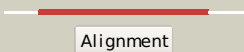

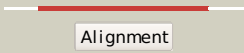







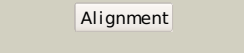

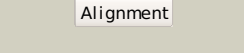

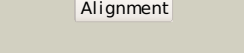



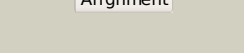

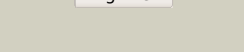



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c8fA_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with2 partially disordered adomet
2	c2yx0A_	 Alignment		99.7	16	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
3	d1tv8a_	 Alignment		99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
4	c3rfaA_	 Alignment		99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
5	c2z2uA_	 Alignment		99.5	18	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
6	c3canA_	 Alignment		99.3	12	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating2 enzyme from bacteroides vulgatus atcc 8482
7	c2a5hC_	 Alignment		99.0	13	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
8	c3t7vA_	 Alignment		98.3	14	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
9	d1olta_	 Alignment		98.2	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
10	d1r30a_	 Alignment		98.2	14	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
11	c1r30A_	 Alignment		98.2	14	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme

12	c3cixA_		Alignment		98.2	15	PDB header: adomet binding protein Chain: A: PDB Molecule: fe-hydrogenase maturase; PDBTitle: x-ray structure of the [fe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
13	c2qgqF_		Alignment		89.8	10	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima.2 northeast structural genomics consortium target vr77
14	c3k8kB_		Alignment		79.7	15	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
15	c2wcsA_		Alignment		77.8	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
16	d1m53a2		Alignment		76.6	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
17	c2qpuB_		Alignment		76.3	13	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
18	d1uoka2		Alignment		74.6	25	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
19	d1gvia3		Alignment		74.5	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
20	d1lwba2		Alignment		74.5	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
21	c1lwba_		Alignment	not modelled	73.3	22	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
22	d1ea9c3		Alignment	not modelled	72.8	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
23	d1ob0a2		Alignment	not modelled	72.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
24	c1ehaA_		Alignment	not modelled	72.0	18	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
25	c3a47A_		Alignment	not modelled	71.9	13	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
26	c2dh3A_		Alignment	not modelled	71.2	15	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
27	d2aaaa2		Alignment	not modelled	70.8	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
28	d1h3ga3		Alignment	not modelled	69.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
29	c1ehaA_		Alignment	not modelled	68.4	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase;

29	c1qnvA	Alignment	not modelled	68.4	14	PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
30	c1gviA	Alignment	not modelled	67.5	22	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
31	d1ua7a2	Alignment	not modelled	67.0	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
32	c1jibA	Alignment	not modelled	66.9	18	PDB header: hydrolase Chain: A: PDB Molecule: neopullulanase; PDBTitle: complex of alpha-amylase ii (tva ii) from thermoactinomyces2 vulgaris r-47 with maltotetraose based on a crystal soaked3 with maltohexaose.
33	d2bhua3	Alignment	not modelled	66.4	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
34	d2guya2	Alignment	not modelled	66.2	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
35	d1wzla3	Alignment	not modelled	66.1	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
36	c1bagA	Alignment	not modelled	66.1	16	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
37	c1m53A	Alignment	not modelled	65.4	25	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
38	d1eh9a3	Alignment	not modelled	64.4	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
39	c2ya0A	Alignment	not modelled	64.1	27	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
40	d1j0ha3	Alignment	not modelled	63.8	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
41	d1ht6a2	Alignment	not modelled	63.7	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
42	c3pzqA	Alignment	not modelled	63.6	13	PDB header: hydrolase Chain: A: PDB Molecule: mannan endo-1,4-beta-mannosidase. glycosyl hydrolase family PDBTitle: structure of the hyperthermostable endo-1,4-beta-d-mannanase from2 thermotoga petrophila rku-1 with maltose and glycerol
43	d1avaa2	Alignment	not modelled	62.1	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
44	c1ea9D	Alignment	not modelled	61.9	16	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltoextrinase; PDBTitle: cyclomaltoextrinase
45	c2aaaA	Alignment	not modelled	61.8	18	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: calcium binding in alpha-amylases: an x-ray diffraction2 study at 2.1 angstroms resolution of two enzymes from3 aspergillus
46	c2by0A	Alignment	not modelled	61.3	12	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
47	d1qhoa4	Alignment	not modelled	60.8	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
48	c3edeB	Alignment	not modelled	60.3	14	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltoextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
49	c2ze0A	Alignment	not modelled	59.8	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
50	c2z1kA	Alignment	not modelled	58.7	25	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
51	d1g5aa2	Alignment	not modelled	58.6	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
52	c3uccA	Alignment	not modelled	57.5	16	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of amylsucrase from deinococcus geothermalis
53	c3m07A	Alignment	not modelled	57.4	18	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha2 amylase from salmonella typhi murium.
54	c1jdaA	Alignment	not modelled	57.3	19	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
55	c3czkA	Alignment	not modelled	55.2	18	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh)

						e322q-2 sucrose complex
56	c3dhuC_	Alignment	not modelled	55.1	12	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
57	c2zidA_	Alignment	not modelled	53.3	17	PDB header: hydrolase Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
58	c1uokA_	Alignment	not modelled	52.5	25	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
59	d1mxga2	Alignment	not modelled	51.3	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
60	d2gipa2	Alignment	not modelled	51.1	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	d1e43a2	Alignment	not modelled	50.6	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
62	c1cygA_	Alignment	not modelled	50.4	20	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
63	c1jgiA_	Alignment	not modelled	50.1	18	PDB header: transferase Chain: A: PDB Molecule: amylsucrase; PDBTitle: crystal structure of the active site mutant glu328gln of2 amylsucrase from neisseria polysaccharea in complex with3 the natural substrate sucrose
64	c1jd7A_	Alignment	not modelled	49.7	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure analysis of the mutant k300r of2 pseudoalteromonas haloplanctis alpha-amylase
65	c3l55B_	Alignment	not modelled	49.7	7	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: b-1,4-endoglucanase/cellulase; PDBTitle: crystal structure of a putative beta-1,4-endoglucanase /2 cellulase from prevotella bryantii
66	c3bmwA_	Alignment	not modelled	49.6	16	PDB header: transferase Chain: A: PDB Molecule: cyclomalto-dextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
67	c2jvmA_	Alignment	not modelled	49.4	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of rhodobacter sphaeroides protein2 rhos4_26430. northeast structural genomics consortium3 target rhr95
68	d1bf2a3	Alignment	not modelled	49.0	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
69	d1pama4	Alignment	not modelled	48.9	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	c1bf2A_	Alignment	not modelled	47.4	8	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
71	c1zjaB_	Alignment	not modelled	47.4	22	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
72	d3bmva4	Alignment	not modelled	47.2	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
73	c2pr7A_	Alignment	not modelled	46.8	21	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
74	d1gcya2	Alignment	not modelled	46.5	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
75	c1bplA_	Alignment	not modelled	46.5	13	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
76	c1m7xC_	Alignment	not modelled	46.4	19	PDB header: transferase Chain: C: PDB Molecule: 1,4-alpha-glucan branching enzyme; PDBTitle: the x-ray crystallographic structure of branching enzyme
77	d1h4pa_	Alignment	not modelled	45.3	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
78	c3icgD_	Alignment	not modelled	43.7	7	PDB header: hydrolase Chain: D: PDB Molecule: endoglucanase d; PDBTitle: crystal structure of the catalytic and carbohydrate binding domain of2 endoglucanase d from clostridium cellulovorans
79	d1m7xa3	Alignment	not modelled	41.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
80	d1cxl4	Alignment	not modelled	40.5	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain

81	d1ud2a2	Alignment	not modelled	39.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
82	c2ya1A	Alignment	not modelled	39.5	27	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
83	c1gcyA	Alignment	not modelled	39.4	23	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
84	d1cgt4	Alignment	not modelled	39.2	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	c2zunB	Alignment	not modelled	38.7	15	PDB header: hydrolase Chain: B: PDB Molecule: 458aa long hypothetical endo-1,4-beta-glucanase; PDBTitle: functional analysis of hyperthermophilic endocellulase from2 the archaeon pyrococcus horikoshii
86	c1hvxA	Alignment	not modelled	37.7	14	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: bacillus stearothermophilus alpha-amylase
87	c1ud8A	Alignment	not modelled	37.4	17	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion
88	c3amlA	Alignment	not modelled	37.2	21	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
89	d1edga	Alignment	not modelled	36.8	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
90	d1gja2	Alignment	not modelled	35.5	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
91	c3blpX	Alignment	not modelled	35.2	17	PDB header: hydrolase Chain: X: PDB Molecule: alpha-amylase 1; PDBTitle: role of aromatic residues in human salivary alpha-amylase
92	d1cyga4	Alignment	not modelled	34.3	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	c1tcmB	Alignment	not modelled	33.8	18	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
94	c3faxA	Alignment	not modelled	33.8	24	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose
95	c2taaA	Alignment	not modelled	33.6	18	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
96	c3aysA	Alignment	not modelled	33.3	13	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: gh5 endoglucanase from a ruminal fungus in complex with cellotriose
97	c1wpcA	Alignment	not modelled	33.2	8	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltohexaosidase; PDBTitle: crystal structure of maltohexaose-producing amylase complexed with2 pseudo-maltononaose
98	d1hvx2	Alignment	not modelled	32.0	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
99	d1eeja1	Alignment	not modelled	31.5	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
100	d1jila3	Alignment	not modelled	31.5	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
101	c2wskA	Alignment	not modelled	29.5	18	PDB header: hydrolase Chain: A: PDB Molecule: glycogen debranching enzyme; PDBTitle: crystal structure of glycogen debranching enzyme glgx from2 escherichia coli k-12
102	d1ecea	Alignment	not modelled	29.3	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
103	c1e40A	Alignment	not modelled	29.0	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: tris/maltotriose complex of chimaeric amylase from b.2 amyloliquefaciens and b. licheniformis at 2.2a
104	c3civA	Alignment	not modelled	28.6	14	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-1,4-mannanase; PDBTitle: crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius
105	d2pb1a1	Alignment	not modelled	28.0	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
106	d2d3na2	Alignment	not modelled	26.9	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
107	c2H5A	Alignment	not modelled	26.7	57	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yutd;

107	c2N3A_	Alignment	not modelled	26.7	37	PDBTitle: solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
108	d1wzaa2	Alignment	not modelled	26.6	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
109	c2vncB_	Alignment	not modelled	25.3	14	PDB header: hydrolase Chain: B: PDB Molecule: glycogen operon protein glgx; PDBTitle: crystal structure of glycogen debranching enzyme trex from2 sulfolobus solfataricus
110	c3zt5D_	Alignment	not modelled	25.1	17	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
111	c2l7xA_	Alignment	not modelled	24.8	30	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: crimean congo hemorrhagic fever gn zinc finger
112	d1adta3	Alignment	not modelled	24.1	31	Fold: Zn-binding domains of ADDBP Superfamily: Zn-binding domains of ADDBP Family: Zn-binding domains of ADDBP
113	c3ib6B_	Alignment	not modelled	24.1	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from listeria2 monocytogenes serotype 4b
114	c1jaeA_	Alignment	not modelled	23.8	13	PDB header: glycosidase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: structure of tenebrio molitor larval alpha-amylase
115	c3qr3B_	Alignment	not modelled	23.5	12	PDB header: hydrolase Chain: B: PDB Molecule: endoglucanase eg-ii; PDBTitle: crystal structure of cel 5a (eg2) from hypocrea jecorina (trichoderma2 reesei)
116	c3amkA_	Alignment	not modelled	22.7	21	PDB header: transferase Chain: A: PDB Molecule: os06g0726400 protein; PDBTitle: structure of the starch branching enzyme i (bei) from oryza sativa l
117	c3k1dA_	Alignment	not modelled	22.7	20	PDB header: transferase Chain: A: PDB Molecule: 1,4-alpha-glucan-branching enzyme; PDBTitle: crystal structure of glycogen branching enzyme synonym: 1,4-alpha-d-2 glucan:1,4-alpha-d-glucan 6-glucosyl-transferase from mycobacterium3 tuberculosis h37rv
118	c3p04A_	Alignment	not modelled	22.3	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8
119	d1g94a2	Alignment	not modelled	21.8	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
120	c3kc2A_	Alignment	not modelled	21.7	25	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae