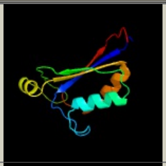
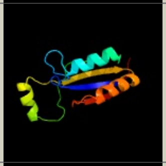
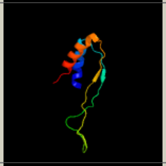
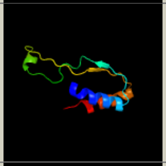
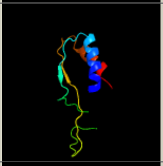
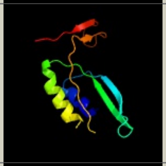
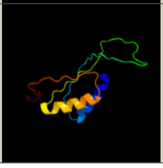
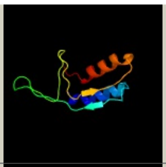
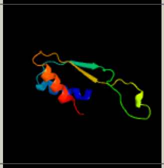
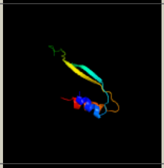
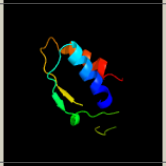
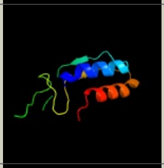
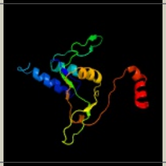
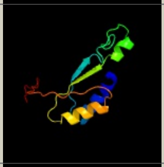
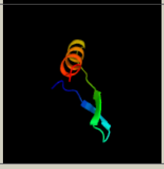
Email	mdejesus@rockefeller.edu
Description	RVBD3071_(-)_3434461_3435570
Date	Thu Aug 8 16:20:24 BST 2019
Unique Job ID	d5c40eb535b821c0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2dclB_	Alignment		100.0	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503; **PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3
2	d1o51a_	Alignment		100.0	25	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**DUF190/COG1993
3	c5d4pA_	Alignment		99.5	16	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein p-ii glnb; **PDBTitle:** structure of cpii bound to adp and bicarbonate, from thiomonas2 intermedia k12
4	d2cz4a1	Alignment		97.1	11	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
5	d2ns1b1	Alignment		94.3	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
6	c2rd5D_	Alignment		94.2	13	**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
7	d1vfja_	Alignment		94.2	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
8	d2piia_	Alignment		93.9	15	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
9	c3o8wA_	Alignment		93.1	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-1); **PDBTitle:** archaeoglobus fulgidus glnk1
10	d1ul3a_	Alignment		91.6	18	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
11	d1qy7a_	Alignment		91.1	12	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein

12	c2j9dG_	Alignment		89.6	10	**PDB header:**membrane transport **Chain:** G: **PDB Molecule:**hypothetical nitrogen regulatory pii-like **PDBTitle:** structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
13	c3mhyC_	Alignment		89.4	18	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**pii-like protein pz; **PDBTitle:** a new pii protein structure
14	c4r25A_	Alignment		87.9	9	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory pii-like protein; **PDBTitle:** structure of b. subtilis glnk
15	c3ncpD_	Alignment		86.9	11	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**nitrogen regulatory protein p-ii (glnb-2); **PDBTitle:** glnk2 from archaeoglobus fulgidus
16	d1hwua_	Alignment		85.7	19	**Fold:**Ferredoxin-like **Superfamily:**GlnB-like **Family:**Prokaryotic signal transducing protein
17	c4usiC_	Alignment		83.3	11	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**nitrogen regulatory protein pii; **PDBTitle:** nitrogen regulatory protein pii from chlamydomonas2 reinhardtii in complex with mgatp and 2-oxoglutarate
18	c1xtzA_	Alignment		81.8	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase; **PDBTitle:** crystal structure of the s. cerevisiae d-ribose-5-phosphate isomerase:2 comparison with the archeal and bacterial enzymes
19	c4ozlA_	Alignment		81.7	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** glnk2 from haloferax mediterranei complexed with amp
20	d2f1fa2	Alignment		79.2	11	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
21	d2fgca1	Alignment	not modelled	79.1	13	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
22	d2pc6a1	Alignment	not modelled	79.1	16	**Fold:**Ferredoxin-like **Superfamily:**ACT-like **Family:**IlvH-like
23	c3bzqA_	Alignment	not modelled	78.0	20	**PDB header:**signaling protein/transcription **Chain:** A: **PDB Molecule:**nitrogen regulatory protein p-ii; **PDBTitle:** high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
24	c2pc6C_	Alignment	not modelled	68.9	15	**PDB header:**lyase **Chain:** C: **PDB Molecule:**probable acetolactate synthase isozyme iii (small subunit); **PDBTitle:** crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
25	c2fgcA_	Alignment	not modelled	68.1	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase, small subunit; **PDBTitle:** crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
26	c2f1fA_	Alignment	not modelled	65.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetolactate synthase isozyme iii small subunit; **PDBTitle:** crystal structure of the regulatory subunit of acetohydroxyacid2 synthase isozyme iii from e. coli
27	c3l7pA_	Alignment	not modelled	46.1	11	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative nitrogen regulatory protein pii; **PDBTitle:** crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
28	d1jnda2	Alignment	not modelled	35.1	29	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain

29	c4lb6B_	Alignment	not modelled	34.4	67	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**protein kinase containing z-dna binding domains; **PDBTitle:** crystal structure of pkz zalpha in complex with ds(cg)6 (tetragonal2 form)
30	d1j3aa_	Alignment	not modelled	32.8	24	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
31	c1s1iM_	Alignment	not modelled	32.8	10	**PDB header:**ribosome **Chain:** M: **PDB Molecule:**60s ribosomal protein l16-a; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
32	c5xaqB_	Alignment	not modelled	32.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 2; **PDBTitle:** crystal structure of animalia-specific trna deacylase from mus2 musculus
33	c3okrC_	Alignment	not modelled	28.5	17	**PDB header:**transferase **Chain:** C: **PDB Molecule:**2-c-methyl-d-erythritol 4-phosphate cytidylyltransferase; **PDBTitle:** structure of mtb apo 2-c-methyl-d-erythritol 4-phosphate2 cytidyltransferase (ispd)
34	c2okvC_	Alignment	not modelled	28.1	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable d-tyrosyl-trna(tyr) deacylase 1; **PDBTitle:** c-myc dna unwinding element binding protein
35	c2zkrj_	Alignment	not modelled	26.5	17	**PDB header:**ribosomal protein/rna **Chain:** J: **PDB Molecule:**rna expansion segment es15 part ii; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
36	c3d5bN_	Alignment	not modelled	26.3	30	**PDB header:**ribosome **Chain:** N: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 50s subunit of one 70s ribosome. the entire crystal3 structure contains two 70s ribosomes as described in remark 400.
37	d1tc5a_	Alignment	not modelled	24.1	16	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
38	c5o60K_	Alignment	not modelled	23.9	30	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
39	c1vw4H_	Alignment	not modelled	23.5	14	**PDB header:**ribosome **Chain:** H: **PDB Molecule:**54s ribosomal protein l23, mitochondrial; **PDBTitle:** structure of the yeast mitochondrial large ribosomal subunit
40	d1hjxa2	Alignment	not modelled	23.1	34	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
41	d2j01n1	Alignment	not modelled	22.9	30	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
42	c3ko7E_	Alignment	not modelled	22.6	15	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** dtd from plasmodium falciparum in complex with d-lysine
43	d1n71a_	Alignment	not modelled	22.4	14	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
44	c4kmfA_	Alignment	not modelled	22.1	33	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**interferon-inducible and double-stranded-dependent eif- **PDBTitle:** crystal structure of zalpha domain from carassius auratus pkz in2 complex with z-dna
45	c4wfaG_	Alignment	not modelled	21.2	25	**PDB header:**ribosome **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** the crystal structure of the large ribosomal subunit of staphylococcus2 aureus in complex with linezolid
46	c5f9pA_	Alignment	not modelled	20.6	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**anthrone oxidase-like protein; **PDBTitle:** crystal structure study of anthrone oxidase-like protein
47	d2aj6a1	Alignment	not modelled	19.7	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
48	d1owqa2	Alignment	not modelled	19.6	31	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
49	c3jxeB_	Alignment	not modelled	19.4	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** crystal structure of pyrococcus horikoshii tryptophanyl-trna2 synthetase in complex with trpamp
50	d2pi6a2	Alignment	not modelled	19.1	31	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
51	c3t9yA_	Alignment	not modelled	18.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase, gnat family; **PDBTitle:** crystal structure of gnat family acetyltransferase staphylococcus2 aureus subsp. aureus usa300_tch1516
52	c2cdh1_	Alignment	not modelled	18.4	15	**PDB header:**transferase **Chain:** 1: **PDB Molecule:**enoyl reductase; **PDBTitle:** architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
						PDB header:transferase **Chain:** B: **PDB Molecule:**predicted s-adenosylmethionine-

53	c1wg8B_	Alignment	not modelled	18.4	20	dependent **PDBTitle:** crystal structure of a predicted s-adenosylmethionine-2 dependent methyltransferase tt1512 from thermus3 thermophilus hb8.
54	d1vf8a2	Alignment	not modelled	18.3	25	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
55	d1prtf_	Alignment	not modelled	18.1	29	**Fold:**OB-fold **Superfamily:**Bacterial enterotoxins **Family:**Bacterial AB5 toxins, B-subunits
56	d2zjrg1	Alignment	not modelled	17.9	33	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
57	c1xjqA_	Alignment	not modelled	17.6	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** adp complex of human paps synthetase 1
58	c2aj6A_	Alignment	not modelled	17.6	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein mw0638; **PDBTitle:** crystal structure of a putative gnat family acetyltransferase (mw0638)2 from staphylococcus aureus subsp. aureus at 1.63 a resolution
59	c5hmnE_	Alignment	not modelled	17.6	14	**PDB header:**transferase **Chain:** E: **PDB Molecule:**aac3-i; **PDBTitle:** crystal structure of an aminoglycoside acetyltransferase hmb0005 from2 an uncultured soil metagenomic sample, unknown active site density3 modeled as polyethylene glycol
60	c5i0cA_	Alignment	not modelled	17.4	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein yjdj; **PDBTitle:** crystal structure of predicted acyltransferase yjdj with acyl-coa n-2 acyltransferase domain from escherichia coli str. k-12
61	c3cf5G_	Alignment	not modelled	16.8	33	**PDB header:**ribosome/antibiotic **Chain:** G: **PDB Molecule:**50s ribosomal protein l13; **PDBTitle:** thiopeptide antibiotic thiostrepton bound to the large ribosomal2 subunit of deinococcus radiodurans
62	d1tfva2	Alignment	not modelled	16.8	48	**Fold:**FKBP-like **Superfamily:**Chitinase insertion domain **Family:**Chitinase insertion domain
63	c2l1iA_	Alignment	not modelled	16.6	20	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hltf protein; **PDBTitle:** nmr structure of the hltf hiran domain
64	c3nohA_	Alignment	not modelled	16.5	20	**PDB header:**peptide binding protein **Chain:** A: **PDB Molecule:**putative peptide binding protein; **PDBTitle:** crystal structure of a putative peptide binding protein (rumgna_00914)2 from ruminococcus gnavus atcc 29149 at 1.60 a resolution
65	c3e0kA_	Alignment	not modelled	16.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**amino-acid acetyltransferase; **PDBTitle:** crystal structure of c-termianl domain of n-acetylglutamate synthase2 from vibrio parahaemolyticus
66	c2dboA_	Alignment	not modelled	15.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**d-tyrosyl-trna(tyr) deacylase; **PDBTitle:** crystal structure of d-tyr-trna(tyr) deacylase from aquifex aeolicus
67	c3jvnA_	Alignment	not modelled	14.3	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** crystal structure of the acetyltransferase vf_1542 from vibrio2 fischeri, northeast structural genomics consortium target vfr136
68	d2gych1	Alignment	not modelled	14.1	30	**Fold:**Ribosomal protein L13 **Superfamily:**Ribosomal protein L13 **Family:**Ribosomal protein L13
69	c3bboL_	Alignment	not modelled	14.0	30	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**ribosomal protein l13; **PDBTitle:** homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome
70	c3ce8A_	Alignment	not modelled	13.3	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative pii-like nitrogen regulatory protein; **PDBTitle:** crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
71	c4bmhA_	Alignment	not modelled	12.4	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** crystal structure of sshat
72	c2reeB_	Alignment	not modelled	12.3	15	**PDB header:**transferase, lyase **Chain:** B: **PDB Molecule:**cura; **PDBTitle:** crystal structure of the loading gnatl domain of cura from lyngbya2 majuscula
73	c5mlcL_	Alignment	not modelled	12.2	30	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**50s ribosomal protein l13, chloroplastic; **PDBTitle:** cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions
74	c3zj0A_	Alignment	not modelled	12.1	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**acetyltransferase; **PDBTitle:** the human o-glcnacase c-terminal domain is a pseudo histone2 acetyltransferase
75	c4ag9B_	Alignment	not modelled	11.5	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glucosamine-6-phosphate n-acetyltransferase; **PDBTitle:** c. elegans glucosamine-6-phosphate n-acetyltransferase (gna1):2 ternary complex with coenzyme a and glcnac
76	d1jkea_	Alignment	not modelled	11.4	24	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
77	c3j3wJ	Alignment	not modelled	11.3	33	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**50s ribosomal protein l13;

		Alignment	not modelled			**PDBTitle:** atomic model of the immature 50s subunit from bacillus subtilis (state2 ii-a)
78	c3hv0A_	Alignment	not modelled	11.3	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase from cryptosporidium parvum
79	d1y7ra1	Alignment	not modelled	11.3	5	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
80	c3iz5K_	Alignment	not modelled	10.7	10	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein l13a (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
81	c3tkaA_	Alignment	not modelled	10.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ribosomal rna small subunit methyltransferase h; **PDBTitle:** crystal structure and solution saxs of methyltransferase rsmh from2 e.coli
82	d1o8bb1	Alignment	not modelled	10.4	19	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
83	c3izcK_	Alignment	not modelled	10.2	11	**PDB header:**ribosome **Chain:** K: **PDB Molecule:**60s ribosomal protein rpl16 (l13p); **PDBTitle:** localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
84	c3j39O_	Alignment	not modelled	10.0	14	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** structure of the d. melanogaster 60s ribosomal proteins
85	c1ypfB_	Alignment	not modelled	9.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**gmp reductase; **PDBTitle:** crystal structure of guac (ba5705) from bacillus anthracis at 1.8 a2 resolution
86	c1vs0A_	Alignment	not modelled	9.5	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the ligase domain from m. tuberculosis ligd at2 2.4a
87	c4fd4B_	Alignment	not modelled	9.1	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**arylalkylamine n-acetyltransferase like 5b; **PDBTitle:** crystal structure of mosquito arylalkylamine n-acetyltransferase like2 5b
88	d1r57a_	Alignment	not modelled	9.0	16	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
89	d1j7ga_	Alignment	not modelled	8.9	18	**Fold:**DTD-like **Superfamily:**DTD-like **Family:**DTD-like
90	c3fynA_	Alignment	not modelled	8.5	11	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**integron gene cassette protein hfx_cass3; **PDBTitle:** crystal structure from the mobile metagenome of cole harbour salt2 marsh: integron cassette protein hfx_cass3
91	d2h6la1	Alignment	not modelled	8.5	7	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**AF0104-like
92	c2v53C_	Alignment	not modelled	8.3	50	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**collagen alpha-1(iii) chain; **PDBTitle:** crystal structure of a sparc-collagen complex
93	c2v53D_	Alignment	not modelled	8.3	50	**PDB header:**cell adhesion **Chain:** D: **PDB Molecule:**collagen alpha-1(iii) chain; **PDBTitle:** crystal structure of a sparc-collagen complex
94	c2v53B_	Alignment	not modelled	8.3	50	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**collagen alpha-1(iii) chain; **PDBTitle:** crystal structure of a sparc-collagen complex
95	c3hzrD_	Alignment	not modelled	8.2	16	**PDB header:**ligase **Chain:** D: **PDB Molecule:**tryptophanyl-trna synthetase; **PDBTitle:** tryptophanyl-trna synthetase homolog from entamoeba histolytica
96	c3sr7C_	Alignment	not modelled	8.2	23	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**isopentenyl-diphosphate delta-isomerase; **PDBTitle:** crystal structure of s. mutans isopentenyl pyrophosphate isomerase
97	c3j3bO_	Alignment	not modelled	8.1	17	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**60s ribosomal protein l13a; **PDBTitle:** structure of the human 60s ribosomal proteins
98	d2fiwa1	Alignment	not modelled	8.0	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
99	c3htnA_	Alignment	not modelled	7.9	7	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative dna binding protein; **PDBTitle:** crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution