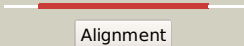

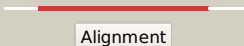

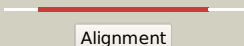







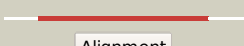











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3028c_fixB_3387086_3388042
Date	Thu Aug 8 16:20:20 BST 2019
Unique Job ID	5263148acc902664

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fahE_	 Alignment		100.0	35	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
2	c1efvA_	 Alignment		100.0	41	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein; PDBTitle: three-dimensional structure of human electron transfer2 flavoprotein to 2.1 a resolution
3	c3clrD_	 Alignment		100.0	33	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein subunit alpha; PDBTitle: crystal structure of the r236a etf mutant from m. methylotrophus
4	c1efpC_	 Alignment		100.0	45	PDB header: electron transport Chain: C: PDB Molecule: protein (electron transfer flavoprotein); PDBTitle: electron transfer flavoprotein (etf) from paracoccus2 denitrificans
5	c4l2iA_	 Alignment		100.0	37	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
6	c5ow0A_	 Alignment		100.0	35	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein, alpha subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
7	c5ol2D_	 Alignment		100.0	34	PDB header: flavoprotein Chain: D: PDB Molecule: electron transfer flavoprotein large subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
8	d1efva2	 Alignment		100.0	69	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
9	d1efpa2	 Alignment		100.0	72	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
10	d3clsd2	 Alignment		100.0	43	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: C-terminal domain of the electron transfer flavoprotein alpha subunit
11	d1efva1	 Alignment		100.0	21	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits

12	c1t9gR_	Alignment		100.0	21	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: electron transfer flavoprotein alpha-subunit, PDBTitle: structure of the human mcad:etf complex
13	d1efpa1	Alignment		100.0	24	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
14	c3ih5A_	Alignment		100.0	25	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: crystal structure of electron transfer flavoprotein alpha-subunit from2 bacteroides thetaiotaomicron
15	d3cisd1	Alignment		100.0	25	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
16	c1o94D_	Alignment		100.0	25	PDB header: electron transport Chain: D: PDB Molecule: electron transfer flavoprotein alpha-subunit; PDBTitle: ternary complex between trimethylamine dehydrogenase and2 electron transferring flavoprotein
17	c3fetA_	Alignment		99.9	21	PDB header: electron transport Chain: A: PDB Molecule: electron transfer flavoprotein subunit alpha related PDBTitle: crystal structure of the electron transfer flavoprotein subunit alpha2 related protein ta0212 from thermoplasma acidophilum
18	c4kpuB_	Alignment		99.9	14	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein alpha/beta-subunit; PDBTitle: electron transferring flavoprotein of acidaminococcus fermentans:2 towards a mechanism of flavin-based electron bifurcation
19	c5ol2E_	Alignment		99.9	13	PDB header: flavoprotein Chain: E: PDB Molecule: electron transfer flavoprotein small subunit; PDBTitle: the electron transferring flavoprotein/butyryl-coa dehydrogenase2 complex from clostridium difficile
20	c6fahB_	Alignment		99.8	17	PDB header: flavoprotein Chain: B: PDB Molecule: caffeyl-coa reductase-etf complex subunit card; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
21	d3clsc1	Alignment	not modelled	99.8	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
22	d1efyb_	Alignment	not modelled	99.8	18	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
23	d1efpb_	Alignment	not modelled	99.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
24	d1o94c_	Alignment	not modelled	99.8	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: ETFP subunits
25	c5ow0B_	Alignment	not modelled	99.7	16	PDB header: electron transport Chain: B: PDB Molecule: electron transfer flavoprotein, beta subunit; PDBTitle: crystal structure of an electron transfer flavoprotein from2 geobacillus metallireducens
26	d1t9ba1	Alignment	not modelled	98.6	17	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
27	d1ozha1	Alignment	not modelled	98.5	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
28	d2ez9a1	Alignment	not modelled	98.4	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
						Fold: DHS-like NAD/FAD-binding domain

29	d2ji7a1	Alignment	not modelled	98.1	18	Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
30	d2ih1a1	Alignment	not modelled	98.0	18	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
31	c4rj1B	Alignment	not modelled	97.7	15	PDB header: lyase Chain: B: PDB Molecule: acetolactate synthase; PDBTitle: acetolactate synthase from bacillus subtilis bound to thdp - crystal2 form ii
32	d1q6za1	Alignment	not modelled	97.6	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
33	c1ozhD	Alignment	not modelled	97.6	21	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 unusual3 intermediate.
34	c2q27B	Alignment	not modelled	97.6	9	PDB header: lyase Chain: B: PDB Molecule: oxalyl-coa decarboxylase; PDBTitle: crystal structure of oxalyl-coa decarboxylase from escherichia coli
35	d1ybha1	Alignment	not modelled	97.6	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
36	d2dja1	Alignment	not modelled	97.5	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
37	c1powA	Alignment	not modelled	97.3	15	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
38	c2ji6B	Alignment	not modelled	97.2	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
39	c2pgnA	Alignment	not modelled	97.2	21	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
40	c2djaA	Alignment	not modelled	97.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: crystal structure of pyruvate oxidase from aerococcus2 viridans containing fad
41	c3lq1A	Alignment	not modelled	97.1	13	PDB header: transferase 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
42	c3eyaE	Alignment	not modelled	97.0	15	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
43	c1t9dB	Alignment	not modelled	96.9	19	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase, mitochondrial; PDBTitle: crystal structure of yeast acetohydroxyacid synthase in complex with a2 sulfonyleurea herbicide, metsulfuron methyl
44	c2ag1A	Alignment	not modelled	96.8	17	PDB header: lyase Chain: A: PDB Molecule: benzaldehyde lyase; PDBTitle: crystal structure of benzaldehyde lyase (bal)- semet
45	c1yi1A	Alignment	not modelled	96.7	17	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase; PDBTitle: crystal structure of arabidopsis thaliana acetohydroxyacid synthase in2 complex with a sulfonyleurea herbicide, tribenuron methyl
46	c2panF	Alignment	not modelled	96.7	16	PDB header: lyase Chain: F: PDB Molecule: glyoxylate carboligase; PDBTitle: crystal structure of e. coli glyoxylate carboligase
47	c5ahkB	Alignment	not modelled	96.7	15	PDB header: transferase Chain: B: PDB Molecule: acetolactate synthase ii, large subunit; PDBTitle: crystal structure of acetohydroxy acid synthase pf5 from2 pseudomonas protegens
48	c4q9dA	Alignment	not modelled	96.6	22	PDB header: lyase Chain: A: PDB Molecule: benzoylformate decarboxylase; PDBTitle: x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
49	c3ey9B	Alignment	not modelled	96.5	17	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
50	c1upaC	Alignment	not modelled	96.4	18	PDB header: synthase Chain: C: PDB Molecule: carboxyethylarginine synthase; PDBTitle: carboxyethylarginine synthase from streptomyces2 clavuligerus (semet structure)
51	d1uana	Alignment	not modelled	96.2	16	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
52	d1pvda1	Alignment	not modelled	96.2	14	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
53	c4i5iA	Alignment	not modelled	96.2	21	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of the sirt1 catalytic domain bound to

						nad and an2 ex527 analog
54	d1m2ka_	Alignment	not modelled	96.1	25	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
55	c2v3wC_	Alignment	not modelled	96.1	17	PDB header: lyase Chain: C: PDB Molecule: benzoylformate decarboxylase; PDBTitle: crystal structure of the benzoylformate decarboxylase variant I461a2 from pseudomonas putida
56	d1ma3a_	Alignment	not modelled	96.0	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
57	c2ixdB_	Alignment	not modelled	95.9	10	PDB header: hydrolase Chain: B: PDB Molecule: Imbe-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
58	c1jscA_	Alignment	not modelled	95.8	16	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
59	c2x7jA_	Alignment	not modelled	95.7	12	PDB header: transferase Chain: A: PDB Molecule: 2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene PDBTitle: structure of the menaquinone biosynthesis protein mend from2 bacillus subtilis
60	d1zpdA1	Alignment	not modelled	95.7	19	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
61	d1yc5a1	Alignment	not modelled	95.6	29	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
62	c4k9qB_	Alignment	not modelled	95.5	18	PDB header: lyase Chain: B: PDB Molecule: benzoylformate decarboxylase; PDBTitle: the crystal structure of benzoylformate decarboxylase from2 polynucleobacter necessarius
63	c5bmoB_	Alignment	not modelled	95.2	13	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein Inmx; PDBTitle: Inmx protein, a putative glcnac-pi de-n-acetylase from streptomyces2 atroolivaceus
64	d2b4ya1	Alignment	not modelled	94.9	16	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
65	c3k35D_	Alignment	not modelled	94.4	24	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
66	c3qlsC_	Alignment	not modelled	94.3	23	PDB header: hydrolase Chain: C: PDB Molecule: nad-dependent deacetylase sirtuin-3, PDBTitle: crystal structure of human sirt3
67	c5cgzA_	Alignment	not modelled	94.3	19	PDB header: lyase Chain: A: PDB Molecule: 4-oxalmesaconate hydratase; PDBTitle: crystal structure of galb, the 4-carboxy-2-hydroxymuconate hydratase,2 from pseudomonas putida kt2440
68	c5fyqB_	Alignment	not modelled	94.0	20	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent protein deacetylase sirtuin-2; PDBTitle: sirt2 in complex with a 13-mer trifluoroacetylated ran peptide
69	c5ol0B_	Alignment	not modelled	94.0	23	PDB header: hydrolase Chain: B: PDB Molecule: putative silent information regulator 2,putative silent PDBTitle: structure of leishmania infantum silent information regulator 22 related protein 1 (lisir2rp1) in complex with acetylated p53 peptide
70	c1zpdA_	Alignment	not modelled	94.0	19	PDB header: alcohol fermentation Chain: A: PDB Molecule: pyruvate decarboxylase; PDBTitle: pyruvate decarboxylase from zymomonas mobilis
71	c2vbiF_	Alignment	not modelled	93.7	17	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
72	c3zg6A_	Alignment	not modelled	93.7	25	PDB header: hydrolase/inhibitor Chain: A: PDB Molecule: nad-dependent protein deacetylase sirtuin-6; PDBTitle: the novel de-long chain fatty acid function of human sirt6
73	c3pkIF_	Alignment	not modelled	93.6	27	PDB header: hydrolase Chain: F: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: human sirt6 crystal structure in complex with adp ribose
74	c3we7A_	Alignment	not modelled	92.7	16	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph0499; PDBTitle: crystal structure of diacetylchitobiose deacetylase from pyrococcus2 horikoshii
75	c1q14A_	Alignment	not modelled	92.5	23	PDB header: hydrolase Chain: A: PDB Molecule: hst2 protein; PDBTitle: structure and autoregulation of the yeast hst2 homolog of sir2
76	c5oj7A_	Alignment	not modelled	92.5	14	PDB header: hydrolase Chain: A: PDB Molecule: nad-dependent protein deacetylase; PDBTitle: sirtuin 4 orthologue from xenopus tropicalis in complex with adp-2 ribose
77	d1q1aa_	Alignment	not modelled	92.0	23	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
78	d1s5pa_	Alignment	not modelled	91.4	22	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
						Fold: DHS-like NAD/FAD-binding domain

