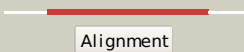

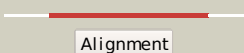

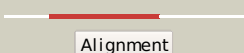

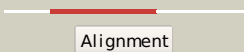
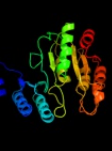
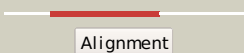

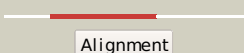

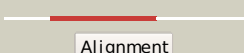

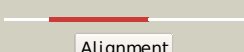

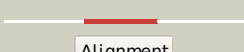

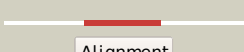

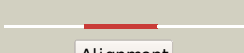



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3dmyA_</a>	 Alignment		100.0	39	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> protein fdra; <b>PDBTitle:</b> crystal structure of a predicated acyl-coa synthetase from e.coli
2	<a href="#">c2csuB_</a>	 Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
3	<a href="#">c3mwdB_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
4	<a href="#">c2nu8D_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase
5	<a href="#">c2fpgA_</a>	 Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [gdp-forming] alpha-chain, <b>PDBTitle:</b> crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
6	<a href="#">c2yv2A_</a>	 Alignment		100.0	28	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
7	<a href="#">c1oi7A_</a>	 Alignment		100.0	24	<b>PDB header:</b> synthetase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa synthetase alpha chain; <b>PDBTitle:</b> the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
8	<a href="#">c2yv1A_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> succinyl-coa ligase [adp-forming] subunit alpha; <b>PDBTitle:</b> crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
9	<a href="#">d2nu7a2</a>	 Alignment		100.0	27	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
10	<a href="#">d1euca2</a>	 Alignment		100.0	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
11	<a href="#">d1oi7a2</a>	 Alignment		100.0	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains

12	<a href="#">d2csua2</a>	Alignment		100.0	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
13	<a href="#">d2csua3</a>	Alignment		99.9	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
14	<a href="#">d2nu7b1</a>	Alignment		99.8	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
15	<a href="#">d1eucb1</a>	Alignment		99.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
16	<a href="#">c2nu9E_</a>	Alignment		99.5	12	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> succinyl-coa synthetase beta chain; <b>PDBTitle:</b> c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
17	<a href="#">c1eucB_</a>	Alignment		99.4	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> succinyl-coa synthetase, beta chain; <b>PDBTitle:</b> crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
18	<a href="#">d2csua1</a>	Alignment		99.4	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
19	<a href="#">c2duwA_</a>	Alignment		99.4	19	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
20	<a href="#">d1y81a1</a>	Alignment		99.2	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
21	<a href="#">d1iuka_</a>	Alignment	not modelled	99.2	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
22	<a href="#">d2d59a1</a>	Alignment		99.1	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
23	<a href="#">d1oi7a1</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
24	<a href="#">d2nu7a1</a>	Alignment	not modelled	99.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
25	<a href="#">d1euca1</a>	Alignment	not modelled	99.0	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
26	<a href="#">c3ff4A_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of uncharacterized protein chu_1412
27	<a href="#">c3mwdA_</a>	Alignment	not modelled	97.8	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-citrate synthase; <b>PDBTitle:</b> truncated human atp-citrate lyase with citrate bound
28	<a href="#">c3m2tA_</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase;

28	<a href="#">c3m2A</a>	Alignment	not modelled	97.4	11	<b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum <b>PDB header:</b> oxidoreductase
29	<a href="#">c3dtyA</a>	Alignment	not modelled	97.4	20	<b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from pseudomonas2 syringae
30	<a href="#">c2q4eB</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase at4g09670; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
31	<a href="#">c3ec7C</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
32	<a href="#">c3fd8A</a>	Alignment	not modelled	97.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
33	<a href="#">c3rbvA</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
34	<a href="#">c2ixaA</a>	Alignment	not modelled	97.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> a-zyyme, n-acetylgalactosaminidase
35	<a href="#">c3e9mC</a>	Alignment	not modelled	97.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
36	<a href="#">c3moiA</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
37	<a href="#">c1zh8B</a>	Alignment	not modelled	97.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
38	<a href="#">c3ip3D</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, putative; <b>PDBTitle:</b> structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
39	<a href="#">c3nt5B</a>	Alignment	not modelled	97.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
40	<a href="#">d1zh8a1</a>	Alignment	not modelled	97.2	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	<a href="#">c2o48X</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> dimeric dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of mammalian dimeric dihydrodiol dehydrogenase
42	<a href="#">c2p2sA</a>	Alignment	not modelled	97.2	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
43	<a href="#">c3ezyB</a>	Alignment	not modelled	97.2	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
44	<a href="#">d1h6da1</a>	Alignment	not modelled	97.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	<a href="#">c3oqbF</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
46	<a href="#">c1lc3A</a>	Alignment	not modelled	97.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> biliverdin reductase a; <b>PDBTitle:</b> crystal structure of a biliverdin reductase enzyme-cofactor2 complex
47	<a href="#">d1lc0a1</a>	Alignment	not modelled	97.1	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	<a href="#">d1ydw1</a>	Alignment	not modelled	97.1	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	<a href="#">c3btuD</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> transcription protein <b>Chain:</b> D: <b>PDB Molecule:</b> galactose/lactose metabolism regulatory protein <b>PDBTitle:</b> crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
50	<a href="#">c3evnA</a>	Alignment	not modelled	97.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
51	<a href="#">c1evjC</a>	Alignment	not modelled	97.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
52	<a href="#">c3e18A</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative nadph-dependent

53	<a href="#">c3db2C_</a>	Alignment	not modelled	97.1	15	oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
54	<a href="#">c1ofgF_</a>	Alignment	not modelled	97.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
55	<a href="#">c1h6dL_</a>	Alignment	not modelled	97.0	17	<b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose <b>PDBTitle:</b> oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
56	<a href="#">c3e82A_</a>	Alignment	not modelled	97.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
57	<a href="#">c3q2kB_</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaC
58	<a href="#">c2glxD_</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
59	<a href="#">c2axqA_</a>	Alignment	not modelled	97.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
60	<a href="#">c3do5A_</a>	Alignment	not modelled	97.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
61	<a href="#">c3gfgB_</a>	Alignment	not modelled	97.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized oxidoreductase yvaa; <b>PDBTitle:</b> structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
62	<a href="#">c2ho3D_</a>	Alignment	not modelled	96.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase, gfo/ldh/moca family from2 streptococcus pneumoniae
63	<a href="#">c3f4lF_</a>	Alignment	not modelled	96.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative oxidoreductase yhhx; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
64	<a href="#">dlryda1</a>	Alignment	not modelled	96.9	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	<a href="#">c3kuxA_</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from yersinia pestis
66	<a href="#">dlxeaa1</a>	Alignment	not modelled	96.8	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
67	<a href="#">clxeaD_</a>	Alignment	not modelled	96.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of a gfo/ldh/moca family oxidoreductase2 from vibrio cholerae
68	<a href="#">c3clab_</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
69	<a href="#">c3fhIC_</a>	Alignment	not modelled	96.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
70	<a href="#">cldrwA_</a>	Alignment	not modelled	96.8	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
71	<a href="#">cle5lA_</a>	Alignment	not modelled	96.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
72	<a href="#">c3bioB_</a>	Alignment	not modelled	96.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, gfo/ldh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase (gfo/ldh/moca family member) from2 porphyromonas gingivalis w83
73	<a href="#">c3v5nA_</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from sinorhizobium meliloti
74	<a href="#">c3euwB_</a>	Alignment	not modelled	96.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
75	<a href="#">c3ceaA_</a>	Alignment	not modelled	96.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
76	<a href="#">c3oa0B_</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide biosynthesis protein wbbp; <b>PDBTitle:</b> crystal structure of the wlbA (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnaC
77	<a href="#">dlj5pa4</a>	Alignment	not modelled	96.4	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> wbbp;

78	<a href="#">c3oa2B_</a>	Alignment	not modelled	96.4	11	<b>PDBTitle:</b> crystal structure of the wlbA (wbpb) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
79	<a href="#">d2nvwa1</a>	Alignment	not modelled	96.2	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
80	<a href="#">c2dc1A_</a>	Alignment	not modelled	96.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
81	<a href="#">d1diha1</a>	Alignment	not modelled	95.6	6	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
82	<a href="#">c1j5pA_</a>	Alignment	not modelled	95.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
83	<a href="#">d1tltA1</a>	Alignment	not modelled	95.3	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
84	<a href="#">c2nvwB_</a>	Alignment	not modelled	95.3	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> galactose/lactose metabolism regulatory protein <b>PDBTitle:</b> crystal scture of transcriptional regulator gal80p from2 klyveromymes lactis
85	<a href="#">c3ketA_</a>	Alignment	not modelled	95.3	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
86	<a href="#">c1tltB_</a>	Alignment	not modelled	95.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase (virulence factor mvim homolog); <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
87	<a href="#">c2z2vA_</a>	Alignment	not modelled	95.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688; <b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
88	<a href="#">c3ijpA_</a>	Alignment	not modelled	95.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
89	<a href="#">d1f06a1</a>	Alignment	not modelled	94.4	7	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
90	<a href="#">d1ebfa1</a>	Alignment	not modelled	94.2	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
91	<a href="#">d1e5qa1</a>	Alignment	not modelled	93.1	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
92	<a href="#">c2p4qA_</a>	Alignment	not modelled	93.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating 1; <b>PDBTitle:</b> crystal structure analysis of gnd1 in saccharomyces cerevisiae
93	<a href="#">c2dt5A_</a>	Alignment	not modelled	93.0	12	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> at-rich dna-binding protein; <b>PDBTitle:</b> crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
94	<a href="#">c3ic5A_</a>	Alignment	not modelled	93.0	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
95	<a href="#">c3dapB_</a>	Alignment	not modelled	92.8	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelic acid dehydrogenase; <b>PDBTitle:</b> c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
96	<a href="#">c3uuwB_</a>	Alignment	not modelled	92.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase with nad(p)-binding rossmann-fold <b>PDBTitle:</b> 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
97	<a href="#">c3bezC_</a>	Alignment	not modelled	92.6	27	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> protease 4; <b>PDBTitle:</b> crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
98	<a href="#">d2dt5a2</a>	Alignment	not modelled	92.4	9	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Transcriptional repressor Rex, C-terminal domain
99	<a href="#">c1pgjA_</a>	Alignment	not modelled	92.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
100	<a href="#">c3fwnB_</a>	Alignment	not modelled	92.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
101	<a href="#">c1pggA_</a>	Alignment	not modelled	91.6	14	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase:



						implications for nadp3 specificity and the enzyme mechanism
102	<a href="#">c2iz1C_</a>	Alignment	not modelled	91.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
103	<a href="#">c2ejwB_</a>	Alignment	not modelled	90.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase from thermus thermophilus hb8
104	<a href="#">c2vt2A_</a>	Alignment	not modelled	90.4	12	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> structure and functional properties of the bacillus2 subtilis transcriptional repressor rex
105	<a href="#">c1yl7F_</a>	Alignment	not modelled	90.1	7	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> the crystal structure of mycobacterium tuberculosis2 dihydrodipicolinate reductase (rv2773c) in complex with nadh (crystal3 form c)
106	<a href="#">c1vm6B_</a>	Alignment	not modelled	89.9	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase (tm1520) from2 thermotoga maritima at 2.27 a resolution
107	<a href="#">c3c8mA_</a>	Alignment	not modelled	89.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
108	<a href="#">c3mtjA_</a>	Alignment	not modelled	89.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
109	<a href="#">d1vm6a3</a>	Alignment	not modelled	89.4	8	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
110	<a href="#">d1yl7a1</a>	Alignment	not modelled	89.3	8	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	<a href="#">c2vbiF_</a>	Alignment	not modelled	88.6	18	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> holostructure of pyruvate decarboxylase from acetobacter2 pasteurianus
112	<a href="#">c2iexA_</a>	Alignment	not modelled	88.5	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroxynapthoic acid synthetase; <b>PDBTitle:</b> crystal structure of dihydroxynapthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
113	<a href="#">c1zpdA_</a>	Alignment	not modelled	87.7	20	<b>PDB header:</b> alcohol fermentation <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate decarboxylase; <b>PDBTitle:</b> pyruvate decarboxylase from zymomonas mobilis
114	<a href="#">d1zpd2</a>	Alignment	not modelled	87.7	21	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module
115	<a href="#">c2ozpA_</a>	Alignment	not modelled	86.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetyl-gamma-glutamyl-phosphate reductase; <b>PDBTitle:</b> crystal structure of n-acetyl-gamma-glutamyl-phosphate reductase2 (tha1904) from thermus thermophilus
116	<a href="#">c1ebuA_</a>	Alignment	not modelled	86.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase complex with nad analogue and l-2 homoserine
117	<a href="#">d2b3ya2</a>	Alignment	not modelled	85.9	25	<b>Fold:</b> Aconitase iron-sulfur domain <b>Superfamily:</b> Aconitase iron-sulfur domain <b>Family:</b> Aconitase iron-sulfur domain
118	<a href="#">c1mb4B_</a>	Alignment	not modelled	85.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate semialdehyde dehydrogenase2 from vibrio cholerae with nadp and s-methyl-l-cysteine3 sulfoxide
119	<a href="#">d2g0ta1</a>	Alignment	not modelled	84.8	22	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nitrogenase iron protein-like
120	<a href="#">d1ovma2</a>	Alignment	not modelled	84.0	17	<b>Fold:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Superfamily:</b> Thiamin diphosphate-binding fold (THDP-binding) <b>Family:</b> Pyruvate oxidase and decarboxylase Pyr module