

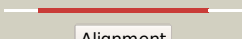













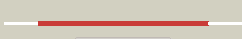






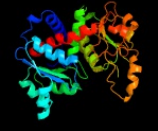









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1656_(argF_1869929_1870852
Date	Fri Aug 2 13:30:25 BST 2019
Unique Job ID	0b0c2ed8eeaed729

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2p2gD_	 Alignment		100.0	99	PDB header: transferase Chain: D; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
2	c4amuB_	 Alignment		100.0	33	PDB header: transferase Chain: B; PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group
3	c1fvoB_	 Alignment		100.0	41	PDB header: transferase Chain: B; PDB Molecule: ornithine transcarbamylase; PDBTitle: crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
4	c2otcA_	 Alignment		100.0	39	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
5	c2w37A_	 Alignment		100.0	37	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase, catabolic; PDBTitle: crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
6	c1a1sA_	 Alignment		100.0	49	PDB header: transcarbamylase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: ornithine carbamoyltransferase from pyrococcus furiosus
7	c3updA_	 Alignment		100.0	38	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
8	c1ortD_	 Alignment		100.0	38	PDB header: transferase Chain: D; PDB Molecule: ornithine transcarbamoylase; PDBTitle: ornithine transcarbamoylase from pseudomonas aeruginosa
9	c3txxD_	 Alignment		100.0	35	PDB header: transferase Chain: D; PDB Molecule: putrescine carbamoyltransferase; PDBTitle: crystal structure of putrescine transcarbamylase from enterococcus2 faecalis
10	c1v1vA_	 Alignment		100.0	40	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
11	c4oh7B_	 Alignment		100.0	48	PDB header: transferase Chain: B; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from brucella2 melitensis

12	c3tpfF	Alignment		100.0	38	PDB header: transferase Chain: F; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
13	c3grfA	Alignment		100.0	37	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
14	c1ml4A	Alignment		100.0	27	PDB header: transferase Chain: A; PDB Molecule: aspartate transcarbamoylase; PDBTitle: the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
15	c1zq2A	Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
16	c3gd5D	Alignment		100.0	52	PDB header: transferase Chain: D; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
17	c2ef0A	Alignment		100.0	44	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
18	c1pg5A	Alignment		100.0	24	PDB header: transferase Chain: A; PDB Molecule: aspartate carbamoyltransferase; PDBTitle: crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfobolus3 acidocaldarius
19	c5g1oF	Alignment		100.0	29	PDB header: transferase Chain: F; PDB Molecule: cad protein; PDBTitle: aspartate transcarbamoylase domain of human cad in apo form
20	c3sdsA	Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase, mitochondrial; PDBTitle: crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
21	c2rgwD	Alignment	not modelled	100.0	26	PDB header: transferase Chain: D; PDB Molecule: aspartate carbamoyltransferase; PDBTitle: catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
22	c4ep1B	Alignment	not modelled	100.0	44	PDB header: transferase Chain: B; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of anabolic ornithine carbamoyltransferase from2 bacillus anthracis
23	c4f2gA	Alignment	not modelled	100.0	44	PDB header: transferase Chain: A; PDB Molecule: ornithine carbamoyltransferase 1; PDBTitle: the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
24	c5nnqA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: ctatc; PDBTitle: aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
25	c1js1Z	Alignment	not modelled	100.0	28	PDB header: transferase Chain: Z; PDB Molecule: transcarbamylase; PDBTitle: crystal structure of a new transcarbamylase from the anaerobic2 bacterium bacteroides fragilis at 2.0 a resolution
26	d1tuga1	Alignment	not modelled	100.0	33	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
27	c5ilqA	Alignment	not modelled	100.0	26	PDB header: transferase Chain: A; PDB Molecule: aspartate carbamoyltransferase; PDBTitle: crystal structure of truncated unliganded aspartate transcarbamoylase2 from plasmodium falciparum
28	c2at2B	Alignment	not modelled	100.0	27	PDB header: transferase Chain: B; PDB Molecule: aspartate carbamoyltransferase; PDBTitle: molecular structure of bacillus subtilis aspartate2 transcarbamoylase at 3.0 angstroms resolution
29	c2vfkA	Alignment	not modelled	100.0	24	PDB header: transferase Chain: A; PDB Molecule: aspartate/ornithine carbamoyltransferase;

29	c4y18A	Alignment	not modelled	100.0	24	PDBTitle: crystal structure of a putative transcarbamoylase from2 enterococcus faecalis PDB header: hydrolase/transferase
30	c3d6nB	Alignment	not modelled	100.0	26	Chain: B; PDB Molecule: aspartate carbamoyltransferase; PDBTitle: crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
31	c4iv5E	Alignment	not modelled	100.0	28	PDB header: transferase Chain: E; PDB Molecule: aspartate carbamoyltransferase, putative; PDBTitle: x-ray crystal structure of a putative aspartate carbamoyltransferase2 from trypanosoma cruzi
32	c3q98A	Alignment	not modelled	100.0	25	PDB header: transferase Chain: A; PDB Molecule: transcarbamylase; PDBTitle: structure of ygew encoded protein from e. coli
33	c3lxmC	Alignment	not modelled	100.0	36	PDB header: transferase Chain: C; PDB Molecule: aspartate carbamoyltransferase; PDBTitle: 2.00 angstrom resolution crystal structure of a catalytic subunit of2 an aspartate carbamoyltransferase (pyrb) from yersinia pestis co92
34	d1otha1	Alignment	not modelled	100.0	42	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
35	d1dxha2	Alignment	not modelled	100.0	37	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
36	d1duvg2	Alignment	not modelled	100.0	36	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
37	d1otha2	Alignment	not modelled	100.0	41	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
38	d1pvva2	Alignment	not modelled	100.0	49	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
39	d1pvva1	Alignment	not modelled	100.0	48	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
40	d1vlva1	Alignment	not modelled	100.0	43	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
41	d1duvg1	Alignment	not modelled	100.0	42	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
42	d1ml4a1	Alignment	not modelled	100.0	34	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
43	d1dxha1	Alignment	not modelled	100.0	39	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
44	d1pg5a1	Alignment	not modelled	100.0	30	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
45	d2at2a1	Alignment	not modelled	100.0	35	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
46	d1vlva2	Alignment	not modelled	100.0	38	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
47	d1js1x1	Alignment	not modelled	100.0	28	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
48	d1ekxa1	Alignment	not modelled	100.0	37	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
49	d1ml4a2	Alignment	not modelled	100.0	21	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
50	d1ekxa2	Alignment	not modelled	100.0	24	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
51	d1pg5a2	Alignment	not modelled	100.0	18	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
52	d2at2a2	Alignment	not modelled	100.0	19	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
53	d1js1x2	Alignment	not modelled	100.0	25	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
54	d2atca2	Alignment	not modelled	100.0	23	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
55	c3oneA	Alignment	not modelled	98.3	20	PDB header: hydrolase/hydrolase substrate Chain: A; PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
56	c5v96A	Alignment	not modelled	98.3	19	PDB header: hydrolase Chain: A; PDB Molecule: s-adenosyl-l-homocysteine hydrolase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase

						from2 naegleria fowleri with bound nad and adenosine
57	c3d4oA_	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
58	c1xdwA_	Alignment	not modelled	98.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nad+-dependent (r)-2-hydroxyglutarate PDBTitle: nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
59	c3n58D_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: D: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
60	c3gvpB_	Alignment	not modelled	98.1	19	PDB header: hydrolase Chain: B: PDB Molecule: adenosylhomocysteinase 3; PDBTitle: human sahh-like domain of human adenosylhomocysteinase 3
61	c1d4fD_	Alignment	not modelled	98.0	22	PDB header: hydrolase Chain: D: PDB Molecule: s-adenosylhomocysteine hydrolase; PDBTitle: crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
62	c3dhyC_	Alignment	not modelled	97.9	23	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
63	c5hm8C_	Alignment	not modelled	97.8	21	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
64	c2rirA_	Alignment	not modelled	97.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
65	c3fn4A_	Alignment	not modelled	97.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
66	c2dbqA_	Alignment	not modelled	97.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
67	c3oetF_	Alignment	not modelled	97.7	22	PDB header: oxidoreductase Chain: F: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: d-erythronate-4-phosphate dehydrogenase complexed with nad
68	c3l07B_	Alignment	not modelled	97.7	18	PDB header: oxidoreductase,hydrolase Chain: B: PDB Molecule: bifunctional protein fold; PDBTitle: methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
69	c3x2fA_	Alignment	not modelled	97.7	20	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: a thermophilic s-adenosylhomocysteine hydrolase
70	c3wwyA_	Alignment	not modelled	97.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: the crystal structure of d-lactate dehydrogenase from fusobacterium2 nucleatum subsp. nucleatum
71	c6aphA_	Alignment	not modelled	97.7	21	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
72	c3n7uD_	Alignment	not modelled	97.7	20	PDB header: oxidoreductase Chain: D: PDB Molecule: formate dehydrogenase; PDBTitle: nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
73	c3k5pA_	Alignment	not modelled	97.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
74	c6f3oC_	Alignment	not modelled	97.6	22	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
75	c4g2nA_	Alignment	not modelled	97.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; PDBTitle: crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
76	c5j23D_	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-hydroxyacid dehydrogenase; PDBTitle: crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium melloti in complex3 with 2'-phospho- adp-ribose
77	c2o4cB_	Alignment	not modelled	97.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
78	c4a26B_	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
79	c3kboB_	Alignment	not modelled	97.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate/hydroxypyruvate reductase a; PDBTitle: 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex

						with nadp
80	c1ybaC	Alignment	not modelled	97.6	20	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
81	c4cukA	Alignment	not modelled	97.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: structure of salmonella d-lactate dehydrogenase in complex2 with nadh
82	c2j6iC	Alignment	not modelled	97.6	19	PDB header: oxidoreductase Chain: C: PDB Molecule: formate dehydrogenase; PDBTitle: candida boidinii formate dehydrogenase (fdh) c-terminal mutant
83	c3wnvA	Alignment	not modelled	97.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glyoxylate reductase; PDBTitle: crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
84	c3gg9C	Alignment	not modelled	97.6	24	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
85	c5dt9A	Alignment	not modelled	97.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: erythronate-4-phosphate dehydrogenase; PDBTitle: crystal structure of a putative d-erythronate-4-phosphate2 dehydrogenase from vibrio cholerae
86	c4lswA	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase protein; PDBTitle: crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonigenium vulgare y25
87	d1mx3a1	Alignment	not modelled	97.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
88	c2gcaB	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glyoxylate reductase/hydroxypyruvate reductase; PDBTitle: ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
89	c1v8bA	Alignment	not modelled	97.5	21	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of a hydrolase
90	c2nacA	Alignment	not modelled	97.5	17	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
91	c3wwzB	Alignment	not modelled	97.5	20	PDB header: oxidoreductase Chain: B: PDB Molecule: d-lactate dehydrogenase (fermentative); PDBTitle: the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
92	c3bazA	Alignment	not modelled	97.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyphenylpyruvate reductase; PDBTitle: structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
93	c4zqbB	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nadp-dependent dehydrogenase; PDBTitle: crystal structure of nadp-dependent dehydrogenase from2 rhodobactersphaeroides in complex with nadp and sulfate
94	c2omeA	Alignment	not modelled	97.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
95	c6ih2B	Alignment	not modelled	97.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphite dehydrogenase; PDBTitle: crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
96	c1gdhA	Alignment	not modelled	97.5	16	PDB header: oxidoreductase(choh (d)-nad(p)+ (a)) Chain: A: PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
97	c1ygyA	Alignment	not modelled	97.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
98	c1j4aA	Alignment	not modelled	97.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
99	c4e5kC	Alignment	not modelled	97.4	15	PDB header: oxidoreductase Chain: C: PDB Molecule: phosphite dehydrogenase (thermostable variant); PDBTitle: thermostable phosphite dehydrogenase in complex with nad and sulfite
100	c1qp8A	Alignment	not modelled	97.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: formate dehydrogenase; PDBTitle: crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
101	c2cukC	Alignment	not modelled	97.4	22	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerate dehydrogenase/glyoxylate reductase; PDBTitle: crystal structure of tt0316 protein from thermus thermophilus hb8
102	d2naca1	Alignment	not modelled	97.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
103	c2g76A	Alignment	not modelled	97.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of human 3-phosphoglycerate dehydrogenase
104	c4dgsA	Alignment	not modelled	97.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase; PDBTitle: the crystals structure of dehydrogenase from rhizobium

						melliloti
105	d1gdha1	Alignment	not modelled	97.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
106	d1gpja2	Alignment	not modelled	97.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
107	c2pi1C_	Alignment	not modelled	97.3	16	PDB header: oxidoreductase Chain: C: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
108	c5mh5A_	Alignment	not modelled	97.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: d-2-hydroxyacid dehydrogenase; PDBTitle: d-2-hydroxyacid dehydrogenases (d2-hdh) from haloferax mediterranei in2 complex with 2-keto-hexanoic acid and nadp+ (1.4 a resolution)
109	c3gvxA_	Alignment	not modelled	97.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerate dehydrogenase related protein; PDBTitle: crystal structure of glycerate dehydrogenase related2 protein from thermoplasma acidophilum
110	d1qp8a1	Alignment	not modelled	97.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
111	c2w2kB_	Alignment	not modelled	97.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: d-mandelate dehydrogenase; PDBTitle: crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
112	c3evtA_	Alignment	not modelled	97.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoglycerate dehydrogenase; PDBTitle: crystal structure of phosphoglycerate dehydrogenase from lactobacillus2 plantarum
113	d1li4a1	Alignment	not modelled	97.3	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
114	c5tx7A_	Alignment	not modelled	97.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-isomer specific 2-hydroxyacid dehydrogenase family PDBTitle: crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
115	d1sc6a1	Alignment	not modelled	97.2	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
116	c4njmA_	Alignment	not modelled	97.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase, putative; PDBTitle: crystal structure of phosphoglycerate bound 3-phosphoglycerate2 dehydrogenase in entamoeba histolytica
117	c1b0aA_	Alignment	not modelled	97.2	18	PDB header: oxidoreductase,hydrolase Chain: A: PDB Molecule: protein (fold bifunctional protein); PDBTitle: 5,10, methylene-tetrahydropholate2 dehydrogenase/cyclohydrolase from e coli.
118	c2ek1A_	Alignment	not modelled	97.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: structure of st1218 protein from sulfolobus tokodaii
119	c3d64A_	Alignment	not modelled	97.2	25	PDB header: hydrolase Chain: A: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
120	d2dlda1	Alignment	not modelled	97.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain