:</b> the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
94	<a href="#">c2h5gA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta-1-pyrroline-5-carboxylate synthetase; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate synthetase
95	<a href="#">d1vlua_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
96	<a href="#">c1vlvB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyl phosphate reductase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
97	<a href="#">c4g07A_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> the crystal structure of the c366s mutant of hdh from brucella suis
98	<a href="#">d1k75a_</a>	Alignment	not modelled	98.0	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> L-histidinol dehydrogenase HisD

99	<a href="#">c4gicB_</a>	 Alignment	not modelled	97.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
100	<a href="#">c6an0A_</a>	 Alignment	not modelled	97.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol dehydrogenase; <b>PDBTitle:</b> crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
101	<a href="#">c5vldC_</a>	 Alignment	not modelled	97.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> histidinol dehydrogenase, chloroplastic; <b>PDBTitle:</b> crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
102	<a href="#">c3v42A_</a>	 Alignment	not modelled	69.3	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> folliculin; <b>PDBTitle:</b> crystal structure of renal tumor suppressor protein, folliculin
103	<a href="#">d1s7ia_</a>	 Alignment	not modelled	43.4	8	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> Dimeric alpha+beta barrel <b>Family:</b> DGPF domain (Pfam 04946)
104	<a href="#">c3jtpB_</a>	 Alignment	not modelled	38.9	13	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> adapter protein meca 1; <b>PDBTitle:</b> crystal structure of the c-terminal domain of meca
105	<a href="#">c2yukA_</a>	 Alignment	not modelled	28.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> myeloid/lymphoid or mixed-lineage leukemia <b>PDBTitle:</b> solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
106	<a href="#">d1a9xa2</a>	 Alignment	not modelled	25.2	17	<b>Fold:</b> Methylglyoxal synthase-like <b>Superfamily:</b> Methylglyoxal synthase-like <b>Family:</b> Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
107	<a href="#">c1usdA_</a>	 Alignment	not modelled	24.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> vasodilator-stimulated phosphoprotein; <b>PDBTitle:</b> human vasp tetramerisation domain l352m
108	<a href="#">c2yvqA_</a>	 Alignment	not modelled	23.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> carbamoyl-phosphate synthase; <b>PDBTitle:</b> crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
109	<a href="#">c5e3eB_</a>	 Alignment	not modelled	22.6	18	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> large exoprotein involved in heme utilization or adhesion; <b>PDBTitle:</b> crystal structure of cdia-ct/cdiI complex from y. kristensenii 33638
110	<a href="#">c5vweA_</a>	 Alignment	not modelled	22.2	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> fact complex subunit ssrp1; <b>PDBTitle:</b> solution nmr structure of the hmg domain of human fact complex subunit2 ssrp1
111	<a href="#">c2crjA_</a>	 Alignment	not modelled	21.9	10	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> swi/snf-related matrix-associated actin- <b>PDBTitle:</b> solution structure of the hmg domain of mouse hmg domain2 protein hmgx2