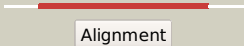

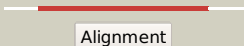

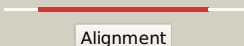




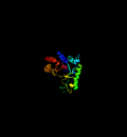


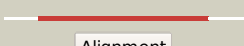












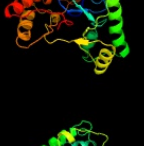


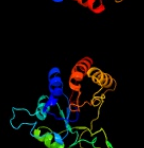

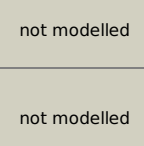


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0784 (-)_878641_879327
Date	Fri Jul 26 01:50:36 BST 2019
Unique Job ID	ce6cfa7558b0c860

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qbuD_	 Alignment		100.0	14	PDB header: hydrolase Chain: D; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of putative peptidoglycan deacetylase (hp0310) from2 helicobacter pylori
2	dlz7aa1	 Alignment		100.0	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: PA1517-like
3	c3rxzA_	 Alignment		100.0	16	PDB header: hydrolase Chain: A; PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
4	c3s6oD_	 Alignment		100.0	15	PDB header: hydrolase Chain: D; PDB Molecule: polysaccharide deacetylase family protein; PDBTitle: crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
5	c2c1iA_	 Alignment		100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: peptidoglycan glcnac deacetylase; PDBTitle: structure of streptococcus pneumoniae peptidoglycan deacetylase2 (sppgda) d 275 n mutant.
6	c4nz3A_	 Alignment		100.0	15	PDB header: hydrolase Chain: A; PDB Molecule: deacetylase da1; PDBTitle: structure of vibrio cholerae chitin de-n-acetylase in complex with2 di(n-acetyl-d-glucosamine) (cbs) in p 21 21 21
7	c2w3zA_	 Alignment		100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
8	c1w17A_	 Alignment		100.0	13	PDB header: hydrolase Chain: A; PDB Molecule: probable polysaccharide deacetylase pdaa; PDBTitle: structure of bacillus subtilis pdaa, a family 4 carbohydrate esterase.
9	c5jp6A_	 Alignment		100.0	12	PDB header: hydrolase Chain: A; PDB Molecule: putative polysaccharide deacetylase; PDBTitle: bdellovibrio bacteriovorus peptidoglycan deacetylase bd3279
10	c4m1bA_	 Alignment		100.0	14	PDB header: hydrolase Chain: A; PDB Molecule: polysaccharide deacetylase; PDBTitle: structural determination of ba0150, a polysaccharide deacetylase from2 bacillus anthracis
11	dlny1a_	 Alignment		100.0	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase

12	d2cc0a1	Alignment		100.0	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
13	d2iw0a1	Alignment		100.0	10	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
14	c5lgcA	Alignment		100.0	16	PDB header: hydrolase Chain: A: PDB Molecule: arce4a; PDBTitle: t48 deacetylase with substrate
15	c4l1gB	Alignment		100.0	11	PDB header: hydrolase Chain: B: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the bc1960 peptidoglycan n-acetylglucosamine2 deacetylase from bacillus cereus
16	c5ncdA	Alignment		100.0	11	PDB header: hydrolase Chain: A: PDB Molecule: peptidoglycan n-acetylglucosamine deacetylase; PDBTitle: crystal structure of the polysaccharide deacetylase bc1974 from2 bacillus cereus in complex with (2s)-2-amino-5-3 (diaminomethylideneamino)-n-hydroxypentanamide
17	d2j13a1	Alignment		100.0	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
18	c2iw0A	Alignment		99.9	10	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
19	d2c71a1	Alignment		99.9	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
20	d2c1ia1	Alignment		99.9	13	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: NodB-like polysaccharide deacetylase
21	c2y8uA	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: a. nidulans chitin deacetylase
22	c2vyoA	Alignment	not modelled	99.9	11	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase domain-containing protein PDBTitle: chitin deacetylase family member from encephalitozoon cuniculi
23	c5z34A	Alignment	not modelled	99.9	13	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: the structure of a chitin deacetylase from bombyx mori provide the2 first insight into insect chitin deacetylation mechanism
24	d2nlya1	Alignment	not modelled	99.9	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: Divergent polysaccharide deacetylase
25	c5znsA	Alignment	not modelled	99.9	10	PDB header: hydrolase Chain: A: PDB Molecule: chitin deacetylase; PDBTitle: insect chitin deacetylase
26	c4wcjA	Alignment	not modelled	99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: structure of icab from ammonifex degensii
27	c6dq3B	Alignment	not modelled	99.8	9	PDB header: hydrolase Chain: B: PDB Molecule: polysaccharide deacetylase; PDBTitle: streptococcus pyogenes deacetylase pdi in complex with acetate
28	c4f9dA	Alignment	not modelled	99.7	9	PDB header: hydrolase Chain: A: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: structure of escherichia coli pgab 42-655 in complex with nickel

