
































Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1493_(mutB)_1684011_1686263
Date	Fri Aug 2 13:30:07 BST 2019
Unique Job ID	81a0a142e93fe71c

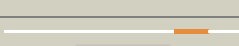
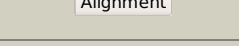



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1e1cA_	 Alignment		100.0	71	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
2	c3bicA_	 Alignment		100.0	62	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
3	c6reqB_	 Alignment		100.0	23	PDB header: isomerase Chain: B: PDB Molecule: protein (methylmalonyl-coa mutase); PDBTitle: methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
4	d7rega1	 Alignment		100.0	72	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
5	c4r3uB_	 Alignment		100.0	41	PDB header: isomerase Chain: B: PDB Molecule: 2-hydroxyisobutyryl-coa mutase large subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
6	c4xc8B_	 Alignment		100.0	35	PDB header: isomerase Chain: B: PDB Molecule: isobutyryl-coa mutase fused; PDBTitle: isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
7	d7reqb1	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Methylmalonyl-CoA mutase, N-terminal (CoA-binding) domain
8	d7reqb2	 Alignment		100.0	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
9	d7rega2	 Alignment		100.0	69	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
10	d1ccwa_	 Alignment		99.6	26	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
11	c1xrsB_	 Alignment		99.4	24	PDB header: isomerase Chain: B: PDB Molecule: d-lysine 5,6-aminomutase beta subunit; PDBTitle: crystal structure of lysine 5,6-aminomutase in complex with plp,2 cobalamin, and 5'-deoxyadenosine

12	d1xrsb1	Alignment		99.4	25	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
13	c2yxba	Alignment		99.3	47	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
14	d1fmfa	Alignment		99.2	28	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
15	c3koxA	Alignment		99.2	18	PDB header: metal binding protein Chain: A: PDB Molecule: d-ornithine aminomutase e component; PDBTitle: crystal structure of ornithine 4,5 aminomutase in complex with 2,4-2 diaminobutyrate (anaerobic)
16	c4r3uD	Alignment		99.1	40	PDB header: isomerase Chain: D: PDB Molecule: 2-hydroxyisobutyryl-coa mutase small subunit; PDBTitle: crystal structure of 2-hydroxyisobutyryl-coa mutase
17	c1bmtB	Alignment		99.0	17	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of2 the b12-binding domains of methionine synthase
18	c4jgiB	Alignment		99.0	21	PDB header: protein binding Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: 1.5 angstrom crystal structure of a novel cobalamin-binding protein2 from desulfitobacterium hafniense dcb-2
19	c1y80A	Alignment		98.9	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from moorella2 thermoacetica
20	c3ezxA	Alignment		98.9	18	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
21	c4hh3C	Alignment	not modelled	98.7	16	PDB header: flavoprotein/transcription Chain: C: PDB Molecule: appa protein; PDBTitle: structure of the appa-ppsr2 core complex from rb. sphaeroides
22	d1ccwb	Alignment	not modelled	98.7	15	Fold: TIM beta/alpha-barrel Superfamily: Cobalamin (vitamin B12)-dependent enzymes Family: Glutamate mutase, large subunit
23	c1k98A	Alignment	not modelled	98.7	15	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
24	d3bula2	Alignment	not modelled	98.6	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
25	c2i2xD	Alignment	not modelled	98.5	14	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtabc from methanosarcina barkeri
26	c3whpA	Alignment	not modelled	97.6	18	PDB header: gene regulation Chain: A: PDB Molecule: probable transcriptional regulator; PDBTitle: crystal structure of the c-terminal domain of themus thermophilus litr2 in complex with cobalamin
27	c5c8eC	Alignment	not modelled	97.2	18	PDB header: transcription regulator/dna Chain: C: PDB Molecule: light-dependent transcriptional regulator carh; PDBTitle: crystal structure of thermus thermophilus carh bound to2 adenosylcobalamin and a 26-bp dna segment
28	c4hh0B	Alignment	not modelled	96.7	15	PDB header: flavoprotein,signaling protein Chain: B: PDB Molecule: appa protein; PDBTitle: dark-state structure of appa c20s without the cys-rich region from rb.2 sphaeroides

29	c3eywA	Alignment	not modelled	96.0	17	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
30	c1zfiA	Alignment	not modelled	95.8	21	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
31	c2b7pA	Alignment	not modelled	95.6	15	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
32	d1krwa	Alignment	not modelled	95.6	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
33	d1o4ua1	Alignment	not modelled	95.5	16	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
34	c4fxsA	Alignment	not modelled	95.2	24	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
35	c1o4uA	Alignment	not modelled	95.2	13	PDB header: transferase Chain: A: PDB Molecule: type ii quinolinic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
36	c4z87B	Alignment	not modelled	95.1	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: structure of the imp dehydrogenase from ashbya gossypii bound to gdp
37	d1qpoa1	Alignment	not modelled	95.1	10	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
38	d1zesal	Alignment	not modelled	95.1	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
39	d1wa3a1	Alignment	not modelled	94.9	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
40	d1yioa2	Alignment	not modelled	94.8	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
41	d1ys7a2	Alignment	not modelled	94.7	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
42	c5x8oA	Alignment	not modelled	94.7	24	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of gmp reductase from trypanosoma brucei with2 guanosine 5'-triphosphate
43	c1ytkA	Alignment	not modelled	94.3	29	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase from thermoplasma PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase from2 thermoplasma acidophilum with nicotinate mononucleotide
44	c2jbmA	Alignment	not modelled	94.2	16	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
45	d1ytda1	Alignment	not modelled	93.9	29	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
46	c4bk9B	Alignment	not modelled	93.8	9	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
47	c4qpiC	Alignment	not modelled	93.7	15	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
48	c1ys7B	Alignment	not modelled	93.7	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulatory protein prra; PDBTitle: crystal structure of the response regulator protein prra complexed2 with mg2+
49	c3tsmB	Alignment	not modelled	93.5	19	PDB header: lyase Chain: B: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of indole-3-glycerol phosphate synthase from2 brucella melitensis
50	d1qapa1	Alignment	not modelled	93.5	13	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
51	c3tsdA	Alignment	not modelled	93.3	20	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 PDB header: transcription

52	c5uicA_	Alignment	not modelled	93.2	12	Chain: A: PDB Molecule: two-component response regulator; PDBTitle: structure of the francisella response regulator receiver domain, qseb
53	d1jbea_	Alignment	not modelled	93.1	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
54	c2c3zA_	Alignment	not modelled	93.1	19	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 <i>Sulfolobus solfataricus</i>
55	c4qccA_	Alignment	not modelled	93.1	21	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
56	c3qjaA_	Alignment	not modelled	93.0	20	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
57	c4q33F_	Alignment	not modelled	92.5	22	PDB header: oxidoreductase Chain: F: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of inosine 5'-monophosphate dehydrogenase from2 <i>Clostridium perfringens</i> complexed with imp and a110
58	d1mvoa_	Alignment	not modelled	92.4	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
59	c5upxA_	Alignment	not modelled	92.3	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of the catalytic domain of the inosine monophosphate2 dehydrogenase from <i>Listeria monocytogenes</i> in the presence of3 xanthosine monophosphate
60	c3l0gD_	Alignment	not modelled	92.1	15	PDB header: transferase Chain: D: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide pyrophosphorylase from2 <i>Ehrlichia chaffeensis</i> at 2.05a resolution
61	c3nhzA_	Alignment	not modelled	92.1	12	PDB header: dna binding protein Chain: A: PDB Molecule: two component system transcriptional regulator mtra; PDBTitle: structure of n-terminal domain of mtra
62	c6bmaA_	Alignment	not modelled	92.0	16	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: the crystal structure of indole-3-glycerol phosphate synthase from2 <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> nctc 11168
63	d1zfja1	Alignment	not modelled	91.8	19	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
64	c4ff0B_	Alignment	not modelled	91.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inosine 5'-monophosphate dehydrogenase from <i>Vibrio cholerae</i> , deletion2 mutant, complexed with imp
65	d1vzwa1	Alignment	not modelled	91.5	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
66	d1thfd_	Alignment	not modelled	91.5	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
67	c6me1A_	Alignment	not modelled	91.0	20	PDB header: ligase Chain: A: PDB Molecule: succinate--coa ligase subunit alpha; PDBTitle: succinyl-coa synthase from <i>Campylobacter jejuni</i>
68	c1qpoA_	Alignment	not modelled	90.7	13	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apoenzyme from2 <i>Mycobacterium tuberculosis</i>
69	d1j5ta_	Alignment	not modelled	90.7	18	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
70	c4af0B_	Alignment	not modelled	90.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of cryptococcal inosine monophosphate2 dehydrogenase
71	c5huoH_	Alignment	not modelled	90.4	15	PDB header: transferase Chain: H: PDB Molecule: nicotinate-nucleotide diphosphorylase (carboxylating); PDBTitle: crystal structure of nadc deletion mutant in c2221 space group
72	c3hdvB_	Alignment	not modelled	90.3	17	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 <i>Pseudomonas putida</i>
73	c3cfyA_	Alignment	not modelled	90.3	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxo repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxo repressor2 protein from <i>Vibrio parahaemolyticus</i>
74	c6ifhA_	Alignment	not modelled	90.2	13	PDB header: transferase Chain: A: PDB Molecule: sporulation initiation phosphotransferase f; PDBTitle: unphosphorylated spoOf from <i>Paenisporsarcina</i> sp. tg-14
75	c4xtiA_	Alignment	not modelled	90.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine-5'-monophosphate dehydrogenase,inosine-5'- PDBTitle: structure of imp dehydrogenase of <i>Ashbya gossypii</i> with imp bound to2 the active site

76	c4jc0B_	 Alignment	not modelled	90.0	13	PDB header: transferase Chain: B: PDB Molecule: ribosomal protein s12 methylthiotransferase rimo; PDBTitle: crystal structure of thermotoga maritima holo rimo in complex with2 pentasulfide, northeast structural genomics consortium target vr77
77	c4e38A_	 Alignment	not modelled	89.8	17	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)
78	d2ayxa1	 Alignment	not modelled	89.7	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
79	d1y0ea_	 Alignment	not modelled	89.6	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
80	d1a53a_	 Alignment	not modelled	89.4	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
81	d1ka9f_	 Alignment	not modelled	89.3	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
82	c3ktoA_	 Alignment	not modelled	88.9	11	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
83	c3jteA_	 Alignment	not modelled	88.8	16	PDB header: protein binding Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver domain protein from2 clostridium thermocellum
84	c4dqwb_	 Alignment	not modelled	88.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure analysis of pa3770
85	d1jr1a1	 Alignment	not modelled	88.4	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
86	c5b69A_	 Alignment	not modelled	88.3	10	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
87	c3snkA_	 Alignment	not modelled	88.2	11	PDB header: signaling protein Chain: A: PDB Molecule: response regulator chey-like protein; PDBTitle: crystal structure of a response regulator chey-like protein (mll6475)2 from mesorhizobium loti at 2.02 a resolution
88	d1dbwa_	 Alignment	not modelled	88.2	21	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
89	c4mz1A_	 Alignment	not modelled	88.1	18	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
90	c1x1oC_	 Alignment	not modelled	88.1	19	PDB header: transferase Chain: C: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of project id tt0268 from thermus thermophilus hb8
91	c3tdmD_	 Alignment	not modelled	87.9	13	PDB header: de novo protein Chain: D: PDB Molecule: computationally designed two-fold symmetric tim-barrel PDBTitle: computationally designed tim-barrel protein, halfplr
92	c1zn2A_	 Alignment	not modelled	87.8	12	PDB header: transcription regulator Chain: A: PDB Molecule: response regulatory protein; PDBTitle: low resolution structure of response regulator styr
93	d1i4na_	 Alignment	not modelled	87.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
94	c3pajA_	 Alignment	not modelled	87.5	12	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
95	d2nu7b1	 Alignment	not modelled	87.3	15	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
96	c5zknA_	Alignment	not modelled	86.8	18	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
97	c1qapA_	Alignment	not modelled	86.8	12	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
98	c2qr3A_	Alignment	not modelled	86.6	10	PDB header: transcription regulator; Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
99	d1u0sy_	Alignment	not modelled	86.5	11	Fold: Flavodoxin-like Superfamily: CheY-like

						Family: CheY-related
100	d1ny5a1	Alignment	not modelled	86.2	11	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
101	d1peya	Alignment	not modelled	86.2	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
102	d1wbha1	Alignment	not modelled	85.9	24	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
103	c3tqvA	Alignment	not modelled	85.8	13	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from <i>2 francisella tularensis</i> .
104	d1jcna1	Alignment	not modelled	85.8	18	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
105	c6gk9C	Alignment	not modelled	85.7	24	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: inhibited structure of <i>impdh</i> from <i>pseudomonas aeruginosa</i>
106	d1qkka	Alignment	not modelled	85.4	19	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
107	c5zjnB	Alignment	not modelled	85.4	18	PDB header: isomerase Chain: B: PDB Molecule: putative n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate-2-epimerase from <i>vibrio2 cholerae</i> with n-acetylmannosamine-6-phosphate
108	c2fpgA	Alignment	not modelled	85.2	13	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [gdp-forming] alpha-chain, PDBTitle: crystal structure of pig gtp-specific succinyl-coa synthetase in <i>2 complex</i> with gdp
109	c4nu7C	Alignment	not modelled	85.2	17	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from <i>2 toxoplasma gondii</i> .
110	c2zwmA	Alignment	not modelled	85.2	9	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein <i>ycyf</i> ; PDBTitle: crystal structure of <i>ycyf</i> receiver domain from <i>bacillus2 subtilis</i>
111	d2a9pa1	Alignment	not modelled	85.0	10	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
112	d1piia2	Alignment	not modelled	85.0	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
113	c4avfD	Alignment	not modelled	84.9	22	PDB header: oxidoreductase Chain: D: PDB Molecule: inosine-5'-monophosphate dehydrogenase; PDBTitle: crystal structure of <i>pseudomonas aeruginosa</i> inosine 5'-2 monophosphate dehydrogenase
114	c3b8iF	Alignment	not modelled	84.8	17	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from <i>pseudomonas2 aeruginosa</i> (pa4872) in complex with oxalate and <i>mg2+</i> .
115	c2yv1A	Alignment	not modelled	84.8	22	PDB header: ligase Chain: A: PDB Molecule: succinyl-coa ligase [adp-forming] subunit alpha; PDBTitle: crystal structure of succinyl-coa synthetase alpha chain from <i>2 methanocaldococcus jannaschii dsm 2661</i>
116	c5n2pA	Alignment	not modelled	84.6	17	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: <i>sulfolobus solfataricus</i> tryptophan synthase a
117	c2jk1A	Alignment	not modelled	84.5	17	PDB header: dna-binding Chain: A: PDB Molecule: hydrogenase transcriptional regulatory protein <i>hupr1</i> ; PDBTitle: crystal structure of the wild-type <i>hupr</i> receiver domain
118	d1xhfa1	Alignment	not modelled	84.2	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
119	d1leepa	Alignment	not modelled	83.9	17	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
120	d1vrda1	Alignment	not modelled	83.9	25	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)