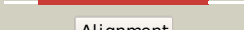
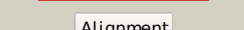
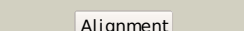


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3pajA_	 Alignment		100.0	62	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
2	c1qapA_	 Alignment		100.0	86	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
3	c3l0gD_	 Alignment		100.0	39	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
4	c1qpoA_	 Alignment		100.0	42	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
5	c2b7pA_	 Alignment		100.0	36	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
6	c1x1oC_	 Alignment		100.0	48	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermophilus hb8
7	c3tqvA_	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
8	c2jbmA_	 Alignment		100.0	34	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
9	c3gnnA_	 Alignment		100.0	50	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
10	c3c2vA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of the quinolinate phosphoribosyl2 transferase (bna6) from saccharomyces cerevisiae complexed3 with prpp and the inhibitor phthalate
11	c1o4uA_	 Alignment		100.0	34	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

12	c1ytkA	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase from thermoplasma PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide
13	d1qapa1	Alignment		100.0	89	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
14	d1qpoa1	Alignment		100.0	48	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
15	c2i14B	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus
16	d1o4ua1	Alignment		100.0	41	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
17	c2f7fA	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase, putative; PDBTitle: crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
18	d1qapa2	Alignment		100.0	83	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
19	d2i14a1	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
20	d1ytda1	Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
21	c1yirA	Alignment	not modelled	100.0	18	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase 2; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
22	c2e5cA	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: nicotinamide phosphoribosyltransferase; PDBTitle: crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
23	d1qpoa2	Alignment	not modelled	99.9	33	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
24	c1vlpA	Alignment	not modelled	99.9	12	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
25	c2im5C	Alignment	not modelled	99.9	15	PDB header: transferase Chain: C: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase2 from porphyromonas gingivalis
26	c3os4A	Alignment	not modelled	99.9	14	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
27	d1o4ua2	Alignment	not modelled	99.9	25	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
28	d2f7fa1	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like

						Family: NadC C-terminal domain-like
29	c1ybeA_	Alignment	not modelled	99.9	12	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
30	d1yira1	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
31	d1ybea1	Alignment	not modelled	99.7	12	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
32	d1vlpa2	Alignment	not modelled	99.6	13	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
33	d1ytda2	Alignment	not modelled	99.4	17	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
34	d2i14a2	Alignment	not modelled	99.2	22	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
35	c1yadD_	Alignment	not modelled	98.7	22	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
36	d2f7fa2	Alignment	not modelled	98.6	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
37	c2v82A_	Alignment	not modelled	98.6	13	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
38	d1xi3a_	Alignment	not modelled	98.5	30	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
39	d1vhca_	Alignment	not modelled	98.5	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	d1wa3a1	Alignment	not modelled	98.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
41	d2tpsa_	Alignment	not modelled	98.4	15	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
42	c3o63B_	Alignment	not modelled	98.3	13	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
43	d1wbha1	Alignment	not modelled	98.3	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
44	c2c3zA_	Alignment	not modelled	98.2	18	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 sulfobolus solfataricus
45	d1a53a_	Alignment	not modelled	98.2	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
46	d1yxya1	Alignment	not modelled	98.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
47	c2yw3E_	Alignment	not modelled	98.1	16	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
48	c3labA_	Alignment	not modelled	98.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdp (2-keto-3-deoxy-6-phosphogluconate) PDBTitle: crystal structure of a putative kdp (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
49	c3qjaA_	Alignment	not modelled	98.0	24	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
50	d1y0ea_	Alignment	not modelled	98.0	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
51	d1mxsa_	Alignment	not modelled	98.0	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
52	d1o0ya_	Alignment	not modelled	98.0	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: isomerase Chain: B: PDB Molecule: n-acetylmannosamine-6-phosphate 2-

53	c3igsB_	Alignment	not modelled	98.0	15	epimerase 2; PDBTitle: structure of the salmonella enterica n-acetylmannosamine-6-phosphate 2-epimerase
54	c1zfjA_	Alignment	not modelled	97.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from <i>Streptococcus pyogenes</i>
55	d1vc4a_	Alignment	not modelled	97.9	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
56	c3q58A_	Alignment	not modelled	97.9	11	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from <i>Salmonella</i> 2 enterica
57	d1eepa_	Alignment	not modelled	97.9	13	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
58	c2cdh1_	Alignment	not modelled	97.8	19	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
59	d1zfja1_	Alignment	not modelled	97.8	11	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
60	c3ceuA_	Alignment	not modelled	97.8	19	PDB header: transferase Chain: A: PDB Molecule: thiamine phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamine phosphate pyrophosphorylase2 (bt 0647) from <i>Bacteroides thetaiotaomicron</i> . northeast3 structural genomics consortium target btr268
61	d1ub3a_	Alignment	not modelled	97.8	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
62	c3oa3A_	Alignment	not modelled	97.8	17	PDB header: lyase Chain: A: PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from <i>Coccidioides immitis</i>
63	c2rduA_	Alignment	not modelled	97.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with 2 glyoxylate
64	d2flia1_	Alignment	not modelled	97.7	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
65	c3ngjC_	Alignment	not modelled	97.7	20	PDB header: lyase Chain: C: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from <i>Entamoeba histolytica</i>
66	d1wv2a_	Alignment	not modelled	97.7	16	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
67	d1jr1a1_	Alignment	not modelled	97.7	12	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
68	c3exsB_	Alignment	not modelled	97.7	15	PDB header: lyase Chain: B: PDB Molecule: rmpd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from <i>Streptococcus mutans</i> in 2 complex with d-r5p
69	c1jcnA_	Alignment	not modelled	97.7	15	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
70	c2e77B_	Alignment	not modelled	97.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
71	d1piia2_	Alignment	not modelled	97.7	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
72	c3inpA_	Alignment	not modelled	97.7	16	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 <i>Francisella tularensis</i> .
73	c3ng3A_	Alignment	not modelled	97.6	15	PDB header: lyase Chain: A: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of deoxyribose phosphate aldolase from <i>Mycobacterium avium</i> 104 in a schiff base with an unknown aldehyde
74	c1vrda_	Alignment	not modelled	97.6	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine-5'-monophosphate dehydrogenase (tm1347)2 from <i>Thermotoga maritima</i> at 2.18 a resolution
75	d1tb3a1_	Alignment	not modelled	97.6	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
76	d1vrda1_	Alignment	not modelled	97.6	21	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
77	d1mzha_	Alignment	not modelled	97.6	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: isomerase

78	c2h6rG_	Alignment	not modelled	97.5	13	Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
79	c3r2gA_	Alignment	not modelled	97.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine 5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5' monophosphate dehydrogenase from2 legionella pneumophila
80	c3khjE_	Alignment	not modelled	97.5	11	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
81	c3qc3B_	Alignment	not modelled	97.5	16	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
82	d1goxa_	Alignment	not modelled	97.5	19	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	c2gjlA_	Alignment	not modelled	97.5	22	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein pa1024; PDBTitle: crystal structure of 2-nitropropane dioxygenase
84	c3nm3D_	Alignment	not modelled	97.5	17	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
85	c2z6jB_	Alignment	not modelled	97.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acp reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
86	d1rpxa_	Alignment	not modelled	97.4	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
87	d1n7ka_	Alignment	not modelled	97.4	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
88	c2htmB_	Alignment	not modelled	97.4	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
89	d1jcna1	Alignment	not modelled	97.4	14	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
90	d1tqxa_	Alignment	not modelled	97.4	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
91	d1i4na_	Alignment	not modelled	97.4	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
92	c1piiA_	Alignment	not modelled	97.4	16	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:3 indoleglycerolphosphate synthase from escherichia coli4 refined at 2.0 angstroms resolution
93	d1hg3a_	Alignment	not modelled	97.3	15	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
94	d1q6oa_	Alignment	not modelled	97.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
95	d1xm3a_	Alignment	not modelled	97.3	11	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
96	c3bo9B_	Alignment	not modelled	97.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
97	d1j5ta_	Alignment	not modelled	97.3	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
98	d1vlpa1	Alignment	not modelled	97.3	9	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
99	c1kbiB_	Alignment	not modelled	97.2	20	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
100	c1znnF_	Alignment	not modelled	97.2	23	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
101	c3bw2A_	Alignment	not modelled	97.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitropropane dioxygenase; PDBTitle: crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
102	c1ypfB_	Alignment	not modelled	97.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: gmp reductase; PDBTitle: crystal structure of guac (ba5705) from bacillus anthracis

					at 1.8 a2 resolution
103	d1pvna1	Alignment	not modelled	97.2	19 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
104	c2a7rD	Alignment	not modelled	97.2	19 PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
105	d1kbial	Alignment	not modelled	97.1	19 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
106	d1vcva1	Alignment	not modelled	97.1	16 Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
107	d1tqja	Alignment	not modelled	97.0	15 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
108	d1w0ma	Alignment	not modelled	97.0	15 Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
109	d1qopa	Alignment	not modelled	97.0	19 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
110	d1p4ca	Alignment	not modelled	97.0	20 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
111	d1hl1ya	Alignment	not modelled	96.9	16 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
112	c3f4wA	Alignment	not modelled	96.9	19 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
113	c2a7nA	Alignment	not modelled	96.9	20 PDB header: oxidoreductase Chain: A: PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
114	c2w6rA	Alignment	not modelled	96.9	21 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
115	c2qr6A	Alignment	not modelled	96.9	17 PDB header: oxidoreductase Chain: A: PDB Molecule: imp dehydrogenase/gmp reductase; PDBTitle: crystal structure of imp dehydrogenase/gmp reductase-like protein2 (np_599840.1) from corynebacterium glutamicum atcc 13032 kitasato at3 1.50 a resolution
116	c2qiwa	Alignment	not modelled	96.8	19 PDB header: transferase Chain: A: PDB Molecule: pep phosphonmutase; PDBTitle: crystal structure of a putative phosphoenolpyruvate phosphonmutase2 (ncgl1015, cgl1060) from corynebacterium glutamicum atcc 13032 at3 1.80 a resolution
117	c3ffsC	Alignment	not modelled	96.8	14 PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
118	c1me9A	Alignment	not modelled	96.8	20 PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh) from2 tritrichomonas foetus with imp bound
119	c3ct7E	Alignment	not modelled	96.8	18 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
120	d1ybea2	Alignment	not modelled	96.8	13 Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like