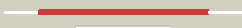









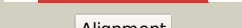

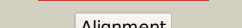

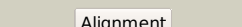

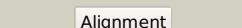

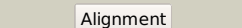





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1603_(hisA)_1803301_1804038
Date	Fri Aug 2 13:30:19 BST 2019
Unique Job ID	cc8d95d165b65ffd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1qo2a_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
2	c4axkB_	 Alignment		100.0	62	PDB header: isomerase Chain: B: PDB Molecule: 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) PDBTitle: crystal structure of subhisa from the thermophile corynebacterium2 efficiens
3	d1jvna1	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
4	c4x2rA_	 Alignment		100.0	66	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
5	c2y85D_	 Alignment		100.0	100	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdp
6	c1jvnB_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
7	c4qj1A_	 Alignment		100.0	29	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).
8	d1h5ya_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
9	c4wd0A_	 Alignment		100.0	62	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of hisap form arthrobacter aurescens
10	d1vzwa1	 Alignment		100.0	69	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
11	c3tdnB_	 Alignment		100.0	23	PDB header: de novo protein Chain: B: PDB Molecule: flr symmetric alpha-beta tim barrel; PDBTitle: computationally designed two-fold symmetric tim-barrel protein, flr

12	d1thfd_	Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
13	c5aheA_	Alignment		100.0	32	PDB header: isomerase Chain: A: PDB Molecule: PDBTitle: crystal structure of salmonella enterica hisa
14	d1ka9f_	Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
15	c2agkA_	Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: structure of s. cerevisiae his6 protein
16	c2w6rA_	Alignment		100.0	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
17	d1znnal	Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: PdxS-like
18	c1znnF_	Alignment		100.0	18	PDB header: biosynthetic protein Chain: F: PDB Molecule: plp synthase; PDBTitle: structure of the synthase subunit of plp synthase
19	c4ml9A_	Alignment		100.0	18	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
20	c3tsmB_	Alignment		100.0	14	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
21	c3qjaA_	Alignment	not modelled	100.0	22	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
22	c6bmaA_	Alignment	not modelled	100.0	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
23	d1a53a_	Alignment	not modelled	99.9	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
24	d1vc4a_	Alignment	not modelled	99.9	22	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
25	c2c3zA_	Alignment	not modelled	99.9	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
26	c1piiA_	Alignment	not modelled	99.9	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
27	d1i4na_	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
28	d1j5ta_	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes

29	c3tdmD	Alignment	not modelled	99.9	24	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfflr
30	d1pia2	Alignment	not modelled	99.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
31	c5umfB	Alignment	not modelled	99.8	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
32	d2flia1	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
33	c3q58A	Alignment	not modelled	99.8	18	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
34	d1tqja	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
35	d1h1ya	Alignment	not modelled	99.8	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
36	c3igsB	Alignment	not modelled	99.8	16	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
37	c5zjnB	Alignment	not modelled	99.8	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
38	c4utwB	Alignment	not modelled	99.8	17	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	d1y0ea	Alignment	not modelled	99.7	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
40	d1yxya1	Alignment	not modelled	99.7	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
41	d1rpxa	Alignment	not modelled	99.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
42	c5zknA	Alignment	not modelled	99.7	15	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
43	c3inpA	Alignment	not modelled	99.7	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.
44	c3vkbA	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: moeo5; PDBTitle: crystal structure of moeo5 soaked with fspp overnight
45	c6ei9A	Alignment	not modelled	99.6	23	PDB header: flavoprotein Chain: A: PDB Molecule: trna-dihydrouridine synthase b; PDBTitle: crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
46	c5n2pA	Alignment	not modelled	99.6	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: sulfobolus solfataricus tryptophan synthase a
47	c5b69A	Alignment	not modelled	99.6	14	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylglyceryl phosphate synthase; PDBTitle: crystal structure of geranylgeranylglyceryl phosphate synthase2 complexed with an g-1-p from thermoplasma acidophilum
48	d1vhna	Alignment	not modelled	99.6	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
49	c3w9zA	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine synthase c; PDBTitle: crystal structure of dusc
50	c4e38A	Alignment	not modelled	99.6	15	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)
51	d1xm3a	Alignment	not modelled	99.6	15	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
52	c4xp7A	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trna-dihydrouridine(20) synthase [nad(p+)]-like; PDBTitle: crystal structure of human trna dihydrouridine synthase 2 PDB header: de novo protein Chain: X: PDB Molecule: beta/aloha-barrel protein based on 1thf

53	c3cwoX	Alignment	not modelled	99.5	20	and 1tmv; PDBTitle: a beta/alpha-barrel built by the combination of fragments from 2 different folds
54	d1wbha1	Alignment	not modelled	99.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
55	c6oviA	Alignment	not modelled	99.5	12	PDB header: lyase Chain: A: PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with 2 pyruvate captured at low ph as a covalent carbinolamine intermediate
56	d1qopa	Alignment	not modelled	99.5	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
57	c4nu7C	Alignment	not modelled	99.5	13	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from <i>Toxoplasma gondii</i> .
58	c3b0vD	Alignment	not modelled	99.5	24	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from <i>Thermus thermophilus</i> in complex with trna
59	d1rd5a	Alignment	not modelled	99.5	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
60	c4n6eA	Alignment	not modelled	99.4	18	PDB header: lyase/biosynthetic protein Chain: A: PDB Molecule: putative thiosugar synthase; PDBTitle: crystal structure of amycolatopsis orientalis bexx/cyso complex
61	d1vhca	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
62	c3qc3B	Alignment	not modelled	99.4	17	PDB header: isomerase Chain: B: PDB Molecule: d-ribulose-5-phosphate-3-epimerase; PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from <i>Homo sapiens</i> at 2.20 Å resolution
63	d1wa3a1	Alignment	not modelled	99.4	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
64	c2v82A	Alignment	not modelled	99.4	17	PDB header: lyase Chain: A: PDB Molecule: 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; PDBTitle: kdpgal complexed to kdpgal
65	d1tqxa	Alignment	not modelled	99.4	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
66	c5z9yB	Alignment	not modelled	99.4	18	PDB header: transferase Chain: B: PDB Molecule: thiazole synthase; PDBTitle: crystal structure of mycobacterium tuberculosis thiazole synthase2 (thig) complexed with dxp
67	d1mxsa	Alignment	not modelled	99.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
68	c1zfaA	Alignment	not modelled	99.4	15	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>
69	c3ct7E	Alignment	not modelled	99.3	12	PDB header: isomerase Chain: E: PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from <i>Escherichia coli</i> k-12
70	c4bk9B	Alignment	not modelled	99.3	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 from <i>Zymomonas mobilis</i> atcc 29191
71	d1xcfa	Alignment	not modelled	99.3	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
72	c4qccA	Alignment	not modelled	99.3	17	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
73	c3labA	Alignment	not modelled	99.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative kdpq (2-keto-3-deoxy-6-phosphogluconate) aldolase; PDBTitle: crystal structure of a putative kdpq (2-keto-3-deoxy-6-2-phosphogluconate) aldolase from <i>Oleispira antarctica</i>
74	c3vndD	Alignment	not modelled	99.2	18	PDB header: lyase Chain: D: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-subunit from the 2 psychrophile <i>Shewanella frigidimarina</i> k14-2
75	c3navB	Alignment	not modelled	99.2	16	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from <i>Vibrio cholerae</i> o1 biovar el tor str. n16961
76	c5kzmA	Alignment	not modelled	99.2	12	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha-beta chain complex from <i>Francisella tularensis</i>
77	c4fxsa	Alignment	not modelled	99.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from <i>Vibrio cholerae</i> complexed2 with imp and mycophenolic acid
						Fold: TIM beta/alpha-barrel

78	d1w0ma_	Alignment	not modelled	99.2	19	Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
79	d1geqa_	Alignment	not modelled	99.2	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
80	c6nkeA_	Alignment	not modelled	99.2	11	PDB header: transferase Chain: A: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: wild-type gggps from thermoplasma volcanium
81	d1xi3a_	Alignment	not modelled	99.2	20	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
82	c2ekcA_	Alignment	not modelled	99.2	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
83	c4z87B_	Alignment	not modelled	99.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
84	c3thaB_	Alignment	not modelled	99.1	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
85	d2tpsa_	Alignment	not modelled	99.1	15	Fold: TIM beta/alpha-barrel Superfamily: Thiamin phosphate synthase Family: Thiamin phosphate synthase
86	c2z6jB_	Alignment	not modelled	99.1	21	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
87	c5cssA_	Alignment	not modelled	99.1	8	PDB header: isomerase Chain: A: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase from thermoplasma2 acidophilum with glycerol 3-phosphate
88	c5x8oA_	Alignment	not modelled	99.1	23	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
89	c3khjE_	Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
90	c2h6rG_	Alignment	not modelled	99.1	15	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
91	c3tsdA_	Alignment	not modelled	99.1	17	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
92	d1hg3a_	Alignment	not modelled	99.1	13	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
93	d1wv2a_	Alignment	not modelled	99.1	18	Fold: TIM beta/alpha-barrel Superfamily: ThiG-like Family: ThiG-like
94	c3f4wA_	Alignment	not modelled	99.1	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
95	c3qr7A_	Alignment	not modelled	99.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
96	c3bo9B_	Alignment	not modelled	99.1	21	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	c3o63B_	Alignment	not modelled	99.1	22	PDB header: transferase Chain: B: PDB Molecule: probable thiamine-phosphate pyrophosphorylase; PDBTitle: crystal structure of thiamin phosphate synthase from mycobacterium2 tuberculosis
98	c2htmB_	Alignment	not modelled	99.0	19	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
99	c3ajxA_	Alignment	not modelled	99.0	21	PDB header: lyase Chain: A: PDB Molecule: 3-hexulose-6-phosphate synthase; PDBTitle: crystal structure of 3-hexulose-6-phosphate synthase
100	c4af0B_	Alignment	not modelled	99.0	26	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
101	c3r2gA_	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 from2 legionella pneumophila
102	c4iqiB_	Alignment	not modelled	99.0	19	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 PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
103	c4dqwb_	Alignment	not modelled	99.0	20
104	c4fejA_	Alignment	not modelled	99.0	12
105	c2rdtA_	Alignment	not modelled	99.0	23
106	c2gjlA_	Alignment	not modelled	99.0	22
107	d1jcna1	Alignment	not modelled	99.0	24
108	c3ffsC_	Alignment	not modelled	99.0	29
109	c5ey5A_	Alignment	not modelled	99.0	17
110	c3cu2A_	Alignment	not modelled	99.0	14
111	c4mm1E_	Alignment	not modelled	99.0	17
112	c4zqrD_	Alignment	not modelled	99.0	24
113	c2qr6A_	Alignment	not modelled	99.0	19
114	d1pvna1	Alignment	not modelled	99.0	20
115	c4q33F_	Alignment	not modelled	98.9	18
116	c4ff0B_	Alignment	not modelled	98.9	18
117	c5kinC_	Alignment	not modelled	98.9	16
118	d1gtea2	Alignment	not modelled	98.9	15
119	c2yw3E_	Alignment	not modelled	98.9	18
120	d1zfja1	Alignment	not modelled	98.9	16