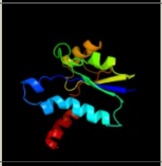
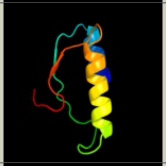
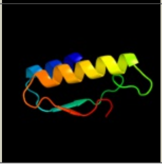
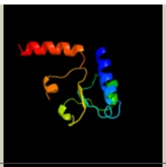
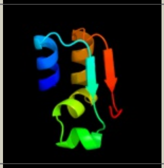
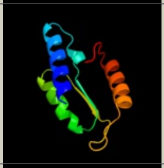
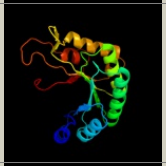
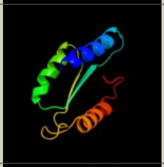
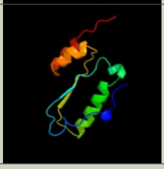
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P23871
Date	Thu Jan 5 11:40:08 GMT 2012
Unique Job ID	77dd8afbddb42741

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1lbqa_	Alignment		100.0	27	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
2	d2hrca1	Alignment		100.0	28	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
3	d2hk6a1	Alignment		100.0	25	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
4	c2xvzA_	Alignment		100.0	17	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**chelatase, putative; **PDBTitle:** cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
5	d1qgoa_	Alignment		100.0	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Cobalt chelatase CbiK
6	c2jh3C_	Alignment		99.8	17	**PDB header:**ribosomal protein **Chain:** C: **PDB Molecule:**ribosomal protein s2-related protein; **PDBTitle:** the crystal structure of dr2241 from deinococcus2 radiodurans at 1.9 a resolution reveals a multi-domain3 protein with structural similarity to chelatases but also4 with two additional novel domains
7	c3lyhB_	Alignment		99.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**cobalamin (vitamin b12) biosynthesis cbix protein; **PDBTitle:** crystal structure of putative cobalamin (vitamin b12) biosynthesis2 cbix protein (yp_958415.1) from marinobacter aquaeolei vt8 at 1.60 a3 resolution
8	c1tjnA_	Alignment		99.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**sirohydrochlorin cobaltochelatase; **PDBTitle:** crystal structure of hypothetical protein af0721 from archaeoglobus2 fulgidus
9	d1tjna_	Alignment		99.2	16	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**CbiX-like
10	c2csuB_	Alignment		87.0	23	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
11	d2csua1	Alignment		85.1	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain

12	c3ke8A_	Alignment		75.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
13	d2d59a1	Alignment		72.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
14	d1efpb_	Alignment		71.8	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
15	c3ewbX_	Alignment		70.7	13	**PDB header:**transferase **Chain:** X: **PDB Molecule:**2-isopropylmalate synthase; **PDBTitle:** crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
16	c3hjtB_	Alignment		68.4	16	**PDB header:**cell adhesion, transport protein **Chain:** B: **PDB Molecule:**lmb; **PDBTitle:** structure of laminin binding protein (lmb) of streptococcus2 agalactiae a bifunctional protein with adhesin and metal3 transporting activity
17	d1yj5a1	Alignment		67.1	12	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**phosphatase domain of polynucleotide kinase
18	d1o94c_	Alignment		67.0	14	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
19	d3clsc1	Alignment		66.6	12	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
20	d1pzxa_	Alignment		66.4	11	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
21	c2qniA_	Alignment	not modelled	66.3	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
22	d1tipa_	Alignment	not modelled	65.4	13	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
23	d1k6ma2	Alignment	not modelled	65.4	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
24	c2yv2A_	Alignment	not modelled	63.3	12	**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
25	c3navB_	Alignment	not modelled	62.0	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
26	c2nu8D_	Alignment	not modelled	61.8	14	**PDB header:**ligase **Chain:** D: **PDB Molecule:**succinyl-coa ligase [adp-forming] subunit alpha; **PDBTitle:** c123at mutant of e. coli succinyl-coa synthetase
27	c2ov3A_	Alignment	not modelled	61.8	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**periplasmic binding protein component of an abc **PDBTitle:** crystal structure of 138-173 znua deletion mutant plus zinc2 bound
28	c3lupA_	Alignment	not modelled	61.6	20	**PDB header:**structure genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** crystal structure of fatty acid binding degv family protein sag13422 from streptococcus agalactiae

