



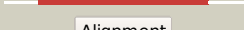

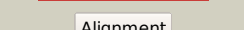

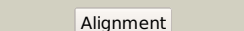




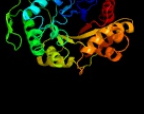
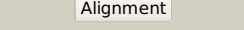

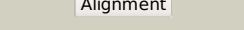

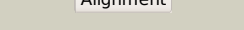

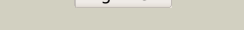



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0132c_fgd2_159698_160780
Date	Tue Jul 23 14:50:17 BST 2019
Unique Job ID	c6838d729730169b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rhca_	 Alignment		100.0	32	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
2	c3c8nB_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: B: PDB Molecule: probable f420-dependent glucose-6-phosphate dehydrogenase PDBTitle: crystal structure of apo-fgd1 from mycobacterium tuberculosis
3	d1ezwa_	 Alignment		100.0	23	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
4	d1luca_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
5	c5tlcA_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: dibenzothiophene desulfurization enzyme a; PDBTitle: crystal structure of bdsa from bacillus subtilis wu-s2b
6	d1nqka_	 Alignment		100.0	22	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
7	c1z69D_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: D: PDB Molecule: coenzyme f420-dependent n(5),n(10)- PDBTitle: crystal structure of methylenetetrahydromethanopterin2 reductase (mer) in complex with coenzyme f420
8	c1tvIA_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein ytnj; PDBTitle: structure of ytnj from bacillus subtilis
9	d1tvla_	 Alignment		100.0	18	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Ssud-like monooxygenases
10	c3raoB_	 Alignment		100.0	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus atcc 10987.
11	c5wanA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrimidine monooxygenase ruta; PDBTitle: crystal structure of a flavoenzyme ruta in the pyrimidine catabolic2 pathway

12	c3sdoB_	Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase; PDBTitle: structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei
13	d1lucb_	Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Bacterial luciferase (alkanal monooxygenase)
14	c5dqpA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: edta monooxygenase; PDBTitle: edta monooxygenase (emoa) from chelativorans sp. bnc1
15	c2wgkA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 3,6-diketocamphane 1,6 monooxygenase; PDBTitle: type ii baeyer-villiger monooxygenase oxygenating2 constituent of 3,6-diketocamphane 1,6 monooxygenase from3 pseudomonas putida
16	c2i7gA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
17	c2b81D_	Alignment		100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: luciferase-like monooxygenase; PDBTitle: crystal structure of the luciferase-like monooxygenase from bacillus2 cereus
18	c3b9nB_	Alignment		100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: alkane monooxygenase; PDBTitle: crystal structure of long-chain alkane monooxygenase (lada)
19	c5w4zA_	Alignment		100.0	23	PDB header: flavoprotein Chain: A: PDB Molecule: riboflavin lyase; PDBTitle: crystal structure of riboflavin lyase (rcae) with modified fmn and2 substrate riboflavin
20	d1f07a_	Alignment		100.0	26	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: F420 dependent oxidoreductases
21	c6friD_	Alignment	not modelled	100.0	11	PDB header: oxidoreductase Chain: D: PDB Molecule: alkanal monooxygenase beta chain; PDBTitle: structure of luxb from photobacterium leiognathi
22	c6ak1B_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dimethyl-sulfide monooxygenase; PDBTitle: crystal structure of dmoa from hyphomicrobium sulfonivorans
23	d1nfpa_	Alignment	not modelled	99.9	20	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
24	d1fvpa_	Alignment	not modelled	99.2	17	Fold: TIM beta/alpha-barrel Superfamily: Bacterial luciferase-like Family: Non-fluorescent flavoprotein (luxF, FP390)
25	c3b8iF_	Alignment	not modelled	75.9	17	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+.
26	d1s2wa_	Alignment	not modelled	73.4	15	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/Isocitrate lyase-like
27	d1o5ka_	Alignment	not modelled	73.3	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
28	c3fa4D_	Alignment	not modelled	72.6	14	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 PDB header: lyase

29	c1zlpA	Alignment	not modelled	72.2	11	Chain: A: PDB Molecule: petal death protein; PDBTitle: petal death protein psr132 with cysteine-linked glutaraldehyde forming2 a thiohemiacetal adduct
30	c3qy6A	Alignment	not modelled	72.1	26	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase ywqe; PDBTitle: crystal structures of ywqe from bacillus subtilis and cpsb from2 streptococcus pneumoniae, unique metal-dependent tyrosine3 phosphatases
31	d1muma	Alignment	not modelled	69.9	19	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
32	c2ze3A	Alignment	not modelled	68.9	19	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
33	c3eooL	Alignment	not modelled	68.4	17	PDB header: lyase Chain: L: PDB Molecule: methylisocitrate lyase; PDBTitle: 2.9a crystal structure of methyl-isocitrate lyase from2 burkholderia pseudomallei
34	d1ujqa	Alignment	not modelled	68.3	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate mutase/isocitrate lyase-like
35	c3lyeA	Alignment	not modelled	66.8	18	PDB header: hydrolase Chain: A: PDB Molecule: oxaloacetate acetyl hydrolase; PDBTitle: crystal structure of oxaloacetate acetylhydrolase
36	c2qiwa	Alignment	not modelled	65.4	14	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
37	c2hjpA	Alignment	not modelled	64.5	19	PDB header: hydrolase Chain: A: PDB Molecule: phosphonopyruvate hydrolase; PDBTitle: crystal structure of phosphonopyruvate hydrolase complex with2 phosphonopyruvate and mg++
38	c3ih1A	Alignment	not modelled	61.1	16	PDB header: lyase Chain: A: PDB Molecule: methylisocitrate lyase; PDBTitle: crystal structure of carboxyvinyl-carboxyphosphonate phosphorylmutase2 from bacillus anthracis
39	c2ehhE	Alignment	not modelled	60.4	8	PDB header: lyase Chain: E: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
40	d2d69a1	Alignment	not modelled	60.0	6	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
41	c6mqhA	Alignment	not modelled	58.5	7	PDB header: lyase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
42	c2r8wB	Alignment	not modelled	56.3	19	PDB header: lyase Chain: B: PDB Molecule: agr_c_1641p; PDBTitle: the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
43	c4lsbA	Alignment	not modelled	55.6	26	PDB header: lyase Chain: A: PDB Molecule: lyase/mutase; PDBTitle: crystal structure of a putative lyase/mutase from burkholderia2 cenocepacia j2315
44	c3d0cB	Alignment	not modelled	55.0	7	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
45	c3pueA	Alignment	not modelled	53.4	9	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
46	d2a6na1	Alignment	not modelled	53.3	5	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
47	c4ur7B	Alignment	not modelled	50.9	17	PDB header: lyase Chain: B: PDB Molecule: keto-deoxy-d-galactarate dehydratase; PDBTitle: crystal structure of keto-deoxy-d-galactarate dehydratase2 complexed with pyruvate
48	c4n4qD	Alignment	not modelled	50.7	7	PDB header: lyase Chain: D: PDB Molecule: acylneuraminate lyase; PDBTitle: crystal structure of n-acetylneuraminate lyase from mycoplasma2 synoviae, crystal form ii
49	c4mg4G	Alignment	not modelled	50.2	17	PDB header: unknown function Chain: G: PDB Molecule: phosphonmutase; PDBTitle: crystal structure of a putative phosphonmutase from burkholderia2 cenocepacia j2315
50	c3g0sA	Alignment	not modelled	48.3	5	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from salmonella typhimurium lt2
51	d1xxxa1	Alignment	not modelled	48.0	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
52	d1m3ua	Alignment	not modelled	47.7	14	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Ketopantoate hydroxymethyltransferase PanB
53	c6hunA	Alignment	not modelled	47.5	10	PDB header: photosynthesis Chain: A: PDB Molecule: ribulose bisphosphate carboxylase; PDBTitle: dimeric archeal rubisco from hyperthermus butylicus
54	c5uncB	Alignment	not modelled	46.5	14	PDB header: isomerase Chain: B: PDB Molecule: phosphoenolpyruvate phosphomutase;

54	c3unfB	Alignment	not modelled	46.5	14	PDBTitle: the crystal structure of phosphoenolpyruvate phosphomutase from <i>Streptomyces platensis</i> subsp. <i>rosaceus</i> PDB header: lyase
55	c3noeA	Alignment	not modelled	46.0	12	Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Pseudomonas aeruginosa</i> PDB header: lyase
56	c3lerA	Alignment	not modelled	45.1	12	Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Campylobacter jejuni</i> subsp. <i>jejuni</i> nctc 11168 PDB header: lyase
57	c3eb2A	Alignment	not modelled	44.2	10	Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Pseudomonas palustris</i> at 2.0 Å resolution PDB header: lyase
58	c3qfeB	Alignment	not modelled	43.9	11	Chain: B: PDB Molecule: putative dihydrodipicolinate synthase family protein; PDBTitle: crystal structures of a putative dihydrodipicolinate synthase family 2 protein from <i>Coccidioides immitis</i> PDB header: lyase
59	c4xkyC	Alignment	not modelled	43.3	10	Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from the commensal bacterium <i>Bacteroides thetaiotaomicron</i> at 2.1 Å resolution PDB header: lyase
60	c3n2xB	Alignment	not modelled	43.0	10	Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the 2 dihydrodipicolinic acid synthase family from <i>E. coli</i> K12 in complex 3 with pyruvate PDB header: lyase
61	c3daqB	Alignment	not modelled	42.9	7	Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant <i>Staphylococcus aureus</i> PDB header: lyase
62	c6daoB	Alignment	not modelled	42.7	5	Chain: B: PDB Molecule: trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; PDBTitle: native wt selenomethionine PDB header: lyase
63	c4nq1B	Alignment	not modelled	42.2	9	Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate synthase; PDBTitle: <i>Legionella pneumophila</i> dihydrodipicolinate synthase with first 2 substrate pyruvate bound in the active site PDB header: lyase
64	c4i7vD	Alignment	not modelled	42.0	12	Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: <i>Agrobacterium tumefaciens</i> dhdp5 with pyruvate PDB header: lyase
65	c3cprB	Alignment	not modelled	41.9	17	Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of <i>Corynebacterium glutamicum</i> 2 dihydrodipicolinate synthase to 2.2 Å resolution PDB header: lyase
66	c4ah7C	Alignment	not modelled	40.7	5	Chain: C: PDB Molecule: n-acetylneuraminase lyase; PDBTitle: structure of wild type <i>Staphylococcus aureus</i> n-acetylneuraminic acid 2 lyase in complex with pyruvate PDB header: hydrolase
67	c1bf2A	Alignment	not modelled	40.5	8	Chain: A: PDB Molecule: isoamylase; PDBTitle: structure of <i>Pseudomonas isoamylase</i> PDB header: hydrolase
68	c2v9dB	Alignment	not modelled	39.3	10	Chain: B: PDB Molecule: yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the 2 dihydrodipicolinic acid synthase family from <i>E. coli</i> K12 PDB header: lyase
69	c2vc6A	Alignment	not modelled	39.2	12	Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of Mosa from <i>S. meliloti</i> with pyruvate bound PDB header: lyase
70	c2yxgD	Alignment	not modelled	39.0	17	Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa) PDB header: lyase
71	c3e96B	Alignment	not modelled	38.8	13	Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from <i>Bacillus clausii</i> PDB header: lyase (carbon-carbon)
72	c1rcxH	Alignment	not modelled	37.8	11	Chain: H: PDB Molecule: ribulose bisphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach Rubisco in complex with its substrate 2 ribulose-1,5-bisphosphate PDB header: lyase
73	c4uxdC	Alignment	not modelled	37.7	5	Chain: C: PDB Molecule: 2-dehydro-3-deoxy-D-gluconate/2-dehydro-3-deoxy- PDBTitle: 2-keto 3-deoxygluconate aldolase from <i>Picrophilus torridus</i> PDB header: lyase
74	d8ruca1	Alignment	not modelled	37.1	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain PDB header: lyase
75	c3na8A	Alignment	not modelled	37.0	16	Chain: A: PDB Molecule: putative dihydrodipicolinate synthetase; PDBTitle: crystal structure of a putative dihydrodipicolinate synthetase from <i>Pseudomonas aeruginosa</i> PDB header: hydrolase
76	c2wjeA	Alignment	not modelled	36.7	12	Chain: A: PDB Molecule: tyrosine-protein phosphatase cpsb; PDBTitle: crystal structure of the tyrosine phosphatase cps4b from <i>Staphylococcus pneumoniae</i> tigr4. PDB header: hydrolase
77	c3dcpB	Alignment	not modelled	35.0	15	Chain: B: PDB Molecule: histidinol-phosphatase; PDBTitle: crystal structure of the putative histidinol phosphatase Hisk from <i>Listeria monocytogenes</i> . northeast structural genomics consortium 3 target lmr141. PDB header: hydrolase
78	c3fkkA	Alignment	not modelled	34.9	12	Chain: A: PDB Molecule: l-2-keto-3-deoxyarabonate dehydratase; PDBTitle: structure of l-2-keto-3-deoxyarabonate dehydratase PDB header: lyase

79	c3bi8A_	Alignment	not modelled	34.9	9	Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: structure of dihydrodipicolinate synthase from clostridium2 botulinum
80	c2h90A_	Alignment	not modelled	34.8	32	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
81	c5ud6B_	Alignment	not modelled	34.3	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from cyanidioschyzon merolae with lysine2 bound
82	c3fluD_	Alignment	not modelled	33.4	17	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
83	d1ht6a2	Alignment	not modelled	33.3	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
84	c5zmyF_	Alignment	not modelled	32.4	23	PDB header: hydrolase Chain: F: PDB Molecule: cis-epoxysuccinate hydrolase; PDBTitle: crystal structure of a cis-epoxysuccinate hydrolase producing d(-)-2 tartaric acids
85	c5ui3C_	Alignment	not modelled	32.4	8	PDB header: lyase Chain: C: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dhds from chlamydomonas reinhardtii
86	c1ps9A_	Alignment	not modelled	32.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
87	c3si9B_	Alignment	not modelled	32.1	16	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
88	d1uoka2	Alignment	not modelled	32.1	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
89	c4icnB_	Alignment	not modelled	31.4	10	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: dihydrodipicolinate synthase from shewanella benthica
90	d1f74a_	Alignment	not modelled	31.4	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
91	d1wdda1	Alignment	not modelled	30.1	14	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
92	c2yb1A_	Alignment	not modelled	30.1	16	PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: structure of an amidohydrolase from chromobacterium violaceum (efi2 target efi-500202) with bound mn, amp and phosphate.
93	c2ya0A_	Alignment	not modelled	29.9	16	PDB header: hydrolase Chain: A: PDB Molecule: putative alkaline amylopullulanase; PDBTitle: catalytic module of the multi-modular glycogen-degrading pneumococcal2 virulence factor spua
94	c3m07A_	Alignment	not modelled	29.3	12	PDB header: unknown function Chain: A: PDB Molecule: putative alpha amylase; PDBTitle: 1.4 angstrom resolution crystal structure of putative alpha amylase2 from salmonella typhimurium.
95	d1ykwa1	Alignment	not modelled	29.2	9	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
96	c6h4eB_	Alignment	not modelled	29.1	13	PDB header: lyase Chain: B: PDB Molecule: putative n-acetylneuraminatase lyase; PDBTitle: proteus mirabilis n-acetylneuraminatase lyase
97	d1z41a1	Alignment	not modelled	29.0	24	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
98	c3qfwB_	Alignment	not modelled	28.7	9	PDB header: lyase Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase large PDBTitle: crystal structure of rubisco-like protein from rhodospseudomonas2 palustris
99	d1lwha2	Alignment	not modelled	28.6	19	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
100	c1rldB_	Alignment	not modelled	28.6	14	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
101	c6daqA_	Alignment	not modelled	27.8	7	PDB header: lyase Chain: A: PDB Molecule: phdj; PDBTitle: phdj bound to substrate intermediate
102	d1g5aa2	Alignment	not modelled	27.2	12	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
103	c6k0aC_	Alignment	not modelled	27.0	4	PDB header: rna binding protein/rna Chain: C: PDB Molecule: ribonuclease p protein component 3; PDBTitle: cryo-em structure of an archaeal ribonuclease p
104	c2d69B_	Alignment	not modelled	26.5	5	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)

105	c2by0A_	Alignment	not modelled	26.5	8	PDB header: hydrolase Chain: A: PDB Molecule: maltooligosyltrehalose trehalohydrolase; PDBTitle: is radiation damage dependent on the dose-rate used during2 macromolecular crystallography data collection
106	c5zxbB_	Alignment	not modelled	26.5	23	PDB header: hydrolase Chain: B: PDB Molecule: cyclic maltosyl-maltose hydrolase; PDBTitle: cyclic alpha-maltosyl-(1->6)-maltose hydrolase from arthrobacter2 globiformis, ligand-free form
107	c3b4uB_	Alignment	not modelled	26.4	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
108	c1ehaA_	Alignment	not modelled	26.4	16	PDB header: hydrolase Chain: A: PDB Molecule: glycosyltrehalose trehalohydrolase; PDBTitle: crystal structure of glycosyltrehalose trehalohydrolase from2 sulfolobus solfataricus
109	d1xkya1	Alignment	not modelled	26.4	10	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
110	d1m53a2	Alignment	not modelled	26.3	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
111	d1wzla3	Alignment	not modelled	25.7	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
112	d1avaa2	Alignment	not modelled	25.7	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
113	c3nwrA_	Alignment	not modelled	25.7	14	PDB header: lyase Chain: A: PDB Molecule: a rubisco-like protein; PDBTitle: crystal structure of a rubisco-like protein from burkholderia fungorum
114	d1bxba_	Alignment	not modelled	25.4	18	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Xylose isomerase
115	c4mwaA_	Alignment	not modelled	25.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
116	c4b5nA_	Alignment	not modelled	25.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, fmn-binding; PDBTitle: crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
117	c3gr7A_	Alignment	not modelled	25.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh\;flavin oxidoreductase; PDBTitle: structure of oye from geobacillus kaustophilus, hexagonal crystal form
118	d1ea9c3	Alignment	not modelled	24.6	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
119	c4a3uB_	Alignment	not modelled	24.5	28	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh\;flavin oxidoreductase/nadh oxidase; PDBTitle: x-structure of the old yellow enzyme homologue from zymomonas mobilis2 (ncr)
120	d1gvia3	Alignment	not modelled	24.2	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain