

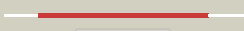







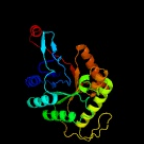



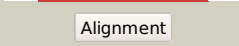






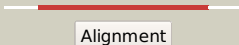
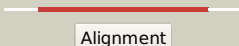

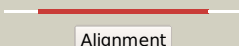



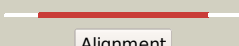

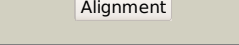
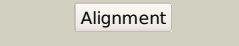

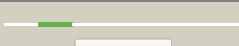
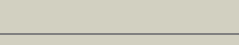
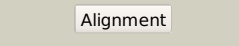


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2161c (-) _2422279_2423145
Date	Mon Aug 5 13:25:28 BST 2019
Unique Job ID	dff964c1de603bca

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2b81D_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
2	<a href="#">c5tlcA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme a; <b>PDBTitle:</b> crystal structure of bdsa from bacillus subtilis wu-s2b
3	<a href="#">d1lucb_</a>	 Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
4	<a href="#">d1luca_</a>	 Alignment		100.0	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
5	<a href="#">c5w4zA_</a>	 Alignment		100.0	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin lyase; <b>PDBTitle:</b> crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
6	<a href="#">c6friD_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alkanal monooxygenase beta chain; <b>PDBTitle:</b> structure of luxb from photobacterium leiognathi
7	<a href="#">c3sdoB_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrotriacetate monooxygenase; <b>PDBTitle:</b> structure of a nitrotriacetate monooxygenase from burkholderia2 pseudomallei
8	<a href="#">d1tvla_</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
9	<a href="#">c1tvIA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
10	<a href="#">d1ezwa_</a>	 Alignment		100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
11	<a href="#">c3b9nB_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkane monooxygenase; <b>PDBTitle:</b> crystal structure of long-chain alkane monooxygenase (lada)

12	<a href="#">c1z69D</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> coenzyme f420-dependent n(5),n(10)- <b>PDBTitle:</b> crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
13	<a href="#">c6ak1B</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyl-sulfide monooxygenase; <b>PDBTitle:</b> crystal structure of dmoa from hyphomicrobium sulfonivorans
14	<a href="#">c5dqpA</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> edta monooxygenase; <b>PDBTitle:</b> edta monooxygenase (emoa) from chelativorans sp. bnc1
15	<a href="#">c3raoB</a>	 Alignment		100.0	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
16	<a href="#">c2wgkA</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,6-diketocamphane 1,6 monooxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
17	<a href="#">c2i7qA</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
18	<a href="#">d1f07a</a>	 Alignment		100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
19	<a href="#">d1rhca</a>	 Alignment		100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
20	<a href="#">c3c8nB</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable f420-dependent glucose-6-phosphate dehydrogenase <b>PDBTitle:</b> crystal structure of apo-fgd1 from mycobacterium tuberculosis
21	<a href="#">c5wanA</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine monooxygenase ruta; <b>PDBTitle:</b> crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
22	<a href="#">d1nqka</a>	 Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
23	<a href="#">d1nfpa</a>	 Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
24	<a href="#">d1fvpa</a>	 Alignment	not modelled	97.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
25	<a href="#">c3dcpB</a>	 Alignment	not modelled	59.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
26	<a href="#">c4ovxA</a>	 Alignment	not modelled	56.0	32	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
27	<a href="#">c3e38A</a>	 Alignment	not modelled	53.7	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> two-domain protein containing predicted php-like metal- <b>PDBTitle:</b> crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution <b>PDB header:</b> lyase

28	<a href="#">c3fa4D_</a>	Alignment	not modelled	52.6	17	<b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
29	<a href="#">c2yb1A_</a>	Alignment	not modelled	52.4	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
30	<a href="#">c1zlpA_</a>	Alignment	not modelled	50.3	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
31	<a href="#">d1uoua2</a>	Alignment	not modelled	50.0	16	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
32	<a href="#">c2zvrA_</a>	Alignment	not modelled	49.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein tm_0416; <b>PDBTitle:</b> crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
33	<a href="#">c2w9mB_</a>	Alignment	not modelled	47.3	11	<b>PDB header:</b> dna replication <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase x; <b>PDBTitle:</b> structure of family x dna polymerase from deinococcus2 radiodurans
34	<a href="#">d1xp3a1</a>	Alignment	not modelled	47.2	7	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
35	<a href="#">d1m5wa_</a>	Alignment	not modelled	46.2	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
36	<a href="#">c5dlcC_</a>	Alignment	not modelled	46.0	33	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa
37	<a href="#">c4lsbA_</a>	Alignment	not modelled	45.6	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
38	<a href="#">c3qy6A_</a>	Alignment	not modelled	44.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase ywqe; <b>PDBTitle:</b> crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
39	<a href="#">c3d0cB_</a>	Alignment	not modelled	44.4	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
40	<a href="#">d1m65a_</a>	Alignment	not modelled	41.2	10	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
41	<a href="#">c3e0fA_</a>	Alignment	not modelled	39.7	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative metal-dependent phosphoesterase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution
42	<a href="#">c3vniC_</a>	Alignment	not modelled	38.4	11	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> xylose isomerase domain protein tim barrel; <b>PDBTitle:</b> crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketohexose sugars
43	<a href="#">c2hjpA_</a>	Alignment	not modelled	37.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
44	<a href="#">c2yz5B_</a>	Alignment	not modelled	37.1	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol phosphatase; <b>PDBTitle:</b> histidinol phosphate phosphatase complexed with phosphate
45	<a href="#">c2x7vA_</a>	Alignment	not modelled	36.7	7	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
46	<a href="#">c3ih1A_</a>	Alignment	not modelled	36.7	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
47	<a href="#">c3e96B_</a>	Alignment	not modelled	36.4	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
48	<a href="#">c2ze3A_</a>	Alignment	not modelled	36.2	25	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
49	<a href="#">d1thfd_</a>	Alignment	not modelled	35.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
50	<a href="#">c3gk0H_</a>	Alignment	not modelled	35.7	18	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
51	<a href="#">c4gx9A_</a>	Alignment	not modelled	35.1	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit epsilon,dna polymerase iii <b>PDBTitle:</b> crystal structure of a dna polymerase iii alpha-epsilon

						chimera
52	<a href="#">c3lyeA</a>	Alignment	not modelled	34.6	47	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
53	<a href="#">c4ur7B</a>	Alignment	not modelled	33.5	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> keto-deoxy-d-galactarate dehydratase; <b>PDBTitle:</b> crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
54	<a href="#">c6k0aC</a>	Alignment	not modelled	32.1	11	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease p protein component 3; <b>PDBTitle:</b> cryo-em structure of an archaeal ribonuclease p
55	<a href="#">d1s2wa</a>	Alignment	not modelled	32.0	33	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
56	<a href="#">c3b8iF</a>	Alignment	not modelled	31.2	12	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+
57	<a href="#">c5zhzA</a>	Alignment	not modelled	29.7	29	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of the apurinic/aprimidinic endonuclease iv from2 mycobacterium tuberculosis
58	<a href="#">d1m3ua</a>	Alignment	not modelled	27.3	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
59	<a href="#">c5i4rA</a>	Alignment	not modelled	27.2	11	<b>PDB header:</b> toxin/antitoxin <b>Chain:</b> A: <b>PDB Molecule:</b> contact-dependent inhibitor a; <b>PDBTitle:</b> contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
60	<a href="#">d1oy0a</a>	Alignment	not modelled	27.0	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
61	<a href="#">d1brwa2</a>	Alignment	not modelled	26.9	18	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
62	<a href="#">c2wjeA</a>	Alignment	not modelled	26.5	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase cpsb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase cps4b from2 stptococcus pneumoniae tigr4.
63	<a href="#">c3o6cA</a>	Alignment	not modelled	26.2	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
64	<a href="#">d1o5ka</a>	Alignment	not modelled	25.4	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
65	<a href="#">c3auoB</a>	Alignment	not modelled	24.8	15	<b>PDB header:</b> transferase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase beta family (x family); <b>PDBTitle:</b> dna polymerase x from thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp
66	<a href="#">c2y85D</a>	Alignment	not modelled	24.7	10	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosyl isomerase a; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
67	<a href="#">c3obeB</a>	Alignment	not modelled	24.3	10	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
68	<a href="#">d1ka9f</a>	Alignment	not modelled	24.2	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
69	<a href="#">c3cnyA</a>	Alignment	not modelled	23.7	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> inositol catabolism protein iole; <b>PDBTitle:</b> crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
70	<a href="#">c4cngB</a>	Alignment	not modelled	23.3	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spou rrna methylase; <b>PDBTitle:</b> crystal structure of sulfobolus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
71	<a href="#">c2qiWA</a>	Alignment	not modelled	22.4	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonmutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncg11015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
72	<a href="#">c2anuA</a>	Alignment	not modelled	21.6	15	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0559; <b>PDBTitle:</b> crystal structure of predicted metal-dependent phosphoesterase (php2 family) (tm0559) from thermotoga maritima at 2.40 a resolution
73	<a href="#">d2anuA1</a>	Alignment	not modelled	21.6	15	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
74	<a href="#">d1muma</a>	Alignment	not modelled	21.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
75	<a href="#">c3tdmD</a>	Alignment	not modelled	21.1	19	<b>PDB header:</b> de novo protein <b>Chain:</b> D: <b>PDB Molecule:</b> computationally designed two-fold symmetric tim-barrel <b>PDBTitle:</b> computationally designed tim-barrel protein, halfllr
76	<a href="#">c4wd0A</a>	Alignment	not modelled	19.8	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-

76	<a href="#">c4w0vA</a>	Alignment	not modelled	19.8	10	phosphoribosylamino) <b>PDBTitle:</b> crystal structure of hisap form arthrobacter aureus
77	<a href="#">d2a6na1</a>	Alignment	not modelled	19.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
78	<a href="#">c3bh1A</a>	Alignment	not modelled	18.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0371 protein dip2346; <b>PDBTitle:</b> crystal structure of protein dip2346 from corynebacterium diphtheriae
79	<a href="#">c4qj1A</a>	Alignment	not modelled	17.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) <b>PDBTitle:</b> crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
80	<a href="#">c3dx5A</a>	Alignment	not modelled	15.9	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein asbf; <b>PDBTitle:</b> crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
81	<a href="#">d1ujqa</a>	Alignment	not modelled	15.6	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
82	<a href="#">c3eooL</a>	Alignment	not modelled	15.6	19	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
83	<a href="#">d1xxa1</a>	Alignment	not modelled	14.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
84	<a href="#">d1x7fa2</a>	Alignment	not modelled	14.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Outer surface protein, N-terminal domain
85	<a href="#">c4mg4G</a>	Alignment	not modelled	14.3	17	<b>PDB header:</b> unknown function <b>Chain:</b> G: <b>PDB Molecule:</b> phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphonomutase from burkholderia2 cenocepacia j2315
86	<a href="#">d1e8ca2</a>	Alignment	not modelled	14.2	12	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
87	<a href="#">c3ez4B</a>	Alignment	not modelled	14.1	12	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyl-2-oxobutanoate hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of 3-methyl-2-oxobutanoate hydroxymethyltransferase2 from burkholderia pseudomallei
88	<a href="#">d1oyaa</a>	Alignment	not modelled	13.8	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
89	<a href="#">c3orsD</a>	Alignment	not modelled	13.7	10	<b>PDB header:</b> isomerase,biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
90	<a href="#">c3umuA</a>	Alignment	not modelled	13.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> crystal structure of l-histidinol phosphate phosphatase (hisk) from2 lactococcus lactis subsp. lactis il1403 complexed with zn, phosphate3 and l-histidinol
91	<a href="#">d1z41a1</a>	Alignment	not modelled	13.1	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
92	<a href="#">c3i4eA</a>	Alignment	not modelled	13.0	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> isocitrate lyase; <b>PDBTitle:</b> crystal structure of isocitrate lyase from burkholderia2 pseudomallei
93	<a href="#">d1w3ia</a>	Alignment	not modelled	12.7	5	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
94	<a href="#">c3f55A</a>	Alignment	not modelled	12.7	21	<b>PDB header:</b> hydrolase, allergen <b>Chain:</b> A: <b>PDB Molecule:</b> beta-1,3-glucanase; <b>PDBTitle:</b> crystal structure of the native endo beta-1,3-glucanase (hev b 2), a2 major allergen from hevea brasiliensis (space group p41)
95	<a href="#">d1vzwa1</a>	Alignment	not modelled	12.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phoshate binding barrel <b>Family:</b> Histidine biosynthesis enzymes
96	<a href="#">c6ahuJ</a>	Alignment	not modelled	12.3	7	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> ribonuclease p protein subunit p30; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p with mature trna
97	<a href="#">d1viza</a>	Alignment	not modelled	12.0	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
98	<a href="#">c3fkkA</a>	Alignment	not modelled	11.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase; <b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
99	<a href="#">c5aheA</a>	Alignment	not modelled	11.8	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> crystal structure of salmonella enterica hisa