29	c3ha2B_	Alignment	not modelled	59.8	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-quinone reductase; **PDBTitle:** crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
30	c2p10D_	Alignment	not modelled	59.0	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
31	c1k6mA_	Alignment	not modelled	58.9	17	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
32	c2fpgA_	Alignment	not modelled	58.0	4	**PDB header:**ligase **Chain:** A: **PDB Molecule:**succinyl-coa ligase [gdp-forming] alpha-chain, **PDBTitle:** crystal structure of pig gtp-specific succinyl-coa2 synthetase in complex with gdp
33	d1bifa2	Alignment	not modelled	57.8	13	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
34	d1g01a_	Alignment	not modelled	56.4	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
35	c3d4iD_	Alignment	not modelled	56.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**sts-2 protein; **PDBTitle:** crystal structure of the 2h-phosphatase domain of sts-2
36	d2p10a1	Alignment	not modelled	54.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**Mll9387-like
37	c3ff4A_	Alignment	not modelled	53.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein chu_1412
38	c2ekcA_	Alignment	not modelled	53.2	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
39	d1y81a1	Alignment	not modelled	53.0	27	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
40	d1qzua_	Alignment	not modelled	51.0	25	**Fold:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Superfamily:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD **Family:**Homo-oligomeric flavin-containing Cys decarboxylases, HFCD
41	c3dnfB_	Alignment	not modelled	50.8	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
42	d1h2ea_	Alignment	not modelled	50.4	14	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
43	c3zvmA_	Alignment	not modelled	46.7	12	**PDB header:**hydrolase/transferase/dna **Chain:** A: **PDB Molecule:**bifunctional polynucleotide phosphatase/kinase; **PDBTitle:** the structural basis for substrate recognition by mammalian2 polynucleotide kinase 3' phosphatase
44	c3nyiA_	Alignment	not modelled	46.4	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**fat acid-binding protein; **PDBTitle:** the crystal structure of a fat acid (stearic acid)-binding protein2 from eubacterium ventriosum atcc 27560.
45	c3c7tB_	Alignment	not modelled	45.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ecdysteroid-phosphate phosphatase; **PDBTitle:** crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
46	d1nh8a2	Alignment	not modelled	45.5	13	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
47	d1fzta_	Alignment	not modelled	45.4	10	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
48	d1qopa_	Alignment	not modelled	45.1	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
49	c1qzuB_	Alignment	not modelled	44.7	25	**PDB header:**lyase **Chain:** B: **PDB Molecule:**hypothetical protein mds018; **PDBTitle:** crystal structure of human phosphopantothenoylcysteine decarboxylase
50	d1ujpa_	Alignment	not modelled	42.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
51	c3mwdB_	Alignment	not modelled	42.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
52	c1oi7A_	Alignment	not modelled	42.7	12	**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
53	d1psza_	Alignment	not modelled	41.9	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor

						Family: TroA-like
54	d1v9ca_	Alignment	not modelled	39.9	14	**Fold:**Flavodoxin-like **Superfamily:**Precorrin-8X methylmutase CbiC/CobH **Family:**Precorrin-8X methylmutase CbiC/CobH
55	c3jr7A_	Alignment	not modelled	39.9	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized egv family protein cog1307; **PDBTitle:** the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
56	c3fdjA_	Alignment	not modelled	38.8	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**degv family protein; **PDBTitle:** the structure of a degv family protein from eubacterium eligens.
57	c2duwA_	Alignment	not modelled	38.7	16	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
58	d1yqha1	Alignment	not modelled	37.2	15	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
59	c3pl5A_	Alignment	not modelled	37.1	9	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** fatty acid binding protein
60	c3ipwA_	Alignment	not modelled	36.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
61	c2yv1A_	Alignment	not modelled	36.3	12	**PDB header:**ligase **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
62	d1iuka_	Alignment	not modelled	36.0	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
63	d1h3da2	Alignment	not modelled	35.2	25	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
64	c1yj5B_	Alignment	not modelled	34.2	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**5' polynucleotide kinase-3' phosphatase catalytic domain; **PDBTitle:** molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
65	d1vk8a_	Alignment	not modelled	33.6	13	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
66	d2hhja1	Alignment	not modelled	33.2	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
67	c3rfaA_	Alignment	not modelled	32.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ribosomal rna large subunit methyltransferase n; **PDBTitle:** x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
68	d1vh3a_	Alignment	not modelled	32.7	9	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylytransferase
69	c2hk1D_	Alignment	not modelled	32.2	7	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**d-psicose 3-epimerase; **PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
70	c2ou4C_	Alignment	not modelled	32.1	12	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase; **PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
71	d3er7a1	Alignment	not modelled	30.2	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Exig0174-like
72	c2a6pA_	Alignment	not modelled	30.1	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible phosphoglycerate mutase gpm2; **PDBTitle:** structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis
73	c3e2vA_	Alignment	not modelled	29.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
74	d2ae8a1	Alignment	not modelled	29.3	14	**Fold:**Ribosomal protein S5 domain 2-like **Superfamily:**Ribosomal protein S5 domain 2-like **Family:**Imidazole glycerol phosphate dehydratase
75	c1o57A_	Alignment	not modelled	28.8	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pur operon repressor; **PDBTitle:** crystal structure of the purine operon repressor of2 bacillus subtilis
76	d7reqb2	Alignment	not modelled	28.6	13	**Fold:**Flavodoxin-like **Superfamily:**Cobalamin (vitamin B12)-binding domain **Family:**Cobalamin (vitamin B12)-binding domain
77	d2dlda2	Alignment	not modelled	28.4	24	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
						Fold:DAK1/DegV-like

78	d1mgpa_	Alignment	not modelled	28.1	19	**Superfamily:**DAK1/DegV-like **Family:**DegV-like
79	c1mgpA_	Alignment	not modelled	28.1	19	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
80	d2b8ea1	Alignment	not modelled	27.6	9	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Meta-cation ATPase, catalytic domain P
81	d1ycga1	Alignment	not modelled	27.2	14	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
82	c2i6oA_	Alignment	not modelled	27.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**sulfolobus solfataricus protein tyrosine **PDBTitle:** crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
83	d1v37a_	Alignment	not modelled	26.8	19	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
84	c2ae8C_	Alignment	not modelled	26.3	14	**PDB header:**lyase **Chain:** C: **PDB Molecule:**imidazoleglycerol-phosphate dehydratase; **PDBTitle:** crystal structure of imidazoleglycerol-phosphate dehydratase from2 staphylococcus aureus subsp. aureus n315
85	d1e5da1	Alignment	not modelled	26.3	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
86	c3e9eB_	Alignment	not modelled	25.6	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
87	c3dmyA_	Alignment	not modelled	25.2	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein fdra; **PDBTitle:** crystal structure of a predicated acyl-coa synthetase from e.coli
88	c3bdkB_	Alignment	not modelled	24.2	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
89	c2hmcA_	Alignment	not modelled	23.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
90	c3rpeA_	Alignment	not modelled	23.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
91	c3dcyA_	Alignment	not modelled	23.5	13	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
92	d1lxna_	Alignment	not modelled	23.0	16	**Fold:**Ferredoxin-like **Superfamily:**MTH1187/YkoF-like **Family:**MTH1187-like
93	d1efvb_	Alignment	not modelled	22.6	15	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Adenine nucleotide alpha hydrolases-like **Family:**ETFP subunits
94	c3eywA_	Alignment	not modelled	21.7	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
95	d1pq4a_	Alignment	not modelled	21.7	12	**Fold:**Chelatase-like **Superfamily:**"Helical backbone" metal receptor **Family:**TroA-like
96	d1fpza_	Alignment	not modelled	21.5	12	**Fold:**(Phosphotyrosine protein) phosphatases II **Superfamily:**(Phosphotyrosine protein) phosphatases II **Family:**Dual specificity phosphatase-like
97	d1bqca_	Alignment	not modelled	21.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
98	c3pnnA_	Alignment	not modelled	21.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a glycosyltransferase from porphyromonas2 gingivalis w83
99	c3guwB_	Alignment	not modelled	21.0	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_1765; **PDBTitle:** crystal structure of the tatd-like protein (af1765) from2 archaeoglobus fulgidus, northeast structural genomics3 consortium target gr121
100	c2c4kD_	Alignment	not modelled	20.8	13	**PDB header:**regulatory protein **Chain:** D: **PDB Molecule:**phosphoribosyl pyrophosphate synthetase- **PDBTitle:** crystal structure of human phosphoribosylpyrophosphate2 synthetase-associated protein 39 (pap39)
101	d1vica_	Alignment	not modelled	20.6	8	**Fold:**Nucleotide-diphospho-sugar transferases **Superfamily:**Nucleotide-diphospho-sugar transferases **Family:**Cytidylyltransferase