

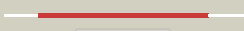



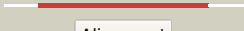

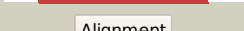





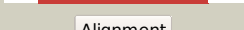

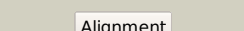

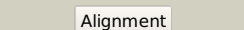





Phyre2

Email: mdejesus@rockefeller.edu
 Description: RVBD0414c_(thiE)_500353_501021
 Date: Tue Jul 23 14:50:48 BST 2019
 Unique Job ID: 4f3a795105bd914e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3o63B_	 Alignment		100.0	95	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
2	c3nm3D_	 Alignment		100.0	30	PDB header: transferase Chain: D: PDB Molecule: thiamine biosynthetic bifunctional enzyme; PDBTitle: the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosynthesis of eukaryotes
3	d2tpsa_	 Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
4	d1xi3a_	 Alignment		100.0	35	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
5	c1yadD_	 Alignment		100.0	27	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
6	c3ceuA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: thiamine phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamine phosphate pyrophosphorylase (bt_0647)2 from bacteroides thetaiotaomicron. northeast structural genomics3 consortium target btr268
7	c4bk9B_	 Alignment		100.0	19	PDB header: lyase Chain: B: PDB Molecule: 2-dehydro-3-deoxyphosphogluconate aldolase/4-hydroxy-2-oxo PDBTitle: crystal structure of 2-keto-3-deoxy-6-phospho-gluconate aldolase from2 zymomonas mobilis atcc 29191
8	d1wa3a1	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
9	c2v82A_	 Alignment		100.0	16	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
10	c4e38A_	 Alignment		99.9	16	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
11	d1vhca_	 Alignment		99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

12	d1mxsa_	Alignment		99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
13	c2yw3E_	Alignment		99.9	23	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
14	d1wbha1	Alignment		99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
15	c3labA_	Alignment		99.9	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpg (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpg (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
16	c6oviA_	Alignment		99.9	17	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with 2 pyruvate captured at low ph as a covalent carbinolamine intermediate
17	c3qc3B_	Alignment		99.9	18	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	c5umfB_	Alignment		99.9	19	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
19	d1tqxa_	Alignment		99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
20	d1rd5a_	Alignment		99.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
21	d1rpxa_	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
22	c3inpA_	Alignment	not modelled	99.9	15	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
23	c4qccA_	Alignment	not modelled	99.9	19	PDB header: structural protein, lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase, peptidyl- PDBTitle: structure of a cube-shaped, highly porous protein cage designed by 2 fusing symmetric oligomeric domains
24	d2flia1	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
25	d1h1ya_	Alignment	not modelled	99.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
26	d1qopa_	Alignment	not modelled	99.9	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
27	d1tqja_	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
28	c4nu7C_	Alignment	not modelled	99.9	18	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from 2 toxoplasma gondii.

29	d1wv2a_	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
30	d1vc4a_	Alignment	not modelled	99.9	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
31	c5n2pA_	Alignment	not modelled	99.9	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
32	c6bmaA_	Alignment	not modelled	99.9	17	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
33	c3tsmB_	Alignment	not modelled	99.9	18	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
34	c3qjaA_	Alignment	not modelled	99.8	23	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
35	c3igsB_	Alignment	not modelled	99.8	21	PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate2 2-epimerase
36	c5zjnB_	Alignment	not modelled	99.8	15	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from vibrio2 cholerae with n-acetylmannosamine-6-phosphate
37	c5b69A_	Alignment	not modelled	99.8	16	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: crystal structure of geranylgeranyl glyceryl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
38	c4utwB_	Alignment	not modelled	99.8	18	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structural characterisation of nane, mannac6p c2 epimerase,2 from clostridium perfringens
39	c5zknA_	Alignment	not modelled	99.8	16	PDB header: isomerase Chain: A: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate 2-epimerase from2 fusobacterium nucleatum
40	d1piia2	Alignment	not modelled	99.8	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
41	c3q58A_	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
42	d1y0ea_	Alignment	not modelled	99.8	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
43	d1a53a_	Alignment	not modelled	99.8	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
44	c3cu2A_	Alignment	not modelled	99.8	11	PDB header: isomerase Chain: A: PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
45	d1yxya1	Alignment	not modelled	99.8	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
46	c3ct7E_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
47	c3vndD_	Alignment	not modelled	99.8	15	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
48	d1xcfa_	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
49	c2c3zA_	Alignment	not modelled	99.8	11	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
50	c5kzmA_	Alignment	not modelled	99.8	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from2 francisella tularensis
51	c6nkeA_	Alignment	not modelled	99.8	15	PDB header: transferase Chain: A: PDB Molecule: geranylgeranyl glyceryl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
52	c3f4wA_	Alignment	not modelled	99.8	20	PDB header: synthase, lyase Chain: A: PDB Molecule: putative hexulose 6 phosphate synthase; PDBTitle: the 1.65a crystal structure of 3-hexulose-6-phosphate2 synthase from salmonella typhimurium
53	c3navB_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan

						synthase from2 vibrio cholerae o1 biovar el tor str. n16961
54	d1i4na_	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
55	c2ekcA_	Alignment	not modelled	99.8	13	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
56	c5ey5A_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: lbcats-a; PDBTitle: lbcats
57	d1j5ta_	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
58	c5z9yB_	Alignment	not modelled	99.7	21	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
59	c3thaB_	Alignment	not modelled	99.7	11	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
60	d1q6oa_	Alignment	not modelled	99.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
61	c4n6eA_	Alignment	not modelled	99.7	18	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
62	d1geqa_	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
63	c3ajxA_	Alignment	not modelled	99.7	26	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
64	c1piiA_	Alignment	not modelled	99.7	18	PDB header: bifunctional(isomerase and synthase) Chain: A: PDB Molecule: n-(5'phosphoribosyl)anthranilate isomerase; PDBTitle: three-dimensional structure of the bifunctional enzyme2 phosphoribosylanthranilate isomerase: indoleglycerolphosphate3 synthase from escherichia coli refined at 2.0 angstroms resolution
65	c4ml9A_	Alignment	not modelled	99.7	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized tim barrel protein with the2 conserved phosphate binding site fromsebaldeella termitidis
66	c5tchG_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
67	c5k9xA_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
68	d1ujpa_	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
69	c5kinC_	Alignment	not modelled	99.6	11	PDB header: lyase Chain: C: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha beta complex from2 streptococcus pneumoniae
70	c3exsB_	Alignment	not modelled	99.6	16	PDB header: lyase Chain: B: PDB Molecule: rrmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
71	d1o4ua1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
72	d2czda1	Alignment	not modelled	99.6	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
73	d1h5ya_	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
74	d1ka9f_	Alignment	not modelled	99.6	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
75	c3jr2D_	Alignment	not modelled	99.5	13	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbh; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
76	c5cssA_	Alignment	not modelled	99.5	16	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate
77	d1zna1	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
78	c1znnF_	Alignment	not modelled	99.5	18	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
79	c4jejA_	Alignment	not modelled	99.5	13	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylglyceryl phosphate synthase;

						PDBTitle: gggps from flavobacterium johnsoniae
80	d1w0ma_	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
81	d1thfd_	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
82	d1xm3a_	Alignment	not modelled	99.5	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
83	c4axkB_	Alignment	not modelled	99.4	17	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5'-phosphoribosylamino)] PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
84	d1hg3a_	Alignment	not modelled	99.4	20	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
85	d1qpoa1	Alignment	not modelled	99.4	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
86	c2htmB_	Alignment	not modelled	99.4	23	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
87	c2y85D_	Alignment	not modelled	99.4	21	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdp
88	c4x2rA_	Alignment	not modelled	99.4	17	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)] PDBTitle: crystal structure of pria from actinomyces urogenitalis
89	c3vkbA_	Alignment	not modelled	99.4	15	PDB header: transferase Chain: A: PDB Molecule: moeo5; PDBTitle: crystal structure of moeo5 soaked with fspp overnight
90	d1qapa1	Alignment	not modelled	99.3	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
91	c3gndC_	Alignment	not modelled	99.3	21	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
92	c4iqiB_	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-(acyl-carrier-protein) reductase ii; PDBTitle: crystal structure of porphyromonas gingivalis enoyl-acyl reductase ii2 (fabk) with cofactors nadph and fmn
93	c4muzA_	Alignment	not modelled	99.3	15	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 archaeoglobus fulgidus complexed with inhibitor bmp
94	c2w6rA_	Alignment	not modelled	99.3	16	PDB header: lyase Chain: A: PDB Molecule: imidazole glycerol phosphate synthase subunit PDBTitle: crystal structure of an artificial (ba)8-barrel protein2 designed from identical half barrels
95	c2qjhH_	Alignment	not modelled	99.2	20	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
96	c4wd0A_	Alignment	not modelled	99.2	17	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)] PDBTitle: crystal structure of hisap from arthrobacter aurescens
97	c2h6rG_	Alignment	not modelled	99.2	21	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
98	c2b7pA_	Alignment	not modelled	99.2	19	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
99	c1x1oC_	Alignment	not modelled	99.2	18	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
100	c3ru6C_	Alignment	not modelled	99.2	11	PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
101	c2z6jB_	Alignment	not modelled	99.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acyl reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
102	c2giiA_	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
103	c2jbmA_	Alignment	not modelled	99.1	20	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
104	c5huoH_	Alignment	not modelled	99.1	12	PDB header: transferase Chain: H: PDB Molecule: nicotinate-nucleotide diphosphorylase (carboxylating);

						PDBTitle: crystal structure of nadc deletion mutant in c2221 space group
105	c1o4uA	Alignment	not modelled	99.1	17	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
106	d1vzwa1	Alignment	not modelled	99.1	25	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
107	c4z87B	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
108	c4gj1A	Alignment	not modelled	99.1	11	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)2 methylideneamino] imidazole-4-carboxamide isomerase (hisa).
109	d1oixa	Alignment	not modelled	99.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
110	d1eixa	Alignment	not modelled	99.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
111	c3bo9B	Alignment	not modelled	99.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkane dioxygenase; PDBTitle: crystal structure of putative nitroalkane dioxygenase (tm0800) from thermotoga maritima at 2.71 a resolution
112	c5aheA	Alignment	not modelled	99.0	12	PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa
113	c2cdh1	Alignment	not modelled	99.0	13	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty acid synthase at 5 angstrom resolution.
114	c5ismF	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: F: PDB Molecule: fmn-dependent nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase (so_0471) from shewanella2 oneidensis mr-1
115	c3tsdA	Alignment	not modelled	99.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from bacillus anthracis str. ames complexed with xmp
116	c5x8oA	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
117	c3l0gD	Alignment	not modelled	99.0	12	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from ehrlichia chaffeensis at 2.05a resolution
118	c1qapA	Alignment	not modelled	99.0	15	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
119	c3khjE	Alignment	not modelled	99.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
120	c3tqvA	Alignment	not modelled	99.0	13	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from francisella tularensis.