Email	l.a.kelley@imperial.ac.uk
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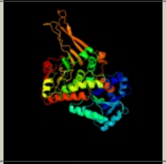
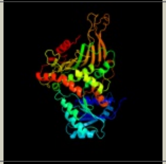
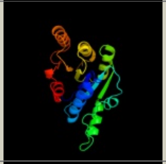
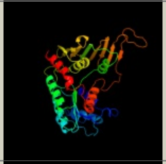
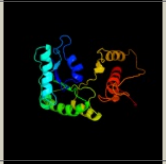
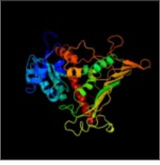
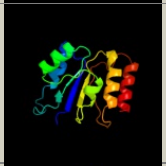
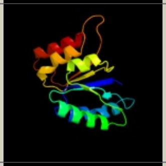
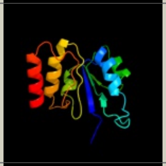
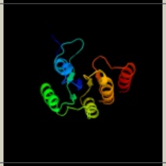
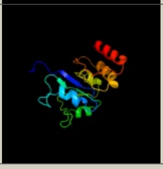
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2bhlB_	Alignment		100.0	37	**PDB header:**oxidoreductase (choh(d)-nadp) **Chain:** B: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose-6-phosphate dehydrogenase2 (deletion variant) complexed with glucose-6-phosphate
2	c1h9aA_	Alignment		100.0	33	**PDB header:**oxidoreductase (choh(d) - nad(p)) **Chain:** A: **PDB Molecule:**glucose 6-phosphate 1-dehydrogenase; **PDBTitle:** complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from l. mesenteroides with coenzyme nadp
3	c1qkiE_	Alignment		100.0	36	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**glucose-6-phosphate 1-dehydrogenase; **PDBTitle:** x-ray structure of human glucose 6-phosphate dehydrogenase2 (variant canton r459l) complexed with structural nadp+
4	d1qkia2	Alignment		100.0	41	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
5	d1h9aa2	Alignment		100.0	34	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Glucose 6-phosphate dehydrogenase-like
6	d1h9aa1	Alignment		100.0	30	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
7	d1qkia1	Alignment		100.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
8	c3m2tA_	Alignment		97.8	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
9	c3btuD_	Alignment		97.8	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]
10	d2nvwa1	Alignment		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
11	c3kuxA_	Alignment		97.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis

12	c3e18A_	Alignment		97.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of nad-binding protein from listeria innocua
13	c3ezyB_	Alignment		97.4	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
14	c3db2C_	Alignment		97.4	19	**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
15	c1zh8B_	Alignment		97.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
16	c3gfgB_	Alignment		97.3	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uncharacterized oxidoreductase yvaa; **PDBTitle:** structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
17	d1h6da1	Alignment		97.3	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
18	c3euwB_	Alignment		97.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
19	c1evjC_	Alignment		97.2	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
20	c2nvwB_	Alignment		97.1	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**galactose/lactose metabolism regulatory protein **PDBTitle:** crystal sctucture of transcriptional regulator gal80p from2 kluyveromymes lactis
21	c3ec7C_	Alignment	not modelled	97.0	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative dehydrogenase; **PDBTitle:** crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
22	c3e82A_	Alignment	not modelled	97.0	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
23	c3uuwB_	Alignment	not modelled	97.0	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.
24	c2glxD_	Alignment	not modelled	96.9	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1,5-anhydro-d-fructose reductase; **PDBTitle:** crystal structure analysis of bacterial 1,5-af reductase
25	c3c1aB_	Alignment	not modelled	96.8	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
26	c3fd8A_	Alignment	not modelled	96.7	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
27	c1ofgF_	Alignment	not modelled	96.7	16	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**glucose-fructose oxidoreductase; **PDBTitle:** glucose-fructose oxidoreductase
28	c1h6dL_	Alignment	not modelled	96.7	16	**PDB header:**protein translocation **Chain:** L: **PDB Molecule:**precursor form of glucose-fructose **PDBTitle:** oxidized precursor form of glucose-fructose

						oxidoreductase2 from zymomonas mobilis complexed with glycerol
29	c3nt5B_	Alignment	not modelled	96.7	13	**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
30	c3f4lF_	Alignment	not modelled	96.6	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
31	c3rbvA_	Alignment	not modelled	96.6	13	**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
32	d1zh8a1	Alignment	not modelled	96.6	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
33	c3e9mC_	Alignment	not modelled	96.5	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
34	c2o48X_	Alignment	not modelled	96.3	13	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**dimeric dihydrodiol dehydrogenase; **PDBTitle:** crystal structure of mammalian dimeric dihydrodiol dehydrogenase
35	c3dtyA_	Alignment	not modelled	96.2	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from pseudomonas2 syringae
36	d1ryda1	Alignment	not modelled	96.2	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
37	c2ho3D_	Alignment	not modelled	96.2	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
38	c3ceaA_	Alignment	not modelled	96.2	13	**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
39	c2q4eB_	Alignment	not modelled	95.8	20	**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
40	c3moiA_	Alignment	not modelled	95.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
41	d1ydwa1	Alignment	not modelled	95.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
42	c3oa0B_	Alignment	not modelled	94.9	16	**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	c3oqbF_	Alignment	not modelled	94.8	20	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
44	c3fhlC_	Alignment	not modelled	94.6	19	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
45	c1lc3A_	Alignment	not modelled	94.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**biliverdin reductase a; **PDBTitle:** crystal structure of a biliverdin reductase enzyme-cofactor2 complex
46	c1xeaD_	Alignment	not modelled	94.0	10	**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
47	c3q2kB_	Alignment	not modelled	94.0	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
48	c1tltB_	Alignment	not modelled	93.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase (virulence factor mvim homolog); **PDBTitle:** crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
49	c3oa2B_	Alignment	not modelled	93.6	17	**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
50	c3ip3D_	Alignment	not modelled	93.6	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase, putative; **PDBTitle:** structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
51	d1tlta1	Alignment	not modelled	93.4	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	d1xeaa1	Alignment	not modelled	93.4	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						PDB header:hydrolase

53	c2ixaA_	Alignment	not modelled	93.0	18	**Chain:** A: **PDB Molecule:**alpha-n-acetylgalactosaminidase; **PDBTitle:** a-zyme, n-acetylgalactosaminidase
54	d1lc0a1	Alignment	not modelled	92.4	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
55	c3evnA_	Alignment	not modelled	91.5	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
56	d1oi7a1	Alignment	not modelled	90.2	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
57	c3v5nA_	Alignment	not modelled	89.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** the crystal structure of oxidoreductase from sinorhizobium meliloti
58	c2zcuA_	Alignment	not modelled	89.4	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized oxidoreductase ytfg; **PDBTitle:** crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
59	d1xgka_	Alignment	not modelled	86.9	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
60	c2vrcD_	Alignment	not modelled	86.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**triphenylmethane reductase; **PDBTitle:** crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
61	c2c20D_	Alignment	not modelled	81.5	24	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of udp-glucose 4-epimerase
62	d2nu7a1	Alignment	not modelled	79.5	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
63	c2v6gA_	Alignment	not modelled	79.0	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**progesterone 5-beta-reductase; **PDBTitle:** structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
64	d1wvga1	Alignment	not modelled	77.0	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
65	c2gn9B_	Alignment	not modelled	74.5	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**udp-glcnac c6 dehydratase; **PDBTitle:** crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
66	c1t2aC_	Alignment	not modelled	73.5	17	**PDB header:**structural genomics,lyase **Chain:** C: **PDB Molecule:**gdp-mannose 4,6 dehydratase; **PDBTitle:** crystal structure of human gdp-d-mannose 4,6-dehydratase
67	d1t2aa_	Alignment	not modelled	73.5	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
68	c2z1mC_	Alignment	not modelled	68.0	17	**PDB header:**lyase **Chain:** C: **PDB Molecule:**gdp-d-mannose dehydratase; **PDBTitle:** crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
69	d1db3a_	Alignment	not modelled	67.0	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
70	d1x1na1	Alignment	not modelled	65.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
71	d1z45a2	Alignment	not modelled	64.6	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
72	d1tz7a1	Alignment	not modelled	63.5	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	d1eswa_	Alignment	not modelled	61.0	30	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	d1rkxa_	Alignment	not modelled	60.7	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
75	d1udca_	Alignment	not modelled	59.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
76	c2qx7A_	Alignment	not modelled	57.5	16	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
77	d2q46a1	Alignment	not modelled	55.9	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
78	c2iodD_	Alignment	not modelled	55.4	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydroflavonol 4-reductase; **PDBTitle:** binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
79	c3enkB_	Alignment	not modelled	54.8	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** 1.9a crystal structure of udp-glucose 4-epimerase from2 burkholderia pseudomallei

