

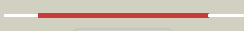




























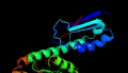









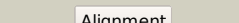

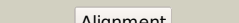


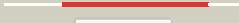
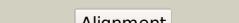


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1596_(nadC)_1797395_1798252
Date	Fri Aug 2 13:30:18 BST 2019
Unique Job ID	191e1c4eb08e6c44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1qpoA	Alignment 		100.0	100	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
2	c3pajA	Alignment 		100.0	40	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
3	c1qapA	Alignment 		100.0	43	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
4	c2b7pA	Alignment 		100.0	37	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
5	c3l0gD	Alignment 		100.0	37	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
6	c1x1oC	Alignment 		100.0	48	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
7	c5huoH	Alignment 		100.0	37	PDB header: transferase Chain: H: PDB Molecule: nicotinate-nucleotide diphosphorylase (carboxylating); PDBTitle: crystal structure of nadc deletion mutant in c2221 space group
8	c2jbmA	Alignment 		100.0	33	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
9	c3tqvA	Alignment 		100.0	37	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
10	c1o4uA	Alignment 		100.0	31	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
11	c3c2vA	Alignment 		100.0	32	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of the quinolinate phosphoribosyl transferase (bna6)2 from saccharomyces cerevisiae complexed with prpp and the inhibitor3 phthalate

12	c3gnnA	 Alignment		100.0	41	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
13	clytkA	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase from thermoplasma PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide
14	d1qpoa1	 Alignment		100.0	100	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
15	d1qapa1	 Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
16	c2i14B	 Alignment		100.0	21	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus
17	d1o4ua1	 Alignment		100.0	36	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
18	c2f7fA	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase, putative; PDBTitle: crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
19	d1qpoa2	 Alignment		100.0	100	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
20	c4yubB	 Alignment		100.0	24	PDB header: ligase Chain: B: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of human nicotinic acid phosphoribosyltransferase
21	d2i14a1	 Alignment	not modelled	100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
22	d1ytda1	 Alignment	not modelled	100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
23	c1yirA	 Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase 2; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
24	c2e5cA	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: nicotinamide phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
25	d1qapa2	 Alignment	not modelled	99.9	35	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
26	c1vlpA	 Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a putative nicotinate phosphoribosyltransferase2 (yor209c, npt1) from saccharomyces cerevisiae at 1.75 a resolution
27	c4hl7A	 Alignment	not modelled	99.9	13	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase (target2 nysgr-026035) from vibrio cholerae
28	c3os4A	 Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis

29	d1o4ua2	Alignment	not modelled	99.9	26	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
30	c2im5C	Alignment	not modelled	99.9	16	PDB header: transferase Chain: C: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase from2 porphyromonas gingivalis
31	d2f7fa1	Alignment	not modelled	99.9	18	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
32	c1ybeA	Alignment	not modelled	99.8	13	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
33	d1ybea1	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
34	d1yira1	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
35	d1vpa2	Alignment	not modelled	99.5	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
36	d1ytda2	Alignment	not modelled	99.4	21	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
37	d2i14a2	Alignment	not modelled	99.1	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
38	c1yadD	Alignment	not modelled	99.0	19	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
39	c6oviA	Alignment	not modelled	98.9	13	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
40	c4bk9B	Alignment	not modelled	98.9	14	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
41	c2v82A	Alignment	not modelled	98.9	8	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
42	d2tpsa	Alignment	not modelled	98.9	15	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
43	d1wa3a1	Alignment	not modelled	98.8	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
44	c3o63B	Alignment	not modelled	98.8	14	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
45	d1vhca	Alignment	not modelled	98.8	8	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
46	d1wbha1	Alignment	not modelled	98.8	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
47	c4e38A	Alignment	not modelled	98.7	12	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)
48	d1xi3a	Alignment	not modelled	98.7	20	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
49	c3labA	Alignment	not modelled	98.7	10	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
50	d1mxsa	Alignment	not modelled	98.7	7	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
51	d2f7fa2	Alignment	not modelled	98.7	21	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
52	c3ceuA	Alignment	not modelled	98.6	11	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
53	c4qccA	Alignment	not modelled	98.6	9	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 by2 fusing symmetric oligomeric domains

54	c2yw3E	Alignment	not modelled	98.6	13	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase/2-deydro-3- PDBTitle: crystal structure analysis of the 4-hydroxy-2-oxoglutarate aldolase/2-2 deydro-3-deoxyphosphogluconate aldolase from tthb1
55	c3nm3D	Alignment	not modelled	98.4	13	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
56	c1zfa	Alignment	not modelled	98.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
57	c5zknA	Alignment	not modelled	98.3	9	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
58	d1yxya1	Alignment	not modelled	98.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
59	c3tsmB	Alignment	not modelled	98.3	11	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
60	d2flia1	Alignment	not modelled	98.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
61	d1y0ea	Alignment	not modelled	98.3	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
62	c3exsB	Alignment	not modelled	98.2	17	PDB header: lyase Chain: B: PDB Molecule: rmpp (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
63	c2c3zA	Alignment	not modelled	98.2	13	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
64	c6bmaA	Alignment	not modelled	98.2	15	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
65	c5upxA	Alignment	not modelled	98.2	11	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from listeria monocytogenes in the presence of3 xanthosine monophosphate
66	d1tqxa	Alignment	not modelled	98.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
67	c4utwB	Alignment	not modelled	98.2	12	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
68	d1a53a	Alignment	not modelled	98.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
69	c3qc3B	Alignment	not modelled	98.2	15	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
70	d1zfja1	Alignment	not modelled	98.2	12	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
71	c3inpA	Alignment	not modelled	98.2	14	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.
72	d1vc4a	Alignment	not modelled	98.2	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
73	d1eepa	Alignment	not modelled	98.2	11	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
74	c3qjaA	Alignment	not modelled	98.2	17	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
75	c4avfD	Alignment	not modelled	98.2	15	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of pseudomonas aeruginosa inosine 5'-2 monophosphate dehydrogenase
76	c4q33F	Alignment	not modelled	98.2	11	PDB header: oxidoreductase Chain: F: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5'-monophosphate dehydrogenase from2 clostridium perfringens complexed with imp and a110
77	c4mz1A	Alignment	not modelled	98.1	14	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a internal deletion of cbs domain from

						campylobacter jejuni complexed3 with inhibitor compound p12
78	c4af0B_	Alignment	not modelled	98.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
79	c3oa3A_	Alignment	not modelled	98.1	13	PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
80	c4z87B_	Alignment	not modelled	98.1	13	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
81	c4dqwb_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
82	c5n2pA_	Alignment	not modelled	98.1	12	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
83	c4ff0B_	Alignment	not modelled	98.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae, deletion2 mutant, complexed with imp
84	c4fxsA_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycophenolic acid
85	c3igsB_	Alignment	not modelled	98.1	15	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
86	c6gk9C_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of impdh from pseudomonas aeruginosa
87	c4xbsA_	Alignment	not modelled	98.1	14	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: 2-deoxyribose-5-phosphate aldolase mutant - e78k
88	d1jr1a1	Alignment	not modelled	98.1	12	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
89	c1vrdA_	Alignment	not modelled	98.1	18	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
90	c1jcnA_	Alignment	not modelled	98.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
91	c4mjmD_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the inosine 5'-monophosphate dehydrogenase, with2 a short internal deletion of cbs domain from bacillus anthracis str.3 ames
92	d1rpxa_	Alignment	not modelled	98.1	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
93	c5umfB_	Alignment	not modelled	98.1	16	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
94	d1vrda1	Alignment	not modelled	98.1	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
95	c5zjnB_	Alignment	not modelled	98.0	14	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
96	c4xtiA_	Alignment	not modelled	98.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: structure of imp dehydrogenase of ashbya gossypii with imp bound to2 the active site
97	d1wv2a_	Alignment	not modelled	98.0	14	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
98	c4n6eA_	Alignment	not modelled	98.0	13	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
99	c3f4wA_	Alignment	not modelled	98.0	17	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
100	d1jcna1	Alignment	not modelled	98.0	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)

101	c3tsdA_	Alignment	not modelled	98.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase from2 bacillus anthracis str. ames complexed with xmp
102	c3cu2A_	Alignment	not modelled	98.0	12	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
103	c4ml9A_	Alignment	not modelled	98.0	21	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 fromsebalbella termitidis
104	c2rdtA_	Alignment	not modelled	98.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase (go) in complex with cdst
105	c4zqrD_	Alignment	not modelled	98.0	16	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
106	d1h1ya_	Alignment	not modelled	98.0	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
107	d1o0ya_	Alignment	not modelled	98.0	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
108	c1fcbA_	Alignment	not modelled	97.9	14	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
109	c2e77B_	Alignment	not modelled	97.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
110	c6a0gA_	Alignment	not modelled	97.9	16	PDB header: flavoprotein Chain: A: PDB Molecule: 4-hydroxymandelate oxidase; PDBTitle: the crystal structure of mandelate oxidase mutant y128f with b-2 phenyllactate
111	c3ct7E_	Alignment	not modelled	97.9	13	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
112	c3khjE_	Alignment	not modelled	97.9	9	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
113	c2rduA_	Alignment	not modelled	97.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
114	d1q6oa_	Alignment	not modelled	97.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
115	c3r2gA_	Alignment	not modelled	97.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
116	c3q58A_	Alignment	not modelled	97.9	13	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
117	c3sr7C_	Alignment	not modelled	97.9	12	PDB header: isomerase Chain: C: PDB Molecule: isopentenyl-diphosphate delta-isomerase; PDBTitle: crystal structure of s. mutans isopentenyl pyrophosphate isomerase
118	d1kbia1	Alignment	not modelled	97.9	9	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
119	c1kbiB_	Alignment	not modelled	97.9	9	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
120	c6bkaA_	Alignment	not modelled	97.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nitronate monooxygenase; PDBTitle: crystal structure of nitronate monooxygenase from cyberlindnera2 saturnus