Phyre2

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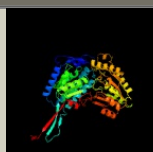
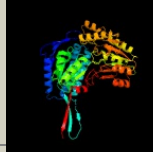
Description	RVBD0458_(-)_549678_551201
Date	Tue Jul 23 14:50:53 BST 2019
Unique Job ID	e3ba81bf015d2a08

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ed6B_	Alignment		100.0	35	**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
2	c2d4eB_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**5-carboxymethyl-2-hydroxymuconate semialdehyde **PDBTitle:** crystal structure of the hpcc from thermus thermophilus hb8
3	d1a4sa_	Alignment		100.0	36	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
4	c3u4jB_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 sinorhizobium meliloti
5	c6fk3B_	Alignment		100.0	32	**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)
6	c4go4E_	Alignment		100.0	39	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative gamma-hydroxymuconic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of pnpe in complex with nicotinamide adenine2 dinucleotide
7	c2ve5H_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** H: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
8	c4o5hD_	Alignment		100.0	42	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**phenylacetaldehyde dehydrogenase; **PDBTitle:** x-ray crystal structure of a putative phenylacetaldehyde dehydrogenase2 from burkholderia cenocepacia
9	d1bxsa_	Alignment		100.0	40	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
10	c4pt3C_	Alignment		100.0	43	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** nadph complex structure of aldehyde dehydrogenase from bacillus cereus
11	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

12	d1o9ja_	Alignment		100.0	39	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
13	c3iwkB_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aminoaldehyde dehydrogenase; **PDBTitle:** crystal structure of aminoaldehyde dehydrogenase 1 from pisum sativum2 (psamadh1)
14	c5izdE_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**d-glyceraldehyde dehydrogenase (nadp(+)); **PDBTitle:** wild-type glyceraldehyde dehydrogenase from thermoplasma acidophilum2 in complex with nadp
15	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
16	c5ur2C_	Alignment		100.0	27	**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
17	d1wnda_	Alignment		100.0	37	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
18	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
19	c4dalB_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative aldehyde dehydrogenase; **PDBTitle:** crystal structure of putative aldehyde dehydrogenase from2 sinorhizobium meliloti 1021
20	c6mvtA_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** structure of a bacterial aldh16 complexed with nadh
21	c4pxlB_	Alignment	not modelled	100.0	40	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**cytosolic aldehyde dehydrogenase rf2c; **PDBTitle:** structure of zm aldh2-3 (rf2c) in complex with nad
22	c3r31A_	Alignment	not modelled	100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**betaine aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
23	d1o04a_	Alignment	not modelled	100.0	43	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
24	c4i25B_	Alignment	not modelled	100.0	38	**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
25	c3k2wD_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**betaine-aldehyde dehydrogenase; **PDBTitle:** crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
26	d1ag8a_	Alignment	not modelled	100.0	43	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
27	c3rh9A_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase (nad(p)(+)); **PDBTitle:** the crystal structure of oxidoreductase from marinobacter aquaeolei
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**1-pyrroline-5-carboxylate dehydrogenase

28	c3qanB_	Alignment	not modelled	100.0	31	1; **PDBTitle:** crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
29	c3i44A_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
30	d1uzba_	Alignment	not modelled	100.0	30	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
31	c3ek1C_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
32	c3b4wA_	Alignment	not modelled	100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
33	c1t90B_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable methylmalonate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of methylmalonate semialdehyde dehydrogenase from2 bacillus subtilis
34	c4jz6A_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**salicylaldehyde dehydrogenase nahf; **PDBTitle:** crystal structure of a salicylaldehyde dehydrogenase from pseudomonas2 putida g7 complexed with salicylaldehyde
35	c4zz7E_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**methylmalonate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of methylmalonate-semialdehyde dehydrogenase (dddc)2 from oceanimonas doudoroffii
36	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
37	c5x5uB_	Alignment	not modelled	100.0	32	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alpha-ketoglutaric semialdehyde dehydrogenase; **PDBTitle:** crystal strcuture of alpha-ketoglutarate-semialdehyde dehydrogenase2 (kgsadh) complexed with nad
38	c4pxnB_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of zm aldh7 in complex with nad
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	c4h73E_	Alignment	not modelled	100.0	30	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** thermostable aldehyde dehydrogenase from pyrobaculum sp. complexed2 with nadp+
41	c4qyjD_	Alignment	not modelled	100.0	37	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** structure of phenylacetaldehyde dehydrogenase from pseudomonas putida2 s12
42	c3jz4C_	Alignment	not modelled	100.0	34	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**succinate-semialdehyde dehydrogenase [nadp+]; **PDBTitle:** crystal structure of e. coli nadp dependent enzyme
43	c6dbbA_	Alignment	not modelled	100.0	22	**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
44	c4e4gF_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**methylmalonate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of putative methylmalonate-semialdehyde2 dehydrogenase from sinorhizobium meliloti 1021
45	d1ky8a_	Alignment	not modelled	100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
46	d1euha_	Alignment	not modelled	100.0	28	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
47	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
48	c4lihG_	Alignment	not modelled	100.0	41	**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
49	c4knaA_	Alignment	not modelled	100.0	28	**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
50	c2w8qA_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase, **PDBTitle:** the crystal structure of human ssadh in complex with ssa.
						PDB header:oxidoreductase **Chain:** B: **PDB Molecule:**bifunctional protein puta;

51	c5kf6B_	Alignment	not modelled	100.0	27	**PDBTitle:** structure of proline utilization a from sinorhizobium meliloti2 complexed with l-tetrahydrofuroic acid and nad+ in space group p21
52	c4idmA_	Alignment	not modelled	100.0	23	**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
53	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 covelent complex with nadph
54	c5u0mB_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**n-succinylglutamate 5-semialdehyde dehydrogenase; **PDBTitle:** fatty aldehyde dehydrogenase from marinobacter aquaeolei vt8 and2 cofactor complex
55	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
56	c2hg2A_	Alignment	not modelled	100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase a; **PDBTitle:** structure of lactaldehyde dehydrogenase
57	d1bi9a_	Alignment	not modelled	100.0	41	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
58	c4i3wC_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**aldehyde dehydrogenase (nad+); **PDBTitle:** structure of phosphonoacetaldehyde dehydrogenase in complex with2 gylceraldehyde-3-phosphate and cofactor nad+
59	c3ju8B_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**succinylglutamic semialdehyde dehydrogenase; **PDBTitle:** crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
60	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
61	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
62	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
63	c4itaA_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**succinate-semialdehyde dehydrogenase; **PDBTitle:** structure of bacterial enzyme in complex with cofactor
64	c3hazA_	Alignment	not modelled	100.0	27	**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	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
66	c3vz0B_	Alignment	not modelled	100.0	28	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nad-dependent aldehyde dehydrogenase; **PDBTitle:** structural insights into cofactor and substrate selection by gox0499
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	40	**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	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
70	c3r64A_	Alignment	not modelled	100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad dependent benzaldehyde dehydrogenase; **PDBTitle:** crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
71	c4h7nA_	Alignment	not modelled	100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** the structure of putative aldehyde dehydrogenase puta from anabaena2 variabilis.
72	c5iuuA_	Alignment	not modelled	100.0	40	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase family protein; **PDBTitle:** crystal structure of indole-3-acetaldehyde dehydrogenase in apo form
73	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
74	c6d97B_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldehyde dehydrogenase 12;

74	c6d97B_	Alignment	not modelled	100.0	18	**PDBTitle:** structure of aldehyde dehydrogenase 12 (aldh12) from zea mays
75	d1ad3a_	Alignment	not modelled	100.0	24	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
76	c4oe4A_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**delta-1-pyrroline-5-carboxylate dehydrogenase, **PDBTitle:** crystal structure of yeast aldh4a1 complexed with nad+
77	c4qgkB_	Alignment	not modelled	100.0	23	**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	26	**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	c5nnoA_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** structure of tbaldh3 complexed with nad and an3057 aldehyde
80	c5ux5C_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase/transferase **Chain:** C: **PDB Molecule:**bifunctional protein proline utilization a (puta); **PDBTitle:** structure of proline utilization a (puta) from corynebacterium2 freiburgense
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	c3v9iD_	Alignment	not modelled	100.0	23	**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
83	d1ez0a_	Alignment	not modelled	100.0	20	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
84	c5ujuA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad-dependent aldehyde dehydrogenase; **PDBTitle:** crystal structure of nad-dependent aldehyde dehydrogenase from2 burkholderia multivorans
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	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**acetaldehyde dehydrogenase (acetylating); **PDBTitle:** crystal structure of an acetylating aldehyde dehydrogenase from2 geobacillus thermoglucosidasius
87	c4c3sA_	Alignment	not modelled	100.0	18	**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	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	16	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
90	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.
91	c5jfnA_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aldehyde dehydrogenase; **PDBTitle:** crystal structure of rhodopseudomonas palustris propionaldehyde2 dehydrogenase with bound coa and acylated cys330
92	c3my7A_	Alignment	not modelled	100.0	16	**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	22	**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	19	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**ALDH-like
96	c1vluB_	Alignment	not modelled	100.0	18	**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	18	**Fold:**ALDH-like **Superfamily:**ALDH-like **Family:**L-histidinol dehydrogenase HisD
						PDB header:oxidoreductase

98	c5vldC_	Alignment	not modelled	98.4	15	**Chain:** C: **PDB Molecule:**histidinol dehydrogenase, chloroplastic; **PDBTitle:** crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
99	c6an0A_	Alignment	not modelled	98.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histidinol dehydrogenase; **PDBTitle:** crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis
100	c4g07A_	Alignment	not modelled	98.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**histidinol dehydrogenase; **PDBTitle:** the crystal structure of the c366s mutant of hdh from brucella suis
101	c4gicB_	Alignment	not modelled	97.9	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
102	c3v42A_	Alignment	not modelled	62.3	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**folliculin; **PDBTitle:** crystal structure of renal tumor suppressor protein, folliculin
103	d1s7ia_	Alignment	not modelled	56.4	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
104	c3jtpB_	Alignment	not modelled	29.3	24	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**adapter protein meca 1; **PDBTitle:** crystal structure of the c-terminal domain of meca
105	c2yukA_	Alignment	not modelled	29.0	26	**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
106	d1k99a_	Alignment	not modelled	26.6	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
107	c2crjA_	Alignment	not modelled	26.2	18	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
108	c2l69A_	Alignment	not modelled	25.1	15	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
109	c2eqzA_	Alignment	not modelled	24.2	8	**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
110	d1j3xa_	Alignment	not modelled	23.4	8	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
111	c1j3xA_	Alignment	not modelled	23.4	8	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**high mobility group protein 2; **PDBTitle:** solution structure of the n-terminal domain of the hmgb2
112	c3fghA_	Alignment	not modelled	22.9	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
113	c3oqbF_	Alignment	not modelled	22.3	11	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
114	d1h6da1	Alignment	not modelled	21.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
115	c1k98A_	Alignment	not modelled	21.6	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methionine synthase; **PDBTitle:** adomet complex of meth c-terminal fragment
116	c2ec4A_	Alignment	not modelled	20.6	10	**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