80	c2p5uC_	Alignment	not modelled	53.7	13	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**udp-glucose 4-epimerase; **PDBTitle:** crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
81	c3e48B_	Alignment	not modelled	53.2	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative nucleoside-diphosphate-sugar epimerase; **PDBTitle:** crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
82	c3mjsA_	Alignment	not modelled	52.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**amphb; **PDBTitle:** structure of a-type ketoreductases from modular polyketide synthase
83	c2pk3B_	Alignment	not modelled	52.2	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gdp-6-deoxy-d-lyxo-4-hexulose reductase; **PDBTitle:** crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
84	c3slgB_	Alignment	not modelled	51.6	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pbgp3 protein; **PDBTitle:** crystal structure of pbgp3 protein from burkholderia pseudomallei
85	d1i24a_	Alignment	not modelled	51.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
86	d2blla1	Alignment	not modelled	50.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
87	d1n7ha_	Alignment	not modelled	48.2	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
88	c2q1wC_	Alignment	not modelled	47.6	23	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
89	d1euca1	Alignment	not modelled	47.3	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
90	c3qvoA_	Alignment	not modelled	46.6	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**nmra family protein; **PDBTitle:** structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
91	c2p2sA_	Alignment	not modelled	44.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
92	c3r6dA_	Alignment	not modelled	43.9	17	**PDB header:**lyase, isomerase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of nad-dependent epimerase/dehydratase from2 veillonella parvula dsm 2008 with cz-methylated lysine
93	d1bxka_	Alignment	not modelled	43.8	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
94	d1orra_	Alignment	not modelled	42.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
95	c1e5lA_	Alignment	not modelled	41.3	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
96	c3h2sA_	Alignment	not modelled	40.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative nadh-flavin reductase; **PDBTitle:** crystal structure of the q03b84 protein from lactobacillus2 casei. northeast structural genomics consortium target3 lcr19.
97	c3ay3C_	Alignment	not modelled	38.3	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nad-dependent epimerase/dehydratase; **PDBTitle:** crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
98	d1gy8a_	Alignment	not modelled	35.1	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
99	c2p4hX_	Alignment	not modelled	35.1	30	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**vestitone reductase; **PDBTitle:** crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
100	c1j5pA_	Alignment	not modelled	34.8	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aspartate dehydrogenase; **PDBTitle:** crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
101	c2axqA_	Alignment	not modelled	34.8	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
102	d1vl0a_	Alignment	not modelled	34.2	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
103	c3dqpA_	Alignment	not modelled	32.5	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase ylbe; **PDBTitle:** crystal structure of the oxidoreductase ylbe from2 lactococcus lactis, northeast structural genomics3 consortium target kr121.
						PDB header:isomerase, lyase **Chain:** A: **PDB Molecule:**nad-dependent epimerase/dehydratase;

104	c3dhnA_	Alignment	not modelled	32.4	33	**PDBTitle:** crystal structure of the putative epimerase q89z24_bactn2 from bacteroides thetaiotaomicron. northeast structural3 genomics consortium target btr310.
105	c2ggsB_	Alignment	not modelled	32.3	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**273aa long hypothetical dtdp-4-dehydrorhamnose **PDBTitle:** crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
106	c3ew7A_	Alignment	not modelled	31.8	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lmo0794 protein; **PDBTitle:** crystal structure of the lmo0794 protein from listeria2 monocytogenes. northeast structural genomics consortium3 target lmr162.
107	c1z7eC_	Alignment	not modelled	31.3	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protein arna; **PDBTitle:** crystal structure of full length arna
108	c2pzlB_	Alignment	not modelled	30.8	16	**PDB header:**sugar binding protein **Chain:** B: **PDB Molecule:**putative nucleotide sugar epimerase/ dehydratase; **PDBTitle:** crystal structure of the bordetella bronchiseptica enzyme2 wbmg in complex with nad and udp
109	c3th6B_	Alignment	not modelled	30.5	20	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from rhipicephalus2 (boophilus) microplus.
110	d1n2sa_	Alignment	not modelled	30.3	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
111	d1ebfa1	Alignment	not modelled	29.7	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
112	d1rpna_	Alignment	not modelled	29.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
113	c3rfxB_	Alignment	not modelled	29.2	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**uronate dehydrogenase; **PDBTitle:** crystal structure of uronate dehydrogenase from agrobacterium2 tumefaciens, y136a mutant complexed with nad
114	c3sc6F_	Alignment	not modelled	27.8	30	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**dtdp-4-dehydrorhamnose reductase; **PDBTitle:** 2.65 angstrom resolution crystal structure of dtdp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
115	d1nnxa_	Alignment	not modelled	27.5	60	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
116	c2vz8B_	Alignment	not modelled	27.4	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**fatty acid synthase; **PDBTitle:** crystal structure of mammalian fatty acid synthase
117	c1n7gB_	Alignment	not modelled	27.1	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gdp-d-mannose-4,6-dehydratase; **PDBTitle:** crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
118	d1ek6a_	Alignment	not modelled	27.1	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	c2ysrA_	Alignment	not modelled	26.6	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**dep domain-containing protein 1; **PDBTitle:** solution structure of the dep domain from human dep domain-2 containing protein 1
120	c3kxqB_	Alignment	not modelled	26.2	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase from bartonella2 henselae at 1.6a resolution