Phyre^2

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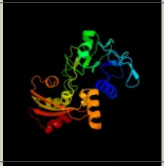
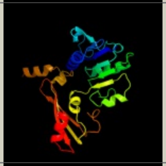
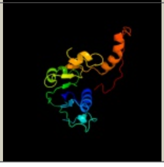
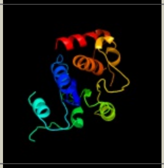
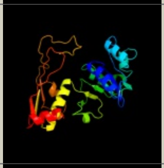
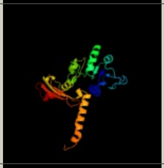
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nvmB_	Alignment		100.0	78	**PDB header:**lyase/oxidoreductase **Chain:** B: **PDB Molecule:**acetaldehyde dehydrogenase (acylating); **PDBTitle:** crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
2	d1nvmb1	Alignment		100.0	67	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
3	d1nvmb2	Alignment		100.0	81	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
4	c1b7gO_	Alignment		99.5	17	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase); **PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase
5	c3kubA_	Alignment		99.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semi-aldehyde dehydrogenase complexed2 with glycerol and phosphate of mycobacterium tuberculosis h37rv
6	c1cf2Q_	Alignment		99.4	18	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**protein (glyceraldehyde-3-phosphate **PDBTitle:** three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus
7	c2qz9B_	Alignment		99.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
8	d2hjsa1	Alignment		99.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
9	c2czcD_	Alignment		99.4	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
10	c2hjsA_	Alignment		99.3	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**usg-1 protein homolog; **PDBTitle:** the structure of a probable aspartate-semialdehyde dehydrogenase from2 pseudomonas aeruginosa
11	c2ozpA_	Alignment		99.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus

12	d1t4ba1	Alignment		99.2	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
13	d1cf2o1	Alignment		99.2	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
14	c2gz3D_	Alignment		99.1	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**aspartate beta-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate semialdehyde dehydrogenase (asadh) from2 streptococcus pneumoniae complexed with nadp and aspartate-3 semialdehyde
15	c1ys4A_	Alignment		99.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
16	c2yyyB_	Alignment		99.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
17	c1t4bB_	Alignment		99.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.
18	d2gz1a1	Alignment		98.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
19	c2yv3B_	Alignment		98.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
20	c2ep5B_	Alignment		98.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**350aa long hypothetical aspartate-semialdehyde **PDBTitle:** structural study of project id st1242 from sulfolobus tokodaii strain7
21	c3uw3A_	Alignment	not modelled	98.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
22	c1s7cA_	Alignment	not modelled	98.8	18	**PDB header:**structural genomics, oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase a; **PDBTitle:** crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
23	c2gd1P_	Alignment	not modelled	98.8	17	**PDB header:**oxidoreductase(aldehyde(d)-nad(a)) **Chain:** P: **PDB Molecule:**apo-d-glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophillus
24	c2q49B_	Alignment	not modelled	98.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at2g19940
25	c1mb4B_	Alignment	not modelled	98.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 from vibrio cholerae with nadp and s-methyl-l-cysteine3 sulfoxide
26	c2g17A_	Alignment	not modelled	98.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** the structure of n-acetyl-gamma-glutamyl-phosphate reductase from2 salmonella typhimurium.
						PDB header:oxidoreductase

27	c1rm4O_	Alignment	not modelled	98.5	17	**Chain:** O: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase a; **PDBTitle:** crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
28	c2pkrI_	Alignment	not modelled	98.5	17	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase aor; **PDBTitle:** crystal structure of (a+cte)4 chimeric form of2 photosyntetic glyceraldehyde-3-phosphate dehydrogenase,3 complexed with nadp
29	c2i5pO_	Alignment	not modelled	98.5	19	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
30	c3h9eA_	Alignment	not modelled	98.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:** **PDBTitle:** crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
31	c2d2iO_	Alignment	not modelled	98.5	17	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
32	c3e18A_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
33	c3sthA_	Alignment	not modelled	98.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
34	c3cieC_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
35	c3rbvA_	Alignment	not modelled	98.3	18	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
36	c3gfgB_	Alignment	not modelled	98.3	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
37	c2ep7B_	Alignment	not modelled	98.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** structural study of project id aq_1065 from aquifex aeolicus vf5
38	c3ceaA_	Alignment	not modelled	98.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**myo-inositol 2-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
39	c1hdgO_	Alignment	not modelled	98.3	20	**PDB header:**oxidoreductase (aldehyd(d)-nad(a)) **Chain:** O: **PDB Molecule:**holo-d-glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** the crystal structure of holo-glyceraldehyde-3-phosphate dehydrogenase2 from the hyperthermophilic bacterium thermotoga maritima at 2.53 angstroms resolution
40	c3ec7C_	Alignment	not modelled	98.3	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
41	c1h6dL_	Alignment	not modelled	98.2	17	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
42	c3docD_	Alignment	not modelled	98.2	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis
43	c3b20R_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase (nadp+); **PDBTitle:** crystal structure analysis of dehydrogenase complexed with nad
44	c1ofgF_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
45	c3m2tA_	Alignment	not modelled	98.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
46	c2x5kO_	Alignment	not modelled	98.2	15	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**d-erythrose-4-phosphate dehydrogenase; **PDBTitle:** structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
47	d2czca2	Alignment	not modelled	98.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	c1evjC_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
						PDB header:oxidoreductase

