



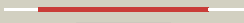



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ofgF_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
2	c1h6dL_	 Alignment		100.0	24	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
3	c3oqbF_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
4	c3moiA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
5	c2glxD_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
6	c1evjC_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
7	c3ceaA_	 Alignment		100.0	19	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
8	c3ezyB_	 Alignment		100.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
9	c3q2kB_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wiba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glnaca
10	c3db2C_	 Alignment		100.0	20	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
11	c3e18A_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua

12	c3kuxA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
13	c2nvwB_	Alignment		100.0	17	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal scture of transcriptional regulator gal80p from2 kluyveromymes lactis
14	c3euwB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
15	c3gfgB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
16	c3dtyA_	Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
17	c1zh8B_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
18	c3btuD_	Alignment		100.0	16	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]
19	c3e9mC_	Alignment		100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
20	c3fd8A_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
21	c3nt5B_	Alignment	not modelled	100.0	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
22	c2q4eB_	Alignment	not modelled	100.0	17	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
23	c2o48X_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
24	c3ip3D_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
25	c3evnA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
26	c3fhIC_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
27	c3ec7C_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
28	c3f4IF_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2

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29	c3rbvA_	Alignment	not modelled	100.0	24	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
30	c2p2sA_	Alignment	not modelled	100.0	17	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
31	c3m2tA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
32	c3e82A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
33	c2ixaA_	Alignment	not modelled	100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyyme, n-acetylgalactosaminidase
34	c3v5nA_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
35	c1xeaD_	Alignment	not modelled	100.0	15	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
36	c1tltB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
37	c3uuwB_	Alignment	not modelled	100.0	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.
38	c2ho3D_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/ldh/moca family from2 streptococcus pneumoniae
39	c3c1aB_	Alignment	not modelled	100.0	19	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
40	c3oa2B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: wbpb; PDBTitle: crystal structure of the wlba (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
41	c1lc3A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
42	c3oa0B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: lipopolysaccharide biosynthesis protein wbpb; PDBTitle: crystal structure of the wlba (wbpb) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcna
43	dlh6da1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	dlryda1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d2nvwa1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	dlzh8a1	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
47	dlydwa1	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	dlxea1	Alignment	not modelled	100.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	dl1ta1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	dl1c0a1	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
51	c1j5pA_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
52	dlf06a1	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

53	c3dapB	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and 2 the inhibitor 5s-isoxazoline
54	c2dc1A	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
55	c1ebuA	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
56	dloi7a1	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
57	d2nu7a1	Alignment	not modelled	99.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
58	c3do5A	Alignment	not modelled	99.8	21	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
59	d1ebfa1	Alignment	not modelled	99.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
60	c3mtjA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
61	dlj5pa4	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
62	d1euca1	Alignment	not modelled	99.7	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
63	d2nvwa2	Alignment	not modelled	99.7	14	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
64	c3bioB	Alignment	not modelled	99.7	18	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
65	d1zh8a2	Alignment	not modelled	99.6	20	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
66	d2dt5a2	Alignment	not modelled	99.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain
67	d1h6da2	Alignment	not modelled	99.6	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
68	c2axqA	Alignment	not modelled	99.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
69	c3ketA	Alignment	not modelled	99.5	15	PDB header: transcription/dna Chain: A: PDB Molecule: redox-sensing transcriptional repressor rex; PDBTitle: crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
70	d1e5qa1	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
71	d1ydwA2	Alignment	not modelled	99.5	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
72	c1drwA	Alignment	not modelled	99.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
73	c3ic5A	Alignment	not modelled	99.4	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
74	c1e5lA	Alignment	not modelled	99.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
75	c2ejwB	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8
76	d1ompa	Alignment	not modelled	99.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like
77	c2yv1A	Alignment	not modelled	99.3	11	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
78	c2dt5A	Alignment	not modelled	99.3	13	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein;

78	c2v0A_	Alignment	not modelled	99.3	15	PDBTitle: crystal structure of tha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: probable ornithine cyclodeaminase; PDBTitle: the crystal structure of probable ornithine cyclodeaminase from2 bordetella pertussis tohamai
79	c3hdjA_	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mu-crystallin homolog; PDBTitle: crystal structure of human mu_crystallin at 2.6 angstrom
80	c2i99A_	Alignment	not modelled	99.1	16	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
81	c1r0lD_	Alignment	not modelled	99.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
82	c3c8mA_	Alignment	not modelled	99.0	15	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
83	c3a14B_	Alignment	not modelled	98.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
84	c2z2vA_	Alignment	not modelled	98.9	18	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
85	d1xea2	Alignment	not modelled	98.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
86	c3l6dB_	Alignment	not modelled	98.8	13	PDB header: ligase Chain: D: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase
87	c2nu8D_	Alignment	not modelled	98.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
88	c3ijpA_	Alignment	not modelled	98.8	16	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
89	c2czcD_	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
90	c3fwnB_	Alignment	not modelled	98.7	5	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
91	c2jcyA_	Alignment	not modelled	98.7	23	PDB header: synthetase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
92	c1oi7A_	Alignment	not modelled	98.7	16	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
93	c2uyyD_	Alignment	not modelled	98.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
94	c3cumA_	Alignment	not modelled	98.7	24	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
95	c2ozpA_	Alignment	not modelled	98.7	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d1cf2o1	Alignment	not modelled	98.7	25	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
97	c2yv2A_	Alignment	not modelled	98.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
98	c3dl1B_	Alignment	not modelled	98.6	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	d1dih1	Alignment	not modelled	98.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
100	c3b1fA_	Alignment	not modelled	98.6	11	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
101	c3ingA_	Alignment	not modelled	98.6	18	

102	d1r0ka2	Alignment	not modelled	98.6	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
103	c3g0oA	Alignment	not modelled	98.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
104	c2iz1C	Alignment	not modelled	98.6	8	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
105	c1pgiA	Alignment	not modelled	98.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
106	c1b7gO	Alignment	not modelled	98.6	20	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
107	c2eghA	Alignment	not modelled	98.6	16	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
108	c3ckyA	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
109	c2p4qA	Alignment	not modelled	98.6	9	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
110	c3dzbA	Alignment	not modelled	98.6	10	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
111	c1yl7F	Alignment	not modelled	98.5	20	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)
112	c3gt0A	Alignment	not modelled	98.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
113	c1vpdA	Alignment	not modelled	98.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
114	c3qhaB	Alignment	not modelled	98.5	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
115	d2ahra2	Alignment	not modelled	98.5	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
116	d1yl7a1	Alignment	not modelled	98.4	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
117	c2ph5A	Alignment	not modelled	98.4	14	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
118	c1pgqA	Alignment	not modelled	98.4	9	PDB header: oxidoreductase (choh(d)-nadp+(a)) Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
119	c1nvmB	Alignment	not modelled	98.4	20	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
120	d1yqga2	Alignment	not modelled	98.4	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain