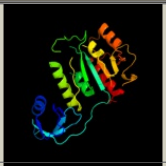
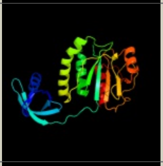
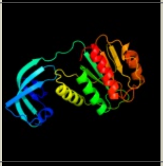
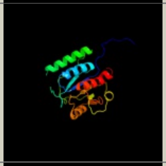
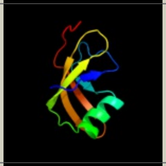
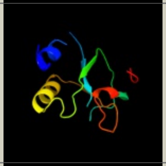
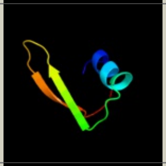
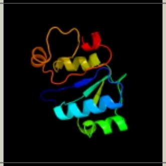
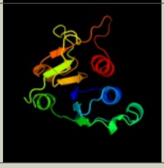
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P0AGL7
Date	Thu Jan 5 11:29:27 GMT 2012
Unique Job ID	c11fef9c70c14452

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vhyB_	Alignment		100.0	63	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein hi0303; **PDBTitle:** crystal structure of haemophilus influenzae protein hi0303, pfam2 duf558
2	c1vhkA_	Alignment		100.0	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yqeu; **PDBTitle:** crystal structure of an hypothetical protein
3	c3kw2A_	Alignment		100.0	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable r-rna methyltransferase; **PDBTitle:** crystal structure of probable rrna-methyltransferase from2 porphyromonas gingivalis
4	c2egwB_	Alignment		100.0	25	**PDB header:**rna methyltransferase **Chain:** B: **PDB Molecule:**upf0088 protein aq_165; **PDBTitle:** crystal structure of rrna methyltransferase with sah ligand
5	c1z85B_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**hypothetical protein tm1380; **PDBTitle:** crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
6	d1nxza2	Alignment		100.0	73	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
7	c2cx8B_	Alignment		100.0	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**methyl transferase; **PDBTitle:** crystal structure of methyltransferase with ligand(sah)
8	d1vhka2	Alignment		100.0	33	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
9	d1v6za2	Alignment		100.0	31	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YggJ C-terminal domain-like
10	d1nxza1	Alignment		99.7	51	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
11	d1vhka1	Alignment		99.5	19	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like

12	d2qmma1	Alignment		96.4	20	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like
13	c3ai9X_	Alignment		96.2	16	**PDB header:**transferase **Chain:** X: **PDB Molecule:**upf0217 protein mj1640; **PDBTitle:** crystal structure of duf358 protein reveals a putative spout-class2 rrna methyltransferase
14	d1v6za1	Alignment		95.9	28	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**YggJ N-terminal domain-like
15	c1k3rA_	Alignment		93.9	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein mt0001; **PDBTitle:** crystal structure of the methyltransferase with a knot from2 methanobacterium thermoautotrophicum
16	d1gz0a1	Alignment		93.8	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
17	d1ipaa1	Alignment		93.6	14	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
18	c1gz0G_	Alignment		93.2	11	**PDB header:**transferase **Chain:** G: **PDB Molecule:**hypothetical trna/rrna methyltransferase yjfh; **PDBTitle:** 23s ribosomal rna g2251 2'o-methyltransferase rlmb
19	c1x7pB_	Alignment		92.9	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna methyltransferase; **PDBTitle:** crystal structure of the spou methyltransferase avirb from2 streptomyces viridochromogenes in complex with the cofactor adomet
20	c1zjrA_	Alignment		92.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna (guanosine-2'-o-)-methyltransferase; **PDBTitle:** crystal structure of a. aeolicus trmh/spou trna modifying enzyme
21	c2ha8A_	Alignment	not modelled	92.5	13	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**tar (hiv-1) rna loop binding protein; **PDBTitle:** methyltransferase domain of human tar (hiv-1) rna binding2 protein 1
22	c2h6rG_	Alignment	not modelled	91.9	15	**PDB header:**isomerase **Chain:** G: **PDB Molecule:**triosephosphate isomerase; **PDBTitle:** crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
23	c3ktyA_	Alignment	not modelled	91.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable methyltransferase; **PDBTitle:** crystal structure of probable methyltransferase from bordetella2 pertussis tohama i
24	c2i6dA_	Alignment	not modelled	91.0	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna methyltransferase, trmh family; **PDBTitle:** the structure of a putative rna methyltransferase of the trmh family2 from porphyromonas gingivalis.
25	c3onpA_	Alignment	not modelled	90.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna/rrna methyltransferase (spou); **PDBTitle:** crystal structure of trna/rrna methyltransferase spou from rhodobacter2 sphaeroides
26	c3l8uA_	Alignment	not modelled	89.1	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative rrna methylase; **PDBTitle:** crystal structure of smu.1707c, a putative rrna methyltransferase from2 streptococcus mutans ua159
27	c3ilkB_	Alignment	not modelled	88.5	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized trna/rrna methyltransferase hi0380; **PDBTitle:** the structure of a probable methylase family protein from haemophilus2 influenzae rd kw20
28	d1mxia_	Alignment	not modelled	87.6	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase

29	d1v2xa_	Alignment	not modelled	87.4	15	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**SpoU-like RNA 2'-O ribose methyltransferase
30	c3ic6A_	Alignment	not modelled	86.0	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative methylase family protein; **PDBTitle:** crystal structure of putative methylase family protein from neisseria2 gonorrhoeae
31	d1mxsa_	Alignment	not modelled	83.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
32	d1wbha1	Alignment	not modelled	82.6	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
33	d1k3ra2	Alignment	not modelled	82.2	19	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**Hypothetical protein MTH1 (MT0001), dimerisation domain
34	c1ipaA_	Alignment	not modelled	80.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rna 2'-o-ribose methyltransferase; **PDBTitle:** crystal structure of rna 2'-o ribose methyltransferase
35	d1rpxa_	Alignment	not modelled	77.9	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
36	c2qiwA_	Alignment	not modelled	76.6	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pep phosphonomutase; **PDBTitle:** crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
37	c2c3zA_	Alignment	not modelled	75.7	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
38	d2flia1	Alignment	not modelled	70.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
39	c2v82A_	Alignment	not modelled	68.7	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**2-dehydro-3-deoxy-6-phosphogalactonate aldolase; **PDBTitle:** kdpgal complexed to kdpgal
40	d1a53a_	Alignment	not modelled	67.9	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
41	c3inpA_	Alignment	not modelled	67.4	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**d-ribulose-phosphate 3-epimerase; **PDBTitle:** 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
42	c3gyqB_	Alignment	not modelled	67.3	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**rrna (adenosine-2'-o-)-methyltransferase; **PDBTitle:** structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
43	d1j5ta_	Alignment	not modelled	67.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
44	c3qjaA_	Alignment	not modelled	66.1	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**indole-3-glycerol phosphate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
45	d1vhca_	Alignment	not modelled	65.0	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
46	c3db3A_	Alignment	not modelled	64.1	8	**PDB header:**ligase **Chain:** A: **PDB Molecule:**e3 ubiquitin-protein ligase uhrf1; **PDBTitle:** crystal structure of the tandem tudor domains of the e3 ubiquitin-2 protein ligase uhrf1 in complex with trimethylated histone h3-k93 peptide
47	c3e5yB_	Alignment	not modelled	63.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**trmh family rna methyltransferase; **PDBTitle:** crystal structure of trmh family rna methyltransferase from2 burkholderia pseudomallei
48	d1znna1	Alignment	not modelled	63.3	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**PdxS-like
49	c3igsB_	Alignment	not modelled	60.2	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase 2; **PDBTitle:** structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
50	c1znnF_	Alignment	not modelled	59.7	14	**PDB header:**biosynthetic protein **Chain:** F: **PDB Molecule:**plp synthase; **PDBTitle:** structure of the synthase subunit of plp synthase
51	c2e6zA_	Alignment	not modelled	53.2	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt5; **PDBTitle:** solution structure of the second kow motif of human2 transcription elongation factor spt5
52	d1piia2	Alignment	not modelled	49.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
53	d1ns5a_	Alignment	not modelled	48.5	21	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
54	c2e5pA_	Alignment	not modelled	47.5	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 1; **PDBTitle:** solution structure of the tudor domain of phd finger2

						protein 1 (phf1 protein)
55	c2eqmA_	Alignment	not modelled	46.4	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1 [homo sapiens]
