





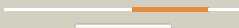










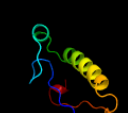







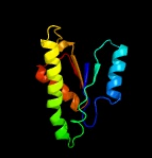
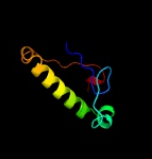
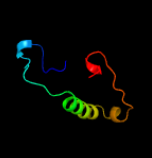





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1069c_(-)_1192515_1194278
Date	Wed Jul 31 22:05:14 BST 2019
Unique Job ID	aef10f1185c4b804

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1cexa_	 Alignment		93.2	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
2	c3gbsA_	 Alignment		91.1	18	PDB header: hydrolase Chain: A: PDB Molecule: cutinase 1; PDBTitle: crystal structure of aspergillus oryzae cutinase
3	d1ivya_	 Alignment		90.8	29	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Serine carboxypeptidase-like
4	d1tcaa_	 Alignment		89.5	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
5	c1gxsC_	 Alignment		89.3	16	PDB header: lyase Chain: C: PDB Molecule: p-(s)-hydroxymandelonitrile lyase chain a; PDBTitle: crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
6	c3dd5F_	 Alignment		88.3	19	PDB header: hydrolase Chain: F: PDB Molecule: cutinase; PDBTitle: glomerella cingulata e600-cutinase complex
7	c3mveB_	 Alignment		86.3	9	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vw1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
8	c4psdA_	 Alignment		83.9	18	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate esterase family 5; PDBTitle: structure of trichoderma reesei cutinase native form.
9	d1wpxa1	 Alignment		83.8	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Serine carboxypeptidase-like
10	c5x88A_	 Alignment		78.0	18	PDB header: hydrolase Chain: A: PDB Molecule: cutinase; PDBTitle: a crystal structure of cutinases from malbranchea cinnamomea
11	c5d8mA_	 Alignment		77.0	16	PDB header: hydrolase Chain: A: PDB Molecule: metagenomic carboxyl esterase mgs0156; PDBTitle: crystal structure of the metagenomic carboxyl esterase mgs0156

12	d1gpla2	Alignment		77.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
13	d1gya_	Alignment		76.4	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
14	c3d0kA_	Alignment		76.0	17	PDB header: hydrolase Chain: A: PDB Molecule: putative poly(3-hydroxybutyrate) depolymerase lpqc; PDBTitle: crystal structure of the lpqc, poly(3-hydroxybutyrate) depolymerase2 from bordetella parapertussis
15	d1etha2	Alignment		75.9	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
16	c4az3A_	Alignment		75.7	27	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal protective protein 32 kda chain; PDBTitle: crystal structure of cathepsin a, complexed with 15a
17	d1ac5a_	Alignment		73.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Serine carboxypeptidase-like
18	d1r88a_	Alignment		72.1	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
19	d1f0na_	Alignment		72.0	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
20	d1rp1a2	Alignment		70.5	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
21	c5xk2A_	Alignment	not modelled	70.5	22	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
22	d1qoza_	Alignment	not modelled	69.3	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
23	c2pplA_	Alignment	not modelled	67.9	17	PDB header: hydrolase Chain: A: PDB Molecule: pancreatic lipase-related protein 1; PDBTitle: human pancreatic lipase-related protein 1
24	d1hpla2	Alignment	not modelled	65.2	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
25	d3b5ea1	Alignment	not modelled	65.0	16	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase/thioesterase 1
26	d1tiaa_	Alignment	not modelled	63.9	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
27	d1sfra_	Alignment	not modelled	62.9	12	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
28	c3g7nA_	Alignment	not modelled	62.4	17	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
29	c1gplA_	Alignment	not modelled	62.2	16	PDB header: serine esterase Chain: A: PDB Molecule: rp2 lipase;

						PDBTitle: rp2 lipase
30	c5gw8A_	Alignment	not modelled	62.2	20	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
31	c1rp1A_	Alignment	not modelled	61.9	15	PDB header: hydrolase Chain: A; PDB Molecule: pancreatic lipase related protein 1; PDBTitle: dog pancreatic lipase related protein 1
32	c4ww4B_	Alignment	not modelled	61.8	24	PDB header: hydrolase Chain: B; PDB Molecule: ruvb-like 2; PDBTitle: double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
33	c2veoA_	Alignment	not modelled	61.4	13	PDB header: hydrolase Chain: A; PDB Molecule: lipase a; PDBTitle: x-ray structure of candida antarctica lipase a in its closed state.
34	c4h18D_	Alignment	not modelled	61.1	9	PDB header: transferase Chain: D; PDB Molecule: cmt1; PDBTitle: three dimensional structure of corynomycoloyl tranferase c
35	c5f2hA_	Alignment	not modelled	60.2	16	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: 2.75 angstrom resolution crystal structure of uncharacterized protein2 from bacillus cereus atcc 10987
36	d1lpbb2	Alignment	not modelled	59.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
37	c3ed1E_	Alignment	not modelled	59.4	13	PDB header: hydrolase receptor Chain: E; PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
38	c5x6sB_	Alignment	not modelled	58.9	13	PDB header: hydrolase Chain: B; PDB Molecule: acetyl/xylan esterase a; PDBTitle: acetyl xylan esterase from aspergillus awamori
39	c2zyiB_	Alignment	not modelled	58.4	10	PDB header: hydrolase Chain: B; PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
40	d1uwca_	Alignment	not modelled	57.4	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
41	d1bu8a2	Alignment	not modelled	56.5	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Pancreatic lipase, N-terminal domain
42	c4hxgl_	Alignment	not modelled	56.2	14	PDB header: hydrolase Chain: J; PDB Molecule: putative uncharacterized protein ph0594; PDBTitle: pyrococcus horikoshii acylaminoacyl peptidase (orthorhombic crystal2 form)
43	d1g66a_	Alignment	not modelled	55.3	18	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Cutinase-like
44	d2jbwa1	Alignment	not modelled	54.8	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
45	c3uuuA_	Alignment	not modelled	54.5	17	PDB header: hydrolase Chain: A; PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
46	c3icvA_	Alignment	not modelled	53.7	15	PDB header: hydrolase Chain: A; PDB Molecule: lipase b; PDBTitle: structural consequences of a circular permutation on lipase b from2 candida antarctica
47	c1hplB_	Alignment	not modelled	53.0	15	PDB header: hydrolase(carboxylic esterase) Chain: B; PDB Molecule: lipase; PDBTitle: horse pancreatic lipase. the crystal structure at 2.3 angstroms2 resolution
48	c2pvsB_	Alignment	not modelled	52.4	13	PDB header: hydrolase Chain: B; PDB Molecule: pancreatic lipase-related protein 2; PDBTitle: structure of human pancreatic lipase related protein 22 mutant n336q
49	c3ajaaA_	Alignment	not modelled	50.7	12	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of msmeg_6394
50	c2qruA_	Alignment	not modelled	49.9	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an alpha/beta hydrolase superfamily protein from2 enterococcus faecalis
51	c2jwbB_	Alignment	not modelled	46.8	14	PDB header: hydrolase Chain: B; PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
52	c3oaaC_	Alignment	not modelled	45.4	20	PDB header: hydrolase/transport protein Chain: C; PDB Molecule: atp synthase subunit alpha; PDBTitle: structure of the e.coli f1-atp synthase inhibited by subunit epsilon
53	c4qnnC_	Alignment	not modelled	43.5	16	PDB header: hydrolase Chain: C; PDB Molecule: phospholipase a 1 from hornet(vespa basalis) venom; PDBTitle: crystal structure of phospholipase a 1 from hornet(vespa basalis)2 venom
54	c3o0dF_	Alignment	not modelled	43.0	18	PDB header: hydrolase Chain: F; PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
55	c2qeqA_	Alianment	not modelled	42.4	15	PDB header: hydrolase Chain: A; PDB Molecule: flavivirin protease ns3 catalytic subunit;

						PDBTitle: crystal structure of kunjin virus ns3 helicase
56	c2v6jA	Alignment	not modelled	40.4	23	PDB header: hydrolase Chain: A: PDB Molecule: rna helicase; PDBTitle: kokobera virus helicase: mutant met47thr
57	c3wiaA	Alignment	not modelled	40.4	19	PDB header: hydrolase Chain: A: PDB Molecule: oxidized polyvinyl alcohol hydrolase; PDBTitle: crystal structure of soph native
58	c3lcrA	Alignment	not modelled	38.6	15	PDB header: hydrolase Chain: A: PDB Molecule: tautomycetin biosynthetic pks; PDBTitle: thioesterase from tautomycetin biosynthetic pathway
59	c3ep1A	Alignment	not modelled	38.2	36	PDB header: transferase/rna Chain: A: PDB Molecule: trna isopentenyltransferase; PDBTitle: crystallographic snapshots of eukaryotic2 dimethylallyltransferase acting on trna: insight into trna3 recognition and reaction mechanism
60	d1ejja	Alignment	not modelled	37.6	20	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
61	c4z8zA	Alignment	not modelled	36.1	12	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the hypothetical protein from ruminiclostridium2 thermocellum atcc 27405
62	c2vijA	Alignment	not modelled	35.6	20	PDB header: hydrolase Chain: A: PDB Molecule: phospholipase a1-igamma; PDBTitle: crystal structure of phospholipase a1
63	d2bmfa2	Alignment	not modelled	35.2	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
64	c3llmB	Alignment	not modelled	34.9	36	PDB header: hydrolase Chain: B: PDB Molecule: atp-dependent rna helicase a; PDBTitle: crystal structure analysis of a rna helicase
65	c1bcrA	Alignment	not modelled	34.8	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine carboxypeptidase ii; PDBTitle: complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
66	c5g59A	Alignment	not modelled	34.3	11	PDB header: structural protein Chain: A: PDB Molecule: esterase; PDBTitle: structure of the pyrococcus furiosus esterase pf2001 with space group2 p3121
67	c3n01A	Alignment	not modelled	33.5	21	PDB header: transferase Chain: A: PDB Molecule: serine hydroxymethyltransferase; PDBTitle: crystal structure of serine hydroxymethyltransferase from2 campylobacter jejuni
68	c2cxaA	Alignment	not modelled	33.5	55	PDB header: transferase Chain: A: PDB Molecule: leucyl/phenylalanyl-trna-protein transferase; PDBTitle: crystal structure of leucyl/phenylalanyl-trna protein2 transferase from escherichia coli
69	d2cxaa1	Alignment	not modelled	33.5	55	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: LFTR-like
70	c3exaD	Alignment	not modelled	33.4	31	PDB header: transferase Chain: D: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: crystal structure of the full-length trna isopentenylpyrophosphate2 transferase (bh2366) from bacillus halodurans, northeast structural3 genomics consortium target bhr41.
71	c4h69A	Alignment	not modelled	33.4	42	PDB header: isomerase Chain: A: PDB Molecule: allene oxide cyclase; PDBTitle: crystal structure of the allene oxide cyclase 2 from physcomitrella2 patens complexed with substrate analog
72	d1k8qa	Alignment	not modelled	32.9	23	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
73	c3fcxA	Alignment	not modelled	32.9	11	PDB header: hydrolase Chain: A: PDB Molecule: s-formylglutathione hydrolase; PDBTitle: crystal structure of human esterase d
74	d1lbqa	Alignment	not modelled	32.7	18	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatae
75	d1dqza	Alignment	not modelled	32.2	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Mycobacterial antigens
76	d3tgla	Alignment	not modelled	31.6	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
77	c3fnbB	Alignment	not modelled	31.0	14	PDB header: hydrolase Chain: B: PDB Molecule: acylaminoacyl peptidase smu_737; PDBTitle: crystal structure of acylaminoacyl peptidase smu_737 from2 streptococcus mutans ua159
78	c3etcB	Alignment	not modelled	31.0	9	PDB header: ligase Chain: B: PDB Molecule: amp-binding protein; PDBTitle: 2.1 a structure of acyl-adenylate synthetase from methanosarcina2 acetivorans containing a link between lys256 and cys298
79	c2z83A	Alignment	not modelled	30.7	21	PDB header: viral protein Chain: A: PDB Molecule: helicase/nucleoside triphosphatase; PDBTitle: crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
						Fold: alpha/beta-Hydrolases

80	d1higa_	Alignment	not modelled	30.2	22	Superfamily: alpha/beta-Hydrolases Family: Gastric lipase
81	c6e7kB_	Alignment	not modelled	30.0	13	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein lipase; PDBTitle: structure of the lipoprotein lipase gpibp1 complex that mediates2 plasma triglyceride hydrolysis
82	c3hkB_	Alignment	not modelled	30.0	22	PDB header: hydrolase Chain: B: PDB Molecule: acyl-coenzyme a thioesterase 2, mitochondrial; PDBTitle: crystal structure of human mitochondrial acyl-coa thioesterase (acot2)
83	d1a1va1	Alignment	not modelled	29.6	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
84	c6q45C_	Alignment	not modelled	29.4	15	PDB header: hydrolase Chain: C: PDB Molecule: atp synthase subunit alpha; PDBTitle: f1-atpase from fusobacterium nucleatum
85	c4nfb_	Alignment	not modelled	29.3	16	PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
86	c3h2iA_	Alignment	not modelled	29.1	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of n228w mutant of the rice cell wall2 degrading esterase lipa from xanthomonas oryzae
87	c4zrsA_	Alignment	not modelled	28.6	14	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of a cloned feruloyl esterase from a soil2 metagenomic library
88	d1jmkc_	Alignment	not modelled	27.9	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
89	c3a8tA_	Alignment	not modelled	27.7	33	PDB header: transferase Chain: A: PDB Molecule: adenylate isopentenyltransferase; PDBTitle: plant adenylate isopentenyltransferase in complex with atp
90	d1qe3a_	Alignment	not modelled	27.7	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Acetylcholinesterase-like
91	c3g8yA_	Alignment	not modelled	27.3	15	PDB header: hydrolase Chain: A: PDB Molecule: susd/ragb-associated esterase-like protein; PDBTitle: crystal structure of a putative hydrolase (bvu_4111) from bacteroides2 vulgatus atcc 8482 at 1.90 a resolution
92	c3e4dD_	Alignment	not modelled	26.7	26	PDB header: hydrolase Chain: D: PDB Molecule: esterase d; PDBTitle: structural and kinetic study of an s-formylglutathione hydrolase from2 agrobacterium tumefaciens
93	c3hc7A_	Alignment	not modelled	26.7	13	PDB header: cell adhesion Chain: A: PDB Molecule: gene 12 protein; PDBTitle: crystal structure of lysin b from mycobacteriophage d29
94	c3crqA_	Alignment	not modelled	26.6	17	PDB header: transferase Chain: A: PDB Molecule: trna delta(2)-isopentenylpyrophosphate PDBTitle: structure of trna dimethylallyltransferase: rna2 modification through a channel
95	c1j9zB_	Alignment	not modelled	26.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
96	c3k2iA_	Alignment	not modelled	25.6	31	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coenzyme a thioesterase 4; PDBTitle: human acyl-coenzyme a thioesterase 4
97	c4ct4B_	Alignment	not modelled	25.4	27	PDB header: rna binding protein Chain: B: PDB Molecule: probable atp-dependent rna helicase ddx6; PDBTitle: cnot1 mif4g domain - ddx6 complex
98	d1tiba_	Alignment	not modelled	25.2	13	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
99	c5agaA_	Alignment	not modelled	24.6	19	PDB header: transferase Chain: A: PDB Molecule: dna polymerase theta; PDBTitle: crystal structure of the helicase domain of human dna2 polymerase theta in complex with amppnp
100	c3fozB_	Alignment	not modelled	24.5	17	PDB header: transferase/rna Chain: B: PDB Molecule: trna delta(2)-isopentenylpyrophosphate transferase; PDBTitle: structure of e. coli isopentenyl-trna transferase in complex with e.2 coli trna(phe)
101	d1mo2a_	Alignment	not modelled	24.4	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Thioesterase domain of polypeptide, polyketide and fatty acid synthases
102	c1mo2A_	Alignment	not modelled	24.4	17	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase, modules 5 and 6; PDBTitle: thioesterase domain from 6-deoxyerythronolide synthase (debs te), ph2 8.5
103	d1jifa_	Alignment	not modelled	24.3	10	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
104	c4nwzA_	Alignment	not modelled	24.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulfide oxidoreductase; PDBTitle: structure of bacterial type ii nadh dehydrogenase from2 caldalkalibacillus thermarum at 2.5a resolution
105	c4i1xA_	Alignment	not modelled	24.0	20	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase from helicobacter

						pylori 26695
106	d2gm3a1	Alignment	not modelled	24.0	11	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: Universal stress protein-like
107	c5thmA	Alignment	not modelled	23.9	21	PDB header: hydrolase Chain: A; PDB Molecule: esterase-6; PDBTitle: esterase-6 from drosophila melanogaster
108	c3hteC	Alignment	not modelled	23.9	14	PDB header: motor protein Chain: C; PDB Molecule: atp-dependent clp protease atp-binding subunit clpX; PDBTitle: crystal structure of nucleotide-free hexameric clpX
109	d2qtva3	Alignment	not modelled	23.8	21	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
110	c3ngmB	Alignment	not modelled	23.5	25	PDB header: hydrolase Chain: B; PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
111	c2czqB	Alignment	not modelled	23.2	15	PDB header: hydrolase Chain: B; PDB Molecule: cutinase-like protein; PDBTitle: a novel cutinase-like protein from cryptococcus sp.
112	c4i5iA	Alignment	not modelled	22.5	21	PDB header: hydrolase Chain: A; PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of the sirt1 catalytic domain bound to nad and an2 ex527 analog
113	c2jlrA	Alignment	not modelled	22.4	14	PDB header: hydrolase Chain: A; PDB Molecule: serine protease subunit ns3; PDBTitle: dengue virus 4 ns3 helicase in complex with amppnp
114	c5t4oA	Alignment	not modelled	22.4	23	PDB header: hydrolase Chain: A; PDB Molecule: atp synthase subunit alpha; PDBTitle: autoinhibited e. coli atp synthase state 1
115	c1s2mA	Alignment	not modelled	22.2	20	PDB header: rna binding protein Chain: A; PDB Molecule: putative atp-dependent rna helicase dhh1; PDBTitle: crystal structure of the dead box protein dhh1p
116	c3eiqD	Alignment	not modelled	22.1	27	PDB header: hydrolase/antitumor protein Chain: D; PDB Molecule: eukaryotic initiation factor 4a-i; PDBTitle: crystal structure of pdcd4-eif4a
117	c5n4kA	Alignment	not modelled	22.1	21	PDB header: rna binding protein Chain: A; PDB Molecule: nucleoprotein; PDBTitle: n-terminal domain of a human coronavirus nl63 nucleocapsid protein
118	c6gunB	Alignment	not modelled	21.9	13	PDB header: hydrolase Chain: B; PDB Molecule: estb from aspergillus nidulans; PDBTitle: siderophore hydrolase estb from aspergillus nidulans
119	d2bxxa1	Alignment	not modelled	21.9	22	Fold: Coronavirus RNA-binding domain Superfamily: Coronavirus RNA-binding domain Family: Coronavirus RNA-binding domain
120	c4oylC	Alignment	not modelled	21.5	15	PDB header: hydrolase Chain: C; PDB Molecule: cutinase; PDBTitle: humicola insolens cutinase in complex with mono-ethylphosphate