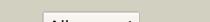
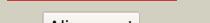
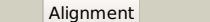
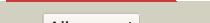
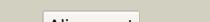
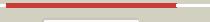


Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD3293_(pcd)_3673599_3675083
Date	Thu Aug 8 16:20:50 BST 2019
Unique Job ID	8dca28a2b04fa09d

Detailed template information

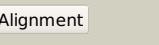
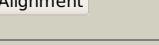
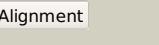
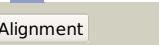
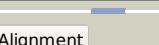
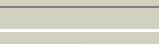
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2jg7G_			100.0	48	PDB header: oxidoreductase Chain: G; PDB Molecule: antiquitin; PDBTitle: crystal structure of seabream antiquitin and elucidation of its substrate specificity
2	c6fk3B_			100.0	35	PDB header: oxidoreductase 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)
3	c4f9iA_			100.0	27	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
4	c6dbbA_			100.0	61	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
5	c5ur2C_			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
6	d1a4sa_			100.0	29	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
7	c3ed6B_			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
8	c4pxnb_			100.0	46	PDB header: oxidoreductase Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: structure of zm aldh7 in complex with nad
9	c2d4eB_			100.0	30	PDB header: oxidoreductase Chain: B; PDB Molecule: 5-carboxymethyl-2-hydroxymuconate semialdehyde PDBTitle: crystal structure of the hpcc from thermus thermophilus hb8
10	c4o5hD_			100.0	32	PDB header: oxidoreductase Chain: D; PDB Molecule: phenylacetaldehyde dehydrogenase; PDBTitle: x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
11	c3u4jb_			100.0	33	PDB header: oxidoreductase Chain: B; PDB Molecule: nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from sinorhizobium meliloti

12	c1t90B_	Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: probable methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate semialdehyde dehydrogenase from2 bacillus subtilis
13	c4go4E_	Alignment		100.0	29	PDB header: oxidoreductase Chain: E: PDB Molecule: putative gamma-hydroxymuconic semialdehyde dehydrogenase; PDBTitle: crystal structure of pnpe in complex with nicotinamide adenine2 dinucleotide
14	c4zz7E_	Alignment		100.0	29	PDB header: oxidoreductase Chain: E: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of methylmalonate-semialdehyde dehydrogenase (dddc)2 from oceanimonas doudoroffii
15	c3ganB_	Alignment		100.0	27	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
16	c3iwkB_	Alignment		100.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: aminoaldehyde dehydrogenase; PDBTitle: crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
17	c4jz6A_	Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: salicylaldehyde dehydrogenase nahf; PDBTitle: crystal structure of a salicylaldehyde dehydrogenase from pseudomonas2 putida g7 complexed with salicylaldehyde
18	c5izdE_	Alignment		100.0	29	PDB header: oxidoreductase Chain: E: PDB Molecule: d-glyceraldehyde dehydrogenase (nadp(+)); PDBTitle: wild-type glyceraldehyde dehydrogenase from thermoplasma acidophilum2 in complex with nadp
19	d1bxsa_	Alignment		100.0	29	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
20	c4h73E_	Alignment		100.0	29	PDB header: oxidoreductase Chain: E: PDB Molecule: aldehyde dehydrogenase; PDBTitle: thermostable aldehyde dehydrogenase from pyrobaculum sp. complexed2 with nadp+
21	c5kf6B_	Alignment	not modelled	100.0	32	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
22	d1wnda_	Alignment	not modelled	100.0	31	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
23	d1o9ja_	Alignment	not modelled	100.0	29	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
24	c6mvta_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a bacterial aldh16 complexed with nadh
25	c2o2qA_	Alignment	not modelled	100.0	31	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
26	c4e4gF_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: F: PDB Molecule: methylmalonate-semialdehyde dehydrogenase; PDBTitle: crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
27	c3rh9A_	Alignment	not modelled	100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate-semialdehyde dehydrogenase (nad(p)(+)); PDBTitle: the crystal structure of oxidoreductase from marinobacter aquaeolei
28	c2ve5H_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: H: PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa

29	c4dalB_	Alignment	not modelled	100.0	28	PDB header: oxidoreductase Chain: B; PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of putative aldehyde dehydrogenase from2 sinorhizobium meliloti 1021
30	c3ek1C_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: C; PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
31	c5x5uB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B; PDB Molecule: alpha-ketoglutaric semialdehyde dehydrogenase; PDBTitle: crystal strcuture of alpha-ketoglutarate-semialdehyde dehydrogenase2 (kgsadh) complexed with nad
32	c5u0mB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B; PDB Molecule: n-succinylglutamate 5-semialdehyde dehydrogenase; PDBTitle: fatty aldehyde dehydrogenase from marinobacter aquaeolei vt8 and2 cofactor complex
33	d1uzba_	Alignment	not modelled	100.0	27	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
34	c4pt3C_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: C; PDB Molecule: aldehyde dehydrogenase; PDBTitle: nadph complex structure of aldehyde dehydrogenase from bacillus cereus
35	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
36	c3ifgH_	Alignment	not modelled	100.0	29	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
37	d1o04a_	Alignment	not modelled	100.0	28	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
38	c4pxIB_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: B; PDB Molecule: cytosolic aldehyde dehydrogenase rf2c; PDBTitle: structure of zm aldh2-3 (rf2c) in complex with nad
39	c4i25B_	Alignment	not modelled	100.0	28	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
40	c4yweE_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: E; PDB Molecule: putative aldehyde dehydrogenase; PDBTitle: crystal structure of a putative aldehyde dehydrogenase from2 burkholderia cenocepacia
41	d1ky8a_	Alignment	not modelled	100.0	28	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
42	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
43	d1ag8a_	Alignment	not modelled	100.0	28	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
44	c2w8qA_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A; PDB Molecule: succinate-semialdehyde dehydrogenase, PDBTitle: the crystal structure of human ssadh in complex with ssa.
45	c3b4wA_	Alignment	not modelled	100.0	29	PDB header: oxidoreductase Chain: A; PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
46	c3r31A_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: A; PDB Molecule: betaine aldehyde dehydrogenase; PDBTitle: crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
47	c3prlD_	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
48	c3jz4C_	Alignment	not modelled	100.0	32	PDB header: oxidoreductase Chain: C; PDB Molecule: succinate-semialdehyde dehydrogenase [nadp+]; PDBTitle: crystal structure of e. coli nadp dependent enzyme
49	d1euha_	Alignment	not modelled	100.0	26	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
50	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 vietnamensis
51	c4qyjD_	Alignment	not modelled	100.0	31	PDB header: oxidoreductase Chain: D; PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
52	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
						PDB header: oxidoreductase

53	c3ju8B	Alignment	not modelled	100.0	30	<p>Chain: B: PDB Molecule:succinylglutamic semialdehyde dehydrogenase; PDBTitle: crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.</p>
54	c4ohtB	Alignment	not modelled	100.0	24	<p>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</p>
55	c3haza	Alignment	not modelled	100.0	32	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:proline dehydrogenase; PDBTitle: crystal structure of bifunctional proline utilization a2 (puta) protein</p>
56	c3i44A	Alignment	not modelled	100.0	25	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution</p>
57	c4lihG	Alignment	not modelled	100.0	30	<p>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</p>
58	c2hg2A	Alignment	not modelled	100.0	31	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:aldehyde dehydrogenase a; PDBTitle: structure of lactaldehyde dehydrogenase</p>
59	c4idmA	Alignment	not modelled	100.0	24	<p>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</p>
60	c4itaA	Alignment	not modelled	100.0	31	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:succinate-semialdehyde dehydrogenase; PDBTitle: structure of bacterial enzyme in complex with cofactor</p>
61	c5mz5A	Alignment	not modelled	100.0	28	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:aldh21); PDBTitle: crystal structure of aldehyde dehydrogenase 21 (aldh21) from2 phycomitrella patens in its apoform</p>
62	c3rosA	Alignment	not modelled	100.0	26	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:nad-dependent aldehyde dehydrogenase; PDBTitle: crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus</p>
63	c3vz0B	Alignment	not modelled	100.0	28	<p>PDB header:oxidoreductase Chain: B: PDB Molecule:putative nad-dependent aldehyde dehydrogenase; PDBTitle: structural insights into cofactor and substrate selection by gox0499</p>
64	c4h7nA	Alignment	not modelled	100.0	25	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:aldehyde dehydrogenase; PDBTitle: the structure of putative aldehyde dehydrogenase puta from anaerobea2 variabilis.</p>
65	c4i3wC	Alignment	not modelled	100.0	30	<p>PDB header:oxidoreductase Chain: C: PDB Molecule:aldehyde dehydrogenase (nad+); PDBTitle: structure of phosphonoacetaldehyde dehydrogenase in complex with2 glyceraldehyde-3-phosphate and cofactor nad+</p>
66	c3pqaA	Alignment	not modelled	100.0	27	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:lactaldehyde dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661</p>
67	c3efvC	Alignment	not modelled	100.0	28	<p>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</p>
68	d1bi9a	Alignment	not modelled	100.0	29	<p>Fold:ALDH-like Superfamily:ALDH-like Family:ALDH-like</p>
69	c2vroB	Alignment	not modelled	100.0	22	<p>PDB header:oxidoreductase Chain: B: PDB Molecule:aldehyde dehydrogenase; PDBTitle: crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400</p>
70	c5tjrE	Alignment	not modelled	100.0	28	<p>PDB header:oxidoreductase Chain: E: PDB Molecule:methylmalonate-semialdehyde dehydrogenase; PDBTitle: x-ray crystal structure of a methylmalonate semialdehyde dehydrogenase2 from pseudomonas sp. aac</p>
71	c3r64A	Alignment	not modelled	100.0	29	<p>PDB header:oxidoreductase Chain: A: PDB Molecule:nad dependent benzaldehyde dehydrogenase; PDBTitle: crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum</p>
72	d1ad3a	Alignment	not modelled	100.0	20	<p>Fold:ALDH-like Superfamily:ALDH-like Family:ALDH-like</p>
73	c4qgkB	Alignment	not modelled	100.0	20	<p>PDB header:oxidoreductase Chain: B: PDB Molecule:fatty aldehyde dehydrogenase; PDBTitle: structure of the human sjogren larsson syndrome enzyme fatty aldehyde2 dehydrogenase (faldh)</p>
74	c5ux5C	Alignment	not modelled	100.0	24	<p>PDB header:oxidoreductase/transferase Chain: C: PDB Molecule:bifunctional protein proline utilization a (puta); PDBTitle: structure of proline utilization a (puta) from corynebacterium2 freiburgense</p>
75	c5fhzF	Alignment	not modelled	100.0	30	<p>PDB header:oxidoreductase Chain: F: PDB Molecule:aldehyde dehydrogenase family 1 member a3; PDBTitle: human aldehyde dehydrogenase 1a3 complexed with nad(+) and retinoic2 acid</p>
						<p>Fold:ALDH-like</p>

