



















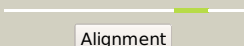
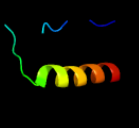


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2676c_(-)_2991943_2992638
Date	Wed Aug 7 12:50:32 BST 2019
Unique Job ID	fb61e8b6b207d384

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4wvsE_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: E; PDB Molecule: putative heme-dependent peroxidase lmo2113; PDBTitle: structure of chlorite dismutase-like protein from listeria2 monocytogenes
2	c3nn4C_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: C; PDB Molecule: chlorite dismutase; PDBTitle: structure of chlorite dismutase from candidatus nitrospira defluviu2 r173k mutant
3	d1t0tv_	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
4	d1vdha_	 Alignment		100.0	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
5	c5a13j_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: J; PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of chlorite dismutase from2 magnetospirillum sp. in complex with thiocyanate
6	c2vxhf_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: F; PDB Molecule: chlorite dismutase; PDBTitle: the crystal structure of chlorite dismutase: a detox enzyme2 producing molecular oxygen
7	c3dtzB_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: putative chlorite dismutase ta0507; PDBTitle: crystal structure of putative chlorite dismutase ta0507
8	c3qpiA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutases from nitrobacter2 winogradskyi
9	c5k8zB_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: B; PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutase from cyanothece sp.2 pcc7425 (ph 8.5)
10	d2cfxa2	 Alignment		69.2	18	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
11	c30a5A_	 Alignment		65.7	14	PDB header: hydrolase Chain: A; PDB Molecule: chi1; PDBTitle: the structure of chi1, a chitinase from yersinia entomophaga

12	c4a5qC_	Alignment		65.7	14	PDB header: hydrolase Chain: C; PDB Molecule: chi1; PDBTitle: crystal structure of the chitinase chi1 fitted into the 3d structure2 of the yersinia entomophaga toxin complex
13	c3pohA_	Alignment		60.8	18	PDB header: hydrolase Chain: A; PDB Molecule: endo-beta-n-acetylglucosaminidase f1; PDBTitle: crystal structure of an endo-beta-n-acetylglucosaminidase (bt_3987)2 from bacteroides thetaiotaomicron vpi-5482 at 1.55 a resolution
14	c4hhuA_	Alignment		57.4	17	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: or280; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
15	c3b9eA_	Alignment		56.1	21	PDB header: hydrolase Chain: A; PDB Molecule: chitinase a; PDBTitle: crystal structure of inactive mutant e315m chitinase a from2 vibrio harveyi
16	c6bt9B_	Alignment		54.6	18	PDB header: hydrolase Chain: B; PDB Molecule: chitinase; PDBTitle: chitinase chia74 from bacillus thuringiensis
17	d2iiza1	Alignment		52.7	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Dyp-type peroxidase-like
18	c1rd6A_	Alignment		50.8	29	PDB header: hydrolase Chain: A; PDB Molecule: chitinase a; PDBTitle: crystal structure of s. marcescens chitinase a mutant w167a
19	c5zl9A_	Alignment		50.3	29	PDB header: hydrolase Chain: A; PDB Molecule: chitinase ab; PDBTitle: engineered chitinase, smchiab-fysfv
20	c5gztB_	Alignment		48.4	14	PDB header: hydrolase Chain: B; PDB Molecule: chitinase; PDBTitle: crystal structure of chitinase chiw from paenibacillus sp. str. fpu-72 reveals a novel type of bacterial cell-surface-expressed multi-3 modular enzyme machinery
21	d1edqa2	Alignment	not modelled	47.6	31	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
22	c5z5mB_	Alignment	not modelled	47.2	19	PDB header: lyase Chain: B; PDB Molecule: predicted protein; PDBTitle: crystal structure of (s)-allantoin synthase
23	c3simA_	Alignment	not modelled	46.7	23	PDB header: hydrolase Chain: A; PDB Molecule: protein, family 18 chitinase; PDBTitle: crystallographic structure analysis of family 18 chitinase from crocus2 vernus
24	d2o8ia1	Alignment	not modelled	46.5	17	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
25	c4txgA_	Alignment	not modelled	46.1	21	PDB header: hydrolase Chain: A; PDB Molecule: chitinase; PDBTitle: crystal structure of a family gh18 chitinase from chromobacterium2 violaceum
26	d1kfwal	Alignment	not modelled	45.8	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
27	c4rl3A_	Alignment	not modelled	45.8	23	PDB header: hydrolase Chain: A; PDB Molecule: chitinase a; PDBTitle: crystal structure of the catalytic domain of a family gh18 chitinase2 from fern, peteris ryukyensis
28	c2y8vB_	Alignment	not modelled	45.1	33	PDB header: hydrolase Chain: B; PDB Molecule: class iii chitinase, putative; PDBTitle: structure of chitinase, chic, from aspergillus fumigatus.
		Alignment				PDB header: hydrolase Chain: X; PDB Molecule: endo-n-acetyl-beta-d-glucosaminidase;

29	c4ac1X	Alignment	not modelled	45.1	29	PDBTitle: the structure of a fungal endo-beta-n-acetylglucosaminidase from2 glycosyl hydrolase family 18, at 1.3a resolution
30	d2cyva2	Alignment	not modelled	42.8	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
31	c4axnB	Alignment	not modelled	42.5	14	PDB header: hydrolase Chain: B: PDB Molecule: chitinase c1; PDBTitle: hallmarks of processive and non-processive glycoside hydrolases2 revealed from computational and crystallographic studies of the3 serratia marcescens chitinases
32	c5jxuA	Alignment	not modelled	42.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase family; PDBTitle: structural basis for the catalytic activity of thermomonospora curvata2 heme-containing dyp-type peroxidase.
33	c5df0A	Alignment	not modelled	41.0	29	PDB header: hydrolase Chain: A: PDB Molecule: ac-chia; PDBTitle: crystal structure of acmnpv chitinase a in complex with chitotrio-2 thiazoline dithioamide
34	c4grcA	Alignment	not modelled	40.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative membrane protein; PDBTitle: crystal structure of dyp-type peroxidase (sco2276) from streptomyces2 coelicolor
35	c4gs1A	Alignment	not modelled	36.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: dyp-type peroxidase; PDBTitle: crystal structure of dyp-type peroxidase from thermobifida2 cellulositytica
36	c3qnsA	Alignment	not modelled	36.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dyp peroxidase; PDBTitle: dypb from rhodococcus jostii rha1, crystal form 2
37	c3ianA	Alignment	not modelled	36.4	18	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of a chitinase from lactococcus lactis subsp. lactis
38	c2djwF	Alignment	not modelled	35.1	16	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
39	c2q37A	Alignment	not modelled	33.7	9	PDB header: plant protein, lyase Chain: A: PDB Molecule: ohcu decarboxylase; PDBTitle: crystal structure of ohcu decarboxylase in the presence of2 (s)-allantoin
40	d2q37a1	Alignment	not modelled	33.7	9	Fold: UraD-like Superfamily: UraD-Like Family: UraD-like
41	c2zbcH	Alignment	not modelled	33.6	16	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
42	d2ebna	Alignment	not modelled	33.5	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
43	c2e1aD	Alignment	not modelled	32.3	14	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
44	d1w9pa1	Alignment	not modelled	31.4	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
45	c6qzoG	Alignment	not modelled	31.1	20	PDB header: oxidoreductase Chain: G: PDB Molecule: peroxidase; PDBTitle: crystal structure of dyp-type peroxidase from cellulomonas bogoriensis
46	c4q6tA	Alignment	not modelled	30.4	10	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 18; PDBTitle: the crystal structure of a class v chitinase from pseudomonas2 fluorescens pf-5
47	c5gzvA	Alignment	not modelled	30.1	12	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of chitinase chiw from paenibacillus sp. str. fpu-72 reveals a novel type of bacterial cell-surface-expressed multi-3 modular enzyme machinery
48	d1s2xa	Alignment	not modelled	30.0	21	Fold: STAT-like Superfamily: Cag-Z Family: Cag-Z
49	c1s2xA	Alignment	not modelled	30.0	21	PDB header: unknown function Chain: A: PDB Molecule: cag-z; PDBTitle: crystal structure of cag-z from helicobacter pylori
50	c3n12A	Alignment	not modelled	28.2	24	PDB header: hydrolase Chain: A: PDB Molecule: chitinase a; PDBTitle: crystal stricture of chitinase in complex with zinc atoms from2 bacillus cereus nctu2
51	d1nara	Alignment	not modelled	27.9	23	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
52	c3cz8A	Alignment	not modelled	27.6	20	PDB header: hydrolase Chain: A: PDB Molecule: putative sporulation-specific glycosylase ydhd; PDBTitle: crystal structure of putative sporulation-specific glycosylase ydhd2 from bacillus subtilis
53	c1kfwA	Alignment	not modelled	27.5	21	PDB header: hydrolase Chain: A: PDB Molecule: chitinase b; PDBTitle: structure of catalytic domain of psychrophilic chitinase b from2 arthrobacter tad20

54	c5ja1B_	Alignment	not modelled	26.6	11	PDB header: ligase Chain: B: PDB Molecule: enterobactin biosynthesis protein ybdz; PDBTitle: entf, a terminal nonribosomal peptide synthetase module bound to the2 mbth-like protein ybdz
55	c5wmmB_	Alignment	not modelled	26.5	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: mbth homologue; PDBTitle: crystal structure of an adenylation domain interrupted by a2 methylation domain (ama4) from nonribosomal peptide synthetase tios
56	c5de0D_	Alignment	not modelled	26.2	19	PDB header: oxidoreductase Chain: D: PDB Molecule: deferrochelataase; PDBTitle: dye-decolorizing protein from v. cholerae
57	c4s3kA_	Alignment	not modelled	25.8	8	PDB header: hydrolase Chain: A: PDB Molecule: spore germination protein yaah; PDBTitle: crystal structure of the bacillus megaterium qm b1551 spore cortex-2 lytic enzyme sle1
58	c3ebvA_	Alignment	not modelled	25.6	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: chinitase a; PDBTitle: crystal structure of putative chitinase a from streptomyces2 coelicolor.
59	d1edta_	Alignment	not modelled	25.4	29	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
60	c4s3jC_	Alignment	not modelled	25.4	12	PDB header: hydrolase Chain: C: PDB Molecule: cortical-lytic enzyme; PDBTitle: crystal structure of the bacillus cereus spore cortex-lytic enzyme2 sle1
61	c2khrA_	Alignment	not modelled	25.2	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: protein mbth; PDBTitle: solution structure of rv2377c, a mbth-like protein from mycobacterium2 tuberculosis
62	d2pstx1	Alignment	not modelled	25.1	11	Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like
63	c4hmcA_	Alignment	not modelled	24.8	13	PDB header: hydrolase Chain: A: PDB Molecule: chitinase 60; PDBTitle: crystal structure of cold-adapted chitinase from moritella marina
64	c2wx6B_	Alignment	not modelled	24.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxidase ycdb; PDBTitle: x-ray crystallographic structure of e. coli apo-efeb
65	c5exkG_	Alignment	not modelled	23.5	17	PDB header: transferase Chain: G: PDB Molecule: lipoyl synthase; PDBTitle: crystal structure of m. tuberculosis lipoyl synthase with 6-2 thiooctanoyl peptide intermediate
66	c3bxwB_	Alignment	not modelled	23.1	9	PDB header: hydrolase Chain: B: PDB Molecule: chitinase domain-containing protein 1; PDBTitle: crystal structure of stabilin-1 interacting chitinase-like protein,2 si-clp
67	c5hbfB_	Alignment	not modelled	23.1	24	PDB header: hydrolase Chain: B: PDB Molecule: chitotriosidase-1; PDBTitle: crystal structure of human full-length chitotriosidase (chit1)
68	d2gpfa1	Alignment	not modelled	23.0	11	Fold: Mbth/L9 domain-like Superfamily: Mbth-like Family: Mbth-like
69	c5u89B_	Alignment	not modelled	22.7	8	PDB header: hydrolase/inhibitor Chain: B: PDB Molecule: mbth domain protein; PDBTitle: crystal structure of a cross-module fragment from the dimodular nrps2 dhbf
70	c6idnA_	Alignment	not modelled	22.0	16	PDB header: plant protein Chain: A: PDB Molecule: icchi, a glycosylated chitinase; PDBTitle: crystal structure of icchi chitinase from ipomoea carnea
71	c6dkuA_	Alignment	not modelled	21.6	22	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory2 domain
72	c4e0eB_	Alignment	not modelled	21.5	39	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a duf4450 family protein (bt_4147) from2 bacteroides thetaiotaomicron vpi-5482 at 2.90 a resolution
73	c2exuA_	Alignment	not modelled	20.8	17	PDB header: transcription Chain: A: PDB Molecule: transcription initiation protein spt4/spt5; PDBTitle: crystal structure of saccharomyces cerevisiae transcription elongation2 factors spt4-spt5ngn domain
74	c4gt2A_	Alignment	not modelled	20.3	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein sco3963; PDBTitle: crystal structure of dyp-type peroxidase (sco3963) from streptomyces2 coelicolor
75	c6eu1O_	Alignment	not modelled	20.3	50	PDB header: transcription Chain: Q: PDB Molecule: dna-directed rna polymerase iii subunit rpc7; PDBTitle: rna polymerase iii - open dna complex (oc-pol3)
76	c1itxA_	Alignment	not modelled	20.3	17	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase; PDBTitle: catalytic domain of chitinase a1 from bacillus circulans wl-12
77	c4w5uA_	Alignment	not modelled	20.2	31	PDB header: hydrolase Chain: A: PDB Molecule: chitinase; PDBTitle: crystal structure of chitinase 40 from thermophilic bacteria2 streptomyces thermoviolaceus.
78	c3qokA_	Alignment	not modelled	20.1	24	PDB header: hydrolase Chain: A: PDB Molecule: putative chitinase ii; PDBTitle: crystal structure of putative chitinase ii from klebsiella pneumoniae
79	c4gu7C_	Alignment	not modelled	19.8	20	PDB header: oxidoreductase Chain: C: PDB Molecule: putative uncharacterized protein sco7193; PDBTitle: crystal structure of dyp-type peroxidase (sco7193) from streptomyces2 coelicolor

80	c2n5xA	Alignment	not modelled	19.8	21	PDB header: chaperone Chain: A; PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: c-terminal domain of cdc37 cochaperone
81	c3oheA	Alignment	not modelled	19.4	28	PDB header: hydrolase Chain: A; PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
82	d1wiza	Alignment	not modelled	19.4	23	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: CUT domain
83	d1i1ga2	Alignment	not modelled	19.2	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
84	c3w4rA	Alignment	not modelled	19.2	23	PDB header: hydrolase Chain: A; PDB Molecule: chitinase; PDBTitle: crystal structure of an insect chitinase from the asian corn borer,2 ostrinia furnacalis
85	c2uy2A	Alignment	not modelled	18.7	16	PDB header: hydrolase Chain: A; PDB Molecule: endochitinase; PDBTitle: sccts1_apo crystal structure
86	c1ur8B	Alignment	not modelled	18.7	19	PDB header: hydrolase Chain: B; PDB Molecule: chitinase b; PDBTitle: interactions of a family 18 chitinase with the designed inhibitor2 hm508, and its degradation product, chitobiono-delta-lactone
87	c1jneA	Alignment	not modelled	18.4	17	PDB header: hormone/growth factor Chain: A; PDB Molecule: imaginal disc growth factor-2; PDBTitle: crystal structure of imaginal disc growth factor-2
88	c4k2jB	Alignment	not modelled	18.3	8	PDB header: dna binding protein, viral protein Chain: B; PDB Molecule: kshv (hhv-8) latency-associated nuclear antigen (lana); PDBTitle: decameric ring structure of kshv (hhv-8) latency-associated nuclear2 antigen (lana) dna binding domain
89	c2kwuA	Alignment	not modelled	18.2	35	PDB header: protein binding/signaling protein Chain: A; PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
90	d1itxa1	Alignment	not modelled	18.2	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
91	d2gvka1	Alignment	not modelled	18.2	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Dyp-type peroxidase-like
92	d1goia2	Alignment	not modelled	17.7	22	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
93	c5evfA	Alignment	not modelled	17.6	71	PDB header: unknown function Chain: A; PDB Molecule: francisella virulence factor; PDBTitle: crystal structure of a francisella virulence factor fvfa in the2 hexagonal form
94	d1vf8a1	Alignment	not modelled	17.4	14	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
95	c1yseA	Alignment	not modelled	16.9	23	PDB header: dna binding protein Chain: A; PDB Molecule: dna-binding protein satb1; PDBTitle: solution structure of the mar-binding domain of satb1
96	d1l7a1	Alignment	not modelled	16.8	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
97	d1cnva	Alignment	not modelled	16.5	8	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Type II chitinase
98	c5fmzB	Alignment	not modelled	16.5	28	PDB header: transcription Chain: B; PDB Molecule: rna-directed rna polymerase catalytic subunit; PDBTitle: crystal structure of influenza b polymerase with bound 5' vrna
99	c2lpdA	Alignment	not modelled	16.4	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: solution structure of a mbth-like protein from burkholderia2 pseudomallei, the etiological agent responsible for melioidosis,3 seattle structural genomics center for infectious disease target4 bupsa.13472.b