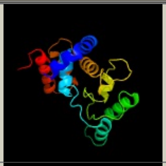
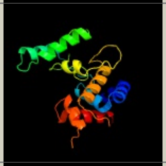
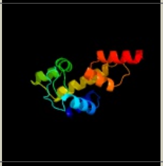
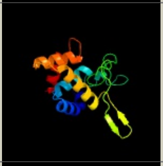
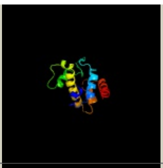
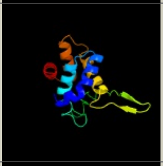
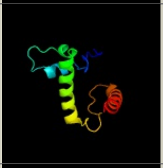
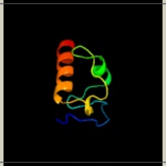
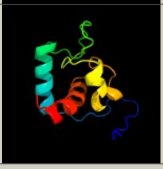
Email	mdejesus@rockefeller.edu
Description	RVBD1022_(lpqU)_1143740_1144471
Date	Wed Jul 31 22:05:09 BST 2019
Unique Job ID	ad3d055db708aeb2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5anzA_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**soluble lytic transglycosylase b3; **PDBTitle:** crystal structure of sltb3 from pseudomonas aeruginosa.
2	d1qusa_	Alignment		100.0	25	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
3	c4anrA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble lytic transglycosylase b; **PDBTitle:** crystal structure of soluble lytic transglycosylase sltb12 from pseudomonas aeruginosa
4	c4oz9A_	Alignment		99.6	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**membrane-bound lytic murein transglycosylase f; **PDBTitle:** crystal structure of mltf from pseudomonas aeruginosa complexed with2 isoleucine
5	c3w6dB_	Alignment		99.6	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lysozyme-like chitinolytic enzyme; **PDBTitle:** crystal structure of catalytic domain of chitinase from ralstonia sp.2 a-471 (e141q) in complex with tetrasaccharide
6	d1qsaa2	Alignment		99.5	22	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**Bacterial muramidase, catalytic domain
7	c4cfoB_	Alignment		99.5	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**mltc; **PDBTitle:** structure of lytic transglycosylase mltc from escherichia2 coli in complex with tetrasaccharide at 2.9 a resolution.
8	c2y8pA_	Alignment		99.5	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**endo-type membrane-bound lytic murein transglycosylase a; **PDBTitle:** crystal structure of an outer membrane-anchored endolytic2 peptidoglycan lytic transglycosylase (mlte) from3 escherichia coli
9	d1gbsa_	Alignment		99.5	30	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**G-type lysozyme
10	c3gxkB_	Alignment		99.4	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**goose-type lysozyme 1; **PDBTitle:** the crystal structure of g-type lysozyme from atlantic cod (gadus2 morhua l.) in complex with nag oligomers sheds new light on substrate3 binding and the catalytic mechanism. native structure to 1.9
11	c6fcqA_	Alignment		99.4	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**soluble lytic murein transglycosylase; **PDBTitle:** the x-ray structure of lytic transglycosylase slt inactive mutant2 e503q from pseudomonas aeruginosa in complex with bulgecin a

12	c1slyA_	Alignment		99.3	19	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**70-kda soluble lytic transglycosylase; **PDBTitle:** complex of the 70-kda soluble lytic transglycosylase with2 bulgecin a
13	c3mgwA_	Alignment		99.3	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme g; **PDBTitle:** thermodynamics and structure of a salmon cold-active goose-type2 lysozyme
14	c6cfcA_	Alignment		99.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of soluble lytic transglycosylase cj0843 of2 campylobacter jejuni in complex with bulgecin a
15	c4xp8A_	Alignment		97.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**etga protein; **PDBTitle:** structure of etga d60n mutant
16	c4fdyA_	Alignment		97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**similar to lipoprotein, nlp/p60 family; **PDBTitle:** crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
17	c4hpeA_	Alignment		97.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell wall hydrolase tn916-like,ctn1-orf17; **PDBTitle:** crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution
18	c3bkhA_	Alignment		94.9	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
19	c4ow1A_	Alignment		93.7	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfc; **PDBTitle:** crystal structure of resuscitation promoting factor c
20	c1xsfA_	Alignment		90.8	17	**PDB header:**cell cycle, hydrolase **Chain:** A: **PDB Molecule:**probable resuscitation-promoting factor rpfb; **PDBTitle:** solution structure of a resuscitation promoting factor2 domain from mycobacterium tuberculosis
21	d1xsfa1	Alignment	not modelled	90.7	20	**Fold:**Lysozyme-like **Superfamily:**Lysozyme-like **Family:**RPF-like
22	c5e27B_	Alignment	not modelled	89.5	19	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** the structure of resuscitation promoting factor b from m. tuberculosis2 reveals unexpected ubiquitin-like domains
23	c4qdnA_	Alignment	not modelled	86.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellar protein flgj [peptidoglycan hydrolase]; **PDBTitle:** crystal structure of the endo-beta-n-acetylglucosaminidase from2 thermotoga maritima
24	c3eo5A_	Alignment	not modelled	86.1	18	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**resuscitation-promoting factor rpfb; **PDBTitle:** crystal structure of the resuscitation promoting factor rpfb
25	c2zycA_	Alignment	not modelled	61.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** crystal structure of peptidoglycan hydrolase from2 sphingomonas sp. a1
26	c3fi7A_	Alignment	not modelled	59.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lmo1076 protein; **PDBTitle:** crystal structure of the autolysin auto (lmo1076) from listeria2 monocytogenes, catalytic domain
27	c1zy7A_	Alignment	not modelled	37.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna-specific adenosine deaminase b1, isoform **PDBTitle:** crystal structure of the catalytic domain of an adenosine2 deaminase that acts on rna (hadar2) bound to inositol3 hexakisphosphate (ihp)
						PDB header:dna binding protein

28	c2kngA_	Alignment	not modelled	30.0	25	**Chain:** A: **PDB Molecule:**protein lsr2; **PDBTitle:** solution structure of c-domain of lsr2
29	c5nm7A_	Alignment	not modelled	26.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan-binding domain 1; **PDBTitle:** crystal structure of burkholderia ap3 phage endolysin
30	d1twla_	Alignment	not modelled	26.5	29	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
31	c5dn4A_	Alignment	not modelled	26.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan hydrolase flgj; **PDBTitle:** structure of the glycoside hydrolase domain from salmonella2 typhimurium flgj
32	c5odvB_	Alignment	not modelled	22.9	11	**PDB header:**virus **Chain:** B: **PDB Molecule:**coat protein; **PDBTitle:** structure of watermelon mosaic virus potyvirus.
33	c5wrtB_	Alignment	not modelled	22.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**soluble inorganic pyrophosphatase; **PDBTitle:** crystal structure of type i inorganic pyrophosphatase from toxoplasma2 gondii.
34	c3p0dD_	Alignment	not modelled	20.9	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**glycoside hydrolase family 9; **PDBTitle:** crystal structure of a multimodular ternary protein complex from2 clostridium thermocellum
35	c5m2oB_	Alignment	not modelled	19.5	31	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**group i dockerin; **PDBTitle:** r. flavefaciens' third scab cohesin in complex with a group 1 dockerin
36	c5c5vB_	Alignment	not modelled	17.1	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**acidocalcisomal pyrophosphatase; **PDBTitle:** recombinant inorganic pyrophosphatase from t brucei brucei
37	c4mfkA_	Alignment	not modelled	15.9	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein tcp24; **PDBTitle:** the crystal structure of acyltransferase in complex with decanoyl-coa
38	c4uyqB_	Alignment	not modelled	15.2	7	**PDB header:**cell adhesion/protein binding **Chain:** B: **PDB Molecule:**cellulosomal scaffoldin adaptor protein b; **PDBTitle:** high resolution structure of the third cohesin scac in complex with2 the scab dockerin with a mutation in the c-terminal helix (in to si)3 from acetivibrio cellulolyticus displaying a type i interaction.
39	c2auwB_	Alignment	not modelled	14.2	27	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hypothetical protein ne0471; **PDBTitle:** crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
40	c5wruA_	Alignment	not modelled	14.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable inorganic pyrophosphatase; **PDBTitle:** crystal structure of type i inorganic pyrophosphatase from p2 falciparum
41	c2ediA_	Alignment	not modelled	12.7	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**nedd8-conjugating enzyme ube2f; **PDBTitle:** solution structure of the uq_con domain from human nedd8-2 conjugating enzyme nce2
42	c3d63B_	Alignment	not modelled	12.6	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei
43	c3jzaB_	Alignment	not modelled	12.5	71	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**uncharacterized protein drra; **PDBTitle:** crystal structure of human rab1b in complex with the gef domain of2 drra/sidm from legionella pneumophila
44	c3t9aA_	Alignment	not modelled	12.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**inositol pyrophosphate kinase; **PDBTitle:** crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
45	c1ygzC_	Alignment	not modelled	12.2	36	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from helicobacter2 pylori
46	c6c45A_	Alignment	not modelled	12.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of human inorganic pyrophosphatase in the p2121212 space group
47	c3iynM_	Alignment	not modelled	12.0	23	**PDB header:**virus **Chain:** M: **PDB Molecule:**penton base protein; **PDBTitle:** 3.6-angstrom cryoem structure of human adenovirus type 5
48	c3ld3A_	Alignment	not modelled	11.6	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution
49	d1bt3a_	Alignment	not modelled	11.4	14	**Fold:**Di-copper centre-containing domain **Superfamily:**Di-copper centre-containing domain **Family:**Catechol oxidase
50	c4qlzA_	Alignment	not modelled	10.2	25	**PDB header:**hydrolase, metal binding protein **Chain:** A: **PDB Molecule:**sjchgc07024 protein; **PDBTitle:** the structure of inorganic pyrophosphatase from schistosoma japonicum
51	c5yanB_	Alignment	not modelled	9.8	44	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**collagen; **PDBTitle:** deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
52	d1fuia1	Alignment	not modelled	9.4	17	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**FucI/AraA C-terminal domain-like **Family:**L-fucose isomerase, C-terminal domain
53	d1i40a_	Alignment	not modelled	9.2	36	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase

54	c3emjL_	Alignment	not modelled	9.1	36	**PDB header:**hydrolase **Chain:** L: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form)
55	c5nrmB_	Alignment	not modelled	8.9	17	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**doccel5: type i dockerin repeat domain from a. **PDBTitle:** crystal structure of the sixth cohesin from acetivibrio2 cellulolyticus' scaffoldin b in complex with cel5 dockerin s51i, l52n3 mutant
56	c4lugA_	Alignment	not modelled	8.3	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase ppa1 from arabidopsis2 thaliana
57	c3n6oB_	Alignment	not modelled	8.2	71	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**guanine nucleotide exchange factor; **PDBTitle:** crystal structure of the gef and p4m domain of drra/sidm from2 legionella pneumophila
58	c3lo0A_	Alignment	not modelled	8.2	45	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
59	c2zuxA_	Alignment	not modelled	8.2	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**yesw protein; **PDBTitle:** crystal structure of rhamnogalacturonan lyase yesw2 complexed with rhamnose
60	d1qeza_	Alignment	not modelled	8.2	36	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
61	c3mx7A_	Alignment	not modelled	8.0	29	**PDB header:**apoptosis **Chain:** A: **PDB Molecule:**fas apoptotic inhibitory molecule 1; **PDBTitle:** crystal structure analysis of human faim-ntd
62	c5teaF_	Alignment	not modelled	8.0	36	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of an inorganic pyrophosphatase from neisseria2 gonorrhoeae
63	c3tr4C_	Alignment	not modelled	7.9	27	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** structure of an inorganic pyrophosphatase (ppa) from coxiella burnetii
64	d1e9ga_	Alignment	not modelled	7.9	25	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
65	d1gk8a1	Alignment	not modelled	7.9	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
66	c3k8kB_	Alignment	not modelled	7.8	22	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**alpha-amylase, susg; **PDBTitle:** crystal structure of susg
67	d1wdda1	Alignment	not modelled	7.8	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
68	c3fq3H_	Alignment	not modelled	7.8	27	**PDB header:**hydrolase **Chain:** H: **PDB Molecule:**inorganic pyrophosphatase:bacterial/archaeal inorganic **PDBTitle:** crystal structure of inorganic phosphatase from brucella melitensis
69	c6n1cB_	Alignment	not modelled	7.6	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** crystal structure of inorganic pyrophosphatase from legionella2 pneumophila philadelphia 1
70	c1rldB_	Alignment	not modelled	7.3	9	**PDB header:**lyase(carbon-carbon) **Chain:** B: **PDB Molecule:**ribulose 1,5 bisphosphate carboxylase/oxygenase (large **PDBTitle:** solid-state phase transition in the crystal structure of ribulose 1,5-2 biphosphate carboxylase(slash)oxygenase
71	d2prda_	Alignment	not modelled	7.3	36	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
72	c3ul4B_	Alignment	not modelled	7.1	17	**PDB header:**cell adhesion/protein binding **Chain:** B: **PDB Molecule:**cellulosome enzyme, dockerin type i; **PDBTitle:** crystal structure of coh-olpa(cthe_3080)-doc918(cthe_0918) complex: a2 novel type i cohesin-dockerin complex from clostridium thermocellum3 attc 27405
73	d1dvoa_	Alignment	not modelled	7.0	23	**Fold:**FinO-like **Superfamily:**FinO-like **Family:**FinO-like
74	c4z12A_	Alignment	not modelled	6.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**aurone synthase; **PDBTitle:** recombinantly expressed latent aurone synthase (polyphenol oxidase)2 co-crystallized with hexatungstotellurate(vi)
75	d2cp5a1	Alignment	not modelled	6.8	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
76	c4dh2B_	Alignment	not modelled	6.5	7	**PDB header:**cell adhesion/protein binding **Chain:** B: **PDB Molecule:**dockerin type 1; **PDBTitle:** crystal structure of coh-olpc(cthe_0452)-doc435(cthe_0435) complex: a2 novel type i cohesin-dockerin complex from clostridium thermocellum3 attc 27405
77	c2n9zA_	Alignment	not modelled	6.1	67	**PDB header:**toxin **Chain:** A: **PDB Molecule:**tau-theraphotoxin-hs1a; **PDBTitle:** solution structure of k1 lobe of double-knot toxin
78	d1ohzb_	Alignment	not modelled	6.0	9	**Fold:**Type I dockerin domain **Superfamily:**Type I dockerin domain **Family:**Type I dockerin domain

79	c2l23A_	Alignment	not modelled	6.0	43	**PDB header:**transcription **Chain:** A: **PDB Molecule:**mediator of rna polymerase ii transcription subunit 25; **PDBTitle:** nmr structure of the acid (activator interacting domain) of the human2 mediator med25 protein
80	c2uxsA_	Alignment	not modelled	6.0	36	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**inorganic pyrophosphatase; **PDBTitle:** 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
81	c3lq9B_	Alignment	not modelled	6.0	16	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**dna-damage-inducible transcript 4 protein; **PDBTitle:** crystal structure of human redd1, a hypoxia-induced regulator of mtor
82	c3ca8B_	Alignment	not modelled	5.9	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein ydcf; **PDBTitle:** crystal structure of escherichia coli ydcf, an s-adenosyl-l-methionine2 utilizing enzyme
83	d1ej7l1	Alignment	not modelled	5.9	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**RuBisCo, C-terminal domain **Family:**RuBisCo, large subunit, C-terminal domain
84	d1udea_	Alignment	not modelled	5.9	36	**Fold:**OB-fold **Superfamily:**Inorganic pyrophosphatase **Family:**Inorganic pyrophosphatase
85	d2cp6a1	Alignment	not modelled	5.6	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
86	c2lyiA_	Alignment	not modelled	5.5	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**protein (entity); **PDBTitle:** repetitive domain (rp) of aciniform spidroin 1 from nephila2 antipodiana
87	c5lxvB_	Alignment	not modelled	5.5	23	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**carbohydrate-binding protein wp_009985128; **PDBTitle:** crystal structure of ruminococcus flavefaciens scaffoldin c cohesin in2 complex with a dockerin from an uncharacterized cbm-containing3 protein
88	c5jxpA_	Alignment	not modelled	5.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**asp/glu-specific dipeptidyl-peptidase; **PDBTitle:** crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
89	c2y3nB_	Alignment	not modelled	5.4	23	**PDB header:**structrual protein/hydrolase **Chain:** B: **PDB Molecule:**cellulosomal family-48 processive glycoside hydrolase; **PDBTitle:** type ii cohesin-dockerin domain from bacteroides cellolosolvens
90	d1twfa_	Alignment	not modelled	5.3	13	**Fold:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Superfamily:**beta and beta-prime subunits of DNA dependent RNA-polymerase **Family:**RNA-polymerase beta-prime
91	d2coya1	Alignment	not modelled	5.3	26	**Fold:**SH3-like barrel **Superfamily:**Cap-Gly domain **Family:**Cap-Gly domain
92	d1jata_	Alignment	not modelled	5.3	20	**Fold:**UBC-like **Superfamily:**UBC-like **Family:**UBC-related
93	c4piaA_	Alignment	not modelled	5.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**autolysin e; **PDBTitle:** crystal structure of s. aureus autolysin e
94	d1ou8a_	Alignment	not modelled	5.2	15	**Fold:**SspB-like **Superfamily:**SspB-like **Family:**Stringent starvation protein B, SspB