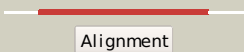

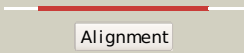







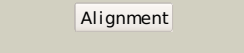



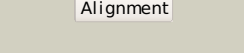



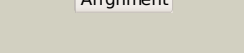

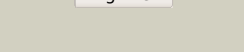



Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v9dB_	 Alignment		100.0	99	PDB header: lyase Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the dihydrodipicolinic acid synthase family from e. coli k12
2	c3n2xB_	 Alignment		100.0	100	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the dihydrodipicolinic acid synthase family from e. coli k12 in complex with pyruvate
3	c3g0sA_	 Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
4	d2a6na1	 Alignment		100.0	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
5	c3si9B_	 Alignment		100.0	28	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
6	d1xxa1	 Alignment		100.0	25	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
7	c3fluD_	 Alignment		100.0	32	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
8	c3noeA_	 Alignment		100.0	30	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
9	c3bi8A_	 Alignment		100.0	30	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
10	d1o5ka_	 Alignment		100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
11	c2ehhE_	 Alignment		100.0	27	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus

29	c3dz1A_	Alignment	not modelled	100.0	19	Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
30	c3e96B_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 bacillus clausii
31	d1w3ia_	Alignment	not modelled	100.0	27	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
32	c3d0cB_	Alignment	not modelled	100.0	23	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 oceanobacillus iheyensis at 1.9 a resolution
33	c2r94B_	Alignment	not modelled	100.0	29	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
34	c3qfeB_	Alignment	not modelled	100.0	26	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
35	c2hmcA_	Alignment	not modelled	100.0	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
36	c2nuxB_	Alignment	not modelled	100.0	25	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
37	c3b4uB_	Alignment	not modelled	100.0	24	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
38	c2pcqA_	Alignment	not modelled	100.0	29	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthase; PDBTitle: crystal structure of putative dihydrodipicolinate synthase (ttha0737)2 from thermus thermophilus hb8
39	d1muma_	Alignment	not modelled	98.3	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
40	c3lyeA_	Alignment	not modelled	98.2	17	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
41	d1ujqa_	Alignment	not modelled	98.0	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
42	c2ze3A_	Alignment	not modelled	98.0	20	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
43	c3eool_	Alignment	not modelled	98.0	22	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
44	c3ih1A_	Alignment	not modelled	97.9	15	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
45	c1zlpA_	Alignment	not modelled	97.9	20	PDB header: lyase Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
46	c3b8iF_	Alignment	not modelled	97.9	22	PDB header: lyase Chain: F: PDB Molecule: pa4872 oxaloacetate decarboxylase; PDBTitle: crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+
47	c3fa4D_	Alignment	not modelled	97.8	15	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
48	d1s2wa_	Alignment	not modelled	97.8	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
49	c2qiwa_	Alignment	not modelled	97.8	23	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
50	c2hjpA_	Alignment	not modelled	97.7	15	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
51	d1xcfa_	Alignment	not modelled	97.6	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
52	c3thaB_	Alignment	not modelled	97.2	13	PDB header: lyase Chain: B: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: tryptophan synthase subunit alpha from campylobacter jejuni.
53	d1rblal	Alignment	not modelled	97.1	8	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
						Fold: TIM beta/alpha-barrel

54	d1j5ta_	Alignment	not modelled	97.1	15	Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
55	c3gr7A_	Alignment	not modelled	97.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal2 crystal form
56	c3ez4B_	Alignment	not modelled	97.0	27	PDB header: transferase Chain: B: PDB Molecule: 3-methyl-2-oxobutanoate hydroxymethyltransferase; PDBTitle: crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
57	d1geqa_	Alignment	not modelled	96.9	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
58	d1ps9a1	Alignment	not modelled	96.9	22	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
59	d1qopa_	Alignment	not modelled	96.9	16	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
60	d8ruca1	Alignment	not modelled	96.9	6	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
61	c2h90A_	Alignment	not modelled	96.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
62	c3navB_	Alignment	not modelled	96.8	16	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
63	c3bolB_	Alignment	not modelled	96.7	18	PDB header: transferase Chain: B: PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
64	c2d69B_	Alignment	not modelled	96.7	13	PDB header: lyase Chain: B: PDB Molecule: ribulose biphosphate 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)
65	c1ps9A_	Alignment	not modelled	96.7	21	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
66	d2d69a1	Alignment	not modelled	96.7	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
67	c3nwrA_	Alignment	not modelled	96.7	16	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
68	d1piia2	Alignment	not modelled	96.6	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
69	d1svda1	Alignment	not modelled	96.6	8	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
70	dlyxya1	Alignment	not modelled	96.6	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
71	c1rcxH_	Alignment	not modelled	96.5	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
72	dloy0a_	Alignment	not modelled	96.5	26	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
73	dlykwa1	Alignment	not modelled	96.5	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
74	d1f61a_	Alignment	not modelled	96.4	22	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
75	c3fk4A_	Alignment	not modelled	96.4	20	PDB header: isomerase Chain: A: PDB Molecule: rubisco-like protein; PDBTitle: crystal structure of rubisco-like protein from bacillus2 cereus atcc 14579
76	d1wdda1	Alignment	not modelled	96.4	7	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
77	c3hf3A_	Alignment	not modelled	96.3	17	PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
78	d1tv5a1	Alignment	not modelled	96.3	12	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
79	c1tv5A_	Alignment	not modelled	96.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase homolog, mitochondrial; PDBTitle: plasmodium falciparum dihydroorotate dehydrogenase with a bound2 inhibitor
						Fold: TIM beta/alpha-barrel

80	dlf76a_	Alignment	not modelled	96.3	18	Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
81	dlz41a1	Alignment	not modelled	96.2	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
82	dlgeha1	Alignment	not modelled	96.2	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
83	dlqvfa_	Alignment	not modelled	96.2	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
84	c1telA_	Alignment	not modelled	96.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ribulose biphosphate carboxylase, large subunit; PDBTitle: crystal structure of a rubisco-like protein from chlorobium2 tepidum
85	c2rduA_	Alignment	not modelled	96.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
86	c3irsB_	Alignment	not modelled	96.1	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bb4693; PDBTitle: crystal structure of uncharacterized tim-barrel protein bb4693 from2 bordetella bronchiseptica
87	c3nurA_	Alignment	not modelled	96.1	16	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
88	c2e77B_	Alignment	not modelled	96.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate complex
89	c2cdh1_	Alignment	not modelled	96.0	16	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
90	dlvyra_	Alignment	not modelled	96.0	11	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
91	c2ekcA_	Alignment	not modelled	95.9	14	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
92	dlrd5a_	Alignment	not modelled	95.9	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
93	c3k30B_	Alignment	not modelled	95.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardioes simplex
94	d2f6ka1	Alignment	not modelled	95.9	15	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
95	c3gndC_	Alignment	not modelled	95.8	18	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDBTitle: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
96	dlbxna1	Alignment	not modelled	95.8	12	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
97	dlgoxa_	Alignment	not modelled	95.8	18	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	c2zviB_	Alignment	not modelled	95.8	14	PDB header: isomerase Chain: B: PDB Molecule: 2,3-diketo-5-methylthiopentyl-1-phosphate PDBTitle: crystal structure of 2,3-diketo-5-methylthiopentyl-1-2 phosphate enolase from bacillus subtilis
99	dlm3ua_	Alignment	not modelled	95.7	24	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
100	cljcnA_	Alignment	not modelled	95.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
101	dltb3a1	Alignment	not modelled	95.6	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
102	dlbwva1	Alignment	not modelled	95.6	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
103	dlid3ga_	Alignment	not modelled	95.5	17	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
104	d2q02a1	Alignment	not modelled	95.5	10	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loli-like
105	c2c3zA_	Alignment	not modelled	95.4	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 sulfobolus solfataricus
						Fold: TIM beta/alpha-barrel

106	d1to3a_	Alignment	not modelled	95.4	17	Superfamily: Aldolase Family: Class I aldolase
107	c3sqsA_	Alignment	not modelled	95.4	11	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12
108	c1rldB_	Alignment	not modelled	95.4	13	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 biphosphate carboxylase(/slash)oxygenase
109	c2qjhH_	Alignment	not modelled	95.3	17	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
110	d1jpma1	Alignment	not modelled	95.3	18	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
111	c2iswB_	Alignment	not modelled	95.3	19	PDB header: lyase Chain: B: PDB Molecule: putative fructose-1,6-bisphosphate aldolase; PDBTitle: structure of giardia fructose-1,6-biphosphate aldolase in2 complex with phosphoglycolohydroxamate
112	d1rpxa_	Alignment	not modelled	95.3	13	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
113	c1djnb_	Alignment	not modelled	95.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylphilus methylotrophus (sp.3 w3a1)
114	c1kbiB_	Alignment	not modelled	95.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: cytochrome b2; PDBTitle: crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
115	c3qfwB_	Alignment	not modelled	95.2	14	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
116	d1ej7l1	Alignment	not modelled	95.2	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
117	c2oemA_	Alignment	not modelled	95.2	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-diketohexane 1-phosphate
118	c2ftpA_	Alignment	not modelled	95.1	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
119	c3stgA_	Alignment	not modelled	94.9	13	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
120	c2fptA_	Alignment	not modelled	94.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroorotate dehydrogenase, mitochondrial; PDBTitle: dual binding mode of a novel series of dhodh inhibitors