



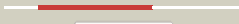









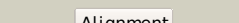

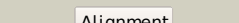



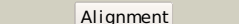

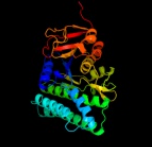


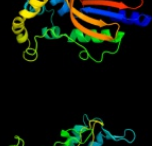

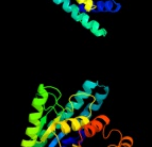


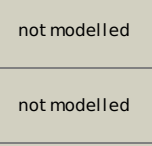


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cdqB_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
2	c3c1nA_	 Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
3	c2j0wA_	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
4	c3l76B_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
5	c3ab4K_	 Alignment		100.0	32	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
6	c3mtjA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
7	c1ebuA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
8	c3do5A_	 Alignment		100.0	25	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
9	c3c8mA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
10	c3ingA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
11	c2ejwB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8

12	d2cdqa1	Alignment		100.0	31	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
13	d2j0wa1	Alignment		100.0	34	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
14	d2hmfa1	Alignment		100.0	36	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
15	d1ebfa2	Alignment		100.0	35	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like
16	c3k4yB	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: isopentenyl phosphate kinase; PDBTitle: crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
17	c2e9yA	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: carbamate kinase; PDBTitle: crystal structure of project ape1968 from aeropyrum pernix k1
18	d1ybda1	Alignment		100.0	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
19	c3ek5A	Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: uridylate kinase; PDBTitle: unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
20	d1e19a	Alignment		99.9	14	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
21	c3ll9A	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: isopentenyl phosphate kinase; PDBTitle: x-ray structures of isopentenyl phosphate kinase
22	d2bnea1	Alignment	not modelled	99.9	26	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
23	d1gs5a	Alignment	not modelled	99.9	17	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
24	d2a1fa1	Alignment	not modelled	99.9	26	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
25	c2rd5A	Alignment	not modelled	99.9	18	PDB header: protein binding Chain: A: PDB Molecule: acetylglutamate kinase-like protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
26	d1z9da1	Alignment	not modelled	99.9	22	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
27	c2dtjA	Alignment	not modelled	99.9	30	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
28	d2bufa1	Alignment	not modelled	99.9	17	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
29	d2brxa1	Alignment	not modelled	99.9	29	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like

						Family:PyrH-like
30	c3nwyB	Alignment	not modelled	99.9	26	PDB header: transferase Chain: B: PDB Molecule: uridylylate kinase; PDBTitle: structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
31	d2ij9a1	Alignment	not modelled	99.9	30	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
32	c2zhoB	Alignment	not modelled	99.9	28	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
33	d1b7ba	Alignment	not modelled	99.9	16	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
34	c2jixC	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: uridylylate kinase; PDBTitle: the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
35	c3l15C	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyl kinase related protein; PDBTitle: crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
36	c3l86A	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: acetylglutamate kinase; PDBTitle: the crystal structure of smu.665 from streptococcus mutans ua159
37	c2re1A	Alignment	not modelled	99.9	29	PDB header: transferase Chain: A: PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
38	c2eqxA	Alignment	not modelled	99.9	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative acetylglutamate kinase; PDBTitle: crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
39	d1ebfa1	Alignment	not modelled	99.9	27	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	c2va1A	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: uridylylate kinase; PDBTitle: crystal structure of ump kinase from ureaplasma parvum
41	d2btya1	Alignment	not modelled	99.9	21	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
42	d2akoa1	Alignment	not modelled	99.9	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
43	c2j4kC	Alignment	not modelled	99.9	19	PDB header: transferase Chain: C: PDB Molecule: uridylylate kinase; PDBTitle: crystal structure of uridylylate kinase from sulfolobus2 solfataricus in complex with ump to 2.2 angstrom3 resolution
44	c2v5hB	Alignment	not modelled	99.9	16	PDB header: transcription Chain: B: PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
45	c3mahA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
46	c2w21A	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
47	c3d40A	Alignment	not modelled	99.8	19	PDB header: transferase Chain: A: PDB Molecule: foma protein; PDBTitle: crystal structure of fosfomicin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
48	d2ap9a1	Alignment	not modelled	99.8	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
49	c2ogxB	Alignment	not modelled	99.8	25	PDB header: metal binding protein Chain: B: PDB Molecule: molybdenum storage protein subunit beta; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
50	c3kzfc	Alignment	not modelled	99.8	22	PDB header: transferase Chain: C: PDB Molecule: carbamate kinase; PDBTitle: structure of giardia carbamate kinase
51	c2j5tf	Alignment	not modelled	99.8	20	PDB header: transferase Chain: F: PDB Molecule: glutamate 5-kinase; PDBTitle: glutamate 5-kinase from escherichia coli complexed with2 glutamate
52	c2ogxA	Alignment	not modelled	99.8	25	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
53	c2f06B	Alignment	not modelled	99.7	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
54	d2hmfa2	Alignment	not modelled	99.5	43	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
						PDB header: transferase

55	c2r98A_	Alignment	not modelled	99.5	18	Chain: A: PDB Molecule: putative acetylglutamate synthase; PDBTitle: crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
56	d2cdqa3	Alignment	not modelled	99.5	30	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
57	d2hmfa3	Alignment	not modelled	99.5	27	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
58	d2j0wa3	Alignment	not modelled	99.4	28	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
59	c2dc1A_	Alignment	not modelled	99.2	25	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
60	c1r0lD_	Alignment	not modelled	99.2	18	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
61	c2eghA_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
62	c3a14B_	Alignment	not modelled	99.1	10	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
63	c2jcyA_	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium3 tuberculosis
64	d1j5pa4	Alignment	not modelled	99.1	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	d1q0qa2	Alignment	not modelled	99.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	d1r0ka2	Alignment	not modelled	99.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	d2cdqa2	Alignment	not modelled	98.9	24	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
68	c3ceaA_	Alignment	not modelled	98.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
69	c3e18A_	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
70	c3gfgB_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
71	d2j0wa2	Alignment	not modelled	98.8	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
72	c1zh8B_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
73	c3ec7C_	Alignment	not modelled	98.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
74	c3e9mC_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
75	c1j5pA_	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
76	c3kuxA_	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
77	c3evnA_	Alignment	not modelled	98.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
78	c2ixaA_	Alignment	not modelled	98.7	15	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyyme, n-acetylgalactosaminidase
79	c3euwB_	Alignment	not modelled	98.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032

80	c1h6dL_	Alignment	not modelled	98.6	16	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose PDBTitle: oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
81	c3db2C_	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
82	c1lc3A_	Alignment	not modelled	98.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
83	c1ofgF_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
84	c3fd8A_	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
85	c2o48X_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
86	c3fhIC_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
87	c3v5nA_	Alignment	not modelled	98.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
88	c3nt5B_	Alignment	not modelled	98.6	16	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
89	c3bioB_	Alignment	not modelled	98.6	21	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
90	c3q2kB_	Alignment	not modelled	98.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glnaca
91	c3ezyB_	Alignment	not modelled	98.6	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
92	d1ydwa1	Alignment	not modelled	98.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
93	c2nvwB_	Alignment	not modelled	98.6	12	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctucture of transcriptional regulator gal80p from2 kluyveromyces lactis
94	c3rbvA_	Alignment	not modelled	98.6	19	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
95	c2ho3D_	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/ldh/moca family from2 streptococcus pneumoniae
96	c3dtyA_	Alignment	not modelled	98.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
97	c3e82A_	Alignment	not modelled	98.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
98	c2q4eB_	Alignment	not modelled	98.5	15	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
99	c3moiA_	Alignment	not modelled	98.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
100	c3f4lF_	Alignment	not modelled	98.4	14	PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
101	c3c1aB_	Alignment	not modelled	98.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
102	c3m2tA_	Alignment	not modelled	98.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
103	c2glxD_	Alignment	not modelled	98.4	13	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
104	c1evjC_	Alignment	not modelled	98.4	16	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase

					(gfor)2 delta1-22 s64d
105	c2axqA_	Alignment	not modelled	98.4	19 PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
106	d1f06a1	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
107	c2p2sA_	Alignment	not modelled	98.3	16 PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
108	c3btuD_	Alignment	not modelled	98.3	13 PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
109	d1zh8a1	Alignment	not modelled	98.3	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	c3dapB_	Alignment	not modelled	98.3	18 PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
111	c3oqbF_	Alignment	not modelled	98.3	16 PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
112	c1e5lA_	Alignment	not modelled	98.2	19 PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
113	d1t1ta1	Alignment	not modelled	98.2	13 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
114	c3ip3D_	Alignment	not modelled	98.1	17 PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
115	c1xeaD_	Alignment	not modelled	98.1	18 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
116	d1lc0a1	Alignment	not modelled	98.1	21 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
117	c1drwA_	Alignment	not modelled	98.1	16 PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
118	d2nvwa1	Alignment	not modelled	98.1	14 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
119	c3uuwB_	Alignment	not modelled	98.1	18 PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
120	d1h6da1	Alignment	not modelled	98.1	18 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain