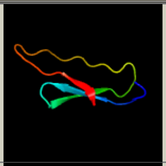
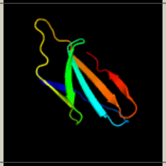
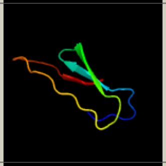
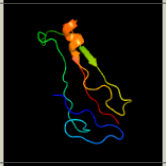
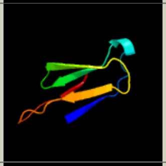
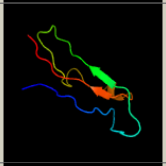
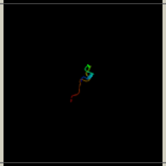
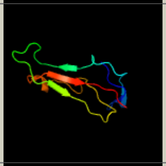
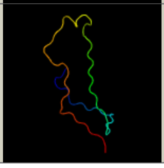
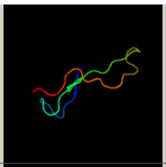
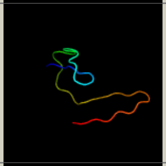
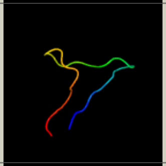
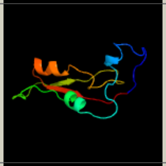
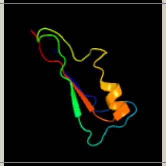
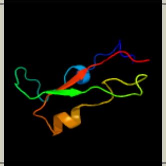
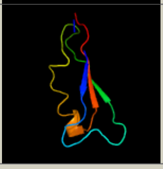
Email	mdejesus@rockefeller.edu
Description	RVBD2330c_(lppP)_2603705_2604232
Date	Mon Aug 5 13:25:48 BST 2019
Unique Job ID	3de962f479b9cddf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pe9D_	Alignment		76.7	18	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
2	c3pdgA_	Alignment		68.4	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
3	c3pe9B_	Alignment		67.3	21	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
4	d1ukca_	Alignment		44.0	13	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
5	c5a2gB_	Alignment		43.1	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**carboxylic ester hydrolase; **PDBTitle:** an esterase from anaerobic clostridium hathewayi can2 hydrolyze aliphatic aromatic polyesters
6	c3pe9C_	Alignment		38.0	18	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
7	c3pe9A_	Alignment		38.0	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**fibronectin(iii)-like module; **PDBTitle:** structures of clostridium thermocellum cbha fibronectin(iii)-like2 modules
8	c5w1uA_	Alignment		36.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylic ester hydrolase; **PDBTitle:** culex quinquefasciatus carboxylesterase b2
9	c6chgB_	Alignment		36.5	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**klla0c10945p; **PDBTitle:** crystal structure of the yeast compass catalytic module
10	c4fg5B_	Alignment		35.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**e3 alpha-esterase-7 caboxylesterase; **PDBTitle:** crystal structure of the alpha-esterase-7 carboxylesterase, e3, from2 lucilia cuprina
11	c4hg6B_	Alignment		32.3	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**cellulose synthase subunit b; **PDBTitle:** structure of a cellulose synthase - cellulose translocation2 intermediate

12	d1v0ea1	Alignment		32.1	18	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Endo-alpha-sialidase
13	c4xw3B_	Alignment		30.5	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx1; **PDBTitle:** crystal structure of the spry domain of the human dead-box protein2 ddx1
14	c6i2tC_	Alignment		29.9	10	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**cholinesterase; **PDBTitle:** cryoem reconstruction of full-length, fully-glycosylated human2 butyrylcholinesterase tetramer
15	c2pm8A_	Alignment		29.7	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cholinesterase; **PDBTitle:** crystal structure of recombinant full length human2 butyrylcholinesterase
16	c4p9lA_	Alignment		26.0	8	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ryanodine receptor 2; **PDBTitle:** crystal structure of mouse ryanodine receptor 2 spry2 domain (1080-2 1253) disease mutant a1107m
17	c4bdtA_	Alignment		25.1	17	**PDB header:**hydrolase/inhibitor **Chain:** A: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** human acetylcholinesterase in complex with huprine w and fasciculin 2
18	d1p0ia_	Alignment		24.9	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
19	d1llfa_	Alignment		23.3	6	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
20	d2ha2a1	Alignment		22.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
21	d1qe3a_	Alignment	not modelled	22.2	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
22	d1f8ua_	Alignment	not modelled	21.0	19	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
23	c1f8uA_	Alignment	not modelled	21.0	19	**PDB header:**hydrolase/toxin **Chain:** A: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** crystal structure of mutant e202q of human acetylcholinesterase2 complexed with green mamba venom peptide fasciculin-ii
24	d2fnja1	Alignment	not modelled	19.0	19	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
25	d1dx4a_	Alignment	not modelled	18.8	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
26	c3r87A_	Alignment	not modelled	17.2	8	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of orf6 protein from photobacterium profundum
27	d1ggbh1	Alignment	not modelled	16.6	11	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
28	d2bcea_	Alignment	not modelled	16.4	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
						Fold: Immunoglobulin-like beta-sandwich

29	d2ij0c1	Alignment	not modelled	16.4	14	**Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
30	c5f21B_	Alignment	not modelled	16.3	11	**PDB header:**hydrolase/immune system **Chain:** B: **PDB Molecule:**nanobody mu375; **PDBTitle:** human cd38 in complex with nanobody mu375
31	c2ogsA_	Alignment	not modelled	16.2	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable carboxylesterase est50; **PDBTitle:** crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
32	d1pj5a1	Alignment	not modelled	16.0	11	**Fold:**Elongation factor/aminomethyltransferase common domain **Superfamily:**Aminomethyltransferase beta-barrel domain **Family:**Aminomethyltransferase beta-barrel domain
33	d2afja1	Alignment	not modelled	15.8	13	**Fold:**Concanavalin A-like lectins/glucanases **Superfamily:**Concanavalin A-like lectins/glucanases **Family:**SPRY domain
34	c2yyoA_	Alignment	not modelled	15.8	27	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**spry domain-containing protein 3; **PDBTitle:** crystal sturcture of human spry domain
35	c5dleD_	Alignment	not modelled	15.0	33	**PDB header:**transferase **Chain:** D: **PDB Molecule:**pts system, fructose-specific iiabc component; **PDBTitle:** crystal structure from a domain (thr161-f265) from fructose-specific2 iiabc component (pts system) from borrelia burgdorferi
36	c6bx3K_	Alignment	not modelled	15.0	28	**PDB header:**gene regulation/transferase **Chain:** K: **PDB Molecule:**compass component bre2; **PDBTitle:** structure of histone h3k4 methyltransferase
37	d1ymme1	Alignment	not modelled	14.9	12	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
38	c6e2hD_	Alignment	not modelled	14.5	14	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**set1/ash2 histone methyltransferase complex subunit ash2; **PDBTitle:** crystal structure of human ash2l (spry domain and sdi motif) in2 complex with full length dpy-30
39	c2m1zA_	Alignment	not modelled	14.1	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lmo0427 protein; **PDBTitle:** solution structure of uncharacterized protein lmo0427
40	d2hfda1	Alignment	not modelled	13.7	25	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
41	d1thga_	Alignment	not modelled	13.6	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
42	c5e24D_	Alignment	not modelled	13.2	25	**PDB header:**transport/dna binding/dna **Chain:** D: **PDB Molecule:**protein hairless; **PDBTitle:** structure of the su(h)-hairless-dna repressor complex
43	c5gsfA_	Alignment	not modelled	12.9	44	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**roseltide rt1; **PDBTitle:** structure of roseltide rt1
44	d1mieh1	Alignment	not modelled	12.5	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
45	c5zt3A_	Alignment	not modelled	12.5	21	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**wa352; **PDBTitle:** crystal structure of wa352 from oryza sativa
46	c2qsiB_	Alignment	not modelled	12.1	25	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
47	c5sxyA_	Alignment	not modelled	12.0	19	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**bifunctional coenzyme pqq synthesis protein c/d; **PDBTitle:** the solution nmr structure for the pqqd truncation of methylobacterium2 extorquens pqqcd representing a functional and stand-alone3 ribosomally synthesized and post-translational modified (ripp)4 recognition element (rre)
48	c3g2bA_	Alignment	not modelled	12.0	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**coenzyme pqq synthesis protein d; **PDBTitle:** crystal structure of pqqd from xanthomonas campestris
49	d1crla_	Alignment	not modelled	11.9	8	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
50	d1k4ya_	Alignment	not modelled	11.8	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
51	d1lr0a_	Alignment	not modelled	11.7	19	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TolA
52	c2kyrA_	Alignment	not modelled	11.4	33	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
53	c1v0eB_	Alignment	not modelled	11.1	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**endo-alpha-sialidase; **PDBTitle:** endosialidase of bacteriophage k1f

54	c4mqtB_	Alignment	not modelled	10.8	14	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**nanobody 9-8; **PDBTitle:** structure of active human m2 muscarinic acetylcholine receptor bound2 to the agonist iperoxo and allosteric modulator ly2119620
55	d1gpla1	Alignment	not modelled	10.4	16	**Fold:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Superfamily:**Lipase/lipooxygenase domain (PLAT/LH2 domain) **Family:**Colipase-binding domain
56	c2a7yA_	Alignment	not modelled	10.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein rv2302/mt2359; **PDBTitle:** solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
57	d2a7ya1	Alignment	not modelled	10.2	15	**Fold:**SH3-like barrel **Superfamily:**Cell growth inhibitor/plasmid maintenance toxic component **Family:**Rv2302-like
58	d1f6wa_	Alignment	not modelled	10.1	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
59	c4p9jC_	Alignment	not modelled	9.7	12	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**ryanodine receptor 1; **PDBTitle:** crystal structure of rabbit ryanodine receptor 1 spry2 domain (1070-2 1246)
60	c4crrA_	Alignment	not modelled	9.6	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-1,3-beta-glucanase, family gh16; **PDBTitle:** crystal structure of the c-terminal cbm6 of lamc a marine2 laminarianse from zobellia galactanivorans
61	c2grxC_	Alignment	not modelled	9.3	29	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**protein tonb; **PDBTitle:** crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
62	d1ea5a_	Alignment	not modelled	9.2	15	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
63	d1yrza2	Alignment	not modelled	9.0	11	**Fold:**5-bladed beta-propeller **Superfamily:**Arabinanase/levansucrase/invertase **Family:**alpha-L-arabinanase-like
64	c2w6cX_	Alignment	not modelled	8.8	15	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**acetylcholinesterase; **PDBTitle:** ache in complex with a bis-(-)-nor-meptazinol derivative
65	c5zc2B_	Alignment	not modelled	8.8	15	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**p-hydroxyphenylacetate 3-hydroxylase, reductase component; **PDBTitle:** acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
66	c4qt6A_	Alignment	not modelled	8.7	7	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**probable e3 ubiquitin-protein ligase herc1; **PDBTitle:** crystal structure of the spry domain of human herc1
67	c2m2kA_	Alignment	not modelled	8.5	35	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hasb protein; **PDBTitle:** the structure of hasb ctd
68	d2gskb1	Alignment	not modelled	8.4	29	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
69	d1gz7a_	Alignment	not modelled	8.3	11	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
70	c4fbrA_	Alignment	not modelled	8.1	25	**PDB header:**carbohydrate binding protein **Chain:** A: **PDB Molecule:**myxobacterial hemagglutinin; **PDBTitle:** crystal structure of the myxococcus xanthus hemagglutinin (mbha)
71	d2fnjb1	Alignment	not modelled	8.1	18	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ubiquitin-related
72	c5jiaH_	Alignment	not modelled	7.8	13	**PDB header:**ran-binding protein **Chain:** H: **PDB Molecule:**ran-binding protein 10; **PDBTitle:** the crystal structure of ius-spry domain from ranbp10
73	d1pjwa_	Alignment	not modelled	7.4	18	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**E set domains **Family:**Class II viral fusion proteins C-terminal domain
74	c6a4mA_	Alignment	not modelled	7.4	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uric acid degradation bifunctional protein pucl; **PDBTitle:** structure of urate oxidase from bacillus subtilis 168
75	d2h7ca1	Alignment	not modelled	7.2	18	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Acetylcholinesterase-like
76	c5b42A_	Alignment	not modelled	6.9	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna mismatch repair protein mutl; **PDBTitle:** crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
77	d1inva_	Alignment	not modelled	6.8	17	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
78	d1j2ga2	Alignment	not modelled	6.7	25	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
79	d2ibaa2	Alignment	not modelled	6.6	33	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**Urate oxidase (uricase)
						PDB header:hydrolase

80	c4mj3B_	Alignment	not modelled	6.5	17	**Chain:** B: **PDB Molecule:**haloalkane dehalogenase; **PDBTitle:** haloalkane dehalogenase dmra from mycobacterium rhodesiae js60
81	c4hizA_	Alignment	not modelled	6.2	19	**PDB header:**hydrolase,viral protein **Chain:** A: **PDB Molecule:**endosialidase; **PDBTitle:** phage phi92 endosialidase
82	d1xoya_	Alignment	not modelled	6.2	17	**Fold:**Galactose-binding domain-like **Superfamily:**Galactose-binding domain-like **Family:**Hypothetical protein AT3g04780/F7O18 27
83	c5c33B_	Alignment	not modelled	6.1	14	**PDB header:**contractile protein **Chain:** B: **PDB Molecule:**ryanodine receptor 2; **PDBTitle:** crystal structure of mouse ryanodine receptor 2 spry1 domain
84	c6qe7A_	Alignment	not modelled	6.1	11	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**anti-sigma factor domain-containing protein; **PDBTitle:** anti-sigma factor domain-containing protein
85	c4eigB_	Alignment	not modelled	5.9	8	**PDB header:**oxidoreductase/immune system **Chain:** B: **PDB Molecule:**ca1698 camel antibody fragment; **PDBTitle:** ca1698 camel antibody fragment in complex with dhfr
86	d2esve1	Alignment	not modelled	5.8	15	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
87	c3ktbD_	Alignment	not modelled	5.8	71	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**arsenical resistance operon trans-acting repressor; **PDBTitle:** crystal structure of arsenical resistance operon trans-acting2 repressor from bacteroides vulgatus atcc 8482
88	d1igih1	Alignment	not modelled	5.7	7	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
89	d43c9b_	Alignment	not modelled	5.6	13	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**Immunoglobulin **Family:**V set domains (antibody variable domain-like)
90	c3tojA_	Alignment	not modelled	5.6	14	**PDB header:**transcription **Chain:** A: **PDB Molecule:**set1/ash2 histone methyltransferase complex subunit ash2; **PDBTitle:** structure of the spry domain of human ash2l
91	c2ys2A_	Alignment	not modelled	5.6	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytoplasmic tyrosine-protein kinase bmx; **PDBTitle:** solution structure of the btk motif of human cytoplasmic2 tyrosine-protein kinase bmx
92	d1bcoa1	Alignment	not modelled	5.6	4	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
93	d1u07a_	Alignment	not modelled	5.4	29	**Fold:**TolA/TonB C-terminal domain **Superfamily:**TolA/TonB C-terminal domain **Family:**TonB
94	c3npfB_	Alignment	not modelled	5.4	43	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative dipeptidyl-peptidase vi; **PDBTitle:** crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
95	c5lw8A_	Alignment	not modelled	5.3	35	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**protein tonb; **PDBTitle:** nmr solution structure of helicobacter pylori tonb-ctd (residues 194-2 285)
96	c2kaoA_	Alignment	not modelled	5.3	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase b1; **PDBTitle:** structure of reduced mouse methionine sulfoxide reductase b12 (sec95cys mutant)
97	c2xivA_	Alignment	not modelled	5.2	29	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**hypothetical invasion protein; **PDBTitle:** structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
98	d1w7ab4	Alignment	not modelled	5.1	33	**Fold:**MutS N-terminal domain-like **Superfamily:**DNA repair protein MutS, domain I **Family:**DNA repair protein MutS, domain I
99	c4ffyH_	Alignment	not modelled	5.1	10	**PDB header:**immune system/viral protein **Chain:** H: **PDB Molecule:**denv1-e111 single chain variable fragment (heavy chain); **PDBTitle:** crystal structure of denv1-e111 single chain variable fragment bound2 to denv-1 diii, strain 16007.