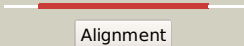

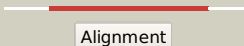

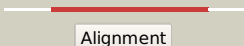







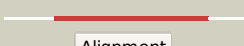















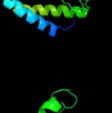

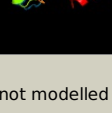


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2361c_(-) _2642588_2643478
Date	Mon Aug 5 13:25:51 BST 2019
Unique Job ID	a1c1b1019f096ef2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vg2C_	 Alignment		100.0	100	PDB header: transferase Chain: C: PDB Molecule: undecaprenyl pyrophosphate synthetase; PDBTitle: rv2361 with ipp
2	c4h8eA_	 Alignment		100.0	40	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of s. aureus undecaprenyl diphosphate synthase in complex2 with fpp and sulfate
3	c4q9mA_	 Alignment		100.0	42	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: isoprenyl transferase; PDBTitle: crystal structure of upps in complex with fpp and an allosteric2 inhibitor
4	c5hc7A_	 Alignment		100.0	39	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: prenyltransferase for protein; PDBTitle: crystal structure of lavandulyl diphosphate synthase from lavandula x2 intermedia in complex with s-thiolo-isopentenylidiphosphate
5	c2vfwB_	 Alignment		100.0	35	PDB header: transferase Chain: B: PDB Molecule: short-chain z-isoprenyl diphosphate synthetase; PDBTitle: rv1086 native
6	d1ueha_	 Alignment		100.0	40	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase
7	c5guKA_	 Alignment		100.0	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: cyclolavandulyl diphosphate synthase; PDBTitle: crystal structure of apo form of cyclolavandulyl diphosphate synthase2 (clds) from streptomyces sp. cl190
8	c5hxpA_	 Alignment		100.0	37	PDB header: transferase Chain: A: PDB Molecule: (2z,6z)-farnesyl diphosphate synthase, chloroplastic; PDBTitle: crystal structure of z,z-farnesyl diphosphate synthase (d71m, e75a and2 h103y mutants) complexed with ipp
9	c1jp3A_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: structure of e.coli undecaprenyl pyrophosphate synthase
10	c5xk9F_	 Alignment		100.0	22	PDB header: transferase Chain: F: PDB Molecule: undecaprenyl diphosphate synthase; PDBTitle: crystal structure of isosesquilandulyl diphosphate synthase from2 streptomyces sp. strain cnh-189 in complex with gssp and dmapp
11	d1f75a_	 Alignment		100.0	38	Fold: Undecaprenyl diphosphate synthase Superfamily: Undecaprenyl diphosphate synthase Family: Undecaprenyl diphosphate synthase

12	c6acsA_	Alignment		100.0	36	PDB header: transferase Chain: A; PDB Molecule: ditrans,polycis-undecaprenyl-diphosphate synthase ((2e,6e)-) PDBTitle: poly-cis-prenyltransferase
13	c2d2rA_	Alignment		100.0	35	PDB header: transferase Chain: A; PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of helicobacter pylori undecaprenyl pyrophosphate2 synthase
14	c3ugsB_	Alignment		100.0	36	PDB header: transferase Chain: B; PDB Molecule: undecaprenyl pyrophosphate synthase; PDBTitle: crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni
15	c6jcnB_	Alignment		100.0	18	PDB header: transferase Chain: B; PDB Molecule: dehydrodolichyl diphosphate synthase complex subunit nus1; PDBTitle: yeast dehydrodolichyl diphosphate synthase complex subunit nus1
16	c4cmxB_	Alignment		98.7	15	PDB header: nuclear protein Chain: B; PDB Molecule: rv3378c; PDBTitle: crystal structure of rv3378c
17	c4k3zA_	Alignment		94.9	10	PDB header: oxidoreductase Chain: A; PDB Molecule: d-erythrose 4-phosphate dehydrogenase; PDBTitle: crystal structure of d-erythrose 4-phosphate dehydrogenase from2 brucella melitensis, solved by iodide sad
18	c3cnyA_	Alignment		94.7	6	PDB header: biosynthetic protein Chain: A; PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
19	c3qxbB_	Alignment		94.4	13	PDB header: isomerase Chain: B; PDB Molecule: putative xylose isomerase; PDBTitle: crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution
20	c3bdkB_	Alignment		94.3	14	PDB header: lyase Chain: B; PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
21	c3dx5A_	Alignment	not modelled	93.8	10	PDB header: lyase Chain: A; PDB Molecule: uncharacterized protein asbf; PDBTitle: crystal structure of the probable 3-dhs dehydratase asbf involved in2 the petrobactin synthesis from bacillus anthracis
22	d1tz9a_	Alignment	not modelled	93.4	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
23	c2hk1D_	Alignment	not modelled	93.2	13	PDB header: isomerase Chain: D; PDB Molecule: d-psicose 3-epimerase; PDBTitle: crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose
24	c2zdsB_	Alignment	not modelled	93.1	11	PDB header: dna binding protein Chain: B; PDB Molecule: putative dna-binding protein; PDBTitle: crystal structure of sco6571 from streptomyces coelicolor a3(2)
25	c2ou4C_	Alignment	not modelled	92.9	15	PDB header: isomerase Chain: C; PDB Molecule: d-tagatose 3-epimerase; PDBTitle: crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii
26	c3cqbB_	Alignment	not modelled	92.3	12	PDB header: isomerase Chain: B; PDB Molecule: l-ribulose-5-phosphate 3-epimerase ulae; PDBTitle: crystal structure of l-xylulose-5-phosphate 3-epimerase ulae (form b)2 complex with zn2+ and sulfate
27	c3b4uB_	Alignment	not modelled	91.1	11	PDB header: lyase Chain: B; PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
28	c3vniC_	Alignment	not modelled	90.9	13	PDB header: isomerase Chain: C; PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structures of d-psicose 3-epimerase from clostridium2 cellulolyticum h10 and its complex with ketoheose

						sugars
29	c5zfsA	Alignment	not modelled	89.9	16	PDB header: isomerase Chain: A: PDB Molecule: d-allulose-3-epimerase; PDBTitle: crystal structure of arthrobacter globiformis m30 sugar epimerase2 which can produce d-allulose from d-fructose
30	c3vylB	Alignment	not modelled	89.6	13	PDB header: isomerase Chain: B: PDB Molecule: l-ribulose 3-epimerase; PDBTitle: structure of l-ribulose 3-epimerase
31	d1i60a	Alignment	not modelled	88.9	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: loll-like
32	c5tnvA	Alignment	not modelled	88.2	10	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family protein 2; PDBTitle: crystal structure of a xylose isomerase-like tim barrel protein from2 mycobacterium smegmatis in complex with magnesium
33	c2rfgB	Alignment	not modelled	86.7	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
34	c3kwsB	Alignment	not modelled	86.4	10	PDB header: isomerase Chain: B: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_001305149.1) from2 parabacteroides distasonis atcc 8503 at 1.68 a resolution
35	c3s5oA	Alignment	not modelled	85.9	10	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
36	c3ngfA	Alignment	not modelled	85.5	10	PDB header: isomerase Chain: A: PDB Molecule: ap endonuclease, family 2; PDBTitle: crystal structure of ap endonuclease, family 2 from brucella2 melitensis
37	c3cprB	Alignment	not modelled	80.7	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
38	c2qtzA	Alignment	not modelled	80.1	11	PDB header: oxidoreductase Chain: A: PDB Molecule: methionine synthase reductase; PDBTitle: crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
39	c2zvrA	Alignment	not modelled	79.9	11	PDB header: isomerase Chain: A: PDB Molecule: uncharacterized protein tm_0416; PDBTitle: crystal structure of a d-tagatose 3-epimerase-related protein from2 thermotoga maritima
40	c6j7aB	Alignment	not modelled	79.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: heme oxygenase 1,nadph--cytochrome p450 reductase; PDBTitle: fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
41	c3tc3B	Alignment	not modelled	79.4	15	PDB header: hydrolase Chain: B: PDB Molecule: uv damage endonuclease; PDBTitle: crystal structure of sacuvde
42	c3qfeB	Alignment	not modelled	79.3	13	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
43	c3eb2A	Alignment	not modelled	79.2	17	PDB header: lyase Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
44	c2x7vA	Alignment	not modelled	79.0	10	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
45	c2nuxB	Alignment	not modelled	78.3	19	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 sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
46	c3fluD	Alignment	not modelled	78.2	18	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
47	c6daqA	Alignment	not modelled	77.7	14	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
48	c1j9zB	Alignment	not modelled	77.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nadph-cytochrome p450 reductase; PDBTitle: cypor-w677g
49	c2v9dB	Alignment	not modelled	76.8	12	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
50	c5iq5A	Alignment	not modelled	76.8	12	PDB header: viral protein Chain: A: PDB Molecule: macro domain; PDBTitle: nmr solution structure of mayaro virus macro domain
51	d1hl2a	Alignment	not modelled	76.7	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
52	d1bxbA	Alignment	not modelled	74.2	11	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
53	c3nqaA	Alignment	not modelled	73.5	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase;

53	c3t06A	Alignment	not modelled	73.3	13	PDBTitle: crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa PDB header: isomerase
54	c3ktcB	Alignment	not modelled	72.3	11	Chain: B: PDB Molecule: xylose isomerase; PDBTitle: crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
55	c3pueA	Alignment	not modelled	72.3	16	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
56	c3si9B	Alignment	not modelled	72.1	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
57	c3h5dD	Alignment	not modelled	72.1	15	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from drug-resistant streptococcus2 pneumoniae
58	c3daqB	Alignment	not modelled	71.9	11	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
59	c4ovxA	Alignment	not modelled	71.7	16	PDB header: isomerase Chain: A: PDB Molecule: xylose isomerase domain protein tim barrel; PDBTitle: crystal structure of xylose isomerase domain protein from planctomyces2 limnophilus dsm 3776
60	c5afdA	Alignment	not modelled	71.3	19	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: native structure of n-acetylneuraminatase lyase (sialic acid aldolase)2 from aliivibrio salmonicida
61	d2ebfx2	Alignment	not modelled	71.2	17	Fold: EreA/ChaN-like Superfamily: EreA/ChaN-like Family: PMT domain-like
62	c2ksnA	Alignment	not modelled	69.7	23	PDB header: signaling protein Chain: A: PDB Molecule: ubiquitin domain-containing protein 2; PDBTitle: solution structure of the n-terminal domain of dc-ubp/ubtd2
63	c5n6yD	Alignment	not modelled	69.5	14	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
64	c3g0sA	Alignment	not modelled	69.4	11	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
65	c3gqeA	Alignment	not modelled	69.2	10	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3; PDBTitle: crystal structure of macro domain of venezuelan equine encephalitis2 virus
66	c5gxuA	Alignment	not modelled	68.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph--cytochrome p450 reductase 2; PDBTitle: crystal structure of arabidopsis atr2
67	c4uxdC	Alignment	not modelled	67.2	11	PDB header: lyase Chain: C: PDB Molecule: 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from picrophilus torridus
68	d1xxa1	Alignment	not modelled	67.1	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
69	c2vc6A	Alignment	not modelled	66.5	17	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of mosa from s. meliloti with pyruvate bound
70	c3n2xB	Alignment	not modelled	64.5	11	PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
71	c3fkkA	Alignment	not modelled	64.4	13	PDB header: lyase Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase
72	c3bi8A	Alignment	not modelled	64.3	11	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
73	d1k77a	Alignment	not modelled	64.3	19	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Hypothetical protein YgbM (EC1530)
74	c5ak1A	Alignment	not modelled	63.2	15	PDB header: hydrolase Chain: A: PDB Molecule: carbohydrate binding family 6; PDBTitle: the penta-modular cellulosomal arabinoxylanase ctxyl5a2 structure as revealed by x-ray crystallography
75	c3ju2A	Alignment	not modelled	62.8	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
76	c2yxgD	Alignment	not modelled	61.8	15	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
77	c2qw5B	Alignment	not modelled	61.5	7	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
						PDB header: lyase

78	c3lciA_	Alignment	not modelled	60.7	17	Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
79	c3lmzA_	Alignment	not modelled	60.6	9	PDB header: isomerase Chain: A: PDB Molecule: putative sugar isomerase; PDBTitle: crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distazonis atcc 8503 at 1.44 a resolution
80	c2bpoA_	Alignment	not modelled	60.0	15	PDB header: reductase Chain: A: PDB Molecule: nadh-cytochrom p450 reductase; PDBTitle: crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
81	d1xima_	Alignment	not modelled	59.1	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
82	c2ehhE_	Alignment	not modelled	58.2	13	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
83	c5ud6B_	Alignment	not modelled	57.2	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from cyanidioschyzon merolae with lysine2 bound
84	c3lerA_	Alignment	not modelled	56.7	19	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc_11168
85	c3q71A_	Alignment	not modelled	56.6	14	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (ard8) - macro domain 2 in complex with adenosine-5-2 diphosphoribose
86	c5ktiA_	Alignment	not modelled	56.5	15	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
87	c3d0cB_	Alignment	not modelled	56.3	13	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
88	c5hmqE_	Alignment	not modelled	56.1	12	PDB header: lyase Chain: E: PDB Molecule: 4-hydroxyphenylpyruvate dioxygenase; PDBTitle: xylose isomerase-like tim barrel/4-hydroxyphenylpyruvate dioxygenase2 fusion protein
89	c3wqoB_	Alignment	not modelled	54.8	19	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein mj1311; PDBTitle: crystal structure of d-tagatose 3-epimerase-like protein
90	d1zr5a1	Alignment	not modelled	54.5	9	Fold: Macro domain-like Superfamily: Macro domain-like Family: Macro domain
91	c3e96B_	Alignment	not modelled	53.7	9	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
92	d1xkya1	Alignment	not modelled	53.5	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	c6mqhA_	Alignment	not modelled	52.9	17	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
94	c3aamA_	Alignment	not modelled	52.3	16	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease iv; PDBTitle: crystal structure of endonuclease iv from thermus thermophilus hb8
95	c1ddiA_	Alignment	not modelled	52.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: crystal structure of sir-fp60
96	c2r8wB_	Alignment	not modelled	51.4	13	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
97	d1o5ka_	Alignment	not modelled	51.1	13	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
98	d1bxca_	Alignment	not modelled	51.1	13	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
99	c4i7vD_	Alignment	not modelled	50.6	16	PDB header: biosynthetic protein Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: agrobacterium tumefaciens dhbps with pyruvate
100	c5kivA_	Alignment	not modelled	50.3	16	PDB header: hydrolase Chain: A: PDB Molecule: protein-adp-ribose hydrolase; PDBTitle: crystal structure of saumacro (sav0325)
101	c5mrjA_	Alignment	not modelled	50.2	15	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylanase; PDBTitle: crystal structure of endo-1,4-beta-xylanase-like protein from2 acremonium chrysogenum
102	c5c54D_	Alignment	not modelled	49.9	13	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase/n-acetylneuraminate lyase; PDBTitle: crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
103	d2a6na1	Alignment	not modelled	49.8	12	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
						PDB header: lyase

104	c4ur7B_	Alignment	not modelled	47.9	7	Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
105	c3p6A_	Alignment	not modelled	47.3	6	PDB header: isomerase Chain: A: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distansoni atcc 8503 at 1.85 a resolution
106	d1bg4a_	Alignment	not modelled	47.3	9	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
107	c3zddA_	Alignment	not modelled	47.0	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
108	c5hqcA_	Alignment	not modelled	46.5	13	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 97 enzyme; PDBTitle: a glycoside hydrolase family 97 enzyme r171k variant from2 pseudoalteromonas sp. strain k8
109	c3dz1A_	Alignment	not modelled	46.3	14	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
110	d1qh8a_	Alignment	not modelled	45.9	11	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
111	c6daoB_	Alignment	not modelled	45.8	15	PDB header: lyase Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: nahe wt selenomethionine
112	c2zq0B_	Alignment	not modelled	45.5	12	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase subb); PDBTitle: crystal structure of subb complexed with acarbose
113	c4xv0A_	Alignment	not modelled	45.0	11	PDB header: hydrolase Chain: A: PDB Molecule: beta-xylanase; PDBTitle: crystal structure of an endo-beta-1,4-xylanase (glycoside hydrolase2 family 10/gh10) enzyme from trichoderma reesei
114	c5ui3C_	Alignment	not modelled	44.9	16	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhbps from chlamydomonas reinhardtii
115	d1yvka1	Alignment	not modelled	43.7	17	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-acetyl transferase, NAT
116	c4ah7C_	Alignment	not modelled	43.1	19	PDB header: lyase Chain: C: PDB Molecule: n-acetylneuraminatase lyase; PDBTitle: structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
117	c2lr8A_	Alignment	not modelled	42.7	18	PDB header: apoptosis Chain: A: PDB Molecule: casp8-associated protein 2; PDBTitle: solution nmr structure of casp8-associated protein 2 from homo2 sapiens, northeast structural genomics consortium (nesg) target3 hr8150a
118	c4nq1B_	Alignment	not modelled	42.7	11	PDB header: lyase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
119	c3bzjA_	Alignment	not modelled	42.3	12	PDB header: hydrolase Chain: A: PDB Molecule: uv endonuclease; PDBTitle: uvde k229l
120	c4ablA_	Alignment	not modelled	41.9	15	PDB header: transferase Chain: A: PDB Molecule: poly [adp-ribose] polymerase 14; PDBTitle: human parp14 (artd8, bal2) - macro domain 3