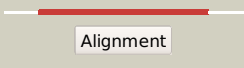

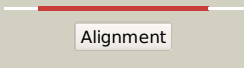

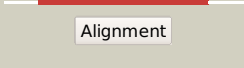

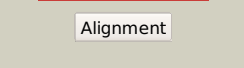

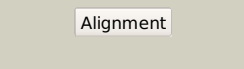
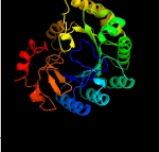
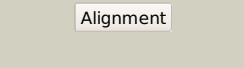
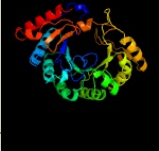
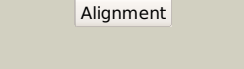

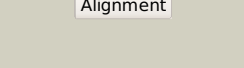
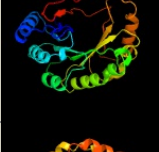
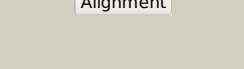

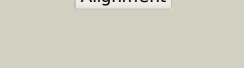
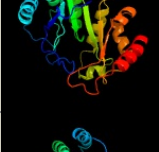
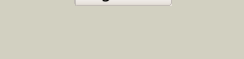


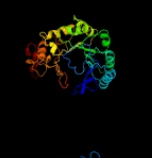
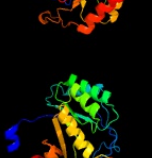


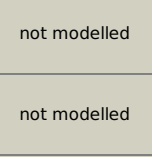


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0693_(pqqE)_792160_793335
Date	Fri Jul 26 01:50:26 BST 2019
Unique Job ID	463ee29e13e7e4fd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5v1tA_			100.0	18	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
2	c4k39A_			100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmecepe with bound adomet and cp18cys peptide
3	c6c8vA_			100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
4	c5wggA_			100.0	21	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
5	c6efnA_			100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
6	d1tv8a_			100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
7	c4m7tA_			100.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
8	c6b4cH_			100.0	15	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
9	c5vs1B_			100.0	16	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)
10	c2yx0A_			99.9	14	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
11	c3c8fA_			99.9	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

12	c5th5C_	Alignment		99.8	17	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
13	c2a5hC_	Alignment		99.7	20	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).
14	c2z2uA_	Alignment		99.7	19	PDB header: metal binding protein Chain: A; PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
15	c3canA_	Alignment		99.7	16	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
16	c4wxcC_	Alignment		99.7	17	PDB header: lyase Chain: C; PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydgc: a maturase of the [fefe]-hydrogenase
17	c6fz6B_	Alignment		99.7	16	PDB header: transferase Chain: B; PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
18	c3t7vA_	Alignment		99.6	13	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
19	c3rfaB_	Alignment		99.6	15	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
20	c4u0pB_	Alignment		99.6	13	PDB header: transferase Chain: B; PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
21	c5exkG_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
22	c1r30A_	Alignment	not modelled	99.6	15	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
23	d1r30a_	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
24	c3cixA_	Alignment	not modelled	99.6	11	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
25	c4njka_	Alignment	not modelled	99.6	21	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+
26	c3rfaA_	Alignment	not modelled	99.6	15	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
27	c4rtbA_	Alignment	not modelled	99.5	16	PDB header: lyase Chain: A; PDB Molecule: hydgc protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydgc from2 carboxydotherrmus hydrogenoformans
28	c6nhlB_	Alignment	not modelled	99.5	20	PDB header: lyase Chain: B; PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli

29	c4jc0B_	Alignment	not modelled	99.5	11	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
30	d1olta_	Alignment	not modelled	99.5	12	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
31	c6fd2B_	Alignment	not modelled	99.1	14	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
32	c4r33A_	Alignment	not modelled	99.1	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
33	c5l7jA_	Alignment	not modelled	98.8	12	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
34	c5ul4A_	Alignment	not modelled	98.7	16	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
35	c2qgqF_	Alignment	not modelled	98.7	9	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
36	c6qk7C_	Alignment	not modelled	98.4	12	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
37	c4fheA_	Alignment	not modelled	98.3	13	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
38	c6iazA_	Alignment	not modelled	96.9	13	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
39	c3ivuB_	Alignment	not modelled	96.4	15	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
40	c3rmjB_	Alignment	not modelled	95.1	13	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
41	c3ewbX_	Alignment	not modelled	94.7	16	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
42	c5hqca_	Alignment	not modelled	91.0	21	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 97 enzyme; PDBTitle: a glycoside hydrolase family 97 enzyme r171k variant from2 pseudoalteromonas sp. strain k8
43	c6e1jB_	Alignment	not modelled	90.8	12	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
44	c1ydoC_	Alignment	not modelled	90.3	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.
45	c3eegB_	Alignment	not modelled	89.8	14	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
46	c2ftpA_	Alignment	not modelled	88.1	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
47	c4uxdC_	Alignment	not modelled	85.9	14	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
48	c5xfmD_	Alignment	not modelled	83.9	15	PDB header: hydrolase Chain: D: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of beta-arabinopyranosidase
49	c2cw6B_	Alignment	not modelled	83.2	14	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
50	c2zq0B_	Alignment	not modelled	82.7	18	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase sub); PDBTitle: crystal structure of sub complexed with acarbose
51	c2i9wA_	Alignment	not modelled	81.7	17	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a sec-c motif containing protein (psyc_2064) from2 psychrobacter arcticus at 1.75 a resolution
52	c1nouA_	Alignment	not modelled	81.2	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
						Fold: TIM beta/alpha-barrel

53	d1yhta1	Alignment	not modelled	78.0	21	Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
54	c3lmyA	Alignment	not modelled	77.7	13	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
55	c1ozbl	Alignment	not modelled	77.6	11	PDB header: protein transport Chain: I: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
56	d1ozbi	Alignment	not modelled	77.6	11	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
57	c1ozbj	Alignment	not modelled	77.5	11	PDB header: protein transport Chain: J: PDB Molecule: preprotein translocase seca subunit; PDBTitle: crystal structure of secb complexed with seca c-terminus
58	c1sx0A	Alignment	not modelled	76.5	16	PDB header: protein transport Chain: A: PDB Molecule: seca; PDBTitle: solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
59	c1sx1A	Alignment	not modelled	76.3	16	PDB header: protein transport Chain: A: PDB Molecule: seca; PDBTitle: solution nmr structure and x-ray absorption analysis of the2 c-terminal zinc-binding domain of the seca atpase
60	c3rpmA	Alignment	not modelled	76.1	16	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetyl-hexosaminidase; PDBTitle: crystal structure of the first gh20 domain of a novel beta-n-acetyl-2 hexosaminidase strh from streptococcus pneumoniae r6
61	c5oarB	Alignment	not modelled	75.9	21	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
62	c1ydnA	Alignment	not modelled	73.2	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.
63	c4ov9A	Alignment	not modelled	70.9	12	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
64	c1qbaA	Alignment	not modelled	70.5	27	PDB header: glycosyl hydrolase Chain: A: PDB Molecule: chitobiase; PDBTitle: bacterial chitobiase, glycosyl hydrolase family 20
65	c1sr9A	Alignment	not modelled	70.4	10	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
66	c3dz1A	Alignment	not modelled	69.9	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
67	d1tm6a	Alignment	not modelled	68.6	12	Fold: Sec-C motif Superfamily: Sec-C motif Family: Sec-C motif
68	c1tm6A	Alignment	not modelled	68.6	12	PDB header: protein transport Chain: A: PDB Molecule: preprotein translocase seca subunit; PDBTitle: nmr structure of the free zinc binding c-terminal domain of2 seca
69	c6ezrA	Alignment	not modelled	67.7	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylglucosaminidase nag2; PDBTitle: crystal structure of gh20 exo beta-n-acetylglucosaminidase from vibrio2 harveyi
70	c3rcnA	Alignment	not modelled	67.4	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aurescens
71	d1nowa1	Alignment	not modelled	66.4	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
72	c3hf3A	Alignment	not modelled	64.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
73	c3e96B	Alignment	not modelled	63.8	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
74	c4ur7B	Alignment	not modelled	63.7	15	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
75	c2ylaA	Alignment	not modelled	63.6	17	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
76	c3fkkA	Alignment	not modelled	63.5	11	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
77	d1mioa	Alignment	not modelled	62.6	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
78	c1m04A	Alignment	not modelled	59.7	27	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcna)
79	c3iwpK	Alignment	not modelled	59.3	9	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein

						cutc
80	c2gxE	Alignment	not modelled	59.3	17	PDB header: hydrolase Chain: E: PDB Molecule: beta-hexosaminidase alpha chain; PDBTitle: crystallographic structure of human beta-hexosaminidase a
81	d1jaka1	Alignment	not modelled	58.0	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
82	c3ct7E	Alignment	not modelled	57.8	14	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
83	c3bleA	Alignment	not modelled	56.1	14	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
84	c4pysB	Alignment	not modelled	56.0	25	PDB header: hydrolase Chain: B: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: the crystal structure of beta-n-acetylhexosaminidase from bacteroides2 fragilis nctc 9343
85	c2d2rA	Alignment	not modelled	55.8	11	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
86	c3b4uB	Alignment	not modelled	54.2	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
87	c6je8A	Alignment	not modelled	53.8	23	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
88	c3n2xB	Alignment	not modelled	53.3	17	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
89	c4h04B	Alignment	not modelled	53.1	17	PDB header: hydrolase Chain: B: PDB Molecule: lacto-n-biosidase; PDBTitle: lacto-n-biosidase from bifidobacterium bifidum
90	c3d0cB	Alignment	not modelled	52.7	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
91	c3gh7A	Alignment	not modelled	51.8	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus sp. ts122 in complex with galnac
92	c1pjtB	Alignment	not modelled	50.8	11	PDB header: transferase/oxidoreductase/lyase Chain: B: PDB Molecule: siroheme synthase; PDBTitle: the structure of the ser128ala point-mutant variant of cysg, the2 multifunctional methyltransferase/dehydrogenase/ferrochelatae for3 siroheme synthesis
93	c3ndcB	Alignment	not modelled	49.9	14	PDB header: transferase Chain: B: PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
94	c3nsnA	Alignment	not modelled	49.7	15	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
95	d2gjxa1	Alignment	not modelled	49.3	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
96	c5hw4C	Alignment	not modelled	49.1	13	PDB header: transferase Chain: C: PDB Molecule: ribosomal rna small subunit methyltransferase i; PDBTitle: crystal structure of escherichia coli 16s rrna methyltransferase rsmi2 in complex with adomet
97	c4nu7C	Alignment	not modelled	48.9	7	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
98	c4i7vD	Alignment	not modelled	47.7	15	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhps with pyruvate
99	c1ps9A	Alignment	not modelled	47.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
100	c3hpxB	Alignment	not modelled	47.4	11	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)
101	c2r8wB	Alignment	not modelled	47.4	16	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
102	c5d88A	Alignment	not modelled	47.3	20	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
103	c3cprB	Alignment	not modelled	44.1	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
104	c2hmcA	Alignment	not modelled	43.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase;

104	c2im1A_	Alignment	not modelled	43.8	10	PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
105	d1yx1a1	Alignment	not modelled	43.2	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
106	c3na8A_	Alignment	not modelled	43.0	15	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
107	c4r9xB_	Alignment	not modelled	41.7	13	PDB header: metal transport Chain: B: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of putative copper homeostasis protein cutc from2 bacillus anthracis
108	c3a24A_	Alignment	not modelled	40.9	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
109	c2knpA_	Alignment	not modelled	40.5	50	PDB header: unknown function Chain: A: PDB Molecule: mcocc-1; PDBTitle: isolation and characterization of peptides from momordica2 cochinchinensis seeds.
110	d1vyra_	Alignment	not modelled	40.4	11	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
111	d1vhna_	Alignment	not modelled	40.3	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
112	c5zmyF_	Alignment	not modelled	40.2	10	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
113	d1twda_	Alignment	not modelled	39.9	10	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
114	c2h90A_	Alignment	not modelled	39.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
115	c3kc2A_	Alignment	not modelled	39.3	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
116	c5ud6B_	Alignment	not modelled	38.3	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhfps from cyanidioschyzon merolae with lysine2 bound
117	d1cbfa_	Alignment	not modelled	38.3	11	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase
118	c1cbfA_	Alignment	not modelled	38.3	11	PDB header: methyltransferase Chain: A: PDB Molecule: cobalt-precorrin-4 transmethylase; PDBTitle: the x-ray structure of a cobalamin biosynthetic enzyme, cobalt2 precorrin-4 methyltransferase, cbif
119	c3hh1D_	Alignment	not modelled	38.2	19	PDB header: transferase Chain: D: PDB Molecule: tetrapyrrole methylase family protein; PDBTitle: the structure of a tetrapyrrole methylase family protein domain from2 chlorobium tepidum t1s
120	d1m1na_	Alignment	not modelled	38.0	9	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein