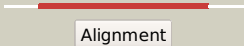

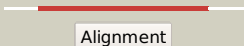

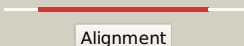







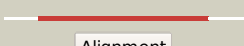
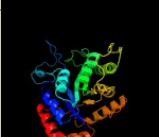








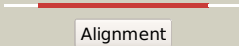

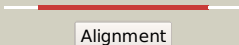

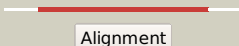



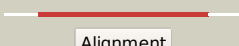

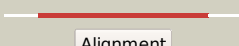

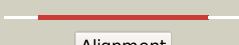





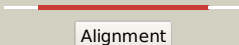
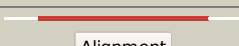



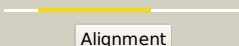
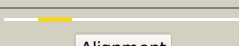
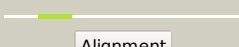


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0953c_(-)_1064118_1064966
Date	Fri Jul 26 01:50:54 BST 2019
Unique Job ID	e67a75324bb83a47

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2b81D_</a>	 Alignment		100.0	19	<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="#">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)
3	<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)
4	<a href="#">c6friD_</a>	 Alignment		100.0	17	<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
5	<a href="#">d1ezwa_</a>	 Alignment		100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
6	<a href="#">c3raoB_</a>	 Alignment		100.0	27	<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.
7	<a href="#">c5tlcA_</a>	 Alignment		100.0	22	<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
8	<a href="#">c3sdoB_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nitrilotriacetate monooxygenase; <b>PDBTitle:</b> structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
9	<a href="#">c1z69D_</a>	 Alignment		100.0	22	<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
10	<a href="#">c2i7gA_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
11	<a href="#">c5w4zA_</a>	 Alignment		100.0	24	<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

12	<a href="#">d1tvla_</a>	 Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
13	<a href="#">c1tvA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
14	<a href="#">d1nqka_</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
15	<a href="#">c3c8nB_</a>	 Alignment		100.0	25	<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
16	<a href="#">c2wgkA_</a>	 Alignment		100.0	20	<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="#">d1f07a_</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
18	<a href="#">c5dqpa_</a>	 Alignment		100.0	23	<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
19	<a href="#">c6ak1B_</a>	 Alignment		100.0	22	<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
20	<a href="#">c3b9nB_</a>	 Alignment		100.0	19	<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)
21	<a href="#">c5wanA_</a>	 Alignment	not modelled	100.0	24	<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="#">d1rhca_</a>	 Alignment	not modelled	100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
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	97.4	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (luxF, FP390)
25	<a href="#">c3cqkB_</a>	 Alignment	not modelled	81.4	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ribulose-5-phosphate 3-epimerase ulae; <b>PDBTitle:</b> crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
26	<a href="#">c3vniC_</a>	 Alignment	not modelled	75.9	13	<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
27	<a href="#">c3wqoB_</a>	 Alignment	not modelled	73.9	15	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein mj1311; <b>PDBTitle:</b> crystal structure of d-tagatose 3-epimerase-like protein
28	<a href="#">c4ovxA_</a>	 Alignment	not modelled	67.7	23	<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
29	<a href="#">d1xp3a1</a>	Alignment	not modelled	67.2	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Endonuclease IV
30	<a href="#">d1i60a_</a>	Alignment	not modelled	61.9	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> loll-like
31	<a href="#">c3vndD_</a>	Alignment	not modelled	57.3	18	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-subunit from the2 psychrophile shewanella frigidimarina k14-2
32	<a href="#">c2x7vA_</a>	Alignment	not modelled	56.1	14	<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
33	<a href="#">c2zvrA_</a>	Alignment	not modelled	51.4	29	<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
34	<a href="#">c3ih1A_</a>	Alignment	not modelled	50.3	15	<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
35	<a href="#">c2ekcA_</a>	Alignment	not modelled	49.6	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> structural study of project id aq_1548 from aquifex aeolicus vf5
36	<a href="#">d1m3ua_</a>	Alignment	not modelled	47.8	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
37	<a href="#">c1zlpA_</a>	Alignment	not modelled	46.9	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
38	<a href="#">d1m5wa_</a>	Alignment	not modelled	46.3	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
39	<a href="#">c4ur7B_</a>	Alignment	not modelled	45.2	13	<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
40	<a href="#">c5uncB_</a>	Alignment	not modelled	44.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoenolpyruvate phosphomutase; <b>PDBTitle:</b> the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
41	<a href="#">c3obeB_</a>	Alignment	not modelled	44.8	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
42	<a href="#">c3gk0H_</a>	Alignment	not modelled	44.5	24	<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
43	<a href="#">c3dcpB_</a>	Alignment	not modelled	44.2	11	<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.
44	<a href="#">c2yb1A_</a>	Alignment	not modelled	43.4	20	<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.
45	<a href="#">c3dx5A_</a>	Alignment	not modelled	42.7	19	<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
46	<a href="#">c6gvbC_</a>	Alignment	not modelled	42.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> exo-beta-1,4-mannosidase; <b>PDBTitle:</b> crystal structure of cutibacterium acnes exo-beta-1,4-mannosidase
47	<a href="#">c3qy6A_</a>	Alignment	not modelled	41.7	33	<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
48	<a href="#">c3e38A_</a>	Alignment	not modelled	41.6	23	<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
49	<a href="#">c5dlcC_</a>	Alignment	not modelled	39.3	30	<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
50	<a href="#">c2ze3A_</a>	Alignment	not modelled	36.6	16	<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
51	<a href="#">c2qiwa_</a>	Alignment	not modelled	36.2	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pep phosphonomutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncgj1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
52	<a href="#">c3lyeA_</a>	Alignment	not modelled	33.1	16	<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="#">c4lsbA_</a>	Alignment	not modelled	32.4	31	<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
54	<a href="#">c5kzmA_</a>	Alignment	not modelled	32.4	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
55	<a href="#">c4k3zA_</a>	Alignment	not modelled	28.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-erythrose 4-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
56	<a href="#">c3ju2A_</a>	Alignment	not modelled	28.4	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein smc04130; <b>PDBTitle:</b> crystal structure of protein smc04130 from sinorhizobium meliloti 1021
57	<a href="#">c5kinC_</a>	Alignment	not modelled	28.4	23	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
58	<a href="#">d1x7fa2</a>	Alignment	not modelled	26.9	21	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Outer surface protein, N-terminal domain
59	<a href="#">c5zhzA_</a>	Alignment	not modelled	26.8	25	<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
60	<a href="#">c3ngfA_</a>	Alignment	not modelled	26.8	23	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ap endonuclease, family 2; <b>PDBTitle:</b> crystal structure of ap endonuclease, family 2 from brucella2 melitensis
61	<a href="#">c4cngB_</a>	Alignment	not modelled	26.0	26	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> spou rrna methylase; <b>PDBTitle:</b> crystal structure of sulfobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
62	<a href="#">c5i4rA_</a>	Alignment	not modelled	25.8	17	<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)
63	<a href="#">c2w9mB_</a>	Alignment	not modelled	25.5	17	<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
64	<a href="#">c4fioA_</a>	Alignment	not modelled	25.4	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methenyltetrahydromethanopterin cyclohydrolase; <b>PDBTitle:</b> crystal structure of methenyltetrahydromethanopterin cyclohydrolase2 from methanobrevibacter ruminantium
65	<a href="#">d1m65a_</a>	Alignment	not modelled	24.5	17	<b>Fold:</b> 7-stranded beta/alpha barrel <b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
66	<a href="#">c5tchG_</a>	Alignment	not modelled	24.1	25	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
67	<a href="#">c2jimH_</a>	Alignment	not modelled	24.0	9	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> glycosyl transferase, group 1 family protein; <b>PDBTitle:</b> crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
68	<a href="#">c3l23A_</a>	Alignment	not modelled	23.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar phosphate isomerase/epimerase; <b>PDBTitle:</b> crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
69	<a href="#">d1ujqa_</a>	Alignment	not modelled	23.4	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
70	<a href="#">c4gx9A_</a>	Alignment	not modelled	23.2	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
71	<a href="#">c3e0fA_</a>	Alignment	not modelled	23.0	20	<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
72	<a href="#">c2p0oA_</a>	Alignment	not modelled	22.5	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein duf871; <b>PDBTitle:</b> crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
73	<a href="#">c3auoB_</a>	Alignment	not modelled	22.1	23	<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
74	<a href="#">c3ez4B_</a>	Alignment	not modelled	21.8	9	<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
75	<a href="#">d1qlma_</a>	Alignment	not modelled	21.4	22	<b>Fold:</b> Methenyltetrahydromethanopterin cyclohydrolase <b>Superfamily:</b> Methenyltetrahydromethanopterin cyclohydrolase <b>Family:</b> Methenyltetrahydromethanopterin cyclohydrolase
76	<a href="#">c6k0aC_</a>	Alignment	not modelled	21.2	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

77	<a href="#">c3bh1A</a>	Alignment	not modelled	20.3	30	<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
78	<a href="#">d1yx1a1</a>	Alignment	not modelled	20.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> KguE-like
79	<a href="#">d1uoua2</a>	Alignment	not modelled	19.9	20	<b>Fold:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Superfamily:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain <b>Family:</b> Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
80	<a href="#">c5zfsA</a>	Alignment	not modelled	18.1	13	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> d-allulose-3-epimerase; <b>PDBTitle:</b> crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
81	<a href="#">c3lmzA</a>	Alignment	not modelled	17.5	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative sugar isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
82	<a href="#">c3o6cA</a>	Alignment	not modelled	17.2	19	<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
83	<a href="#">d1oyaa</a>	Alignment	not modelled	16.7	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
84	<a href="#">c2yz5B</a>	Alignment	not modelled	15.3	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
85	<a href="#">d1z41a1</a>	Alignment	not modelled	15.1	29	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
86	<a href="#">d1k77a</a>	Alignment	not modelled	14.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Xylose isomerase-like <b>Family:</b> Hypothetical protein YgbM (EC1530)
87	<a href="#">c6bmaA</a>	Alignment	not modelled	14.5	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
88	<a href="#">c1x7fA</a>	Alignment	not modelled	14.1	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> outer surface protein; <b>PDBTitle:</b> crystal structure of an uncharacterized b. cereus protein
89	<a href="#">c6ahuJ</a>	Alignment	not modelled	13.6	13	<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
90	<a href="#">c5dxxA</a>	Alignment	not modelled	13.4	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> artemisinic aldehyde delta(11(13)) reductase; <b>PDBTitle:</b> crystal structure of dbr2
91	<a href="#">c3qxbB</a>	Alignment	not modelled	13.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative xylose isomerase; <b>PDBTitle:</b> crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
92	<a href="#">d1gwja</a>	Alignment	not modelled	12.6	35	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
93	<a href="#">d1vyra</a>	Alignment	not modelled	12.6	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
94	<a href="#">c4a3uB</a>	Alignment	not modelled	12.5	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nahd\flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
95	<a href="#">c4tmcB</a>	Alignment	not modelled	12.4	24	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> old yellow enzyme; <b>PDBTitle:</b> crystal structure of old yellow enzyme from candida macedoniensis2 aku4588 complexed with p-hydroxybenzaldehyde
96	<a href="#">c6mp2B</a>	Alignment	not modelled	12.1	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> blman5b; <b>PDBTitle:</b> crystal structure of blman5b solved by siras
97	<a href="#">c2gq8A</a>	Alignment	not modelled	12.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> structure of sye1, an oye homologue from s. ondeidensis, in complex2 with p-hydroxyacetophenone
98	<a href="#">c2h90A</a>	Alignment	not modelled	11.6	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
99	<a href="#">c4b5nA</a>	Alignment	not modelled	11.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> crystal structure of oxidized shewanella yellow enzyme 4 (sye4)