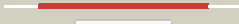



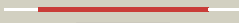










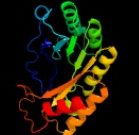



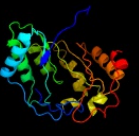




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2218_(lipA)_2485281_2486216
Date	Mon Aug 5 13:25:34 BST 2019
Unique Job ID	2ed0dd86d06fefb4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5exkG	 Alignment		100.0	100	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
2	c4u0pB	 Alignment		100.0	45	PDB header: transferase Chain: B; PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
3	c4jc0B	 Alignment		100.0	13	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
4	c3cixA	 Alignment		100.0	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
5	c1r30A	 Alignment		99.9	19	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
6	d1r30a	 Alignment		99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase
7	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
8	c3t7vA	 Alignment		99.9	14	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
9	c2qgaF	 Alignment		99.9	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
10	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
11	c6fd2B	 Alignment		99.9	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

12	d1olta_	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
13	c4r33A_	Alignment		99.8	16	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
14	c5l7jA_	Alignment		99.8	10	PDB header: translation Chain: A: PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
15	c6qk7C_	Alignment		99.8	18	PDB header: translation Chain: C: PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
16	c5ul4A_	Alignment		99.8	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
17	d1tv8a_	Alignment		99.7	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
18	c5v1tA_	Alignment		99.7	9	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
19	c6iazA_	Alignment		99.7	14	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
20	c5vslB_	Alignment		99.7	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)
21	c3rfaB_	Alignment	not modelled	99.6	14	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
22	c6efnA_	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
23	c4k39A_	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmece with bound adomet and cp18cys peptide
24	c3c8fA_	Alignment	not modelled	99.6	13	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
25	c3rfaA_	Alignment	not modelled	99.5	14	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	c6b4cH_	Alignment	not modelled	99.5	13	PDB header: antiviral protein Chain: H: PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
27	c2yx0A_	Alignment	not modelled	99.5	17	PDB header: metal binding protein Chain: A: PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
						PDB header: transferase Chain: B: PDB Molecule: probable dual-specificity rna

28	c6fz6B_	Alignment	not modelled	99.4	17	methyltransferase rimn; PDBTitle: crystal structure of a radical sam methyltransferase from <i>Sphaerobacter thermophilus</i>
29	c2a5hC_	Alignment	not modelled	99.4	17	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 from <i>Clostridium subterminale</i> sb4, with michaelis analog (l-alpha-lysine 3 external aldimine form of pyridoxal-5'-phosphate).
30	c5wggA_	Alignment	not modelled	99.1	12	PDB header: peptide binding protein Chain: A: PDB Molecule: radical sam domain protein; PDBTitle: structural insights into thioether bond formation in the biosynthesis of sactipeptides
31	c4fheA_	Alignment	not modelled	99.1	9	PDB header: lyase Chain: A: PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
32	c6c8vA_	Alignment	not modelled	98.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from <i>Methylobacterium extorquens</i>
33	c5th5C_	Alignment	not modelled	98.9	11	PDB header: lyase Chain: C: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from <i>Bacillus subtilis</i> with 6-carboxypterin-2 5'-deoxyadenosyl ester bound
34	c4m7tA_	Alignment	not modelled	98.7	13	PDB header: metal binding protein Chain: A: PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
35	c3canA_	Alignment	not modelled	98.4	13	PDB header: lyase activator Chain: A: PDB Molecule: pyruvate-formate lyase-activating enzyme; PDBTitle: crystal structure of a domain of pyruvate-formate lyase-activating 2 enzyme from <i>Bacteroides vulgatus</i> atcc 8482
36	c2z2uA_	Alignment	not modelled	98.1	12	PDB header: metal binding protein Chain: A: PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
37	c3ivuB_	Alignment	not modelled	98.1	13	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
38	d1nvma2	Alignment	not modelled	98.1	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
39	c3rmjB_	Alignment	not modelled	98.1	16	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from <i>Neisseria meningitidis</i>
40	c1nvmG_	Alignment	not modelled	98.0	10	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
41	c6nhlB_	Alignment	not modelled	98.0	12	PDB header: lyase Chain: B: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from <i>Escherichia coli</i>
42	c2cw6B_	Alignment	not modelled	98.0	12	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into 2 catalysis and the molecular basis for 3 hydroxymethylglutaric aciduria
43	c4njka_	Alignment	not modelled	97.9	16	PDB header: lyase Chain: A: PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from <i>Burkholderia multivorans</i> in complex 2 with adomet, 7-carboxy-7-deazaguanine, and mg2+
44	c3ewbX_	Alignment	not modelled	97.9	15	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate 2 synthase from <i>Listeria monocytogenes</i>
45	c4jn6C_	Alignment	not modelled	97.9	13	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from <i>Mycobacterium tuberculosis</i> hrv37
46	c2ftpA_	Alignment	not modelled	97.8	19	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from <i>Pseudomonas aeruginosa</i>
47	c3bleA_	Alignment	not modelled	97.7	15	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from <i>Leptospira interrogans</i> ; PDBTitle: crystal structure of the catalytic domain of licms in complexed with 2 malonate
48	c1ydoC_	Alignment	not modelled	97.7	13	PDB header: lyase Chain: C: PDB Molecule: hmg-coa lyase; PDBTitle: crystal structure of the <i>Bacillus subtilis</i> hmg-coa lyase, northeast 2 structural genomics target sr181.
49	c3eegB_	Alignment	not modelled	97.6	10	PDB header: transferase Chain: B: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from <i>Cytophaga hutchinsonii</i>
50	c1ydnA_	Alignment	not modelled	97.5	12	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from <i>Brucella melitensis</i> , 2 northeast structural genomics target lr35.
51	c6e1jB_	Alignment	not modelled	97.5	12	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from <i>Brassica juncea</i>
						PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase;

