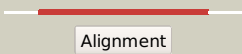

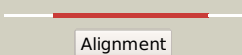

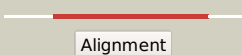

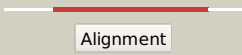

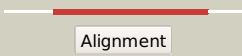

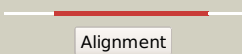

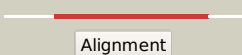

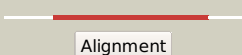

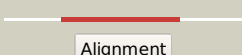

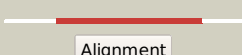







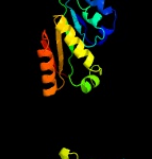
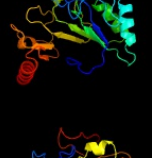
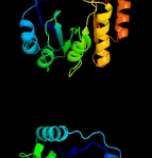

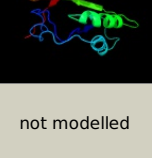


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1681_(moeX)_1905257_1906249
Date	Fri Aug 2 13:30:28 BST 2019
Unique Job ID	3bdc8b088f4ba888

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6efnA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
2	c5v1tA_	 Alignment		100.0	16	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
3	d1tv8a_	 Alignment		100.0	19	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
4	c5wggA_	 Alignment		100.0	19	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	c4k39A_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
6	c6b4cH_	 Alignment		100.0	20	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
7	c5vslB_	 Alignment		100.0	14	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)
8	c6c8vA_	 Alignment		99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
9	c2yx0A_	 Alignment		99.9	16	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
10	c3c8fA_	 Alignment		99.9	15	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
11	c5th5C_	 Alignment		99.9	14	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

12	c4wxcC_	Alignment		99.9	18	PDB header: lyase Chain: C: PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
13	c4m7tA_	Alignment		99.9	16	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
14	c3t7vA_	Alignment		99.8	13	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
15	c2a5hC_	Alignment		99.8	15	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).
16	c3canA_	Alignment		99.8	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
17	c4njka_	Alignment		99.8	15	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+
18	c4u0pB_	Alignment		99.7	15	PDB header: transferase Chain: B: PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
19	c5exkG_	Alignment		99.7	16	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
20	c3rfaB_	Alignment		99.7	19	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	c1r30A_	Alignment	not modelled	99.7	15	PDB header: transferase Chain: A: PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
22	d1r30a_	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
23	c6fz6B_	Alignment	not modelled	99.7	20	PDB header: transferase Chain: B: PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
24	c2z2uA_	Alignment	not modelled	99.7	17	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaical tyw1
25	c3rfaA_	Alignment	not modelled	99.7	19	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
26	c4rtbA_	Alignment	not modelled	99.7	19	PDB header: lyase Chain: A: PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrmus hydrogenoformans
27	c3cixA_	Alignment	not modelled	99.7	18	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
28	c6nhIB_	Alignment	not modelled	99.7	17	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	99.6	10	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	14	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
31	c4r33A_	Alignment	not modelled	99.5	20	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
32	c6fd2B_	Alignment	not modelled	99.4	16	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
33	c5ul4A_	Alignment	not modelled	99.1	17	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
34	c5l7jA_	Alignment	not modelled	99.1	11	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
35	c2qggF_	Alignment	not modelled	99.0	11	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	98.9	15	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
37	c4fheA_	Alignment	not modelled	98.7	9	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
38	c6iazA_	Alignment	not modelled	98.4	9	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	98.0	12	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
40	c3rmjB_	Alignment	not modelled	97.8	11	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
41	c2ftpA_	Alignment	not modelled	97.1	12	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
42	c2cw6B_	Alignment	not modelled	96.9	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
43	c3ewbX_	Alignment	not modelled	96.8	12	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
44	c6e1jB_	Alignment	not modelled	96.8	13	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
45	c3eegB_	Alignment	not modelled	96.6	15	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
46	c1ydnA_	Alignment	not modelled	96.6	11	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.
47	c1ydoC_	Alignment	not modelled	96.5	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.
48	c3bleA_	Alignment	not modelled	96.5	11	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
49	c3hpxB_	Alignment	not modelled	96.1	15	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)
50	c2zyfA_	Alignment	not modelled	95.6	7	PDB header: transferase Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermophilus2 complexed with magnesium ion and alpha-ketoglutarate
51	c1sr9A_	Alignment	not modelled	95.4	17	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
52	c4ov9A_	Alignment	not modelled	94.6	10	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-

						2 isopropylmalate
53	c5zmyf_	Alignment	not modelled	94.3	14	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
54	c1nvmG_	Alignment	not modelled	94.1	9	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
55	c4jn6C_	Alignment	not modelled	93.8	18	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	c3a9iA_	Alignment	not modelled	93.1	7	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
57	d1nvma2	Alignment	not modelled	92.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
58	c5tnvA_	Alignment	not modelled	88.7	13	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
59	c1ps9A_	Alignment	not modelled	84.8	7	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
60	d1yhta1	Alignment	not modelled	84.6	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
61	d1z41a1	Alignment	not modelled	83.0	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
62	c4lrtC_	Alignment	not modelled	82.6	17	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
63	d1ps9a1	Alignment	not modelled	81.8	7	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
64	c3hf3A_	Alignment	not modelled	80.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
65	c5oarB_	Alignment	not modelled	80.1	11	PDB header: hydrolase Chain: B: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of native beta-n-acetylhexosaminidase isolated from2 aspergillus oryzae
66	c2h90A_	Alignment	not modelled	79.9	10	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
67	d1sr9a2	Alignment	not modelled	78.6	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
68	c3gr7A_	Alignment	not modelled	78.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
69	c3dxiB_	Alignment	not modelled	77.7	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 (bvj_2661) from bacteroides vulgatus
70	c3gh7A_	Alignment	not modelled	76.5	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase; PDBTitle: crystal structure of beta-hexosaminidase from paenibacillus sp. ts122 in complex with galnac
71	c2y7eA_	Alignment	not modelled	76.3	14	PDB header: lyase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from candidatus cloacamonas acidaminovorans (tetragonal form)
72	c2yl8A_	Alignment	not modelled	75.9	20	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
73	d1n7ka_	Alignment	not modelled	74.9	21	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
74	d1nowa1	Alignment	not modelled	74.1	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
75	c2nx9B_	Alignment	not modelled	73.5	17	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
76	c1nouA_	Alignment	not modelled	73.4	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase beta chain; PDBTitle: native human lysosomal beta-hexosaminidase isoform b
77	c3cprB_	Alignment	not modelled	72.2	15	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase;

77	c3cp1B_	Alignment	not modelled	72.2	13	PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution PDB header: hydrolase
78	c3rpmA_	Alignment	not modelled	71.8	20	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
79	d1jaka1	Alignment	not modelled	70.3	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
80	c5ocsB_	Alignment	not modelled	69.3	10	PDB header: flavoprotein Chain: B; PDB Molecule: putative nadh-depndent flavin oxidoreductase; PDBTitle: ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
81	c1pjtB_	Alignment	not modelled	68.8	22	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
82	c3chvA_	Alignment	not modelled	68.0	10	PDB header: metal binding protein Chain: A; PDB Molecule: prokaryotic domain of unknown function (duf849) with a tim PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
83	c3ndcB_	Alignment	not modelled	67.7	15	PDB header: transferase Chain: B; PDB Molecule: precorrin-4 c(11)-methyltransferase; PDBTitle: crystal structure of precorrin-4 c11-methyltransferase from2 rhodobacter capsulatus
84	c2ylaA_	Alignment	not modelled	66.7	22	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
85	c1m04A_	Alignment	not modelled	66.4	20	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: mutant streptomyces plicatus beta-hexosaminidase (d313n) in complex2 with product (glcnae)
86	c3e02A_	Alignment	not modelled	66.0	17	PDB header: metal binding protein Chain: A; PDB Molecule: uncharacterized protein duf849; PDBTitle: crystal structure of a duf849 family protein (bx_e_c0271) from2 burkholderia xenovorans lb400 at 1.90 a resolution
87	c3lciA_	Alignment	not modelled	65.6	23	PDB header: lyase Chain: A; PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
88	c3lmyA_	Alignment	not modelled	65.4	15	PDB header: hydrolase Chain: A; PDB Molecule: beta-hexosaminidase subunit beta; PDBTitle: the crystal structure of beta-hexosaminidase b in complex with2 pyrimethamine
89	c2bpbB_	Alignment	not modelled	65.3	19	PDB header: oxidoreductase Chain: B; PDB Molecule: sulfite:cytochrome c oxidoreductase subunit b; PDBTitle: sulfite dehydrogenase from starkeya novella
90	d2gjxa1	Alignment	not modelled	64.7	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-N-acetylhexosaminidase catalytic domain
91	d2g0wa1	Alignment	not modelled	64.0	6	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: !loll-like
92	c3aytA_	Alignment	not modelled	63.9	19	PDB header: unknown function Chain: A; PDB Molecule: putative uncharacterized protein tthb071; PDBTitle: tthb071 protein from thermus thermophilus hb8
93	c5ks8F_	Alignment	not modelled	63.4	15	PDB header: ligase Chain: F; PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
94	d1v93a_	Alignment	not modelled	63.3	13	Fold: TIM beta/alpha-barrel Superfamily: FAD-linked oxidoreductase Family: Methylenetetrahydrofolate reductase
95	c6je8A_	Alignment	not modelled	63.1	18	PDB header: hydrolase Chain: A; PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of a beta-n-acetylhexosaminidase
96	c6ei9A_	Alignment	not modelled	62.5	20	PDB header: flavoprotein Chain: A; PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
97	c2iswB_	Alignment	not modelled	61.8	15	PDB header: lyase Chain: B; PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
98	c4ovxA_	Alignment	not modelled	61.4	9	PDB header: isomerase Chain: A; PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
99	c6aaavA_	Alignment	not modelled	61.3	20	PDB header: hydrolase Chain: A; PDB Molecule: alpha-glucosyltransferase; PDBTitle: crystal structure of alpha-glucosyl transfer enzyme, xgta at 1.722 angstrom resolution
100	c1rr2A_	Alignment	not modelled	60.8	16	PDB header: transferase Chain: A; PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
101	d1vyra_	Alignment	not modelled	60.7	9	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases

102	c2dh3A_	Alignment	not modelled	59.1	14	PDB header: transport protein, signaling protein Chain: A: PDB Molecule: 4f2 cell-surface antigen heavy chain; PDBTitle: crystal structure of human ed-4f2hc
103	c2r8wB_	Alignment	not modelled	58.9	13	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
104	c6h4eB_	Alignment	not modelled	58.5	13	PDB header: lyase Chain: B: PDB Molecule: putative n-acetylneuraminate lyase; PDBTitle: proteus mirabilis n-acetylneuraminate lyase
105	d2a6na1	Alignment	not modelled	58.4	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
106	c5hqca_	Alignment	not modelled	58.3	18	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
107	c3no5C_	Alignment	not modelled	58.0	12	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pfam duf849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
108	c4i7vD_	Alignment	not modelled	57.9	13	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhds with pyruvate
109	d1yx1a1	Alignment	not modelled	57.7	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
110	c5m99A_	Alignment	not modelled	57.1	18	PDB header: hydrolase Chain: A: PDB Molecule: alpha-amylase; PDBTitle: functional characterization and crystal structure of thermostable2 amylase from thermotoga petrophila, reveals high thermostability and3 an archaic form of dimerization
111	c5ks8D_	Alignment	not modelled	56.8	15	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
112	c3b4uB_	Alignment	not modelled	56.4	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
113	c2zq0B_	Alignment	not modelled	56.2	13	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase sub); PDBTitle: crystal structure of sub complexed with acarbose
114	c6oviA_	Alignment	not modelled	56.0	13	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
115	c3rcnA_	Alignment	not modelled	55.9	22	PDB header: hydrolase Chain: A: PDB Molecule: beta-n-acetylhexosaminidase; PDBTitle: crystal structure of beta-n-acetylhexosaminidase from arthrobacter2 aureus
116	c3atyA_	Alignment	not modelled	55.9	8	PDB header: oxidoreductase Chain: A: PDB Molecule: prostaglandin f2a synthase; PDBTitle: crystal structure of tcoye
117	c3fkka_	Alignment	not modelled	55.4	13	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
118	c5zcbA_	Alignment	not modelled	55.0	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase
119	c3w9za_	Alignment	not modelled	54.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
120	d1s4da_	Alignment	not modelled	54.8	25	Fold: Tetrapyrrole methylase Superfamily: Tetrapyrrole methylase Family: Tetrapyrrole methylase