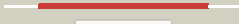



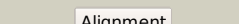






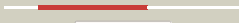











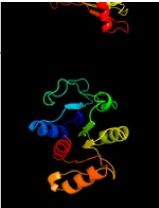

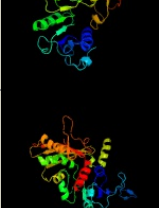



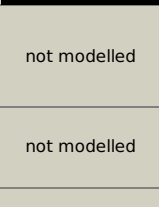
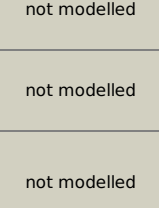


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3535c (-) _3973768_3974679
Date	Fri Aug 9 18:20:21 BST 2019
Unique Job ID	2f3b0d223242718c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4jn6B_</a>	 Alignment		100.0	100	<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
2	<a href="#">c1nvmB_</a>	 Alignment		100.0	58	<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
3	<a href="#">d1nvmB1</a>	 Alignment		100.0	49	<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
4	<a href="#">d1nvmB2</a>	 Alignment		100.0	61	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> GAPDH-like
5	<a href="#">c1b7gO_</a>	 Alignment		99.6	17	<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
6	<a href="#">c3kubA_</a>	 Alignment		99.6	15	<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
7	<a href="#">c1cf2O_</a>	 Alignment		99.5	16	<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
8	<a href="#">c2qz9B_</a>	 Alignment		99.5	21	<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
9	<a href="#">d2hjsa1</a>	 Alignment		99.5	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
10	<a href="#">c2czcD_</a>	 Alignment		99.5	17	<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
11	<a href="#">c2hjsA_</a>	 Alignment		99.5	20	<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
12	<a href="#">c2ozpA_</a>	 Alignment		99.4	16	<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
13	<a href="#">d1t4ba1</a>	Alignment		99.4	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
14	<a href="#">d1cf2o1</a>	Alignment		99.3	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
15	<a href="#">c4dpkB</a>	Alignment		99.3	15 <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
16	<a href="#">c2yv3B</a>	Alignment		99.3	19 <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
17	<a href="#">c2yvyB</a>	Alignment		99.2	18 <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
18	<a href="#">c1ys4A</a>	Alignment		99.1	16 <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
19	<a href="#">c5jw6A</a>	Alignment		99.1	17 <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
20	<a href="#">c2gz3D</a>	Alignment		99.1	16 <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
21	<a href="#">c2ep5B</a>	Alignment	not modelled	99.1	14 <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
22	<a href="#">c1t4bB</a>	Alignment	not modelled	99.1	13 <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.
23	<a href="#">c5cefA</a>	Alignment	not modelled	99.0	15 <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
24	<a href="#">d2gz1a1</a>	Alignment	not modelled	99.0	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
25	<a href="#">c2g17A</a>	Alignment	not modelled	99.0	19 <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.
26	<a href="#">c1mb4B</a>	Alignment	not modelled	99.0	19 <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
27	<a href="#">c2gd1P</a>	Alignment	not modelled	99.0	17 <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
28	<a href="#">c4zhsC</a>	Alignment	not modelled	99.0	13 <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 <b>PDB header:</b> structural genomics, oxidoreductase

29	<a href="#">c1s7cA_</a>	Alignment	not modelled	99.0	23	<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
30	<a href="#">c2q49B_</a>	Alignment	not modelled	98.9	12	<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
31	<a href="#">c4wojB_</a>	Alignment	not modelled	98.9	16	<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
32	<a href="#">c3uw3A_</a>	Alignment	not modelled	98.9	17	<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
33	<a href="#">c2i5pO_</a>	Alignment	not modelled	98.8	19	<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
34	<a href="#">c3sthA_</a>	Alignment	not modelled	98.8	17	<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
35	<a href="#">c2d2iO_</a>	Alignment	not modelled	98.8	19	<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+
36	<a href="#">c5ur0B_</a>	Alignment	not modelled	98.8	18	<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
37	<a href="#">c2pkrl_</a>	Alignment	not modelled	98.7	20	<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
38	<a href="#">c3h9eO_</a>	Alignment	not modelled	98.7	18	<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
39	<a href="#">c1hdgO_</a>	Alignment	not modelled	98.7	19	<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
40	<a href="#">c2x5kO_</a>	Alignment	not modelled	98.6	16	<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
41	<a href="#">c1rm4O_</a>	Alignment	not modelled	98.6	20	<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
42	<a href="#">c4qx6A_</a>	Alignment	not modelled	98.6	19	<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
43	<a href="#">c3b20R_</a>	Alignment	not modelled	98.6	18	<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"
44	<a href="#">c4dibF_</a>	Alignment	not modelled	98.6	19	<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
45	<a href="#">c6norB_</a>	Alignment	not modelled	98.6	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nad dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
46	<a href="#">c2ep7B_</a>	Alignment	not modelled	98.6	26	<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
47	<a href="#">c5j9gB_</a>	Alignment	not modelled	98.6	18	<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
48	<a href="#">c3e18A_</a>	Alignment	not modelled	98.6	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua
49	<a href="#">c5kt0A_</a>	Alignment	not modelled	98.5	19	<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.
50	<a href="#">c3cieC_</a>	Alignment	not modelled	98.5	17	<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
51	<a href="#">c3docD_</a>	Alignment	not modelled	98.5	17	<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
52	<a href="#">c3upyB_</a>	Alignment	not modelled	98.5	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
53	<a href="#">c3wb9A_</a>	Alignment	not modelled	98.5	19	<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
54	<a href="#">c4hadD_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
55	<a href="#">c3wzgB_</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structure of meso-dapdh q154l/t173i/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
56	<a href="#">d2czca2</a>	Alignment	not modelled	98.5	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
57	<a href="#">c5uibA_</a>	Alignment	not modelled	98.4	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase protein; <b>PDBTitle:</b> crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
58	<a href="#">c2b4rQ_</a>	Alignment	not modelled	98.4	15	<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
59	<a href="#">c3wycB_</a>	Alignment	not modelled	98.4	15	<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
60	<a href="#">c6iauB_</a>	Alignment	not modelled	98.4	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
61	<a href="#">c1cerC_</a>	Alignment	not modelled	98.4	18	<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 thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
62	<a href="#">c6ok4A_</a>	Alignment	not modelled	98.4	25	<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
63	<a href="#">c3db2C_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative nadph-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
64	<a href="#">c4mkzA_</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
65	<a href="#">c2dc1A_</a>	Alignment	not modelled	98.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
66	<a href="#">d2g17a1</a>	Alignment	not modelled	98.4	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
67	<a href="#">c5b3uB_</a>	Alignment	not modelled	98.4	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> biliverdin reductase; <b>PDBTitle:</b> crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
68	<a href="#">c3hq4R_</a>	Alignment	not modelled	98.4	24	<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
69	<a href="#">c3rbvA_</a>	Alignment	not modelled	98.4	20	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata in complex with nadp
70	<a href="#">c3ceaA_</a>	Alignment	not modelled	98.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> glyceraldehyde 3-phosphate

71	<a href="#">c1ihxD_</a>	Alignment	not modelled	98.3	18	dehydrogenase; <b>PDBTitle:</b> crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
72	<a href="#">c3e9mC_</a>	Alignment	not modelled	98.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
73	<a href="#">c2q4eB_</a>	Alignment	not modelled	98.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase at4g09670; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
74	<a href="#">c4f3yA_</a>	Alignment	not modelled	98.3	17	<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
75	<a href="#">c2qlxD_</a>	Alignment	not modelled	98.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
76	<a href="#">c1xeaD_</a>	Alignment	not modelled	98.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
77	<a href="#">c2i3aD_</a>	Alignment	not modelled	98.3	19	<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
78	<a href="#">c1vknC_</a>	Alignment	not modelled	98.3	17	<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
79	<a href="#">c3hskB_</a>	Alignment	not modelled	98.3	18	<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
80	<a href="#">c3bioB_</a>	Alignment	not modelled	98.3	23	<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
81	<a href="#">d2q49a1</a>	Alignment	not modelled	98.3	9	<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="#">c3euwB_</a>	Alignment	not modelled	98.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
83	<a href="#">c3ec7C_</a>	Alignment	not modelled	98.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
84	<a href="#">c1h6dL_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
85	<a href="#">c3dapB_</a>	Alignment	not modelled	98.2	17	<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="#">c3evnA_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
87	<a href="#">c6iaqA_</a>	Alignment	not modelled	98.2	19	<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
88	<a href="#">c1drwA_</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
89	<a href="#">c1ofgF_</a>	Alignment	not modelled	98.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
90	<a href="#">c5ugjC_</a>	Alignment	not modelled	98.2	20	<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
91	<a href="#">d1vkna1</a>	Alignment	not modelled	98.2	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
92	<a href="#">c1evjC_</a>	Alignment	not modelled	98.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
93	<a href="#">c1obfO_</a>	Alignment	not modelled	98.2	15	<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.
94	<a href="#">c4ew6A_</a>	Alignment	not modelled	98.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactose-1-dehydrogenase protein; <b>PDBTitle:</b> crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
95	<a href="#">c3ezyB_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima

96	<a href="#">d1f06a1</a>	Alignment	not modelled	98.2	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
97	<a href="#">c3fd8A</a>	Alignment	not modelled	98.1	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
98	<a href="#">c4gqaC</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad binding oxidoreductase; <b>PDBTitle:</b> crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
99	<a href="#">c4hktA</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
100	<a href="#">c2o48X</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> dimeric dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of mammalian dimeric dihydrodiol dehydrogenase
101	<a href="#">d1mb4a1</a>	Alignment	not modelled	98.1	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
102	<a href="#">d2dt5a2</a>	Alignment	not modelled	98.1	22	<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
103	<a href="#">c1zh8B</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
104	<a href="#">c3gfgB</a>	Alignment	not modelled	98.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized oxidoreductase yvaa; <b>PDBTitle:</b> structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
105	<a href="#">c6jnkA</a>	Alignment	not modelled	98.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose 1-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
106	<a href="#">c3q2kB</a>	Alignment	not modelled	98.1	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna
107	<a href="#">c3dtyA</a>	Alignment	not modelled	98.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from pseudomonas2 syringae
108	<a href="#">c3m2tA</a>	Alignment	not modelled	98.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum
109	<a href="#">d1dssg1</a>	Alignment	not modelled	98.0	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
110	<a href="#">c3kuxA</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from yersinia pestis
111	<a href="#">c2ho3D</a>	Alignment	not modelled	98.0	19	<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
112	<a href="#">c5a06E</a>	Alignment	not modelled	98.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aldose-aldose oxidoreductase; <b>PDBTitle:</b> crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
113	<a href="#">c2p2sA</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
114	<a href="#">c4h3vA</a>	Alignment	not modelled	98.0	26	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase domain protein; <b>PDBTitle:</b> crystal structure of oxidoreductase domain protein from kribbella2 flavida
115	<a href="#">d2cvoa1</a>	Alignment	not modelled	98.0	11	<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
116	<a href="#">c3nt5B</a>	Alignment	not modelled	98.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
117	<a href="#">c5yabD</a>	Alignment	not modelled	98.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> scyllo-inositol dehydrogenase with l-glucose dehydrogenase <b>PDBTitle:</b> crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
118	<a href="#">c5tenH</a>	Alignment	not modelled	98.0	12	<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
119	<a href="#">c3hjaB</a>	Alignment	not modelled	97.9	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

120	<a href="#">c3ic5A_</a>	Alignment	not modelled	97.9	19	<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 pomeroyi.
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