49	c3fd8A_	Alignment	not modelled	98.2	19	**Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
50	c3dapB_	Alignment	not modelled	98.2	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
51	c3e9mC_	Alignment	not modelled	98.1	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
52	c2q4eB_	Alignment	not modelled	98.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable oxidoreductase at4g09670; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
53	c1xeaD_	Alignment	not modelled	98.1	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
54	c2dc1A_	Alignment	not modelled	98.1	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
55	c3evnA_	Alignment	not modelled	98.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
56	c2b4rQ_	Alignment	not modelled	98.1	16	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
57	c1cerC_	Alignment	not modelled	98.1	18	**PDB header:**oxidoreductase (aldehyde(d)-nad(a)) **Chain:** C: **PDB Molecule:**holo-d-glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
58	c3hskB_	Alignment	not modelled	98.1	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
59	d1f06a1	Alignment	not modelled	98.1	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	c2glxD_	Alignment	not modelled	98.1	24	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
61	c1ihxD_	Alignment	not modelled	98.0	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of two d-glyceraldehyde-3-phosphate2 dehydrogenase complexes: a case of asymmetry
62	c1vknC_	Alignment	not modelled	98.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tm1782) from thermotoga maritima at 1.80 a resolution
63	c1zh8B_	Alignment	not modelled	98.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
64	c3q2kB_	Alignment	not modelled	98.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
65	d2q49a1	Alignment	not modelled	98.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c3hq4R_	Alignment	not modelled	98.0	22	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
67	c3db2C_	Alignment	not modelled	98.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative nadph-dependent oxidoreductase; **PDBTitle:** crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
68	c3bioB_	Alignment	not modelled	98.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
69	c3kuxA_	Alignment	not modelled	98.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
70	c3nt5B_	Alignment	not modelled	98.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; **PDBTitle:** crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
71	c3moiA_	Alignment	not modelled	98.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50

72	d1zh8a1	Alignment	not modelled	98.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
73	c3ezyB_	Alignment	not modelled	97.9	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
74	c3euwB_	Alignment	not modelled	97.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
75	c3uuwB_	Alignment	not modelled	97.9	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase with nad(p)-binding rossmann-fold **PDBTitle:** 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
76	d1vkna1	Alignment	not modelled	97.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	d1h6da1	Alignment	not modelled	97.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
78	c3e82A_	Alignment	not modelled	97.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
79	c2o48X_	Alignment	not modelled	97.8	12	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
80	c3hjaB_	Alignment	not modelled	97.8	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
81	c1obfO_	Alignment	not modelled	97.8	16	**PDB header:**glycolytic pathway **Chain:** O: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** the crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from alcaligenes xylosoxidans at 1.73 resolution.
82	c2p2sA_	Alignment	not modelled	97.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
83	c2i3aD_	Alignment	not modelled	97.7	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (rv1652) from mycobacterium tuberculosis
84	d1ebfa1	Alignment	not modelled	97.7	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
85	c1drwA_	Alignment	not modelled	97.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
86	d2g17a1	Alignment	not modelled	97.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
87	c3ktdC_	Alignment	not modelled	97.7	21	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
88	d2cvoa1	Alignment	not modelled	97.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
89	d1ydwa1	Alignment	not modelled	97.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	d2dt5a2	Alignment	not modelled	97.7	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
91	d1ryda1	Alignment	not modelled	97.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
92	c3f4lF_	Alignment	not modelled	97.6	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**putative oxidoreductase yhhx; **PDBTitle:** crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
93	c1ebuA_	Alignment	not modelled	97.6	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase complex with nad analogue and l-2 homoserine
94	c3do5A_	Alignment	not modelled	97.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
95	d1dssg1	Alignment	not modelled	97.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						Fold:NAD(P)-binding Rossmann-fold domains

96	d1tlta1	Alignment	not modelled	97.6	17	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	d1mb4a1	Alignment	not modelled	97.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
98	c3v5nA_	Alignment	not modelled	97.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
99	d1euca1	Alignment	not modelled	97.6	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
100	c1tltB_	Alignment	not modelled	97.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
101	c3ketA_	Alignment	not modelled	97.6	17	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
102	d2nvwa1	Alignment	not modelled	97.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
103	c3ic5A_	Alignment	not modelled	97.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
104	c3fhlC_	Alignment	not modelled	97.5	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
105	c2ho3D_	Alignment	not modelled	97.5	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
106	c2ixaA_	Alignment	not modelled	97.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
107	c1lc3A_	Alignment	not modelled	97.5	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
108	d1gpja2	Alignment	not modelled	97.5	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
109	c3c1aB_	Alignment	not modelled	97.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
110	c3a14B_	Alignment	not modelled	97.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of dxr from thermotoga maritima, in complex with2 nadph
111	d1pqua1	Alignment	not modelled	97.4	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
112	c2dt5A_	Alignment	not modelled	97.4	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
113	c3dtyA_	Alignment	not modelled	97.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
114	c1gpjA_	Alignment	not modelled	97.4	23	**PDB header:**reductase **Chain:** A: **PDB Molecule:**glutamyl-trna reductase; **PDBTitle:** glutamyl-trna reductase from methanopyrus kandleri
115	c2nvwB_	Alignment	not modelled	97.2	13	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
116	c2jcyA_	Alignment	not modelled	97.2	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
117	c2axqA_	Alignment	not modelled	97.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
118	d1xeaa1	Alignment	not modelled	97.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
119	c3mtjA_	Alignment	not modelled	97.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
						PDB header:oxidoreductase

120	c2graA_	Alignment	not modelled	97.1	16	**Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase 1; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp