


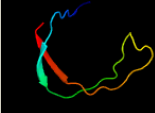

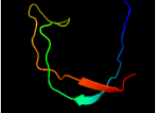
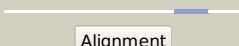

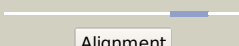
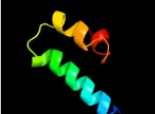
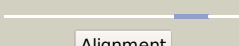
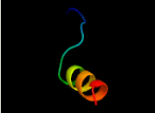
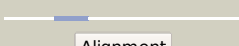

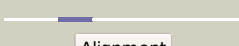
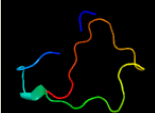



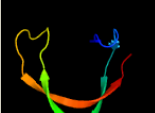

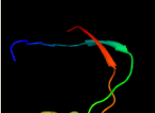











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2033c_(-)_2280248_2281090
Date	Mon Aug 5 13:25:14 BST 2019
Unique Job ID	d0070485defb6b6b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4r36A_	 Alignment		28.2	22	PDB header: transferase Chain: A: PDB Molecule: putative acyl-[acyl-carrier-protein]--udp-n-acetylglucosamine2 acyltransferase from bacteroides fragilis 9343
2	c4wxlB_	 Alignment		24.4	27	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure analysis of lpxa, a udp-n-acetylglucosamine2 complex with actinonin
3	d2defa_	 Alignment		24.0	22	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
4	c5xxeD_	 Alignment		23.4	32	PDB header: dna binding protein Chain: D: PDB Molecule: protection of telomeres protein tpz1; PDBTitle: crystal structure of poz1 and tpz1
5	d2jf2a1	 Alignment		23.0	17	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: UDP N-acetylglucosamine acyltransferase
6	c5xxeC_	 Alignment		22.8	32	PDB header: dna binding protein Chain: C: PDB Molecule: protection of telomeres protein tpz1; PDBTitle: crystal structure of poz1 and tpz1
7	c4cg4D_	 Alignment		21.1	22	PDB header: actin-binding protein Chain: D: PDB Molecule: pyrin; PDBTitle: crystal structure of the chs-b30.2 domains of trim20
8	c3mmlD_	 Alignment		17.6	32	PDB header: hydrolase Chain: D: PDB Molecule: allophanate hydrolase subunit 1; PDBTitle: allophanate hydrolase complex from mycobacterium smegmatis, msmeg0435-2 msmeg0436
9	c6e1jB_	 Alignment		16.2	20	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
10	c3qu1B_	 Alignment		14.0	27	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: peptide deformylase 2; PDBTitle: peptide deformylase from vibrio cholerae
11	d1xeoa1	 Alignment		14.0	22	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase

12	c5j46A_	Alignment		14.0	22	PDB header: hydrolase Chain: A; PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from burkholderia2 multivorans
13	c2kdcC_	Alignment		13.7	19	PDB header: transferase Chain: C; PDB Molecule: diacylglycerol kinase; PDBTitle: nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
14	c2epgB_	Alignment		12.4	48	PDB header: ligase Chain: B; PDB Molecule: hypothetical protein ttha1785; PDBTitle: crystal structure of ttha1785
15	c5ip0C_	Alignment		11.8	13	PDB header: structural protein Chain: C; PDB Molecule: pha granule-associated protein; PDBTitle: pha binding protein phap (phasin)
16	c6flnE_	Alignment		11.4	22	PDB header: protein binding Chain: E; PDB Molecule: e3 ubiquitin/isg15 ligase trim25; PDBTitle: crystal structure of the human trim25 coiled-coil and pryspry domains
17	c5vwxB_	Alignment		11.1	60	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h0-h3glt
18	c5vwxD_	Alignment		11.1	60	PDB header: apoptosis Chain: D; PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h0-h3glt
19	d1e3oc2	Alignment		11.1	29	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
20	c2e6iA_	Alignment		11.0	38	PDB header: transferase Chain: A; PDB Molecule: tyrosine-protein kinase itk/tsk; PDBTitle: solution structure of the btk motif of tyrosine-protein2 kinase itk from human
21	c2w3tA_	Alignment	not modelled	10.8	22	PDB header: hydrolase Chain: A; PDB Molecule: peptide deformylase; PDBTitle: chloro complex of the ni-form of e.coli deformylase
22	d1wz3a1	Alignment	not modelled	10.7	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: APG12-like
23	c3w1sC_	Alignment	not modelled	10.4	31	PDB header: ligase Chain: C; PDB Molecule: ubiquitin-like protein atg12; PDBTitle: crystal structure of saccharomyces cerevisiae atg12-atg5 conjugate2 bound to the n-terminal domain of atg16
24	c5vx3F_	Alignment	not modelled	10.3	64	PDB header: apoptosis Chain: F; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
25	c5vx3D_	Alignment	not modelled	10.3	64	PDB header: apoptosis Chain: D; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
26	c5vx3H_	Alignment	not modelled	10.2	64	PDB header: apoptosis Chain: H; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
27	d1uhua_	Alignment	not modelled	10.1	44	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: MMLV matrix protein-like
28	d1au7a2	Alignment	not modelled	10.0	21	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: POU-specific domain
29	c5vx0B_	Alignment	not modelled	9.7	64	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-like protein 11;

						PDBTitle: bak in complex with bim-h3glg
30	c5vwyB_	Alignment	not modelled	9.7	64	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h3pc-rt
31	c5vx2D_	Alignment	not modelled	9.7	64	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim-h3pc-rt
32	c5vx2B_	Alignment	not modelled	9.6	64	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim-h3pc-rt
33	c5vx0D_	Alignment	not modelled	9.6	64	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3glg
34	c5vx3B_	Alignment	not modelled	9.5	64	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
35	c3chtA_	Alignment	not modelled	9.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: p-aminobenzoate n-oxygenase; PDBTitle: crystal structure of di-iron aurf with partially bound ligand
36	c1ws1A_	Alignment	not modelled	8.7	27	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase 1; PDBTitle: structure analysis of peptide deformylase from bacillus2 cereus
37	c2phcB_	Alignment	not modelled	8.4	30	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
38	d1uc2a_	Alignment	not modelled	8.3	45	Fold: Hypothetical protein PH1602 Superfamily: Hypothetical protein PH1602 Family: Hypothetical protein PH1602
39	c3uwaA_	Alignment	not modelled	8.2	14	PDB header: hydrolase Chain: A: PDB Molecule: riia-riib membrane-associated protein; PDBTitle: crystal structure of a probable peptide deformylase from synechococcus2 phage s-ssm7
40	c2yy8B_	Alignment	not modelled	8.1	39	PDB header: transferase Chain: B: PDB Molecule: upf0106 protein ph0461; PDBTitle: crystal structure of archaeal trna-methylase for position2 56 (atrm56) from pyrococcus horikoshii, complexed with s-3 adenosyl-l-methionine
41	c3ib7A_	Alignment	not modelled	8.0	20	PDB header: hydrolase Chain: A: PDB Molecule: icc protein; PDBTitle: crystal structure of full length rv0805
42	d2fca1	Alignment	not modelled	7.9	60	Fold: Toprim domain Superfamily: Toprim domain Family: Toprim domain
43	c2k1hA_	Alignment	not modelled	7.6	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ser13; PDBTitle: solution nmr structure of ser13 from staphylococcus epidermidis.2 northeast structural genomics consortium target ser13
44	d3proc2	Alignment	not modelled	7.4	31	Fold: Alpha-lytic protease prodomain-like Superfamily: Alpha-lytic protease prodomain Family: Alpha-lytic protease prodomain
45	c3rxvA_	Alignment	not modelled	7.4	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nif3 protein; PDBTitle: crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
46	d1rl4a_	Alignment	not modelled	7.1	27	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
47	d1ksqa_	Alignment	not modelled	7.0	36	Fold: TB module/8-cys domain Superfamily: TB module/8-cys domain Family: TB module/8-cys domain
48	c6cazaA_	Alignment	not modelled	7.0	24	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of a peptide deformylase from legionella pneumophila
49	c2ynmD_	Alignment	not modelled	7.0	23	PDB header: oxidoreductase Chain: D: PDB Molecule: light-independent protochlorophyllide reductase subunit b; PDBTitle: structure of the adpxalf3-stabilized transition state of the2 nitrogenase-like dark-operative protochlorophyllide oxidoreductase3 complex from prochlorococcus marinus with its substrate4 protochlorophyllide a
50	c5jxxC_	Alignment	not modelled	6.8	17	PDB header: transferase Chain: C: PDB Molecule: acyl-[acyl-carrier-protein]-udp-n-acetylglucosamine o- PDBTitle: crystal structure of udp-n-acetylglucosamine o-acyltransferase (lpxa)2 from moraxella catarrhalis rh4.
51	c5lz3B_	Alignment	not modelled	6.7	47	PDB header: antiviral protein Chain: B: PDB Molecule: 3a; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of aichivirus a
52	c2m89A_	Alignment	not modelled	6.6	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: aha1 domain protein; PDBTitle: solution structure of the aha1 dimer from colwellia psychrerythraea
53	c3ocaB_	Alignment	not modelled	6.6	27	PDB header: hydrolase Chain: B: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of peptide deformylase from ehrlichia chaffeensis
54	d1mn8a_	Alignment	not modelled	6.5	44	Fold: Retroviral matrix proteins Superfamily: Retroviral matrix proteins Family: MMLV matrix protein-like

55	c3j9vC_	Alignment	not modelled	6.5	28	PDB header: hydrolase Chain: C: PDB Molecule: v-type proton atpase catalytic subunit a; PDBTitle: yeast v-atpase state 3
56	d2phcb1	Alignment	not modelled	6.1	29	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like
57	d1whwa_	Alignment	not modelled	6.1	10	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
58	c2r5iL_	Alignment	not modelled	6.0	47	PDB header: viral protein Chain: L: PDB Molecule: l1 protein; PDBTitle: pentamer structure of major capsid protein l1 of human papilloma virus2 type 18
59	d2f09a1	Alignment	not modelled	5.9	15	Fold: Streptavidin-like Superfamily: YdhA-like Family: YdhA-like
60	c2lghA_	Alignment	not modelled	5.9	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the ahsa1-like protein aha_2358 from2 aeromonas hydrophila refined with nh rdcs, northeast structural3 genomics consortium target ahr99.
61	c3cp8C_	Alignment	not modelled	5.8	50	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
62	d1avaa2	Alignment	not modelled	5.8	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
63	c3cpmA_	Alignment	not modelled	5.8	20	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase, chloroplast; PDBTitle: plant peptide deformylase pdf1b crystal structure
64	c3oepA_	Alignment	not modelled	5.8	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein ttha0988; PDBTitle: crystal structure of ttha0988 in space group p43212
65	c3e3uA_	Alignment	not modelled	5.7	29	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor
66	d1dzla_	Alignment	not modelled	5.6	60	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group I dsDNA viruses Family: Papovaviridae-like VP
67	c1dzlA_	Alignment	not modelled	5.6	60	PDB header: virus Chain: A: PDB Molecule: late major capsid protein l1; PDBTitle: l1 protein of human papillomavirus 16
68	d1h3na1	Alignment	not modelled	5.6	26	Fold: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Superfamily: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases Family: Anticodon-binding domain of a subclass of class I aminoacyl-tRNA synthetases
69	c4mjgB_	Alignment	not modelled	5.6	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf4853 family protein (actodo_00621) from2 actinomyces odontolyticus atcc 17982 at 2.65 a resolution
70	c2ew7A_	Alignment	not modelled	5.5	20	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of helicobacter pylori peptide deformylase
71	c4e06l_	Alignment	not modelled	5.4	83	PDB header: hydrolase/hydrolase inhibitor Chain: l: PDB Molecule: salivary anti-thrombin peptide anophelin; PDBTitle: anophelin from the malaria vector inhibits thrombin through a novel2 reverse-binding mechanism
72	d1ix1a_	Alignment	not modelled	5.3	18	Fold: Peptide deformylase Superfamily: Peptide deformylase Family: Peptide deformylase
73	c3j6rC_	Alignment	not modelled	5.3	60	PDB header: virus Chain: C: PDB Molecule: major capsid protein l1; PDBTitle: electron cryo-microscopy of human papillomavirus type 16 capsid
74	c5ii6A_	Alignment	not modelled	5.2	20	PDB header: cell adhesion Chain: A: PDB Molecule: zona pellucida sperm-binding protein 2; PDBTitle: crystal structure of the zp-n1 domain of mouse sperm receptor zp2 at2 0.95 a resolution
75	c5tgtA_	Alignment	not modelled	5.2	25	PDB header: ligase Chain: A: PDB Molecule: glutamate--trna ligase; PDBTitle: crystal structure of glytamyl-trna synthetase glurs from pseudomonas2 aeruginosa
76	c3g5rA_	Alignment	not modelled	5.2	43	PDB header: transferase Chain: A: PDB Molecule: methylenetetrahydrofolate--trna-(uracil-5-)- PDBTitle: crystal structure of thermus thermophilus trmfo in complex with2 tetrahydrofolate
77	c4e8wA_	Alignment	not modelled	5.2	32	PDB header: transferase/transferase inhibitor Chain: A: PDB Molecule: d-beta-d-heptose 7-phosphate kinase; PDBTitle: crystal structure of burkholderia cenocepacia hlda in complex with an2 atp-competitive inhibitor
78	c3n0rA_	Alignment	not modelled	5.1	21	PDB header: signaling protein Chain: A: PDB Molecule: response regulator; PDBTitle: structure of the phyr stress response regulator at 1.25 angstrom2 resolution
79	c3ziuA_	Alignment	not modelled	5.1	8	PDB header: ligase Chain: A: PDB Molecule: leucyl-trna synthetase; PDBTitle: crystal structure of mycoplasma mobile leucyl-trna2 synthetase with leu-ams in the active site