29	c5bu6B	Alignment	not modelled	99.7	15	PDB header: hydrolase Chain: B: PDB Molecule: bpsb (pgab), poly-beta-1,6-n-acetyl-d-glucosamine n- PDBTitle: structure of bpsb deaceylase domain from bordetella bronchiseptica
30	c4u10B	Alignment	not modelled	99.6	13	PDB header: hydrolase Chain: B: PDB Molecule: poly-beta-1,6-n-acetyl-d-glucosamine n-deacetylase; PDBTitle: probing the structure and mechanism of de-n-acetylase from2 aggregatibacter actinomycetemcomitans
31	c6go1A	Alignment	not modelled	99.4	9	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase-like protein; PDBTitle: crystal structure of a bacillus anthracis peptidoglycan deacetylase
32	c4hd5A	Alignment	not modelled	99.1	10	PDB header: hydrolase Chain: A: PDB Molecule: polysaccharide deacetylase; PDBTitle: crystal structure of bc0361, a polysaccharide deacetylase from2 bacillus cereus
33	d1k1xa3	Alignment	not modelled	99.0	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: 4-alpha-glucanotransferase, N-terminal domain
34	c1k1yA	Alignment	not modelled	98.8	12	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of thermococcus litoralis 4-alpha-glucanotransferase2 complexed with acarbose
35	d2b5dx2	Alignment	not modelled	98.5	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
36	c2b5dX	Alignment	not modelled	98.4	15	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of the novel alpha-amylase amyc from thermotoga2 maritima
37	c2qv5A	Alignment	not modelled	98.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu2773; PDBTitle: crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
38	c5wu7A	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of gh57-type branching enzyme from hyperthermophilic2 archaeon pyrococcus horikoshii
39	c3n92A	Alignment	not modelled	97.5	13	PDB header: transferase Chain: A: PDB Molecule: alpha-amylase, gh57 family; PDBTitle: crystal structure of tk1436, a gh57 branching enzyme from2 hyperthermophilic archaeon thermococcus kodakaraensis, in complex3 with glucose
40	c1ufaA	Alignment	not modelled	97.1	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: tt1467 protein; PDBTitle: crystal structure of tt1467 from thermus thermophilus hb8
41	d1ufaa2	Alignment	not modelled	96.9	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: AmyC N-terminal domain-like
42	c2wyhA	Alignment	not modelled	96.4	11	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase; PDBTitle: structure of the streptococcus pyogenes family gh38 alpha-2 mannosidase
43	c3hftA	Alignment	not modelled	96.3	11	PDB header: hydrolase Chain: A: PDB Molecule: wbms, polysaccharide deacetylase involved in o-antigen PDBTitle: crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
44	c2ow7A	Alignment	not modelled	93.2	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase 2; PDBTitle: golgi alpha-mannosidase ii complex with (1r,6s,7r,8s)-1-2 thioniabicyclo[4.3.0]nonan-7,8-diol chloride
45	c1o7dA	Alignment	not modelled	93.1	13	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-mannosidase; PDBTitle: the structure of the bovine lysosomal a-mannosidase suggests a novel2 mechanism for low ph activation
46	c2hk1D	Alignment	not modelled	92.7	7	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
47	c1htyA	Alignment	not modelled	92.5	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase ii; PDBTitle: golgi alpha-mannosidase ii
48	d2b7oa1	Alignment	not modelled	91.8	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
49	c5hudA	Alignment	not modelled	91.2	17	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) PDBTitle: non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
50	c6bmcA	Alignment	not modelled	91.0	20	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
51	c5uxmA	Alignment	not modelled	90.9	12	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
52	d3bvua3	Alignment	not modelled	90.3	16	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: alpha-mannosidase

53	c2o7vA	Alignment	not modelled	89.2	9	PDB header: hydrolase Chain: A: PDB Molecule: cxe carboxylesterase; PDBTitle: carboxylesterase aecxe1 from actinidia eriantha covalently inhibited2 by paraoxon
54	d1i60a	Alignment	not modelled	88.1	9	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
55	c5zfsA	Alignment	not modelled	85.7	12	PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
56	c3ktcB	Alignment	not modelled	83.7	8	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
57	c3kwsB	Alignment	not modelled	82.3	9	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
58	c6b9pA	Alignment	not modelled	81.4	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase from canavalia ensiformis (jack bean); PDBTitle: structure of gh 38 jack bean alpha-mannosidase in complex with a 36-2 valent iminosugar cluster inhibitor
59	c5oljA	Alignment	not modelled	79.3	15	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of porphyromonas gingivalis dipeptidyl peptidase 4
60	d2g0wa1	Alignment	not modelled	77.6	9	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
61	d1muwa	Alignment	not modelled	77.5	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
62	d1u4na	Alignment	not modelled	77.4	7	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
63	c3obeB	Alignment	not modelled	76.5	11	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
64	c4ob7A	Alignment	not modelled	75.9	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: crystal structure of esterase rppe mutant w187h
65	c4v2iB	Alignment	not modelled	75.7	11	PDB header: hydrolase Chain: B: PDB Molecule: esterase/lipase; PDBTitle: biochemical characterization and structural analysis of a2 new cold-active and salt tolerant esterase from the marine3 bacterium thalassospira sp
66	c3d7rB	Alignment	not modelled	74.6	13	PDB header: hydrolase Chain: B: PDB Molecule: esterase; PDBTitle: crystal structure of a putative esterase from staphylococcus aureus
67	c3cqkB	Alignment	not modelled	74.4	11	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
68	d1bxca	Alignment	not modelled	73.8	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
69	d1jia	Alignment	not modelled	72.6	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
70	c2ou4C	Alignment	not modelled	72.0	10	PDB header: isomerase Chain: C: PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
71	c5jd5A	Alignment	not modelled	71.7	16	PDB header: hydrolase Chain: A: PDB Molecule: mgs-mile3; PDBTitle: crystal structure of mgs-mile3, an alpha/beta hydrolase enzyme from2 the metagenome of pyrene-phenanthrene enrichment culture with3 sediment sample of milazzo harbor, italy
72	c3vylB	Alignment	not modelled	71.1	10	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
73	c2g5tA	Alignment	not modelled	70.7	8	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: crystal structure of human dipeptidyl peptidase iv (dppiv) complexed2 with cyanopyrrolidine (c5-pro-pro) inhibitor 21ag
74	c4krxB	Alignment	not modelled	70.6	13	PDB header: hydrolase Chain: B: PDB Molecule: acetyl esterase; PDBTitle: structure of aes from e. coli
75	c2f46A	Alignment	not modelled	70.6	14	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative phosphatase (nma1982) from neisseria2 meningitidis z2491 at 1.41 a resolution
76	c3aikB	Alignment	not modelled	69.4	7	PDB header: hydrolase Chain: B: PDB Molecule: 303aa long hypothetical esterase; PDBTitle: crystal structure of a hsl-like carboxylesterase from sulfobolus2 tokodaii
77	c4xvcG	Alignment	not modelled	68.9	20	PDB header: hydrolase Chain: G: PDB Molecule: esterase e40; PDBTitle: crystal structure of an esterase from the bacterial