76	d1ez0a	Alignment	not modelled	100.0	21	Superfamily: ALDH-like Family: ALDH-like
77	c5nnoA	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of tbaldh3 complexed with nad and an3057 aldehyde
78	c4oe4A	Alignment	not modelled	100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: delta-1-pyrroline-5-carboxylate dehydrogenase, PDBTitle: crystal structure of yeast aldh4a1 complexed with nad+
79	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
80	c5iuuA	Alignment	not modelled	100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase family protein; PDBTitle: crystal structure of indole-3-acetaldehyde dehydrogenase in apo form
81	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
82	c4dngB	Alignment	not modelled	100.0	30	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
83	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
84	c3v9iD	Alignment	not modelled	100.0	24	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
85	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
86	c5j78B	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acetylating); PDBTitle: crystal structure of an acetylating aldehyde dehydrogenase from2 geobacillus thermoglucosidarius
87	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
88	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
89	c5jfna	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: crystal structure of rhodopseudomonas palustris propionaldehyde2 dehydrogenase with bound coa and acylated cys330
90	d1o20a	Alignment	not modelled	100.0	20	Fold: ALDH-like Superfamily: ALDH-like Family: ALDH-like
91	c4jbeA	Alignment	not modelled	100.0	20	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	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
93	c4ghkB	Alignment	not modelled	100.0	19	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	18	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	18	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	98.4	19	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD
98	c4gicB	Alignment	not modelled	97.7	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
99	c6an0A	Alignment	not modelled	97.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
						PDB header: oxidoreductase

100	c4g07A		Alignment	not modelled	97.5	20	Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
101	c5vldC		Alignment	not modelled	96.8	17	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	d1s7ia		Alignment	not modelled	46.2	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
103	c2yvgA		Alignment	not modelled	41.8	15	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
104	d1a9xa2		Alignment	not modelled	32.3	7	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
105	c2ec4A		Alignment	not modelled	31.5	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: fas-associated factor 1; PDBTitle: solution structure of the uas domain from human fas-2 associated factor 1
106	c5n9mA		Alignment	not modelled	29.4	13	PDB header: transferase Chain: A: PDB Molecule: cobyric acid synthase; PDBTitle: crystal structure of gatd - a glutamine amidotransferase from staphylococcus aureus involved in peptidoglycan amidation
107	c3jtpB		Alignment	not modelled	22.8	20	PDB header: protein binding Chain: B: PDB Molecule: adapter protein meca 1; PDBTitle: crystal structure of the c-terminal domain of meca
108	c4ksaD		Alignment	not modelled	22.2	21	PDB header: lyase Chain: D: PDB Molecule: malonyl-coa decarboxylase; PDBTitle: crystal structure of malonyl-coa decarboxylase from rhodopseudomonas2 palustris, northeast structural genomics consortium target rpr127
109	c1u57A		Alignment	not modelled	21.5	36	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: nmr structure of the (345-392)gag sequence from hiv-1