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Description	P20605
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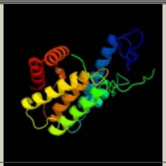
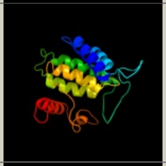
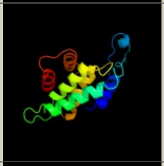
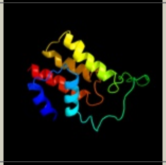
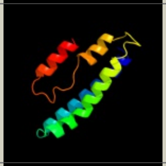
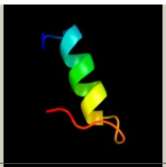
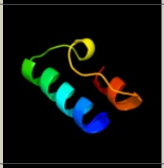
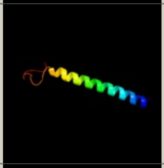
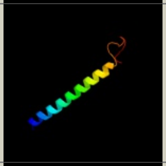
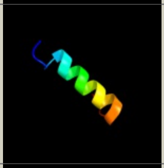
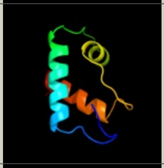
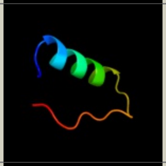
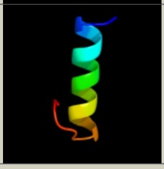
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vzaD_	Alignment		100.0	32	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**cell filamentation protein; **PDBTitle:** type iv secretion system effector protein bepa
2	d2f6sa1	Alignment		100.0	24	**Fold:**Fic-like **Superfamily:**Fic-like **Family:**Fic-like
3	c2f6sA_	Alignment		100.0	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cell filamentation protein, putative; **PDBTitle:** structure of cell filamentation protein (fic) from helicobacter pylori
4	d2g03a1	Alignment		100.0	26	**Fold:**Fic-like **Superfamily:**Fic-like **Family:**Fic-like
5	c3cucB_	Alignment		100.0	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**protein of unknown function with a fic domain; **PDBTitle:** crystal structure of a fic domain containing signaling protein2 (bt_2513) from bacteroides thetaiotaomicron vpi-5482 at 2.71 a3 resolution
6	c3eqxB_	Alignment		99.9	12	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**fic domain containing transcriptional regulator; **PDBTitle:** crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
7	c3n3vA_	Alignment		99.9	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenosine monophosphate-protein transferase ibpa; **PDBTitle:** crystal structure of ibpafic2-h3717a in complex with adenylylated2 cdc42
8	c3dd7A_	Alignment		99.1	12	**PDB header:**ribosome inhibitor **Chain:** A: **PDB Molecule:**death on curing protein; **PDBTitle:** structure of doch66y in complex with the c-terminal domain of phd
9	c3letB_	Alignment		98.3	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenosine monophosphate-protein transferase vops; **PDBTitle:** crystal structure of fic domain containing ampylator, vops
10	d1s0pa_	Alignment		83.0	13	**Fold:**N-terminal domain of adenylylcyclase associated protein, CAP **Superfamily:**N-terminal domain of adenylylcyclase associated protein, CAP **Family:**N-terminal domain of adenylylcyclase associated protein, CAP
11	d3etja2	Alignment		59.7	33	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like

12	d1yl7a1	Alignment		30.7	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
13	c1yn9B_	Alignment		26.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**polynucleotide 5'-phosphatase; **PDBTitle:** crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
14	d1s2xa_	Alignment		23.0	15	**Fold:**STAT-like **Superfamily:**Cag-Z **Family:**Cag-Z
15	c1s2xA_	Alignment		23.0	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**cag-z; **PDBTitle:** crystal structure of cag-z from helicobacter pylori
16	c2imgA_	Alignment		22.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 23; **PDBTitle:** crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
17	c3awfC_	Alignment		21.2	10	**PDB header:**hydrolase, membrane protein **Chain:** C: **PDB Molecule:**voltage-sensor containing phosphatase; **PDBTitle:** crystal structure of pten-like domain of ci-vsp (236-576)
18	c3rgqA_	Alignment		20.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein-tyrosine phosphatase mitochondrial 1; **PDBTitle:** crystal structure of ptpmt1 in complex with pi(5)p
19	d1hdgo1	Alignment		19.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
20	d1ohea2	Alignment		18.4	14	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
21	d1diha1	Alignment	not modelled	18.3	26	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
22	c1yl7F_	Alignment	not modelled	18.1	23	**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)
23	c2vfwB_	Alignment	not modelled	17.4	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**short-chain z-isoprenyl diphosphate synthetase; **PDBTitle:** rv1086 native
24	c3ijpA_	Alignment	not modelled	17.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
25	c2vg2C_	Alignment	not modelled	16.9	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**undecaprenyl pyrophosphate synthetase; **PDBTitle:** rv2361 with ipp
26	d1u8fo1	Alignment	not modelled	16.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
27	d1j0xo1	Alignment	not modelled	16.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
28	c2gwoC_	Alignment	not modelled	15.1	17	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**dual specificity protein phosphatase 13; **PDBTitle:** crystal structure of tmdp

29	d1mkpa_	Alignment	not modelled	15.0	9	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
30	d1i32a1	Alignment	not modelled	14.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
31	d1ggaa1	Alignment	not modelled	14.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
32	d1k3ta1	Alignment	not modelled	13.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
33	c2d2rA_	Alignment	not modelled	13.5	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
34	d3gpdg1	Alignment	not modelled	13.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
35	c2wgpA_	Alignment	not modelled	13.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 14; **PDBTitle:** crystal structure of human dual specificity phosphatase 14
36	c2y96A_	Alignment	not modelled	13.0	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase dupd1; **PDBTitle:** structure of human dual-specificity phosphatase 27
37	c3ihtB_	Alignment	not modelled	13.0	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**s-adenosyl-l-methionine methyl transferase; **PDBTitle:** crystal structure of s-adenosyl-l-methionine methyl transferase2 (yp_165822.1) from silicibacter pomeroyi dss-3 at 1.80 a resolution
38	d1ueha_	Alignment	not modelled	12.7	25	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
39	c1zzwA_	Alignment	not modelled	12.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of catalytic domain of human map kinase2 phosphatase 5
40	d1vm6a3	Alignment	not modelled	11.9	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	c3h2zA_	Alignment	not modelled	11.7	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
42	c1wrmA_	Alignment	not modelled	11.5	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 22; **PDBTitle:** crystal structure of jsp-1
43	c2c46B_	Alignment	not modelled	11.5	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** crystal structure of the human rna guanylyltransferase and2 5'-phosphatase
44	d2j0141	Alignment	not modelled	11.4	44	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
45	c2j034_	Alignment	not modelled	11.4	44	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** structure of the thermus thermophilus 70s ribosome2 complexed with mrna, trna and paromomycin (part 4 of 4).3 this file contains the 50s subunit from molecule ii.
46	c2e0tA_	Alignment	not modelled	11.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase 26; **PDBTitle:** crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
47	c2i6oA_	Alignment	not modelled	11.2	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfolobus solfataricus protein tyrosine **PDBTitle:** crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
48	d1rm4a1	Alignment	not modelled	11.1	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	c3emuA_	Alignment	not modelled	10.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**leucine rich repeat and phosphatase domain **PDBTitle:** crystal structure of a leucine rich repeat and phosphatase2 domain containing protein from entamoeba histolytica
50	c1i32D_	Alignment	not modelled	10.9	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
51	c1jp3A_	Alignment	not modelled	10.7	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**undecaprenyl pyrophosphate synthase; **PDBTitle:** structure of e.coli undecaprenyl pyrophosphate synthase
52	c3qvoA_	Alignment	not modelled	10.6	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nmra family protein; **PDBTitle:** structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
53	c2p1nD	Alignment	not modelled	10.3	10	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a;

53	c2p1nD_	Alignment	not modelled	10.3	10	**PDBTitle:** mechanism of auxin perception by the tir1 ubiquitin ligase
54	c2r0bA_	Alignment	not modelled	10.1	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine/threonine/tyrosine-interacting protein; **PDBTitle:** crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
55	c2nt2C_	Alignment	not modelled	9.7	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein phosphatase slingshot homolog 2; **PDBTitle:** crystal structure of slingshot phosphatase 2
56	c1hdgO_	Alignment	not modelled	9.6	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
57	c2g6zB_	Alignment	not modelled	9.5	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dual specificity protein phosphatase 5; **PDBTitle:** crystal structure of human dusp5
58	c1drwA_	Alignment	not modelled	9.3	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
59	d2b4ro1	Alignment	not modelled	9.0	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	c3h2sA_	Alignment	not modelled	8.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh-flavin reductase; **PDBTitle:** crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
61	d1vs6z1	Alignment	not modelled	8.5	44	**Fold:**L28p-like **Superfamily:**L28p-like **Family:**Ribosomal protein L31p
62	d1cf2o1	Alignment	not modelled	8.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
63	d1bf4a_	Alignment	not modelled	8.4	30	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**"Histone-like" proteins from archaea
64	d1dssg1	Alignment	not modelled	8.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	d1hdoa_	Alignment	not modelled	8.2	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
66	c2hcmA_	Alignment	not modelled	8.1	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
67	c3cieC_	Alignment	not modelled	7.9	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
68	c3ew7A_	Alignment	not modelled	7.9	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo0794 protein; **PDBTitle:** crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
69	d1m3ga_	Alignment	not modelled	7.7	17	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
70	c2oudA_	Alignment	not modelled	7.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase 10; **PDBTitle:** crystal structure of the catalytic domain of human mkp5
71	c1yz4A_	Alignment	not modelled	7.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity phosphatase-like 15 isoform a; **PDBTitle:** crystal structure of dusp15
72	d2hf5a1	Alignment	not modelled	7.6	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
73	d1vhra_	Alignment	not modelled	7.6	13	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
74	c3s4oB_	Alignment	not modelled	7.5	17	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein tyrosine phosphatase-like protein; **PDBTitle:** protein tyrosine phosphatase (putative) from leishmania major
75	c3hq4R_	Alignment	not modelled	7.4	14	**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
76	c2b664_	Alignment	not modelled	7.4	44	**PDB header:**ribosome **Chain:** 4: **PDB Molecule:**50s ribosomal protein l31; **PDBTitle:** 50s ribosomal subunit from a crystal structure of release factor rf1,2 trnas and mrna bound to the ribosome. this file contains the 50s3 subunit from a crystal structure of release factor rf1, trnas and4 mrna bound to the ribosome and is described in remark 400

77	d2pkqo1	Alignment	not modelled	7.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
78	c3bbo1_	Alignment	not modelled	7.4	44	**PDB header:**ribosome **Chain:** 1: **PDB Molecule:**ribosomal protein l31; **PDBTitle:** homology model for the spinach chloroplast 50s subunit2 fitted to 9.4a cryo-em map of the 70s chlororibosome
79	d1gado1	Alignment	not modelled	7.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	c2d2iO_	Alignment	not modelled	7.1	22	**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+
81	d1obfo1	Alignment	not modelled	7.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	d1f75a_	Alignment	not modelled	7.0	25	**Fold:**Undecaprenyl diphosphate synthase **Superfamily:**Undecaprenyl diphosphate synthase **Family:**Undecaprenyl diphosphate synthase
83	c1yx7A_	Alignment	not modelled	6.9	5	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calsensin; **PDBTitle:** nmr structure of calsensin, energy minimized average2 structure.
84	c1vm6B_	Alignment	not modelled	6.6	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
85	c3nmeA_	Alignment	not modelled	6.6	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sex4 glucan phosphatase; **PDBTitle:** structure of a plant phosphatase
86	c2ep7B_	Alignment	not modelled	6.6	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** structural study of project id aq_1065 from aquifex aeolicus vf5
87	c3e8xA_	Alignment	not modelled	6.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative nad-dependent epimerase/dehydratase; **PDBTitle:** putative nad-dependent epimerase/dehydratase from bacillus halodurans.
88	c3docD_	Alignment	not modelled	6.3	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of trka glyceraldehyde-3-phosphate2 dehydrogenase from brucella melitensis
89	c2b4rQ_	Alignment	not modelled	6.2	19	**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
90	c2i5pO_	Alignment	not modelled	6.2	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
91	d1i9sa_	Alignment	not modelled	6.2	8	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
92	c2jx3A_	Alignment	not modelled	6.1	33	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein dek; **PDBTitle:** nmr solution structure of the n-terminal domain of dek
93	c3sthA_	Alignment	not modelled	6.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
94	c2hwyB_	Alignment	not modelled	6.0	33	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**protein smg5; **PDBTitle:** structure of pin domain of human smg5.
95	d3cmco1	Alignment	not modelled	5.8	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	c3n0aA_	Alignment	not modelled	5.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase auxilin; **PDBTitle:** crystal structure of auxilin (40-400)
97	c2aucC_	Alignment	not modelled	5.7	17	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**myosin a tail interacting protein; **PDBTitle:** structure of the plasmodium mtip-myoa complex, a key component of the2 parasite invasion motor
98	c2p4dA_	Alignment	not modelled	5.6	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dual specificity protein phosphatase; **PDBTitle:** structure-assisted discovery of variola major h12 phosphatase inhibitors
99	c3oakC_	Alignment	not modelled	5.5	60	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of a spn1 (iws1)-spt6 complex