56	d1y71a1	Alignment	not modelled	45.7	20	**Fold:**SH3-like barrel **Superfamily:**Kinase-associated protein B-like **Family:**Kinase-associated protein B-like
57	d1i4na_	Alignment	not modelled	44.6	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
58	d1wa3a1	Alignment	not modelled	44.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
59	c3iz5Y_	Alignment	not modelled	43.7	13	**PDB header:**ribosome **Chain:** Y: **PDB Molecule:**60s ribosomal protein l26 (l24p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
60	d1to0a_	Alignment	not modelled	43.0	13	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
61	d2csua1	Alignment	not modelled	39.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
62	d3bbda1	Alignment	not modelled	39.7	17	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**EMG1/NEP1-like
63	d1vc4a_	Alignment	not modelled	38.8	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
64	d1sf8a_	Alignment	not modelled	38.5	6	**Fold:**HSP90 C-terminal domain **Superfamily:**HSP90 C-terminal domain **Family:**HSP90 C-terminal domain
65	c2equA_	Alignment	not modelled	38.5	15	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**phd finger protein 20-like 1; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 20-like 1
66	c1yadD_	Alignment	not modelled	38.2	12	**PDB header:**transcription **Chain:** D: **PDB Molecule:**regulatory protein teni; **PDBTitle:** structure of teni from bacillus subtilis
67	c2eqjA_	Alignment	not modelled	37.9	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**metal-response element-binding transcription **PDBTitle:** solution structure of the tudor domain of metal-response2 element-binding transcription factor 2
68	d1d9ea_	Alignment	not modelled	37.3	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
69	c2csuB_	Alignment	not modelled	37.3	14	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**457aa long hypothetical protein; **PDBTitle:** crystal structure of ph0766 from pyrococcus horikoshii ot3
70	d1w0ma_	Alignment	not modelled	36.1	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Triosephosphate isomerase (TIM) **Family:**Triosephosphate isomerase (TIM)
71	c2jvvA_	Alignment	not modelled	35.8	24	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of e. coli nusg carboxyterminal domain
72	c2kvqG_	Alignment	not modelled	35.8	24	**PDB header:**transcription **Chain:** G: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** solution structure of nuse:nusg-ctd complex
73	d1xi3a_	Alignment	not modelled	35.8	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
74	d1te7a_	Alignment	not modelled	35.8	12	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**yqfB-like
75	c2yw3E_	Alignment	not modelled	35.7	19	**PDB header:**lyase **Chain:** E: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- **PDBTitle:** crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
76	d1q6oa_	Alignment	not modelled	35.6	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Decarboxylase
77	c2zpaB_	Alignment	not modelled	35.1	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein ypfi; **PDBTitle:** crystal structure of trna(met) cytidine acetyltransferase
78	c3sz8D_	Alignment	not modelled	34.9	9	**PDB header:**transferase **Chain:** D: **PDB Molecule:**2-dehydro-3-deoxyphosphooctonate aldolase 2; **PDBTitle:** crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
79	c3qiiA_	Alignment	not modelled	34.0	11	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 2 of human phd finger protein 20
						Fold:TIM beta/alpha-barrel

80	d1tqja_	Alignment	not modelled	33.4	13	**Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
81	d1xm3a_	Alignment	not modelled	33.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**ThiG-like **Family:**ThiG-like
82	c2xk0A_	Alignment	not modelled	33.3	3	**PDB header:**transcription **Chain:** A: **PDB Molecule:**polycomb protein pcl; **PDBTitle:** solution structure of the tudor domain from drosophila2 polycomblike (pcl)
83	c3qc3B_	Alignment	not modelled	32.5	15	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**d-ribulose-5-phosphate-3-epimerase; **PDBTitle:** crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
84	d1nz9a_	Alignment	not modelled	32.1	21	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
85	d1vr4a1	Alignment	not modelled	30.6	14	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
86	c3ih1A_	Alignment	not modelled	28.9	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**methylisocitrate lyase; **PDBTitle:** crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
87	d1vh0a_	Alignment	not modelled	28.9	10	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
88	d1vqot1	Alignment	not modelled	28.6	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
89	d2do3a1	Alignment	not modelled	28.3	13	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**SPT5 KOW domain-like
90	c2qjhH_	Alignment	not modelled	27.0	12	**PDB header:**lyase **Chain:** H: **PDB Molecule:**putative aldolase mj0400; **PDBTitle:** m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
91	c3o63B_	Alignment	not modelled	27.0	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thiamine-phosphate pyrophosphorylase; **PDBTitle:** crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
92	c3dx5A_	Alignment	not modelled	27.0	10	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uncharacterized protein asbf; **PDBTitle:** crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
93	d1nppa2	Alignment	not modelled	27.0	15	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**N-utilization substance G protein NusG, C-terminal domain
94	d1wjsa_	Alignment	not modelled	26.6	9	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
95	c3ajxA_	Alignment	not modelled	26.4	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-hexulose-6-phosphate synthase; **PDBTitle:** crystal structure of 3-hexulose-6-phosphate synthase
96	d2tpsa_	Alignment	not modelled	26.4	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Thiamin phosphate synthase **Family:**Thiamin phosphate synthase
97	d1y2ia_	Alignment	not modelled	26.0	17	**Fold:**Dodecin subunit-like **Superfamily:**YbjQ-like **Family:**YbjQ-like
98	c1y2iC_	Alignment	not modelled	26.0	17	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**hypothetical protein s0862; **PDBTitle:** crystal structure of mcsg target apc27401 from shigella2 flexneri
99	c3navB_	Alignment	not modelled	26.0	16	**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
100	d1i60a_	Alignment	not modelled	25.7	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**IolI-like
101	d2zjrr1	Alignment	not modelled	25.3	17	**Fold:**SH3-like barrel **Superfamily:**Translation proteins SH3-like domain **Family:**Ribosomal proteins L24p and L21e
102	c3qkbB_	Alignment	not modelled	25.1	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
103	c3exsB_	Alignment	not modelled	24.7	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**rmpd (hexulose-6-phosphate synthase); **PDBTitle:** crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
104	c3q1jA_	Alignment	not modelled	24.7	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 20; **PDBTitle:** crystal structure of tudor domain 1 of human phd finger protein 20
105	c3p8bB_	Alignment	not modelled	24.1	22	**PDB header:**transferase/transcription **Chain:** B: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** x-ray crystal structure of pyrococcus furiosus transcription2 elongation factor spt4/5
						PDB header:synthase, lyase

106	c3f4wA_	Alignment	not modelled	23.9	18	**Chain:** A: **PDB Molecule:**putative hexulose 6 phosphate synthase; **PDBTitle:** the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
107	c2xhcA_	Alignment	not modelled	23.8	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription antitermination protein nusg; **PDBTitle:** crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
108	d1o54a_	Alignment	not modelled	23.3	24	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**tRNA(1-methyladenosine) methyltransferase-like
109	d1wgsa_	Alignment	not modelled	22.8	13	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo barrel domain
110	d1wjqa_	Alignment	not modelled	22.7	16	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**MBT repeat
111	c3lyeA_	Alignment	not modelled	22.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oxaloacetate acetyl hydrolase; **PDBTitle:** crystal structure of oxaloacetate acetylhydrolase
112	d2d59a1	Alignment	not modelled	22.5	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
113	c2kw8A_	Alignment	not modelled	22.4	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lpxtg-site transpeptidase family protein; **PDBTitle:** solution structure of bacillus anthracis sortase a (srta)2 transpeptidase
114	c3q58A_	Alignment	not modelled	22.3	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**n-acetylmannosamine-6-phosphate 2-epimerase; **PDBTitle:** structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
115	d2nu7a1	Alignment	not modelled	22.2	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**CoA-binding domain
116	c2e5qA_	Alignment	not modelled	22.0	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**phd finger protein 19; **PDBTitle:** solution structure of the tudor domain of phd finger2 protein 19, isoform b [homo sapiens]
117	d1o6da_	Alignment	not modelled	21.5	18	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**YbeA-like
118	d1o60a_	Alignment	not modelled	21.4	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
119	c2rd5D_	Alignment	not modelled	20.8	10	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**pii protein; **PDBTitle:** structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
120	d2qwva1	Alignment	not modelled	20.7	17	**Fold:**alpha/beta knot **Superfamily:**alpha/beta knot **Family:**AF1056-like