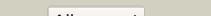
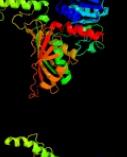
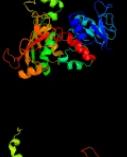
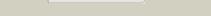
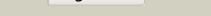
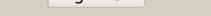


# Phyre<sup>2</sup>

Email mdejesus@rockefeller.edu  
 Description RVBD3708c\_(asd)\_4151358\_4152395  
 Date Fri Aug 9 18:20:40 BST 2019  
 Unique Job ID 74a479a945239e24

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3kubA_</a>			100.0	100	<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
2	<a href="#">c2gz3D_</a>			100.0	39	<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
3	<a href="#">c2qz9B_</a>			100.0	44	<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
4	<a href="#">c2hjsA_</a>			100.0	35	<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
5	<a href="#">c1mb4B_</a>			100.0	25	<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 vibrio2 cholerae with nadp and s-methyl-l-cysteine sulfoxide
6	<a href="#">c2yv3B_</a>			100.0	44	<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
7	<a href="#">c3uw3A_</a>			100.0	26	<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
8	<a href="#">c1t4bB_</a>			100.0	27	<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.
9	<a href="#">c4wojB_</a>			100.0	27	<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
10	<a href="#">c2i3aD_</a>			100.0	24	<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
11	<a href="#">c5jw6A_</a>			100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> cystal structure of aspartate semialdehyde dehydrogenase from2 aspergillus fumigatus

12	<a href="#">c4dpkB</a>			100.0	27	<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
13	<a href="#">c1vknC</a>			100.0	21	<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
14	<a href="#">c2ozpA</a>			100.0	23	<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
15	<a href="#">c5cefA</a>			100.0	31	<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
16	<a href="#">c2q49B</a>			100.0	22	<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
17	<a href="#">c4zhsC</a>			100.0	31	<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
18	<a href="#">c3hskB</a>			100.0	34	<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
19	<a href="#">c2g17A</a>			100.0	24	<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.
20	<a href="#">c2ep5B</a>			100.0	33	<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 sulfolobus tokodaii strain7
21	<a href="#">clys4A</a>		not modelled	100.0	33	<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 methanococcus jannaschii
22	<a href="#">c2gd1P</a>		not modelled	100.0	22	<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
23	<a href="#">d2gz1a2</a>		not modelled	100.0	33	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
24	<a href="#">d2hjsa2</a>		not modelled	100.0	32	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
25	<a href="#">d1pqua2</a>		not modelled	100.0	28	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
26	<a href="#">d1mb4a2</a>		not modelled	100.0	27	<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="#">d1t4ba2</a>		not modelled	100.0	30	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like <b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> glyceraldehyde-3-phosphate

28	<a href="#">c3sthA_</a>	Alignment	not modelled	100.0	24	<p>dehydrogenase;  <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase from <i>Toxoplasma gondii</i></p> <p><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 <i>Escherichia coli</i></p>
29	<a href="#">c1s7cA_</a>	Alignment	not modelled	100.0	19	<p><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 nadp from <i>Synechococcus elongatus</i>"</p>
30	<a href="#">c3b20R_</a>	Alignment	not modelled	100.0	23	<p><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 <i>Methanothermus fervidus</i></p>
31	<a href="#">c1cf2O_</a>	Alignment	not modelled	100.0	16	<p><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 <i>Synechococcus</i> sp. complexed3 with nadp+</p>
32	<a href="#">c2d2iO_</a>	Alignment	not modelled	100.0	22	<p><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 <i>Synechococcus</i> sp. complexed3 with nadp+</p>
33	<a href="#">c1b7gO_</a>	Alignment	not modelled	100.0	16	<p><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</p>
34	<a href="#">c1hdgO_</a>	Alignment	not modelled	100.0	21	<p><b>PDB header:</b> oxidoreductase (aldehyd(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 <i>Thermotoga maritima</i> at 2.53 angstroms resolution</p>
35	<a href="#">c1rm4O_</a>	Alignment	not modelled	100.0	19	<p><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</p>
36	<a href="#">c2pkrl_</a>	Alignment	not modelled	100.0	19	<p><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</p>
37	<a href="#">c2x5kO_</a>	Alignment	not modelled	100.0	20	<p><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 <i>E. coli</i></p>
38	<a href="#">c3cieC_</a>	Alignment	not modelled	100.0	21	<p><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 <i>Cryptosporidium parvum</i></p>
39	<a href="#">c1cerC_</a>	Alignment	not modelled	100.0	21	<p><b>PDB header:</b> oxidoreductase (aldehyde(d)-nad(a))  <b>Chain:</b> C: <b>PDB Molecule:</b>holo-d-glyceraldehyde-3-phosphate dehydrogenase;  <b>PDBTitle:</b> determinants of enzyme thermostability observed in the2 molecular structure of <i>Thermus aquaticus</i> d-glyceraldehyde-3-phosphate dehydrogenase at 2.5 angstroms resolution</p>
40	<a href="#">c2yyyB_</a>	Alignment	not modelled	100.0	15	<p><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</p>
41	<a href="#">c5j9gB_</a>	Alignment	not modelled	100.0	18	<p><b>PDB header:</b> oxidoreductase  <b>Chain:</b> B: <b>PDB Molecule:</b>glyceraldehyde-3-p dehydrogenase;  <b>PDBTitle:</b> structure of <i>Lactobacillus acidophilus</i> glyceraldehyde-3-phosphate2 dehydrogenase at 2.21 angstrom resolution</p>
42	<a href="#">d2gz1a1</a>	Alignment	not modelled	100.0	41	<p><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</p>
43	<a href="#">c3docD_</a>	Alignment	not modelled	100.0	20	<p><b>PDB header:</b> oxidoreductase  <b>Chain:</b> D: <b>PDB Molecule:</b>glyceraldehyde 3-phosphate dehydrogenase;  <b>PDBTitle:</b> crystal structure of <i>TrkA</i> glyceraldehyde-3-phosphate dehydrogenase2 from <i>Brucella melitensis</i></p>
44	<a href="#">c6ok4A_</a>	Alignment	not modelled	100.0	21	<p><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 <i>Chlamydia trachomatis</i> with bound nad</p>
45	<a href="#">c4qx6A_</a>	Alignment	not modelled	100.0	20	<p><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 from <i>Streptococcus agalactiae</i> nema316 at 2.46 angstrom resolution</p>
46	<a href="#">c2b4rQ_</a>	Alignment	not modelled	100.0	19	<p><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 from <i>Plasmodium falciparum</i> at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site</p>
47	<a href="#">c3h9eO_</a>	Alignment	not modelled	100.0	21	<p><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</p>

						glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
48	<a href="#">d2hjsa1</a>	Alignment	not modelled	100.0	35	<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
49	<a href="#">c4dibF_</a>	Alignment	not modelled	100.0	22	<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
50	<a href="#">c5ur0B_</a>	Alignment	not modelled	100.0	17	<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
51	<a href="#">c2czcD_</a>	Alignment	not modelled	100.0	20	<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
52	<a href="#">c3hq4R_</a>	Alignment	not modelled	100.0	19	<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
53	<a href="#">d2q49a1</a>	Alignment	not modelled	100.0	19	<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
54	<a href="#">d2g17a1</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
55	<a href="#">c1ihxD_</a>	Alignment	not modelled	100.0	20	<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
56	<a href="#">c3hjaB_</a>	Alignment	not modelled	100.0	20	<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
57	<a href="#">c2ep7B_</a>	Alignment	not modelled	100.0	20	<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
58	<a href="#">d1vkna1</a>	Alignment	not modelled	100.0	19	<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
59	<a href="#">c2i5pO_</a>	Alignment	not modelled	100.0	22	<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
60	<a href="#">d2cvoa1</a>	Alignment	not modelled	100.0	20	<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
61	<a href="#">c1obfO_</a>	Alignment	not modelled	100.0	19	<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 xylosoxidans at 1.7 a3 resolution.
62	<a href="#">d2cvoa2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
63	<a href="#">d1t4ba1</a>	Alignment	not modelled	100.0	24	<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
64	<a href="#">d1mb4a1</a>	Alignment	not modelled	100.0	26	<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
65	<a href="#">d1pqua1</a>	Alignment	not modelled	100.0	23	<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
66	<a href="#">c5ld5C_</a>	Alignment	not modelled	100.0	22	<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
67	<a href="#">d1vkna2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
68	<a href="#">d2q49a2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
69	<a href="#">c1i32D_</a>	Alignment	not modelled	100.0	20	<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 <b>Fold:</b> FwdE/GAPDH domain-like

