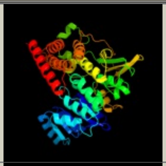
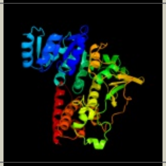
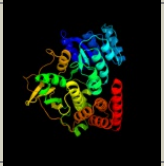
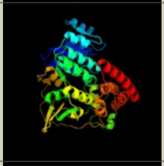
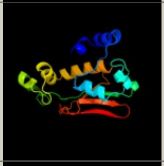
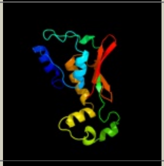
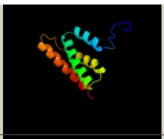
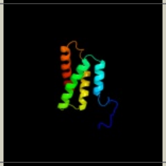
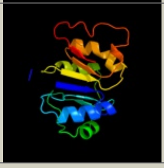
Email	l.a.kelley@imperial.ac.uk
Description	P45568
Date	Thu Jan 5 12:03:20 GMT 2012
Unique Job ID	92cfff81d18d49a4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2eghA_	Alignment		100.0	100	**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
2	c3au9A_	Alignment		100.0	36	**PDB header:**isomerase/isomerase inhibitor **Chain:** A: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** crystal structure of the quaternary complex-1 of an isomerase
3	c1k5hB_	Alignment		100.0	100	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**1-deoxy-d-xylulose-5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose-5-phosphate reductoisomerase
4	c2jcyA_	Alignment		100.0	41	**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
5	c1r0lD_	Alignment		100.0	51	**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
6	c3a14B_	Alignment		100.0	35	**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
7	d1q0qa3	Alignment		100.0	100	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
8	d1r0ka3	Alignment		100.0	61	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Dihydrodipicolinate reductase-like
9	d1q0qa2	Alignment		100.0	86	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
10	d1r0ka2	Alignment		100.0	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
11	d1t1ra2	Alignment		100.0	100	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain

12	d1q0qa1		Alignment		100.0	100	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
13	d1r0ka1		Alignment		100.0	43	**Fold:**Left-handed superhelix **Superfamily:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain **Family:**1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain
14	c3mtjA_		Alignment		99.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
15	c3c8mA_		Alignment		99.7	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
16	c3do5A_		Alignment		99.6	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
17	c2ejwB_		Alignment		99.5	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase from thermus thermophilus hb8
18	c3ingA_		Alignment		99.5	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
19	c1ebuA_		Alignment		99.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** homoserine dehydrogenase complex with nad analogue and l-2 homoserine
20	d1ebfa1		Alignment		99.0	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
21	c3moiA_		Alignment	not modelled	99.0	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
22	c3nt5B_		Alignment	not modelled	99.0	21	**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
23	c2axqA_		Alignment	not modelled	98.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
24	c3db2C_		Alignment	not modelled	98.9	15	**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
25	c3e9mC_		Alignment	not modelled	98.8	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
26	c1e5lA_		Alignment	not modelled	98.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
27	c3m2tA_		Alignment	not modelled	98.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
28	c3ezyB_		Alignment	not modelled	98.8	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414

						from2 thermotoga maritima
29	c3evnA_	Alignment	not modelled	98.8	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
30	c2glxD_	Alignment	not modelled	98.8	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
31	c2ixaA_	Alignment	not modelled	98.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
32	c3dtyA_	Alignment	not modelled	98.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
33	c2dc1A_	Alignment	not modelled	98.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
34	c3q2kB_	Alignment	not modelled	98.7	15	**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
35	c3e18A_	Alignment	not modelled	98.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
36	d1zh8a1	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
37	c1zh8B_	Alignment	not modelled	98.6	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
38	c1ofgF_	Alignment	not modelled	98.6	18	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
39	c1h6dL_	Alignment	not modelled	98.6	18	**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
40	c2o48X_	Alignment	not modelled	98.5	17	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
41	c1cf2Q_	Alignment	not modelled	98.5	16	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**protein (glyceraldehyde-3-phosphate **PDBTitle:** three-dimensional structure of d-glyceraldehyde-3-phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus
42	c1xeaD_	Alignment	not modelled	98.5	13	**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
43	c3euwB_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
44	c1evjC_	Alignment	not modelled	98.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
45	c3oa0B_	Alignment	not modelled	98.5	19	**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
46	c3fd8A_	Alignment	not modelled	98.5	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
47	c3ec7C_	Alignment	not modelled	98.4	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
48	c2q4eB_	Alignment	not modelled	98.4	13	**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
49	d1j5pa4	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
50	d1ydwa1	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
51	c3btuD_	Alignment	not modelled	98.4	14	**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]
52	c2ho3D_	Alignment	not modelled	98.4	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
53	c3ceaA_	Alignment	not modelled	98.4	14	**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

54	d1cf2o1	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
55	c3v5nA_	Alignment	not modelled	98.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
56	c3c1aB_	Alignment	not modelled	98.3	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
57	c3gfgB_	Alignment	not modelled	98.3	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
58	c2p2sA_	Alignment	not modelled	98.3	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
59	c1b7gO_	Alignment	not modelled	98.3	13	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**protein (glyceraldehyde 3-phosphate dehydrogenase); **PDBTitle:** glyceraldehyde 3-phosphate dehydrogenase
60	d1f06a1	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
61	c3fhlC_	Alignment	not modelled	98.3	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
62	c3f4lF_	Alignment	not modelled	98.3	18	**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
63	c3rbvA_	Alignment	not modelled	98.2	24	**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
64	c3e82A_	Alignment	not modelled	98.2	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
65	d1e5qa1	Alignment	not modelled	98.2	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
66	c2czcD_	Alignment	not modelled	98.2	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
67	c2z2vA_	Alignment	not modelled	98.1	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
68	c1j5pA_	Alignment	not modelled	98.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate dehydrogenase; **PDBTitle:** crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
69	c3kuxA_	Alignment	not modelled	98.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
70	c3dapB_	Alignment	not modelled	98.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**diaminopimelic acid dehydrogenase; **PDBTitle:** c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
71	c2nvwB_	Alignment	not modelled	98.1	12	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
72	c3oa2B_	Alignment	not modelled	98.1	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
73	c1lc3A_	Alignment	not modelled	98.1	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
74	d1pqua1	Alignment	not modelled	98.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	d1ryda1	Alignment	not modelled	98.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
76	d2nvwa1	Alignment	not modelled	98.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
77	c2ozpA_	Alignment	not modelled	98.0	17	**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
						Fold:NAD(P)-binding Rossmann-fold domains

78	d1h6da1	Alignment	not modelled	98.0	19	**Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
79	c2ph5A_	Alignment	not modelled	97.9	15	**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
80	d2g17a1	Alignment	not modelled	97.9	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	c2g17A_	Alignment	not modelled	97.9	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n-acetyl-gamma-glutamyl-phosphate reductase; **PDBTitle:** the structure of n-acetyl-gamma-glutamyl-phosphate reductase from2 salmonella typhimurium.
82	c3ip3D_	Alignment	not modelled	97.9	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
83	c3ic5A_	Alignment	not modelled	97.9	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
84	c3hq4R_	Alignment	not modelled	97.9	21	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of c151s mutant of glyceraldehyde-3-phosphate2 dehydrogenase 1 (gapdh1) complexed with nad from staphylococcus3 aureus mrsa252 at 2.2 angstrom resolution
85	d1oi7a1	Alignment	not modelled	97.8	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
86	c3hskB_	Alignment	not modelled	97.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** crystal structure of aspartate semialdehyde dehydrogenase2 with nadp from candida albicans
87	d1t4ba1	Alignment	not modelled	97.8	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	c1drwA_	Alignment	not modelled	97.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrodipicolinate reductase; **PDBTitle:** escherichia coli dhpr/nhdh complex
89	c3bioB_	Alignment	not modelled	97.8	24	**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
90	d2czca2	Alignment	not modelled	97.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
91	c2ep5B_	Alignment	not modelled	97.7	23	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**350aa long hypothetical aspartate-semialdehyde **PDBTitle:** structural study of project id st1242 from sulfolobus tokodaii strain7
92	d2nu7a1	Alignment	not modelled	97.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
93	c2yyyB_	Alignment	not modelled	97.7	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase
94	c3oqbF_	Alignment	not modelled	97.7	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
95	d1xeaa1	Alignment	not modelled	97.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
96	d1tlta1	Alignment	not modelled	97.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	c2gd1P_	Alignment	not modelled	97.6	16	**PDB header:**oxidoreductase(aldehyde(d)-nad(a)) **Chain:** P: **PDB Molecule:**apo-d-glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** coenzyme-induced conformational changes in glyceraldehyde-3-2 phosphate dehydrogenase from bacillus stearothermophillus
98	c1t4bB_	Alignment	not modelled	97.6	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** 1.6 angstrom structure of esherichia coli aspartate-2 semialdehyde dehydrogenase.
99	c1s7cA_	Alignment	not modelled	97.6	17	**PDB header:**structural genomics, oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase a; **PDBTitle:** crystal structure of mes buffer bound form of glyceraldehyde 3-2 phosphate dehydrogenase from escherichia coli
100	c1rm4O_	Alignment	not modelled	97.5	18	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase a; **PDBTitle:** crystal structure of recombinant photosynthetic glyceraldehyde-3-2 phosphate dehydrogenase a4 isoform, complexed with nadp
						PDB header:oxidoreductase

101	c2b4rQ_	Alignment	not modelled	97.5	17	**Chain:** Q: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
102	c3ketA_	Alignment	not modelled	97.5	19	**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
103	c3sthA_	Alignment	not modelled	97.5	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 toxoplasma gondii
104	c1ys4A_	Alignment	not modelled	97.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate-semialdehyde dehydrogenase; **PDBTitle:** structure of aspartate-semialdehyde dehydrogenase from2 methanococcus jannaschii
105	c2i5pO_	Alignment	not modelled	97.5	15	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate2 dehydrogenase isoform 1 from k. marxianus
106	c3uuwB_	Alignment	not modelled	97.4	16	**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.
107	c2x5kO_	Alignment	not modelled	97.4	18	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**d-erythrose-4-phosphate dehydrogenase; **PDBTitle:** structure of an active site mutant of the d-erythrose-4-phosphate2 dehydrogenase from e. coli
108	c3b20R_	Alignment	not modelled	97.4	16	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase (nadp+); **PDBTitle:** crystal structure analysis of dehydrogenase complexed with nad
109	d1b7go1	Alignment	not modelled	97.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	c2d2iO_	Alignment	not modelled	97.4	17	**PDB header:**oxidoreductase **Chain:** O: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** crystal structure of nadp-dependent glyceraldehyde-3-2 phosphate dehydrogenase from synechococcus sp. complexed3 with nadp+
111	c2pkrI_	Alignment	not modelled	97.4	18	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase aor; **PDBTitle:** crystal structure of (a+cte)4 chimeric form of2 photosyntetic glyceraldehyde-3-phosphate dehydrogenase,3 complexed with nadp
112	d1vkna1	Alignment	not modelled	97.4	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
113	d1euca1	Alignment	not modelled	97.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
114	c2ep7B_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** structural study of project id aq_1065 from aquifex aeolicus vf5
115	d2gz1a1	Alignment	not modelled	97.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
116	c3h9eA_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:** **PDBTitle:** crystal structure of human sperm-specific glyceraldehyde-3-phosphate2 dehydrogenase (gapds) complex with nad and phosphate
117	d1t1ra3	Alignment	not modelled	97.3	100	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
118	c3cieC_	Alignment	not modelled	97.2	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
119	d1mb4a1	Alignment	not modelled	97.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
120	d2q49a1	Alignment	not modelled	97.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain