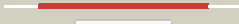



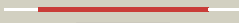




























Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0423c_(thiC)_508585_510228
 Date Tue Jul 23 14:50:49 BST 2019
 Unique Job ID 5f213627e4665b3e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4s2aA_	 Alignment		100.0	69	PDB header: lyase Chain: A: PDB Molecule: phosphomethylpyrimidine synthase; PDBTitle: crystal structure of caulobacter crescentus thic with fe4s4 cluster at2 remote site (holo form)
2	c4s28A_	 Alignment		100.0	68	PDB header: lyase Chain: A: PDB Molecule: phosphomethylpyrimidine synthase, chloroplastic; PDBTitle: crystal structure of arabidopsis thaliana thic with bound2 aminoimidazole ribonucleotide, s-adenosylhomocysteine, fe4s4 cluster3 and fe
3	c3epmB_	 Alignment		100.0	69	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiamine biosynthesis protein thic; PDBTitle: crystal structure of caulobacter crescentus thic
4	c4n7qA_	 Alignment		100.0	68	PDB header: lyase Chain: A: PDB Molecule: phosphomethylpyrimidine synthase, chloroplastic; PDBTitle: crystal structure of eukaryotic thic from a. thaliana
5	c4mwaA_	 Alignment		96.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
6	c3pnzD_	 Alignment		95.7	14	PDB header: hydrolase Chain: D: PDB Molecule: phosphotriesterase family protein; PDBTitle: crystal structure of the lactonase lmo2620 from listeria monocytogenes
7	c6cluC_	 Alignment		93.6	17	PDB header: antimicrobial protein Chain: C: PDB Molecule: dihydropteroate synthase; PDBTitle: staphylococcus aureus dihydropteroate synthase (sadhps) f17l e208k2 double mutant structure
8	c5hmqE_	 Alignment		92.5	17	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
9	d3bofa1	 Alignment		91.1	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
10	c4djeE_	 Alignment		90.0	16	PDB header: transferase/vitamin-binding protein Chain: E: PDB Molecule: corrinoide/iron-sulfur protein large subunit; PDBTitle: crystal structure of folate-bound corrinoide iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
11	c2hjpA_	 Alignment		90.0	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++

12	c3bolB_	Alignment		89.0	18	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
13	c4o1fB_	Alignment		88.8	19	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
14	c5visB_	Alignment		88.7	19	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.
15	d1h1ya_	Alignment		88.5	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
16	c2zvrA_	Alignment		86.9	13	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
17	c3qc3B_	Alignment		86.9	17	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
18	c5a06E_	Alignment		86.8	16	PDB header: oxidoreductase Chain: E: PDB Molecule: aldose-aldose oxidoreductase; PDBTitle: crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
19	d1ad1a_	Alignment		85.8	18	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
20	d1rxda_	Alignment		85.2	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
21	d2flia1	Alignment	not modelled	84.7	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
22	c3db2C_	Alignment	not modelled	84.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
23	c5uncB_	Alignment	not modelled	84.5	15	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase; PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from2 streptomyces platensis subsp. rosaceus
24	c6omzA_	Alignment	not modelled	84.4	18	PDB header: ligase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from mycobacterium2 smegmatis with bound 6-hydroxymethylpterin-monophosphate
25	d2q02a1	Alignment	not modelled	84.3	16	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
26	c2c46B_	Alignment	not modelled	84.1	17	PDB header: transferase Chain: B: PDB Molecule: mrna capping enzyme; PDBTitle: crystal structure of the human rna guanylyltransferase and 5'-2' phosphatase
27	c5xw4A_	Alignment	not modelled	84.1	18	PDB header: cell cycle Chain: A: PDB Molecule: tyrosine-protein phosphatase cdc14; PDBTitle: crystal structure of budding yeast cdc14p (wild type) in the apo state
						Fold: TIM beta/alpha-barrel

28	d1n7ka_	Alignment	not modelled	83.8	18	Superfamily: Aldolase Family: Class I aldolase
29	d1i60a_	Alignment	not modelled	83.8	14	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
30	c3gkaB_	Alignment	not modelled	83.3	25	PDB header: oxidoreductase Chain: B: PDB Molecule: n-ethylmaleimide reductase; PDBTitle: crystal structure of n-ethylmaleimidine reductase from2 burkholderia pseudomallei
31	c3k13A_	Alignment	not modelled	82.9	16	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
32	c5b3uB_	Alignment	not modelled	82.8	13	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
33	c3w9zA_	Alignment	not modelled	82.4	19	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
34	d1sfla_	Alignment	not modelled	81.8	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
35	c2o7qA_	Alignment	not modelled	81.7	25	PDB header: oxidoreductase,transferase Chain: A: PDB Molecule: bifunctional 3-dehydroquinate dehydratase/shikimate PDBTitle: crystal structure of the a. thaliana dhq-dehydroshikimate-sdh-2 shikimate-nadp(h)
36	c4zqrD_	Alignment	not modelled	81.2	19	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from mycobacterium tuberculosis
37	c2y0fD_	Alignment	not modelled	80.6	18	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispq) from thermus thermophilus hb27
38	d1f6ya_	Alignment	not modelled	79.9	14	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
39	d1ub3a_	Alignment	not modelled	79.5	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	c3q2kB_	Alignment	not modelled	79.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna
41	c4gmfD_	Alignment	not modelled	79.1	20	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazolanyl imine reductase from yersinia2 enterocolitica (irp3)
42	c5dbul_	Alignment	not modelled	79.0	25	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
43	c4ot7A_	Alignment	not modelled	78.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of a variant of ncr from zymomonas mobilis
44	c3d0cB_	Alignment	not modelled	78.7	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
45	c5uurA_	Alignment	not modelled	78.2	21	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: xanthomonas albilineans dihydropteroate synthase with 4-aminobenzoic2 acid
46	c3gr7A_	Alignment	not modelled	78.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
47	c1tx2A_	Alignment	not modelled	77.8	19	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
48	d1tx2a_	Alignment	not modelled	77.8	19	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
49	c6ei9A_	Alignment	not modelled	77.7	19	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
50	c5tnvA_	Alignment	not modelled	76.2	14	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
51	d1tqja_	Alignment	not modelled	75.4	29	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
52	c1vliA_	Alignment	not modelled	75.3	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution

53	c2vc7A_	Alignment	not modelled	75.3	12	PDB header: hydrolase Chain: A: PDB Molecule: aryldialkylphosphatase; PDBTitle: structural basis for natural lactonase and promiscuous2 phosphotriesterase activities
54	c6norB_	Alignment	not modelled	75.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
55	c3k2gA_	Alignment	not modelled	75.2	15	PDB header: resiniferatoxin binding protein Chain: A: PDB Molecule: resiniferatoxin-binding, phosphotriesterase- PDBTitle: crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
56	c3cqkB_	Alignment	not modelled	74.8	12	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
57	c4gqaC_	Alignment	not modelled	74.1	14	PDB header: oxidoreductase Chain: C: PDB Molecule: nad binding oxidoreductase; PDBTitle: crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
58	c3ih1A_	Alignment	not modelled	73.6	17	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
59	d1ccwb_	Alignment	not modelled	73.1	20	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Glutamate mutase, large subunit
60	c4qnwA_	Alignment	not modelled	73.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: chanoclavine-i aldehyde reductase; PDBTitle: crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
61	c2glxD_	Alignment	not modelled	73.0	24	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
62	c4wd0A_	Alignment	not modelled	73.0	21	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of hisap form arthrobacter aurescens
63	c3rbvA_	Alignment	not modelled	73.0	17	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
64	d2qtvA4	Alignment	not modelled	72.8	23	Fold: Gelsolin-like Superfamily: C-terminal, gelsolin-like domain of Sec23/24 Family: C-terminal, gelsolin-like domain of Sec23/24
65	c2hg4A_	Alignment	not modelled	72.7	17	PDB header: transferase Chain: A: PDB Molecule: 6-deoxyerythronolide b synthase; PDBTitle: structure of the ketosynthase-acyltransferase didomain of module 52 from debs.
66	c3l9cA_	Alignment	not modelled	72.4	17	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: the crystal structure of smu.777 from streptococcus mutans ua159
67	d2zdra2	Alignment	not modelled	72.2	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
68	c3rgqA_	Alignment	not modelled	71.8	16	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
69	c3ngfA_	Alignment	not modelled	71.5	11	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis
70	c2imgA_	Alignment	not modelled	70.7	21	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
71	d1ryda1	Alignment	not modelled	70.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
72	d1h6za1	Alignment	not modelled	70.2	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
73	c3khdC_	Alignment	not modelled	70.1	15	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
74	d1vhna_	Alignment	not modelled	69.2	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
75	c1zlpA_	Alignment	not modelled	68.9	15	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
76	d1vlia2	Alignment	not modelled	68.6	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
77	c3s4oB_	Alignment	not modelled	68.5	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major
78	c3hf3A_	Alignment	not modelled	67.4	24	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01 PDB header: oxidoreductase

79	c3nt5B_	Alignment	not modelled	67.2	11	Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
80	d1o0ya_	Alignment	not modelled	67.1	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
81	d1ajza_	Alignment	not modelled	66.8	19	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
82	c3b0vD_	Alignment	not modelled	66.8	28	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
83	c2vefB_	Alignment	not modelled	66.3	19	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
84	c4hktA_	Alignment	not modelled	66.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
85	c3euwB_	Alignment	not modelled	65.5	9	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
86	c4miyB_	Alignment	not modelled	64.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
87	c2yciX_	Alignment	not modelled	64.6	18	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
88	d1gkra2	Alignment	not modelled	63.7	16	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Hydantoinase (dihydropyrimidinase), catalytic domain
89	c2i6oA_	Alignment	not modelled	63.6	18	PDB header: hydrolase Chain: A: PDB Molecule: sulfolobus solfataricus protein tyrosine PDBTitle: crystal structure of the complex of the archaeal sulfolobus2 ptp-fold phosphatase with phosphopeptides n-g-(p)y-k-n
90	c5uibA_	Alignment	not modelled	63.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase protein; PDBTitle: crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
91	c1vrdA_	Alignment	not modelled	63.3	26	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from thermotoga maritima at 2.18 a resolution
92	c4rdzA_	Alignment	not modelled	63.2	13	PDB header: hydrolase Chain: A: PDB Molecule: parathion hydrolase; PDBTitle: crystal structure of vmolac in p64 space group
93	d1xbta1	Alignment	not modelled	63.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Type II thymidine kinase
94	c3noeA_	Alignment	not modelled	62.3	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
95	c1ps9A_	Alignment	not modelled	62.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
96	c3fd8A_	Alignment	not modelled	61.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
97	c3p6IA_	Alignment	not modelled	61.9	16	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distansonic atcc 8503 at 1.85 a resolution
98	c5umfB_	Alignment	not modelled	61.9	25	PDB header: isomerase Chain: B: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: crystal structure of a ribulose-phosphate 3-epimerase from neisseria2 gonorrhoeae with bound phosphate
99	d1vbga1	Alignment	not modelled	61.8	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
100	c2q4eB_	Alignment	not modelled	61.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
101	c1h6dL_	Alignment	not modelled	61.8	17	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose PDBTitle: oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
102	c1ofgF_	Alignment	not modelled	61.8	17	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
103	c3daqB_	Alignment	not modelled	61.7	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from

						methicillin-2 resistant staphylococcus aureus
104	c3eooL_	Alignment	not modelled	61.2	13	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
105	d1ohea2	Alignment	not modelled	60.9	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
106	c5yabD_	Alignment	not modelled	60.7	14	PDB header: oxidoreductase Chain: D: PDB Molecule: scyllo-inositol dehydrogenase with l-glucose dehydrogenase PDBTitle: crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
107	c3ngiC_	Alignment	not modelled	60.4	20	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
108	c4xp7A_	Alignment	not modelled	60.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p)+]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2
109	d1kbla1	Alignment	not modelled	59.9	13	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate phosphate dikinase, C-terminal domain
110	c3nsnA_	Alignment	not modelled	59.8	22	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylglucosaminidase; PDBTitle: crystal structure of insect beta-n-acetyl-d-hexosaminidase ofhex12 complexed with tmg-chitotriomycin
111	d1qt1a_	Alignment	not modelled	59.7	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
112	c4xbsA_	Alignment	not modelled	59.5	22	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
113	c6c8vA_	Alignment	not modelled	59.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme pqq synthesis protein e; PDBTitle: x-ray structure of pqqe from methylobacterium extorquens
114	d1a3xa2	Alignment	not modelled	58.9	18	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
115	d1rpxa_	Alignment	not modelled	58.8	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
116	c2dzaA_	Alignment	not modelled	58.6	18	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate
117	c3fokH_	Alignment	not modelled	58.3	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cgl0159; PDBTitle: crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
118	c5ncrA_	Alignment	not modelled	57.6	13	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine phosphatase; PDBTitle: oh1 from the orf virus: a tyrosine phosphatase that displays distinct2 structural features and triple substrate specificity
119	c3e18A_	Alignment	not modelled	57.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
120	d1mzha_	Alignment	not modelled	57.0	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase