



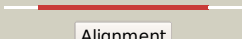

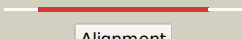













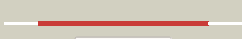












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1652_(argC)_1865583_1866641
Date	Fri Aug 2 13:30:24 BST 2019
Unique Job ID	b318d51199afaa99

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2i3aD_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (rv1652) from mycobacterium tuberculosis
2	<a href="#">c2q49B_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
3	<a href="#">c1vknC_</a>	 Alignment		100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tm1782) from thermotoga maritima at 1.80 a resolution
4	<a href="#">c2ozpA_</a>	 Alignment		100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
5	<a href="#">c2g17A_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> the structure of n-acetyl-gamma-glutamyl-phosphate reductase from2 salmonella typhimurium.
6	<a href="#">c4dpgB_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> malonyl-coa/succinyl-coa reductase; <b>PDBTitle:</b> structure of malonyl-coenzyme a reductase from crenarchaeota
7	<a href="#">c2gz3D_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aspartate beta-semialdehyde dehydrogenase; <b>PDBTitle:</b> structure of aspartate semialdehyde dehydrogenase (asadh) from2 streptococcus pneumoniae complexed with nadp and aspartate-3 semialdehyde
8	<a href="#">c5jw6A_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase from2 aspergillus fumigatus
9	<a href="#">c1mb4B_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase from vibrio cholerae with nadp and s-methyl-l-cysteine sulfoxide
10	<a href="#">c1t4bB_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> 1.6 angstrom structure of escherichia coli aspartate-2 semialdehyde dehydrogenase.
11	<a href="#">c4wojB_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate semialdehyde dehydrogenase; <b>PDBTitle:</b> aspartate semialdehyde dehydrogenase from francisella tularensis

12	<a href="#">c3kubA</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semi-aldehyde dehydrogenase complexed2 with glycerol and phosphate of mycobacterium tuberculosis h37rv
13	<a href="#">c5cefA</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase from2 cryptococcus neoformans
14	<a href="#">c2hjsA</a>	Alignment		100.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> usg-1 protein homolog; <b>PDBTitle:</b> the structure of a probable aspartate-semialdehyde dehydrogenase from2 pseudomonas aeruginosa
15	<a href="#">c3hskB</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase with nadp2 from candida albicans
16	<a href="#">c2ep5B</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 350aa long hypothetical aspartate-semialdehyde <b>PDBTitle:</b> structural study of project id st1242 from sulfobolus tokodaii strain7
17	<a href="#">c3uw3A</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
18	<a href="#">c4zhsC</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> aspartate semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase from2 trichophyton rubrum
19	<a href="#">c2qz9B</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
20	<a href="#">c2yv3B</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
21	<a href="#">c1ys4A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> structure of aspartate-semialdehyde dehydrogenase from methanococcus2 jannaschii
22	<a href="#">d2q49a1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	<a href="#">c2gd1P</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase(aldehyde(d)-nad(a)) <b>Chain:</b> P: <b>PDB Molecule:</b> apo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophilus
24	<a href="#">d2g17a1</a>	Alignment	not modelled	100.0	29	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
25	<a href="#">d2cvoa1</a>	Alignment	not modelled	100.0	36	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
26	<a href="#">d2cvoa2</a>	Alignment	not modelled	100.0	37	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
27	<a href="#">d1vkn1</a>	Alignment	not modelled	100.0	34	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	<a href="#">d1vkn2</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like

29	<a href="#">d2q49a2</a>	Alignment	not modelled	100.0	39	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
30	<a href="#">c3sthA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
31	<a href="#">d2g17a2</a>	Alignment	not modelled	100.0	40	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
32	<a href="#">c1cf2Q</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> protein (glyceraldehyde-3-phosphate dehydrogenase); <b>PDBTitle:</b> three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon methanothermus3 fervidus
33	<a href="#">c1b7gO</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> protein (glyceraldehyde 3-phosphate dehydrogenase); <b>PDBTitle:</b> glyceraldehyde 3-phosphate dehydrogenase
34	<a href="#">d2hjsa2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
35	<a href="#">d2hjsa1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
36	<a href="#">c1s7cA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> structural genomics, oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
37	<a href="#">d2gz1a1</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
38	<a href="#">c2czcD</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
39	<a href="#">c2yyyB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
40	<a href="#">d1t4ba1</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	<a href="#">d1pqua2</a>	Alignment	not modelled	100.0	22	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
42	<a href="#">d1t4ba2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
43	<a href="#">d1mb4a2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
44	<a href="#">d2gz1a2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
45	<a href="#">d1mb4a1</a>	Alignment	not modelled	100.0	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	<a href="#">d1pqua1</a>	Alignment	not modelled	100.0	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	<a href="#">c3b20R</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase2 complexed with nadfrom synechococcus elongatus"
48	<a href="#">c1hdgO</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase (aldehy(d)-nad(a)) <b>Chain:</b> O: <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution
49	<a href="#">c2d2iO</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
50	<a href="#">c3cieC</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
						<b>PDB header:</b> oxidoreductase (aldehyde(d)-nad(a)) <b>Chain:</b> C: <b>PDB Molecule:</b> holo-d-glyceraldehyde-3-phosphate

51	<a href="#">c1cerC</a>	Alignment	not modelled	100.0	15	dehydrogenase; <b>PDBTitle:</b> determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3-phosphate dehydrogenase at 2.5 angstroms resolution
52	<a href="#">c1rm4O</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase a; <b>PDBTitle:</b> crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
53	<a href="#">c2x5kO</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> d-erythrose-4-phosphate dehydrogenase; <b>PDBTitle:</b> structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
54	<a href="#">c2pkrl</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase aor; <b>PDBTitle:</b> crystal structure of (a+cte)4 chimeric form of photosynthetic2 glyceraldehyde-3-phosphate dehydrogenase, complexed with nadp
55	<a href="#">c5ur0B</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystallographic structure of glyceraldehyde-3-phosphate dehydrogenase2 from naegleria gruberi
56	<a href="#">c6ok4A</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase (gapdh)2 from chlamydia trachomatis with bound nad
57	<a href="#">c5j9gB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-p dehydrogenase; <b>PDBTitle:</b> structure of lactobacillus acidophilus glyceraldehyde-3-phosphate2 dehydrogenase at 2.21 angstrom resolution
58	<a href="#">c4qx6A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 streptococcus agalactiae nem316 at 2.46 angstrom resolution
59	<a href="#">c4dibF</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 bacillus anthracis str. Sterne
60	<a href="#">c3h9eO</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase, testis-specific; <b>PDBTitle:</b> crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
61	<a href="#">c2i5pO</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
62	<a href="#">c2b4rQ</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
63	<a href="#">c3docD</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of trka glyceraldehyde-3-phosphate dehydrogenase2 from brucella melitensis
64	<a href="#">c2ep7B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structural study of project id aq_1065 from aquifex aeolicus vf5
65	<a href="#">c3hq4R</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> R: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
66	<a href="#">c3hjaB</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 borrelia burgdorferi
67	<a href="#">c1ihxD</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
68	<a href="#">c1obfO</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> glycolytic pathway <b>Chain:</b> O: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylooxidans at 1.7 a3 resolution.
69	<a href="#">d1cf2o1</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
70	<a href="#">c5jyfB</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> structures of streptococcus agalactiae gbs gapdh in different2 enzymatic states

71	<a href="#">d1hdgo2</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> Fwde/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
72	<a href="#">d1dssg1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
73	<a href="#">c5ld5C</a>	Alignment	not modelled	99.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of a bacterial dehydrogenase at 2.19 angstroms2 resolution
74	<a href="#">c1i32D</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate dehydrogenase; <b>PDBTitle:</b> leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
75	<a href="#">c3ic5A</a>	Alignment	not modelled	98.9	24	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroiyi.
76	<a href="#">c4ywjB</a>	Alignment	not modelled	98.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
77	<a href="#">c4f3yA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
78	<a href="#">c5z2fA</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
79	<a href="#">c5ugjC</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of htpa reductase from neisseria meningitidis
80	<a href="#">c5tenH</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
81	<a href="#">c2z2vA</a>	Alignment	not modelled	98.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688; <b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
82	<a href="#">c1drwA</a>	Alignment	not modelled	98.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
83	<a href="#">c1nvmB</a>	Alignment	not modelled	98.5	23	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase (acylating); <b>PDBTitle:</b> crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
84	<a href="#">c4jn6B</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> lyase/oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> acetaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
85	<a href="#">c3dapB</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelic acid dehydrogenase; <b>PDBTitle:</b> c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
86	<a href="#">c1e5IA</a>	Alignment	not modelled	98.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
87	<a href="#">c3wgzB</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structure of meso-dapdh q154/t173i/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
88	<a href="#">c5I78A</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminoadipic semialdehyde synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
89	<a href="#">d1nvmB1</a>	Alignment	not modelled	98.4	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	<a href="#">c5kt0A</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
91	<a href="#">c3wb9A</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
92	<a href="#">c2axqA</a>	Alignment	not modelled	98.3	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
93	<a href="#">d1f06a1</a>	Alignment	not modelled	98.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> semialdehyde dehydrogenase nad-binding

94	<a href="#">c5t57A_</a>	Alignment	not modelled	98.3	27	protein; <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
95	<a href="#">d2cmda1</a>	Alignment	not modelled	98.3	21	<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
96	<a href="#">c3wycB_</a>	Alignment	not modelled	98.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase; <b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp
97	<a href="#">c2pv7B_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> isomerase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) <b>PDBTitle:</b> crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
98	<a href="#">c3bioB_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
99	<a href="#">c2dt5A_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> at-rich dna-binding protein; <b>PDBTitle:</b> crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
100	<a href="#">c4e12A_</a>	Alignment	not modelled	98.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diketoreductase; <b>PDBTitle:</b> substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
101	<a href="#">c4xb1B_</a>	Alignment	not modelled	98.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 319aa long hypothetical homoserine dehydrogenase; <b>PDBTitle:</b> hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
102	<a href="#">d1y7ta1</a>	Alignment	not modelled	98.1	19	<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
103	<a href="#">c2f1kD_</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
104	<a href="#">d2f1ka2</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
105	<a href="#">c5zi3A_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> malate dehydrogenase; <b>PDBTitle:</b> mdh3 wild type, apo-form
106	<a href="#">c6iaqA_</a>	Alignment	not modelled	98.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase n-terminus domain-containing <b>PDBTitle:</b> structure of amine dehydrogenase from mycobacterium smegmatis
107	<a href="#">d2dt5a2</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Transcriptional repressor Rex, C-terminal domain
108	<a href="#">d1i36a2</a>	Alignment	not modelled	98.1	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
109	<a href="#">c6g1mA_</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> amine dehydrogenase from petrotoga mobilis; open and closed form
110	<a href="#">c6iauB_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine dehydrogenase; <b>PDBTitle:</b> amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine
111	<a href="#">d1civa1</a>	Alignment	not modelled	98.0	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
112	<a href="#">c2y0dB_</a>	Alignment	not modelled	98.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
113	<a href="#">c3vtfA_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
114	<a href="#">c2ho3D_</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
115	<a href="#">c4uunA_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase; <b>PDBTitle:</b> trichomonas vaginalis lactate dehydrogenase in complex with nadh
116	<a href="#">c3gg2B_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
117	<a href="#">d5mdha1</a>	Alignment	not modelled	98.0	17	<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
118	<a href="#">c3d1lB_</a>	Alignment	not modelled	98.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadp oxidoreductase bf3122; <b>PDBTitle:</b> crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
						<b>PDB header:</b> oxidoreductase

119	<a href="#">c5n2iC_</a>	Alignment	not modelled	98.0	17	<b>Chain:</b> C: <b>PDB Molecule:</b> reduced coenzyme f420:nadp oxidoreductase; <b>PDBTitle:</b> f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
120	<a href="#">c2g5cD_</a>	Alignment	not modelled	98.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from aquifex aeolicus