



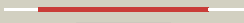




























#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2otcA_</a>	 Alignment		100.0	88	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> ornithine transcarbamoylase complexed with n-2 (phosphonacetyl)-l-ornithine
2	<a href="#">c3updA_</a>	 Alignment		100.0	67	<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
3	<a href="#">c1ortD_</a>	 Alignment		100.0	58	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine transcarbamoylase; <b>PDBTitle:</b> ornithine transcarbamoylase from pseudomonas aeruginosa
4	<a href="#">c2w37A_</a>	 Alignment		100.0	48	<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
5	<a href="#">c1a1sA_</a>	 Alignment		100.0	42	<b>PDB header:</b> transcarbamylase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> ornithine carbamoyltransferase from pyrococcus furiosus
6	<a href="#">c1vlvA_</a>	 Alignment		100.0	46	<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
7	<a href="#">c1fvoB_</a>	 Alignment		100.0	39	<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
8	<a href="#">c1ml4A_</a>	 Alignment		100.0	27	<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
9	<a href="#">c2p2gD_</a>	 Alignment		100.0	40	<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
10	<a href="#">c1zq2A_</a>	 Alignment		100.0	36	<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
11	<a href="#">c3tpfF_</a>	 Alignment		100.0	37	<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

12	<a href="#">d1tuga1</a>	<div><div></div><div>Alignment</div></div>		100.0	27	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
13	<a href="#">c3grfA</a>	<div><div></div><div>Alignment</div></div>		100.0	33	<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
14	<a href="#">c3sdsA</a>	<div><div></div><div>Alignment</div></div>		100.0	34	<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
15	<a href="#">c1pg5A</a>	<div><div></div><div>Alignment</div></div>		100.0	23	<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
16	<a href="#">c2rgwD</a>	<div><div></div><div>Alignment</div></div>		100.0	23	<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
17	<a href="#">c2ef0A</a>	<div><div></div><div>Alignment</div></div>		100.0	42	<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
18	<a href="#">c3gd5D</a>	<div><div></div><div>Alignment</div></div>		100.0	42	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> ornithine carbamoyltransferase; <b>PDBTitle:</b> crystal structure of ornithine carbamoyltransferase from gloeobacter2 violaceus
19	<a href="#">c1js1Z</a>	<div><div></div><div>Alignment</div></div>		100.0	30	<b>PDB header:</b> transferase <b>Chain:</b> Z: <b>PDB Molecule:</b> transcarbamylase; <b>PDBTitle:</b> crystal structure of a new transcarbamylase from the2 anaerobic bacterium bacteroides fragilis at 2.0 a3 resolution
20	<a href="#">c3q98A</a>	<div><div></div><div>Alignment</div></div>		100.0	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transcarbamylase; <b>PDBTitle:</b> structure of ygew encoded protein from e. coli
21	<a href="#">c3d6nB</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	22	<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
22	<a href="#">c2at2B</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	28	<b>PDB header:</b> <b>PDB COMPND:</b>
23	<a href="#">c3lxmC</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	31	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> aspartate carbamoyltransferase; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a catalytic2 subunit of an aspartate carbamoyltransferase (pyrb) from3 yersinia pestis co92
24	<a href="#">d1duvg2</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	87	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
25	<a href="#">d1dxha2</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	55	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
26	<a href="#">d1duvg1</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	89	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
27	<a href="#">d1pvva1</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	43	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
28	<a href="#">d1vlva1</a>	<div><div></div><div>Alignment</div></div>	not modelled	100.0	49	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
		<div><div></div><div></div></div>				<b>Fold:</b> ATC-like

29	<a href="#">d1dxha1</a>	Alignment	not modelled	100.0	62	<b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
30	<a href="#">d1ml4a1</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
31	<a href="#">d1lotha1</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
32	<a href="#">d1ekxa1</a>	Alignment	not modelled	100.0	35	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
33	<a href="#">d1lotha2</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
34	<a href="#">d1pvva2</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
35	<a href="#">d1pg5a1</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
36	<a href="#">d2at2a1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
37	<a href="#">d1vlva2</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
38	<a href="#">d1js1x1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
39	<a href="#">d1ml4a2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
40	<a href="#">d1ekxa2</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
41	<a href="#">d1pg5a2</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
42	<a href="#">d1js1x2</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
43	<a href="#">d2at2a2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
44	<a href="#">d2atca2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
45	<a href="#">c3oneA</a>	Alignment	not modelled	98.4	19	<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
46	<a href="#">c3gvpB</a>	Alignment	not modelled	98.3	17	<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
47	<a href="#">c1d4fD</a>	Alignment	not modelled	98.2	13	<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
48	<a href="#">c3n58D</a>	Alignment	not modelled	98.2	16	<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
49	<a href="#">c3dhyC</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
50	<a href="#">c1xdwA</a>	Alignment	not modelled	98.0	17	<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
51	<a href="#">c3d4oA</a>	Alignment	not modelled	98.0	14	<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
52	<a href="#">c1v8bA</a>	Alignment	not modelled	97.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteinase; <b>PDBTitle:</b> crystal structure of a hydrolase
53	<a href="#">c2j6iC</a>	Alignment	not modelled	97.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> candida boidinii formate dehydrogenase (fdh) c-terminal2 mutant
54	<a href="#">c3n7uD</a>	Alignment	not modelled	97.7	18	<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
55	<a href="#">c3l07B</a>	Alignment	not modelled	97.7	14	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> methylenetetrahydrofolate

