Phyre^2

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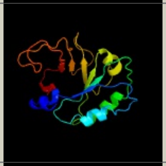
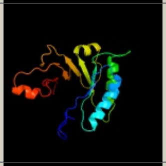
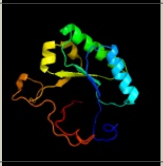
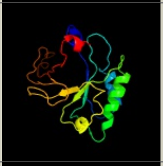
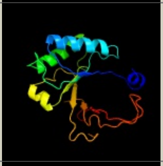
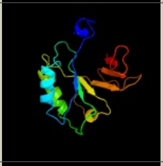
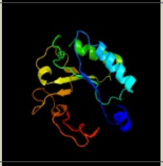
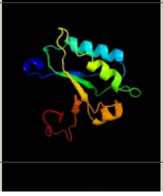
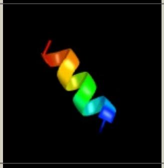
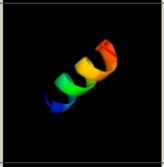
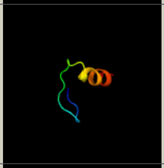
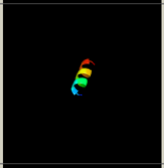
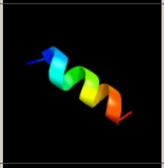
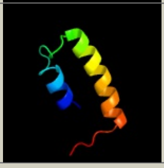
Description	RVBD3766_(-)_4212471_4213160
Date	Fri Aug 9 18:20:47 BST 2019
Unique Job ID	aead0f5bfba05a93

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2nw0B_	Alignment		99.3	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**plyb; **PDBTitle:** crystal structure of a lysin
2	c2wagA_	Alignment		99.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme, putative; **PDBTitle:** the structure of a family 25 glycosyl hydrolase from2 bacillus anthracis.
3	c4jz5A_	Alignment		99.2	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gp26; **PDBTitle:** high-resolution structure of catalytic domain of endolysin ply40 from2 bacteriophage p40 of listeria monocytogenes
4	c4krtA_	Alignment		99.1	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**autolytic lysozyme; **PDBTitle:** x-ray structure of endolysin from clostridium perfringens phage2 phism101
5	d1jfxa_	Alignment		98.9	24	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase
6	c4ff5A_	Alignment		98.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**glycosyl hydrolase 25; **PDBTitle:** structure basis of a novel virulence factor ghip a glycosyl hydrolase2 25 of streptococcus pneumoniae participating in host cell invasion
7	c5a6sA_	Alignment		98.7	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**endolysin; **PDBTitle:** crystal structure of the ctp1l endolysin reveals how its2 activity is regulated by a secondary translation product
8	c5jipB_	Alignment		98.5	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cortical-lytic enzyme; **PDBTitle:** crystal structure of the clostridium perfringens spore cortex lytic2 enzyme slem
9	c2x8rE_	Alignment		98.4	25	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** the structure of a family gh25 lysozyme from aspergillus2 fumigatus
10	c2wwcA_	Alignment		96.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**1,4-beta-n-acetylmuramidase; **PDBTitle:** 3d-structure of the modular autolysin lytc from2 streptococcus pneumoniae in complex with synthetic3 peptidoglycan ligand
11	d2j8ga2	Alignment		95.3	17	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase

12	c2j8fA_	Alignment		94.6	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme; **PDBTitle:** crystal structure of the modular cpl-1 endolysin complexed with a2 peptidoglycan analogue (e94q mutant in complex with a disaccharide-3 pentapeptide)
13	c4b1pJ_	Alignment		60.8	69	**PDB header:**transferase/dna **Chain:** J: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** archaeal rnap-dna binary complex at 4.32ang
14	c4aybQ_	Alignment		60.5	69	**PDB header:**transferase **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase; **PDBTitle:** rnap at 3.2ang
15	d1vaza_	Alignment		59.2	23	**Fold:**NSFL1 (p97 ATPase) cofactor p47, SEP domain **Superfamily:**NSFL1 (p97 ATPase) cofactor p47, SEP domain **Family:**NSFL1 (p97 ATPase) cofactor p47, SEP domain
16	d1ss6a_	Alignment		53.5	23	**Fold:**NSFL1 (p97 ATPase) cofactor p47, SEP domain **Superfamily:**NSFL1 (p97 ATPase) cofactor p47, SEP domain **Family:**NSFL1 (p97 ATPase) cofactor p47, SEP domain
17	c4b1oQ_	Alignment		49.8	69	**PDB header:**transferase/dna **Chain:** Q: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** archaeal rnap-dna binary complex at 4.32ang
18	c2y0sJ_	Alignment		49.6	69	**PDB header:**transferase **Chain:** J: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in p21 space2 group
19	c2y0sQ_	Alignment		49.6	69	**PDB header:**transferase **Chain:** Q: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in p21 space2 group
20	c4e0uB_	Alignment		46.8	39	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cyclic dipeptide n-prenyltransferase; **PDBTitle:** crystal structure of cdpnpt in complex with thiolodiphosphate and (s)-2 benzodiazependione
21	c3hkzZ_	Alignment	not modelled	43.7	62	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
22	c2waqQ_	Alignment	not modelled	42.6	69	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-directed rna2 polymerase
23	c3hkzY_	Alignment	not modelled	40.6	62	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
24	c1q88B_	Alignment	not modelled	37.9	35	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**39 kda initiator binding protein; **PDBTitle:** crystal structure of the c-domain of the t.vaginalis inr2 binding protein, ibp39 (monoclinic form)
25	c3vwbA_	Alignment	not modelled	37.9	13	**PDB header:**transcription/dna **Chain:** A: **PDB Molecule:**virulence regulon transcriptional activator virb; **PDBTitle:** crystal structure of virb core domain (se-met derivative) complexed2 with the cis-acting site (5-bru modifications) upstream icsb promoter
26	c5yaaD_	Alignment	not modelled	37.5	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**meiosis regulator and mrna stability factor 1; **PDBTitle:** crystal structure of marf1 nyn domain from mus musculus
27	c3i4zA_	Alignment	not modelled	37.4	34	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tryptophan dimethylallyltransferase; **PDBTitle:** crystal structure of the dimethylallyl tryptophan synthase fgapt2 from2 aspergillus fumigatus
28	d1q88a_	Alignment	not modelled	37.3	35	**Fold:**39 kda initiator binding protein, IBP39, C-terminal domains **Superfamily:**39 kda initiator binding protein, IBP39, C-terminal

		Alignment				domains **Family:**39 kda initiator binding protein, IBP39, C-terminal domains
29	c3o2kA_	Alignment	not modelled	35.6	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**brevianamide f prenyltransferase; **PDBTitle:** crystal structure of brevianamide f prenyltransferase complexed with2 brevianamide f and dimethylallyl s-thiolodiphosphate
30	c4aczB_	Alignment	not modelled	32.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-alpha-mannosidase; **PDBTitle:** structure of the gh99 endo-alpha-mannosidase from2 bacteroides thetaiotaomicron
31	c5kdaA_	Alignment	not modelled	32.4	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aromatic prenyltransferase; **PDBTitle:** crystal structure of the aromatic prenyltransferase atapt from2 aspergillus terreus a8-4 in complex with dimethylallyl s-3 thiolodiphosphate and genistein
32	c3fdgA_	Alignment	not modelled	32.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dipeptidase ac. metallo peptidase. merops family m19; **PDBTitle:** the crystal structure of the dipeptidase ac, metallo peptidase. merops2 family m19
33	d1vcla3	Alignment	not modelled	24.8	50	**Fold:**Hemolytic lectin CEL-III, C-terminal domain **Superfamily:**Hemolytic lectin CEL-III, C-terminal domain **Family:**Hemolytic lectin CEL-III, C-terminal domain
34	c3d0jA_	Alignment	not modelled	24.3	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ca_c3497; **PDBTitle:** crystal structure of conserved protein of unknown function ca_c34972 from clostridium acetobutylicum atcc 824
35	c4m1pA_	Alignment	not modelled	24.0	27	**PDB header:**transcription repressor **Chain:** A: **PDB Molecule:**copper-sensitive operon repressor (csor); **PDBTitle:** crystal structure of the copper-sensing repressor csor with cu(i) from2 geobacillus thermodenitrificans ng80-2
36	c2mkfA_	Alignment	not modelled	23.4	31	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**brca1-a complex subunit rap80; **PDBTitle:** solution structure of the e81 deletion mutant of the tandem uims of2 rap80
37	c4z80D_	Alignment	not modelled	21.7	63	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**cytoadherence-linked asexual protein; **PDBTitle:** crystal structure of toxoplasma gondii ama4 di-dii-egf1 in complex2 with a 33 aa tgron2l1 peptide
38	c3kgbA_	Alignment	not modelled	21.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase 1/2; **PDBTitle:** crystal structure of thymidylate synthase 1/2 from encephalitozoon2 cuniculi at 2.2 a resolution
39	c4z80C_	Alignment	not modelled	21.5	63	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**cytoadherence-linked asexual protein; **PDBTitle:** crystal structure of toxoplasma gondii ama4 di-dii-egf1 in complex2 with a 33 aa tgron2l1 peptide
40	c4ad2C_	Alignment	not modelled	20.7	14	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**glycosyl hydrolase family 71; **PDBTitle:** structure of the gh99 endo-alpha-mannosidase from bacteroides2 xylanisolvens in complex with glucose-1,3-isofagomine
41	c1cixA_	Alignment	not modelled	20.4	32	**PDB header:**antimicrobial peptide **Chain:** A: **PDB Molecule:**protein (tachystatin a); **PDBTitle:** three-dimensional structure of antimicrobial peptide2 tachystatin a isolated from horseshoe crab
42	d1cixa_	Alignment	not modelled	20.4	32	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**omega toxin-like **Family:**Spider toxins
43	c2ppxA_	Alignment	not modelled	19.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
44	d2ppxa1	Alignment	not modelled	19.9	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
45	c3ix6B_	Alignment	not modelled	19.7	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of thymidylate synthase thya from brucella2 melitensis
46	c5j9iH_	Alignment	not modelled	19.6	13	**PDB header:**antitoxin **Chain:** H: **PDB Molecule:**antitoxin iga-2; **PDBTitle:** crystal structure of the higa2 antitoxin c-terminal domain
47	c4c8qH_	Alignment	not modelled	19.6	19	**PDB header:**transcription **Chain:** H: **PDB Molecule:**dna topoisomerase 2-associated protein pat1; **PDBTitle:** crystal structure of the yeast lsm1-7-pat1 complex
48	d1w3ia_	Alignment	not modelled	19.4	42	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
49	c5jaaB_	Alignment	not modelled	19.2	13	**PDB header:**toxin **Chain:** B: **PDB Molecule:**antitoxin iga-2; **PDBTitle:** crystal structure of the higba2 toxin-antitoxin complex
50	d1f28a_	Alignment	not modelled	18.6	13	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
51	d1r69a_	Alignment	not modelled	18.4	36	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
52	d1bkpa_	Alignment	not modelled	18.1	20	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
53	c3fmyA_	Alignment	not modelled	18.1	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)

54	c4dq1A_	Alignment	not modelled	17.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate synthase; **PDBTitle:** thymidylate synthase from staphylococcus aureus.
55	d1qzfa2	Alignment	not modelled	17.9	17	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
56	c3v8hB_	Alignment	not modelled	17.6	7	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of thymidylate synthase from burkholderia2 thailandensis
57	c6e11F_	Alignment	not modelled	17.3	86	**PDB header:**protein transport **Chain:** F: **PDB Molecule:**exported protein 2; **PDBTitle:** ptex core complex in the resetting (compact) state
58	d1hvya_	Alignment	not modelled	17.2	17	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
59	d1uf2c2	Alignment	not modelled	16.9	44	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Top domain of virus capsid protein
60	d2auwa1	Alignment	not modelled	16.8	33	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE0471 C-terminal domain-like
61	d2croa_	Alignment	not modelled	16.8	29	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
62	c4iswB_	Alignment	not modelled	16.7	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of phosphorylated c.elegans thymidylate synthase in2 complex with dump
63	d1seja2	Alignment	not modelled	16.7	17	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
64	d2g8oa1	Alignment	not modelled	16.6	20	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
65	c5mmjw_	Alignment	not modelled	16.5	19	**PDB header:**ribosome **Chain:** W: **PDB Molecule:** **PDBTitle:** structure of the small subunit of the chloroplast ribosome
66	d1sq8a_	Alignment	not modelled	16.3	36	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
67	d2tsra_	Alignment	not modelled	16.3	13	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
68	c4g9uD_	Alignment	not modelled	16.3	13	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of trichinella spiralis thymidylate synthase2 complexed with dump
69	d1ug2a_	Alignment	not modelled	16.2	26	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
70	c2j0fC_	Alignment	not modelled	16.0	27	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidine phosphorylase; **PDBTitle:** structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
71	c6h4eB_	Alignment	not modelled	15.6	35	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative n-acetylneuraminate lyase; **PDBTitle:** proteus mirabilis n-acetylneuraminate lyase
72	c2aazG_	Alignment	not modelled	15.6	17	**PDB header:**transferase **Chain:** G: **PDB Molecule:**thymidylate synthase; **PDBTitle:** cryptococcus neoformans thymidylate synthase complexed with substrate2 and an antifolate
73	d2a6ca1	Alignment	not modelled	15.4	50	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**NE1354
74	d1utxa_	Alignment	not modelled	15.4	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
75	c6aujC_	Alignment	not modelled	15.3	20	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of thymidylate synthase from elizabethkingia2 anophelis nuhp1
76	c4pu4C_	Alignment	not modelled	15.1	39	**PDB header:**toxin/antitoxin/dna **Chain:** C: **PDB Molecule:**toxin-antitoxin system antidote transcriptional repressor **PDBTitle:** shewanella oneidensis mr-1 toxin antitoxin system hipa, hipb and its2 operator dna complex (space group p21)
77	d1tisa_	Alignment	not modelled	14.9	13	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
78	c1zx4B_	Alignment	not modelled	14.9	27	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**plasmid partition par b protein; **PDBTitle:** structure of parb bound to dna
79	c2ebkA_	Alignment	not modelled	14.5	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**rwd domain-containing protein 3; **PDBTitle:** solution structure of the rwd domain of human rwd domain2 containing protein 3
80	c3pqeD_	Alignment	not modelled	14.5	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**l-lactate dehydrogenase; **PDBTitle:** crystal structure of l-lactate dehydrogenase from bacillus subtilis2 with h171c mutation

81	c2kt9A_	Alignment	not modelled	14.3	11	**PDB header:**ribosomal protein **Chain:** A: **PDB Molecule:**probable 30s ribosomal protein psrp-3; **PDBTitle:** solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
82	d1tswa_	Alignment	not modelled	14.3	19	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
83	d1j3kc_	Alignment	not modelled	13.9	13	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
84	c2hpgB_	Alignment	not modelled	13.3	13	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**abc transporter, periplasmic substrate-binding **PDBTitle:** the crystal structure of a thermophilic trap periplasmic2 binding protein
85	d1xrsb2	Alignment	not modelled	13.2	67	**Fold:**Dodecin subunit-like **Superfamily:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain **Family:**D-lysine 5,6-aminomutase beta subunit KamE, N-terminal domain
86	d1ldma2	Alignment	not modelled	13.0	25	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
87	c3qj7D_	Alignment	not modelled	13.0	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of the mycobacterium tuberculosis thymidylate2 synthase (thya) bound to dump
88	c5c54D_	Alignment	not modelled	12.9	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase/n-acetylneuraminate lyase; **PDBTitle:** crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
89	d1pkxa2	Alignment	not modelled	12.9	39	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC
90	c4bpsA_	Alignment	not modelled	12.8	30	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**fkbo; **PDBTitle:** crystal structure of chorismatase at 1.08 angstrom resolution.
91	c3egyX_	Alignment	not modelled	12.7	24	**PDB header:**transferase **Chain:** X: **PDB Molecule:**thymidylate synthase; **PDBTitle:** crystal structure of human thymidyalte synthase a191k with loop 181-2 197 stabilized in the inactive conformation
92	c2jvlA_	Alignment	not modelled	12.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**trmbf1; **PDBTitle:** nmr structure of the c-terminal domain of mbf1 of trichoderma reesei
93	c3vx8C_	Alignment	not modelled	12.6	30	**PDB header:**ligase **Chain:** C: **PDB Molecule:**autophagy-related protein 3; **PDBTitle:** crystal structure of arabidopsis thaliana atg7ntd-atg3 complex
94	c2wb1Q_	Alignment	not modelled	12.2	67	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
95	d1b5ea_	Alignment	not modelled	12.0	20	**Fold:**Thymidylate synthase/dCMP hydroxymethylase **Superfamily:**Thymidylate synthase/dCMP hydroxymethylase **Family:**Thymidylate synthase/dCMP hydroxymethylase
96	c5z7iC_	Alignment	not modelled	12.0	41	**PDB header:**dna binding protein/dna **Chain:** C: **PDB Molecule:**cell cycle regulatory protein gcra; **PDBTitle:** caulobacter crescentus gcra dna-binding domain(dbd)in complex with2 unmethylated dsdna
97	c2vc6A_	Alignment	not modelled	11.8	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of mosa from s. meliloti with pyruvate bound
98	c3omtA_	Alignment	not modelled	11.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** putative antitoxin component, chu_2935 protein, from xre family from2 prevotella buccae.
99	d1z84a1	Alignment	not modelled	11.8	13	**Fold:**HIT-like **Superfamily:**HIT-like **Family:**Hexose-1-phosphate uridylyltransferase