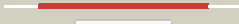



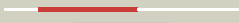



















Phyre2

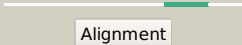
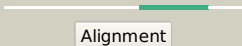
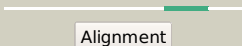
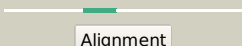


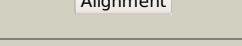

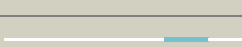


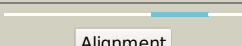

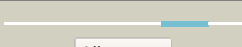
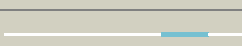


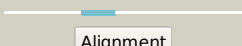


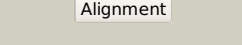
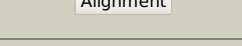
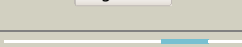


Email	mdejesus@rockefeller.edu
Description	RVBD1415_(ribA2)_1590403_1591680
Date	Wed Jul 31 22:05:52 BST 2019
Unique Job ID	314ca1ecbef54459

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4i14B_	 Alignment		100.0	100	PDB header: hydrolase, lyase Chain: B; PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: crystal structure of mtb-riba2 (rv1415)
2	c6mnzB_	 Alignment		100.0	44	PDB header: lyase Chain: B; PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of ribbx, a two domain 3,4-dihydroxy-2-butanone 4-2 phosphate synthase from a. baumannii.
3	d1k4ia_	 Alignment		100.0	48	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
4	c3mioA_	 Alignment		100.0	100	PDB header: lyase Chain: A; PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: crystal structure of 3,4-dihydroxy-2-butanone 4-phosphate synthase2 domain from mycobacterium tuberculosis at ph 6.00
5	d1g57a_	 Alignment		100.0	47	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
6	d1tksa_	 Alignment		100.0	52	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
7	d1snaa_	 Alignment		100.0	34	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
8	c4ffjA_	 Alignment		100.0	45	PDB header: lyase Chain: A; PDB Molecule: riboflavin biosynthesis protein ribba; PDBTitle: the crystal structure of spdhpbs from s.pneumoniae
9	c4p6dA_	 Alignment		100.0	47	PDB header: lyase Chain: A; PDB Molecule: 3,4-dihydroxy-2-butanone 4-phosphate synthase; PDBTitle: structure of ribb complexed with po4 ion
10	d2bz1a1	 Alignment		100.0	54	Fold: RibA-like Superfamily: RibA-like Family: RibA-like
11	c4ri4B_	 Alignment		100.0	45	PDB header: hydrolase Chain: B; PDB Molecule: gtp cyclohydrolase-2; PDBTitle: crystal structure of gtp cyclohydrolase ii from helicobacter pylori2 26695

12	c3ur8A_	Alignment		87.8	17	PDB header: hydrolase Chain: A: PDB Molecule: glucan endo-1,3-beta-d-glucosidase; PDBTitle: lower-density crystal structure of potato endo-1,3-beta-glucanase
13	d1aq0a_	Alignment		86.3	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
14	d1oi2a_	Alignment		85.9	27	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
15	d1ghsa_	Alignment		85.2	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
16	d1lh0a_	Alignment		84.6	16	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
17	d2cyga1	Alignment		83.7	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
18	c3f55A_	Alignment		82.5	21	PDB header: hydrolase, allergen Chain: A: PDB Molecule: beta-1,3-glucanase; PDBTitle: crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
19	c4fd4B_	Alignment		82.3	22	PDB header: transferase Chain: B: PDB Molecule: arylalkylamine n-acetyltransferase like 5b; PDBTitle: crystal structure of mosquito arylalkylamine n-acetyltransferase like2 5b
20	c1un9B_	Alignment		80.2	33	PDB header: kinase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: crystal structure of the dihydroxyacetone kinase from c.2 freundii in complex with amp-pnp and mg2+
21	c4fq5B_	Alignment	not modelled	78.0	15	PDB header: isomerase Chain: B: PDB Molecule: maleate cis-trans isomerase; PDBTitle: crystal structure of the maleate isomerase iso(c200a) from pseudomonas2 putida s16 with maleate
22	d1un8a4	Alignment	not modelled	74.7	31	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
23	d1u6ma_	Alignment	not modelled	74.2	25	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
24	c2iu6B_	Alignment	not modelled	74.2	25	PDB header: transferase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: regulation of the dha operon of lactococcus lactis
25	d1y0na_	Alignment	not modelled	73.4	29	Fold: YehU-like Superfamily: YehU-like Family: YehU-like
26	d1v96a1	Alignment	not modelled	72.1	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
27	c3te4A_	Alignment	not modelled	71.8	24	PDB header: transferase Chain: A: PDB Molecule: dopamine n acetyltransferase, isoform a; PDBTitle: crystal structure of dopamine n acetyltransferase in complex with2 acetyl-coa from drosophila melanogaster
28	d1n71a_	Alignment	not modelled	71.2	25	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
29	c5ygeA_	Alignment	not modelled	67.8	22	PDB header: transferase Chain: A: PDB Molecule: amino-acid acetyltransferase;

						PDBTitle: arga complexed with acecoa and glutamate
30	d1js3a_	Alignment	not modelled	67.8	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Pyridoxal-dependent decarboxylase
31	c3ct4B_	Alignment	not modelled	65.7	23	PDB header: transferase Chain: B: PDB Molecule: pts-dependent dihydroxyacetone kinase, dihydroxyacetone- PDBTitle: structure of dha-kinase subunit dhak from <i>I. lactis</i>
32	d1y9ka1	Alignment	not modelled	63.6	19	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
33	c2reeB_	Alignment	not modelled	63.5	21	PDB header: transferase, lyase Chain: B: PDB Molecule: cura; PDBTitle: crystal structure of the loading gnat1 domain of cura from <i>lyngbya2 majuscula</i>
34	d2g3aa1	Alignment	not modelled	63.5	26	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
35	c6eeiA_	Alignment	not modelled	60.6	19	PDB header: lyase Chain: A: PDB Molecule: tyrosine decarboxylase 1; PDBTitle: crystal structure of arabidopsis thaliana phenylacetaldehyde synthase2 in complex with l-phenylalanine
36	c4fd5A_	Alignment	not modelled	60.6	25	PDB header: transferase Chain: A: PDB Molecule: arylalkylamine n-acetyltransferase 2; PDBTitle: crystal structure of arylalkylamine n-acetyltransferase 2 from <i>aedes2 aegypti</i>
37	c2g1uA_	Alignment	not modelled	60.3	16	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from <i>thermotoga maritima</i> at 1.50 a resolution
38	d1y9wa1	Alignment	not modelled	59.8	25	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
39	c4obuG_	Alignment	not modelled	59.7	19	PDB header: lyase Chain: G: PDB Molecule: pyridoxal-dependent decarboxylase domain protein; PDBTitle: ruminococcus gnavus tryptophan decarboxylase rumgna_01526 (apo)
40	c3n2IA_	Alignment	not modelled	58.7	17	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from <i>vibrio cholerae</i> o1 biovar eltor3 str. n16961
41	d1y82a1	Alignment	not modelled	56.5	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
42	c6eeqA_	Alignment	not modelled	55.5	28	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of rhodiola rosea 4-hydroxyphenylacetaldehyde2 synthase
43	c3dr8B_	Alignment	not modelled	54.1	26	PDB header: transferase Chain: B: PDB Molecule: ynca; PDBTitle: structure of ynca, a putative acetyltransferase from <i>salmonella2 typhimurium</i> with its cofactor acetyl-coa
44	c6eewC_	Alignment	not modelled	52.8	19	PDB header: lyase Chain: C: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of catharanthus roseus tryptophan decarboxylase in2 complex with l-tryptophan
45	c3zihB_	Alignment	not modelled	52.7	14	PDB header: cell cycle Chain: B: PDB Molecule: cell division protein sepf; PDBTitle: bacillus subtilis sepf, c-terminal domain
46	c3p04A_	Alignment	not modelled	52.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from <i>corynebacterium glutamicum.2</i> northeast structural genomics consortium target cgr8
47	c5f56A_	Alignment	not modelled	51.3	20	PDB header: dna binding protein/dna Chain: A: PDB Molecule: single-stranded-dna-specific exonuclease; PDBTitle: structure of recj complexed with dna and ssb-ct
48	d1ko7a1	Alignment	not modelled	49.6	16	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phoshatase HprK N-terminal domain
49	c3p04B_	Alignment	not modelled	49.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from <i>corynebacterium glutamicum.2</i> northeast structural genomics consortium target cgr8
50	d1tiqa_	Alignment	not modelled	48.8	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
51	c6ao7A_	Alignment	not modelled	48.3	18	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase; PDBTitle: crystal structure of a gnat family acetyltransferase from2 elizabethkingia anophelis with acetyl-coa bound
52	c4ritB_	Alignment	not modelled	47.9	30	PDB header: lyase Chain: B: PDB Molecule: pyridoxal-dependent decarboxylase; PDBTitle: the yellow crystal structure of pyridoxal-dependent decarboxylase from2 sphaerobacter thermophilus dsm 20745
53	c5o5cD_	Alignment	not modelled	47.1	19	PDB header: lyase Chain: D: PDB Molecule: putative decarboxylase involved in desferrioxamine PDBTitle: the crystal structure of dfoj, the desferrioxamine biosynthetic2 pathway lysine decarboxylase from the fire blight disease pathogen3 erwinia amylovora
54	c4efzB_	Alignment	not modelled	46.8	24	PDB header: hydrolase Chain: B: PDB Molecule: metallo-beta-lactamase family protein; PDBTitle: crystal structure of a hypothetical metallo-beta-lactamase from2 burkholderia pseudomallei

55	c4e0aB	 Alignment	not modelled	45.7	14	PDB header: transferase Chain: B: PDB Molecule: bh1408 protein; PDBTitle: crystal structure of the mutant f44r bh1408 protein from bacillus2 halodurans, northeast structural genomics consortium (nesg) target3 bhr182
56	c2xecD	 Alignment	not modelled	44.7	18	PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to tris
57	c5k18D	 Alignment	not modelled	43.9	28	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: n-terminal acetyltransferase b complex subunit nat3; PDBTitle: the natb acetyltransferase complex bound to bisubstrate inhibitor
58	c6eemB	 Alignment	not modelled	43.3	15	PDB header: lyase Chain: B: PDB Molecule: tyrosine/dopa decarboxylase; PDBTitle: crystal structure of papaver somniferum tyrosine decarboxylase in2 complex with l-tyrosine
59	c5ktaA	 Alignment	not modelled	42.9	10	PDB header: transferase Chain: A: PDB Molecule: fdhc; PDBTitle: apo fdhc- a nucleotide-linked sugar gnat
60	d2cy2a1	 Alignment	not modelled	39.8	28	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
61	c3kc2A	 Alignment	not modelled	39.8	16	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
62	d1hrua	 Alignment	not modelled	39.3	10	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
63	c4e1oC	 Alignment	not modelled	39.3	20	PDB header: lyase Chain: C: PDB Molecule: histidine decarboxylase; PDBTitle: human histidine decarboxylase complex with histidine methyl ester2 (hme)
64	c2oh1A	 Alignment	not modelled	39.1	16	PDB header: transferase Chain: A: PDB Molecule: acetyltransferase, gnat family; PDBTitle: crystal structure of acetyltransferase gnat family (yp_013287.1) from2 listeria monocytogenes 4b f2365 at 1.46 a resolution
65	c3tquD	 Alignment	not modelled	37.6	19	PDB header: hydrolase Chain: D: PDB Molecule: non-canonical purine ntp pyrophosphatase; PDBTitle: structure of a ham1 protein from coxiella burnetii
66	d1k7ka	 Alignment	not modelled	36.8	30	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
67	d1lssa	 Alignment	not modelled	35.5	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
68	c3d8pB	 Alignment	not modelled	35.0	23	PDB header: transferase Chain: B: PDB Molecule: acetyltransferase of gnat family; PDBTitle: crystal structure of acetyltransferase of gnat family (np_373092.1)2 from staphylococcus aureus mu50 at 2.20 a resolution
69	c5k9nB	 Alignment	not modelled	34.9	27	PDB header: transferase Chain: B: PDB Molecule: polyamine n acetyltransferase; PDBTitle: structural and mechanistic analysis of drosophila melanogaster2 polyamine n acetyltransferase, an enzyme that catalyzes the formation3 of n acetylglutamine
70	c3lodA	 Alignment	not modelled	34.8	25	PDB header: transferase Chain: A: PDB Molecule: putative acyl-coa n-acyltransferase; PDBTitle: the crystal structure of the putative acyl-coa n-acyltransferase from2 klebsiella pneumoniae subsp.pneumoniae mgh 78578
71	d2fiaa1	 Alignment	not modelled	34.7	26	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
72	c2okkA	 Alignment	not modelled	34.4	11	PDB header: lyase Chain: A: PDB Molecule: glutamate decarboxylase 2: PDBTitle: the x-ray crystal structure of the 65kda isoform of glutamic acid2 decarboxylase (gad65)
73	c3mjdA	 Alignment	not modelled	34.3	10	PDB header: transferase Chain: A: PDB Molecule: orotate phosphoribosyltransferase; PDBTitle: 1.9 angstrom crystal structure of orotate phosphoribosyltransferase2 (pyre) francisella tularensis.
74	d1i12a	 Alignment	not modelled	34.3	24	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
75	c2q0yA	 Alignment	not modelled	33.8	22	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of gcn5-related n-acetyltransferase (yp_295895.1)2 from ralstonia eutropha jmp134 at 1.80 a resolution
76	c3exnA	 Alignment	not modelled	33.3	16	PDB header: transferase Chain: A: PDB Molecule: probable acetyltransferase; PDBTitle: crystal structure of acetyltransferase from thermus thermophilus hb8
77	c3i9sA	 Alignment	not modelled	33.1	28	PDB header: transferase Chain: A: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
78	c4g6cA	 Alignment	not modelled	32.5	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-hexosaminidase 1; PDBTitle: crystal structure of beta-hexosaminidase 1 from burkholderia2 cenocepacia j2315
79	d2fiwa1	 Alignment	not modelled	32.4	18	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT

80	c3k40B_	Alignment	not modelled	32.3	21	PDB header: lyase Chain: B: PDB Molecule: aromatic-l-amino-acid decarboxylase; PDBTitle: crystal structure of drosophila 3,4-dihydroxyphenylalanine2 decarboxylase
81	d2je8a5	Alignment	not modelled	32.2	10	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
82	c6jr1A_	Alignment	not modelled	31.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,4-dihydroxyphenylacetaldehyde synthase; PDBTitle: crystal structure of drosophila alpha methyl dopa-resistant protein/3,2 4-dihydroxyphenylacetaldehyde synthase
83	d1yvka1	Alignment	not modelled	31.9	16	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
84	c3f8kA_	Alignment	not modelled	31.3	21	PDB header: transferase Chain: A: PDB Molecule: protein acetyltransferase; PDBTitle: crystal structure of protein acetyltransferase (pat) from sulfolobus2 solfataricus
85	d2euia1	Alignment	not modelled	30.9	12	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
86	d1yvoa1	Alignment	not modelled	30.8	30	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
87	d1s3za_	Alignment	not modelled	30.8	29	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
88	d1ohwa_	Alignment	not modelled	29.7	28	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
89	d1o8ca2	Alignment	not modelled	29.3	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
90	c4yskA_	Alignment	not modelled	28.0	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-lactamase domain protein; PDBTitle: crystal structure of apo-form sdoa from pseudomonas putida
91	d1vhsa_	Alignment	not modelled	27.5	27	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
92	d1m65a_	Alignment	not modelled	27.3	17	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: PHP domain
93	c2w61A_	Alignment	not modelled	27.1	19	PDB header: glycoprotein Chain: A: PDB Molecule: glycolipid-anchored surface protein 2; PDBTitle: saccharomyces cerevisiae gas2p apostructure (e176q mutant)
94	d1ghea_	Alignment	not modelled	27.1	27	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
95	c4ua3A_	Alignment	not modelled	26.8	19	PDB header: transferase Chain: A: PDB Molecule: uncharacterized n-acetyltransferase c825.04c; PDBTitle: crystal structure of selenomethionine labeled spnatd
96	c2jlmE_	Alignment	not modelled	26.5	23	PDB header: transferase Chain: E: PDB Molecule: putative phosphinothricin n-acetyltransferase; PDBTitle: structure of a putative acetyltransferase (aciad1637) from2 acinetobacter baylyi adp1
97	c3k9uA_	Alignment	not modelled	26.0	20	PDB header: transferase Chain: A: PDB Molecule: paia acetyltransferase; PDBTitle: crystal structure of paia acetyltransferase (ta0374) from thermoplasma2 acidophilum
98	c4ri1A_	Alignment	not modelled	25.6	14	PDB header: transferase Chain: A: PDB Molecule: udp-4-amino-4,6-dideoxy-n-acetyl-beta-l-altrosamine n- PDBTitle: crystal structure of helicobacter pylori pseudaminic acid biosynthesis2 n -acetyltransferase pseh complex with acetyl-coa
99	c4e8oB_	Alignment	not modelled	25.5	25	PDB header: transferase Chain: B: PDB Molecule: aac(6')-ih protein; PDBTitle: crystal structure of aminoglycoside antibiotic 6'-n-acetyltransferase2 aac(6')-ih from acinetobacter baumannii
100	c4h89A_	Alignment	not modelled	25.4	26	PDB header: transferase Chain: A: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: the structure of a gcn5-related n-acetyltransferase from kribbella2 flavida
101	c5f46A_	Alignment	not modelled	25.3	21	PDB header: transferase Chain: A: PDB Molecule: aminoglycoside acetyltransferase meta-aac0020; PDBTitle: crystal structure of an aminoglycoside acetyltransferase meta-aac00202 from an uncultured soil metagenomic sample, apoenzyme form
102	c2przB_	Alignment	not modelled	24.7	13	PDB header: transferase Chain: B: PDB Molecule: orotate phosphoribosyltransferase 1; PDBTitle: s. cerevisiae orotate phosphoribosyltransferase complexed with omp
103	c1ib1E_	Alignment	not modelled	24.0	21	PDB header: signaling protein/transferase Chain: E: PDB Molecule: serotonin n-acetyltransferase; PDBTitle: crystal structure of the 14-3-3 zeta:serotonin n-acetyltransferase2 complex
104	c2uvpB_	Alignment	not modelled	24.0	17	PDB header: unknown function Chain: B: PDB Molecule: hoba; PDBTitle: crystal structure of hoba (hp1230)from helicobacter pylori
						PDB header: transferase

105	c2qmaB_	Alignment	not modelled	23.6	20	Chain: B: PDB Molecule: diaminobutyrate-pyruvate transaminase and l-2,4- PDBTitle: crystal structure of glutamate decarboxylase domain of 2 diaminobutyrate-pyruvate transaminase and l-2,4-diaminobutyrate3 decarboxylase from vibrio parahaemolyticus
106	c4wv4A_	Alignment	not modelled	23.4	23	PDB header: transcription Chain: A: PDB Molecule: transcription initiation factor tfiid subunit 10; PDBTitle: heterodimer of taf8/taf10
107	c1zswA_	Alignment	not modelled	23.1	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glyoxalase family protein; PDBTitle: crystal structure of bacillus cereus metallo protein from glyoxalase2 family
108	c5tchG_	Alignment	not modelled	23.1	26	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
109	c3iupB_	Alignment	not modelled	23.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadph:quinone oxidoreductase; PDBTitle: crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
110	c2jisA_	Alignment	not modelled	22.9	19	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.
111	c2r1iB_	Alignment	not modelled	22.7	28	PDB header: transferase Chain: B: PDB Molecule: gcn5-related n-acetyltransferase; PDBTitle: crystal structure of putative acetyltransferase (yp_831484.1) from2 arthrobacter sp. fb24 at 1.65 a resolution
112	c2qmlA_	Alignment	not modelled	22.6	28	PDB header: unknown function Chain: A: PDB Molecule: bh2621 protein; PDBTitle: crystal structure of an uncharacterized protein (bh2621) from bacillus2 halodurans at 1.55 a resolution
113	c3e48B_	Alignment	not modelled	22.6	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of a nucleoside-diphosphate-sugar epimerase2 (sav0421) from staphylococcus aureus, northeast structural genomics3 consortium target zr319
114	c3jszA_	Alignment	not modelled	22.3	21	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: legionella pneumophila glucosyltransferase lgt1 n293a with udp-glc
115	c3vthA_	Alignment	not modelled	22.2	27	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
116	d2beia1	Alignment	not modelled	21.9	24	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
117	d1jcua_	Alignment	not modelled	21.8	18	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: YrdC-like
118	c2k5tA_	Alignment	not modelled	21.7	16	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein yhhk; PDBTitle: solution nmr structure of putative n-acetyl transferase2 yhhk from e. coli bound to coenzyme a: northeast3 structural genomics consortium target et106
119	d2hmva1	Alignment	not modelled	21.3	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
120	d1v7ra_	Alignment	not modelled	21.0	17	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)