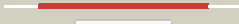



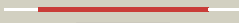

























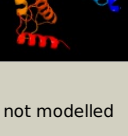


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3377c_(-)_3791028_3792533
Date	Fri Aug 9 18:20:04 BST 2019
Unique Job ID	6ec942d2aff7087a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5bp8A_	 Alignment		100.0	27	PDB header: isomerase Chain: A: PDB Molecule: ent-copalyl diphosphate synthase; PDBTitle: ent-copalyl diphosphate synthase from streptomyces platensis
2	c1w6kA_	 Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: lanosterol synthase; PDBTitle: structure of human osc in complex with lanosterol
3	c1o79A_	 Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: squalene--hopene cyclase; PDBTitle: structures of human oxidosqualene cyclase inhibitors bound to an2 homologous enzyme
4	c3pybB_	 Alignment		100.0	24	PDB header: isomerase Chain: B: PDB Molecule: ent-copalyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of ent-copalyl diphosphate synthase from arabidopsis2 thaliana in complex with 13-aza-13,14-dihydrocopalyl diphosphate
5	c3s9vD_	 Alignment		100.0	25	PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
6	c3p5rB_	 Alignment		100.0	23	PDB header: lyase Chain: B: PDB Molecule: taxadiene synthase; PDBTitle: crystal structure of taxadiene synthase from pacific yew (taxus2 brevifolia) in complex with mg2+ and 2-fluorogeranylgeranyl3 diphosphate
7	c3saeA_	 Alignment		100.0	25	PDB header: lyase Chain: A: PDB Molecule: alpha-bisabolene synthase; PDBTitle: structure of a three-domain sesquiterpene synthase: a prospective2 target for advanced biofuels production
8	d1w6ka1	 Alignment		100.0	19	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
9	d2sqca1	 Alignment		100.0	20	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
10	d2sqca2	 Alignment		100.0	16	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
11	d1w6ka2	 Alignment		99.8	13	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases

12	d3dssb1	Alignment		99.8	15	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
13	d1r76a_	Alignment		99.7	23	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
14	d1qqfa_	Alignment		99.6	13	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
15	c1hzfA_	Alignment		99.5	10	PDB header: immune system Chain: A: PDB Molecule: complement factor c4a; PDBTitle: c4adg fragment of human complement factor c4a
16	d1hzfa_	Alignment		99.5	10	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
17	d1c3da_	Alignment		99.5	14	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Complement components
18	c3e37B_	Alignment		99.4	17	PDB header: transferase Chain: B: PDB Molecule: protein farnesyltransferase subunit beta; PDBTitle: protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5
19	d2h6fb1	Alignment		99.4	18	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
20	d1n4qb_	Alignment		99.4	13	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases
21	c1tnuL_	Alignment	not modelled	99.4	13	PDB header: transferase Chain: L: PDB Molecule: geranylgeranyl transferase type i beta subunit; PDBTitle: rat protein geranylgeranyltransferase type-i complexed with2 a ggpp analog and a gcincckvl peptide derived from rhob
22	c3draB_	Alignment	not modelled	99.4	12	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyltransferase type i beta subunit; PDBTitle: candida albicans protein geranylgeranyltransferase-i2 complexed with ggpp
23	c2pn5A_	Alignment	not modelled	99.3	12	PDB header: immune system Chain: A: PDB Molecule: thioester-containing protein i; PDBTitle: crystal structure of tep1r
24	c4mbgB_	Alignment	not modelled	99.3	12	PDB header: transferase Chain: B: PDB Molecule: caax farnesyltransferase beta subunit ram1; PDBTitle: crystal structure of aspergillus fumigatus protein farnesyltransferase2 binary complex with farnesyldiphosphate
25	c4acqA_	Alignment	not modelled	99.2	16	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: alpha-2-macroglobulin; PDBTitle: alpha-2 macroglobulin
26	c4fxkB_	Alignment	not modelled	99.2	18	PDB header: immune system Chain: B: PDB Molecule: complement c4-a alpha chain; PDBTitle: human complement c4
27	c2pmvB_	Alignment	not modelled	99.2	15	PDB header: transport protein Chain: B: PDB Molecule: gastric intrinsic factor; PDBTitle: crystal structure of human intrinsic factor- cobalamin complex at 2.62 a resolution
28	c4acqC_	Alignment	not modelled	99.2	16	PDB header: hydrolase inhibitor Chain: C: PDB Molecule: alpha-2-macroglobulin;

						PDBTitle: alpha-2 macroglobulin
29	c3g6jB_	Alignment	not modelled	99.2	13	PDB header: immune system Chain: B; PDB Molecule: complement c3 alpha chain; PDBTitle: c3b in complex with a c3b specific fab
30	d1gxma_	Alignment	not modelled	99.2	15	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
31	c2b39B_	Alignment	not modelled	99.2	17	PDB header: immune system Chain: B; PDB Molecule: c3; PDBTitle: structure of mammalian c3 with an intact thioester at 3a resolution
32	c2a73B_	Alignment	not modelled	99.1	11	PDB header: immune system Chain: B; PDB Molecule: complement c3; PDBTitle: human complement component c3
33	c3cu7A_	Alignment	not modelled	99.1	14	PDB header: immune system Chain: A; PDB Molecule: complement c5; PDBTitle: human complement component 5
34	c4a5wA_	Alignment	not modelled	99.1	15	PDB header: immune system Chain: A; PDB Molecule: complement c5; PDBTitle: crystal structure of c5b6
35	c3q7aB_	Alignment	not modelled	99.1	14	PDB header: transferase/transferase inhibitor Chain: B; PDB Molecule: farnesyltransferase beta subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpp and l-778,123
36	c4u48A_	Alignment	not modelled	99.0	13	PDB header: hydrolase inhibitor Chain: A; PDB Molecule: putative inner membrane lipoprotein; PDBTitle: crystal structure of salmonella alpha-2-macroglobulin
37	c4rtdA_	Alignment	not modelled	99.0	15	PDB header: lipid binding protein Chain: A; PDB Molecule: uncharacterized lipoprotein yfhm; PDBTitle: escherichia coli alpha-2-macroglobulin activated by porcine elastase
38	c4ydeB_	Alignment	not modelled	99.0	11	PDB header: transferase Chain: B; PDB Molecule: protein farnesyltransferase/geranylgeranyltransferase type- PDBTitle: crystal structure of candida albicans protein farnesyltransferase2 binary complex with the isoprenoid farnesyl diphosphate
39	c2pmvA_	Alignment	not modelled	98.8	17	PDB header: transport protein Chain: A; PDB Molecule: gastric intrinsic factor; PDBTitle: crystal structure of human intrinsic factor- cobalamin complex at 2.62 a resolution
40	c2v3nA_	Alignment	not modelled	98.5	14	PDB header: transport protein Chain: A; PDB Molecule: transcobalamin-2; PDBTitle: crystallographic analysis of upper axial ligand2 substitutions in cobalamin bound to transcobalamin
41	c4kkiA_	Alignment	not modelled	98.5	21	PDB header: transport protein Chain: A; PDB Molecule: transcobalamin-1; PDBTitle: crystal structure of haptocorrin in complex with cncbl
42	c1ug9A_	Alignment	not modelled	97.9	21	PDB header: hydrolase Chain: A; PDB Molecule: glucodextranase; PDBTitle: crystal structure of glucodextranase from arthrobacter globiformis i42
43	d1ulva1	Alignment	not modelled	97.5	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
44	c1lf6A_	Alignment	not modelled	97.1	12	PDB header: hydrolase Chain: A; PDB Molecule: glucoamylase; PDBTitle: crystal structure of bacterial glucoamylase
45	c2zzrA_	Alignment	not modelled	97.0	13	PDB header: hydrolase Chain: A; PDB Molecule: unsaturated glucuronyl hydrolase; PDBTitle: crystal structure of unsaturated glucuronyl hydrolase from2 streptococcus agalactiae
46	c5zjzC_	Alignment	not modelled	96.9	12	PDB header: lyase Chain: C; PDB Molecule: santalene synthase; PDBTitle: crystal structure of a enzyme from santalum album
47	d1lf6a1	Alignment	not modelled	96.5	12	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Bacterial glucoamylase C-terminal domain-like
48	c5z3dA_	Alignment	not modelled	96.3	15	PDB header: hydrolase Chain: A; PDB Molecule: glycoside hydrolase 15-related protein; PDBTitle: glycosidase f290y
49	c5c05A_	Alignment	not modelled	96.3	12	PDB header: biosynthetic protein Chain: A; PDB Molecule: putative gamma-terpinene synthase; PDBTitle: crystal structure of gamma-terpinene synthase from thymus vulgaris
50	c2ongA_	Alignment	not modelled	96.1	16	PDB header: lyase Chain: A; PDB Molecule: 4s-limonene synthase; PDBTitle: crystal structure of of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp).
