

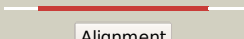

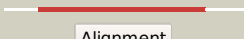













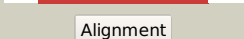









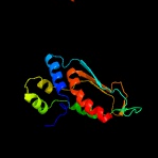




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1330c_(-)_1499219_1500565
Date	Wed Jul 31 22:05:43 BST 2019
Unique Job ID	78c5b099281e4b72

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2f7fA_	 Alignment		100.0	33	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase, putative; PDBTitle: crystal structure of enterococcus faecalis putative nicotinate2 phosphoribosyltransferase, new york structural genomics consortium
2	c4yubB_	 Alignment		100.0	34	PDB header: ligase Chain: B: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of human nicotinic acid phosphoribosyltransferase
3	c1vlpA_	 Alignment		100.0	20	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
4	c4hl7A_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase (target2 nysgr-026035) from vibrio cholerae
5	c2im5C_	 Alignment		100.0	22	PDB header: transferase Chain: C: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase from2 porphyromonas gingivalis
6	c1yirA_	 Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase 2; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
7	c3os4A_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: the crystal structure of nicotinate phosphoribosyltransferase from2 yersinia pestis
8	c1ybeA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
9	c2i14B_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from pyrococcus furiosus
10	c2e5cA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: nicotinamide phosphoribosyltransferase; PDBTitle: crystal structure of human nmprtase complexed with 5'-phosphoribosyl-2 1'-pyrophosphate
11	c1ytkA_	 Alignment		100.0	27	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase from thermoplasma PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide

12	d2f7fa1	Alignment		100.0	34	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
13	d2i14a1	Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
14	d1ytda1	Alignment		100.0	28	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
15	d1yira1	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
16	d1ybea1	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
17	d1vlpa2	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain
18	d2f7fa2	Alignment		100.0	29	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
19	c1x1oC	Alignment		100.0	23	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermophilus hb8
20	c2b7pA	Alignment		100.0	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
21	c1qpoA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyl transferase; PDBTitle: quinolinic acid phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
22	d1vlpa1	Alignment	not modelled	100.0	19	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
23	c3pajA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinic acid phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
24	c3l0gD	Alignment	not modelled	100.0	16	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
25	c5huoH	Alignment	not modelled	100.0	23	PDB header: transferase Chain: H: PDB Molecule: nicotinate-nucleotide diphosphorylase (carboxylating); PDBTitle: crystal structure of nadc deletion mutant in c2221 space group
26	d1ybea2	Alignment	not modelled	100.0	20	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
27	c2jbmA	Alignment	not modelled	100.0	27	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
						Fold: alpha/beta-Hammerhead

28	d1yira2	Alignment	not modelled	100.0	25	Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase N-terminal domain-like
29	c1qapA	Alignment	not modelled	100.0	20	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
30	c3tqvA	Alignment	not modelled	100.0	17	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
31	c1o4uA	Alignment	not modelled	100.0	13	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
32	c3gnnA	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 burkholderi pseudomallei
33	c3c2vA	Alignment	not modelled	100.0	19	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
34	d2i14a2	Alignment	not modelled	100.0	24	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
35	d1ytda2	Alignment	not modelled	100.0	23	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
36	d1qapa1	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
37	d1qpoa1	Alignment	not modelled	99.8	20	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
38	d1o4ua1	Alignment	not modelled	99.5	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
39	d1qpoa2	Alignment	not modelled	97.9	31	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
40	d1qapa2	Alignment	not modelled	97.7	20	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
41	d1o4ua2	Alignment	not modelled	97.2	12	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
42	c6oviA	Alignment	not modelled	95.9	11	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
43	c3tsmB	Alignment	not modelled	94.2	15	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
44	c5umfB	Alignment	not modelled	94.0	14	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
45	d2flia1	Alignment	not modelled	93.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
46	c3qjaA	Alignment	not modelled	92.5	18	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
47	d1rpxa	Alignment	not modelled	92.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
48	d1a53a	Alignment	not modelled	92.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
49	c3inpA	Alignment	not modelled	91.3	9	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.
50	d1xi3a	Alignment	not modelled	91.0	14	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
51	c6bmaA	Alignment	not modelled	91.0	18	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
52	c2c3zA	Alignment	not modelled	90.7	15	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
53	d1vhca	Alignment	not modelled	90.6	15	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

54	c4e38A	Alignment	not modelled	90.6	16	PDB header: lyase Chain: A: PDB Molecule: keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate PDBTitle: crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibrionales bacterium swat-3 (target efi-502156)
55	d1tqxa	Alignment	not modelled	90.3	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
56	c4bk9B	Alignment	not modelled	90.1	12	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
57	c3labA	Alignment	not modelled	90.0	16	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
58	d1wbha1	Alignment	not modelled	89.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
59	c4qccA	Alignment	not modelled	89.5	14	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
60	c3cu2A	Alignment	not modelled	89.5	17	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
61	c3o63B	Alignment	not modelled	88.7	8	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
62	c3qc3B	Alignment	not modelled	88.5	11	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
63	c1e1cA	Alignment	not modelled	87.9	21	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
64	c5aheA	Alignment	not modelled	87.9	35	PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa
65	d2tpsa	Alignment	not modelled	87.4	13	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
66	c4x2rA	Alignment	not modelled	87.2	24	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
67	c1yadD	Alignment	not modelled	86.9	8	PDB header: transcription Chain: D: PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
68	d1tqja	Alignment	not modelled	86.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
69	d1mxsa	Alignment	not modelled	85.8	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
70	d1h1ya	Alignment	not modelled	85.2	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
71	d1ofda2	Alignment	not modelled	85.1	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
72	d1ea0a2	Alignment	not modelled	84.5	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
73	c4nu7C	Alignment	not modelled	84.3	22	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
74	d1qopa	Alignment	not modelled	84.1	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
75	d1hg3a	Alignment	not modelled	84.0	4	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
76	c5n2pA	Alignment	not modelled	83.9	14	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfolobus solfataricus tryptophan synthase a
77	c2h6rG	Alignment	not modelled	82.1	5	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
78	d1wa3a1	Alignment	not modelled	82.0	19	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
79	c3ct7E	Alignment	not modelled	81.7	19	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
80	c2v82A_	Alignment	not modelled	81.1	17	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
81	c3ceuA_	Alignment	not modelled	80.8	8	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
82	c4utwB_	Alignment	not modelled	79.7	10	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
83	d1xcfa_	Alignment	not modelled	78.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
84	c4ml9A_	Alignment	not modelled	78.3	16	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 fromsealdella termitidis
85	c3exsB_	Alignment	not modelled	77.2	16	PDB header: lyase Chain: B: PDB Molecule: rmppd (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
86	c4g1kB_	Alignment	not modelled	75.9	18	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from burkholderia2 thailandensis
87	d1h5ya_	Alignment	not modelled	75.0	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
88	d1thfd_	Alignment	not modelled	73.3	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
89	d7reqa2	Alignment	not modelled	73.1	21	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
90	c2yw3E_	Alignment	not modelled	72.8	17	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
91	d1j5ta_	Alignment	not modelled	72.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
92	c5b69A_	Alignment	not modelled	69.0	15	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: crystal structure of geranylgeranylgeranyl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
93	d1yxva1	Alignment	not modelled	69.0	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
94	d1znnA1	Alignment	not modelled	68.8	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
95	c1znnF_	Alignment	not modelled	68.8	16	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
96	c5zjnB_	Alignment	not modelled	68.4	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
97	c3igsB_	Alignment	not modelled	68.3	11	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
98	c4axkB_	Alignment	not modelled	68.1	19	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
99	d1q6oa_	Alignment	not modelled	66.2	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
100	c2bdqA_	Alignment	not modelled	65.2	16	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis protein cutc from2 streptococcus agalactiae, northeast structural genomics target sar15.
101	d1i4na_	Alignment	not modelled	65.1	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
102	d1vc4a_	Alignment	not modelled	64.9	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
103	d1rd5a_	Alignment	not modelled	64.9	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes

104	d1y0ea_	Alignment	not modelled	64.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
105	c4n6eA_	Alignment	not modelled	63.8	20	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
106	c6nkeA_	Alignment	not modelled	63.6	9	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
107	c2jgqB_	Alignment	not modelled	62.7	13	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
108	d1ka9f_	Alignment	not modelled	62.7	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
109	d1geqa_	Alignment	not modelled	62.3	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
110	c3bicA_	Alignment	not modelled	60.0	14	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
111	c5zknA_	Alignment	not modelled	56.3	10	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
112	d1vzwa1	Alignment	not modelled	55.7	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
113	c3q58A_	Alignment	not modelled	54.7	15	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
114	c4fxsA_	Alignment	not modelled	54.1	30	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from vibrio cholerae complexed2 with imp and mycopenolic acid
115	c3s6dA_	Alignment	not modelled	51.9	23	PDB header: isomerase Chain: A: PDB Molecule: putative triosephosphate isomerase; PDBTitle: crystal structure of a putative triosephosphate isomerase from2 coccidioides immitis
116	c6qssA_	Alignment	not modelled	51.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: malate dehydrogenase; PDBTitle: crystal structure of ignicoccus islandicus malate dehydrogenase co-2 crystallized with 10 mm tb-xo4
117	c3absD_	Alignment	not modelled	50.6	31	PDB header: lyase Chain: D: PDB Molecule: ethanolamine ammonia-lyase light chain; PDBTitle: crystal structure of ethanolamine ammonia-lyase from escherichia coli2 complexed with adeninylpentylcobalamin and ethanolamine
118	d1trea_	Alignment	not modelled	49.4	21	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
119	c4x22A_	Alignment	not modelled	49.2	22	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of leptospira interrogans triosephosphate isomerase2 (litim)
120	c3tdmD_	Alignment	not modelled	49.2	23	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr