



















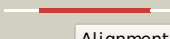









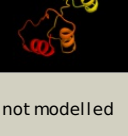


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2zdra2	 Alignment		97.8	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
2	c1vliA_	 Alignment		97.8	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: spore coat polysaccharide biosynthesis protein spse; PDBTitle: crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
3	d1vlia2	 Alignment		97.8	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: NeuB-like
4	c1xuzA_	 Alignment		97.6	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: polysialic acid capsule biosynthesis protein siac; PDBTitle: crystal structure analysis of sialic acid synthase (neub)from2 neisseria meningitidis, bound to mn2+, phosphoenolpyruvate, and n-3 acetyl mannosaminitol
5	c3qjaA_	 Alignment		97.3	17	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form
6	c2c3zA_	 Alignment		97.2	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
7	c3igsB_	 Alignment		97.2	10	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
8	c3ktsA_	 Alignment		96.8	9	PDB header: transcriptional regulator Chain: A: PDB Molecule: glycerol uptake operon antiterminator regulatory protein; PDBTitle: crystal structure of glycerol uptake operon antiterminator regulatory2 protein from listeria monocytogenes str. 4b f2365
9	d1geqa_	 Alignment		96.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
10	d1a53a_	 Alignment		96.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
11	c3g8rA_	 Alignment		96.5	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: probable spore coat polysaccharide biosynthesis protein e; PDBTitle: crystal structure of putative spore coat polysaccharide biosynthesis2 protein e from chromobacterium violaceum atcc 12472

12	c2ekcA_	Alignment		96.0	15	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
13	c3q58A_	Alignment		95.9	14	PDB header: isomerase Chain: A: PDB Molecule: n-acetylmannosamine-6-phosphate 2-epimerase; PDBTitle: structure of n-acetylmannosamine-6-phosphate epimerase from salmonella2 enterica
14	c3thaB_	Alignment		95.9	16	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
15	c3lyeA_	Alignment		95.8	11	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
16	d1ujpa_	Alignment		95.8	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
17	c2bdqA_	Alignment		95.7	13	PDB header: metal transport Chain: A: PDB Molecule: copper homeostasis protein cutc; PDBTitle: crystal structure of the putative copper homeostasis2 protein cutc from streptococcus agalactiae, northeast3 strucural genomics target sar15.
18	d1vkfa_	Alignment		95.7	14	Fold: TIM beta/alpha-barrel Superfamily: GlpP-like Family: GlpP-like
19	d1e0ta2	Alignment		95.6	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
20	c3navB_	Alignment		95.2	14	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of an alpha subunit of tryptophan synthase from2 vibrio cholerae o1 biovar el tor str. n16961
21	d1o60a_	Alignment	not modelled	95.1	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
22	d1j5ta_	Alignment	not modelled	95.1	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
23	d1qopa_	Alignment	not modelled	95.0	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
24	d1i4na_	Alignment	not modelled	95.0	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
25	d1piia2	Alignment	not modelled	94.9	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
26	c3iwpK_	Alignment	not modelled	94.7	18	PDB header: metal binding protein Chain: K: PDB Molecule: copper homeostasis protein cutc homolog; PDBTitle: crystal structure of human copper homeostasis protein cutc
27	d1tqxa_	Alignment	not modelled	94.6	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
28	d1yxa1	Alignment	not modelled	94.5	10	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
						Fold: TIM beta/alpha-barrel

29	d1xcfa_	Alignment	not modelled	94.5	11	Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
30	c3ivuB_	Alignment	not modelled	94.5	12	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
31	d1d9ea_	Alignment	not modelled	94.4	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
32	d1vc4a_	Alignment	not modelled	94.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
33	c3qr7A_	Alignment	not modelled	94.2	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
34	d1x7fa2	Alignment	not modelled	94.1	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Outer surface protein, N-terminal domain
35	d1o1za_	Alignment	not modelled	94.1	12	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
36	c3sz8D_	Alignment	not modelled	94.1	10	PDB header: transferase Chain: D: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase 2; PDBTitle: crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
37	d1pkla2	Alignment	not modelled	93.9	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
38	c2p0oA_	Alignment	not modelled	93.9	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein duf871; PDBTitle: crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
39	d2g50a2	Alignment	not modelled	93.9	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
40	c2z6jB_	Alignment	not modelled	93.8	14	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
41	c2oemA_	Alignment	not modelled	93.8	17	PDB header: isomerase Chain: A: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; PDBTitle: crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketoheptane 1-phosphate
42	c3fk4A_	Alignment	not modelled	93.7	20	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
43	d1h5ya_	Alignment	not modelled	93.6	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
44	c2o55A_	Alignment	not modelled	93.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative glycerophosphodiester phosphodiesterase; PDBTitle: crystal structure of a putative glycerophosphodiester2 phosphodiesterase from galdieria sulphuraria
45	d1w3ia_	Alignment	not modelled	93.5	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
46	d1muma_	Alignment	not modelled	93.4	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
47	d1s2wa_	Alignment	not modelled	93.3	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
48	c1e0tD_	Alignment	not modelled	93.3	18	PDB header: phosphotransferase Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: r292d mutant of e. coli pyruvate kinase
49	d1mxsa_	Alignment	not modelled	93.3	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
50	c3l12A_	Alignment	not modelled	93.2	17	PDB header: hydrolase Chain: A: PDB Molecule: putative glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (yp_165505.1) from silicibacter pomeroyi dss-3 at3 1.60 a resolution
51	c3pg8B_	Alignment	not modelled	93.2	15	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
52	d1vzwa1	Alignment	not modelled	93.1	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
53	c2r94B_	Alignment	not modelled	93.0	11	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
						Fold: TIM beta/alpha-barrel

54	d1vd6a1	Alignment	not modelled	93.0	18	Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
55	c2pz0B	Alignment	not modelled	93.0	11	PDB header: hydrolase Chain: B: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of glycerophosphodiester phosphodiesterase (gdpd)2 from t. tengcongensis
56	c3inpA	Alignment	not modelled	93.0	11	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.
57	d1q6oa	Alignment	not modelled	93.0	7	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
58	c3exsB	Alignment	not modelled	92.9	12	PDB header: lyase Chain: B: PDB Molecule: rmpp (hexulose-6-phosphate synthase); PDBTitle: crystal structure of kgpdc from streptococcus mutans in2 complex with d-r5p
59	d1h1ya	Alignment	not modelled	92.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
60	d1liua2	Alignment	not modelled	92.9	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
61	c2ze3A	Alignment	not modelled	92.7	14	PDB header: isomerase Chain: A: PDB Molecule: dfa0005; PDBTitle: crystal structure of dfa0005 complexed with alpha-ketoglutarate: a2 novel member of the icl/pepm superfamily from alkali-tolerant3 deinococcus ficus
62	c1x7fA	Alignment	not modelled	92.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: outer surface protein; PDBTitle: crystal structure of an uncharacterized b. cereus protein
63	c3kruC	Alignment	not modelled	92.6	15	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh:flavin oxidoreductase/nadh oxidase; PDBTitle: crystal structure of the thermostable old yellow enzyme from2 thermoanaerobacter pseudethanolicus e39
64	d1rd5a	Alignment	not modelled	92.6	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
65	c3rlhA	Alignment	not modelled	92.6	14	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d lisisctox-alphaia1a; PDBTitle: crystal structure of a class ii phospholipase d from loxosceles2 intermedia venom
66	c2rfgB	Alignment	not modelled	92.5	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
67	c3fa4D	Alignment	not modelled	92.5	10	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
68	c3gndC	Alignment	not modelled	92.5	13	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
69	d1w0ma	Alignment	not modelled	92.3	13	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
70	d1wbha1	Alignment	not modelled	92.2	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
71	d2d69a1	Alignment	not modelled	92.1	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
72	d1zcca1	Alignment	not modelled	92.0	6	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
73	c3t7vA	Alignment	not modelled	91.9	14	PDB header: transferase Chain: A: PDB Molecule: methylornithine synthase pylb; PDBTitle: crystal structure of methylornithine synthase (pylb)
74	c1jdaA	Alignment	not modelled	91.9	18	PDB header: hydrolase Chain: A: PDB Molecule: 1,4-alpha maltotetrahydrolase; PDBTitle: maltotetraose-forming exo-amylase
75	c3jr2D	Alignment	not modelled	91.8	13	PDB header: biosynthetic protein Chain: D: PDB Molecule: hexulose-6-phosphate synthase sgbb; PDBTitle: x-ray crystal structure of the mg-bound 3-keto-l-gulonate-6-phosphate2 decarboxylase from vibrio cholerae o1 biovar el tor str. n16961
76	c2y85D	Alignment	not modelled	91.8	11	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdp
77	c3hf3A	Alignment	not modelled	91.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
78	c3ih1A	Alignment	not modelled	91.6	11	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
79	c3ez4B	Alignment	not modelled	91.6	12	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase;

						PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
80	c3khdC_	Alignment	not modelled	91.5	17	PDB header: transferase Chain: C: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pff1300w.
81	c3t07D_	Alignment	not modelled	91.4	20	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
82	c2hmcA_	Alignment	not modelled	91.4	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
83	c1t5aB_	Alignment	not modelled	91.3	21	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
84	c2qiwa_	Alignment	not modelled	91.3	13	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
85	d1y0ea_	Alignment	not modelled	91.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: NanE-like
86	c2nuxB_	Alignment	not modelled	91.0	9	PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
87	d1a3xa2	Alignment	not modelled	91.0	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase
88	d1vhca_	Alignment	not modelled	90.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
89	d1yda1	Alignment	not modelled	90.6	8	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Glycerophosphoryl diester phosphodiesterase
90	c1ydyA_	Alignment	not modelled	90.6	8	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of periplasmic glycerophosphodiester2 phosphodiesterase from escherichia coli
91	c3bleA_	Alignment	not modelled	90.3	17	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in2 complexed with malonate
92	c3qfwB_	Alignment	not modelled	90.2	13	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
93	d1twda_	Alignment	not modelled	90.2	14	Fold: TIM beta/alpha-barrel Superfamily: CutC-like Family: CutC-like
94	c3ks6A_	Alignment	not modelled	90.1	8	PDB header: hydrolase Chain: A: PDB Molecule: glycerophosphoryl diester phosphodiesterase; PDBTitle: crystal structure of putative glycerophosphoryl diester2 phosphodiesterase (17743486) from agrobacterium tumefaciens3 str. c58 (dupont) at 1.80 a resolution
95	d1svda1	Alignment	not modelled	89.9	9	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
96	d8ruca1	Alignment	not modelled	89.9	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
97	c3f4wA_	Alignment	not modelled	89.7	14	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
98	c3qvqB_	Alignment	not modelled	89.5	8	PDB header: hydrolase Chain: B: PDB Molecule: phosphodiesterase olei02445; PDBTitle: the structure of an oleispira antarctica phosphodiesterase olei024452 in complex with the product sn-glycerol-3-phosphate
99	d1ykwa1	Alignment	not modelled	89.5	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
100	c1aqfB_	Alignment	not modelled	89.5	20	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase; PDBTitle: pyruvate kinase from rabbit muscle with mg, k, and l-2 phospholactate
101	d1vhna_	Alignment	not modelled	89.5	10	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
102	d3dhp2	Alignment	not modelled	89.3	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
103	c2cw6B_	Alignment	not modelled	89.3	12	PDB header: lyase Chain: B: PDB Molecule: hydroxymethylglutaryl-coa lyase, mitochondrial; PDBTitle: crystal structure of human hmg-coa lyase: insights into2 catalysis and the molecular basis for3 hydroxymethylglutaric

						aciduria
104	c3si9B_	Alignment	not modelled	89.2	9	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
105	c3rlgA_	Alignment	not modelled	89.2	14	PDB header: hydrolase Chain: A: PDB Molecule: sphingomyelin phosphodiesterase d lisictox-alpha1a1a; PDBTitle: crystal structure of loxosceles intermedia phospholipase d isoform 12 h12a mutant
106	c1kwgA_	Alignment	not modelled	89.2	25	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of thermus thermophilus a4 beta-galactosidase
107	c3stgA_	Alignment	not modelled	89.1	8	PDB header: transferase Chain: A: PDB Molecule: 2-dehydro-3-deoxyphosphooctonate aldolase; PDBTitle: crystal structure of a58p, del(n59), and loop 7 truncated mutant of 3-2 deoxy-d-manno-octulosonate 8-phosphate synthase (kdo8ps) from3 neisseria meningitidis
108	c3e96B_	Alignment	not modelled	89.0	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
109	c1zfpA_	Alignment	not modelled	89.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase; PDBTitle: inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
110	d1geha1	Alignment	not modelled	88.9	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
111	c1ps9A_	Alignment	not modelled	88.9	23	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
112	c2qygC_	Alignment	not modelled	88.9	15	PDB header: unknown function Chain: C: PDB Molecule: ribulose bisphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodopseudomonas2 palustris
113	c3nwrA_	Alignment	not modelled	88.8	11	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
114	c3g0sA_	Alignment	not modelled	88.8	10	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
115	c1zlpA_	Alignment	not modelled	88.8	13	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
116	c1o4uA_	Alignment	not modelled	88.8	14	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
117	d1qpoa1	Alignment	not modelled	88.8	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
118	d1o4ua1	Alignment	not modelled	88.8	14	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
119	c2jbmA_	Alignment	not modelled	88.6	21	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
120	d1rpxa_	Alignment	not modelled	88.6	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase