























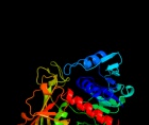









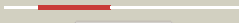

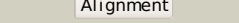


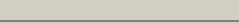



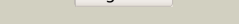
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2x5kO_	 Alignment		100.0	99	PDB header: oxidoreductase Chain: O: PDB Molecule: d-erythrose-4-phosphate dehydrogenase; PDBTitle: structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
2	c1obfO_	 Alignment		100.0	49	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.
3	c2d2iO_	 Alignment		100.0	44	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+
4	c1i32D_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
5	c3b20R_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure analysis of dehydrogenase complexed with nad
6	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
7	c1rm4O_	 Alignment		100.0	41	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
8	c1hdqO_	 Alignment		100.0	45	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
9	c2pkrl_	 Alignment		100.0	41	PDB header: oxidoreductase Chain: I: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase aor; PDBTitle: crystal structure of (a+cte)4 chimeric form of2 photosynthetic glyceraldehyde-3-phosphate dehydrogenase,3 complexed with nadp
10	c3hq4R_	 Alignment		100.0	41	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
11	c2ep7B_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5
						PDB header: oxidoreductase

12	c2b4rQ	Alignment		100.0	40	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
13	c3cieC	Alignment		100.0	36	PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
14	c1cerC	Alignment		100.0	43	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
15	c3h9eA	Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
16	c3hjaB	Alignment		100.0	42	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
17	c1ihxD	Alignment		100.0	36	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
18	c1s7cA	Alignment		100.0	40	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	c3sthA	Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
20	c2i5pO	Alignment		100.0	39	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
21	c2gd1P	Alignment	not modelled	100.0	45	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 stearothermophilus
22	c2yyvB	Alignment	not modelled	100.0	15	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	15	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	15	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
25	d1rm4a2	Alignment	not modelled	100.0	42	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
26	d3cmco2	Alignment	not modelled	100.0	42	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
27	d1gado2	Alignment	not modelled	100.0	35	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
28	d2h4r2	Alignment	not modelled	100.0	38	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-

28	d2u4fo2	Alignment	not modelled	100.0	38	terminal domain Family: GAPDH-like
29	d1u8fo2	Alignment	not modelled	100.0	36	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
30	d2pkqo2	Alignment	not modelled	100.0	44	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
31	d3gpdg2	Alignment	not modelled	100.0	34	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
32	d1ggaa2	Alignment	not modelled	100.0	33	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
33	d1dssg2	Alignment	not modelled	100.0	33	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
34	d1i32a2	Alignment	not modelled	100.0	35	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
35	d1hdgo2	Alignment	not modelled	100.0	41	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
36	d2g82a2	Alignment	not modelled	100.0	42	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
37	d1k3ta2	Alignment	not modelled	100.0	34	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
38	d1obfo2	Alignment	not modelled	100.0	44	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
39	c2czcD	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
40	d3cmco1	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
41	d1hdgo1	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
42	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
43	d1obfo1	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
44	d1gado1	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
45	d1k3ta1	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
46	d1u8fo1	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
47	d1rm4a1	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
48	d2g82a1	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	d3gpdg1	Alignment	not modelled	100.0	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d1vc2a1	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
51	d1j0xo1	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
52	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
53	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

54	d1dssg1	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
55	d2b4ro1	Alignment	not modelled	100.0	42	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	22	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	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 350aa long hypothetical aspartate-semialdehyde PDBTitle: structural study of project id st1242 from sulfolobus tokodaii strain7
58	c2gz3D_	Alignment	not modelled	100.0	19	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
59	c2yv3B_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
60	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
61	c2q17A_	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.
62	clys4A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
63	c3kubA_	Alignment	not modelled	100.0	22	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
64	c1t4bB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: 1.6 angstrom structure of escherichia coli aspartate-2 semialdehyde dehydrogenase.
65	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
66	c2q49B_	Alignment	not modelled	100.0	16	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
67	c2ozpA_	Alignment	not modelled	100.0	14	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
68	c2hjsA_	Alignment	not modelled	100.0	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
69	d1cf2o1	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
70	c2i3aD_	Alignment	not modelled	100.0	15	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	18	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	13	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	99.9	23	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	21	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
75	d1t4ba2	Alignment	not modelled	99.9	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
76	d1mb4a2	Alignment	not modelled	99.9	15	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
						Fold: FwdE/GAPDH domain-like

77	d2gz1a2	Alignment	not modelled	99.9	15	Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
78	d2czca2	Alignment	not modelled	99.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
79	d2hjsa1	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
80	d1mb4a1	Alignment	not modelled	99.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	d1t4ba1	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
82	d2hjsa2	Alignment	not modelled	99.8	13	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
83	d1pqua1	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
84	d2g17a1	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	d2cvoa1	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	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
87	d1cf2o2	Alignment	not modelled	99.6	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
88	d1b7go2	Alignment	not modelled	99.6	19	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
89	d2q49a1	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
90	d1b7go1	Alignment	not modelled	99.5	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
91	d2czca1	Alignment	not modelled	99.5	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
92	d2cvoa2	Alignment	not modelled	99.4	10	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
93	c1nvmb	Alignment	not modelled	98.7	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	98.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
95	c3ijpA	Alignment	not modelled	98.4	17	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	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	c3euwB	Alignment	not modelled	98.2	16	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
98	c3dapB	Alignment	not modelled	98.2	28	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
99	c3fd8A	Alignment	not modelled	98.2	22	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
100	d1f06a1	Alignment	not modelled	98.2	32	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
101	c3bioB	Alignment	not modelled	98.1	27	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
102	c2dc1A	Alignment	not modelled	98.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus

103	d1diha1	 Alignment	not modelled	98.1	26	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
104	c3mtjA	 Alignment	not modelled	98.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
105	c3nt5B	 Alignment	not modelled	98.0	21	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
106	c3a14B	 Alignment	not modelled	98.0	16	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
107	d1r0ka2	 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
108	c3do5A	 Alignment	not modelled	97.9	20	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
109	c2z2vA	 Alignment	not modelled	97.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
110	c1yl7F	 Alignment	not modelled	97.9	25	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)
111	c1r0lD	 Alignment	not modelled	97.9	13	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
112	c1ebuA	 Alignment	not modelled	97.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
113	d1vm6a3	 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
114	c3moiA	 Alignment	not modelled	97.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
115	c1j5pA	 Alignment	not modelled	97.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
116	c1vm6B	 Alignment	not modelled	97.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
117	c3ic5A	 Alignment	not modelled	97.8	24	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	c2ixaA	 Alignment	not modelled	97.8	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyyme, n-acetylgalactosaminidase
119	d1yl7a1	 Alignment	not modelled	97.8	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
120	c2ejwB	 Alignment	not modelled	97.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8