						hormone-sensitive2 lipase (hsl) family
78	c3ed1E	Alignment	not modelled	67.3	9	PDB header: hydrolase receptor Chain: E: PDB Molecule: gibberellin receptor gid1; PDBTitle: crystal structure of rice gid1 complexed with ga3
79	c3fakA	Alignment	not modelled	66.7	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: structural and functional analysis of a hormone-sensitive2 lipase like este5 from a metagenome library
80	c5l8sD	Alignment	not modelled	65.9	13	PDB header: hydrolase Chain: D: PDB Molecule: amino acyl peptidase; PDBTitle: the crystal structure of a cold-adapted acylaminoacyl peptidase2 reveals a novel quaternary architecture based on the arm-exchange3 mechanism
81	c6aaeA	Alignment	not modelled	65.6	20	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: crystal structure of chloramphenicol-metabolizaing enzyme estdl136
82	c2wirB	Alignment	not modelled	64.6	5	PDB header: hydrolase Chain: B: PDB Molecule: alpha/beta hydrolase fold-3 domain protein; PDBTitle: hyperthermophilic esterase from the archeon pyrobaculum2 calidifontis
83	c5jd4D	Alignment	not modelled	63.9	5	PDB header: hydrolase Chain: D: PDB Molecule: lae6; PDBTitle: crystal structure of lae6 ser161ala mutant, an alpha/beta hydrolase2 enzyme from the metagenome of lake arreo, spain
84	c6gl2A	Alignment	not modelled	63.9	18	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase, family gh5; PDBTitle: structure of zgengagh5_4 wild type at 1.2 angstrom resolution
85	c4q05A	Alignment	not modelled	63.7	15	PDB header: hydrolase Chain: A: PDB Molecule: esterase e25; PDBTitle: crystal structure of an esterase e25
86	c5miiD	Alignment	not modelled	63.1	9	PDB header: hydrolase Chain: D: PDB Molecule: carboxyl esterase 2; PDBTitle: crystal structure of carboxyl esterase 2 (tmelest2) from mycorrhizal2 fungus tuber melanosporum
87	c4q3oB	Alignment	not modelled	62.9	18	PDB header: hydrolase Chain: B: PDB Molecule: mgs-mt1; PDBTitle: crystal structure of mgs-mt1, an alpha/beta hydrolase enzyme from a2 lake matapan deep-sea metagenome library
88	c2ecfA	Alignment	not modelled	62.7	13	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl peptidase iv; PDBTitle: crystal structure of dipeptidyl aminopeptidase iv from2 stentrophomonas maltophilia
89	c1vjqB	Alignment	not modelled	62.1	22	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
90	c3wj2A	Alignment	not modelled	62.0	7	PDB header: hydrolase Chain: A: PDB Molecule: carboxylesterase; PDBTitle: crystal structure of estfa (fe-lacking apo form)
91	c4wy8A	Alignment	not modelled	61.9	9	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
92	c2qtbB	Alignment	not modelled	60.5	8	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl peptidase 4; PDBTitle: human dipeptidyl peptidase iv/cd26 in complex with a 4-aryl2 cyclohexylalanine inhibitor
93	c3ju2A	Alignment	not modelled	60.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
94	c3ga7A	Alignment	not modelled	59.9	13	PDB header: hydrolase Chain: A: PDB Molecule: acetyl esterase; PDBTitle: 1.55 angstrom crystal structure of an acetyl esterase from salmonella2 typhimurium
95	c3azqA	Alignment	not modelled	59.0	17	PDB header: hydrolase Chain: A: PDB Molecule: aminopeptidase; PDBTitle: crystal structure of puromycin hydrolase s511a mutant complexed with2 pgg
96	d1lzlA	Alignment	not modelled	58.9	9	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
97	c4wy5A	Alignment	not modelled	56.7	7	PDB header: hydrolase Chain: A: PDB Molecule: esterase; PDBTitle: structural analysis of two fungal esterases from rhizomucor miehei2 explaining their substrate specificity
98	c5jm0A	Alignment	not modelled	56.5	10	PDB header: hydrolase Chain: A: PDB Molecule: alpha-mannosidase,alpha-mannosidase,alpha-mannosidase; PDBTitle: structure of the s. cerevisiae alpha-mannosidase 1
99	c1xfdD	Alignment	not modelled	55.9	6	PDB header: membrane protein Chain: D: PDB Molecule: dipeptidyl aminopeptidase-like protein 6; PDBTitle: structure of a human a-type potassium channel accelerating factor2 dppx, a member of the dipeptidyl aminopeptidase family
100	c4ypvA	Alignment	not modelled	54.5	13	PDB header: hydrolase Chain: A: PDB Molecule: est8; PDBTitle: high-resolution structure of a metagenome-derived esterase est8
101	c4zi5A	Alignment	not modelled	53.3	17	PDB header: hydrolase Chain: A: PDB Molecule: p91; PDBTitle: crystal structure of dienelactone hydrolase-like promiscuous2 phosphotriesterase p91 from metagenomic libraries
102	c3vniC	Alignment	not modelled	51.3	8	PDB header: isomerase Chain: C: PDB Molecule: xylose isomerase domain protein tim barrel;

102	c5vnc_	Alignment	not modelled	51.5	0	PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
103	d1rxda_	Alignment	not modelled	51.2	16	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
104	c3dnmA_	Alignment	not modelled	51.0	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase/lipase; PDBTitle: crystal structure hormone-sensitive lipase from a2 metagenome library
105	c5l2pD_	Alignment	not modelled	50.5	17	PDB header: hydrolase Chain: D: PDB Molecule: arylesterase; PDBTitle: structure of arylesterase
106	d2q02a1	Alignment	not modelled	46.8	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
107	d2l5ia1	Alignment	not modelled	46.4	15	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: YdjC-like
108	c4ovxA_	Alignment	not modelled	45.1	11	PDB header: isomerase Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
109	c5jrlC_	Alignment	not modelled	44.8	10	PDB header: hydrolase Chain: C: PDB Molecule: dipeptidyl aminopeptidases/acylaminoacyl-peptidases-like PDBTitle: crystal structure of the sphingopyxin i lasso peptide isopeptidase2 spi-isop (native)
110	c2k6xA_	Alignment	not modelled	44.4	12	PDB header: transcription Chain: A: PDB Molecule: rna polymerase sigma factor rpod; PDBTitle: autoregulation of a group 1 bacterial sigma factor involves2 the formation of a region 1.1- induced compacted structure
111	c5yznA_	Alignment	not modelled	43.5	21	PDB header: hydrolase Chain: A: PDB Molecule: acyl-peptide hydrolase, putative; PDBTitle: crystal structure of s9 peptidase (active form) from deinococcus2 radiodurans r1
112	c3gk0H_	Alignment	not modelled	42.7	27	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
113	d2pbdp1	Alignment	not modelled	40.9	0	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
114	c3cnyA_	Alignment	not modelled	40.2	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
115	c1z68A_	Alignment	not modelled	39.8	10	PDB header: lyase Chain: A: PDB Molecule: fibroblast activation protein, alpha subunit; PDBTitle: crystal structure of human fibroblast activation protein alpha
116	d1pnea_	Alignment	not modelled	39.4	0	Fold: Profilin-like Superfamily: Profilin (actin-binding protein) Family: Profilin (actin-binding protein)
117	c2eepA_	Alignment	not modelled	39.4	12	PDB header: hydrolase Chain: A: PDB Molecule: dipeptidyl aminopeptidase iv, putative; PDBTitle: prolyl tripeptidyl aminopeptidase complexed with an inhibitor
118	c2zshA_	Alignment	not modelled	37.9	13	PDB header: hormone receptor Chain: A: PDB Molecule: probable gibberellin receptor gid111; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
119	c5hc4A_	Alignment	not modelled	37.2	7	PDB header: hydrolase Chain: A: PDB Molecule: lipolytic enzyme; PDBTitle: structure of esterase est22
120	c4wj1B_	Alignment	not modelled	36.8	8	PDB header: membrane protein Chain: B: PDB Molecule: inactive dipeptidyl peptidase 10; PDBTitle: structure of human dipeptidyl peptidase 10 (dppy): a modulator of2 neuronal kv4 channels