

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f4lF_	 Alignment		100.0	99	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
2	c3kuxA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
3	c3fd8A_	 Alignment		100.0	49	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
4	c3gfgB_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: B; PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
5	c3oqbF_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: F; PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
6	c3fhlC_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: C; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
7	c3moiA_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
8	c2glxD_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: D; PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
9	c3e82A_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A; PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
10	c3e18A_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
11	c1ofgF_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: F; PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase

12	c1h6dL_	Alignment		100.0	20	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
13	c3euwB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
14	c3db2C_	Alignment		100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfotobacterium hafniense dcb-2 at 1.70 a3 resolution
15	c3ezyB_	Alignment		100.0	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
16	c3q2kB_	Alignment		100.0	20	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
17	c2o48X_	Alignment		100.0	19	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
18	c1eviC_	Alignment		100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
19	c2q4eB_	Alignment		100.0	15	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
20	c1zh8B_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
21	c3nt5B_	Alignment	not modelled	100.0	15	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
22	c3e9mC_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
23	c3dtyA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
24	c3v5nA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
25	c3evnA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
26	c3ip3D_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from2 thermotoga maritima
27	c3rbvA_	Alignment	not modelled	100.0	20	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
28	c3ceaA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase

						(np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
29	c3m2tA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
30	c3btuD_	Alignment	not modelled	100.0	19	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]
31	c3ec7C_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
32	c2nvwB_	Alignment	not modelled	100.0	16	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctucture of transcriptional regulator gal80p from2 kluyveromyces lactis
33	c2p2sA_	Alignment	not modelled	100.0	15	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
34	c2ixaA_	Alignment	not modelled	100.0	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetyl galactosaminidase; PDBTitle: a-zyyme, n-acetyl galactosaminidase
35	c2ho3D_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
36	c1xeaD_	Alignment	not modelled	100.0	14	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
37	c3c1aB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
38	c3uuwB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
39	c1titB_	Alignment	not modelled	100.0	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)
40	c3oa2B_	Alignment	not modelled	100.0	18	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
41	c1lc3A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
42	c3oa0B_	Alignment	not modelled	100.0	18	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-glnaca
43	d1h6da1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
44	d1ryda1	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d1zh8a1	Alignment	not modelled	100.0	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	d2nvwa1	Alignment	not modelled	100.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
47	d1ydw1	Alignment	not modelled	100.0	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	d1xea1	Alignment	not modelled	100.0	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
49	d1tita1	Alignment	not modelled	100.0	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
50	d1lc0a1	Alignment	not modelled	100.0	25	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceral dehyde-3-phosphate dehydrogenase-like, N-terminal domain
51	c1j5pA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
52	d1f06a1	Alignment	not modelled	99.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

78	c2yv1A	Alignment	not modelled	99.2	15	Chain: A: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 methanocaldococcus jannaschii dsm 2661
79	c2dt5A	Alignment	not modelled	99.2	13	PDB header: dna binding protein Chain: A: PDB Molecule: at-rich dna-binding protein; PDBTitle: crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
80	c2i99A	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: mu-crystallin homolog; PDBTitle: crystal structure of human mu_crystallin at 2.6 angstrom
81	c3a14B	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
82	c2z2vA	Alignment	not modelled	98.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
83	d1xeaa2	Alignment	not modelled	98.9	8	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
84	c3c8mA	Alignment	not modelled	98.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
85	c2jcyA	Alignment	not modelled	98.8	13	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
86	c1b7gO	Alignment	not modelled	98.8	12	PDB header: oxidoreductase Chain: O: PDB Molecule: protein (glyceraldehyde 3-phosphate dehydrogenase); PDBTitle: glyceraldehyde 3-phosphate dehydrogenase
87	c3ijpA	Alignment	not modelled	98.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from2 bartonella henselae at 2.0a resolution
88	c2nu8D	Alignment	not modelled	98.7	12	PDB header: ligase Chain: D: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase
89	c1oi7A	Alignment	not modelled	98.7	15	PDB header: synthetase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
90	c1r0ID	Alignment	not modelled	98.7	16	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
91	d1cf2o1	Alignment	not modelled	98.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
92	c3l6dB	Alignment	not modelled	98.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
93	c3cumA	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
94	c3dzbA	Alignment	not modelled	98.6	9	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
95	c3b1fA	Alignment	not modelled	98.6	8	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
96	c2yv2A	Alignment	not modelled	98.6	16	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from2 aeropyrum pernix k1
97	c2czcD	Alignment	not modelled	98.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: glyceraldehyde-3-phosphate dehydrogenase; PDBTitle: crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 pyrococcus horikoshii ot3
98	d1yl7a1	Alignment	not modelled	98.5	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
99	d1dihA1	Alignment	not modelled	98.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
100	c3gt0A	Alignment	not modelled	98.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
101	c2p4qA	Alignment	not modelled	98.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces

					cerevisiae
102	c2ozpA	Alignment	not modelled	98.5	9 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
103	c1yl7F	Alignment	not modelled	98.5	17 PDB header: oxidoreductase Chain: F: PDB Molecule: dihydroadipicinate reductase; PDBTitle: the crystal structure of mycobacterium tuberculosis2 dihydroadipicinate reductase (rv2773c) in complex with nadh (crystal3 form c)
104	c3ingA	Alignment	not modelled	98.4	16 PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from thermoplasma acidophilum at 1.95 a resolution
105	c1cf2Q	Alignment	not modelled	98.4	13 PDB header: oxidoreductase Chain: Q: PDB Molecule: protein (glyceraldehyde-3-phosphate phosphate2 dehydrogenase from the hyperthermophilic archaeon3 methanothermus fervidus
106	c3d1lB	Alignment	not modelled	98.4	23 PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from bacteroides fragilis
107	c2eghA	Alignment	not modelled	98.4	17 PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
108	c3fwnB	Alignment	not modelled	98.4	12 PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
109	c3ckyA	Alignment	not modelled	98.4	13 PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
110	d2czca2	Alignment	not modelled	98.4	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	c2iz1C	Alignment	not modelled	98.4	17 PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
112	c1vpdA	Alignment	not modelled	98.4	12 PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
113	d1q0qa2	Alignment	not modelled	98.3	17 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
114	c3triB	Alignment	not modelled	98.3	16 PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
115	c3qsgA	Alignment	not modelled	98.3	12 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-binding phosphogluconate dehydrogenase-like protein; PDBTitle: crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
116	c2ph5A	Alignment	not modelled	98.3	11 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
117	c1pgiA	Alignment	not modelled	98.3	15 PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
118	c3g0oA	Alignment	not modelled	98.3	11 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
119	c2izzE	Alignment	not modelled	98.3	8 PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate2 reductase
120	d1i36a2	Alignment	not modelled	98.2	15 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain