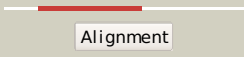
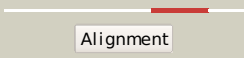
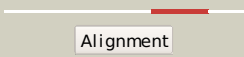
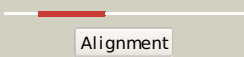
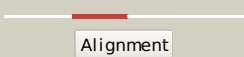
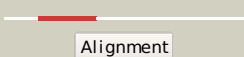
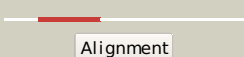
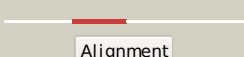
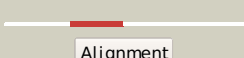
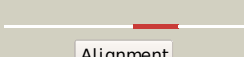
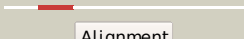
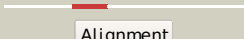
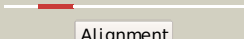
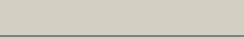
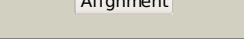
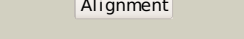
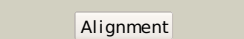
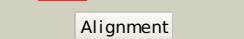
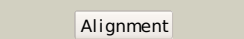
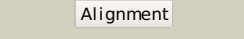
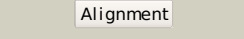


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1k98A_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
2	c3bolB_	 Alignment		100.0	29	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from <i>thermotoga maritima</i> complexed with zn2+
3	d1mska_	 Alignment		100.0	100	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Methionine synthase SAM-binding domain
4	c2o2kA_	 Alignment		100.0	49	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: crystal structure of the activation domain of human2 methionine synthase isoform/mutant d963e/k1071n
5	d1umya_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
6	c3k13A_	 Alignment		100.0	64	PDB header: transferase Chain: A: PDB Molecule: 5-methyltetrahydrofolate-homocysteine methyltransferase; PDBTitle: structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from <i>bacteroides thetaiotaomicron</i>
7	d3bofa2	 Alignment		100.0	33	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
8	d1lt7a_	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
9	c2yciX_	 Alignment		100.0	25	PDB header: transferase Chain: X: PDB Molecule: 5-methyltetrahydrofolate corrinoid/iron sulfur protein PDBTitle: methyltransferase native
10	d3bofa1	 Alignment		100.0	24	Fold: TIM beta/alpha-barrel Superfamily: Dihydropterolate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
11	c1bmtB_	 Alignment		100.0	100	PDB header: methyltransferase Chain: B: PDB Molecule: methionine synthase; PDBTitle: how a protein binds b12: a 3.0 angstrom x-ray structure of 2 the b12-binding domains of methionine synthase

12	dlf6ya_	Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Methyltetrahydrofolate-utilizing methyltransferases
13	c2i2xD_	Alignment		100.0	32	PDB header: transferase Chain: D: PDB Molecule: methyltransferase 1; PDBTitle: crystal structure of methanol:cobalamin methyltransferase complex2 mtac from methanosarcina barkeri
14	c3ezxA_	Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: monomethylamine corrinoid protein 1; PDBTitle: structure of methanosarcina barkeri monomethylamine2 corrinoid protein
15	d3bula2	Alignment		100.0	99	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
16	c1xrsB_	Alignment		100.0	19	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
17	c1tx2A_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: dhps, dihydropteroate synthase; PDBTitle: dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
18	d1tx2a_	Alignment		100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
19	d1j6ra_	Alignment		100.0	17	Fold: Methionine synthase activation domain-like Superfamily: Methionine synthase activation domain-like Family: Hypothetical protein TM0269
20	d1ad1a_	Alignment		100.0	20	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
21	d1ajza_	Alignment	not modelled	100.0	21	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
22	c2y5sA_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of burkholderia cenocepacia dihydropteroate2 synthase complexed with 7,8-dihydropteroate.
23	d1xrsb1	Alignment	not modelled	99.9	19	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
24	c3tr9A_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: structure of a dihydropteroate synthase (folp) in complex with pteroi2 acid from coxiella burnetii
25	c2vp8A_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase 2; PDBTitle: structure of mycobacterium tuberculosis rv1207
26	d1eyea_	Alignment	not modelled	99.9	19	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
27	c2dzaA_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: dihydropteroate synthase; PDBTitle: crystal structure of dihydropteroate synthase from thermus2 thermophilus hb8 in complex with 4-aminobenzoate PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iiii)-binding protein from2 moorella thermoacetica
28	c1y80A_	Alignment	not modelled	99.9	30	Fold: Methionine synthase domain-like

29	d3bula1	Alignment	not modelled	99.9	99	Superfamily: Methionine synthase domain Family: Methionine synthase domain
30	c2h9aB	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase, iron- PDBTitle: corrinoid iron-sulfur protein
31	c2vefB	Alignment	not modelled	99.8	27	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase; PDBTitle: dihydropteroate synthase from streptococcus pneumoniae
32	d7reqa2	Alignment	not modelled	99.8	16	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
33	d1ccwa	Alignment	not modelled	99.8	22	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
34	d1fmfa	Alignment	not modelled	99.7	20	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
35	c2yxbA	Alignment	not modelled	99.6	18	PDB header: isomerase Chain: A: PDB Molecule: coenzyme b12-dependent mutase; PDBTitle: crystal structure of the methylmalonyl-coa mutase alpha-subunit from2 aeropyrum pernix
36	c2h9aA	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron- PDBTitle: corrinoid iron-sulfur protein
37	c3mcnA	Alignment	not modelled	99.3	19	PDB header: transferase Chain: A: PDB Molecule: 2-amino-4-hydroxy-6-hydroxymethyl dihydropteridine PDBTitle: crystal structure of the 6-hydroxymethyl-7,8-dihydropterin2 pyrophosphokinase dihydropteroate synthase bifunctional enzyme from3 francisella tularensis
38	c2bmbA	Alignment	not modelled	99.3	19	PDB header: transferase Chain: A: PDB Molecule: folic acid synthesis protein fol1; PDBTitle: x-ray structure of the bifunctional 6-hydroxymethyl-7,8-2 dihydroxypterin pyrophosphokinase dihydropteroate synthase3 from saccharomyces cerevisiae
39	c3bicA	Alignment	not modelled	99.1	13	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase, mitochondrial precursor; PDBTitle: crystal structure of human methylmalonyl-coa mutase
40	c3noyA	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
41	c3koxA	Alignment	not modelled	98.4	29	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)
42	c1e1cA	Alignment	not modelled	97.8	17	PDB header: isomerase Chain: A: PDB Molecule: methylmalonyl-coa mutase alpha chain; PDBTitle: methylmalonyl-coa mutase h244a mutant
43	d1ka9f	Alignment	not modelled	97.4	19	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
44	d1xxxa1	Alignment	not modelled	96.4	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
45	c2v9dB	Alignment	not modelled	96.4	14	PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
46	c3s5oA	Alignment	not modelled	96.3	15	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; PDBTitle: crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate
47	c3n2xB	Alignment	not modelled	96.2	15	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
48	c2ehhE	Alignment	not modelled	96.1	13	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
49	c3fkA	Alignment	not modelled	96.0	13	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
50	c2r8wB	Alignment	not modelled	95.9	12	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
51	c3si9B	Alignment	not modelled	95.8	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
52	d1h5ya	Alignment	not modelled	95.7	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
53	c3e96B	Alignment	not modelled	95.7	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
54	d1o5ka	Alignment	not modelled	95.7	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase

						Family: Class I aldolase
55	c3noeA	Alignment	not modelled	95.6	10	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
56	c3daqB	Alignment	not modelled	95.6	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
57	c2vc6A	Alignment	not modelled	95.5	12	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
58	c3eb2A	Alignment	not modelled	95.4	17	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
59	c2fdsA	Alignment	not modelled	95.3	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: orotidine-monophosphate-decarboxylase; PDBTitle: crystal structure of plasmodium berghei orotidine 5'-2 monophosphate decarboxylase (ortholog of plasmodium3 falciparum pf10_0225)
60	d2fdsa1	Alignment	not modelled	95.3	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
61	c3bi8A	Alignment	not modelled	95.3	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
62	d1xkya1	Alignment	not modelled	95.1	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
63	c3na8A	Alignment	not modelled	94.9	16	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
64	c3g0sA	Alignment	not modelled	94.8	12	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
65	c3lerA	Alignment	not modelled	94.8	12	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
66	c2qw5B	Alignment	not modelled	94.8	17	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
67	d2a6na1	Alignment	not modelled	94.7	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
68	c2qyqC	Alignment	not modelled	94.5	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
69	c2oemA	Alignment	not modelled	94.3	18	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-diketohehexane 1-phosphate
70	c3fluD	Alignment	not modelled	94.2	13	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
71	c6reqB	Alignment	not modelled	94.2	14	PDB header: isomerase Chain: B: PDB Molecule: protein (methylmalonyl-coa mutase); PDBTitle: methylmalonyl-coa mutase, 3-carboxypropyl-coa inhibitor complex
72	d1u1ha2	Alignment	not modelled	93.8	15	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Cobalamin-independent methionine synthase
73	c2nx9B	Alignment	not modelled	93.7	18	PDB header: lyase Chain: B: PDB Molecule: oxaloacetate decarboxylase 2, subunit alpha; PDBTitle: crystal structure of the carboxyltransferase domain of the2 oxaloacetate decarboxylase na+ pump from vibrio cholerae
74	c3qfwB	Alignment	not modelled	93.6	19	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodopseudomonas2 palustris
75	d2ffca1	Alignment	not modelled	93.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Decarboxylase
76	c3qfeB	Alignment	not modelled	93.2	16	PDB header: lyase Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
77	c3cprB	Alignment	not modelled	93.2	20	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
78	c2yxgD	Alignment	not modelled	92.9	10	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)

79	c2d69B_	 Alignment	not modelled	92.9	15	PDB header: lyase Chain: B: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
80	d1jvna1	 Alignment	not modelled	92.7	21	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
81	c2rfgB_	 Alignment	not modelled	92.6	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
82	d1vhna_	 Alignment	not modelled	92.4	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
83	c2y0fD_	 Alignment	not modelled	92.1	20	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
84	c1jvnB_	 Alignment	not modelled	91.8	19	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
85	c2y85D_	 Alignment	not modelled	91.8	17	PDB header: isomerase Chain: D: PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
86	c1telA_	 Alignment	not modelled	91.7	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose bisphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
87	d1qh8b_	 Alignment	not modelled	91.7	13	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
88	c2r94B_	 Alignment	not modelled	91.7	16	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
89	d1ykwa1	 Alignment	not modelled	91.1	16	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
90	d2q8za1	 Alignment	not modelled	91.0	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Decarboxylase
91	d1m1na_	 Alignment	not modelled	91.0	14	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
92	d1hl2a_	 Alignment	not modelled	90.8	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	d2d69a1	 Alignment	not modelled	90.7	17	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
94	c3obkH_	 Alignment	not modelled	90.7	18	PDB header: lyase Chain: H: PDB Molecule: delta-aminolevulinic acid dehydratase; PDBTitle: crystal structure of delta-aminolevulinic acid dehydratase2 (porphobilinogen synthase) from toxoplasma gondii me49 in complex3 with the reaction product porphobilinogen
95	c3d0cB_	 Alignment	not modelled	90.5	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
96	d1thfd_	 Alignment	not modelled	90.2	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Histidine biosynthesis enzymes
97	c3dz1A_	 Alignment	not modelled	90.1	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 1.87a resolution
98	d1f74a_	 Alignment	not modelled	89.7	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	d1m1nb_	 Alignment	not modelled	89.6	13	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
100	d1rd5a_	 Alignment	not modelled	89.5	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: Tryptophan biosynthesis enzymes
101	d7reqb2	 Alignment	not modelled	89.3	17	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
102	c3r89A_	 Alignment	not modelled	89.2	16	PDB header: lyase Chain: A: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5-phosphate decarboxylase from2 anaerococcus prevotii dsm 20548
103	c3eo0L_	 Alignment	not modelled	89.2	23	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
		 Alignment				Fold: TIM beta/alpha-barrel

104	d1muma_	Alignment	not modelled	89.2	18	Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
105	d8ruca1	Alignment	not modelled	89.1	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
106	c3pueA_	Alignment	not modelled	89.0	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dihydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
107	d1o66a_	Alignment	not modelled	88.6	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
108	c3b0vD_	Alignment	not modelled	88.4	17	PDB header: oxidoreductase/rna Chain: D: PDB Molecule: trna-dihydrouridine synthase; PDBTitle: trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
109	c3qw3B_	Alignment	not modelled	87.8	16	PDB header: transferase, lyase Chain: B: PDB Molecule: orotidine-5-phosphate decarboxylase/orotate PDBTitle: structure of leishmania donovani omp decarboxylase
110	c3nwrA_	Alignment	not modelled	87.3	17	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
111	c3lciA_	Alignment	not modelled	86.6	13	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
112	c1rldB_	Alignment	not modelled	86.5	21	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose 1,5 bisphosphate carboxylase/oxygenase (large PDBTitle: solid-state phase transition in the crystal structure of ribulose 1,5-2 biposphate carboxylase(/slash)oxygenase
113	d1wdda1	Alignment	not modelled	86.2	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
114	c3lmaC_	Alignment	not modelled	85.9	19	PDB header: membrane protein Chain: C: PDB Molecule: stage v sporulation protein ad (spovad); PDBTitle: crystal structure of the stage v sporulation protein ad2 (spovad) from bacillus licheniformis. northeast structural3 genomics consortium target bir6.
115	c3ru6C_	Alignment	not modelled	85.8	10	PDB header: lyase Chain: C: PDB Molecule: orotidine 5'-phosphate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of orotidine 5'-phosphate2 decarboxylase (pyrf) from campylobacter jejuni subsp. jejuni nctc3 11168
116	d1vzwa1	Alignment	not modelled	85.7	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
117	c1rcxH_	Alignment	not modelled	85.6	12	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach rubisco in complex with its substrate2 ribulose-1,5-bisphosphate
118	c1ypxA_	Alignment	not modelled	85.4	13	PDB header: transferase Chain: A: PDB Molecule: putative vitamin-b12 independent methionine synthase family PDBTitle: crystal structure of the putative vitamin-b12 independent methionine2 synthase from listeria monocytogenes, northeast structural genomics3 target lmr13
119	c3lyeA_	Alignment	not modelled	84.9	15	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
120	c2ftpA_	Alignment	not modelled	84.3	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa