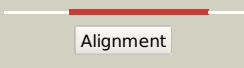

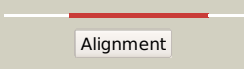
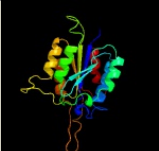
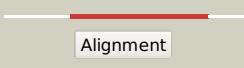

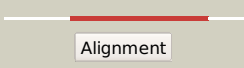
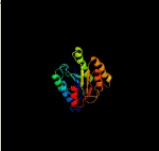
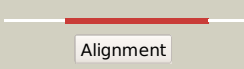

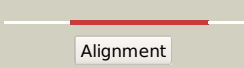

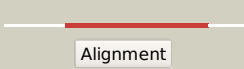

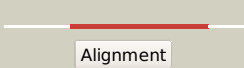
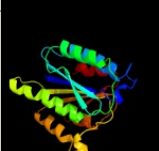
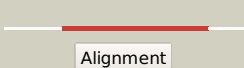
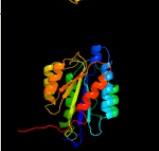
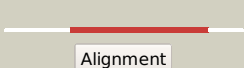

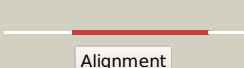












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1481 (-) _1671383_1672390
Date	Fri Aug 2 13:30:06 BST 2019
Unique Job ID	09ad2dd531c1035f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4rckB_	 Alignment		100.0	26	PDB header: membrane protein Chain: B; PDB Molecule: hypothetical membrane spanning protein; PDBTitle: crystal structure of uncharacterized membrane spanning protein from2 vibrio fischeri
2	c3ibsA_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: conserved hypothetical protein batb; PDBTitle: crystal structure of conserved hypothetical protein batb from2 bacteroides thetaiotaomicron
3	c6nmIE_	 Alignment		100.0	17	PDB header: transcription Chain: E; PDB Molecule: general transcription factor iih subunit 2, p44; PDBTitle: cryo-em structure of the human tfiih core complex
4	c6o9l6_	 Alignment		99.9	18	PDB header: transcription/dna Chain: 6; PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
5	c4fx5A_	 Alignment		99.9	22	PDB header: blood clotting Chain: A; PDB Molecule: von willebrand factor type a; PDBTitle: von willebrand factor type a from catenulispora acidiphila
6	c5iy70_	 Alignment		99.9	14	PDB header: transcription, transferase/dna Chain: 0; PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the open state
7	c5a8jA_	 Alignment		99.9	20	PDB header: transcription Chain: A; PDB Molecule: vwa2; PDBTitle: crystal structure of the arnb paralog vwa2 from2 sulfobolus acidocaldarius
8	c4wfqA_	 Alignment		99.9	16	PDB header: transcription Chain: A; PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: crystal structure of tfiih subunit
9	c6fpzA_	 Alignment		99.9	15	PDB header: structural protein Chain: A; PDB Molecule: inter-alpha-trypsin inhibitor heavy chain h1; PDBTitle: inter-alpha-inhibitor heavy chain 1, d298a
10	c5oqj6_	 Alignment		99.9	16	PDB header: transcription Chain: 6; PDB Molecule: suppressor of stem-loop protein 1; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
11	c1rs0A_	 Alignment		99.9	19	PDB header: hydrolase Chain: A; PDB Molecule: complement factor b; PDBTitle: crystal structure analysis of the bb segment of factor b2 complexed with di-isopropyl-phosphate (dip)

12	d2ok5a1	Alignment		99.9	17	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
13	c2ok5A_	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: complement factor b; PDBTitle: human complement factor b
14	c2i6sA_	Alignment		99.8	19	PDB header: hydrolase Chain: A: PDB Molecule: complement c2a fragment; PDBTitle: complement component c2a
15	c4b4tW_	Alignment		99.8	24	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: near-atomic resolution structural model of the yeast 26s proteasome
16	c2x5nA_	Alignment		99.8	20	PDB header: nuclear protein Chain: A: PDB Molecule: 26s proteasome regulatory subunit rpn10; PDBTitle: crystal structure of the sprpn10 vwa domain
17	c5gjqW_	Alignment		99.8	22	PDB header: hydrolase Chain: W: PDB Molecule: 26s proteasome non-atpase regulatory subunit 4; PDBTitle: structure of the human 26s proteasome bound to usp14-ubal
18	c3jbrF_	Alignment		99.8	15	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
19	d1jeyb2	Alignment		99.8	15	Fold: vWA-like Superfamily: vWA-like Family: Ku80 subunit N-terminal domain
20	c5gjfF_	Alignment		99.8	15	PDB header: membrane protein Chain: F: PDB Molecule: voltage-dependent calcium channel subunit alpha-2/delta-1; PDBTitle: structure of the mammalian voltage-gated calcium channel cav1.12 complex at near atomic resolution
21	c2b2xB_	Alignment	not modelled	99.8	17	PDB header: immune system Chain: B: PDB Molecule: integrin alpha-1; PDBTitle: vla1 rdeltah i-domain complexed with a quadruple mutant of the aqc22 fab
22	c4hqnb_	Alignment	not modelled	99.8	16	PDB header: cell adhesion Chain: B: PDB Molecule: sporozoite surface protein 2; PDBTitle: crystal structure of manganese-loaded plasmodium vivax trap protein
23	c3n2nC_	Alignment	not modelled	99.8	15	PDB header: toxin receptor Chain: C: PDB Molecule: anthrax toxin receptor 1; PDBTitle: the crystal structure of tumor endothelial marker 8 (tem8)2 extracellular domain
24	c2x31F_	Alignment	not modelled	99.8	20	PDB header: ligase Chain: F: PDB Molecule: magnesium-chelatase 60 kda subunit; PDBTitle: modelling of the complex between subunits bchi and bchd of magnesium2 chelatase based on single-particle cryo-em reconstruction at 7.5 ang
25	d1n3ya_	Alignment	not modelled	99.7	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
26	d1jeya2	Alignment	not modelled	99.7	17	Fold: vWA-like Superfamily: vWA-like Family: Ku70 subunit N-terminal domain
27	c2iueA_	Alignment	not modelled	99.7	14	PDB header: membrane protein Chain: A: PDB Molecule: pactolus i-domain; PDBTitle: pactolus i-domain: functional switching of the rossmann2 fold
28	d1v7pc_	Alignment	not modelled	99.7	19	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain

29	d1ijba_	Alignment	not modelled	99.7	8	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
30	d1u0oc1	Alignment	not modelled	99.7	8	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
31	d1shux_	Alignment	not modelled	99.7	20	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
32	c4hqfA_	Alignment	not modelled	99.7	16	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-related anonymous protein, trap; PDBTitle: crystal structure of plasmodium falciparum trap, i4 form
33	d1ck4a_	Alignment	not modelled	99.7	13	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
34	d1pt6a_	Alignment	not modelled	99.7	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
35	d1atza_	Alignment	not modelled	99.7	15	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
36	d1pd0a3	Alignment	not modelled	99.7	16	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
37	d1q0pa_	Alignment	not modelled	99.7	18	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
38	c5e6rA_	Alignment	not modelled	99.7	16	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-I; PDBTitle: structures of leukocyte integrin alb2: the ai domain, the headpiece,2 and the pocket for the internal ligand
39	d1mf7a_	Alignment	not modelled	99.7	14	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
40	d1yvra2	Alignment	not modelled	99.6	13	Fold: vWA-like Superfamily: vWA-like Family: RoRNP C-terminal domain-like
41	c3txaA_	Alignment	not modelled	99.6	28	PDB header: cell adhesion Chain: A: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
42	c3gxbB_	Alignment	not modelled	99.6	11	PDB header: cell adhesion Chain: B: PDB Molecule: von willebrand factor; PDBTitle: crystal structure of wvf a2 domain
43	c4cnbA_	Alignment	not modelled	99.6	17	PDB header: structural protein Chain: A: PDB Molecule: proximal thread matrix protein 1; PDBTitle: structure of proximal thread matrix protein 1 (ptmp1) from the2 mussel byssus - crystal form 2
44	c3tw0D_	Alignment	not modelled	99.6	28	PDB header: cell adhesion Chain: D: PDB Molecule: cell wall surface anchor family protein; PDBTitle: structural analysis of adhesive tip pilin, gbs104 from group b2 streptococcus agalactiae
45	c2xggB_	Alignment	not modelled	99.6	15	PDB header: hydrolase Chain: B: PDB Molecule: microneme protein 2; PDBTitle: structure of toxoplasma gondii micronemal protein 2 a_i2 domain
46	c4okuA_	Alignment	not modelled	99.6	15	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein mic2; PDBTitle: structure of toxoplasma gondii promic2
47	c4ihkA_	Alignment	not modelled	99.6	13	PDB header: cell adhesion Chain: A: PDB Molecule: collagen alpha3(vi); PDBTitle: crystal structure of the collagen vi alpha3 n5 domain r1061q
48	d1mjna_	Alignment	not modelled	99.5	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
49	c2nvoA_	Alignment	not modelled	99.4	15	PDB header: rna binding protein Chain: A: PDB Molecule: ro sixty-related protein, rsr; PDBTitle: crystal structure of deinococcus radiodurans ro (rsr) protein
50	d1tyeb2	Alignment	not modelled	99.4	16	Fold: vWA-like Superfamily: vWA-like Family: Integrin A (or I) domain
51	c1jeyB_	Alignment	not modelled	99.3	13	PDB header: dna binding protein/dna Chain: B: PDB Molecule: ku80; PDBTitle: crystal structure of the ku heterodimer bound to dna
52	c6bxjA_	Alignment	not modelled	99.3	18	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: structure of a single-chain beta3 integrin
53	c6djpB_	Alignment	not modelled	99.2	15	PDB header: membrane protein Chain: B: PDB Molecule: integrin beta-8; PDBTitle: integrin alpha-v beta-8 in complex with the fabs 8b8 and 68
54	c6bxfA_	Alignment	not modelled	99.2	19	PDB header: cell adhesion Chain: A: PDB Molecule: chimera protein of integrin beta-3 and integrin alpha-I; PDBTitle: crystal structure of an extended b3 integrin I33
55	c3vi3D_	Alignment	not modelled	99.2	17	PDB header: cell adhesion/immune system Chain: D: PDB Molecule: integrin beta-1; PDBTitle: crystal structure of alpha5beta1 integrin headpiece (ligand-free form)

56	c6nmiF_	Alignment	not modelled	99.2	14	PDB header: transcription Chain: F: PDB Molecule: general transcription factor iih subunit 3, p34; PDBTitle: cryo-em structure of the human tfiih core complex
57	c3v4pB_	Alignment	not modelled	99.1	16	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-7; PDBTitle: crystal structure of a4b7 headpiece complexed with fab act-1
58	c4um9D_	Alignment	not modelled	99.1	21	PDB header: immune system Chain: D: PDB Molecule: integrin beta-6; PDBTitle: crystal structure of alpha v beta 6 with peptide
59	c1pd0A_	Alignment	not modelled	99.1	16	PDB header: transport protein Chain: A: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the copii coat subunit, sec24.2 complexed with a peptide from the snare protein sed53 (yeast syntaxin-5)
60	c3fcuB_	Alignment	not modelled	99.0	16	PDB header: cell adhesion/blood clotting Chain: B: PDB Molecule: integrin beta-3; PDBTitle: structure of headpiece of integrin aiibb3 in open conformation
61	c3egxB_	Alignment	not modelled	98.9	25	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24a; PDBTitle: crystal structure of the mammalian copii-coat protein sec23a/24a2 complexed with the snare protein sec22b and bound to the transport3 signal sequence of the snare protein bet1
62	c1m2vB_	Alignment	not modelled	98.9	18	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24; PDBTitle: crystal structure of the yeast sec23/24 heterodimer
63	c1u8cB_	Alignment	not modelled	98.8	15	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: a novel adaptation of the integrin psi domain revealed from its2 crystal structure
64	c1m2oA_	Alignment	not modelled	98.8	23	PDB header: protein transport/signaling protein Chain: A: PDB Molecule: protein transport protein sec23; PDBTitle: crystal structure of the sec23-sar1 complex
65	c3eg9B_	Alignment	not modelled	98.8	24	PDB header: protein transport Chain: B: PDB Molecule: sec24 related gene family, member d; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
66	d2qtva3	Alignment	not modelled	98.8	28	Fold: vWA-like Superfamily: vWA-like Family: Trunk domain of Sec23/24
67	c3eg9A_	Alignment	not modelled	98.8	23	PDB header: protein transport Chain: A: PDB Molecule: protein transport protein sec23a; PDBTitle: crystal structure of the mammalian copii-coat protein sec23/24 bound2 to the transport signal sequence of membrin
68	c3eh2B_	Alignment	not modelled	98.8	25	PDB header: protein transport Chain: B: PDB Molecule: protein transport protein sec24c; PDBTitle: crystal structure of the human copii-coat protein sec24c
69	c3ragA_	Alignment	not modelled	98.7	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein aaci_0196 from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
70	c3k71G_	Alignment	not modelled	98.6	12	PDB header: cell adhesion Chain: G: PDB Molecule: integrin alpha-x; PDBTitle: structure of integrin alphax beta2 ectodomain
71	c1jeqA_	Alignment	not modelled	98.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: ku70; PDBTitle: crystal structure of the ku heterodimer
72	c3ijeB_	Alignment	not modelled	98.6	15	PDB header: protein binding Chain: B: PDB Molecule: integrin beta-3; PDBTitle: crystal structure of the complete integrin alphavbeta3 ectodomain plus2 an alpha/beta transmembrane fragment
73	c5y58E_	Alignment	not modelled	98.4	16	PDB header: rna binding protein Chain: E: PDB Molecule: atp-dependent dna helicase ii subunit 1; PDBTitle: crystal structure of ku70/80 and tlc1
74	c1yvrA_	Alignment	not modelled	98.3	13	PDB header: rna binding protein Chain: A: PDB Molecule: 60-kda ss-a/ro ribonucleoprotein; PDBTitle: ro autoantigen
75	c3k6sB_	Alignment	not modelled	98.2	16	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-2; PDBTitle: structure of integrin alphaxbeta2 ectodomain
76	c5iy63_	Alignment	not modelled	97.7	9	PDB header: transcription, transferase/dna Chain: 3: PDB Molecule: general transcription factor iih subunit 3; PDBTitle: human holo-pic in the closed state
77	c4pn7A_	Alignment	not modelled	97.7	16	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor; PDBTitle: crystal structure of the tfiih p34 n-terminal domain
78	c5y59B_	Alignment	not modelled	97.6	15	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku80 and sir4
79	c5y58D_	Alignment	not modelled	97.5	12	PDB header: rna binding protein Chain: D: PDB Molecule: atp-dependent dna helicase ii subunit 2; PDBTitle: crystal structure of ku70/80 and tlc1
80	c5oqj4_	Alignment	not modelled	97.4	14	PDB header: transcription Chain: 4: PDB Molecule: rna polymerase ii transcription factor b subunit 4; PDBTitle: structure of yeast transcription pre-initiation complex with tfiih
81	c6gvwD_	Alignment	not modelled	96.9	14	PDB header: signaling protein Chain: D: PDB Molecule: brisc and brca1-a complex member 1; PDBTitle: crystal structure of the brca1-a complex
						PDB header: transferase

82	c5ahkB	Alignment	not modelled	94.7	16	Chain: B; PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
83	d1ozha3	Alignment	not modelled	92.7	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
84	d2ihta3	Alignment	not modelled	91.6	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
85	d2ji7a3	Alignment	not modelled	91.3	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
86	d1t9ba3	Alignment	not modelled	91.2	14	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
87	c2pgnA	Alignment	not modelled	90.6	14	PDB header: hydrolase Chain: A; PDB Molecule: cyclohexane-1,2-dione hydrolase (cdh); PDBTitle: the crystal structure of fad and thdp-dependent cyclohexane-1,2-dione2 hydrolase in complex with cyclohexane-1,2-dione
88	d2djia3	Alignment	not modelled	90.5	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
89	c1powA	Alignment	not modelled	90.4	17	PDB header: oxidoreductase(oxygen as acceptor) Chain: A; PDB Molecule: pyruvate oxidase; PDBTitle: the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
90	c1t9dB	Alignment	not modelled	90.2	14	PDB header: transferase Chain: B; PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonylurea herbicide, metsulfuron methyl
91	c3ey9B	Alignment	not modelled	90.0	14	PDB header: oxidoreductase Chain: B; PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic activation of the2 peripheral membrane enzyme pyruvate oxidase from escherichia coli
92	d2ez9a3	Alignment	not modelled	89.0	16	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
93	d1q6za3	Alignment	not modelled	88.0	18	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
94	c2panF	Alignment	not modelled	87.8	15	PDB header: lyase Chain: F; PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
95	c2djia	Alignment	not modelled	86.8	18	PDB header: oxidoreductase Chain: A; PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
96	c3eyaE	Alignment	not modelled	86.2	17	PDB header: oxidoreductase Chain: E; PDB Molecule: pyruvate dehydrogenase [cytochrome]; PDBTitle: structural basis for membrane binding and catalytic2 activation of the peripheral membrane enzyme pyruvate3 oxidase from escherichia coli
97	c1ozhD	Alignment	not modelled	85.9	13	PDB header: lyase Chain: D; PDB Molecule: acetolactate synthase, catabolic; PDBTitle: the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusal3 intermediate.
98	c1upaC	Alignment	not modelled	85.7	17	PDB header: synthase Chain: C; PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
99	c2nxwB	Alignment	not modelled	85.7	14	PDB header: lyase Chain: B; PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 braslense
100	c4rjB	Alignment	not modelled	85.4	17	PDB header: lyase Chain: B; PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
101	c2ag1A	Alignment	not modelled	82.1	15	PDB header: lyase Chain: A; PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
102	d1jsca3	Alignment	not modelled	82.0	17	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
103	c2jlaD	Alignment	not modelled	81.6	10	PDB header: transferase Chain: D; PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: crystal structure of e.coli mend, 2-succinyl-5-enolpyruvyl-2 6-hydroxy-3-cyclohexadiene-1-carboxylate synthase - semet3 protein
104	c2v3wC	Alignment	not modelled	78.5	18	PDB header: lyase Chain: C; PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant l461a2 from pseudomonas putida
105	c2q27B	Alignment	not modelled	77.2	18	PDB header: lyase Chain: B; PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
106	c2ji6B	Alignment	not modelled	76.9	19	PDB header: lyase Chain: B; PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: x-ray structure of oxalyl-coa decarboxylase in complex with 3-deaza-2 thdp and oxalyl-coa PDB header: transferase

107	c3lq1A_	Alignment	not modelled	76.8	19	Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- PDBTitle: crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
108	c4k9qB_	Alignment	not modelled	76.7	15	PDB header: lyase Chain: B: PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
109	c3mk7F_	Alignment	not modelled	75.9	13	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
110	d1ybha3	Alignment	not modelled	75.4	15	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
111	c5m32p_	Alignment	not modelled	74.7	22	PDB header: hydrolase Chain: P: PDB Molecule: proteasome subunit alpha type-4; PDBTitle: human 26s proteasome in complex with oprozomib
112	c1jscA_	Alignment	not modelled	74.7	18	PDB header: lyase Chain: A: PDB Molecule: acetoxyhydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetoxyhydroxyacid synthase: a target for herbicidal3 inhibitors
113	c1yi1A_	Alignment	not modelled	73.8	16	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetoxyhydroxyacid synthase in2 complex with a sulfonylurea herbicide, tribenuron methyl
114	c4q9dA_	Alignment	not modelled	71.3	18	PDB header: lyase Chain: A: PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
115	d2r8oa2	Alignment	not modelled	63.2	10	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
116	d2ieaa2	Alignment	not modelled	60.0	12	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
117	c4c7vA_	Alignment	not modelled	56.4	14	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: apo transketolase from lactobacillus salivarius at 2.2a resolution
118	d1itza1	Alignment	not modelled	55.4	13	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: TK-like PP module
119	c1zpdA_	Alignment	not modelled	54.2	16	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
120	c3rimA_	Alignment	not modelled	52.2	14	PDB header: transferase Chain: A: PDB Molecule: transketolase; PDBTitle: crystal structure of mycobacterium tuberculosis transketolase2 (rv1449c)