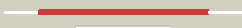























# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1380_(pyrB)_1553238_1554197
Date	Wed Jul 31 22:05:48 BST 2019
Unique Job ID	c1198067b20e54f4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4amuB</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ornithine carbamoyltransferase, catabolic; <b>PDBTitle:</b> structure of ornithine carbamoyltransferase from mycoplasma2 penetrans with a p321 space group
2	<a href="#">c1ml4A</a>	 Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> aspartate transcarbamoylase; <b>PDBTitle:</b> the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
3	<a href="#">c2w37A</a>	 Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ornithine carbamoyltransferase, catabolic; <b>PDBTitle:</b> crystal structure of the hexameric catabolic ornithine2 transcarbamylase from lactobacillus hilgardii
4	<a href="#">c5nngA</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ctatc; <b>PDBTitle:</b> aspartate transcarbamoylase from chaetomium thermophilum cad-like2 bound to carbamoyl phosphate
5	<a href="#">c3updA</a>	 Alignment		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> 2.9 angstrom crystal structure of ornithine carbamoyltransferase2 (argf) from vibrio vulnificus
6	<a href="#">c2otcA</a>	 Alignment		100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
7	<a href="#">c1a1sA</a>	 Alignment		100.0	30	<b>PDB header:</b> transcarbamylase <b>Chain:</b> A; <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> ornithine carbamoyltransferase from pyrococcus furiosus
8	<a href="#">c1ortD</a>	 Alignment		100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> D; <b>PDB Molecule:</b> ornithine transcarbamoylase; <b>PDBTitle:</b> ornithine transcarbamoylase from pseudomonas aeruginosa
9	<a href="#">c5g1oF</a>	 Alignment		100.0	37	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> cad protein; <b>PDBTitle:</b> aspartate transcarbamoylase domain of human cad in apo form
10	<a href="#">d1tuga1</a>	 Alignment		100.0	32	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
11	<a href="#">c1fvoB</a>	 Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> ornithine transcarbamylase; <b>PDBTitle:</b> crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate

12	<a href="#">c1v1vA_</a>	Alignment		100.0	29	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase (tm1097) from2 thermotoga maritima at 2.25 a resolution
13	<a href="#">c4oh7B_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
14	<a href="#">c1pg5A_</a>	Alignment		100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> crystal structure of the unligated (t-state) aspartate2 transcarbamoylase from the extremely thermophilic archaeon sulfolobus3 acidocaldarius
15	<a href="#">c3txxD_</a>	Alignment		100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putrescine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of putrescine transcarbamylase from enterococcus2 faecalis
16	<a href="#">c3d6nB_</a>	Alignment		100.0	35	<b>PDB header:</b> hydrolase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> crystal structure of aquifex dihydroorotase activated by aspartate2 transcarbamoylase
17	<a href="#">c2rgwD_</a>	Alignment		100.0	34	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
18	<a href="#">c2p2gD_</a>	Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
19	<a href="#">c2ef0A_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
20	<a href="#">c3grfA_</a>	Alignment		100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> x-ray structure of ornithine transcarbamoylase from giardia2 lamblia
21	<a href="#">c3sdsA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase, mitochondrial; <b>PDBTitle:</b> crystal structure of a mitochondrial ornithine carbamoyltransferase2 from coccidioides immitis
22	<a href="#">c2at2B_</a>	Alignment	not modelled	100.0	38	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> molecular structure of bacillus subtilis aspartate2 transcarbamoylase at 3.0 angstroms resolution
23	<a href="#">c1js1Z_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> Z: <b>PDB Molecule:</b> transcarbamylase; <b>PDBTitle:</b> crystal structure of a new transcarbamylase from the anaerobic2 bacterium bacteroides fragilis at 2.0 a resolution
24	<a href="#">c4f2gA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase 1; <b>PDBTitle:</b> the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
25	<a href="#">c1zq2A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of n-acetyl-l-ornithine transcarbamylase2 complexed with cp
26	<a href="#">c5ilqA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> crystal structure of truncated unliganded aspartate transcarbamoylase2 from plasmodium falciparum
27	<a href="#">c3tpfF_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
28	<a href="#">c3gd5D_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase;

28	<a href="#">c3g03D</a>	Alignment	not modelled	100.0	31	<b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus <b>PDB header:</b> transferase
29	<a href="#">c4ep1B</a>	Alignment	not modelled	100.0	26	<b>Chain:</b> B; <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of anabolic ornithine carbamoyltransferase from2 bacillus anthracis <b>PDB header:</b> transferase
30	<a href="#">c4iv5E</a>	Alignment	not modelled	100.0	33	<b>Chain:</b> E; <b>PDB Molecule:</b> aspartate carbamoyltransferase, putative; <b>PDBTitle:</b> x-ray crystal structure of a putative aspartate carbamoyltransferase2 from trypanosoma cruzi <b>PDB header:</b> transferase
31	<a href="#">c2yfkA</a>	Alignment	not modelled	100.0	24	<b>Chain:</b> A; <b>PDB Molecule:</b> aspartate/ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of a putative transcarbamoylase from2 enterococcus faecalis <b>PDB header:</b> transferase
32	<a href="#">c3lxmC</a>	Alignment	not modelled	100.0	33	<b>Chain:</b> C; <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a catalytic subunit of2 an aspartate carbamoyltransferase (pyrb) from yersinia pestis co92 <b>PDB header:</b> transferase
33	<a href="#">c3q98A</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> A; <b>PDB Molecule:</b> transcarbamylase; <b>PDBTitle:</b> structure of ygew encoded protein from e. coli <b>PDB header:</b> transferase
34	<a href="#">d1ml4a1</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
35	<a href="#">d1otha1</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
36	<a href="#">d1vlva1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
37	<a href="#">d1duvg1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
38	<a href="#">d1pvva1</a>	Alignment	not modelled	100.0	33	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
39	<a href="#">d1dxha1</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
40	<a href="#">d1ekxa1</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
41	<a href="#">d2at2a1</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
42	<a href="#">d1pg5a1</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
43	<a href="#">d1dxha2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
44	<a href="#">d1duvg2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
45	<a href="#">d1pvva2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
46	<a href="#">d1ml4a2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
47	<a href="#">d1otha2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
48	<a href="#">d1js1x1</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
49	<a href="#">d1ekxa2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
50	<a href="#">d1pg5a2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
51	<a href="#">d1vlva2</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
52	<a href="#">d2at2a2</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
53	<a href="#">d1js1x2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
54	<a href="#">d2atca2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
55	<a href="#">c1d4fD</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> s-adenosylhomocysteine hydrolase; <b>PDBTitle:</b> crystal structure of recombinant rat-liver d244e mutant s-

						2 adenosylhomocysteine hydrolase
56	<a href="#">c3gvpB_</a>	Alignment	not modelled	98.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> adenosylhomocysteinase 3; <b>PDBTitle:</b> human sahh-like domain of human adenosylhomocysteinase 3
57	<a href="#">c3n58D_</a>	Alignment	not modelled	98.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
58	<a href="#">c5v96A_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> s-adenosyl-l-homocysteine hydrolase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 naegleria fowleri with bound nad and adenosine
59	<a href="#">c3oneA_</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> hydrolase/hydrolase substrate <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
60	<a href="#">c3d4oA_</a>	Alignment	not modelled	98.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
61	<a href="#">c2gcgB_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate reductase/hydroxypyruvate reductase; <b>PDBTitle:</b> ternary crystal structure of human glyoxylate2 reductase/hydroxypyruvate reductase
62	<a href="#">c6aphA_</a>	Alignment	not modelled	97.9	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of adenosylhomocysteinase from elizabethkingia2 anophelis nuhp1 in complex with nad and adenosine
63	<a href="#">c5hm8C_</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> 2.85 angstrom crystal structure of s-adenosylhomocysteinase from2 cryptosporidium parvum in complex with adenosine and nad.
64	<a href="#">c6f3oC_</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 pseudomonas aeruginosa complexed with adenine, k+ and zn2+ cations
65	<a href="#">c3n7uD_</a>	Alignment	not modelled	97.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
66	<a href="#">c3x2fA_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> a thermophilic s-adenosylhomocysteine hydrolase
67	<a href="#">c2nacA_</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> oxidoreductase(aldehyde(d),nad+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> high resolution structures of holo and apo formate dehydrogenase
68	<a href="#">c2o4cB_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythronate-4-phosphate dehydrogenase complexed2 with nad
69	<a href="#">c3kboB_</a>	Alignment	not modelled	97.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyoxylate/hydroxypyruvate reductase a; <b>PDBTitle:</b> 2.14 angstrom crystal structure of putative oxidoreductase (ycdw) from2 salmonella typhimurium in complex with nadp
70	<a href="#">d2naca1</a>	Alignment	not modelled	97.7	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
71	<a href="#">c1gdhA_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> oxidoreductase(choh (d)-nad(p)+( a)) <b>Chain:</b> A: <b>PDB Molecule:</b> d-glycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
72	<a href="#">c3fn4A_</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent formate dehydrogenase; <b>PDBTitle:</b> apo-form of nad-dependent formate dehydrogenase from bacterium2 moraxella sp.c-1 in closed conformation
73	<a href="#">c1xdwA_</a>	Alignment	not modelled	97.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad+-dependent (r)-2-hydroxyglutarate <b>PDBTitle:</b> nad+-dependent (r)-2-hydroxyglutarate dehydrogenase from2 acidaminococcus fermentans
74	<a href="#">d1gdha1</a>	Alignment	not modelled	97.6	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
75	<a href="#">c3d64A_</a>	Alignment	not modelled	97.6	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
76	<a href="#">c3oetF_</a>	Alignment	not modelled	97.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> d-erythronate-4-phosphate dehydrogenase complexed with nad
77	<a href="#">c2omeA_</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal-binding protein 2; <b>PDBTitle:</b> crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
78	<a href="#">c2rirA_</a>	Alignment	not modelled	97.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
79	<a href="#">c2dbqA_</a>	Alignment	not modelled	97.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of glyoxylate reductase (ph0597) from pyrococcus2 horikoshii ot3, complexed with nadp (i41)
						<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase;

80	<a href="#">c3dhyC</a>	Alignment	not modelled	97.6	19	<b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and 3 inhibitors
81	<a href="#">d1mx3a1</a>	Alignment	not modelled	97.6	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
82	<a href="#">c3wwzB</a>	Alignment	not modelled	97.6	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-lactate dehydrogenase (fermentative); <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from pseudomonas2 aeruginosa
83	<a href="#">c6ih2B</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphite dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphite dehydrogenase from ralstonia sp. 4506
84	<a href="#">c5j23D</a>	Alignment	not modelled	97.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of nadph-dependent glyoxylate/hydroxypyruvate2 reductase smc04462 (smghrb) from sinorhizobium melloti in complex3 with 2'-phospho- <small>adp</small> -ribose
85	<a href="#">c2j6iC</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> candida boidinii formate dehydrogenase (fdh) c-terminal mutant
86	<a href="#">c5tx7A</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from desulfovibrio vulgaris
87	<a href="#">c4g2nA</a>	Alignment	not modelled	97.5	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of putative d-isomer specific 2-hydroxyacid2 dehydrogenase, nad-binding from polaromonas sp. js6 66
88	<a href="#">c1v8bA</a>	Alignment	not modelled	97.5	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
89	<a href="#">c3k5pA</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
90	<a href="#">c3wnvA</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxylate reductase; <b>PDBTitle:</b> crystal structure of a glyoxylate reductase from paecilomyces2 thermophila
91	<a href="#">c3gg9C</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase oxidoreductase protein; <b>PDBTitle:</b> crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
92	<a href="#">c2pi1C</a>	Alignment	not modelled	97.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-lactate dehydrogenase from aquifex2 aeolicus complexed with nad and lactic acid
93	<a href="#">c4lswA</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyacid dehydrogenase protein; <b>PDBTitle:</b> crystallization and structural analysis of 2-hydroxyacid dehydrogenase2 from ketogulonigenium vulgare y25
94	<a href="#">c2g76A</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of human 3-phosphoglycerate dehydrogenase
95	<a href="#">c1ybaC</a>	Alignment	not modelled	97.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> the active form of phosphoglycerate dehydrogenase
96	<a href="#">c4zgsE</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> putative d-lactate dehydrogenase; <b>PDBTitle:</b> identification of the pyruvate reductase of chlamydomonas reinhardtii
97	<a href="#">c5dt9A</a>	Alignment	not modelled	97.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> erythronate-4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative d-erythronate-4-phosphate2 dehydrogenase from vibrio cholerae
98	<a href="#">c2cukC</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerate dehydrogenase/glyoxylate reductase; <b>PDBTitle:</b> crystal structure of tt0316 protein from thermus thermophilus hb8
99	<a href="#">c6p2iA</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> oxidoreductase, biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycerate dehydrogenase; <b>PDBTitle:</b> acyclic imino acid reductase (bsp5) in complex with nadph and d-arg
100	<a href="#">c2yq4C</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase2 from lactobacillus delbrueckii ssp. bulgaricus
101	<a href="#">c2w2kB</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> d-mandelate dehydrogenase; <b>PDBTitle:</b> crystal structure of the apo forms of rhodotorula graminis2 d-mandelate dehydrogenase at 1.8a.
102	<a href="#">d2llda1</a>	Alignment	not modelled	97.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
103	<a href="#">c4cukA</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> structure of salmonella d-lactate dehydrogenase in complex2 with nadh
						<b>PDB header:</b> oxidoreductase

104	<a href="#">c1ygyA</a>	Alignment	not modelled	97.3	18	<b>Chain:</b> A; <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from <i>Mycobacterium tuberculosis</i>
105	<a href="#">c3bazA</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from <i>Coleus blumei</i> in 2 complex with nadp+
106	<a href="#">c3gvxA</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glycerate dehydrogenase related protein; <b>PDBTitle:</b> crystal structure of glycerate dehydrogenase related 2 protein from <i>Thermoplasma acidophilum</i>
107	<a href="#">d1j4aa1</a>	Alignment	not modelled	97.2	12	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
108	<a href="#">c5mh5A</a>	Alignment	not modelled	97.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-2-hydroxyacid dehydrogenase; <b>PDBTitle:</b> d-2-hydroxyacid dehydrogenases (d2-hdh) from <i>Haloferax mediterranei</i> in 2 complex with 2-keto-hexanoic acid and nadp+ (1.4 Å resolution)
109	<a href="#">c2eklA</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> structure of st1218 protein from <i>Sulfolobus tokodaii</i>
110	<a href="#">c1wwkA</a>	Alignment	not modelled	97.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from <i>Pyrococcus</i> 2 <i>horikoshii</i> ot3
111	<a href="#">c4e5kC</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> phosphite dehydrogenase (thermostable variant); <b>PDBTitle:</b> thermostable phosphite dehydrogenase in complex with nad and sulfite
112	<a href="#">c3evtA</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from <i>Lactobacillus</i> 2 <i>plantarum</i>
113	<a href="#">d1sc6a1</a>	Alignment	not modelled	97.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
114	<a href="#">c3hg7A</a>	Alignment	not modelled	97.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase family <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase 2 family protein from <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> a449
115	<a href="#">c3wwyA</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> the crystal structure of d-lactate dehydrogenase from <i>Fusobacterium</i> 2 <i>nucleatum</i> subsp. <i>nucleatum</i>
116	<a href="#">d1li4a1</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
117	<a href="#">c4zqbB</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nadp-dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent dehydrogenase from 2 <i>Rhodobactersphaeroides</i> in complex with nadp and sulfate
118	<a href="#">c4dgsA</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> the crystals structure of dehydrogenase from <i>Rhizobium meliloti</i>
119	<a href="#">d1qp8a1</a>	Alignment	not modelled	97.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Formate/glycerate dehydrogenases, NAD-domain
120	<a href="#">c4xa8A</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> d-isomer specific 2-hydroxyacid dehydrogenase nad-binding; <b>PDBTitle:</b> crystal structure of d-isomer specific 2-hydroxyacid dehydrogenase 2 from <i>Xanthobacter autotrophicus</i> py2