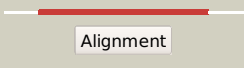

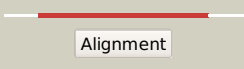

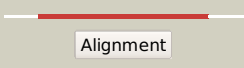

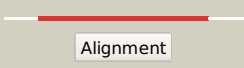

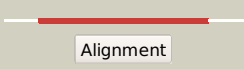

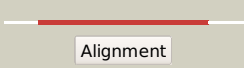

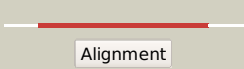

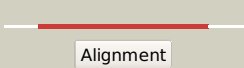

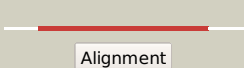

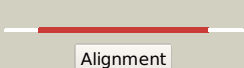

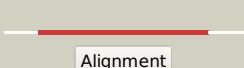

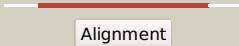

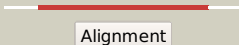

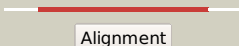



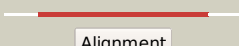

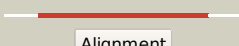

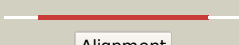






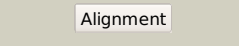
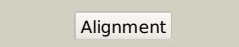



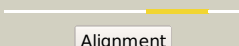



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0791c_(-)_884800_885843
Date	Fri Jul 26 01:50:37 BST 2019
Unique Job ID	25f1c4e790fce035

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3raoB_</a>			100.0	27	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> putative luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
2	<a href="#">c3sdoB_</a>			100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nitrilotriacetate monooxygenase; <b>PDBTitle:</b> structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
3	<a href="#">c1tvIA_</a>			100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> protein ytnj; <b>PDBTitle:</b> structure of ytnj from bacillus subtilis
4	<a href="#">d1tvIA_</a>			100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monooxygenases
5	<a href="#">c5tlcA_</a>			100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> dibenzothiophene desulfurization enzyme a; <b>PDBTitle:</b> crystal structure of bdsa from bacillus subtilis wu-s2b
6	<a href="#">d1luca_</a>			100.0	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monooxygenase)
7	<a href="#">d1ezwa_</a>			100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
8	<a href="#">c5dqpA_</a>			100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> edta monooxygenase; <b>PDBTitle:</b> edta monooxygenase (emoa) from chelativorans sp. bnc1
9	<a href="#">c2b81D_</a>			100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> luciferase-like monooxygenase; <b>PDBTitle:</b> crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
10	<a href="#">c2i7gA_</a>			100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> crystal structure of monooxygenase from agrobacterium tumefaciens
11	<a href="#">c5w4zA_</a>			100.0	22	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> riboflavin lyase; <b>PDBTitle:</b> crystal structure of riboflavin lyase (rcae) with modified fmn and 2 substrate riboflavin

12	<a href="#">c5wanA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine monoxygenase ruta; <b>PDBTitle:</b> crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway
13	<a href="#">d1nqka_</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Ssud-like monoxygenases
14	<a href="#">c1z69D_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> coenzyme f420-dependent n(5),n(10)- <b>PDBTitle:</b> crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
15	<a href="#">c3b9nB_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alkane monoxygenase; <b>PDBTitle:</b> crystal structure of long-chain alkane monoxygenase (lada)
16	<a href="#">d1lucb_</a>	 Alignment		100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Bacterial luciferase (alkanal monoxygenase)
17	<a href="#">c3c8nB_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable f420-dependent glucose-6-phosphate dehydrogenase <b>PDBTitle:</b> crystal structure of apo-fgd1 from mycobacterium tuberculosis
18	<a href="#">c2wgkA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3,6-diketocamphane 1,6 monoxygenase; <b>PDBTitle:</b> type ii baeyer-villiger monoxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monoxygenase from3 pseudomonas putida
19	<a href="#">c6ak1B_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dimethyl-sulfide monoxygenase; <b>PDBTitle:</b> crystal structure of dmoa from hyphomicrobium sulfonivorans
20	<a href="#">c6friD_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alkanal monoxygenase beta chain; <b>PDBTitle:</b> structure of luxb from photobacterium leiognathi
21	<a href="#">d1rhca_</a>	 Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
22	<a href="#">d1f07a_</a>	 Alignment	not modelled	100.0	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> F420 dependent oxidoreductases
23	<a href="#">d1nfpa_</a>	 Alignment	not modelled	99.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (LuxF, FP390)
24	<a href="#">d1fvpa_</a>	 Alignment	not modelled	99.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Bacterial luciferase-like <b>Family:</b> Non-fluorescent flavoprotein (LuxF, FP390)
25	<a href="#">c3qy6A_</a>	 Alignment	not modelled	82.7	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine-protein phosphatase ywqe; <b>PDBTitle:</b> crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
26	<a href="#">d1jpdx1</a>	 Alignment	not modelled	82.4	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
27	<a href="#">c3fa4D_</a>	 Alignment	not modelled	74.4	21	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-dimethylmalate lyase; <b>PDBTitle:</b> crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
28	<a href="#">d1muma_</a>	 Alignment	not modelled	67.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like <b>PDB header:</b> hydrolase

29	<a href="#">c5zmyF_</a>	Alignment	not modelled	67.3	15	<b>Chain:</b> F; <b>PDB Molecule:</b> cis-epoxysuccinate hydrolase; <b>PDBTitle:</b> crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
30	<a href="#">c1zlpA_</a>	Alignment	not modelled	67.3	14	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> petal death protein; <b>PDBTitle:</b> petal death protein psr132 with cysteine-linked glutaraldehyde forming 2 a thiohemiacetal adduct
31	<a href="#">c3eooL_</a>	Alignment	not modelled	66.7	17	<b>PDB header:</b> lyase <b>Chain:</b> L; <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> 2.9a crystal structure of methyl-isocitrate lyase from Burkholderia pseudomallei
32	<a href="#">c3lyeA_</a>	Alignment	not modelled	63.1	19	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> oxaloacetate acetyl hydrolase; <b>PDBTitle:</b> crystal structure of oxaloacetate acetylhydrolase
33	<a href="#">c3b8fF_</a>	Alignment	not modelled	61.2	22	<b>PDB header:</b> lyase <b>Chain:</b> F; <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from Pseudomonas aeruginosa (pa4872) in complex with oxalate and mg2+
34	<a href="#">d1ujqa_</a>	Alignment	not modelled	60.6	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/isocitrate lyase-like
35	<a href="#">c2ze3A_</a>	Alignment	not modelled	60.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> dfa0005; <b>PDBTitle:</b> crystal structure of dfa0005 complexed with alpha-ketoglutarate: a 2 novel member of the icl/pepm superfamily from alkali-tolerant Deinococcus Ficus
36	<a href="#">d1jpmA1</a>	Alignment	not modelled	59.8	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
37	<a href="#">c3ih1A_</a>	Alignment	not modelled	59.7	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> methylisocitrate lyase; <b>PDBTitle:</b> crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase 2 from Bacillus anthracis
38	<a href="#">c2wjeA_</a>	Alignment	not modelled	58.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> tyrosine-protein phosphatase cpsb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase cps4b from Streptococcus pneumoniae tigr4.
39	<a href="#">c3b4uB_</a>	Alignment	not modelled	57.1	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from Agrobacterium tumefaciens str. c58
40	<a href="#">c2r8wB_</a>	Alignment	not modelled	54.9	35	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> agr_c_1641p; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase (atu0899) from Agrobacterium tumefaciens str. c58
41	<a href="#">c2qiwa_</a>	Alignment	not modelled	54.7	8	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> pep phosphonmutase; <b>PDBTitle:</b> crystal structure of a putative phosphoenolpyruvate phosphonmutase 2 (ncgl1015, cgl1060) from Corynebacterium glutamicum atcc 13032 at 3.180 Å resolution
42	<a href="#">c4mg4G_</a>	Alignment	not modelled	51.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> G; <b>PDB Molecule:</b> phosphonmutase; <b>PDBTitle:</b> crystal structure of a putative phosphonmutase from Burkholderia cenocepacia j2315
43	<a href="#">c4lsbA_</a>	Alignment	not modelled	47.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> lyase/mutase; <b>PDBTitle:</b> crystal structure of a putative lyase/mutase from Burkholderia cenocepacia j2315
44	<a href="#">d1o5ka_</a>	Alignment	not modelled	43.5	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
45	<a href="#">c3dcpB_</a>	Alignment	not modelled	43.2	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> histidinol-phosphatase; <b>PDBTitle:</b> crystal structure of the putative histidinol phosphatase Hisk from Listeria monocytogenes. Northeast structural genomics consortium 3 target lmr141.
46	<a href="#">c6k0aC_</a>	Alignment	not modelled	43.0	5	<b>PDB header:</b> rna binding protein/rna <b>Chain:</b> C; <b>PDB Molecule:</b> ribonuclease p protein component 3; <b>PDBTitle:</b> cryo-em structure of an archaeal ribonuclease p
47	<a href="#">c2yb1A_</a>	Alignment	not modelled	42.8	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> amidohydrolase; <b>PDBTitle:</b> structure of an amidohydrolase from Chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
48	<a href="#">c3bh1A_</a>	Alignment	not modelled	41.7	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> upf0371 protein dip2346; <b>PDBTitle:</b> crystal structure of protein dip2346 from Corynebacterium diphtheriae
49	<a href="#">d1tzza1</a>	Alignment	not modelled	41.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
50	<a href="#">c5ud6B_</a>	Alignment	not modelled	40.6	16	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhds from cyanidioschyzon merolae with lysine 2 bound
51	<a href="#">c4mwaA_</a>	Alignment	not modelled	40.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> 1.85 Å crystal structure of Gcpe protein from Bacillus anthracis
52	<a href="#">c3e0fA_</a>	Alignment	not modelled	39.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> putative metal-dependent phosphoesterase; <b>PDBTitle:</b> crystal structure of a putative metal-dependent phosphoesterase 2 (bad_1165) from Bifidobacterium adolescentis atcc 15703 at 2.40 Å resolution
						<b>PDB header:</b> lyase

53	<a href="#">c4nnCA</a>	Alignment	not modelled	37.4	17	<b>Chain:</b> A: <b>PDB Molecule:</b> obca, oxalate biosynthetic component a; <b>PDBTitle:</b> ternary complex of obca with c4-coa adduct and oxalate
54	<a href="#">c3chvA</a>	Alignment	not modelled	35.9	13	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> prokaryotic domain of unknown function (dof849) with a tim <b>PDBTitle:</b> crystal structure of a prokaryotic domain of unknown function (dof849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution
55	<a href="#">c6daqA</a>	Alignment	not modelled	35.9	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phdj; <b>PDBTitle:</b> phdj bound to substrate intermediate
56	<a href="#">c2r94B</a>	Alignment	not modelled	35.4	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; <b>PDBTitle:</b> crystal structure of kd(p)ga from t.tenax
57	<a href="#">c3lerA</a>	Alignment	not modelled	35.1	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
58	<a href="#">c3daqB</a>	Alignment	not modelled	35.1	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
59	<a href="#">d1e8ca2</a>	Alignment	not modelled	33.5	16	<b>Fold:</b> MurD-like peptide ligases, peptide-binding domain <b>Superfamily:</b> MurD-like peptide ligases, peptide-binding domain <b>Family:</b> MurCDEF C-terminal domain
60	<a href="#">c3e96B</a>	Alignment	not modelled	33.4	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
61	<a href="#">c6arhA</a>	Alignment	not modelled	33.3	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> crystal structure of human nal at a resolution of 1.6 angstrom
62	<a href="#">c3no5C</a>	Alignment	not modelled	32.9	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a pfam dof849 domain containing protein2 (reut_a1631) from ralstonia eutropha jmp134 at 1.90 a resolution
63	<a href="#">d1s2wa</a>	Alignment	not modelled	32.5	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
64	<a href="#">d1r0ma1</a>	Alignment	not modelled	31.6	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
65	<a href="#">c6ahuJ</a>	Alignment	not modelled	31.5	15	<b>PDB header:</b> hydrolase/rna <b>Chain:</b> J: <b>PDB Molecule:</b> ribonuclease p protein subunit p30; <b>PDBTitle:</b> cryo-em structure of human ribonuclease p with mature trna
66	<a href="#">c5ktIA</a>	Alignment	not modelled	31.2	23	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
67	<a href="#">c4n4qD</a>	Alignment	not modelled	31.2	10	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate lyase; <b>PDBTitle:</b> crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
68	<a href="#">d2d69a1</a>	Alignment	not modelled	31.1	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain
69	<a href="#">c4exqA</a>	Alignment	not modelled	30.6	13	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
70	<a href="#">d1wuea1</a>	Alignment	not modelled	30.4	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
71	<a href="#">c3bi8A</a>	Alignment	not modelled	30.4	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of dihydrodipicolinate synthase from clostridium2 botulinum
72	<a href="#">c3noyA</a>	Alignment	not modelled	30.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
73	<a href="#">d1wufa1</a>	Alignment	not modelled	29.9	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
74	<a href="#">c4fioA</a>	Alignment	not modelled	29.8	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> methenyltetrahydromethanopterin cyclohydrolase; <b>PDBTitle:</b> crystal structure of methenyltetrahydromethanopterin cyclohydrolase2 from methanobrevibacter ruminantium
75	<a href="#">c4nq1B</a>	Alignment	not modelled	29.0	26	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
76	<a href="#">c3e38A</a>	Alignment	not modelled	28.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> two-domain protein containing predicted php-like metal- <b>PDBTitle:</b> crystal structure of a two-domain protein containing predicted php-2 like metal-dependent phosphoesterase (bvu_3505) from bacteroides3 vulgatus atcc 8482 at 2.20 a resolution
77	<a href="#">d1sjda1</a>	Alignment	not modelled	28.7	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
						<b>Fold:</b> 7-stranded beta/alpha barrel

78	<a href="#">d1m65a_</a>	Alignment	not modelled	28.5	21	<b>Superfamily:</b> PHP domain-like <b>Family:</b> PHP domain
79	<a href="#">c3lciA_</a>	Alignment	not modelled	28.1	30	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w
80	<a href="#">c2yxgD_</a>	Alignment	not modelled	27.8	30	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)
81	<a href="#">c3pueA_</a>	Alignment	not modelled	27.4	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of the complex of dihydrodipicolinate synthase from <i>2 acinetobacter baumannii</i> with lysine at 2.6a resolution
82	<a href="#">c3na8A_</a>	Alignment	not modelled	27.3	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of a putative dihydrodipicolinate synthetase from <i>2 pseudomonas aeruginosa</i>
83	<a href="#">c2hmcA_</a>	Alignment	not modelled	27.3	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from <i>2 agrobacterium tumefaciens</i>
84	<a href="#">d1j93a_</a>	Alignment	not modelled	26.6	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> UROD/MetE-like <b>Family:</b> Uroporphyrinogen decarboxylase, UROD
85	<a href="#">c3qfeB_</a>	Alignment	not modelled	26.4	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dihydrodipicolinate synthase family protein; <b>PDBTitle:</b> crystal structures of a putative dihydrodipicolinate synthase family2 protein from <i>2 coccidioides immitis</i>
86	<a href="#">c2hjpA_</a>	Alignment	not modelled	26.4	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphonopyruvate hydrolase; <b>PDBTitle:</b> crystal structure of phosphonopyruvate hydrolase complex with <i>2 phosphonopyruvate</i> and <i>mg++</i>
87	<a href="#">c3d0cB_</a>	Alignment	not modelled	26.1	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from <i>2 oceanobacillus ihenyensis</i> at 1.9 a resolution
88	<a href="#">c3s5oA_</a>	Alignment	not modelled	26.1	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; <b>PDBTitle:</b> crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to <i>2 pyruvate</i>
89	<a href="#">d1xxxa1</a>	Alignment	not modelled	25.6	8	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
90	<a href="#">c6mqhA_</a>	Alignment	not modelled	25.5	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from <i>2 burkholderia mallei</i>
91	<a href="#">c2ejaB_</a>	Alignment	not modelled	25.4	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> crystal structure of uroporphyrinogen decarboxylase from <i>2 aquifex aeolicus</i>
92	<a href="#">c2v9dB_</a>	Alignment	not modelled	25.2	30	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to <i>2 the dihydrodipicolinic acid synthase family</i> from <i>2 e. coli3 k12</i>
93	<a href="#">c2rfgB_</a>	Alignment	not modelled	24.9	30	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from <i>2 hahella chejuensis</i> at 1.5a resolution
94	<a href="#">c2w9mB_</a>	Alignment	not modelled	24.8	14	<b>PDB header:</b> dna replication <b>Chain:</b> B: <b>PDB Molecule:</b> polymerase x; <b>PDBTitle:</b> structure of family x dna polymerase from <i>2 deinococcus radiodurans</i>
95	<a href="#">c4i7vD_</a>	Alignment	not modelled	24.5	19	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> <i>2 agrobacterium tumefaciens dhps</i> with pyruvate
96	<a href="#">d2mnra1</a>	Alignment	not modelled	24.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
97	<a href="#">c5ui3C_</a>	Alignment	not modelled	24.3	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhps from <i>2 chlamydomonas reinhardtii</i>
98	<a href="#">c2y7eA_</a>	Alignment	not modelled	24.3	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-keto-5-aminohexanoate cleavage enzyme; <b>PDBTitle:</b> crystal structure of the 3-keto-5-aminohexanoate cleavage enzyme2 (kce) from <i>2 candidatus cloacamonas acidaminovorans</i> (tetragonal form)
99	<a href="#">c2yz5B_</a>	Alignment	not modelled	24.1	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> histidinol phosphatase; <b>PDBTitle:</b> histidinol phosphate phosphatase complexed with phosphate
100	<a href="#">c5ocsB_</a>	Alignment	not modelled	22.7	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-dependent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from <i>2 ralstonia cupriavidus metallidurans</i>
101	<a href="#">c3fkkA_</a>	Alignment	not modelled	22.6	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase; <b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
102	<a href="#">c4ah7C_</a>	Alignment	not modelled	22.6	19	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> structure of wild type <i>2 staphylococcus aureus</i> n-acetylneuraminic acid2 lyase in complex with pyruvate

103	<a href="#">c2vc6A_</a>	Alignment	not modelled	22.2	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of mosa from s. melliloti with pyruvate bound
104	<a href="#">c4b5nA_</a>	Alignment	not modelled	22.1	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, frn-binding; <b>PDBTitle:</b> crystal structure of oxidized shewanella yellow enzyme 4 (sy4)
105	<a href="#">c5ikyA_</a>	Alignment	not modelled	21.8	19	<b>PDB header:</b> hydrolase,lyase <b>Chain:</b> A: <b>PDB Molecule:</b> oxalate biosynthetic component 1; <b>PDBTitle:</b> apo structure of obc1, a bifunctional enzyme for quorum sensing-2 dependent oxalogenesis
106	<a href="#">c3eb2A_</a>	Alignment	not modelled	21.5	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 2.0a resolution
107	<a href="#">d2a6na1</a>	Alignment	not modelled	21.5	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
108	<a href="#">d1yeya1</a>	Alignment	not modelled	21.4	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
109	<a href="#">c4dppB_</a>	Alignment	not modelled	21.3	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase 2, chloroplastic; <b>PDBTitle:</b> the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
110	<a href="#">c4zr8B_</a>	Alignment	not modelled	21.2	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uroporphyrinogen decarboxylase; <b>PDBTitle:</b> structure of uroporphyrinogen decarboxylase from acinetobacter2 baumannii
111	<a href="#">d2gl5a1</a>	Alignment	not modelled	21.1	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
112	<a href="#">c3cprB_</a>	Alignment	not modelled	21.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase; <b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
113	<a href="#">d1w3ia_</a>	Alignment	not modelled	21.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
114	<a href="#">c2d69B_</a>	Alignment	not modelled	20.9	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase; <b>PDBTitle:</b> crystal structure of the complex of sulfate ion and octameric2 ribulose-1,5-bisphosphate carboxylase/oxygenase (rubisco) from3 pyrococcus horikoshii ot3 (form-2 crystal)
115	<a href="#">d1e2ka_</a>	Alignment	not modelled	20.7	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
116	<a href="#">c6hunA_</a>	Alignment	not modelled	20.7	14	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase; <b>PDBTitle:</b> dimeric archeal rubisco from hyperthermus butylicus
117	<a href="#">d2gdqa1</a>	Alignment	not modelled	20.4	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
118	<a href="#">c4gx9A_</a>	Alignment	not modelled	20.3	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii subunit epsilon,dna polymerase iii <b>PDBTitle:</b> crystal structure of a dna polymerase iii alpha-epsilon chimera
119	<a href="#">c2nuxB_</a>	Alignment	not modelled	20.2	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate <b>PDBTitle:</b> 2-keto-3-deoxygluconate aldolase from sulfobobus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
120	<a href="#">d1geha1</a>	Alignment	not modelled	20.1	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> RuBisCo, C-terminal domain <b>Family:</b> RuBisCo, large subunit, C-terminal domain