Phyre^2

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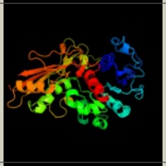
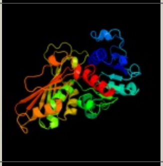
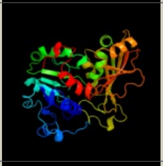
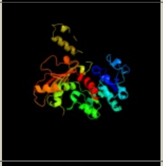
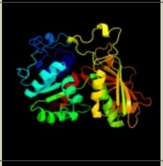
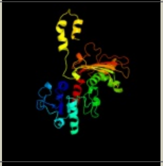
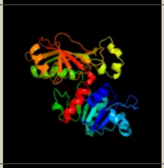
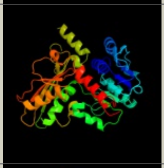
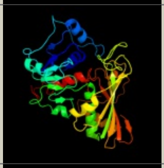
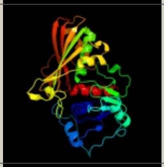
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g17A_	Alignment		100.0	90	**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.
2	c2q49B_	Alignment		100.0	37	**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
3	c2ozpA_	Alignment		100.0	34	**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
4	c2i3aD_	Alignment		100.0	38	**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
5	c1vknC_	Alignment		100.0	37	**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
6	c2ep5B_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**350aa long hypothetical aspartate-semialdehyde **PDBTitle:** structural study of project id st1242 from sulfolobus tokodaii strain7
7	c1mb4B_	Alignment		100.0	15	**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
8	c3hskB_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
9	c1ys4A_	Alignment		100.0	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
10	c1t4bB_	Alignment		100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.
11	c2gz3D_	Alignment		100.0	24	**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

12	c3uw3A_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
13	c3kubA_	Alignment		100.0	25	**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
14	c2yv3B_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
15	c2qz9B_	Alignment		100.0	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
16	c2hjsA_	Alignment		100.0	25	**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
17	c2gd1P_	Alignment		100.0	15	**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
18	c3sthA_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
19	c1s7cA_	Alignment		100.0	14	**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
20	d2g17a1	Alignment		100.0	78	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
21	c3cieC_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
22	d2q49a1	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
23	c1cerC_	Alignment	not modelled	100.0	16	**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
24	c1cf2Q_	Alignment	not modelled	100.0	14	**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
25	c1hdgO_	Alignment	not modelled	100.0	15	**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
26	c1rm4O_	Alignment	not modelled	100.0	13	**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

27	d2cvoa1	Alignment	not modelled	100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	c1b7gO_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase); **PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase
29	c2d2iO_	Alignment	not modelled	100.0	15	**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+
30	c2pkrI_	Alignment	not modelled	100.0	13	**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
31	c3h9eA_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:** **PDBTitle:** crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
32	c2yyyB_	Alignment	not modelled	100.0	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
33	d1vkna1	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
34	c2x5kO_	Alignment	not modelled	100.0	14	**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
35	c2i5pO_	Alignment	not modelled	100.0	14	**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
36	c3docD_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis
37	c2b4rQ_	Alignment	not modelled	100.0	15	**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
38	c2ep7B_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** structural study of project id aq_1065 from aquifex aeolicus vf5
39	c3hq4R_	Alignment	not modelled	100.0	17	**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
40	c2czcD_	Alignment	not modelled	100.0	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
41	c3hjaB_	Alignment	not modelled	100.0	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
42	c1ihxD_	Alignment	not modelled	100.0	11	**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
43	c1obfO_	Alignment	not modelled	100.0	14	**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.
44	d2g17a2	Alignment	not modelled	100.0	92	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
45	d2cvoa2	Alignment	not modelled	100.0	38	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
46	c1i32D_	Alignment	not modelled	100.0	12	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
47	d1vkna2	Alignment	not modelled	100.0	39	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like

48	d2q49a2	Alignment	not modelled	100.0	40	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
49	d2gz1a1	Alignment	not modelled	100.0	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d2hjsa2	Alignment	not modelled	100.0	20	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
51	d2hjsa1	Alignment	not modelled	100.0	29	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	d1pqua2	Alignment	not modelled	100.0	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
53	d1t4ba2	Alignment	not modelled	100.0	26	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
54	d2gz1a2	Alignment	not modelled	100.0	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
55	d1mb4a2	Alignment	not modelled	100.0	24	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
56	d1t4ba1	Alignment	not modelled	100.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	d1pqua1	Alignment	not modelled	100.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
58	d1mb4a1	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
59	d1hdgo2	Alignment	not modelled	99.9	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
60	d1cf2o1	Alignment	not modelled	99.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	d1rm4a2	Alignment	not modelled	99.9	8	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
62	d1dssg1	Alignment	not modelled	99.9	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
63	d1u8fo2	Alignment	not modelled	99.9	12	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
64	d3cmco2	Alignment	not modelled	99.9	12	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
65	d2b4ro2	Alignment	not modelled	99.9	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
66	d1gado2	Alignment	not modelled	99.9	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
67	d1i32a2	Alignment	not modelled	99.9	11	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
68	d1ggaa2	Alignment	not modelled	99.8	8	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
69	d3gpdg2	Alignment	not modelled	99.8	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
70	d2pkqo2	Alignment	not modelled	99.8	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
71	d2g82a2	Alignment	not modelled	99.8	15	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
72	d1dssg2	Alignment	not modelled	99.8	11	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
73	d1gado1	Alignment	not modelled	99.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-

						terminal domain
74	d1k3ta2	Alignment	not modelled	99.8	9	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
75	d3cmco1	Alignment	not modelled	99.8	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	d1obfo2	Alignment	not modelled	99.8	11	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
77	d1j0xo1	Alignment	not modelled	99.8	8	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
78	d1rm4a1	Alignment	not modelled	99.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
79	d1u8fo1	Alignment	not modelled	99.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	d2g82a1	Alignment	not modelled	99.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	d1ggaa1	Alignment	not modelled	99.8	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	d1vc2a1	Alignment	not modelled	99.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	d1k3ta1	Alignment	not modelled	99.7	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
84	d1hdgo1	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
85	d1i32a1	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
86	d2pkqo1	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	d3gpdg1	Alignment	not modelled	99.7	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	d2b4ro1	Alignment	not modelled	99.6	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	d1obfo1	Alignment	not modelled	99.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	c1drwA_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
91	d2czca2	Alignment	not modelled	99.2	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
92	c1nvmB_	Alignment	not modelled	99.1	17	**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
93	c3ijpA_	Alignment	not modelled	99.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
94	c3ic5A_	Alignment	not modelled	99.1	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.
95	c3dapB_	Alignment	not modelled	99.0	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
96	d1diha1	Alignment	not modelled	99.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	d1f06a1	Alignment	not modelled	98.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
98	c2z2vA_	Alignment	not modelled	98.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
99	d1nvmb1	Alignment	not modelled	98.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

99	d1nvmb1	Alignment	not modelled	98.9	16	**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
100	d1b7go1	Alignment	not modelled	98.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
101	c2ho3D_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
102	d1cf2o2	Alignment	not modelled	98.8	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
103	c3bioB_	Alignment	not modelled	98.8	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
104	c3fhlC_	Alignment	not modelled	98.7	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
105	c1e5lA_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
106	d1b7go2	Alignment	not modelled	98.6	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
107	c2dt5A_	Alignment	not modelled	98.6	13	**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
108	c2axqA_	Alignment	not modelled	98.6	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
109	d1q0qa2	Alignment	not modelled	98.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	d2dt5a2	Alignment	not modelled	98.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
111	c3m2tA_	Alignment	not modelled	98.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
112	c2q4eB_	Alignment	not modelled	98.5	11	**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
113	c2ixaA_	Alignment	not modelled	98.5	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
114	c3f4lF_	Alignment	not modelled	98.5	19	**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
115	c3db2C_	Alignment	not modelled	98.5	8	**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
116	c3e18A_	Alignment	not modelled	98.5	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
117	c3do5A_	Alignment	not modelled	98.5	18	**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
118	d2czca1	Alignment	not modelled	98.5	14	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
119	c3a14B_	Alignment	not modelled	98.5	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
120	c3euwB_	Alignment	not modelled	98.5	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032