
















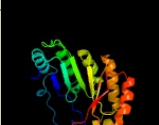


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2388c_(hemN)_2682025_2683152
Date	Mon Aug 5 13:25:54 BST 2019
Unique Job ID	820fd6c1e72e4ff5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1olta_	 Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
2	c5l7jA_	 Alignment		100.0	18	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
3	c6iazA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
4	c6qk7C_	 Alignment		100.0	17	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
5	c4jc0B_	 Alignment		100.0	14	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
6	c6fd2B_	 Alignment		100.0	17	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative apramycin biosynthetic oxidoreductase 4; PDBTitle: radical sam 1,2-diol dehydratase aprd4 in complex with its substrate2 paromamine
7	c3cixA_	 Alignment		100.0	17	PDB header: adomet binding protein Chain: A: PDB Molecule: fefe-hydrogenase maturase; PDBTitle: x-ray structure of the [fefe]-hydrogenase maturase hyde from2 thermotoga maritima in complex with thiocyanate
8	c2qqaF_	 Alignment		99.9	13	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: protein tm_1862; PDBTitle: crystal structure of tm_1862 from thermotoga maritima. northeast2 structural genomics consortium target vr77
9	c3t7vA_	 Alignment		99.9	15	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
10	d1r30a_	 Alignment		99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
11	c1r30A_	 Alignment		99.9	14	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme

12	c5u14A	Alignment		99.9	12	PDB header: metal binding protein Chain: A: PDB Molecule: oxsb protein; PDBTitle: structure of cobalamin-dependent s-adenosylmethionine radical enzyme2 oxsb with aqua-cobalamin and s-adenosylmethionine bound
13	c5exkG	Alignment		99.9	19	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
14	c4wxcC	Alignment		99.9	15	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
15	c4u0pB	Alignment		99.9	13	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
16	c4rtbA	Alignment		99.9	15	PDB header: lyase Chain: A: PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
17	c4r33A	Alignment		99.7	15	PDB header: lyase Chain: A: PDB Molecule: nosl; PDBTitle: x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
18	c5v1tA	Alignment		99.7	17	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
19	d1tv8a	Alignment		99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
20	c3rfaB	Alignment		99.6	11	PDB header: oxidoreductase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase n; PDBTitle: x-ray structure of rlmn from escherichia coli in complex with s-2 adenosylmethionine
21	c3rfaA	Alignment	not modelled	99.6	10	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
22	c6fz6B	Alignment	not modelled	99.6	13	PDB header: transferase Chain: B: PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
23	c4k39A	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
24	c6efnA	Alignment	not modelled	99.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
25	c6b4cH	Alignment	not modelled	99.5	14	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
26	c5vslB	Alignment	not modelled	99.5	15	PDB header: antiviral protein Chain: B: PDB Molecule: radical s-adenosyl methionine domain-containing protein 2; PDBTitle: crystal structure of viperin with bound [4fe-4s] cluster and s-2 adenosylhomocysteine (sah)
27	c3c8fA	Alignment	not modelled	99.5	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate formate-lyase 1-activating enzyme; PDBTitle: 4fe-4s-pyruvate formate-lyase activating enzyme with partially2 disordered adomet
28	c4fheA	Alignment	not modelled	99.4	12	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase;

						PDBTitle: spore photoproduct lyase c140a mutant
29	c2yx0A_	Alignment	not modelled	99.4	12	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
30	c2a5hC_	Alignment	not modelled	99.3	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).
31	c5wggA_	Alignment	not modelled	99.3	14	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis2 of sactipeptides
32	c5th5C_	Alignment	not modelled	98.9	15	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from bacillus subtilis with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
33	c4m7tA_	Alignment	not modelled	98.7	17	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
34	c6c8vA_	Alignment	not modelled	98.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
35	c3canA_	Alignment	not modelled	98.4	15	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
36	c2z2uA_	Alignment	not modelled	98.1	13	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
37	c6nhlB_	Alignment	not modelled	97.8	16	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
38	c4njka_	Alignment	not modelled	97.2	16	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from burkholderia multivorans in complex2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
39	c6e1jB_	Alignment	not modelled	96.7	15	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
40	d1qwga_	Alignment	not modelled	96.4	19	Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
41	c2cw6B_	Alignment	not modelled	95.7	13	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
42	c2ftpA_	Alignment	not modelled	95.2	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
43	c3ivuB_	Alignment	not modelled	95.0	14	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
44	c1nvmG_	Alignment	not modelled	94.5	18	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
45	c3rmjB_	Alignment	not modelled	94.3	13	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
46	c3bleA_	Alignment	not modelled	94.2	12	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
47	c1ydnA_	Alignment	not modelled	93.9	12	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.
48	d1h4pa_	Alignment	not modelled	93.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
49	c1ydoC_	Alignment	not modelled	93.8	11	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.
50	c5ey5A_	Alignment	not modelled	93.5	16	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
51	c5zc2B_	Alignment	not modelled	93.2	22	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
52	d1r7ja_	Alignment	not modelled	92.9	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Archaeal DNA-binding protein

53	c3cyvA	Alignment	not modelled	92.3	11	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from2 shigella flexineri: new insights into its catalytic3 mechanism
54	c2x4hA	Alignment	not modelled	92.2	12	PDB header: transcription Chain: A: PDB Molecule: hypothetical protein sso2273; PDBTitle: crystal structure of the hypothetical protein sso2273 from2 sulfolobus solfataricus
55	c4jn6C	Alignment	not modelled	91.6	19	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
56	d2v7fa1	Alignment	not modelled	91.3	25	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Rps19E-like
57	d1nvma2	Alignment	not modelled	90.8	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
58	c3dx5A	Alignment	not modelled	90.6	5	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
59	c3navB	Alignment	not modelled	90.6	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
60	c3eegB	Alignment	not modelled	90.6	16	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
61	c3vndD	Alignment	not modelled	90.4	15	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
62	d1qopa	Alignment	not modelled	90.4	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
63	c5cviB	Alignment	not modelled	90.3	14	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
64	c6hvgA	Alignment	not modelled	90.2	25	PDB header: transferase Chain: A: PDB Molecule: alternansucrase; PDBTitle: crystal structure of truncated alternansucrase from leuconostoc2 mesenteroides nrri b-1355
65	c3j38T	Alignment	not modelled	90.1	22	PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein s19a; PDBTitle: structure of the d. melanogaster 40s ribosomal proteins
66	c4eacC	Alignment	not modelled	90.1	17	PDB header: lyase Chain: C: PDB Molecule: mannonate dehydratase; PDBTitle: crystal structure of mannonate dehydratase from escherichia coli2 strain k12
67	c6irtA	Alignment	not modelled	90.0	21	PDB header: membrane protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: human lat1-4f2hc complex bound with bch
68	c3j3aT	Alignment	not modelled	89.8	22	PDB header: ribosome Chain: T: PDB Molecule: 40s ribosomal protein s19; PDBTitle: structure of the human 40s ribosomal proteins
69	c3ewbX	Alignment	not modelled	89.8	10	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
70	c3zeyO	Alignment	not modelled	89.6	29	PDB header: ribosome Chain: O: PDB Molecule: ribosomal protein s19, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
71	c5xxuT	Alignment	not modelled	89.5	24	PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein es19; PDBTitle: small subunit of toxoplasma gondii ribosome
72	c3iz6S	Alignment	not modelled	89.5	27	PDB header: ribosome Chain: S: PDB Molecule: 40s ribosomal protein s19 (s19e); PDBTitle: localization of the small subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
73	d1i60a	Alignment	not modelled	89.5	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
74	c1g3wA	Alignment	not modelled	89.4	22	PDB header: gene regulation Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: cd-cys102ser dtxr
75	c5xyiT	Alignment	not modelled	89.2	21	PDB header: ribosome Chain: T: PDB Molecule: ribosomal protein s19e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
76	c1gcyA	Alignment	not modelled	89.2	18	PDB header: hydrolase Chain: A: PDB Molecule: glucan 1,4-alpha-maltotetrahydrolase; PDBTitle: high resolution crystal structure of maltotetraose-forming2 exo-amylase
77	c2zyfA	Alignment	not modelled	89.0	16	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
78	c2dh3A	Alignment	not modelled	89.0	24	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
						Fold: TIM beta/alpha-barrel

79	d1gcya2	Alignment	not modelled	89.0	19	Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
80	c2infB	Alignment	not modelled	88.9	7	PDB header: lyase Chain: B: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from bacillus2 subtilis
81	c5lfcA	Alignment	not modelled	88.6	22	PDB header: transferase Chain: A: PDB Molecule: dsrv; PDBTitle: crystal structure of leuconostoc citreum nrrl b-1299 n-terminally2 truncated dextransucrase dsr-m
82	c2xznT	Alignment	not modelled	88.6	17	PDB header: ribosome Chain: T: PDB Molecule: rps19e; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
83	c2it0A	Alignment	not modelled	88.5	26	PDB header: transcription/dna Chain: A: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of a two-domain ider-dna complex crystal2 form ii
84	c3lmzA	Alignment	not modelled	88.4	15	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distazonis atcc 8503 at 1.44 a resolution
85	c4exqA	Alignment	not modelled	88.4	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
86	d1j93a	Alignment	not modelled	88.4	13	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
87	c3w0kA	Alignment	not modelled	88.4	14	PDB header: hydrolase Chain: A: PDB Molecule: bifunctional endomannanase/endoglucanase; PDBTitle: crystal structure of a glycoside hydrolase
88	c5kzmA	Alignment	not modelled	88.0	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
89	c2qw5B	Alignment	not modelled	87.8	16	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
90	c3wy3A	Alignment	not modelled	87.8	19	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase mutant d202n in complex with2 glucose and glycerol
91	c4o6jA	Alignment	not modelled	87.8	16	PDB header: metal binding protein Chain: A: PDB Molecule: iron-dependent transcription repressor related protein; PDBTitle: crystal structure of t. acidophilum ider
92	d2q02a1	Alignment	not modelled	87.3	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: lolI-like
93	c5cg0B	Alignment	not modelled	87.2	12	PDB header: hydrolase Chain: B: PDB Molecule: beta-glucosidase; PDBTitle: crystal structure of spodoptera frugiperda beta-glycosidase
94	c1f5tA	Alignment	not modelled	87.2	23	PDB header: transcription/dna Chain: A: PDB Molecule: diphtheria toxin repressor; PDBTitle: diphtheria tox repressor (c102d mutant) complexed with2 nickel and dtxr consensus binding sequence
95	c1fx7C	Alignment	not modelled	87.0	29	PDB header: signaling protein Chain: C: PDB Molecule: iron-dependent repressor ider; PDBTitle: crystal structure of the iron-dependent regulator (ider) from2 mycobacterium tuberculosis
96	d2fxaa1	Alignment	not modelled	86.6	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
97	c2bdqA	Alignment	not modelled	86.5	14	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
98	c4ay8B	Alignment	not modelled	86.5	11	PDB header: transferase Chain: B: PDB Molecule: methylcobalamin): coenzyme m methyltransferase; PDBTitle: semet-derivative of a methyltransferase from m. mazei
99	c2zoxA	Alignment	not modelled	86.5	11	PDB header: hydrolase Chain: A: PDB Molecule: cytosolic beta-glucosidase; PDBTitle: crystal structure of the covalent intermediate of human cytosolic2 beta-glucosidase
100	c6az1X	Alignment	not modelled	86.4	24	PDB header: ribosome/antibiotic Chain: X: PDB Molecule: ribosomal protein s19e; PDBTitle: cryo-em structure of the small subunit of leishmania ribosome bound to2 paromomycin
101	d1avaa2	Alignment	not modelled	86.3	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
102	c1e40A	Alignment	not modelled	86.3	10	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
103	c2nx9B	Alignment	not modelled	86.2	16	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

104	d1a3xa2	Alignment	not modelled	86.1	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
105	d1vffa1	Alignment	not modelled	86.1	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Family 1 of glycosyl hydrolase
106	d2pb1a1	Alignment	not modelled	85.8	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
107	c3cqkB	Alignment	not modelled	85.5	15	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
108	c1tcmB	Alignment	not modelled	85.4	18	PDB header: glycosyltransferase Chain: B: PDB Molecule: cyclodextrin glycosyltransferase; PDBTitle: cyclodextrin glycosyltransferase w616a mutant from bacillus2 circulans strain 251
109	c2jepB	Alignment	not modelled	85.4	17	PDB header: hydrolase Chain: B: PDB Molecule: xyloglucanase; PDBTitle: native family 5 xyloglucanase from paenibacillus pabuli
110	c4yheB	Alignment	not modelled	85.2	12	PDB header: hydrolase Chain: B: PDB Molecule: gh5; PDBTitle: native bacteroidetes-affiliated gh5 cellulase linked with a2 polysaccharide utilization locus
111	d1vjza	Alignment	not modelled	85.0	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
112	c2ekcA	Alignment	not modelled	85.0	11	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
113	c5tnvA	Alignment	not modelled	84.8	18	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
114	d1ob0a2	Alignment	not modelled	84.8	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
115	d1hl2a	Alignment	not modelled	84.8	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
116	c1lwhA	Alignment	not modelled	84.7	24	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: crystal structure of t. maritima 4-alpha-glucanotransferase
117	c3g3zA	Alignment	not modelled	84.6	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, marr family; PDBTitle: the structure of nmb1585, a marr family regulator from neisseria2 meningitidis
118	d1j0ha3	Alignment	not modelled	84.5	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	c5x7uA	Alignment	not modelled	84.4	21	PDB header: hydrolase Chain: A: PDB Molecule: trehalose synthase; PDBTitle: trehalose synthase from thermobaculum terrenum
120	c5c54D	Alignment	not modelled	84.3	16	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminate lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum