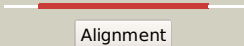

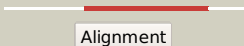

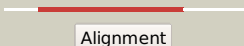







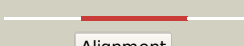











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2733c_(-)_3044996_3046534
Date	Wed Aug 7 12:50:39 BST 2019
Unique Job ID	b445deed34b0fc37

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4jc0B_	 Alignment		100.0	31	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
2	c2qgqF_	 Alignment		100.0	29	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
3	c6fd2B_	 Alignment		100.0	18	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
4	c5ul4A_	 Alignment		100.0	13	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
5	c3cixA_	 Alignment		100.0	15	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
6	d1olta_	 Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Oxygen-independent coproporphyrinogen III oxidase HemN
7	c4u0pB_	 Alignment		100.0	18	PDB header: transferase Chain: B; PDB Molecule: lipoyl synthase 2; PDBTitle: the crystal structure of lipoyl synthase in complex with s-adenosyl2 homocysteine
8	c5exkG_	 Alignment		100.0	18	PDB header: transferase Chain: G; PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
9	c5l7jA_	 Alignment		100.0	16	PDB header: translation Chain: A; PDB Molecule: elp3 family; PDBTitle: crystal structure of elp3 from dehalococcoides mccartyi
10	c3t7vA_	 Alignment		100.0	15	PDB header: transferase Chain: A; PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
11	d1r30a_	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: Biotin synthase

12	c1r30A_	Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: biotin synthase; PDBTitle: the crystal structure of biotin synthase, an s-adenosylmethionine-2 dependent radical enzyme
13	c6iazA_	Alignment		100.0	17	PDB header: transferase Chain: A; PDB Molecule: histone acetyltransferase, elp3 family; PDBTitle: the archaeal methanocaldococcus infernus elp3 with n-terminus deletion2 (1-46)
14	c6qk7C_	Alignment		99.9	17	PDB header: translation Chain: C; PDB Molecule: elongator complex protein 3; PDBTitle: elongator catalytic subcomplex elp123 lobe
15	c4wxcC_	Alignment		99.9	11	PDB header: lyase Chain: C; PDB Molecule: biotin and thiamin synthesis associated; PDBTitle: crystal structure of hydg: a maturase of the [fefe]-hydrogenase
16	c3rfaA_	Alignment		99.9	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
17	c3rfaB_	Alignment		99.9	16	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
18	c4rtbA_	Alignment		99.8	14	PDB header: lyase Chain: A; PDB Molecule: hydg protein; PDBTitle: x-ray structure of the fefe-hydrogenase maturase hydg from2 carboxydotherrnus hydrogenoformans
19	c6fz6B_	Alignment		99.8	15	PDB header: transferase Chain: B; PDB Molecule: probable dual-specificity rna methyltransferase rlmn; PDBTitle: crystal structure of a radical sam methyltransferase from2 sphaerobacter thermophilus
20	c5v1tA_	Alignment		99.8	15	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam; PDBTitle: crystal structure of streptococcus suis suib bound to precursor2 peptide sua
21	c2yx0A_	Alignment	not modelled	99.7	14	PDB header: metal binding protein Chain: A; PDB Molecule: radical sam enzyme; PDBTitle: crystal structure of p. horikoshii tyw1
22	d1tv8a_	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Radical SAM enzymes Family: MoCo biosynthesis proteins
23	c4r33A_	Alignment	not modelled	99.7	14	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
24	c5vslB_	Alignment	not modelled	99.6	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)
25	c2a5hC_	Alignment	not modelled	99.6	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).
26	c3c8fA_	Alignment	not modelled	99.5	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
27	c4fheA_	Alignment	not modelled	99.5	14	PDB header: lyase Chain: A; PDB Molecule: spore photoproduct lyase; PDBTitle: spore photoproduct lyase c140a mutant
						PDB header: oxidoreductase

28	c4k39A	Alignment	not modelled	99.5	10	Chain: A; PDB Molecule: anaerobic sulfatase-maturing enzyme; PDBTitle: native ansmecepe with bound adomet and cp18cys peptide
29	c6efnA	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A; PDB Molecule: sporulation killing factor maturation protein skfb; PDBTitle: structure of a ripp maturase, skfb
30	c6b4cH	Alignment	not modelled	99.4	15	PDB header: antiviral protein Chain: H; PDB Molecule: viperin; PDBTitle: structure of viperin from trichoderma virens
31	c5th5C	Alignment	not modelled	99.2	16	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
32	c5wggA	Alignment	not modelled	99.0	13	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
33	c4m7tA	Alignment	not modelled	98.8	12	PDB header: metal binding protein Chain: A; PDB Molecule: btrn; PDBTitle: crystal structure of btrn in complex with adomet and 2-doia
34	c6c8vA	Alignment	not modelled	98.3	14	PDB header: oxidoreductase Chain: A; PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
35	c6nhlB	Alignment	not modelled	98.1	12	PDB header: lyase Chain: B; PDB Molecule: 7-carboxy-7-deazaguanine synthase; PDBTitle: crystal structure of quee from escherichia coli
36	c2z2uA	Alignment	not modelled	97.6	17	PDB header: metal binding protein Chain: A; PDB Molecule: upf0026 protein mj0257; PDBTitle: crystal structure of archaeal tyw1
37	c4njka	Alignment	not modelled	97.6	11	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+
38	c3canA	Alignment	not modelled	97.5	20	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
39	d7reqa2	Alignment	not modelled	97.3	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
40	c1e1cA	Alignment	not modelled	97.0	17	PDB header: isomerase Chain: A; PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
41	c2ftpA	Alignment	not modelled	96.6	15	PDB header: lyase Chain: A; PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
42	d3bula2	Alignment	not modelled	96.5	11	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
43	d1ccwa	Alignment	not modelled	96.3	13	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
44	c3rmjB	Alignment	not modelled	96.3	13	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of truncated alpha-isopropylmalate synthase from2 neisseria meningitidis
45	c3jvuB	Alignment	not modelled	95.9	11	PDB header: transferase Chain: B; PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
46	c2cw6B	Alignment	not modelled	95.8	12	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
47	c1bmtB	Alignment	not modelled	95.8	13	PDB header: methyltransferase Chain: B; PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
48	c3bicA	Alignment	not modelled	95.5	15	PDB header: isomerase Chain: A; PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
49	c1y80A	Alignment	not modelled	95.5	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
50	c2p10D	Alignment	not modelled	95.2	21	PDB header: hydrolase Chain: D; PDB Molecule: mlI9387 protein; PDBTitle: crystal structure of a putative phosphonopyruvate hydrolase (mlI9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
51	c3ewbX	Alignment	not modelled	95.2	13	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
52	c3eegB	Alignment	not modelled	94.9	11	PDB header: transferase Chain: B; PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of a 2-isopropylmalate synthase from2 cytophaga hutchinsonii
53	c2vxbA	Alignment	not modelled	94.9	17	PDB header: isomerase Chain: A; PDB Molecule: coenzyme b12-dependent mutase;

53	c4yxaA	Alignment	not modelled	94.5	17	PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix PDB header: flavoprotein/transcription
54	c4hh3C	Alignment	not modelled	94.8	20	Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-pps2 core complex from rb. sphaeroides
55	c2i2xD	Alignment	not modelled	94.3	13	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
56	c3bleA	Alignment	not modelled	93.6	10	Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
57	d1f6ya	Alignment	not modelled	93.5	10	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
58	d1tx2a	Alignment	not modelled	93.5	12	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
59	c1tx2A	Alignment	not modelled	93.5	12	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
60	c6reqB	Alignment	not modelled	93.1	15	PDB header: isomerase Chain: B: PDB Molecule: protein (methylmalonyl-coa mutase); PDBTitle: methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
61	c3hpxB	Alignment	not modelled	92.9	14	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)
62	c3ct7E	Alignment	not modelled	92.8	11	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
63	d1fmfa	Alignment	not modelled	92.6	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
64	c3ezxA	Alignment	not modelled	92.5	13	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
65	c1ydnA	Alignment	not modelled	92.3	14	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.
66	c4hh0B	Alignment	not modelled	92.0	17	PDB header: flavoprotein,signaling protein Chain: B: PDB Molecule: appa protein; PDBTitle: dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides
67	d1nvm2	Alignment	not modelled	92.0	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
68	c1nvmG	Alignment	not modelled	91.8	13	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
69	c6omzA	Alignment	not modelled	91.1	13	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
70	d1ajza	Alignment	not modelled	91.1	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
71	c1zfa	Alignment	not modelled	91.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
72	d1ad1a	Alignment	not modelled	90.8	10	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
73	c4e38A	Alignment	not modelled	90.8	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)
74	d1qt1a	Alignment	not modelled	90.7	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
75	c4jgiB	Alignment	not modelled	90.6	17	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
76	c3khdC	Alignment	not modelled	90.0	9	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
77	d1eyea	Alignment	not modelled	90.0	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
78	c1ydoC	Alignment	not modelled	89.9	8	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. PDB header: plant protein

79	c6e1jB_	Alignment	not modelled	89.7	10	Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
80	d1yvca1	Alignment	not modelled	89.1	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
81	c3lu2B_	Alignment	not modelled	88.5	16	PDB header: hydrolase Chain: B: PDB Molecule: lmo2462 protein; PDBTitle: structure of lmo2462, a listeria monocytogenes amidohydrolase family2 putative dipeptidase
82	c6gcsK_	Alignment	not modelled	88.3	13	PDB header: oxidoreductase Chain: K: PDB Molecule: psst subunit (nukm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
83	d1xima_	Alignment	not modelled	87.8	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
84	c4z87B_	Alignment	not modelled	87.8	24	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
85	c3whpA_	Alignment	not modelled	87.6	18	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
86	c5visB_	Alignment	not modelled	87.6	11	PDB header: hydrolase,oxidoreductase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: 1.73 angstrom resolution crystal structure of dihydropteroate synthase2 (folp-smz_b27) from soil uncultured bacterium.
87	d1yeza1	Alignment	not modelled	87.4	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: TRAM domain
88	c4af0B_	Alignment	not modelled	87.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
89	c6oviA_	Alignment	not modelled	87.1	11	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
90	d1k77a_	Alignment	not modelled	86.9	12	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
91	d1h1ya_	Alignment	not modelled	86.7	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
92	c2h1fB_	Alignment	not modelled	86.4	12	PDB header: transferase Chain: B: PDB Molecule: lipopolysaccharide heptosyltransferase-1; PDBTitle: e. coli heptosyltransferase waac with adp
93	d1muwa_	Alignment	not modelled	86.3	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
94	c4fxsA_	Alignment	not modelled	85.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
95	d1liua2	Alignment	not modelled	85.2	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
96	c3tr9A_	Alignment	not modelled	85.2	16	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroiic2 acid from coxiella burnetii
97	c3f6cB_	Alignment	not modelled	84.7	12	PDB header: dna binding protein Chain: B: PDB Molecule: positive transcription regulator evga; PDBTitle: crystal structure of n-terminal domain of positive transcription2 regulator evga from escherichia coli
98	c4ov9A_	Alignment	not modelled	84.4	14	PDB header: transferase Chain: A: PDB Molecule: isopropylmalate synthase; PDBTitle: structure of isopropylmalate synthase binding with alpha-2 isopropylmalate
99	c5uurA_	Alignment	not modelled	84.2	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
100	c4o1fB_	Alignment	not modelled	83.4	14	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
101	c2yw3E_	Alignment	not modelled	83.0	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
102	d2glka1	Alignment	not modelled	82.8	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
103	c3cu2A_	Alignment	not modelled	82.3	13	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution

104	d1mxsa_	Alignment	not modelled	82.1	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
105	d1vhca_	Alignment	not modelled	82.1	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
106	c4fxjB_	Alignment	not modelled	81.7	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
107	c4r3uD_	Alignment	not modelled	81.4	14	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
108	c2yciX_	Alignment	not modelled	81.4	15	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
109	c2zyfA_	Alignment	not modelled	80.7	13	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
110	c2fmoA_	Alignment	not modelled	80.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methylenetetrahydrofolate reductase; PDBTitle: ala177val mutant of e. coli methylenetetrahydrofolate2 reductase
111	c4jn6C_	Alignment	not modelled	79.6	14	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
112	c3qc3B_	Alignment	not modelled	79.6	15	PDB header: isomerase Chain: B: PDB Molecule: d-ribose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
113	c3gveB_	Alignment	not modelled	77.5	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yfkn protein; PDBTitle: crystal structure of calcineurin-like phosphoesterase yfkn from2 bacillus subtilis
114	d7reqb2	Alignment	not modelled	77.3	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
115	c6humK_	Alignment	not modelled	75.3	17	PDB header: proton transport Chain: K: PDB Molecule: nad(p)h-quinone oxidoreductase subunit k; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
116	c6fcgB_	Alignment	not modelled	74.9	12	PDB header: hydrolase Chain: B: PDB Molecule: glycoside hydrolase, gh17 family; PDBTitle: crystal structure of an endo-laminarinase from formosa hel1_33_131
117	d3bofa1	Alignment	not modelled	74.8	10	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
118	c2vefB_	Alignment	not modelled	74.3	14	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
119	c3zu0A_	Alignment	not modelled	74.3	12	PDB header: hydrolase Chain: A: PDB Molecule: nad nucleotidase; PDBTitle: structure of haemophilus influenzae nad nucleotidase (nadr)
120	d1pswa_	Alignment	not modelled	73.6	18	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: ADP-heptose LPS heptosyltransferase II