












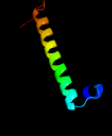





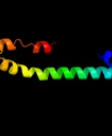


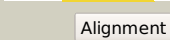




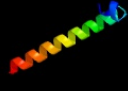





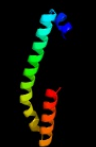



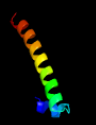


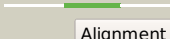





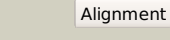


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1772_(-)_2006643_2006954
Date	Fri Aug 2 13:30:38 BST 2019
Unique Job ID	a4b410ce436f5de0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4akkA_	 Alignment		99.5	19	PDB header: transcription Chain: A: PDB Molecule: nitrate regulatory protein; PDBTitle: structure of the nasr transcription antiterminator
2	d1qo0d_	 Alignment		98.7	17	Fold: Flavodoxin-like Superfamily: CheY-like Family: Positive regulator of the amidase operon AmiR
3	d1s8na_	 Alignment		97.4	18	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
4	c4mc8A_	 Alignment		82.5	19	PDB header: lyase Chain: A: PDB Molecule: putative sesquiterpene cyclase; PDBTitle: hedycaryl synthase in complex with hepes
5	c4bbaA_	 Alignment		82.0	13	PDB header: protein-binding protein Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: crystal structure of glucokinase regulatory protein complexed to2 phosphate
6	d1ps1a_	 Alignment		78.9	6	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase
7	d1di1a_	 Alignment		78.5	11	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Aristolochene/pentalenene synthase
8	c3w0ID_	 Alignment		77.1	15	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: glucokinase regulatory protein; PDBTitle: the crystal structure of xenopus glucokinase and glucokinase2 regulatory protein complex
9	c6q4sA_	 Alignment		75.0	16	PDB header: unknown function Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: crystal structure of a-eudesmol synthase
10	c5nx6A_	 Alignment		72.5	11	PDB header: lyase Chain: A: PDB Molecule: pentalenene synthase; PDBTitle: crystal structure of 1,8-cineole synthase from streptomyces2 clavuligerus in complex with 2-fluoroneryl diphosphate
11	c5i1uB_	 Alignment		72.2	20	PDB header: lyase Chain: B: PDB Molecule: germacradien-4-ol synthase; PDBTitle: crystal structure of germacradien-4-ol synthase from streptomyces2 citricolor

12	c4lc9A_	 Alignment		70.3	10	PDB header: transferase/transferase regulator Chain: A: PDB Molecule: glucokinase regulatory protein; PDBTitle: structural basis for regulation of human glucokinase by glucokinase2 regulatory protein
13	c3lg5A_	 Alignment		69.1	14	PDB header: lyase Chain: A: PDB Molecule: epi-isozizaene synthase; PDBTitle: f198a epi-isozizaene synthase: complex with mg, inorganic2 pyrophosphate and benzyl triethyl ammonium cation
14	c3v1vA_	 Alignment		68.2	8	PDB header: lyase Chain: A: PDB Molecule: 2-methylisoborneol synthase; PDBTitle: crystal structure of 2-methylisoborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and geranyl-s-thiolodiphosphate
15	c5ermA_	 Alignment		67.1	13	PDB header: lyase Chain: A: PDB Molecule: fuscococadiene synthase; PDBTitle: crystal structure of cyclization domain of phomopsis amygdali2 fuscococadiene synthase complexed with magnesium ions and pamidronate
16	c5dw7A_	 Alignment		66.8	13	PDB header: lyase Chain: A: PDB Molecule: germacradienol/geosmin synthase; PDBTitle: crystal structure of the unliganded geosmin synthase n-terminal domain2 from streptomyces coelicolor
17	c6egkB_	 Alignment		62.5	8	PDB header: lyase Chain: B: PDB Molecule: cucumene synthase; PDBTitle: t181n cucumene synthase
18	c1tr8A_	 Alignment		61.6	19	PDB header: chaperone Chain: A: PDB Molecule: conserved protein (mth177); PDBTitle: crystal structure of archaeal nascent polypeptide-associated complex2 (aenac)
19	c4okmA_	 Alignment		60.2	18	PDB header: transferase Chain: A: PDB Molecule: terpene synthase metal-binding domain-containing protein; PDBTitle: selinadiene synthase apo and in complex with diphosphate
20	c2oa6B_	 Alignment		58.3	21	PDB header: lyase Chain: B: PDB Molecule: aristolochene synthase; PDBTitle: aristolochene synthase from aspergillus terreus complexed with2 pyrophosphate
21	c3b9tD_	 Alignment	not modelled	55.4	12	PDB header: hydrolase Chain: D: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of predicted acetamidase/formamidase (yp_546212.1)2 from methylobacillus flagellatus kt at 1.58 a resolution
22	c3v1xA_	 Alignment	not modelled	54.8	7	PDB header: lyase Chain: A: PDB Molecule: 2-methylisoborneol synthase; PDBTitle: crystal structure of 2-methylisoborneol synthase from streptomyces2 coelicolor a3(2) in complex with mg2+ and 2-fluorogeranyl diphosphate
23	c5nx4A_	 Alignment	not modelled	52.4	13	PDB header: ligase Chain: A: PDB Molecule: pentalene synthase; PDBTitle: crystal structure of linalool/nerolidol synthase from streptomyces2 clavuligerus
24	d5easa2	 Alignment	not modelled	47.3	13	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain
25	c3mjJD_	 Alignment	not modelled	45.2	4	PDB header: hydrolase Chain: D: PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
26	c4wyhA_	 Alignment	not modelled	42.0	14	PDB header: replication Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of prix from the hyperthermophilic archaeon2 sulfobolus solfataricus
27	c1n20A_	 Alignment	not modelled	41.9	6	PDB header: isomerase Chain: A: PDB Molecule: (+)-bornyl diphosphate synthase; PDBTitle: (+)-bornyl diphosphate synthase: complex with mg and 3-aza-2,3-dihydrogeranyl diphosphate PDB header: hydrolase

28	c2ii1A_	Alignment	not modelled	41.6	15	Chain: A: PDB Molecule: acetamidase; PDBTitle: crystal structure of acetamidase (10172637) from bacillus halodurans2 at 1.95 a resolution
29	c5ubuC_	Alignment	not modelled	40.3	15	PDB header: hydrolase Chain: C: PDB Molecule: putative acetamidase/formamidase; PDBTitle: 2.75 angstrom resolution crystal structure of acetamidase from2 yersinia enterocolitica.
30	c5a0iA_	Alignment	not modelled	38.5	17	PDB header: lyase Chain: A: PDB Molecule: labdane-related diterpene synthase; PDBTitle: crystallographic structure of the bacterial labdane-related diterpene2 synthase lrdc in complex with mg and ppi at 2.57 a resolution.
31	d2f4la1	Alignment	not modelled	38.2	12	Fold: CUB-like Superfamily: Acetamidase/Formamidase-like Family: Acetamidase/Formamidase-like
32	d1n1ba2	Alignment	not modelled	38.0	6	Fold: Terpenoid synthases Superfamily: Terpenoid synthases Family: Terpenoid cyclase C-terminal domain
33	c6edjD_	Alignment	not modelled	36.8	25	PDB header: virus like particle Chain: D: PDB Molecule: external core antigen; PDBTitle: cryo-em structure of woodchuck hepatitis virus capsid
34	c2wknE_	Alignment	not modelled	35.1	16	PDB header: hydrolase Chain: E: PDB Molecule: formamidase; PDBTitle: gamma lactamase from delftia acidovorans
35	c4zq8B_	Alignment	not modelled	34.8	9	PDB header: transferase Chain: B: PDB Molecule: isoprenoid synthase; PDBTitle: crystal structure of a terpene synthase from streptomyces lydicus,2 target efi-540129
36	c3n0fA_	Alignment	not modelled	34.4	9	PDB header: lyase Chain: A: PDB Molecule: isoprene synthase; PDBTitle: crystal structure of isoprene synthase from grey poplar leaves2 (populus x canescens)
37	c6o9qA_	Alignment	not modelled	34.4	6	PDB header: lyase Chain: A: PDB Molecule: sesquisabinene b synthase 1; PDBTitle: wild-type sasqs1
38	c2ongA_	Alignment	not modelled	34.3	3	PDB header: lyase Chain: A: PDB Molecule: 4s-limonene synthase; PDBTitle: crystal structure of of limonene synthase with 2-2 fluorogeranyl diphosphate (fgpp).
39	c2y96A_	Alignment	not modelled	32.5	9	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase dupd1; PDBTitle: structure of human dual-specificity phosphatase 27
40	c5uv1A_	Alignment	not modelled	31.1	7	PDB header: lyase Chain: A: PDB Molecule: (+)-limonene synthase; PDBTitle: crystal structure of (+)-limonene synthase complexed with 2-2 fluorogeranyl diphosphate
41	d1gqta_	Alignment	not modelled	30.9	30	Fold: Hepatitis B viral capsid (hbcag) Superfamily: Hepatitis B viral capsid (hbcag) Family: Hepatitis B viral capsid (hbcag)
42	c1hx9A_	Alignment	not modelled	28.1	12	PDB header: lyase Chain: A: PDB Molecule: 5-epi-aristolochene synthase; PDBTitle: crystal structure of teas w273s form 1
43	d1i9sa_	Alignment	not modelled	23.8	21	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
44	c4jmkA_	Alignment	not modelled	22.9	9	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 8; PDBTitle: structure of dusp8
45	c2j5cB_	Alignment	not modelled	21.7	6	PDB header: lyase Chain: B: PDB Molecule: 1,8-cineole synthase; PDBTitle: rational conversion of substrate and product specificity in a2 monoterpene synthase. structural insights into the molecular basis of3 rapid evolution.
46	c2imgA_	Alignment	not modelled	21.1	22	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
47	c5c05A_	Alignment	not modelled	20.7	6	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative gamma-terpinene synthase; PDBTitle: crystal structure of gamma-terpinene synthase from thymus vulgaris
48	c2hcmA_	Alignment	not modelled	20.4	22	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase; PDBTitle: crystal structure of mouse putative dual specificity phosphatase2 complexed with zinc tungstate, new york structural genomics3 consortium
49	c2nt2C_	Alignment	not modelled	18.2	9	PDB header: hydrolase Chain: C: PDB Molecule: protein phosphatase slingshot homolog 2; PDBTitle: crystal structure of slingshot phosphatase 2
50	c4gaxA_	Alignment	not modelled	18.1	9	PDB header: lyase Chain: A: PDB Molecule: amorpha-4,11-diene synthase; PDBTitle: crystal structure of an alpha-bisabolol synthase mutant
51	c2r0bA_	Alignment	not modelled	17.9	9	PDB header: hydrolase Chain: A: PDB Molecule: serine/threonine/tyrosine-interacting protein; PDBTitle: crystal structure of human tyrosine phosphatase-like2 serine/threonine/tyrosine-interacting protein
52	c5zjC_	Alignment	not modelled	17.7	6	PDB header: lyase Chain: C: PDB Molecule: santalene synthase; PDBTitle: crystal structure of a enzyme from santalum album
53	c3s4oB_	Alignment	not modelled	17.5	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein tyrosine phosphatase-like protein; PDBTitle: protein tyrosine phosphatase (putative) from leishmania major

54	c2esbA	Alignment	not modelled	17.4	9	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 18; PDBTitle: crystal structure of human dusp18
55	c1zzwA	Alignment	not modelled	17.1	13	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of catalytic domain of human map kinase2 phosphatase 5
56	c3s4eA	Alignment	not modelled	16.6	26	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 19; PDBTitle: crystal structure of a novel mitogen-activated protein kinase2 phosphatase, skrp1
57	c3g4dB	Alignment	not modelled	16.4	12	PDB header: lyase Chain: B: PDB Molecule: (+)-delta-cadinene synthase isozyme xc1; PDBTitle: crystal structure of (+)-delta-cadinene synthase from gossypium2 arboreum and evolutionary divergence of metal binding motifs for3 catalysis
58	c6i28A	Alignment	not modelled	16.2	18	PDB header: viral protein Chain: A: PDB Molecule: orf98 ptp-2; PDBTitle: crystal structure of cydia pomonella ptp-2 phosphatase
59	c2oudA	Alignment	not modelled	16.1	13	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 10; PDBTitle: crystal structure of the catalytic domain of human mkp5
60	c3emuA	Alignment	not modelled	16.1	17	PDB header: hydrolase Chain: A: PDB Molecule: leucine rich repeat and phosphatase domain containing PDBTitle: crystal structure of a leucine rich repeat and phosphatase domain2 containing protein from entamoeba histolytica
61	c2gwoC	Alignment	not modelled	16.0	9	PDB header: hydrolase Chain: C: PDB Molecule: dual specificity protein phosphatase 13; PDBTitle: crystal structure of tmpd
62	c2g6zB	Alignment	not modelled	15.3	17	PDB header: hydrolase Chain: B: PDB Molecule: dual specificity protein phosphatase 5; PDBTitle: crystal structure of human dusp5
63	d1ohea2	Alignment	not modelled	15.2	11	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
64	c3rgqA	Alignment	not modelled	14.8	17	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase mitochondrial 1; PDBTitle: crystal structure of ptpmt1 in complex with pi(5)p
65	d1m3ga	Alignment	not modelled	14.0	29	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
66	c2e0tA	Alignment	not modelled	12.8	9	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 26; PDBTitle: crystal structure of catalytic domain of dual specificity phosphatase2 26, ms0830 from homo sapiens
67	c3u5zA	Alignment	not modelled	12.7	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna polymerase accessory protein 62; PDBTitle: structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
68	c2obnA	Alignment	not modelled	12.4	11	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anaebaena2 variabilis atcc 29413 at 2.30 a resolution
69	c2j17A	Alignment	not modelled	12.4	11	PDB header: hydrolase Chain: A: PDB Molecule: tyrosine-protein phosphatase yil113w; PDBTitle: ptyr bound form of sdp-1
70	c2dhmA	Alignment	not modelled	12.3	26	PDB header: protein binding Chain: A: PDB Molecule: protein bola; PDBTitle: solution structure of the bola protein from escherichia coli
71	c1oheA	Alignment	not modelled	12.3	11	PDB header: hydrolase Chain: A: PDB Molecule: cdc14b2 phosphatase; PDBTitle: structure of cdc14b phosphatase with a peptide ligand
72	c1yz4A	Alignment	not modelled	12.1	4	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase-like 15 isoform a; PDBTitle: crystal structure of dusp15
73	c4rd8B	Alignment	not modelled	12.0	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of a functionally-unknown protein from2 legionella pneumophila subsp. pneumophila str. philadelphia 1
74	c1yn9B	Alignment	not modelled	11.9	21	PDB header: hydrolase Chain: B: PDB Molecule: polynucleotide 5'-phosphatase; PDBTitle: crystal structure of baculovirus rna 5'-phosphatase2 complexed with phosphate
75	c3nmeA	Alignment	not modelled	11.7	13	PDB header: hydrolase Chain: A: PDB Molecule: sex4 glucan phosphatase; PDBTitle: structure of a plant phosphatase
76	c5z5bA	Alignment	not modelled	11.6	17	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine phosphatase; PDBTitle: crystal structure of tk-ptp in the g95a mutant form
77	c5xjvA	Alignment	not modelled	11.4	14	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 13 isoform a; PDBTitle: two intermediate states of conformation switch in dual specificity2 phosphatase 13a
78	c4ki9A	Alignment	not modelled	10.9	22	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 12; PDBTitle: crystal structure of the catalytic domain of human dusp12 at 2.0 a2 resolution
79	c1tlqA	Alignment	not modelled	10.9	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ypjq; PDBTitle: crystal structure of protein ypjq from bacillus subtilis, pfam duf64

80	d1ttqa_	Alignment	not modelled	10.9	11	Fold: YutG-like Superfamily: YutG-like Family: YutG-like
81	c6bwqB_	Alignment	not modelled	10.5	14	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
82	d1ku9a_	Alignment	not modelled	10.4	9	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DNA-binding protein Mj223
83	c1wrmA_	Alignment	not modelled	10.2	11	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity phosphatase 22; PDBTitle: crystal structure of jsp-1
84	c4kyrA_	Alignment	not modelled	10.2	17	PDB header: hydrolase, sugar binding protein Chain: A: PDB Molecule: phosphoglucan phosphatase lsf2, chloroplastic; PDBTitle: structure of a product bound plant phosphatase
85	d1nria_	Alignment	not modelled	10.1	17	Fold: SIS domain Superfamily: SIS domain Family: mono-SIS domain
86	c1nriA_	Alignment	not modelled	10.1	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0754; PDBTitle: crystal structure of putative phosphosugar isomerase hi0754 from2 haemophilus influenzae
87	c4hvb0B_	Alignment	not modelled	10.1	15	PDB header: transcription, viral protein Chain: B: PDB Molecule: avtr; PDBTitle: structure and function of avtr, a novel transcriptional regulator from2 a hyperthermophilic archaeal lipothrixvirus
88	d2fxaa1	Alignment	not modelled	9.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
89	d2qsba1	Alignment	not modelled	9.8	16	Fold: Bromodomain-like Superfamily: Ta0600-like Family: Ta0600-like
90	c4yixB_	Alignment	not modelled	9.4	19	PDB header: protein binding Chain: B: PDB Molecule: atp-dependent clp protease adapter protein clps 2; PDBTitle: the structure of agrobacterium tumefaciens clps2 bound to l-2 phenylalaninamide
91	d1mkpa_	Alignment	not modelled	9.2	14	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like
92	c6dnmA_	Alignment	not modelled	8.7	27	PDB header: chaperone Chain: A: PDB Molecule: export chaperone sats; PDBTitle: the crystal structure of sats c-terminal domain
93	c5x3tA_	Alignment	not modelled	8.2	16	PDB header: antitoxin/toxin Chain: A: PDB Molecule: antitoxin vapp26; PDBTitle: vappbc from mycobacterium tuberculosis
94	d1w3ia_	Alignment	not modelled	8.1	11	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
95	d2d6fc1	Alignment	not modelled	7.9	5	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
96	c2l9dA_	Alignment	not modelled	7.8	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of the protein yp_546394.1, the first structural2 representative of the pfam family pf12112
97	c4r30C_	Alignment	not modelled	7.5	14	PDB header: hydrolase Chain: C: PDB Molecule: laforin; PDBTitle: structure of human laforin dual specificity phosphatase domain
98	c3s9vD_	Alignment	not modelled	7.4	9	PDB header: lyase, isomerase Chain: D: PDB Molecule: abietadiene synthase, chloroplastic; PDBTitle: abietadiene synthase from abies grandis
99	c4nyhB_	Alignment	not modelled	7.4	13	PDB header: hydrolase Chain: B: PDB Molecule: rna/rnp complex-1-interacting phosphatase; PDBTitle: orthorhombic crystal form of pir1 dual specificity phosphatase core