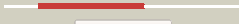

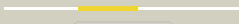







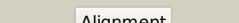

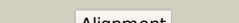




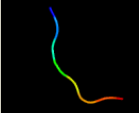

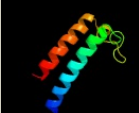




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0470A (-) _561857_562297
Date	Tue Jul 23 14:50:55 BST 2019
Unique Job ID	732a757ed7901428

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4od5C_	 Alignment		99.2	21	PDB header: transferase Chain: C; PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1
2	c3wmmP_	 Alignment		72.7	19	PDB header: photosynthesis Chain: P; PDB Molecule: lh1 beta polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form
3	c3ts7B_	 Alignment		71.2	19	PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of farnesyl diphosphate synthase (target efi-501951)2 from methylococcus capsulatus
4	c3m9uD_	 Alignment		69.5	12	PDB header: transferase Chain: D; PDB Molecule: farnesyl-diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl pyrophosphate synthase from2 lactobacillus brevis atcc 367
5	c2ndjA_	 Alignment		64.7	7	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e member 3; PDBTitle: structural basis for kcne3 and estrogen modulation of the kcnq12 channel
6	c1wrgA_	 Alignment		53.7	17	PDB header: membrane protein Chain: A; PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
7	d1lghb_	 Alignment		49.2	25	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
8	c2zcpA_	 Alignment		45.5	12	PDB header: transferase Chain: A; PDB Molecule: dehydrosqualene synthase; PDBTitle: crystal structure of the c(30) carotenoid dehydrosqualene synthase2 from staphylococcus aureus complexed with farnesyl thiopyrophosphate
9	d1jpya_	 Alignment		41.5	88	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Interleukin 17F, IL-17F
10	c3lomA_	 Alignment		40.1	13	PDB header: transferase Chain: A; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of geranyltransferase from legionella pneumophila
11	c2vxsB_	 Alignment		39.3	75	PDB header: cytokine Chain: B; PDB Molecule: interleukin-17a; PDBTitle: structure of il-17a in complex with a potent, fully human2 neutralising antibody

12	c2k21A_	Alignment		38.5	22	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e PDBTitle: nmr structure of human kcne1 in Impg micelles at ph 6.0 and 2 40 degree c
13	c3m0gB_	Alignment		36.5	16	PDB header: transferase Chain: B; PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of putative farnesyl diphosphate synthase from 2 rhodobacter capsulatus
14	c2m0qA_	Alignment		36.2	22	PDB header: membrane protein Chain: A; PDB Molecule: potassium voltage-gated channel subfamily e member 2; PDBTitle: solution nmr analysis of intact kcne2 in detergent micelles 2 demonstrate a straight transmembrane helix
15	c2ftzA_	Alignment		33.2	14	PDB header: transferase Chain: A; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of geranyltranstransferase (ec 2.5.1.10) (tm0161) 2 from thermotoga maritima at 1.90 a resolution
16	d1ezfa_	Alignment		33.2	15	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Squalene synthase
17	c6et5u_	Alignment		31.9	22	PDB header: photosynthesis Chain: U; PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
18	c4qhuC_	Alignment		31.9	75	PDB header: immune system Chain: C; PDB Molecule: interleukin-17a; PDBTitle: crystal structure of il-17a/fab6785 complex
19	c5xn5A_	Alignment		31.4	22	PDB header: transferase Chain: A; PDB Molecule: os07g0580900 protein; PDBTitle: homo-dimer crystal structure of geranylgeranyl diphosphate synthases 12 from oryza sativa
20	c3oacD_	Alignment		31.3	21	PDB header: transferase Chain: D; PDB Molecule: geranyl diphosphate synthase large subunit; PDBTitle: mint deletion mutant of heterotetrameric geranyl pyrophosphate 2 synthase in complex with ligands
21	c5lysA_	Alignment	not modelled	30.9	19	PDB header: transferase/transferase inhibitor Chain: A; PDB Molecule: phytoene synthase; PDBTitle: crystal structure of a dehydrosqualene synthase in complex with ligand
22	c3npkB_	Alignment	not modelled	27.8	23	PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: the crystal structure of geranyltranstransferase from campylobacter 2 jejuni
23	c2j1oA_	Alignment	not modelled	27.4	14	PDB header: transferase Chain: A; PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: geranylgeranyl diphosphate synthase from sinapis alba
24	c4hd1A_	Alignment	not modelled	26.0	31	PDB header: transferase Chain: A; PDB Molecule: squalene synthase hpnc; PDBTitle: crystal structure of squalene synthase hpnc from alicyclobacillus 2 acidocaldarius
25	d2diga1	Alignment	not modelled	25.4	53	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
26	c4lltB_	Alignment	not modelled	24.8	15	PDB header: transferase Chain: B; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a farnesyl diphosphate synthase from roseobacter 2 denitrificans och 114, target efi-509393, with two ipp and calcium 3 bound in active site
27	c5aypA_	Alignment	not modelled	24.7	16	PDB header: transferase Chain: A; PDB Molecule: farnesyl diphosphate synthase; PDBTitle: crystal structure of bacillus stearothermophilus farnesyl 2 pyrophosphate synthase
28	c3ipiA_	Alignment	not modelled	23.5	12	PDB header: transferase Chain: A; PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of a geranyltranstransferase from the methanosarcina 2 mazei
						Fold: Light-harvesting complex subunits

29	d1jo5a_	Alignment	not modelled	23.3	25	Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
30	c5uxmA_	Alignment	not modelled	23.2	22	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: type ii dah7ps from pseudomonas aeruginosa with trp bound
31	c5hudA_	Alignment	not modelled	22.9	22	PDB header: transferase/isomerase Chain: A: PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate (dahp) PDBTitle: non-covalent complex of and dahp synthase and chorismate mutase from2 corynebacterium glutamicum with bound transition state analog
32	d2b7oa1	Alignment	not modelled	22.0	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class-II DAHP synthetase
33	c6bmcA_	Alignment	not modelled	21.2	11	PDB header: transferase Chain: A: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: the structure of a dimeric type ii dah7ps associated with pyocyanin2 biosynthesis in pseudomonas aeruginosa
34	c3we9A_	Alignment	not modelled	20.7	21	PDB header: transferase Chain: A: PDB Molecule: putative phytoene/squalene synthase yisp; PDBTitle: the crystal structure of yisp from bacillus subtilis subsp. subtilis2 strain 168
35	c3llwA_	Alignment	not modelled	20.3	20	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase (ispa); PDBTitle: crystal structure of geranyltransferase from helicobacter pylori 26695
36	c2aydA_	Alignment	not modelled	20.3	44	PDB header: transcription Chain: A: PDB Molecule: wrky transcription factor 1; PDBTitle: crystal structure of the c-terminal wrky domainof atwrky1, an sa-2 induced and partially npr1-dependent transcription factor
37	c3kraB_	Alignment	not modelled	19.8	13	PDB header: transferase Chain: B: PDB Molecule: geranyl diphosphate synthase small subunit; PDBTitle: mint heterotetrameric geranyl pyrophosphate synthase in complex with2 magnesium
38	c3p8lB_	Alignment	not modelled	19.6	17	PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of polyprenyl synthase from enterococcus faecalis2 v583
39	d1wj2a_	Alignment	not modelled	19.6	38	Fold: WRKY DNA-binding domain Superfamily: WRKY DNA-binding domain Family: WRKY DNA-binding domain
40	c2h8oA_	Alignment	not modelled	19.1	15	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: the 1.6a crystal structure of the geranyltransferase from2 agrobacterium tumefaciens
41	c2azjB_	Alignment	not modelled	19.0	15	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: crystal structure for the mutant d81c of sulfolobus2 solfataricus hexaprenyl pyrophosphate synthase
42	c2lurA_	Alignment	not modelled	19.0	78	PDB header: plant protein Chain: A: PDB Molecule: kalata; PDBTitle: nmr solution structure of kb1[ghrw;23-28]
43	c4lfgB_	Alignment	not modelled	16.9	15	PDB header: transferase Chain: B: PDB Molecule: geranylgeranyl diphosphate synthase; PDBTitle: crystal structure of geranylgeranyl diphosphate synthase sub12742 (target efi-509455) from streptococcus uberis 0140j with bound3 magnesium and isopentyl diphosphate, fully liganded complex;
44	c2digA_	Alignment	not modelled	16.1	44	PDB header: dna binding protein Chain: A: PDB Molecule: lamin-b receptor; PDBTitle: solusion structure of the todor domain of human lamin-b2 receptor
45	c6dhrA_	Alignment	not modelled	15.8	78	PDB header: plant protein Chain: A: PDB Molecule: rivi3; PDBTitle: nmr solution structure of rivi3
46	c3lsnA_	Alignment	not modelled	15.3	15	PDB header: transferase Chain: A: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of putative geranyltranstransferase from pseudomonas2 fluorescens pf-5 complexed with magnesium
47	c2o1oB_	Alignment	not modelled	15.2	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative farnesyl pyrophosphate synthase; PDBTitle: cryptosporidium parvum putative polyprenyl pyrophosphate synthase2 (cgd4_2550) in complex with risedronate.
48	d1rqja_	Alignment	not modelled	15.0	16	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
49	d1rtra_	Alignment	not modelled	14.8	18	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
50	c3ucaB_	Alignment	not modelled	14.7	16	PDB header: transferase Chain: B: PDB Molecule: geranyltranstransferase; PDBTitle: crystal structure of isoprenoid synthase (target efi-501974) from2 clostridium perfringens
51	c3ghnA_	Alignment	not modelled	14.6	38	PDB header: hydrolase Chain: A: PDB Molecule: a disintegrin and metalloproteinase with thrombospondin PDBTitle: crystal structure of the exosite-containing fragment of human adams132 (form-2)
52	c3a9kC_	Alignment	not modelled	14.3	67	PDB header: signaling protein/metal binding protein Chain: C: PDB Molecule: mitogen-activated protein kinase kinase kinase 7- PDBTitle: crystal structure of the mouse tab3-nzf in complex with2 lys63-linked di-ubiquitin

53	d2q80a1	Alignment	not modelled	13.4	8	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Isoprenyl diphosphate synthases
54	d2k4xa1	Alignment	not modelled	12.7	50	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein S27a
55	c1l2yA	Alignment	not modelled	12.3	100	PDB header: de novo protein Chain: A; PDB Molecule: tc5b; PDBTitle: nmr structure of trp-cage miniprotein construct tc5b
56	c1orxA	Alignment	not modelled	12.1	78	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
57	c1rijA	Alignment	not modelled	11.6	100	PDB header: de novo protein Chain: A; PDB Molecule: e6apn1 peptide; PDBTitle: e6-bind trp-cage (e6apn1)
58	c2jofA	Alignment	not modelled	11.6	100	PDB header: de novo protein Chain: A; PDB Molecule: trp-cage; PDBTitle: the trp-cage: optimizing the stability of a globular2 miniprotein
59	d2a1jb1	Alignment	not modelled	11.5	13	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
60	c6ir8A	Alignment	not modelled	11.2	33	PDB header: transcription/dna Chain: A; PDB Molecule: oswrky45; PDBTitle: rice wrky/dna complex
61	c3uc7F	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: F; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
62	c2ll5A	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: A; PDB Molecule: cyclo-tc1; PDBTitle: cyclo-tc1 trp-cage
63	c3uc8C	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: C; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
64	c3uc7B	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: B; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
65	c3uc8A	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: A; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
66	c3uc7A	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: A; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
67	c3uc7C	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: C; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
68	c3uc8B	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: B; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - tetragonal crystal form
69	c3uc7D	Alignment	not modelled	10.8	100	PDB header: de novo protein Chain: D; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
70	c2e8xB	Alignment	not modelled	10.6	17	PDB header: transferase Chain: B; PDB Molecule: geranylgeranyl pyrophosphate synthetase; PDBTitle: s. cerevisiae geranylgeranyl pyrophosphate synthase in2 complex with magnesium and gpp
71	c3uc7E	Alignment	not modelled	10.6	100	PDB header: de novo protein Chain: E; PDB Molecule: cyclo-tc1; PDBTitle: trp-cage cyclo-tc1 - monoclinic crystal form
72	c3wccC	Alignment	not modelled	10.6	15	PDB header: transferase Chain: C; PDB Molecule: farnesyltransferase, putative; PDBTitle: the complex structure of tcsqs with ligand, e5700
73	c2lk1A	Alignment	not modelled	10.5	42	PDB header: rna binding protein Chain: A; PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
74	c2jwmA	Alignment	not modelled	10.4	56	PDB header: plant protein Chain: A; PDB Molecule: kalata-b7; PDBTitle: nmr spatial srtructure of ternary complex kalata b7/mn2+/dpc2 micelle
75	c2lk0A	Alignment	not modelled	10.4	42	PDB header: rna binding protein Chain: A; PDB Molecule: rna-binding protein 5; PDBTitle: solution structure and binding studies of the ranbp2-type zinc finger2 of rbm5
76	c5w3xD	Alignment	not modelled	10.0	38	PDB header: transcription Chain: D; PDB Molecule: disease resistance protein rrs1; PDBTitle: crystal structure of popp2 in complex with ip6, accoa and the wrky2 domain of rrs1-r .
77	d1u5sb2	Alignment	not modelled	10.0	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
78	c1n0zA	Alignment	not modelled	10.0	47	PDB header: transcription Chain: A; PDB Molecule: znf265; PDBTitle: solution structure of the first zinc-finger domain from2 znf265
79	c2mutA	Alignment	not modelled	9.7	13	PDB header: hydrolase Chain: A; PDB Molecule: dna excision repair protein ercc-1; PDBTitle: solution structure of the f231l mutant ercc1-xpf dimerization region PDB header: transferase

80	c3cp6A	Alignment	not modelled	9.6	15	Chain: A; PDB Molecule: farnesyl pyrophosphate synthetase; PDBTitle: crystal structure of human farnesyl diphosphate synthase (t201a2 mutant) complexed with mg and biphosphonate inhibitor
81	c3hkzP	Alignment	not modelled	9.4	50	PDB header: transferase Chain: P; PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
82	c5xj6A	Alignment	not modelled	9.4	18	PDB header: transferase Chain: A; PDB Molecule: glycerol-3-phosphate acyltransferase; PDBTitle: crystal structure of plsy (ygih), an integral membrane glycerol 3-2 phosphate acyltransferase - the glycerol 3-phosphate form
83	d1n1ua	Alignment	not modelled	9.4	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
84	c1n1uA	Alignment	not modelled	9.4	67	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: nmr structure of [ala1,15]kalata b1
85	c2f2iA	Alignment	not modelled	9.1	56	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [p20d,v21k]-kalata b1
86	c5h7yB	Alignment	not modelled	8.9	83	PDB header: hydrolase inhibitor/peptide Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: structure of immunity protein tplei of t6ss from pseudomonas2 aeruginosa complexed with "l" peptide
87	c2ldsA	Alignment	not modelled	8.9	75	PDB header: toxin Chain: A; PDB Molecule: insecticidal toxin lait1; PDBTitle: solution structure of a short-chain lait1 from the venom of scorpion2 liocheles australasiae
88	c3g9yA	Alignment	not modelled	8.8	42	PDB header: transcription/rna Chain: A; PDB Molecule: zinc finger ran-binding domain-containing protein 2; PDBTitle: crystal structure of the second zinc finger from zranb2/znf265 bound2 to 6 nt ssrna sequence agguaa
89	c1nb1A	Alignment	not modelled	8.8	78	PDB header: antibiotic Chain: A; PDB Molecule: kalata b1; PDBTitle: high resolution solution structure of kalata b1
90	d1nb1a	Alignment	not modelled	8.8	78	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
91	d1pt4a	Alignment	not modelled	8.7	56	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Cyclotides Family: Kalata B1
92	c2f2jA	Alignment	not modelled	8.6	56	PDB header: antimicrobial protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: solution structure of [w19k, p20n, v21k]-kalata b1
93	c2m9oA	Alignment	not modelled	8.6	56	PDB header: plant protein Chain: A; PDB Molecule: kalata-b7; PDBTitle: solution structure of kalata b7
94	d2aq0a1	Alignment	not modelled	8.4	18	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
95	c5e8kA	Alignment	not modelled	8.1	18	PDB header: transferase Chain: A; PDB Molecule: geranylgeranyl pyrophosphate synthase 10, mitochondrial; PDBTitle: crystal structure of polyprenyl pyrophosphate synthase 2 from2 arabidopsis thaliana
96	c1kalA	Alignment	not modelled	8.1	100	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: elucidation of the primary and three-dimensional structure2 of the uterotonic polypeptide kalata b1
97	c1jzA	Alignment	not modelled	8.1	78	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
98	c1k48A	Alignment	not modelled	8.1	78	PDB header: plant protein Chain: A; PDB Molecule: kalata b1; PDBTitle: refined structure and disulfide pairing of the kalata b12 peptide
99	c4ttnA	Alignment	not modelled	7.9	78	PDB header: plant protein Chain: A; PDB Molecule: kalata-b1; PDBTitle: quasi-racemic structure of [g6a]kalata b1