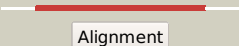



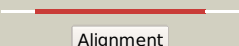





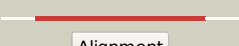















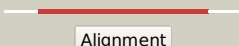

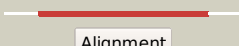

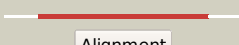

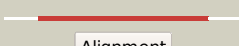








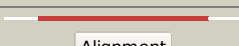
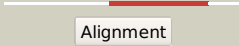


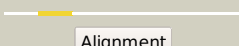

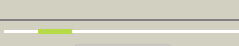


Phyre2

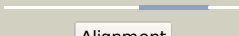

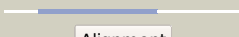



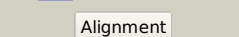
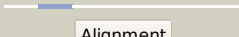

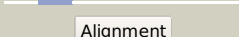


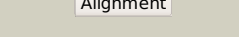
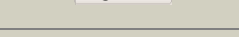


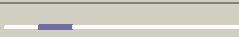



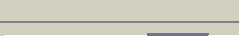

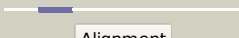

Email	mdejesus@rockefeller.edu
Description	RVBD3079c_(-)_3441767_3442594
Date	Thu Aug 8 16:20:25 BST 2019
Unique Job ID	7d2d4a053c57da23

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2b81D_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
2	c5tlcA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
3	d1luca_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
4	d1lucb_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
5	c3raoB_	 Alignment		100.0	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
6	c5w4zA_	 Alignment		100.0	23	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
7	c3sdoB_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrotriacetate monooxygenase; PDBTitle: structure of a nitrotriacetate monooxygenase from burkholderia2 pseudomallei
8	c1z69D_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
9	c6friD_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
10	d1tvla_	 Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
11	c1tvA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis

12	d1ezwa_	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
13	c3b9nB_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
14	c2i7gA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
15	c5dqpA_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
16	d1f07a_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
17	c3c8nB_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
18	d1rhca_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
19	c5wanA_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
20	c6ak1B_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
21	c2wgkA_	 Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
22	d1nqka_	 Alignment	not modelled	100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
23	d1nfpa_	 Alignment	not modelled	99.2	13	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	 Alignment	not modelled	86.3	10	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c5zfsA_	 Alignment	not modelled	82.4	19	PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
26	c3cqkB_	 Alignment	not modelled	76.7	16	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
27	c3wqoB_	 Alignment	not modelled	72.4	22	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
28	d1xp3a1	 Alignment	not modelled	66.9	7	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV PDB header: isomerase

29	c4ovxA_	Alignment	not modelled	63.5	13	Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
30	c3obeB_	Alignment	not modelled	59.9	16	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
31	c3vniC_	Alignment	not modelled	59.7	14	PDB header: isomerase Chain: C: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with keto-hexose sugars
32	c2zvrA_	Alignment	not modelled	58.5	10	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
33	c2x7vA_	Alignment	not modelled	58.3	11	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
34	c3cnyA_	Alignment	not modelled	57.3	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf1 at 1.85 a3 resolution
35	c2ekcA_	Alignment	not modelled	52.6	18	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
36	c3l23A_	Alignment	not modelled	50.7	16	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
37	c2hk1D_	Alignment	not modelled	47.0	10	PDB header: isomerase Chain: D: PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
38	d1i60a_	Alignment	not modelled	44.8	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
39	d1m5wa_	Alignment	not modelled	37.1	15	Fold: TIM beta/alpha-barrel Superfamily: Pyridoxine 5'-phosphate synthase Family: Pyridoxine 5'-phosphate synthase
40	c3dcpB_	Alignment	not modelled	36.2	16	PDB header: hydrolase Chain: B: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase hisk from2 listeria monocytogenes. northeast structural genomics consortium3 target lmr141.
41	c2yb1A_	Alignment	not modelled	36.1	22	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
42	c3dx5A_	Alignment	not modelled	34.9	16	PDB header: lyase Chain: A: PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
43	c4cngB_	Alignment	not modelled	34.5	3	PDB header: transferase Chain: B: PDB Molecule: spou rna methylase; PDBTitle: crystal structure of sulfolobus acidocaldarius trmj in2 complex with s-adenosyl-l-homocysteine
44	c5i4rA_	Alignment	not modelled	33.6	17	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
45	c3vndD_	Alignment	not modelled	33.3	26	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
46	d1viza_	Alignment	not modelled	32.9	15	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
47	c3gk0H_	Alignment	not modelled	32.7	21	PDB header: transferase Chain: H: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein from2 burkholderia pseudomallei
48	c3e38A_	Alignment	not modelled	31.8	20	PDB header: hydrolase Chain: A: PDB Molecule: two-domain protein containing predicted php-like metal- PDBTitle: 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	c6daqA_	Alignment	not modelled	30.7	10	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
50	d1qlma_	Alignment	not modelled	29.6	18	Fold: Methenyltetrahydromethanopterin cyclohydrolase Superfamily: Methenyltetrahydromethanopterin cyclohydrolase Family: Methenyltetrahydromethanopterin cyclohydrolase
51	c2w9mB_	Alignment	not modelled	27.6	28	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
52	c5dlcC_	Alignment	not modelled	27.4	15	PDB header: transferase Chain: C: PDB Molecule: pyridoxine 5'-phosphate synthase; PDBTitle: x-ray crystal structure of a pyridoxine 5-prime-phosphate synthase2 from pseudomonas aeruginosa

53	c5c54D	 Alignment	not modelled	26.7	21	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminate lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from <i>2 corynebacterium glutamicum</i>
54	c3ju2A	 Alignment	not modelled	25.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from <i>sinorhizobium meliloti 1021</i>
55	c4fioA	 Alignment	not modelled	25.4	21	PDB header: hydrolase Chain: A: PDB Molecule: methenyltetrahydromethanopterin cyclohydrolase; PDBTitle: crystal structure of methenyltetrahydromethanopterin cyclohydrolase2 from <i>methanobrevibacter ruminantium</i>
56	c3lmzA	 Alignment	not modelled	25.1	6	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from <i>2 parabacteroides distazonis atcc 8503 at 1.44 a resolution</i>
57	c3lyeA	 Alignment	not modelled	24.3	27	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
58	c3ih1A	 Alignment	not modelled	23.8	24	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from <i>bacillus anthracis</i>
59	d2q02a1	 Alignment	not modelled	23.7	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
60	c3e0fA	 Alignment	not modelled	23.6	22	PDB header: hydrolase Chain: A: PDB Molecule: putative metal-dependent phosphoesterase; PDBTitle: crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from <i>bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution</i>
61	c6k0aC	 Alignment	not modelled	23.0	11	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
62	c3ikzA	 Alignment	not modelled	22.9	18	PDB header: transferase Chain: A: PDB Molecule: phosphopantetheine adenyltransferase; PDBTitle: crystal structure of phosphopantetheine adenyltransferase from <i>2 burkholderia pseudomallei</i>
63	c1zlpA	 Alignment	not modelled	22.3	33	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming 2 a thiohemiacetal adduct
64	c3eb2A	 Alignment	not modelled	22.2	13	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>2 rhodospseudomonas palustris at 2.0a resolution</i>
65	c4i7vD	 Alignment	not modelled	20.6	15	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhdp5 with pyruvate
66	c3ngfA	 Alignment	not modelled	20.1	13	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from <i>brucella2 melitensis</i>
67	c5tchG	 Alignment	not modelled	20.0	24	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from <i>m. tuberculosis -2 ligand-free form, trpa-g66v mutant</i>
68	c5zhzA	 Alignment	not modelled	19.6	33	PDB header: dna binding protein Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of the apurinic/aprimidinic endonuclease iv from <i>2 mycobacterium tuberculosis</i>
69	c4mg4G	 Alignment	not modelled	19.6	13	PDB header: unknown function Chain: G: PDB Molecule: phosphonomutase; PDBTitle: crystal structure of a putative phosphonomutase from <i>burkholderia2 cenocepacia j2315</i>
70	c2qiwa	 Alignment	not modelled	19.4	25	PDB header: transferase Chain: A: PDB Molecule: pep phosphonomutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonomutase2 (ncg11015, cg11060) from <i>corynebacterium glutamicum atcc 13032 at 3 1.80 a resolution</i>
71	d1m65a	 Alignment	not modelled	19.4	12	Fold: 7-stranded beta/alpha barrel Superfamily: PHP domain-like Family: PHP domain
72	c3auoB	 Alignment	not modelled	19.3	25	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase beta family (x family); PDBTitle: dna polymerase x from <i>thermus thermophilus hb8 ternary complex with 1-2 nt gapped dna and ddgtp</i>
73	d1uoua2	 Alignment	not modelled	19.2	16	Fold: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain Family: Nucleoside phosphorylase/phosphoribosyltransferase catalytic domain
74	c3b4uB	 Alignment	not modelled	19.0	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>agrobacterium2 tumefaciens str. c58</i>
75	d1oy0a	 Alignment	not modelled	19.0	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
76	d1ujqa	 Alignment	not modelled	18.3	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
						PDB header: oxidoreductase

77	c3vtfA_	Alignment	not modelled	18.0	13	Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
78	c3qy6A_	Alignment	not modelled	18.0	20	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
79	c2yxqD_	Alignment	not modelled	17.9	16	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
80	c3gg2B_	Alignment	not modelled	17.9	8	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
81	c3pueA_	Alignment	not modelled	17.7	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
82	c3fluD_	Alignment	not modelled	17.7	11	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
83	c3fkkA_	Alignment	not modelled	17.6	14	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
84	c3s5oA_	Alignment	not modelled	17.2	10	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
85	d1o5ka_	Alignment	not modelled	17.1	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
86	c3noeA_	Alignment	not modelled	17.0	13	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
87	d1e8ca2	Alignment	not modelled	16.8	14	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
88	c3bh1A_	Alignment	not modelled	16.7	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0371 protein dip2346; PDBTitle: crystal structure of protein dip2346 from corynebacterium diphtheriae
89	c6daoB_	Alignment	not modelled	16.6	10	PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
90	c6mqhA_	Alignment	not modelled	16.6	14	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
91	d1x7fa2	Alignment	not modelled	16.4	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
92	c4nq1B_	Alignment	not modelled	16.2	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
93	d1hl2a_	Alignment	not modelled	16.0	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
94	c2nuxB_	Alignment	not modelled	15.8	9	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
95	d1yx1a1	Alignment	not modelled	15.8	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: KguE-like
96	c3x1mC_	Alignment	not modelled	15.5	15	PDB header: transferase Chain: C: PDB Molecule: phosphopantetheine adenyltransferase; PDBTitle: crystal structure of phosphopantetheine adenyltransferase/ppat from2 pseudomonas aeruginosa with coa
97	d1k77a_	Alignment	not modelled	15.3	20	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
98	d1w3ia_	Alignment	not modelled	15.2	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c4n4qD_	Alignment	not modelled	15.2	12	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii