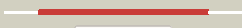



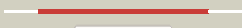




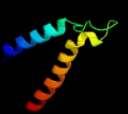





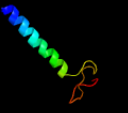



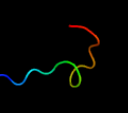


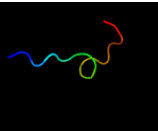




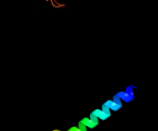

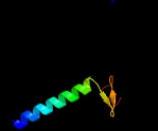
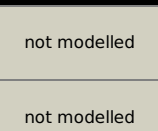


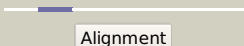
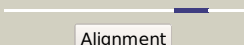


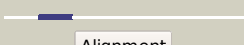
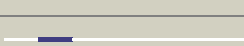

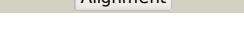
Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1302_rfe_1458301_1459515
Date	Wed Jul 31 22:05:40 BST 2019
Unique Job ID	ec88abc637f2d86f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4j72A_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
2	c5jnqA_	 Alignment		100.0	23	PDB header: transferase/antibiotic Chain: A: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: mray tunicamycin complex
3	c4j72B_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
4	c5levA_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine--dolichyl-phosphate n- PDBTitle: crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminephosphotransferase (dpagt1) (v264g mutant)
5	c6m97A_	 Alignment		45.5	21	PDB header: transport protein Chain: A: PDB Molecule: chimera protein of high affinity copper uptake protein 1 PDBTitle: crystal structure of the high-affinity copper transporter ctr1
6	c4q0pA_	 Alignment		24.7	44	PDB header: isomerase Chain: A: PDB Molecule: l-ribose isomerase; PDBTitle: crystal structure of acinetobacter sp. dl28 l-ribose isomerase in2 complex with l-ribose
7	c5gasN_	 Alignment		21.0	17	PDB header: hydrolase Chain: N: PDB Molecule: archaeal/vacuolar-type h+-atpase subunit i; PDBTitle: thermus thermophilus v/a-atpase, conformation 2
8	d2q7ra1	 Alignment		20.0	16	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain
9	c5un8B_	 Alignment		17.7	27	PDB header: hydrolase Chain: B: PDB Molecule: protein o-glcnacase; PDBTitle: crystal structure of human o-glcnacase in complex with glycopeptide2 p53
10	d2cbia2	 Alignment		17.5	20	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain
11	d2choa2	 Alignment		16.1	27	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: alpha-D-glucuronidase/Hyaluronidase catalytic domain

12	c2cbjA	Alignment		14.9	20	PDB header: hydrolase Chain: A; PDB Molecule: hyaluronidase; PDBTitle: structure of the clostridium perfringens nagj family 84 glycoside2 hydrolase, a homologue of human o-glcnaase in complex with pugnac
13	c2choA	Alignment		14.3	27	PDB header: hydrolase Chain: A; PDB Molecule: glucosaminidase; PDBTitle: bacteroides thetaiotaomicron hexosaminidase with o-2 glcnaase activity
14	c2uuiA	Alignment		14.2	13	PDB header: lyase Chain: A; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
15	d2cpwa1	Alignment		13.2	24	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
16	c2xsbA	Alignment		12.3	33	PDB header: hydrolase Chain: A; PDB Molecule: hyaluronoglucosaminidase; PDBTitle: ogoga pugnac complex
17	c2pnoI	Alignment		12.2	14	PDB header: lyase Chain: I; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
18	c2pnoJ	Alignment		12.2	14	PDB header: lyase Chain: J; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
19	c2pnoE	Alignment		12.2	14	PDB header: lyase Chain: E; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
20	c2pnoL	Alignment		12.2	14	PDB header: lyase Chain: L; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
21	c2pnoH	Alignment	not modelled	12.2	14	PDB header: lyase Chain: H; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
22	c2pnoB	Alignment	not modelled	12.2	14	PDB header: lyase Chain: B; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
23	c2pnoF	Alignment	not modelled	12.2	14	PDB header: lyase Chain: F; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
24	c2pnoG	Alignment	not modelled	12.2	14	PDB header: lyase Chain: G; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
25	c2pnoC	Alignment	not modelled	12.2	14	PDB header: lyase Chain: C; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
26	c2pnoD	Alignment	not modelled	12.2	14	PDB header: lyase Chain: D; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
27	c2pnoK	Alignment	not modelled	12.2	14	PDB header: lyase Chain: K; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
28	c2pnoA	Alignment	not modelled	12.2	14	PDB header: lyase Chain: A; PDB Molecule: leukotriene c4 synthase; PDBTitle: crystal structure of human leukotriene c4 synthase
29	d2uuia1	Alignment	not modelled	12.2	14	Fold: MAPEG domain-like Superfamily: MAPEG domain-like Family: MAPEG domain

30	c2eq7C	 Alignment	not modelled	12.2	20	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate dehydrogenase e2 component; PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
31	c3b29A	 Alignment	not modelled	10.9	14	PDB header: lyase Chain: A: PDB Molecule: leukotriene c4 synthase; PDBTitle: human leukotriene c4 synthase in complex with dodecyl-beta-d-2 selenomaltoside
32	d1uoua1	 Alignment	not modelled	9.3	10	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
33	c5diyB	 Alignment	not modelled	8.0	20	PDB header: hydrolase Chain: B: PDB Molecule: hyaluronidase; PDBTitle: thermobaculum terrenum o-glcnac hydrolase mutant - d120n
34	c2k74A	 Alignment	not modelled	7.5	19	PDB header: membrane protein, oxidoreductase Chain: A: PDB Molecule: disulfide bond formation protein b; PDBTitle: solution nmr structure of dsbb-ubiquinone complex
35	c6aztA	 Alignment	not modelled	7.5	23	PDB header: plant protein Chain: A: PDB Molecule: asparaginyl endopeptidase 1; PDBTitle: asparaginyl endopeptidase 1 bound to aan peptide, a tetrahedral2 intermediate
36	c3bg2A	 Alignment	not modelled	6.9	23	PDB header: hydrolase Chain: A: PDB Molecule: dgtp triphosphohydrolase; PDBTitle: crystal structure of deoxyguanosinetriphosphate triphosphohydrolase2 from flavobacterium sp. med217
37	d2tpta1	 Alignment	not modelled	6.6	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
38	d1brwa1	 Alignment	not modelled	6.5	5	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
39	c2eq8C	 Alignment	not modelled	6.0	38	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
40	d2idaa1	 Alignment	not modelled	5.9	25	Fold: RING/U-box Superfamily: RING/U-box Family: Zf-UBP
41	c4r7qA	 Alignment	not modelled	5.8	9	PDB header: signaling protein Chain: A: PDB Molecule: sensor histidine kinase; PDBTitle: the structure of a sensor domain of a histidine kinase from vibrio2 cholerae o1 biovar eltor str. n16961
42	c1ic9A	 Alignment	not modelled	5.8	50	PDB header: de novo protein Chain: A: PDB Molecule: th10aox; PDBTitle: nmr solution structure of the designed beta-sheet mini-2 protein th10aox
43	c2v1nA	 Alignment	not modelled	5.8	29	PDB header: nuclear protein Chain: A: PDB Molecule: protein kin homolog; PDBTitle: solution structure of the region 51-160 of human kin172 reveals a winged helix fold
44	c1ic1A	 Alignment	not modelled	5.7	50	PDB header: de novo protein Chain: A: PDB Molecule: th1ox; PDBTitle: solution structure of designed beta-sheet mini-protein th1ox
45	c2kdcC	 Alignment	not modelled	5.7	10	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
46	d2pila	 Alignment	not modelled	5.7	25	Fold: Pili subunits Superfamily: Pili subunits Family: Pilin
47	d1ijwc	 Alignment	not modelled	5.6	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
48	c2eq9C	 Alignment	not modelled	5.6	38	PDB header: oxidoreductase Chain: C: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
49	d1o17a1	 Alignment	not modelled	5.6	9	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
50	c2cooA	 Alignment	not modelled	5.6	38	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase component of branched- PDBTitle: solution structure of the e3_binding domain of2 dihydrolipoamide branched chaintransacylase
51	d1y0za	 Alignment	not modelled	5.5	24	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: gamma-Butyrobetaine hydroxylase
52	c1w3dA	 Alignment	not modelled	5.4	31	PDB header: transferase Chain: A: PDB Molecule: dihydrolipoyllysine-residue acetyltransferase component of PDBTitle: nmr structure of the peripheral-subunit binding domain of bacillus2 stearothermophilus e2p
53	d2cyua1	 Alignment	not modelled	5.4	15	Fold: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex Superfamily: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex

						Family: Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
54	c3sokB_	Alignment	not modelled	5.3	29	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
55	c4awaA_	Alignment	not modelled	5.3	19	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: legumain; PDBTitle: crystal structure of active legumain in complex with yvad-cmk2 at ph 5.0
56	d1v8ga1	Alignment	not modelled	5.3	12	Fold: Methionine synthase domain-like Superfamily: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain Family: Nucleoside phosphorylase/phosphoribosyltransferase N-terminal domain
57	d2c42a2	Alignment	not modelled	5.2	46	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
58	c4qoyE_	Alignment	not modelled	5.1	38	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase (dihydrolipoyltransacetylase) PDBTitle: novel binding motif and new flexibility revealed by structural2 analysis of a pyruvate dehydrogenase-dihydrolipoyl acetyltransferase3 sub-complex from the escherichia coli pyruvate dehydrogenase multi-4 enzyme complex
59	c4rymA_	Alignment	not modelled	5.1	12	PDB header: membrane protein Chain: A: PDB Molecule: integral membrane protein; PDBTitle: crystal structure of bctspo iodo type1 monomer
60	c5mlc7_	Alignment	not modelled	5.1	14	PDB header: ribosome Chain: 7: PDB Molecule: psrp5alpha, chloroplastic; PDBTitle: cryo-em structure of the spinach chloroplast ribosome reveals the2 location of plastid-specific ribosomal proteins and extensions