79	d1ovma1	Alignment	not modelled	91.1	12	Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
80	c2w93A	Alignment	not modelled	90.9	22	PDB header: lyase Chain: A: PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate pyruvamide
81	c3jwpA	Alignment	not modelled	90.5	18	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein sir2 homologue; PDBTitle: crystal structure of plasmodium falciparum sir2a (pf13_0152) in2 complex with amp
82	c1ovmC	Alignment	not modelled	89.9	14	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
83	d1j8fa	Alignment	not modelled	89.8	20	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
84	c2jlaD	Alignment	not modelled	87.2	15	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
85	c5a3aA	Alignment	not modelled	86.8	11	PDB header: transferase Chain: A: PDB Molecule: sir2 family protein; PDBTitle: crystal structure of the adp-ribosylating sirtuin (sirtm)2 from streptococcus pyogenes (apo form)
86	c3cf4G	Alignment	not modelled	86.2	10	PDB header: oxidoreductase Chain: G: PDB Molecule: acetyl-coa decarboxylase/synthase epsilon subunit; PDBTitle: structure of the codh component of the m. barkeri acids complex
87	c2hjhB	Alignment	not modelled	85.9	17	PDB header: hydrolase Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
88	c5ks8F	Alignment	not modelled	84.3	19	PDB header: ligase Chain: F: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
89	c4jn6C	Alignment	not modelled	83.8	19	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of the aldolase-dehydrogenase complex from2 mycobacterium tuberculosis hrv37
90	c2vbgB	Alignment	not modelled	83.7	17	PDB header: lyase Chain: B: PDB Molecule: branched-chain alpha-ketoacid decarboxylase; PDBTitle: the complex structure of the branched-chain keto acid2 decarboxylase (kdca) from lactococcus lactis with 2r-1-3 hydroxyethyl-deazathdp
91	c2nxwB	Alignment	not modelled	82.9	17	PDB header: lyase Chain: B: PDB Molecule: phenyl-3-pyruvate decarboxylase; PDBTitle: crystal structure of phenylpyruvate decarboxylase of azospirillum2 brasilense
92	c1ydnA	Alignment	not modelled	82.4	15	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.
93	c2ftpA	Alignment	not modelled	81.9	13	PDB header: lyase Chain: A: PDB Molecule: hydroxymethylglutaryl-coa lyase; PDBTitle: crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
94	c2pn1A	Alignment	not modelled	81.0	14	PDB header: ligase Chain: A: PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exiguobacterium sp. 255-15 at 2.00 a3 resolution
95	c3jvuB	Alignment	not modelled	80.2	14	PDB header: transferase Chain: B: PDB Molecule: homocitrate synthase, mitochondrial; PDBTitle: homocitrate synthase lys4 bound to 2-og
96	c1rr2A	Alignment	not modelled	79.9	18	PDB header: transferase Chain: A: PDB Molecule: transcarboxylase 5s subunit; PDBTitle: propionibacterium shermanii transcarboxylase 5s subunit bound to 2-2 ketobutyric acid
97	c2x3yA	Alignment	not modelled	79.4	14	PDB header: isomerase Chain: A: PDB Molecule: phosphoheptose isomerase; PDBTitle: crystal structure of gmha from burkholderia pseudomallei
98	d1x94a	Alignment	not modelled	79.3	15	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
99	c4lrtC	Alignment	not modelled	79.3	19	PDB header: lyase/oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal and solution structures of the bifunctional enzyme2 (aldolase/aldehyde dehydrogenase) from thermomonospora curvata,3 reveal a cofactor-binding domain motion during nad+ and coa4 accommodation within the shared cofactor-binding site
100	c5ks8D	Alignment	not modelled	79.0	19	PDB header: ligase Chain: D: PDB Molecule: pyruvate carboxylase subunit beta; PDBTitle: crystal structure of two-subunit pyruvate carboxylase from2 methylobacillus flagellatus
101	c6h77B	Alignment	not modelled	78.4	16	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: e1 enzyme for ubiquitin like protein activation in complex with ubl PDB header: hydrolase

102	c3dfmA	Alignment	not modelled	77.3	23	Chain: A: PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
103	c1nvmG	Alignment	not modelled	75.7	21	PDB header: lyase/oxidoreductase Chain: G: PDB Molecule: 4-hydroxy-2-oxovalerate aldolase; PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
104	d1o6ca	Alignment	not modelled	75.7	15	Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDP-N-acetylglucosamine 2-epimerase
105	d1jw9b	Alignment	not modelled	74.7	20	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Molybdenum cofactor biosynthesis protein MoeB
106	c6e1jB	Alignment	not modelled	74.0	14	PDB header: plant protein Chain: B: PDB Molecule: 2-isopropylmalate synthase, a genome specific 1; PDBTitle: crystal structure of methylthioalkylmalate synthase (bjumam1.1) from2 brassica juncea
107	d1nvma2	Alignment	not modelled	72.6	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: HMGL-like
108	c4mm1E	Alignment	not modelled	72.4	22	PDB header: transferase Chain: E: PDB Molecule: geranylgeranylgeranyl phosphate synthase; PDBTitle: gggps from methanothermobacter thermautotrophicus
109	d1q74a	Alignment	not modelled	70.8	22	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
110	c3op1A	Alignment	not modelled	70.3	13	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
111	c5btrB	Alignment	not modelled	69.1	17	PDB header: hydrolase/substrate Chain: B: PDB Molecule: nad-dependent protein deacetylase sirtuin-1; PDBTitle: crystal structure of sirt1 in complex with resveratrol and an amc-2 containing peptide
112	d1moqa	Alignment	not modelled	67.8	16	Fold: SIS domain Superfamily: SIS domain Family: double-SIS domain
113	c4iaoB	Alignment	not modelled	66.3	19	PDB header: hydrolase/transcription Chain: B: PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of sir2 c543s mutant in complex with sid domain of2 sir4
114	c3bleA	Alignment	not modelled	65.7	13	PDB header: transferase Chain: A: PDB Molecule: citramalate synthase from leptospira interrogans; PDBTitle: crystal structure of the catalytic domain of licms in complexed with2 malonate
115	c2ze5A	Alignment	not modelled	63.6	22	PDB header: transferase Chain: A: PDB Molecule: isopentenyl transferase; PDBTitle: crystal structure of adenosine phosphate-isopentenyltransferase
116	c4s12C	Alignment	not modelled	63.2	15	PDB header: lyase Chain: C: PDB Molecule: n-acetylmuramic acid 6-phosphate etherase; PDBTitle: 1.55 angstrom crystal structure of n-acetylmuramic acid 6-phosphate2 etherase from yersinia enterocolitica.
117	d1l1qa	Alignment	not modelled	63.1	14	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
118	c2x0kB	Alignment	not modelled	61.8	18	PDB header: transferase Chain: B: PDB Molecule: riboflavin biosynthesis protein ribf; PDBTitle: crystal structure of modular fad synthetase from2 corynebacterium ammoniagenes
119	c4ffnA	Alignment	not modelled	61.3	29	PDB header: ligase/substrate Chain: A: PDB Molecule: pylc; PDBTitle: pylc in complex with d-ornithine and amppnp
120	c2dy0A	Alignment	not modelled	61.0	17	PDB header: transferase Chain: A: PDB Molecule: adenine phosphoribosyltransferase; PDBTitle: crystal structure of project jw0458 from escherichia coli