						dehydrogenase/methenyltetrahydrofolate2 cyclohydrolase, putative bifunctional protein fold from francisella3 tularensis.
56	<a href="#">c3d64A</a>	Alignment	not modelled	97.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> adenosylhomocysteine; <b>PDBTitle:</b> crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
57	<a href="#">c1ybaC</a>	Alignment	not modelled	97.6	17	<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
58	<a href="#">c3k5pA</a>	Alignment	not modelled	97.6	19	<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
59	<a href="#">c4a26B</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative c-1-tetrahydrofolate synthase, cytoplasmic; <b>PDBTitle:</b> the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
60	<a href="#">c2gcgB</a>	Alignment	not modelled	97.5	20	<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
61	<a href="#">c2dbqA</a>	Alignment	not modelled	97.4	18	<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)
62	<a href="#">c2nacA</a>	Alignment	not modelled	97.4	13	<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
63	<a href="#">c2rirA</a>	Alignment	not modelled	97.4	14	<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
64	<a href="#">d1mx3a1</a>	Alignment	not modelled	97.4	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
65	<a href="#">c2omeA</a>	Alignment	not modelled	97.4	14	<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)
66	<a href="#">c1b0aA</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> oxidoreductase,hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (fold bifunctional protein); <b>PDBTitle:</b> 5,10, methylene-tetrahydrofolate2 dehydrogenase/cyclohydrolase from e coli.
67	<a href="#">c3evtA</a>	Alignment	not modelled	97.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from2 lactobacillus plantarum
68	<a href="#">c1gdhA</a>	Alignment	not modelled	97.3	18	<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
69	<a href="#">c2eklA</a>	Alignment	not modelled	97.2	17	<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 sulfolobus tokodaii
70	<a href="#">c3oetF</a>	Alignment	not modelled	97.2	15	<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
71	<a href="#">c2o4cB</a>	Alignment	not modelled	97.2	15	<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
72	<a href="#">c1gpjA</a>	Alignment	not modelled	97.2	14	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> glutamyl-trna reductase from methanopyrus kandleri
73	<a href="#">c3gg9C</a>	Alignment	not modelled	97.1	18	<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
74	<a href="#">c1dxyA</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-2-hydroxyisocaproate dehydrogenase; <b>PDBTitle:</b> structure of d-2-hydroxyisocaproate dehydrogenase
75	<a href="#">c1j4aA</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-lactate dehydrogenase; <b>PDBTitle:</b> insights into domain closure, substrate specificity and2 catalysis of d-lactate dehydrogenase from lactobacillus3 bulgaricus
76	<a href="#">c3bazA</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxyphenylpyruvate reductase; <b>PDBTitle:</b> structure of hydroxyphenylpyruvate reductase from coleus blumei in2 complex with nadp+
77	<a href="#">c1qp8A</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative formate dehydrogenase from2 pyrobaculum aerophilum
78	<a href="#">c3hg7A</a>	Alignment	not modelled	97.0	16	<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 family protein from aeromonas salmonicida subsp. salmonicida a449
79	<a href="#">d1gpja2</a>	Alignment	not modelled	97.0	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain

80	<a href="#">dlqp8a1</a>	Alignment	not modelled	97.0	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
81	<a href="#">c2pi1C</a>	Alignment	not modelled	96.9	20	<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
82	<a href="#">dlgdha1</a>	Alignment	not modelled	96.9	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
83	<a href="#">c3kboB</a>	Alignment	not modelled	96.9	14	<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
84	<a href="#">c2cukC</a>	Alignment	not modelled	96.9	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
85	<a href="#">c2w2kB</a>	Alignment	not modelled	96.9	16	<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.
86	<a href="#">c3gvxA</a>	Alignment	not modelled	96.8	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 related2 protein from thermoplasma acidophilum
87	<a href="#">d2naca1</a>	Alignment	not modelled	96.8	15	<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
88	<a href="#">d2dl da1</a>	Alignment	not modelled	96.8	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
89	<a href="#">dlsc6a1</a>	Alignment	not modelled	96.8	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
90	<a href="#">dl a4ia1</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
91	<a href="#">c3p2oB</a>	Alignment	not modelled	96.8	17	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
92	<a href="#">c2g76A</a>	Alignment	not modelled	96.7	21	<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
93	<a href="#">c1wwkA</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of phosphoglycerate dehydrogenase from pyrococcus2 horikoshii ot3
94	<a href="#">c1ygyA</a>	Alignment	not modelled	96.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-3-phosphoglycerate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
95	<a href="#">dlb0aa1</a>	Alignment	not modelled	96.6	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Aminoacid dehydrogenase-like, C-terminal domain
96	<a href="#">c4a5oB</a>	Alignment	not modelled	96.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of pseudomonas aeruginosa n5, n10-2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase (fold)
97	<a href="#">dlj4aa1</a>	Alignment	not modelled	96.5	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
98	<a href="#">c3nglA</a>	Alignment	not modelled	96.5	12	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of bifunctional 5,10-methylenetetrahydrofolate2 dehydrogenase / cyclohydrolase from thermoplasma acidophilum
99	<a href="#">dlli4a1</a>	Alignment	not modelled	96.5	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
100	<a href="#">dlpjca1</a>	Alignment	not modelled	96.4	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
101	<a href="#">dl dxya1</a>	Alignment	not modelled	96.3	15	<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
102	<a href="#">c3p2oA</a>	Alignment	not modelled	96.3	18	<b>PDB header:</b> oxidoreductase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional protein fold; <b>PDBTitle:</b> crystal structure of fold bifunctional protein from campylobacter2 jejuni
103	<a href="#">c3g79A</a>	Alignment	not modelled	96.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; <b>PDBTitle:</b> crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
104	<a href="#">dlvgya1</a>	Alignment	not modelled	96.3	21	<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
105	<a href="#">c1u8xX</a>	Alignment	not modelled	96.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> maltose-6'-phosphate glucosidase; <b>PDBTitle:</b> crystal structure of glva from bacillus subtilis, a metal-



					requiring,2 nad-dependent 6-phospho-alpha-glucosidase
106	<a href="#">c1vjta_</a>	Alignment	not modelled	96.1	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
107	<a href="#">d1v8ba1</a>	Alignment	not modelled	96.0	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="#">c3gg2B_</a>	Alignment	not modelled	95.8	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
109	<a href="#">c1l7eC_</a>	Alignment	not modelled	95.7	18 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinamide nucleotide transhydrogenase, <b>PDBTitle:</b> crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
110	<a href="#">d1vjta1</a>	Alignment	not modelled	95.5	23 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
111	<a href="#">d1l7da1</a>	Alignment	not modelled	95.5	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
112	<a href="#">c2d0iC_</a>	Alignment	not modelled	95.4	10 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure ph0520 protein from pyrococcus horikoshii ot3
113	<a href="#">c3oj0A_</a>	Alignment	not modelled	95.4	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamyl-trna reductase; <b>PDBTitle:</b> crystal structure of glutamyl-trna reductase from thermoplasma2 volcanium (nucleotide binding domain)
114	<a href="#">c2y0dB_</a>	Alignment	not modelled	95.4	15 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
115	<a href="#">c1s6yA_</a>	Alignment	not modelled	95.3	22 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phospho-beta-glucosidase; <b>PDBTitle:</b> 2.3a crystal structure of phospho-beta-glucosidase
116	<a href="#">c1a4iB_</a>	Alignment	not modelled	94.9	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> methylenetetrahydrofolate dehydrogenase / <b>PDBTitle:</b> human tetrahydrofolate dehydrogenase / cyclohydrolase
117	<a href="#">c1obbB_</a>	Alignment	not modelled	94.9	18 <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-glucosidase; <b>PDBTitle:</b> alpha-glucosidase a, agla, from thermotoga maritima in2 complex with maltose and nad+
118	<a href="#">c2eezG_</a>	Alignment	not modelled	94.9	20 <b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> alanine dehydrogenase; <b>PDBTitle:</b> crystal structure of alanine dehydrogenase from themus thermophilus
119	<a href="#">d1civa1</a>	Alignment	not modelled	94.8	16 <b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
120	<a href="#">c7mdhA_</a>	Alignment	not modelled	94.8	17 <b>PDB header:</b> chloroplastic malate dehydrogenase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (malate dehydrogenase); <b>PDBTitle:</b> structural basis for light acitvation of a chloroplast enzyme. the2 structure of sorghum nadp-malate dehydrogenase in its oxidized form