Phyre2

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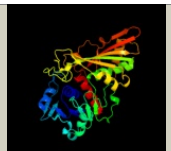
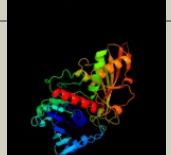
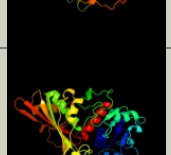
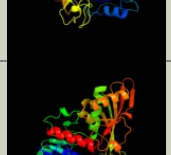
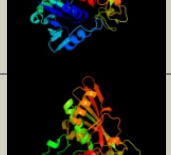
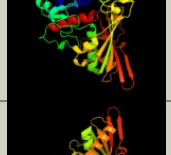
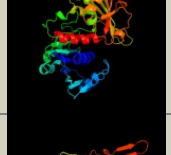
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1i32D_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
2	c3hq4R_	Alignment		100.0	58	**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
3	c2ep7B_	Alignment		100.0	49	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** structural study of project id aq_1065 from aquifex aeolicus vf5
4	c3docD_	Alignment		100.0	48	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis
5	c1ihxD_	Alignment		100.0	48	**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
6	c3h9eA_	Alignment		100.0	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:** **PDBTitle:** crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
7	c1hdgO_	Alignment		100.0	54	**PDB header:**oxidoreductase (aldehy(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
8	c2b4rQ_	Alignment		100.0	45	**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
9	c1obfO_	Alignment		100.0	44	**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.
10	c1rm4O_	Alignment		100.0	45	**PDB header:**oxidoreductase **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
11	c3hjaB_	Alignment		100.0	50	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi

12	c2pkrl_	Alignment		100.0	45	**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
13	c2d2iO_	Alignment		100.0	45	**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+
14	c3cieC_	Alignment		100.0	47	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
15	c3b20R_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase (nadp+); **PDBTitle:** crystal structure analysis of dehydrogenase complexed with nad
16	c1cerC_	Alignment		100.0	50	**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
17	c2x5kO_	Alignment		100.0	40	**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
18	c1s7cA_	Alignment		100.0	46	**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
19	c2i5pO_	Alignment		100.0	48	**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
20	c3sthA_	Alignment		100.0	49	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
21	c2gd1P_	Alignment	not modelled	100.0	52	**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
22	c2yyyB_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
23	c1cf2Q_	Alignment	not modelled	100.0	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
24	c1b7gO_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase); **PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase
25	d1gado2	Alignment	not modelled	100.0	51	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
26	d1u8fo2	Alignment	not modelled	100.0	50	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
27	d3cmco2	Alignment	not modelled	100.0	57	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like

28	c2czcD_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
29	d1rm4a2	Alignment	not modelled	100.0	49	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
30	d2b4ro2	Alignment	not modelled	100.0	52	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
31	d1ggaa2	Alignment	not modelled	100.0	50	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
32	d3gpdg2	Alignment	not modelled	100.0	51	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
33	d1dssg2	Alignment	not modelled	100.0	51	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
34	d1i32a2	Alignment	not modelled	100.0	49	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
35	d1k3ta2	Alignment	not modelled	100.0	49	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
36	d2pkqo2	Alignment	not modelled	100.0	51	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
37	d2g82a2	Alignment	not modelled	100.0	52	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
38	d1hdgo2	Alignment	not modelled	100.0	55	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
39	d1obfo2	Alignment	not modelled	100.0	45	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
40	d3cmco1	Alignment	not modelled	100.0	44	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	d1u8fo1	Alignment	not modelled	100.0	37	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	d1hdgo1	Alignment	not modelled	100.0	48	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	d1j0xo1	Alignment	not modelled	100.0	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	d3gpdg1	Alignment	not modelled	100.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d1gado1	Alignment	not modelled	100.0	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	d2g82a1	Alignment	not modelled	100.0	46	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	d1vc2a1	Alignment	not modelled	100.0	49	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	d1dssg1	Alignment	not modelled	100.0	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	d1rm4a1	Alignment	not modelled	100.0	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d1ggaa1	Alignment	not modelled	100.0	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
51	d1k3ta1	Alignment	not modelled	100.0	38	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	d1obfo1	Alignment	not modelled	100.0	41	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	d2b4ro1	Alignment	not modelled	100.0	40	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

53	d2b4f0i	Alignment	not modelled	100.0	40	**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
54	d1i32a1	Alignment	not modelled	100.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	d2pkqo1	Alignment	not modelled	100.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
56	c2qz9B_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
57	c2ep5B_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**350aa long hypothetical aspartate-semialdehyde **PDBTitle:** structural study of project id st1242 from sulfolobus tokodaii strain7
58	c2yv3B_	Alignment	not modelled	100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
59	c3uw3A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
60	c2g17A_	Alignment	not modelled	100.0	16	**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.
61	c2gz3D_	Alignment	not modelled	100.0	18	**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
62	c1ys4A_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
63	c1t4bB_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** 1.6 angstrom structure of escherichia coli aspartate-2 semialdehyde dehydrogenase.
64	c3kubA_	Alignment	not modelled	100.0	21	**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
65	c2q49B_	Alignment	not modelled	100.0	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
66	c1mb4B_	Alignment	not modelled	100.0	18	**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
67	d1cf2o1	Alignment	not modelled	100.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
68	c2ozpA_	Alignment	not modelled	100.0	15	**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
69	c2hjsA_	Alignment	not modelled	100.0	19	**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
70	c2i3aD_	Alignment	not modelled	100.0	16	**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
71	c3hskB_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
72	c1vknC_	Alignment	not modelled	100.0	15	**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
73	d2gz1a1	Alignment	not modelled	100.0	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
74	d1pqua2	Alignment	not modelled	99.9	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
75	d1t4ba2	Alignment	not modelled	99.9	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
76	d1mb4a2	Alignment	not modelled	99.9	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain

						Family:GAPDH-like
77	d2gz1a2	Alignment	not modelled	99.9	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
78	d2hjsa2	Alignment	not modelled	99.8	18	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
79	d1t4ba1	Alignment	not modelled	99.8	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	d2czca2	Alignment	not modelled	99.8	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	d2hjsa1	Alignment	not modelled	99.8	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	d1pqua1	Alignment	not modelled	99.7	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	d2g17a1	Alignment	not modelled	99.7	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
84	d2cvoa1	Alignment	not modelled	99.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
85	d1mb4a1	Alignment	not modelled	99.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
86	d1vkna1	Alignment	not modelled	99.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
87	d2q49a1	Alignment	not modelled	99.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	d1b7go1	Alignment	not modelled	99.6	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
89	d1cf2o2	Alignment	not modelled	99.6	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
90	d1b7go2	Alignment	not modelled	99.6	17	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
91	d2cvoa2	Alignment	not modelled	99.5	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
92	d2czca1	Alignment	not modelled	99.4	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
93	c1nvmB_	Alignment	not modelled	98.8	16	**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
94	c1drwA_	Alignment	not modelled	98.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
95	c3ijpA_	Alignment	not modelled	98.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
96	d1nvmb1	Alignment	not modelled	98.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	c3bioB_	Alignment	not modelled	98.3	18	**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
98	c2z2vA_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
99	c3dapB_	Alignment	not modelled	98.2	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
100	d1q0qa2	Alignment	not modelled	98.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
101	c3a14B_	Alignment	not modelled	98.2	17	**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
						PDB header:oxidoreductase

102	c2ho3D_	Alignment	not modelled	98.1	21	**Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
103	d1diha1	Alignment	not modelled	98.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
104	d1r0ka2	Alignment	not modelled	98.1	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
105	c2dc1A_	Alignment	not modelled	98.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
106	d1f06a1	Alignment	not modelled	98.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
107	c1yl7F_	Alignment	not modelled	98.1	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
108	c3mtjA_	Alignment	not modelled	98.0	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
109	c1r0lD_	Alignment	not modelled	98.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
110	c3do5A_	Alignment	not modelled	98.0	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
111	d1yl7a1	Alignment	not modelled	98.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
112	c3e9mC_	Alignment	not modelled	98.0	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
113	c3fhlC_	Alignment	not modelled	97.9	24	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
114	c2axqA_	Alignment	not modelled	97.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
115	c2ixaA_	Alignment	not modelled	97.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
116	c3m2tA_	Alignment	not modelled	97.9	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
117	c3ic5A_	Alignment	not modelled	97.9	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
118	d1ydwa1	Alignment	not modelled	97.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
119	c3e18A_	Alignment	not modelled	97.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
120	c3euwB_	Alignment	not modelled	97.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032