70	<a href="#">d2g17a2</a>		not modelled	100.0	23	<b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
71	<a href="#">c5jyfB_</a>		not modelled	100.0	19	<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
72	<a href="#">d1cf2o1</a>		not modelled	99.9	16	<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="#">d1dssg1</a>		not modelled	99.9	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
74	<a href="#">d1hdgo2</a>		not modelled	99.8	20	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
75	<a href="#">d1gad01</a>		not modelled	99.7	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
76	<a href="#">d3cmco1</a>		not modelled	99.7	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
77	<a href="#">d1k3ta1</a>		not modelled	99.7	16	<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
78	<a href="#">d1j0xo1</a>		not modelled	99.7	20	<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
79	<a href="#">d1u8fo1</a>		not modelled	99.7	20	<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
80	<a href="#">d2g82a1</a>		not modelled	99.7	17	<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
81	<a href="#">d1rm4a1</a>		not modelled	99.7	19	<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
82	<a href="#">d1hdg01</a>		not modelled	99.7	20	<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
83	<a href="#">d1ggaal</a>		not modelled	99.7	18	<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
84	<a href="#">d1vc2a1</a>		not modelled	99.7	19	<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
85	<a href="#">d2pkq01</a>		not modelled	99.7	20	<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
86	<a href="#">d1i32a1</a>		not modelled	99.6	20	<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
87	<a href="#">d3gpdg1</a>		not modelled	99.6	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
88	<a href="#">d2b4ro1</a>		not modelled	99.6	19	<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
89	<a href="#">d1obf01</a>		not modelled	99.5	18	<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="#">c4jn6B_</a>		not modelled	99.5	20	<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
91	<a href="#">d1u8fo2</a>		not modelled	99.4	21	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
92	<a href="#">c1nvmB_</a>		not modelled	99.4	17	<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
93	<a href="#">d1rm4a2</a>		not modelled	99.4	19	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
94	<a href="#">d3cmco2</a>		not modelled	99.3	26	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
95	<a href="#">d1gad02</a>		not modelled	99.3	22	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain

						<b>Family:</b> GAPDH-like																																																																																																														
96	<a href="#">d2b4ro2</a>		not modelled	99.3	21	<b>Fold:</b> FwdE/GAPDH domain-like																																																																																																														
97	<a href="#">d1k3ta2</a>		not modelled	99.3	22	<b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain																																																																																																														
98	<a href="#">d1gaa2</a>		not modelled	99.3	22	<b>Family:</b> GAPDH-like																																																																																																														
99	<a href="#">d1i32a2</a>		not modelled	99.3	20	<b>Fold:</b> FwdE/GAPDH domain-like																																																																																																														
100	<a href="#">d3gpdg2</a>		not modelled	99.3	26	<b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain																																																																																																														
101	<a href="#">d2g82a2</a>		not modelled	99.3	21	<b>Family:</b> GAPDH-like																																																																																																														
102	<a href="#">d2pkqo2</a>		not modelled	99.3	23	<b>Fold:</b> FwdE/GAPDH domain-like																																																																																																														
103	<a href="#">d1nvmb1</a>		not modelled	99.3	15	<b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain																																																																																																														
104	<a href="#">d1dssg2</a>		not modelled	99.2	23	<b>Family:</b> GAPDH-like																																																																																																														
105	<a href="#">d1obfo2</a>		not modelled	99.2	21	<b>Fold:</b> FwdE/GAPDH domain-like																																																																																																														
106	<a href="#">c3ic5A_</a>		not modelled	99.0	24	<b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain																																																																																																														
107	<a href="#">d2czca2</a>		not modelled	99.0	16	<b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain																																																																																																														
108	<a href="#">c1drwA_</a>		not modelled	99.0	16	<b>PDB header:</b> oxidoreductase																																																																																																														
						<b>Chain: A: PDB Molecule:</b> putative saccharopine dehydrogenase;																																																																																																														
						<b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.																																																																																																														
109	<a href="#">c5tenH_</a>		not modelled	98.9	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains																																																																																																														
110	<a href="#">c5z2fA_</a>		not modelled	98.9	14	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains																																																																																																														
111	<a href="#">c4ywjb_</a>		not modelled	98.9	14	<b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain																																																																																																														
112	<a href="#">c4f3yA_</a>		not modelled	98.8	14	<b>PDB header:</b> oxidoreductase																																																																																																														
113	<a href="#">c2z2vA_</a>		not modelled	98.8	12	114	<a href="#">c3dapB_</a>		not modelled	98.8	15	<b>Chain: A: PDB Molecule:</b> dihydrodipicolinate reductase;	115	<a href="#">c5ugjc_</a>		not modelled	98.8	17	<b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii	116	<a href="#">d1f06a1</a>		not modelled	98.7	19	<b>PDB header:</b> oxidoreductase	117	<a href="#">c3wycb_</a>		not modelled	98.7	19	118	<a href="#">c3wgzb_</a>		not modelled	98.7	16	<b>Chain: B: PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase;	119	<a href="#">c3wb9A_</a>		not modelled	98.7	14	<b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp+							<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: PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase;							<b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp+							<b>PDB header:</b> oxidoreductase							<b>Chain: A: PDB Molecule:</b> diaminopimelate dehydrogenase;							<b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum							<b>PDB header:</b> oxidoreductase
114	<a href="#">c3dapB_</a>		not modelled	98.8	15	<b>Chain: A: PDB Molecule:</b> dihydrodipicolinate reductase;																																																																																																														
115	<a href="#">c5ugjc_</a>		not modelled	98.8	17	<b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii																																																																																																														
116	<a href="#">d1f06a1</a>		not modelled	98.7	19	<b>PDB header:</b> oxidoreductase																																																																																																														
117	<a href="#">c3wycb_</a>		not modelled	98.7	19	118	<a href="#">c3wgzb_</a>		not modelled	98.7	16	<b>Chain: B: PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase;	119	<a href="#">c3wb9A_</a>		not modelled	98.7	14	<b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp+							<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: PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase;							<b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp+							<b>PDB header:</b> oxidoreductase							<b>Chain: A: PDB Molecule:</b> diaminopimelate dehydrogenase;							<b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum							<b>PDB header:</b> oxidoreductase																											
118	<a href="#">c3wgzb_</a>		not modelled	98.7	16	<b>Chain: B: PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase;																																																																																																														
119	<a href="#">c3wb9A_</a>		not modelled	98.7	14	<b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp+																																																																																																														
						<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: PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase;																																																																																																														
						<b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp+																																																																																																														
						<b>PDB header:</b> oxidoreductase																																																																																																														
						<b>Chain: A: PDB Molecule:</b> diaminopimelate dehydrogenase;																																																																																																														
						<b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum																																																																																																														
						<b>PDB header:</b> oxidoreductase																																																																																																														

120 [c1e5IA\\_](#)

Alignment

not modelled

98.6

13

**Chain: A: PDB Molecule:**saccharopine reductase;**PDBTitle:** apo saccharopine reductase from magnaporthe grisea