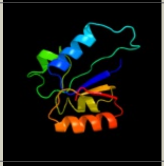
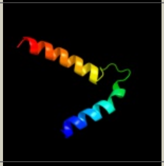
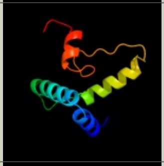
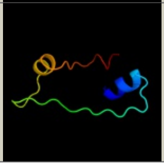
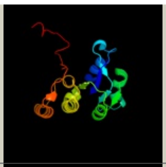
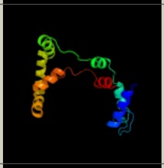
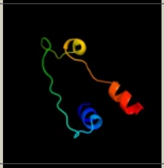
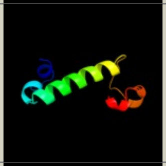
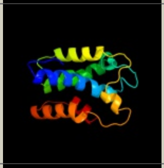
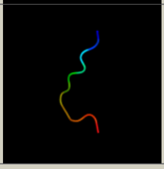
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P77260
Date	Thu Jan 5 12:26:57 GMT 2012
Unique Job ID	c95c53f20a89f7bd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m2wA_	Alignment		100.0	38	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol dehydrogenase; **PDBTitle:** pseudomonas fluorescens mannitol 2-dehydrogenase ternary complex with2 nad and d-mannitol
2	c3h2zA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mannitol-1-phosphate 5-dehydrogenase; **PDBTitle:** the crystal structure of mannitol-1-phosphate dehydrogenase from2 shigella flexneri
3	d1lj8a4	Alignment		100.0	39	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
4	d1lj8a3	Alignment		100.0	36	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**Mannitol 2-dehydrogenase
5	c2axqA_	Alignment		53.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
6	c3mtjA_	Alignment		44.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**homoserine dehydrogenase; **PDBTitle:** the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
7	d1k4ia_	Alignment		43.7	12	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
8	c2ph5A_	Alignment		39.5	17	**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
9	d1gzsb_	Alignment		37.8	11	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
10	c3e59A_	Alignment		35.8	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyoverdine biosynthesis protein pvca; **PDBTitle:** crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
11	d1snna_	Alignment		34.7	22	**Fold:**YrdC/RibB **Superfamily:**YrdC/RibB **Family:**3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB

12	c3euwB_	Alignment		32.9	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
13	d1qusa_	Alignment		32.7	12	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
14	c3mioA_	Alignment		32.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3,4-dihydroxy-2-butanone 4-phosphate synthase; **PDBTitle:** crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
15	c3fggA_	Alignment		28.4	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bce2196; **PDBTitle:** crystal structure of putative ecf-type sigma factor negative effector2 from bacillus cereus
16	d1r0ka2	Alignment		27.6	11	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
17	c3egoB_	Alignment		26.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**probable 2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
18	c3nt5B_	Alignment		23.2	22	**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
19	c1r0lD_	Alignment		21.7	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**1-deoxy-d-xylulose 5-phosphate reductoisomerase; **PDBTitle:** 1-deoxy-d-xylulose 5-phosphate reductoisomerase from2 zymomonas mobilis in complex with nadph
20	d2o8ra3	Alignment		21.5	36	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
21	c1z9bA_	Alignment	not modelled	21.2	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-2; **PDBTitle:** solution structure of the c1-subdomain of bacillus2 stearothermophilus translation initiation factor if2
22	c3ceaA_	Alignment	not modelled	21.0	8	**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
23	c2qytA_	Alignment	not modelled	21.0	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
24	c1e5lA_	Alignment	not modelled	21.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
25	c1ceuA_	Alignment	not modelled	19.7	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hiv-1 regulatory protein n-terminal **PDBTitle:** nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
26	c2o8rA_	Alignment	not modelled	18.6	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis
27	d1v8fa_	Alignment	not modelled	16.7	25	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
28	c2cu2A_	Alignment	not modelled	16.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative mannose-1-phosphate guanylyl transferase; **PDBTitle:** crystal structure of mannose-1-phosphate

						geranyltransferase from2 thermus thermophilus hb8
29	d1ftaa_	Alignment	not modelled	15.8	25	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
30	c2q4eB_	Alignment	not modelled	15.6	16	**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
31	d2py6a1	Alignment	not modelled	15.0	30	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**FkbM-like
32	c2gq1A_	Alignment	not modelled	14.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fructose-1,6-bisphosphatase; **PDBTitle:** crystal structure of recombinant type i fructose-1,6-bisphosphatase2 from escherichia coli complexed with sulfate ions
33	c2fhyL_	Alignment	not modelled	14.7	25	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**fructose-1,6-bisphosphatase 1; **PDBTitle:** structure of human liver fpbase complexed with a novel2 benzoxazole as allosteric inhibitor
34	c3ghyA_	Alignment	not modelled	14.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
35	d2v0fa1	Alignment	not modelled	13.2	40	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
36	c3dapB_	Alignment	not modelled	12.9	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
37	d1e5qa1	Alignment	not modelled	12.4	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
38	c3guzB_	Alignment	not modelled	12.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** structural and substrate-binding studies of pantothenate2 synthenate (ps)provide insights into homotropic inhibition3 by pantoate in ps's
39	c3hn2A_	Alignment	not modelled	12.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
40	c3c7cB_	Alignment	not modelled	11.8	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**octopine dehydrogenase; **PDBTitle:** a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
41	c3omdB_	Alignment	not modelled	11.6	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of unknown function protein from leptospirillum2 rubarum
42	d1uj8a1	Alignment	not modelled	11.2	16	**Fold:**Another 3-helical bundle **Superfamily:**IscX-like **Family:**IscX-like
43	c3n8hA_	Alignment	not modelled	10.6	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine ligase from francisella2 tularensis
44	d2a1jb1	Alignment	not modelled	10.5	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Hef domain-like
45	d1r6ea_	Alignment	not modelled	10.4	14	**Fold:**SopE-like GEF domain **Superfamily:**SopE-like GEF domain **Family:**SopE-like GEF domain
46	c3tbiA_	Alignment	not modelled	10.4	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**rna polymerase-associated protein gp33; **PDBTitle:** crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
47	c2k0rA_	Alignment	not modelled	10.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsbd; **PDBTitle:** solution structure of the c103s mutant of the n-terminal2 domain of dsbd from neisseria meningitidis
48	d1bk4a_	Alignment	not modelled	10.0	25	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
49	c2c9lZ_	Alignment	not modelled	9.8	40	**PDB header:**viral protein **Chain:** Z: **PDB Molecule:**bzlf1 trans-activator protein; **PDBTitle:** structure of the epstein-barr virus zebra protein
50	c2ejcA_	Alignment	not modelled	9.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantoate--beta-alanine ligase; **PDBTitle:** crystal structure of pantoate--beta-alanine ligase (panc)2 from thermotoga maritima
51	d1f06a1	Alignment	not modelled	9.4	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
52	d2cu2a2	Alignment	not modelled	9.3	13	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**mannose-1-phosphate guanylyl transferase
53	d1nuwa_	Alignment	not modelled	9.3	25	**Fold:**Carbohydrate phosphatase **Superfamily:**Carbohydrate phosphatase **Family:**Inositol monophosphatase/fructose-1,6-bisphosphatase-like
54	c3innB_	Alignment	not modelled	9.2	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantoate-beta-alanine-ligase in complex2 with atp at low occupancy at 2.1 a resolution

55	d2oc5a1	Alignment	not modelled	9.0	24	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**PMT1231-like
56	c1yy3A_	Alignment	not modelled	9.0	22	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**s-adenosylmethionine:trna ribosyltransferase- **PDBTitle:** structure of s-adenosylmethionine:trna ribosyltransferase-2 isomerase (quea)
57	d2ouxa1	Alignment	not modelled	8.9	10	**Fold:**alpha-alpha superhelix **Superfamily:**MgtE N-terminal domain-like **Family:**MgtE N-terminal domain-like
58	c3ketA_	Alignment	not modelled	8.8	12	**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
59	c3bjrA_	Alignment	not modelled	8.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative carboxylesterase; **PDBTitle:** crystal structure of a putative carboxylesterase (lp_1002) from2 lactobacillus plantarum wcfs1 at 2.09 a resolution
60	c2qpqC_	Alignment	not modelled	8.7	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
61	c1fi0A_	Alignment	not modelled	8.6	44	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**vpr protein; **PDBTitle:** solution structure of hiv-1 vpr (13-33) peptide in micells
62	c3g17H_	Alignment	not modelled	8.6	12	**PDB header:**structural genomics, unknown function **Chain:** H: **PDB Molecule:**similar to 2-dehydropantoate 2-reductase; **PDBTitle:** structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
63	c2x41A_	Alignment	not modelled	8.3	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-glucosidase; **PDBTitle:** structure of beta-glucosidase 3b from thermotoga neapolitana2 in complex with glucose
64	c2x5sB_	Alignment	not modelled	8.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**mannose-1-phosphate guanylyltransferase; **PDBTitle:** crystal structure of t. maritima gdp-mannose2 pyrophosphorylase in apo state.
65	d1g7sa3	Alignment	not modelled	8.2	16	**Fold:**Initiation factor IF2/eIF5b, domain 3 **Superfamily:**Initiation factor IF2/eIF5b, domain 3 **Family:**Initiation factor IF2/eIF5b, domain 3
66	d1xdpa3	Alignment	not modelled	8.2	50	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
67	d2dt5a2	Alignment	not modelled	8.0	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
68	c3b20R_	Alignment	not modelled	7.4	19	**PDB header:**oxidoreductase **Chain:** R: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase (nadp+); **PDBTitle:** crystal structure analysis of dehydrogenase complexed with nad
69	d1u2ka_	Alignment	not modelled	7.3	26	**Fold:**Heme-dependent peroxidases **Superfamily:**Heme-dependent peroxidases **Family:**Catalase-peroxidase KatG
70	c2k2iB_	Alignment	not modelled	7.3	36	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**sfi1 peptide; **PDBTitle:** nmr solution structure of the c-terminal domain (t94-y172)2 of the human centrin 2 in complex with a repeat sequence of3 human sfi1 (r641-t660)
71	c3h8gC_	Alignment	not modelled	7.3	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cytosol aminopeptidase; **PDBTitle:** bestatin complex structure of leucine aminopeptidase from pseudomonas2 putida
72	d1ihoa_	Alignment	not modelled	7.2	21	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC)
73	c3rrlC_	Alignment	not modelled	7.2	18	**PDB header:**transferase **Chain:** C: **PDB Molecule:**succinyl-coa:3-ketoacid-coenzyme a transferase subunit a; **PDBTitle:** complex structure of 3-oxoadipate coa-transferase subunit a and b from2 helicobacter pylori 26695
74	c1txgA_	Alignment	not modelled	7.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
75	d1o7fa1	Alignment	not modelled	7.0	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**DEP domain
76	c3r24A_	Alignment	not modelled	7.0	50	**PDB header:**transferase, viral protein **Chain:** A: **PDB Molecule:**2'-o-methyl transferase; **PDBTitle:** crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible
77	c1u2jC_	Alignment	not modelled	6.9	26	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**peroxidase/catalase hpi; **PDBTitle:** crystal structure of the c-terminal domain from the2 catalase-peroxidase katg of escherichia coli (p21 21 21)
78	d1t0la_	Alignment	not modelled	6.9	11	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Dimeric isocitrate & isopropylmalate dehydrogenases
						PDB header:structural genomics, unknown function

79	c3ogiC_	Alignment	not modelled	6.8	20	**Chain:** C: **PDB Molecule:**putative esat-6-like protein 6; **PDBTitle:** crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
80	c2d2iO_	Alignment	not modelled	6.7	19	**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+
81	d1mrza2	Alignment	not modelled	6.7	24	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Adenylyltransferase
82	c3tevA_	Alignment	not modelled	6.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hyrolase, family 3; **PDBTitle:** the crystal structure of glycosyl hydrolase from deinococcus2 radiodurans r1
83	d1m9dc_	Alignment	not modelled	6.6	15	**Fold:**Retrovirus capsid protein, N-terminal core domain **Superfamily:**Retrovirus capsid protein, N-terminal core domain **Family:**Retrovirus capsid protein, N-terminal core domain
84	c3fk4A_	Alignment	not modelled	6.3	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rubisco-like protein; **PDBTitle:** crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
85	c2xvtC_	Alignment	not modelled	6.2	33	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**receptor activity-modifying protein 2; **PDBTitle:** structure of the extracellular domain of human ramp2
86	c3ag5A_	Alignment	not modelled	6.2	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pantothenate synthetase; **PDBTitle:** crystal structure of pantothenate synthetase from staphylococcus2 aureus
87	d1veha_	Alignment	not modelled	6.1	25	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Fe-S cluster assembly (FSCA) domain-like **Family:**NifU C-terminal domain-like
88	d2hiqa1	Alignment	not modelled	6.0	16	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Hypothetical protein YdhR
89	c3q2kB_	Alignment	not modelled	5.9	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
90	c2o8sA_	Alignment	not modelled	5.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**agr_c_984p; **PDBTitle:** x-ray crystal structure of protein agr_c_984 from agrobacterium2 tumefaciens. northeast structural genomics consortium target atr120.
91	d1f0xa1	Alignment	not modelled	5.8	38	**Fold:**Ferredoxin-like **Superfamily:**FAD-linked oxidases, C-terminal domain **Family:**D-lactate dehydrogenase
92	c2k8sA_	Alignment	not modelled	5.7	46	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europea: northeast structural3 genomics target net6
93	c2ew2B_	Alignment	not modelled	5.6	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-dehydropantoate 2-reductase, putative; **PDBTitle:** crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
94	d2pg4a1	Alignment	not modelled	5.6	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**F93-like
95	c3f3mA_	Alignment	not modelled	5.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphopantetheine adenylyltransferase; **PDBTitle:** six crystal structures of two phosphopantetheine2 adenylyltransferases reveal an alternative ligand binding3 mode and an associated structural change
96	c1lanA_	Alignment	not modelled	5.5	13	**PDB header:**hydrolase (alpha-aminoacylpeptide) **Chain:** A: **PDB Molecule:**leucine aminopeptidase; **PDBTitle:** leucine aminopeptidase complex with l-leucinal
97	d1vm6a3	Alignment	not modelled	5.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
98	d2ahua2	Alignment	not modelled	5.5	13	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
99	d1hcia1	Alignment	not modelled	5.4	26	**Fold:**Spectrin repeat-like **Superfamily:**Spectrin repeat **Family:**Spectrin repeat