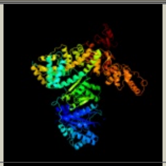
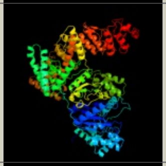
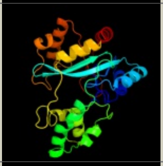
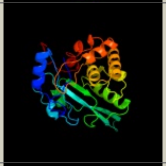
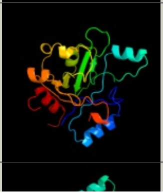
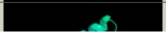
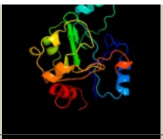
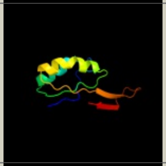
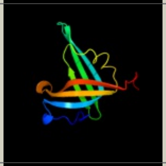
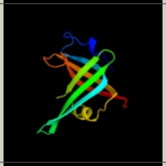
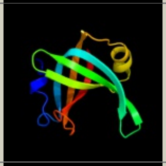
Phyre^2

Email	l.a.kelley@imperial.ac.uk
Description	P10443
Date	Thu Jan 5 11:32:19 GMT 2012
Unique Job ID	42bb57e9b22d4d14

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3e0dA_	Alignment		100.0	42	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase iii subunit alpha; **PDBTitle:** insights into the replisome from the crystral structure of2 the ternary complex of the eubacterial dna polymerase iii3 alpha-subunit
2	c2hnhA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase iii alpha subunit; **PDBTitle:** crystal structure of the catalytic alpha subunit of e. coli2 replicative dna polymerase iii
3	c3f2cA_	Alignment		100.0	27	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**geobacillus kaustophilus dna polc; **PDBTitle:** dna polymerase polc from geobacillus kaustophilus complex with dna,2 dgtp and mn
4	c3e0fA_	Alignment		99.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative metal-dependent phosphoesterase; **PDBTitle:** crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
5	c2wjeA_	Alignment		99.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase cpsb; **PDBTitle:** crystal structure of the tyrosine phosphatase cps4b from2 steptococcus pneumoniae tigr4.
6	c2yb1A_	Alignment		99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amidohydrolase; **PDBTitle:** structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
7	c3qy6A_	Alignment		99.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tyrosine-protein phosphatase ywqe; **PDBTitle:** crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
8	c3dcpB_	Alignment		99.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol-phosphatase; **PDBTitle:** crystal structure of the putative histidinol phosphatase2 hisk from listeria monocytogenes. northeast structural3 genomics consortium target lmr141.
9	c2yz5B_	Alignment		99.6	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**histidinol phosphatase; **PDBTitle:** histidinol phosphate phosphatase complexed with phosphate
10	d1m65a_	Alignment		99.4	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
11	d2anua1	Alignment		99.2	18	**Fold:**7-stranded beta/alpha barrel **Superfamily:**PHP domain-like **Family:**PHP domain
						

12	c2anuA_	Alignment		99.2	18	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm0559; **PDBTitle:** crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution
13	c2w9mB_	Alignment		99.0	16	**PDB header:**dna replication **Chain:** B: **PDB Molecule:**polymerase x; **PDBTitle:** structure of family x dna polymerase from deinococcus2 radiodurans
14	c3e38A_	Alignment		98.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**two-domain protein containing predicted php-like metal- **PDBTitle:** crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
15	d1c0aa1	Alignment		97.9	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
16	c3i7fA_	Alignment		97.8	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** aspartyl trna synthetase from entamoeba histolytica
17	c1b8aB_	Alignment		97.8	16	**PDB header:**ligase **Chain:** B: **PDB Molecule:**protein (aspartyl-trna synthetase); **PDBTitle:** aspartyl-trna synthetase
18	d1b8aa1	Alignment		97.8	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
19	c1x55A_	Alignment		97.7	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase; **PDBTitle:** crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
20	d1e1oa1	Alignment		97.7	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
21	d1gm5a2	Alignment	not modelled	97.7	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**RecG "wedge" domain
22	c1eqrC_	Alignment	not modelled	97.6	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of free aspartyl-trna synthetase from2 escherichia coli
23	c3e9hB_	Alignment	not modelled	97.6	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase from bacillus stearothermophilus2 complexed with l-lysylsulfamoyl adenosine
24	d1bbua1	Alignment	not modelled	97.6	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
25	c1wydB_	Alignment	not modelled	97.6	23	**PDB header:**ligase **Chain:** B: **PDB Molecule:**hypothetical aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from sulfolobus tokodaii
26	c3bjuB_	Alignment	not modelled	97.5	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** crystal structure of tetrameric form of human lysyl-trna2 synthetase
27	d1n9wa1	Alignment	not modelled	97.5	31	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
28	d1l0wa1	Alignment	not modelled	97.5	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
29	c2xgtB	Alignment	not modelled	97.5	18	**PDB header:**ligase **Chain:** B: **PDB Molecule:**asparaginyl-trna synthetase, cytoplasmic;

29	c2xgtB_	Alignment	not modelled	97.5	18	**PDBTitle:** asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
30	c3kf6A_	Alignment	not modelled	97.5	19	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of s. pombe stn1-ten1 complex
31	c3dm3A_	Alignment	not modelled	97.5	22	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor a; **PDBTitle:** crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjr118e
32	c2k50A_	Alignment	not modelled	97.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**replication factor a related protein; **PDBTitle:** solution nmr structure of the replication factor a related2 protein from methanobacterium thermoautotrophicum.3 northeast structural genomics target tr91a.
33	c1efwA_	Alignment	not modelled	97.4	14	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** crystal structure of aspartyl-trna synthetase from thermus2 thermophilus complexed to trnaasp from escherichia coli
34	d1eova1	Alignment	not modelled	97.4	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
35	c3m4qA_	Alignment	not modelled	97.3	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**asparaginyl-trna synthetase, putative; **PDBTitle:** entamoeba histolytica asparaginyl-trna synthetase (asnrs)
36	c1e22A_	Alignment	not modelled	97.3	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**lysyl-trna synthetase; **PDBTitle:** lysyl-trna synthetase (lysu) hexagonal form complexed with2 lysine and the non-hydrolysable atp analogue amp-pcp
37	d2edua1	Alignment	not modelled	97.2	16	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
38	c3e0eA_	Alignment	not modelled	97.2	23	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a; **PDBTitle:** crystal structure of a domain of replication protein a from2 methanococcus maripaludis. northeast structural genomics3 targe mrr110b
39	c1asyA_	Alignment	not modelled	97.1	20	**PDB header:**complex (aminoacyl-trna synthase/trna) **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase; **PDBTitle:** class ii aminoacyl transfer rna synthetases: crystal2 structure of yeast aspartyl-trna synthetase complexed with3 trna asp
40	c1n9wA_	Alignment	not modelled	97.1	33	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**aspartyl-trna synthetase 2; **PDBTitle:** crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
41	d2pi2a1	Alignment	not modelled	96.8	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
42	d1o7ia_	Alignment	not modelled	96.8	19	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
43	c1z9fA_	Alignment	not modelled	96.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of single stranded dna-binding protein (tm0604) from2 thermotoga maritima at 2.60 a resolution
44	c1gm5A_	Alignment	not modelled	96.8	14	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
45	c2pi2A_	Alignment	not modelled	96.7	21	**PDB header:**replication, dna binding protein **Chain:** A: **PDB Molecule:**replication protein a 32 kda subunit; **PDBTitle:** full-length replication protein a subunits rpa14 and rpa32
46	d2i5ha1	Alignment	not modelled	96.7	27	**Fold:**AF1531-like **Superfamily:**AF1531-like **Family:**AF1531-like
47	c2i5hA_	Alignment	not modelled	96.7	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein af1531; **PDBTitle:** crystal structure of af1531 from archaeoglobus fulgidus,2 pfam duf655
48	c3eivB_	Alignment	not modelled	96.4	22	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein 2; **PDBTitle:** crystal structure of single-stranded dna-binding protein2 from streptomyces coelicolor
49	d1xjva1	Alignment	not modelled	96.4	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
50	d1krta_	Alignment	not modelled	96.2	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
51	d1qvca_	Alignment	not modelled	96.2	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
52	c2kenA_	Alignment	not modelled	96.1	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of the ob domain (residues 67-166)2 of mm0293 from methanosarcina mazei. northeast structural3 genomics consortium target mar214a.
53	c3tqyA_	Alignment	not modelled	96.1	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** structure of a single-stranded dna-binding protein (ssb), from2 coxiella burnetii
54	c1ynxA_	Alignment	not modelled	96.1	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**replication factor-a protein 1;

54	c1ynxA_	Alignment	not modelled	96.1	18	**PDBTitle:** solution structure of dna binding domain a (dbd-a) of2 s.cerevisiae replication protein a (rpa)
55	d1v1qa_	Alignment	not modelled	96.0	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
56	c3kf8C_	Alignment	not modelled	95.9	13	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**protein stn1; **PDBTitle:** crystal structure of c. tropicalis stn1-ten1 complex
57	d1eyga_	Alignment	not modelled	95.9	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
58	c2ihfA_	Alignment	not modelled	95.9	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of deletion mutant delta 228-252 r190a of the2 single-stranded dna binding protein from thermus aquaticus
59	d1jmca1	Alignment	not modelled	95.7	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
60	d1jmca2	Alignment	not modelled	95.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
61	c3pgzB_	Alignment	not modelled	95.6	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of a single strand binding protein (ssb) from2 bartonella henselae
62	c1fguA_	Alignment	not modelled	95.6	24	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication protein a 70 kda dna-binding subunit; **PDBTitle:** ssdna-binding domain of the large subunit of replication2 protein a
63	c2k75A_	Alignment	not modelled	95.5	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ta0387; **PDBTitle:** solution nmr structure of the ob domain of ta0387 from2 thermoplasma acidophilum. northeast structural genomics3 consortium target tar80b.
64	c1se8A_	Alignment	not modelled	95.5	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** structure of single-stranded dna-binding protein (ssb) from d.2 radiodurans
65	d1se8a_	Alignment	not modelled	95.5	12	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
66	c1xjvA_	Alignment	not modelled	95.4	12	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**protection of telomeres 1; **PDBTitle:** crystal structure of human pot1 bound to telomeric single-2 stranded dna (ttagggttag)
67	d1ue1a_	Alignment	not modelled	95.4	23	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
68	c2iheA_	Alignment	not modelled	95.0	23	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of wild-type single-stranded dna binding protein2 from thermus aquaticus
69	c3kojA_	Alignment	not modelled	95.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**uncharacterized protein ycf41; **PDBTitle:** crystal structure of the ssb domain of q5n255_synp6 protein2 from synechococcus sp. northeast structural genomics3 consortium target snr59a.
70	c3e0jG_	Alignment	not modelled	94.9	19	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna polymerase subunit delta-2; **PDBTitle:** x-ray structure of the complex of regulatory subunits of2 human dna polymerase delta
71	d3bzka1	Alignment	not modelled	94.9	22	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Tex HhH-containing domain-like
72	d3ulla_	Alignment	not modelled	94.9	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
73	c1k8gC_	Alignment	not modelled	94.7	14	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the n-terminal domain of oxytricha2 nova telomere end binding protein alpha subunit both3 uncomplexed and complexed with telomeric ssdna
74	c2vw9B_	Alignment	not modelled	94.7	15	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**single-stranded dna binding protein; **PDBTitle:** single stranded dna binding protein complex from2 helicobacter pylori
75	d1wjja_	Alignment	not modelled	94.6	22	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
76	c3lgjA_	Alignment	not modelled	94.4	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**single-stranded dna-binding protein; **PDBTitle:** crystal structure of single-stranded binding protein (ssb) from2 bartonella henselae
77	c1s5lu_	Alignment	not modelled	94.2	17	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**photosystem ii 12 kda extrinsic protein; **PDBTitle:** architecture of the photosynthetic oxygen evolving center
78	d1qzga_	Alignment	not modelled	94.2	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
79	d1jb7a1	Alignment	not modelled	93.8	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
						PDB header:dna binding protein

80	c1ue7A_	Alignment	not modelled	93.6	21	**Chain:** A: **PDB Molecule:**single-strand binding protein; **PDBTitle:** crystal structure of the single-stranded dna-binding2 protein from mycobacterium tuberculosis
81	c3fhwB_	Alignment	not modelled	92.5	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**primosomal replication protein n; **PDBTitle:** crystal structure of the protein prib from bordetella parapertussis.2 northeast structural genomics consortium target bpr162.
82	c3k8aA_	Alignment	not modelled	92.4	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative primosomal replication protein; **PDBTitle:** neisseria gonorrhoeae prib
83	d2axtu1	Alignment	not modelled	92.2	17	**Fold:**SAM domain-like **Superfamily:**PsbU/PolX domain-like **Family:**PsbU-like
84	d2duya1	Alignment	not modelled	91.9	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**ComEA-like
85	c1eqqD_	Alignment	not modelled	91.2	20	**PDB header:**replication/rna **Chain:** D: **PDB Molecule:**single stranded dna binding protein; **PDBTitle:** single stranded dna binding protein and ssdna complex
86	c2ekcA_	Alignment	not modelled	89.3	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
87	c2oceA_	Alignment	not modelled	89.3	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
88	d1txya_	Alignment	not modelled	88.7	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
89	c1ph4A_	Alignment	not modelled	87.4	14	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** crystal structure of the oxytricha nova telomere end-binding protein2 complexed with noncognate ssdna ggggttttggcg
90	c1jb7A_	Alignment	not modelled	87.4	14	**PDB header:**dna-binding protein/dna **Chain:** A: **PDB Molecule:**telomere-binding protein alpha subunit; **PDBTitle:** dna g-quartets in a 1.86 a resolution structure of an oxytricha nova2 telomeric protein-dna complex
91	d1sr3a_	Alignment	not modelled	86.7	21	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
92	c3en2A_	Alignment	not modelled	81.8	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable primosomal replication protein n; **PDBTitle:** three-dimensional structure of the protein prib from2 ralstonia solanacearum at the resolution 2.3a. northeast3 structural genomics consortium target rsr213c.
93	d1hl9a2	Alignment	not modelled	79.4	27	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Putative alpha-L-fucosidase, catalytic domain
94	c1wxpA_	Alignment	not modelled	79.0	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**tho complex subunit 1; **PDBTitle:** solution structure of the death domain of nuclear matrix2 protein p84
95	d1j6qa_	Alignment	not modelled	75.7	24	**Fold:**OB-fold **Superfamily:**Heme chaperone CcmE **Family:**Heme chaperone CcmE
96	c1j6qA_	Alignment	not modelled	75.7	24	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**cytochrome c maturation protein e; **PDBTitle:** solution structure and characterization of the heme2 chaperone ccme
97	d2amxa1	Alignment	not modelled	74.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
98	d1nnxa_	Alignment	not modelled	74.1	12	**Fold:**OB-fold **Superfamily:**Hypothetical protein YgiW **Family:**Hypothetical protein YgiW
99	d1vfla1	Alignment	not modelled	72.3	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
100	c3rysA_	Alignment	not modelled	70.9	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosine deaminase 1; **PDBTitle:** the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
101	d2qalk1	Alignment	not modelled	70.6	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Translational machinery components **Family:**Ribosomal protein L18 and S11
102	c3jyvK_	Alignment	not modelled	67.6	28	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**40s ribosomal protein s14(a); **PDBTitle:** structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
103	c3mo4B_	Alignment	not modelled	67.5	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**alpha-1,3/4-fucosidase; **PDBTitle:** the crystal structure of an alpha-(1-3,4)-fucosidase from2 bifidobacterium longum subsp. infantis atcc 15697
104	c1hl8B_	Alignment	not modelled	65.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-l-fucosidase; **PDBTitle:** crystal structure of thermotoga maritima alpha-fucosidase
105	d1rh9a1	Alignment	not modelled	64.3	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases

106	d1ug3a1	Alignment	not modelled	64.2	17	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**MIF4G domain-like
107	d1tg7a5	Alignment	not modelled	62.7	19	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Glycosyl hydrolases family 35 catalytic domain
108	d1ujpa_	Alignment	not modelled	60.7	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
109	d1a4ma_	Alignment	not modelled	60.1	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Adenosine/AMP deaminase
110	c2x6kB_	Alignment	not modelled	60.1	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotidylinositol 3 kinase 59f; **PDBTitle:** the crystal structure of the drosophila class iii pi3-kinase2 vps34 in complex with pi-103
111	d1geqa_	Alignment	not modelled	59.3	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**Tryptophan biosynthesis enzymes
112	c3psiA_	Alignment	not modelled	58.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription elongation factor spt6; **PDBTitle:** crystal structure of the spt6 core domain from saccharomyces2 cerevisiae, form spt6(239-1451)
113	d1wcga1	Alignment	not modelled	58.1	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Family 1 of glycosyl hydrolase
114	d1rpxa_	Alignment	not modelled	57.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Ribulose-phoshate binding barrel **Family:**D-ribulose-5-phosphate 3-epimerase
115	c2dplA_	Alignment	not modelled	56.4	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing] subunit b; **PDBTitle:** crystal structure of the gmp synthase from pyrococcus horikoshii ot3
116	d1i94m_	Alignment	not modelled	55.1	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
117	c3navB_	Alignment	not modelled	54.7	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
118	d1hjqa_	Alignment	not modelled	54.5	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
119	c3pzqA_	Alignment	not modelled	54.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family **PDBTitle:** structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
120	d2v4jc1	Alignment	not modelled	53.9	21	**Fold:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Superfamily:**DsrC, the gamma subunit of dissimilatory sulfite reductase **Family:**DsrC, the gamma subunit of dissimilatory sulfite reductase