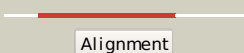
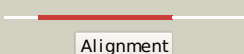
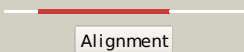
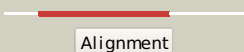
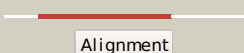
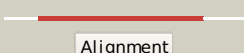
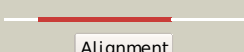
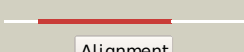
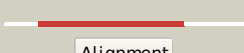
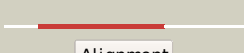
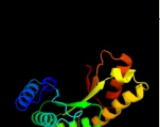
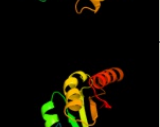


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tv8a_	 Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
2	c2yx0A_	 Alignment		99.9	16	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
3	c3c8fA_	 Alignment		99.8	12	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
4	c1r30A_	 Alignment		99.8	17	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-2 adenosylmethionine-dependent radical enzyme
5	d1r30a_	 Alignment		99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
6	c3t7vA_	 Alignment		99.8	14	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
7	c2a5hC_	 Alignment		99.8	18	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	c3cixA_	 Alignment		99.7	14	PDB header: adomet binding protein Chain: A: PDB Molecule: fe-fe-hydrogenase maturase; PDBTitle: x-ray structure of the [fe-fe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
9	c3rfaA_	 Alignment		99.7	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
10	c2z2uA_	 Alignment		99.5	15	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaean tyw1
11	d1olta_	 Alignment		99.5	13	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN

12	c3canA_	Alignment		99.5	17	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
13	c2qgqF_	Alignment		99.1	9	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	c3ivuB_	Alignment		97.4	12	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
15	c3eegB_	Alignment		95.6	14	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
16	c3ewbX_	Alignment		95.0	9	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-2 isopropylmalate synthase from listeria monocytogenes
17	c2ftpA_	Alignment		92.7	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
18	c1nvmG_	Alignment		91.6	15	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
19	c2cw6B_	Alignment		90.9	9	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric aciduria
20	c3bleA_	Alignment		90.0	13	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in2 complexed with malonate
21	d1nvma2	Alignment	not modelled	89.8	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
22	c1ydnA_	Alignment	not modelled	89.5	10	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
23	c1ydoC_	Alignment	not modelled	87.8	12	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the bacillus subtilis hmg-coa lyase, northeast2 structural genomics target sr181.
24	c1sr9A_	Alignment	not modelled	82.2	10	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
25	c2nx9B_	Alignment	not modelled	82.1	12	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
26	d1qt1a_	Alignment	not modelled	81.1	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
27	c3khdC_	Alignment	not modelled	79.4	11	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
28	c2wcsA_	Alignment	not modelled	75.4	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha amylase, catalytic region; PDBTitle: crystal structure of debranching enzyme from nostoc2 punctiforme (npde)
						Fold: TIM beta/alpha-barrel

29	d1qhoa4	Alignment	not modelled	74.1	15	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
30	c2zyfA	Alignment	not modelled	70.8	12	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermophilus2 complexed with magnesuim ion and alpha-ketoglutarate
31	d2aaaa2	Alignment	not modelled	70.7	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
32	d1muwa	Alignment	not modelled	68.9	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
33	d3bmva4	Alignment	not modelled	68.5	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
34	c1lwhA	Alignment	not modelled	67.6	17	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
35	d1pama4	Alignment	not modelled	66.7	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
36	c1m53A	Alignment	not modelled	66.5	13	PDB header: isomerase Chain: A: PDB Molecule: isomaltulose synthase; PDBTitle: crystal structure of isomaltulose synthase (pali) from2 klebsiella sp. lx3
37	c3hpxB	Alignment	not modelled	65.3	13	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of mycobacterium tuberculosis leua active site2 domain 1-425 (truncation mutant delta:426-644)
38	c3a47A	Alignment	not modelled	64.6	9	PDB header: hydrolase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of isomaltase from saccharomyces cerevisiae
39	d1cgt4	Alignment	not modelled	64.0	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
40	d1bf2a3	Alignment	not modelled	64.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
41	d1h3ga3	Alignment	not modelled	63.7	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
42	d1gjwa2	Alignment	not modelled	63.0	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
43	d1uoka2	Alignment	not modelled	61.5	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
44	d1csla4	Alignment	not modelled	58.4	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
45	c1ea9D	Alignment	not modelled	58.0	13	PDB header: hydrolase Chain: D: PDB Molecule: cyclomaltoextrinase; PDBTitle: cyclomaltoextrinase
46	d1m53a2	Alignment	not modelled	57.5	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
47	c2aaaA	Alignment	not modelled	56.5	10	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
48	d1gvia3	Alignment	not modelled	56.1	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
49	c1uoka	Alignment	not modelled	55.7	16	PDB header: glucosidase Chain: A: PDB Molecule: oligo-1,6-glucosidase; PDBTitle: crystal structure of b. cereus oligo-1,6-glucosidase
50	d2guya2	Alignment	not modelled	54.6	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
51	d1e43a2	Alignment	not modelled	53.6	11	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
52	c1qhoA	Alignment	not modelled	52.3	17	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: five-domain alpha-amylase from bacillus stearothermophilus,2 maltose/acarbose complex
53	d1g5aa2	Alignment	not modelled	52.2	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
54	d1lwha2	Alignment	not modelled	50.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
55	c2ze0A	Alignment	not modelled	50.0	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: alpha-glucosidase gsj
						PDB header: hydrolase

56	c2zidA	Alignment	not modelled	49.7	16	Chain: A: PDB Molecule: dextran glucosidase; PDBTitle: crystal structure of dextran glucosidase e236q complex with2 isomaltotriose
57	c3edeB	Alignment	not modelled	49.7	14	PDB header: hydrolase Chain: B: PDB Molecule: cyclomaltodextrinase; PDBTitle: structural base for cyclodextrin hydrolysis
58	c1bf2A	Alignment	not modelled	48.9	10	PDB header: hydrolase Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of pseudomonas isoamylase
59	c2ya0A	Alignment	not modelled	48.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading2 pneumococcal virulence factor spua
60	d1ob0a2	Alignment	not modelled	48.6	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
61	c3dxiB	Alignment	not modelled	48.6	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bv_u_2661) from bacteroides vulgatus
62	c1gjuA	Alignment	not modelled	48.4	16	PDB header: transferase Chain: A: PDB Molecule: maltodextrin glycosyltransferase; PDBTitle: maltosyltransferase from thermotoga maritima
63	c2qpuB	Alignment	not modelled	47.9	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amylase type a isozyme; PDBTitle: sugar tongs mutant s378p in complex with acarbose
64	d1ea9c3	Alignment	not modelled	47.8	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
65	c1jibA	Alignment	not modelled	46.8	16	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.
66	c2z1kA	Alignment	not modelled	46.4	19	PDB header: hydrolase Chain: A: PDB Molecule: (neo)pullulanase; PDBTitle: crystal structure of ttha1563 from thermus thermophilus hb8
67	d1yhta1	Alignment	not modelled	45.8	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
68	c2zq0B	Alignment	not modelled	45.7	17	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase sub); PDBTitle: crystal structure of subB complexed with acarbose
69	d2gjp a2	Alignment	not modelled	44.5	13	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
70	c2jvfA	Alignment	not modelled	44.1	12	PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein
71	c3czkA	Alignment	not modelled	43.4	16	PDB header: hydrolase Chain: A: PDB Molecule: sucrose hydrolase; PDBTitle: crystal structure analysis of sucrose hydrolase(suh) e322q-2 sucrose complex
72	d1u7pa	Alignment	not modelled	42.9	8	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
73	c1zjaB	Alignment	not modelled	42.8	14	PDB header: isomerase Chain: B: PDB Molecule: trehalulose synthase; PDBTitle: crystal structure of the trehalulose synthase mutb from2 pseudomonas mesoacidophila mx-45 (triclinic form)
74	c1qysA	Alignment	not modelled	42.3	9	PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold
75	d1ua7a2	Alignment	not modelled	42.1	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
76	c3dhuC	Alignment	not modelled	41.9	16	PDB header: hydrolase Chain: C: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of an alpha-amylase from lactobacillus2 plantarum
77	c1ehaA	Alignment	not modelled	41.5	10	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase2 from sulfolobus solfataricus
78	c1gviA	Alignment	not modelled	40.9	15	PDB header: hydrolase Chain: A: PDB Molecule: maltogenic amylase; PDBTitle: thermus maltogenic amylase in complex with beta-cd
79	d1j0ha3	Alignment	not modelled	40.8	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
80	c2taaA	Alignment	not modelled	39.2	11	PDB header: hydrolase (o-glycosyl) Chain: A: PDB Molecule: taka-amylase a; PDBTitle: structure and possible catalytic residues of taka-amylase a
81	d1cyga4	Alignment	not modelled	39.2	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
82	c2dh3A	Alignment	not modelled	38.1	11	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc

83	c3k8kB_	Alignment	not modelled	38.1	19	PDB header: membrane protein Chain: B: PDB Molecule: alpha-amylase, susg; PDBTitle: crystal structure of susg
84	d1ud2a2	Alignment	not modelled	37.4	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
85	c1bagA_	Alignment	not modelled	36.7	17	PDB header: alpha-amylase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: alpha-amylase from bacillus subtilis complexed with2 maltopentaose
86	c1jgiA_	Alignment	not modelled	36.0	12	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
87	c1cygA_	Alignment	not modelled	35.9	10	PDB header: glycosyltransferase Chain: A: PDB Molecule: cyclodextrin glucanotransferase; PDBTitle: cyclodextrin glucanotransferase (e.c.2.4.1.19) (cgtase)
88	c3gh7A_	Alignment	not modelled	35.7	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus2 sp. ts12 in complex with galnac
89	d1jaka1	Alignment	not modelled	34.8	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
90	d1mzha_	Alignment	not modelled	34.6	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	d1z6ma1	Alignment	not modelled	33.8	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbA-like
92	c2yl8A_	Alignment	not modelled	33.7	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: inhibition of the pneumococcal virulence factor strh and2 molecular insights into n-glycan recognition and3 hydrolysis
93	d1ht6a2	Alignment	not modelled	33.7	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
94	c3os4A_	Alignment	not modelled	32.8	12	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
95	c3na8A_	Alignment	not modelled	32.1	17	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
96	c2rfgB_	Alignment	not modelled	31.8	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
97	d1pkla2	Alignment	not modelled	31.7	9	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
98	c3bmwA_	Alignment	not modelled	31.5	13	PDB header: transferase Chain: A: PDB Molecule: cyclomaltoextrin glucanotransferase; PDBTitle: cyclodextrin glycosyl transferase from thermoanaerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
99	c3zt5D_	Alignment	not modelled	31.4	18	PDB header: hydrolase Chain: D: PDB Molecule: putative glucanohydrolase pep1a; PDBTitle: glge isoform 1 from streptomyces coelicolor with maltose2 bound
100	d1yx1a1	Alignment	not modelled	30.2	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
101	c3ngjC_	Alignment	not modelled	30.0	10	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
102	c2ya1A_	Alignment	not modelled	29.7	14	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: product complex of a multi-modular glycogen-degrading2 pneumococcal virulence factor spua
103	d1o0ya_	Alignment	not modelled	29.5	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
104	d1mxga2	Alignment	not modelled	28.5	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
105	d1avaa2	Alignment	not modelled	27.7	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
106	c1bplA_	Alignment	not modelled	27.3	13	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucan-4-glucanohydrolase; PDBTitle: glycosyltransferase
107	d1wzla3	Alignment	not modelled	27.3	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
108	c3faxA_	Alignment	not modelled	27.0	14	PDB header: hydrolase Chain: A: PDB Molecule: reticulocyte binding protein; PDBTitle: the crystal structure of gbs pullulanase sap in complex with2 maltotetraose Fold: TIM beta/alpha-barrel

109	d1yira1	Alignment	not modelled	26.7	14	Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
110	c2kl5A	Alignment	not modelled	25.9	55	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yutd; PDBTitle: solution nmr structure of protein yutd from b.subtilis, northeast2 structural genomics consortium target sr232
111	d1d3ga	Alignment	not modelled	25.5	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	d1nowa1	Alignment	not modelled	25.0	18	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
113	d1mioa	Alignment	not modelled	24.8	8	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
114	c3n2xB	Alignment	not modelled	24.7	19	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
115	c2epoB	Alignment	not modelled	24.6	11	PDB header: hydrolase Chain: B: PDB Molecule: n-acetyl-beta-d-glucosaminidase; PDBTitle: n-acetyl-b-d-glucosaminidase (gcna) from streptococcus gordonii
116	c1e40A	Alignment	not modelled	24.3	11	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
117	d1pbya1	Alignment	not modelled	23.6	13	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
118	d2bhua3	Alignment	not modelled	23.5	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	c1tcmB	Alignment	not modelled	23.4	10	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
120	c1ud8A	Alignment	not modelled	22.8	13	PDB header: hydrolase Chain: A: PDB Molecule: amylase; PDBTitle: crystal structure of amyk38 with lithium ion