51	c3n0fA_	Alignment	not modelled	95.8	19	PDB header: lyase Chain: A; PDB Molecule: isoprene synthase; PDBTitle: crystal structure of isoprene synthase from grey poplar leaves2 (populus x canescens)
52	c6o9qA_	Alignment	not modelled	95.3	10	PDB header: lyase Chain: A; PDB Molecule: sesquisabinene b synthase 1; PDBTitle: wild-type sasqs1
53	d2d5ja1	Alignment	not modelled	94.6	15	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glycosyl Hydrolase Family 88
54	c3wc3A_	Alignment	not modelled	94.6	17	PDB header: hydrolase Chain: A; PDB Molecule: endo-1, 4-beta-glucanase; PDBTitle: crystal structure of endo-1,4-beta-glucanase from eisenia fetida

55	c4gaxA	Alignment	not modelled	94.5	12	PDB header: lyase Chain: A: PDB Molecule: amorpha-4,11-diene synthase; PDBTitle: crystal structure of an alpha-bisabolol synthase mutant
56	c1hx9A	Alignment	not modelled	94.3	12	PDB header: lyase Chain: A: PDB Molecule: 5-epi-aristolochene synthase; PDBTitle: crystal structure of teas w273s form 1
57	c3g4dB	Alignment	not modelled	94.1	16	PDB header: lyase Chain: B: PDB Molecule: (+)-delta-cadinene synthase isozyme xc1; PDBTitle: crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
58	d1g87a1	Alignment	not modelled	93.8	20	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
59	c1n20A	Alignment	not modelled	93.3	10	PDB header: isomerase Chain: A: PDB Molecule: (+)-bornyl diphosphate synthase; PDBTitle: (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,3-dihydrogeranyl diphosphate
60	c3vw5B	Alignment	not modelled	92.4	12	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of sugar epimerase from ruminal bacterium
61	d1ks8a	Alignment	not modelled	92.1	17	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
62	d1gaia	Alignment	not modelled	90.2	16	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase
63	c2yikA	Alignment	not modelled	90.1	15	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: catalytic domain of clostridium thermocellum celt
64	c6fhwB	Alignment	not modelled	89.6	15	PDB header: hydrolase Chain: B: PDB Molecule: glucoamylase p; PDBTitle: structure of hormoconis resiniae glucoamylase
65	c3pmmA	Alignment	not modelled	88.1	18	PDB header: hydrolase Chain: A: PDB Molecule: putative cytoplasmic protein; PDBTitle: the crystal structure of a possible member of gh105 family from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578
66	c2j5cB	Alignment	not modelled	88.0	16	PDB header: lyase Chain: B: PDB Molecule: 1,8-cineole synthase; PDBTitle: rational conversion of substrate and product specificity in a2 monoterpene synthase. structural insights into the molecular basis of3 rapid evolution.
67	c5noaA	Alignment	not modelled	87.6	18	PDB header: hydrolase Chain: A: PDB Molecule: family 88 glycosyl hydrolase; PDBTitle: polysaccharide lyase baccell_00875
68	d1tf4a1	Alignment	not modelled	87.6	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
69	c4ce7B	Alignment	not modelled	86.7	12	PDB header: hydrolase Chain: B: PDB Molecule: unsaturated 3s-rhamnoglucuronyl hydrolase; PDBTitle: crystal structure of a novel unsaturated beta-glucuronyl2 hydrolase enzyme, belonging to family gh105, involved in3 ulvan degradation
70	c5uv1A	Alignment	not modelled	84.2	17	PDB header: lyase Chain: A: PDB Molecule: (+)-limonene synthase; PDBTitle: crystal structure of (+)-limonene synthase complexed with 2-2 fluorogeranyl diphosphate
71	c3k11A	Alignment	not modelled	83.7	9	PDB header: hydrolase Chain: A: PDB Molecule: putative glycosyl hydrolase; PDBTitle: crystal structure of putative glycosyl hydrolase (np_813087.1) from2 bacteroides thetaiotaomicron vpi-5482 at 1.80 a resolution
72	c4pw2A	Alignment	not modelled	80.3	20	PDB header: isomerase Chain: A: PDB Molecule: d-glucuronyl c5 epimerase b; PDBTitle: crystal structure of d-glucuronyl c5 epimerase
73	c6fhvA	Alignment	not modelled	79.4	19	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: crystal structure of penicillium oxalicum glucoamylase
74	c3wiwA	Alignment	not modelled	79.2	14	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase family 88; PDBTitle: crystal structure of unsaturated glucuronyl hydrolase specific for2 heparin
75	c5x32B	Alignment	not modelled	76.6	12	PDB header: isomerase Chain: B: PDB Molecule: n-acylglucosamine 2-epimerase; PDBTitle: crystal structure of d-mannose isomerase
76	c5zigD	Alignment	not modelled	76.5	13	PDB header: isomerase Chain: D: PDB Molecule: cellobiose 2-epimerase; PDBTitle: the structure of cellobiose 2-epimerase from spirochaeta thermophila2 dsm 6192
77	c3wkgA	Alignment	not modelled	75.9	18	PDB header: isomerase Chain: A: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase in complex with2 glucosylmannose
78	c2xfgA	Alignment	not modelled	75.1	18	PDB header: hydrolase/sugar binding protein Chain: A: PDB Molecule: endoglucanase 1; PDBTitle: reassembly and co-crystallization of a family 9 processive2 endoglucanase from separately expressed gh9 and cbm3c3 modules
79	c5zhhB	Alignment	not modelled	75.1	13	PDB header: isomerase Chain: B: PDB Molecule: cellobiose 2-epimerase; PDBTitle: structure of cellobiose 2-epimerase from bacillus thermoamylovorans2 b4167 PDB header: isomerase

80	c3gt5A_	Alignment	not modelled	75.0	12	Chain: A: PDB Molecule: n-acetylglucosamine 2-epimerase; PDBTitle: crystal structure of an n-acetylglucosamine 2-epimerase family protein2 from xylella fastidiosa
81	c2vn4A_	Alignment	not modelled	75.0	19	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: glycoside hydrolase family 15 glucoamylase from hypocrea jecorina
82	d1nc5a_	Alignment	not modelled	73.2	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Hypothetical protein YteR
83	c1js4B_	Alignment	not modelled	72.1	13	PDB header: glycosyl hydrolase Chain: B: PDB Molecule: endo/exocellulase e4; PDBTitle: endo/exocellulase:cellobiose from thermomonospora
84	d1ia6a_	Alignment	not modelled	67.1	13	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Cellulases catalytic domain
85	c1ga2A_	Alignment	not modelled	65.5	23	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase 9g; PDBTitle: the crystal structure of endoglucanase 9g from clostridium2 cellulolyticum complexed with cellobiose
86	c4xuvB_	Alignment	not modelled	64.9	12	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase family 105 protein; PDBTitle: crystal structure of a glycoside hydrolase family 105 (gh105) enzyme2 from thielavia terrestris
87	c3e6uA_	Alignment	not modelled	64.1	10	PDB header: signaling protein Chain: A: PDB Molecule: lanc-like protein 1; PDBTitle: crystal structure of human lanc1
88	d2fbaa1	Alignment	not modelled	61.4	19	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: Glucoamylase
89	c4wu0B_	Alignment	not modelled	61.1	11	PDB header: hydrolase Chain: B: PDB Molecule: similar to yter (bacilus subtilis); PDBTitle: structural analysis of c. acetobutylicum atcc 824 glycoside hydrolase2 from family 105
90	d1whca_	Alignment	not modelled	60.1	11	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
91	d2crna1	Alignment	not modelled	59.6	10	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
92	c4z4IA_	Alignment	not modelled	56.9	11	PDB header: isomerase Chain: A: PDB Molecule: cellobiose 2-epimerase; PDBTitle: crystal structure of cellobiose 2-epimerase from caldicellulosiruptor2 saccharolyticus dsm 8903
93	d5easa1	Alignment	not modelled	56.9	15	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpenoid cyclase N-terminal domain
94	c2crnA_	Alignment	not modelled	56.5	11	PDB header: immune system Chain: A: PDB Molecule: ubash3a protein; PDBTitle: solution structure of the uba domain of human ubash3a2 protein
95	c5u2oA_	Alignment	not modelled	56.0	29	PDB header: hydrolase Chain: A: PDB Molecule: j30 cch; PDBTitle: crystal structure of zn-binding triple mutant of gh family 92 endoglucanase j30
96	c4zlgA_	Alignment	not modelled	55.8	10	PDB header: transferase Chain: A: PDB Molecule: putative b-glycan phosphorylase; PDBTitle: cellobionic acid phosphorylase - gluconic acid complex
97	d1veka_	Alignment	not modelled	55.6	29	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
98	d1n1ba1	Alignment	not modelled	55.0	12	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpenoid cyclase N-terminal domain
99	c4q88B_	Alignment	not modelled	54.8	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: glycosyl hydrolase family 88 from bacteroides vulgatus
100	c6fhnA_	Alignment	not modelled	54.1	8	PDB header: hydrolase Chain: A: PDB Molecule: protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
101	d1rk8c_	Alignment	not modelled	52.2	33	Fold: WW domain-like Superfamily: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain Family: Pym (Within the bgcn gene intron protein, WIBG), N-terminal domain
102	c1rk8C_	Alignment	not modelled	52.2	33	PDB header: translation Chain: C: PDB Molecule: within the bgcn gene intron protein; PDBTitle: structure of the cytosolic protein pym bound to the mago-2 y14 core of the exon junction complex
103	c3x17B_	Alignment	not modelled	51.9	26	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase; PDBTitle: crystal structure of metagenome-derived glycoside hydrolase family 92 endoglucanase
104	c2cpwA_	Alignment	not modelled	50.6	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: cbl-interacting protein sts-1 variant; PDBTitle: solution structure of rsgi ruh-031, a uba domain from human2 cdna
105	c6ex6A_	Alignment	not modelled	50.1	14	PDB header: hydrolase Chain: A: PDB Molecule: six-hairpin glycosidase; PDBTitle: the gh127, beta-arabinofuranosidase, bt3674
106	c3wkaA_	Alignment	not modelled	48.3	16	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase;

						PDBTitle: crystal structure of gh127 beta-l-arabinofuranosidase hypba1 from2 bifidobacterium longum arabinose complex form
107	d2cpwa1	Alignment	not modelled	41.2	13	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
108	c2jyvA_	Alignment	not modelled	41.0	63	PDB header: cytokine Chain: A: PDB Molecule: granulin-2; PDBTitle: human granulin f
109	c4qk0C_	Alignment	not modelled	37.0	19	PDB header: hydrolase Chain: C: PDB Molecule: gh127 beta-l-arabinofuranosidase; PDBTitle: crystal structure of ara127n-se, a gh127 beta-l-arabinofuranosidase2 from geobacillus stearothermophilus t6
110	c2dagA_	Alignment	not modelled	35.7	11	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: solution structure of the first uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
111	c2dakA_	Alignment	not modelled	31.8	14	PDB header: hydrolase Chain: A: PDB Molecule: ubiquitin carboxyl-terminal hydrolase 5; PDBTitle: solution structure of the second uba domain in the human2 ubiquitin specific protease 5 (isopeptidase 5)
112	c1clcA_	Alignment	not modelled	30.0	25	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: endoglucanase celd; ec: 3.2.1.4; PDBTitle: three-dimensional structure of endoglucanase d at 1.92 angstroms resolution
113	c2daiA_	Alignment	not modelled	29.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ubiquitin associated domain containing 1; PDBTitle: solution structure of the first uba domain in the human2 ubiquitin associated domain containing 1 (ubadc1)
114	c5mqoA_	Alignment	not modelled	28.3	4	PDB header: hydrolase Chain: A: PDB Molecule: non-reducing end beta-l-arabinofuranosidase; PDBTitle: glycoside hydrolase bt_1003
115	c6fhjA_	Alignment	not modelled	27.9	9	PDB header: hydrolase Chain: A: PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
116	d1fp3a_	Alignment	not modelled	25.1	11	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase
117	d1wiva_	Alignment	not modelled	24.4	11	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
118	d2afaa1	Alignment	not modelled	22.9	10	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: N-acylglucosamine (NAG) epimerase
119	c3gzkA_	Alignment	not modelled	21.1	16	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: structure of a. acidocaldarius cellulase cela