52	c4lrtC_	Alignment	not modelled	97.4	15	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
53	c2zyfA_	Alignment	not modelled	97.3	12	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
54	c5zmyF_	Alignment	not modelled	97.2	16	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
55	c1rr2A_	Alignment	not modelled	96.9	15	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
56	c2nx9B_	Alignment	not modelled	96.8	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
57	c4ov9A_	Alignment	not modelled	96.5	14	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
58	c1sr9A_	Alignment	not modelled	96.3	9	PDB header: transferase Chain: A: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of leua from mycobacterium tuberculosis
59	c5ks8F_	Alignment	not modelled	96.3	11	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
60	c3a9iA_	Alignment	not modelled	96.2	14	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: homocitrate synthase; PDBTitle: crystal structure of homocitrate synthase from thermus thermophilus2 complexed with lys
61	c5ks8D_	Alignment	not modelled	96.1	12	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
62	c3labA_	Alignment	not modelled	96.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpq (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpq (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
63	c3no5C_	Alignment	not modelled	96.0	10	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
64	c3dxiB_	Alignment	not modelled	96.0	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative aldolase; PDBTitle: crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
65	c4e38A_	Alignment	not modelled	95.9	12	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
66	c3chvA_	Alignment	not modelled	95.8	13	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
67	c5cxsA_	Alignment	not modelled	95.8	18	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of isoform 2 of purine nucleoside phosphorylase2 complexed with mes
68	c3c6cA_	Alignment	not modelled	95.8	11	PDB header: hydrolase Chain: A: PDB Molecule: 3-keto-5-aminohexanoate cleavage enzyme; PDBTitle: crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution
69	c3vndD_	Alignment	not modelled	95.8	19	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
70	c6oviA_	Alignment	not modelled	95.8	15	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
71	d1qopa_	Alignment	not modelled	95.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
72	c5ey5A_	Alignment	not modelled	95.6	14	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
73	c5kzmA_	Alignment	not modelled	95.5	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
74	c2y7eA_	Alignment	not modelled	95.4	13	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)
75	c3navB_	Alignment	not modelled	95.3	16 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
76	d1vhca_	Alignment	not modelled	95.2	16 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
77	c5tchG_	Alignment	not modelled	95.2	21 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
78	d1mxsa_	Alignment	not modelled	95.0	18 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
79	c2ekcA_	Alignment	not modelled	95.0	16 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
80	c3b0vD_	Alignment	not modelled	94.8	15 PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
81	c5k9xA_	Alignment	not modelled	94.8	15 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
82	c4lnaA_	Alignment	not modelled	94.4	16 PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase i from spirosuma2 linguale dsm 74, nysgrc target 029362
83	c4uxdC_	Alignment	not modelled	94.4	16 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
84	c3lerA_	Alignment	not modelled	94.3	14 PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
85	d1wbha1	Alignment	not modelled	94.1	23 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
86	d1ad1a_	Alignment	not modelled	94.1	13 Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
87	c5ifkC_	Alignment	not modelled	93.8	19 PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: purine nucleoside phosphorylase
88	c4nq1B_	Alignment	not modelled	93.4	13 PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
89	c4nsnC_	Alignment	not modelled	93.4	16 PDB header: transferase Chain: C: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from2 porphyromonas gingivalis atcc 33277, nysgrc target 030972,3 orthorhombic symmetry
90	c3khdC_	Alignment	not modelled	93.4	10 PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
91	d3pnpa_	Alignment	not modelled	93.3	21 Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
92	c2p4sA_	Alignment	not modelled	93.3	15 PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: structure of purine nucleoside phosphorylase from anopheles gambiae in2 complex with dadme-immh
93	c6ei9A_	Alignment	not modelled	93.2	11 PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
94	c5afdA_	Alignment	not modelled	93.0	9 PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: native structure of n-acetylneuraminatase lyase (sialic acid aldolase)2 from aliivibrio salmonicida
95	c3e02A_	Alignment	not modelled	93.0	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
96	c3ggsA_	Alignment	not modelled	92.9	18 PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
97	c3hpxB_	Alignment	not modelled	92.6	9 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)
98	c5n2pA_	Alignment	not modelled	92.5	15 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfobolus solfataricus tryptophan synthase a
99	c2yw3E_	Alignment	not modelled	92.4	18 PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
					PDB header: oxidoreductase

100	c3w9zA_	Alignment	not modelled	92.4	16	Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
101	c5ud6B_	Alignment	not modelled	92.3	18	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from cyanidioschyzon merolae with lysine2 bound
102	c2hjpA_	Alignment	not modelled	92.3	16	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
103	c3e49A_	Alignment	not modelled	92.1	17	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf849 with a tim barrel fold; PDBTitle: crystal structure of a prokaryotic domain of unknown function (duf849)2 with a tim barrel fold (bx_e_c0966) from burkholderia xenovorans lb4003 at 1.75 a resolution
104	c1yr3A_	Alignment	not modelled	91.9	15	PDB header: transferase Chain: A: PDB Molecule: xanthosine phosphorylase; PDBTitle: escherichia coli purine nucleoside phosphorylase ii, the product of2 the xapa gene
105	d3bofa1	Alignment	not modelled	91.7	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
106	c4lsbA_	Alignment	not modelled	91.6	18	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
107	c5uurA_	Alignment	not modelled	91.6	14	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
108	d1yxa1	Alignment	not modelled	91.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
109	d1rqba2	Alignment	not modelled	91.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
110	d1ajza_	Alignment	not modelled	91.4	15	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
111	d3bgsa1	Alignment	not modelled	91.4	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
112	c3lotC_	Alignment	not modelled	91.4	12	PDB header: structure genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (np_070038.1) from2 archaeoglobus fulgidus at 1.89 a resolution
113	c3n2xB_	Alignment	not modelled	91.4	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
114	c2r94B_	Alignment	not modelled	91.2	19	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
115	c3lciA_	Alignment	not modelled	91.2	18	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
116	c4rc1B_	Alignment	not modelled	91.0	18	PDB header: unknown function Chain: B: PDB Molecule: upf0264 protein mj1099; PDBTitle: structure of the methanofuran/methanopterin biosynthetic enzyme mj10992 from methanocaldococcus jannaschii with prpp
117	c2ehhE_	Alignment	not modelled	91.0	19	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
118	c3c52B_	Alignment	not modelled	90.9	13	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: class ii fructose-1,6-bisphosphate aldolase from helicobacter pylori2 in complex with phosphoglycolohydroxamic acid, a competitive3 inhibitor
119	c3g0sA_	Alignment	not modelled	90.9	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
120	c1piiA_	Alignment	not modelled	90.8	17	PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5'-phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution