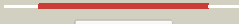



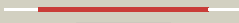



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o48X_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
2	c2ho3D_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/ldh/moca family from <i>Streptococcus pneumoniae</i>
3	c3e9mC_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from <i>Enterococcus faecalis</i>
4	c3evnA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from <i>Streptococcus agalactiae</i> 2603v/r
5	c2glxD_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-D-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
6	c3oqbF_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from <i>Bradyrhizobium japonicum</i> USDA 110
7	c1ofgF_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
8	c1h6dL_	 Alignment		100.0	19	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from <i>Zymomonas mobilis</i> complexed with glycerol
9	c3fd8A_	 Alignment		100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from <i>Enterococcus faecalis</i>
10	c3db2C_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from <i>Desulfitobacterium hafniense</i> dcb-2 at 1.70 Å resolution
11	c3ezyB_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from <i>Thermotoga maritima</i>

12	c3f4lF_	Alignment		100.0	16	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
13	c1zh8B_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
14	c2q4eB_	Alignment		100.0	22	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
15	c3kuxA_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
16	c3euwB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
17	c1evjC_	Alignment		100.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
18	c3qfgB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
19	c3e18A_	Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
20	c3rbvA_	Alignment		100.0	22	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
21	c3q2kB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca
22	c3moiA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
23	c3btuD_	Alignment	not modelled	100.0	15	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]
24	c3fhIC_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
25	c3m2tA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
26	c3ceaA_	Alignment	not modelled	100.0	16	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
27	c3dtyA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
28	c3e82A_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2

						klebsiella pneumoniae
29	c3ec7C_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
30	c1xeaD_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/dh/moca family; PDBTitle: crystal structure of a gfo/dh/moca family oxidoreductase2 from vibrio cholerae
31	c3c1aB_	Alignment	not modelled	100.0	18	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
32	c3nt5B_	Alignment	not modelled	100.0	17	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
33	c3v5nA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
34	c2p2sA_	Alignment	not modelled	100.0	13	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
35	c2nvwB_	Alignment	not modelled	100.0	15	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal scture of transcriptional regulator gal80p from2 kluyveromyces lactis
36	c3ip3D_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
37	c3uuwB_	Alignment	not modelled	100.0	15	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	c2ixaA_	Alignment	not modelled	100.0	12	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyne, n-acetylgalactosaminidase
39	c1titB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
40	c1lc3A_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
41	c3oa2B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: wbp; PDBTitle: crystal structure of the wlba (wbp) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
42	c3oa0B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: lipopolysaccaride biosynthesis protein wbp; PDBTitle: crystal structure of the wlba (wbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glnaca
43	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
44	d1h6da1	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
45	d1zh8a1	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
46	d1ryda1	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	d1ydw1	Alignment	not modelled	100.0	28	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	d1xea1	Alignment	not modelled	99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	d1tita1	Alignment	not modelled	99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	c1j5pA_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
51	d1lc0a1	Alignment	not modelled	99.9	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	d1f06a1	Alignment	not modelled	99.9	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

52	d1rvda1	Alignment	not modelled	99.9	10	Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
53	c3dapB	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
54	c2dc1A	Alignment	not modelled	99.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
55	c1ebuA	Alignment	not modelled	99.8	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
56	d1oi7a1	Alignment	not modelled	99.8	13	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	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
58	c3do5A	Alignment	not modelled	99.7	24	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	99.7	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	d1j5pa4	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	d1euca1	Alignment	not modelled	99.7	9	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
62	c3mtjA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
63	c3bioB	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
64	d2dt5a2	Alignment	not modelled	99.6	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain
65	c2axqA	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
66	d1zh8a2	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
67	c3ketA	Alignment	not modelled	99.5	8	PDB header: transcription/dna rex; 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
68	d2nvwa2	Alignment	not modelled	99.5	13	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
69	c1drwA	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
70	d1e5qa1	Alignment	not modelled	99.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	d1h6da2	Alignment	not modelled	99.4	19	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
72	c1e5lA	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
73	d1lomoa	Alignment	not modelled	99.4	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like
74	d1ydwa2	Alignment	not modelled	99.4	17	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
75	c3ic5A	Alignment	not modelled	99.3	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
76	c2dt5A	Alignment	not modelled	99.3	9	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
77	c2ejwB	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8
						PDB header: structural genomics, unknown function

78	c3hdjA_	Alignment	not modelled	99.3	14	Chain: A: PDB Molecule: probable ornithine cyclodeaminase; PDBTitle: the crystal structure of probable ornithine cyclodeaminase from2 bordetella pertussis tohama i
79	c2i99A_	Alignment	not modelled	99.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: mu-crystallin homolog; PDBTitle: crystal structure of human mu_crystallin at 2.6 angstrom
80	c1b7gO_	Alignment	not modelled	99.1	13	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
81	c2z2vA_	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
82	c2yv1A_	Alignment	not modelled	99.0	12	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
83	d1cf2o1	Alignment	not modelled	98.9	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
84	c3a14B_	Alignment	not modelled	98.9	20	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
85	c3c8mA_	Alignment	not modelled	98.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
86	c1r0lD_	Alignment	not modelled	98.8	14	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
87	c2czcD_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
88	c3ijpA_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
89	c1cf2Q_	Alignment	not modelled	98.7	17	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
90	c3l6dB_	Alignment	not modelled	98.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
91	c3cumA_	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
92	c2ozpA_	Alignment	not modelled	98.7	11	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
93	d1xeaa2	Alignment	not modelled	98.7	10	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
94	c3d1lB_	Alignment	not modelled	98.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
95	c2jcyA_	Alignment	not modelled	98.6	16	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
96	c3g0oA_	Alignment	not modelled	98.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
97	c2nu8D_	Alignment	not modelled	98.6	12	PDB header: ligase Chain: D: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase
98	c3fwnB_	Alignment	not modelled	98.6	9	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
99	c1oi7A_	Alignment	not modelled	98.6	14	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
100	c3dzba_	Alignment	not modelled	98.6	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
						PDB header: oxidoreductase

101	c1pgjA_	Alignment	not modelled	98.6	15	Chain: A: PDB Molecule: 6-phosphoglucanate dehydrogenase; PDBTitle: x-ray structure of 6-phosphoglucanate dehydrogenase from the protozoan2 parasite t. brucei
102	d1q0qa2	Alignment	not modelled	98.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
103	d1yl7a1	Alignment	not modelled	98.5	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
104	c3gt0A_	Alignment	not modelled	98.5	8	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
105	d1diha1	Alignment	not modelled	98.5	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
106	c3ckyA_	Alignment	not modelled	98.5	9	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
107	c3b1fA_	Alignment	not modelled	98.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
108	c1yl7F_	Alignment	not modelled	98.5	11	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)
109	c2ahrB_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
110	c2iz1C_	Alignment	not modelled	98.5	11	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphoglucanate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
111	c2p4qA_	Alignment	not modelled	98.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphoglucanate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
112	c2f1kD_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
113	c3plnA_	Alignment	not modelled	98.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
114	c2ag8A_	Alignment	not modelled	98.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
115	d2ahra2	Alignment	not modelled	98.4	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphoglucanate dehydrogenase-like, N-terminal domain
116	c3dojA_	Alignment	not modelled	98.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
117	cli36A_	Alignment	not modelled	98.4	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
118	c3ingA_	Alignment	not modelled	98.4	18	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
119	c2yv2A_	Alignment	not modelled	98.4	14	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
120	d1r0ka2	Alignment	not modelled	98.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain