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Description	P77376
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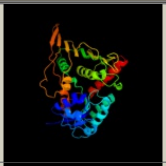
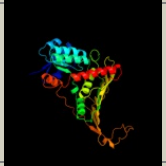
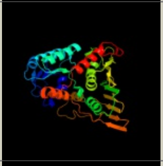
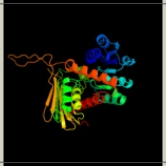
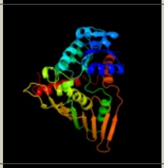
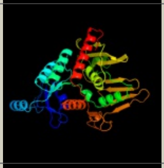
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kuxA_	Alignment		100.0	70	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
2	c3gfgB_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
3	c3e18A_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
4	c3fhlC_	Alignment		100.0	40	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
5	c3e82A_	Alignment		100.0	49	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
6	c3f4lF_	Alignment		100.0	37	**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
7	c1h6dL_	Alignment		100.0	17	**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
8	c1ofgF_	Alignment		100.0	17	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
9	c3oqbF_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
10	c3fd8A_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
11	c3db2C_	Alignment		100.0	17	**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

12	c2glxD_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
13	c3moiA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
14	c3q2kB_	Alignment		100.0	22	**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
15	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
16	c3evnA_	Alignment		100.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
17	c3ezyB_	Alignment		100.0	21	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
18	c3dtyA_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
19	c1zh8B_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
20	c1evjC_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
21	c2q4eB_	Alignment	not modelled	100.0	18	**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
22	c3e9mC_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
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	c3rbvA_	Alignment	not modelled	100.0	21	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**sugar 3-ketoreductase; **PDBTitle:** crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
25	c3btuD_	Alignment	not modelled	100.0	20	**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]
26	c3ceaA_	Alignment	not modelled	100.0	17	**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	c3v5nA_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
28	c3nt5B_	Alignment	not modelled	100.0	18	**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
29	c3m2tA_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
30	c2nvwB_	Alignment	not modelled	100.0	18	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
31	c2p2sA_	Alignment	not modelled	100.0	21	**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
32	c3ec7C_	Alignment	not modelled	100.0	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
33	c3ip3D_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
34	c2ixaA_	Alignment	not modelled	100.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
35	c3c1aB_	Alignment	not modelled	100.0	22	**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
36	c3uuwB_	Alignment	not modelled	100.0	19	**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.
37	c1xeaD_	Alignment	not modelled	100.0	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
38	c2ho3D_	Alignment	not modelled	100.0	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
39	c1tltB_	Alignment	not modelled	100.0	19	**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	16	**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	16	**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
42	c3oa0B_	Alignment	not modelled	100.0	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**lipopolysaccaride biosynthesis protein wbpb; **PDBTitle:** crystal structure of the wlba (wbpb) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnaca
43	d1h6da1	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	d1ryda1	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	d1zh8a1	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	d2nvwa1	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
47	d1ydwa1	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
48	d1xeaa1	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	d1lc0a1	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d1tlta1	Alignment	not modelled	100.0	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
51	c1j5pA_	Alignment	not modelled	99.9	9	**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	d1f06a1	Alignment	not modelled	99.9	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains

52	d1f06a1	Alignment	not modelled	99.9	21	**Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
53	c3dapB_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
54	c2dc1A_	Alignment	not modelled	99.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
55	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
56	d1oi7a1	Alignment	not modelled	99.8	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
57	c1ebuA_	Alignment	not modelled	99.8	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase complex with nad analogue and l-2 homoserine
58	c3mtjA_	Alignment	not modelled	99.8	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
59	d1ebfa1	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
60	d1j5pa4	Alignment	not modelled	99.7	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
61	d1euca1	Alignment	not modelled	99.7	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
62	d1zh8a2	Alignment	not modelled	99.7	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
63	c3do5A_	Alignment	not modelled	99.7	18	**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
64	c3bioB_	Alignment	not modelled	99.7	18	**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
65	d2dt5a2	Alignment	not modelled	99.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
66	d2nvwa2	Alignment	not modelled	99.6	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
67	d1h6da2	Alignment	not modelled	99.6	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
68	c1drwA_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
69	c3ketA_	Alignment	not modelled	99.5	21	**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	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
71	c3ic5A_	Alignment	not modelled	99.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
72	d1e5qa1	Alignment	not modelled	99.4	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
73	c2dt5A_	Alignment	not modelled	99.4	16	**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
74	c2axqA_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
75	c2ejwB_	Alignment	not modelled	99.4	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8
76	c2yv1A_	Alignment	not modelled	99.2	17	**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
77	c1e5lA_	Alignment	not modelled	99.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea

78	c3hdjA_	Alignment	not modelled	99.1	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable ornithine cyclodeaminase; **PDBTitle:** the crystal structure of probable ornithine cyclodeaminase from2 bordetella pertussis tohama i
79	d1omoa_	Alignment	not modelled	99.1	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Ornithine cyclodeaminase-like
80	c2z2vA_	Alignment	not modelled	99.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
81	d1xeaa2	Alignment	not modelled	99.0	9	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
82	c3c8mA_	Alignment	not modelled	98.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
83	c1r0lD_	Alignment	not modelled	98.9	13	**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
84	c2nu8D_	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
85	c3ijpA_	Alignment	not modelled	98.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
86	c2i99A_	Alignment	not modelled	98.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mu-crystallin homolog; **PDBTitle:** crystal structure of human mu_crystallin at 2.6 angstrom
87	d1diha1	Alignment	not modelled	98.7	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	c2ozpA_	Alignment	not modelled	98.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (ttha1904) from thermus thermophilus
89	c3a14B_	Alignment	not modelled	98.7	17	**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
90	c1b7gO_	Alignment	not modelled	98.7	13	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase); **PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase
91	c1oi7A_	Alignment	not modelled	98.7	19	**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	c2czcD_	Alignment	not modelled	98.7	21	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
93	c3l6dB_	Alignment	not modelled	98.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
94	c1yl7F_	Alignment	not modelled	98.6	18	**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)
95	c2yv2A_	Alignment	not modelled	98.6	17	**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
96	c3cumA_	Alignment	not modelled	98.6	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
97	d1cf2o1	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
98	c3ckyA_	Alignment	not modelled	98.6	19	**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
99	c3ingA_	Alignment	not modelled	98.5	17	**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
100	c2p4qA_	Alignment	not modelled	98.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating 1; **PDBTitle:** crystal structure analysis of gnd1 in saccharomyces cerevisiae
101	d1yl7a1	Alignment	not modelled	98.5	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-

						terminal domain
102	c2jcyA_	Alignment	not modelled	98.5	21	**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
103	c3fwnB_	Alignment	not modelled	98.5	12	**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
104	d1nvmb1	Alignment	not modelled	98.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
105	c1nvmB_	Alignment	not modelled	98.5	17	**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
106	c3d1lB_	Alignment	not modelled	98.5	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
107	c3nklA_	Alignment	not modelled	98.5	14	**PDB header:**oxidoreductase/lyase **Chain:** A: **PDB Molecule:**udp-d-quinovosamine 4-dehydrogenase; **PDBTitle:** crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
108	c2eghA_	Alignment	not modelled	98.4	17	**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
109	c3qhaB_	Alignment	not modelled	98.4	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
110	c3g0oA_	Alignment	not modelled	98.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
111	c2uyyD_	Alignment	not modelled	98.4	10	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
112	c1pgjA_	Alignment	not modelled	98.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
113	c2iz1C_	Alignment	not modelled	98.4	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
114	d1tlta2	Alignment	not modelled	98.4	13	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
115	d1r0ka2	Alignment	not modelled	98.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
116	c3b1fA_	Alignment	not modelled	98.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans
117	d1i36a2	Alignment	not modelled	98.4	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
118	c2ph5A_	Alignment	not modelled	98.4	13	**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
119	c1pgqA_	Alignment	not modelled	98.3	11	**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
120	c1vpdA_	Alignment	not modelled	98.3	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]