











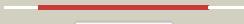



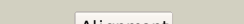

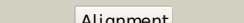

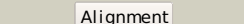

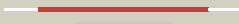

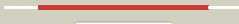



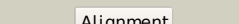
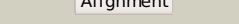




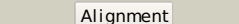
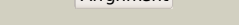
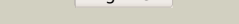
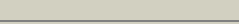
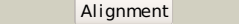



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qz9B_	 Alignment		100.0	48	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 ii from vibrio cholerae
2	c2hjsA_	 Alignment		100.0	37	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
3	c2qz3D_	 Alignment		100.0	33	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
4	c3kubA_	 Alignment		100.0	35	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
5	c2yv3B_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase from thermus2 thermophilus hb8
6	c1mb4B_	 Alignment		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
7	c1t4bB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: 1.6 angstrom structure of escherichia coli aspartate-2 semialdehyde dehydrogenase.
8	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
9	c2i3aD_	 Alignment		100.0	21	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
10	c2q49B_	 Alignment		100.0	19	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
11	c2ozpA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: n-acetyl-gamma-glutamyl-phosphate reductase; PDBTitle: crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus

12	c1vknC_	Alignment		100.0	18	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
13	c2ep5B_	Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 350aa long hypothetical aspartate-semialdehyde PDBTitle: structural study of project id st1242 from sulfolobus tokodaii strain7
14	c2g17A_	Alignment		100.0	21	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.
15	c3hskB_	Alignment		100.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
16	c1ys4A_	Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate-semialdehyde dehydrogenase; PDBTitle: structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
17	c2gd1P_	Alignment		100.0	20	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
18	d2hjsa2	Alignment		100.0	35	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
19	d2gz1a2	Alignment		100.0	28	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
20	d1mb4a2	Alignment		100.0	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
21	d1t4ba2	Alignment	not modelled	100.0	23	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
22	c3sthA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
23	d1pqaa2	Alignment	not modelled	100.0	23	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
24	c1s7cA_	Alignment	not modelled	100.0	20	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
25	c1b7gO_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
26	c1cf2O_	Alignment	not modelled	100.0	18	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
27	c2d2iO_	Alignment	not modelled	100.0	19	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+

28	c1cerC_	 Alignment	not modelled	100.0	17	PDB header: oxidoreductase (aldehyde(d)-nad(a)) dehydrogenase; 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
29	c3cieC_	 Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
30	c1hdgO_	 Alignment	not modelled	100.0	18	PDB header: oxidoreductase (aldehy(d)-nad(a)) dehydrogenase; 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
31	c1rm4O_	 Alignment	not modelled	100.0	16	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
32	c2pkrl_	 Alignment	not modelled	100.0	16	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
33	c2x5kO_	 Alignment	not modelled	100.0	17	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
34	c2czcD_	 Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: D; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
35	d2gz1a1	 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
36	c3h9eA_	 Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A; PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
37	c3docD_	 Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: D; PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis
38	c2yyvB_	 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
39	d2hjsa1	 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
40	c2b4rQ_	 Alignment	not modelled	100.0	17	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
41	d2q49a1	 Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	d2g17a1	 Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
43	c1ihxD_	 Alignment	not modelled	100.0	21	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
44	c3hq4R_	 Alignment	not modelled	100.0	19	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
45	d2cvoa2	 Alignment	not modelled	100.0	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
46	d2cvoa1	 Alignment	not modelled	100.0	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	d1vkna1	 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
48	c2i5pO_	Alignment	not modelled	100.0	21	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 PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: structural study of project id aq_1065 from aquifex aeolicus vf5
49	c2ep7B_	Alignment	not modelled	100.0	16	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.
50	clobfO_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase from borrelia burgdorferi
51	c3hjaB_	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
52	d1t4ba1	Alignment	not modelled	100.0	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C- terminal domain Family: GAPDH-like
53	d2q49a2	Alignment	not modelled	100.0	16	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C- terminal domain Family: GAPDH-like
54	d1vkna2	Alignment	not modelled	100.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
55	d1mb4a1	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
56	d1pqaa1	Alignment	not modelled	100.0	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C- terminal domain Family: GAPDH-like
57	d2g17a2	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde 3-phosphate dehydrogenase; PDBTitle: leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
58	ci132D_	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
59	d1cf2o1	Alignment	not modelled	99.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
60	d1dssg1	Alignment	not modelled	99.8	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C- terminal domain Family: GAPDH-like
61	d1hdgo2	Alignment	not modelled	99.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
62	d3cmco1	Alignment	not modelled	99.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
63	d1gado1	Alignment	not modelled	99.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
64	d1j0xo1	Alignment	not modelled	99.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
65	d1rm4a1	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
66	d1u8fo1	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
67	d1hdgo1	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
68	d1ggaa1	Alignment	not modelled	99.6	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
69	d1k3ta1	Alignment	not modelled	99.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
70	d2pkqo1	Alignment	not modelled	99.5	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
71	d2g82a1	Alignment	not modelled	99.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N- terminal domain
72	c1nvmB_	Alignment	not modelled	99.5	15	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
73	d1vc2a1	Alignment	not modelled	99.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

73	d1vc2a1	Alignment	not modelled	99.3	17	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
74	d3gpdg1	Alignment	not modelled	99.5	17	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
75	d1i32a1	Alignment	not modelled	99.5	15	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
76	d2b4ro1	Alignment	not modelled	99.4	15	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
77	d1obfo1	Alignment	not modelled	99.4	22	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
78	d1nvmb1	Alignment	not modelled	99.4	21	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
79	d2b4ro2	Alignment	not modelled	99.1	17	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
80	d1rm4a2	Alignment	not modelled	99.1	19	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
81	d1u8fo2	Alignment	not modelled	99.1	14	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
82	d1k3ta2	Alignment	not modelled	99.1	17	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
83	d1ggaa2	Alignment	not modelled	99.1	18	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
84	d3cmco2	Alignment	not modelled	99.1	19	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
85	d1gado2	Alignment	not modelled	99.0	15	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
86	d2czca2	Alignment	not modelled	99.0	17	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
87	d1i32a2	Alignment	not modelled	99.0	17	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
88	d3gpdg2	Alignment	not modelled	99.0	14	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
89	c3ic5A_	Alignment	not modelled	99.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroiy.
90	d2g82a2	Alignment	not modelled	98.9	19	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
91	d2pkqo2	Alignment	not modelled	98.9	16	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
92	c1drwA_	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
93	d1dssg2	Alignment	not modelled	98.8	16	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
94	d1obfo2	Alignment	not modelled	98.8	20	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
95	d1b7go2	Alignment	not modelled	98.8	16	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
96	c3dapB_	Alignment	not modelled	98.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
97	d1cf2o2	Alignment	not modelled	98.7	20	Family: GAPDH-like Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain
98	d1f06a1	Alignment	not modelled	98.7	12	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains
						PDB header: oxidoreductase

99	c2z2vA	Alignment	not modelled	98.6	13	Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
100	c3bioB	Alignment	not modelled	98.6	20	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
101	d2dt5a2	Alignment	not modelled	98.4	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain
102	d1b7go1	Alignment	not modelled	98.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
103	d2czca1	Alignment	not modelled	98.4	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
104	c2dt5A	Alignment	not modelled	98.4	19	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of tha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
105	c3e18A	Alignment	not modelled	98.3	8	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
106	c1e5lA	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
107	c3ijpA	Alignment	not modelled	98.3	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
108	c3e9mC	Alignment	not modelled	98.3	15	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
109	c2ixaA	Alignment	not modelled	98.3	24	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyne, n-acetylgalactosaminidase
110	c3evnA	Alignment	not modelled	98.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
111	c1lc3A	Alignment	not modelled	98.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
112	d2nu7a1	Alignment	not modelled	98.2	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
113	d1ebfa1	Alignment	not modelled	98.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
114	c3fh1C	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
115	d1euca1	Alignment	not modelled	98.2	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
116	d1diha1	Alignment	not modelled	98.2	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
117	c2axqA	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
118	c3gfgB	Alignment	not modelled	98.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
119	c1xeaD	Alignment	not modelled	98.1	19	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of a gfo/ldh/moca family oxidoreductase2 from vibrio cholerae
120	c2ph5A	Alignment	not modelled	98.1	20	PDB header: transferase Chain: A: PDB Molecule: homospermidine synthase; PDBTitle: crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54