



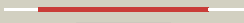


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1s7cA_	 Alignment		100.0	100	PDB header: structural genomics, oxidoreductase Chain: A: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase a; PDBTitle: crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
2	c1i32D_	 Alignment		100.0	55	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
3	c2ep7B_	 Alignment		100.0	52	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5
4	c3hq4R_	 Alignment		100.0	48	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
5	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
6	c2b4rO_	 Alignment		100.0	65	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
7	c1hdgO_	 Alignment		100.0	51	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	c3cieC_	 Alignment		100.0	62	PDB header: oxidoreductase Chain: C: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
9	c2d2iO_	 Alignment		100.0	49	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+
10	c3b20R_	 Alignment		100.0	49	PDB header: oxidoreductase Chain: R: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase (nadp+); PDBTitle: crystal structure analysis of dehydrogenase complexed with nad
11	c3h9eA_	 Alignment		100.0	63	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate

12	c1rm4O_	Alignment		100.0	48	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
13	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
14	c2pkrl_	Alignment		100.0	48	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
15	c3hjaB_	Alignment		100.0	53	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
16	c1ihxD_	Alignment		100.0	66	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
17	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 xylooxidans at 1.73 resolution.
18	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
19	c3sthA_	Alignment		100.0	63	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	66	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	59	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	c2yyyB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
23	c1cf2O_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: Q: PDB Molecule: protein (glyceraldehyde-3-phosphate dehydrogenase); 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	c2czcD_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
26	d1gado2	Alignment	not modelled	100.0	100	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
27	d1rm4a2	Alignment	not modelled	100.0	50	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain

						Family: GAPDH-like
28	d1u8fo2	Alignment	not modelled	100.0	79	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
29	d3cmco2	Alignment	not modelled	100.0	60	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
30	d2b4ro2	Alignment	not modelled	100.0	74	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
31	d3gpdg2	Alignment	not modelled	100.0	78	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
32	d1dssg2	Alignment	not modelled	100.0	79	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
33	d1ggaa2	Alignment	not modelled	100.0	61	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
34	d1i32a2	Alignment	not modelled	100.0	61	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
35	d2pkqo2	Alignment	not modelled	100.0	51	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
36	d1hdgo2	Alignment	not modelled	100.0	50	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
37	d1k3ta2	Alignment	not modelled	100.0	59	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
38	d2g82a2	Alignment	not modelled	100.0	52	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
39	d1gado1	Alignment	not modelled	100.0	92	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	d1obfo2	Alignment	not modelled	100.0	51	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
41	d3cmco1	Alignment	not modelled	100.0	53	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	d1u8fo1	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
43	d1k3ta1	Alignment	not modelled	100.0	43	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	d1ggaa1	Alignment	not modelled	100.0	47	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d1hdgo1	Alignment	not modelled	100.0	45	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	48	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	d1rm4a1	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
49	d3gpdg1	Alignment	not modelled	100.0	47	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d1j0xo1	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
51	c2qz9B	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
52	d1i32a1	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
53	d2b4ro1	Alignment	not modelled	100.0	52	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

53	d2v4f01	Alignment	not modelled	100.0	32	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
54	d1obfo1	Alignment	not modelled	100.0	46	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
55	d1dssg1	Alignment	not modelled	100.0	46	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
56	d2pkqo1	Alignment	not modelled	100.0	41	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
57	c2ep5B_	Alignment	not modelled	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
58	c2g17A_	Alignment	not modelled	100.0	15	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.
59	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
60	c3uw3A_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of an aspartate-semialdehyde dehydrogenase from2 burkholderia thailandensis
61	c2q49B_	Alignment	not modelled	100.0	13	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
62	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 (tha1904) from thermus thermophilus
63	c2gz3D_	Alignment	not modelled	100.0	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
64	c1ys4A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
65	c1t4bB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.
66	c1mb4B_	Alignment	not modelled	100.0	16	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	c3kubA_	Alignment	not modelled	100.0	18	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
68	c2hjsA_	Alignment	not modelled	100.0	18	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	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
70	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
71	c3hskB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
72	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
73	d2gz1a1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
74	d2g17a1	Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	d2cvoa1	Alignment	not modelled	99.9	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	d1vkna1	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-

						terminal domain
77	d2q49a1	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
78	d2hjsa1	Alignment	not modelled	99.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
79	d2cvoa2	Alignment	not modelled	99.9	11	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
80	d2hjsa2	Alignment	not modelled	99.9	16	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
81	d1pqua2	Alignment	not modelled	99.9	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
82	d1mb4a2	Alignment	not modelled	99.9	19	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
83	d1t4ba2	Alignment	not modelled	99.9	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
84	d2gz1a2	Alignment	not modelled	99.9	14	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
85	d1t4ba1	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
86	d1mb4a1	Alignment	not modelled	99.8	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
87	d1pqua1	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
88	d1vkna2	Alignment	not modelled	99.8	11	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
89	d2q49a2	Alignment	not modelled	99.8	9	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
90	d2czca2	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
91	d2g17a2	Alignment	not modelled	99.8	12	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
92	d1cf2o2	Alignment	not modelled	99.5	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
93	d1b7go2	Alignment	not modelled	99.5	21	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
94	d1b7go1	Alignment	not modelled	99.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
95	d2czca1	Alignment	not modelled	99.4	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
96	c1nvmB_	Alignment	not modelled	99.1	19	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
97	c1drwA_	Alignment	not modelled	99.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
98	d1nvmbl	Alignment	not modelled	98.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	c2z2vA_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
100	c3fd8A_	Alignment	not modelled	98.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
101	c3euwB_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
102	c3iinA_	Alignment	not modelled	98.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase;

102	c3jppA	Alignment	not modelled	98.6	19	PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroiyi.
103	c3ic5A	Alignment	not modelled	98.6	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
104	d1f06a1	Alignment	not modelled	98.6	27	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/ldh/moca family member) from2 porphyromonas gingivalis w83
105	c3dapB	Alignment	not modelled	98.6	28	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
106	c3bioB	Alignment	not modelled	98.6	24	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
107	c3e9mC	Alignment	not modelled	98.6	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
108	c3nt5B	Alignment	not modelled	98.4	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
109	c3a14B	Alignment	not modelled	98.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
110	d1dih1	Alignment	not modelled	98.4	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
111	c2dc1A	Alignment	not modelled	98.4	30	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
112	c2axqA	Alignment	not modelled	98.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
113	d2dt5a2	Alignment	not modelled	98.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
114	c3fhlC	Alignment	not modelled	98.3	27	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyyme, n-acetylgalactosaminidase
115	c3e18A	Alignment	not modelled	98.3	28	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
116	c3e82A	Alignment	not modelled	98.3	24	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)
117	c3moiA	Alignment	not modelled	98.3	21	
118	c2ixaA	Alignment	not modelled	98.3	18	
119	c2q4eB	Alignment	not modelled	98.3	20	
120	c1yl7F	Alignment	not modelled	98.3	21	