

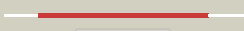




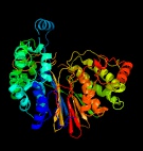

















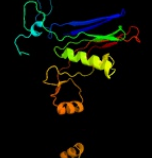




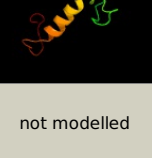


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0773c_(ggtA)_865854_867392
Date	Fri Jul 26 01:50:35 BST 2019
Unique Job ID	fae67a74d313cf65

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4y23A_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: gamma glutamyl transpeptidase,gamma glutamyltranspeptidase; PDBTitle: crystal structure of t399a precursor mutant protein of gamma-glutamyl2 transpeptidase from bacillus licheniformis
2	d2nlza1	 Alignment		100.0	50	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like
3	d2i3oa1	 Alignment		100.0	31	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like
4	c2e0wA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: t391a precursor mutant protein of gamma-glutamyltranspeptidase from2 escherichia coli
5	c2v36A_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase large chain; PDBTitle: crystal structure of gamma-glutamyl transferase from bacillus subtilis
6	c2qm6C_	 Alignment		100.0	28	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
7	c2z8jA_	 Alignment		100.0	29	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark
8	c4gdxA_	 Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase 1 heavy chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
9	c5zjgC_	 Alignment		100.0	31	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyltransferase 1 threonine peptidase. merops PDBTitle: gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly
10	c3g9kD_	 Alignment		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase enzyme capd
11	c2v36D_	 Alignment		100.0	29	PDB header: transferase Chain: D: PDB Molecule: gamma-glutamyltranspeptidase small chain; PDBTitle: crystal structure of gamma-glutamyl transferase from bacillus subtilis

12	c2e0yB_	Alignment		100.0	33	PDB header: transferase Chain: B: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of the samarium derivative of mature gamma-2 glutamyltranspeptidase from escherichia coli
13	c4gdxB_	Alignment		100.0	28	PDB header: hydrolase Chain: B: PDB Molecule: gamma-glutamyltranspeptidase 1 light chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
14	c5zjgD_	Alignment		100.0	29	PDB header: transferase Chain: D: PDB Molecule: gamma-glutamyltransferase 1 threonine peptidase. merops PDBTitle: gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly
15	c2nqoB_	Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of helicobacter pylori gamma-glutamyltranspeptidase
16	c3ga9S_	Alignment		100.0	25	PDB header: hydrolase Chain: S: PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase enzyme capd,2 crystal form ii
17	c1p4vA_	Alignment		95.2	17	PDB header: hydrolase Chain: A: PDB Molecule: n(4)-(beta-n-acetylglucosaminy)l-l-asparaginase PDBTitle: crystal structure of the glycosylasparaginase precursor2 d151n mutant with glycine
18	c1apyA_	Alignment		94.8	33	PDB header: hydrolase Chain: A: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase
19	c1t3mA_	Alignment		94.6	26	PDB header: hydrolase Chain: A: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
20	c3cuqA_	Alignment		94.1	20	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
21	c2gezE_	Alignment	not modelled	94.0	25	PDB header: hydrolase Chain: E: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
22	c4pu6A_	Alignment	not modelled	94.0	20	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase alpha subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with k+ cations
23	c2zmeA_	Alignment	not modelled	93.8	20	PDB header: protein transport Chain: A: PDB Molecule: vacuolar-sorting protein snf8; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
24	c2zakB_	Alignment	not modelled	93.3	26	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase precursor; PDBTitle: orthorhombic crystal structure of precursor e. coli isoaspartyl2 peptidase/l-asparaginase (ecaiii) with active-site t179a mutation
25	c2gacA_	Alignment	not modelled	92.6	26	PDB header: hydrolase Chain: A: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
26	c2a8lB_	Alignment	not modelled	91.9	31	PDB header: hydrolase Chain: B: PDB Molecule: threonine aspartase 1; PDBTitle: crystal structure of human taspase1 (t234a mutant)
27	c1u5tA_	Alignment	not modelled	89.6	21	PDB header: transport protein Chain: A: PDB Molecule: appears to be functionally related to snf7; PDBTitle: structure of the escrt-ii endosomal trafficking complex
28	c4gduB_	Alignment	not modelled	88.3	14	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of sulfate-bound human l-asparaginase protein

29	c1apzB	Alignment	not modelled	84.0	20	PDB header: complex (hydrolase/peptide) Chain: B: PDB Molecule: aspartylglucosaminidase; PDBTitle: human aspartylglucosaminidase complex with reaction product
30	d1u5ta1	Alignment	not modelled	83.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
31	c2gacD	Alignment	not modelled	70.6	20	PDB header: hydrolase Chain: D: PDB Molecule: glycosylasparaginase; PDBTitle: t152c mutant glycosylasparaginase from flavobacterium2 meningosepticum
32	c1w7pD	Alignment	not modelled	68.6	34	PDB header: protein transport Chain: D: PDB Molecule: vps36p, ylr417w; PDBTitle: the crystal structure of endosomal complex escrt-ii2 (vps22/vps25/vps36)
33	c2zalD	Alignment	not modelled	67.5	19	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
34	c1u5tB	Alignment	not modelled	65.4	28	PDB header: transport protein Chain: B: PDB Molecule: defective in vacuolar protein sorting; vps36p; PDBTitle: structure of the escrt-ii endosomal trafficking complex
35	c2zmeB	Alignment	not modelled	62.6	22	PDB header: protein transport Chain: B: PDB Molecule: vacuolar protein-sorting-associated protein 36; PDBTitle: integrated structural and functional model of the human escrt-ii2 complex
36	c1jn9B	Alignment	not modelled	59.1	20	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: structure of putative asparaginase encoded by escherichia coli ybik2 gene
37	c1t3mD	Alignment	not modelled	59.1	20	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
38	c1t3mB	Alignment	not modelled	59.1	20	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: structure of the isoaspartyl peptidase with l-asparaginase2 activity from e. coli
39	c1k2xD	Alignment	not modelled	53.7	20	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
40	c1jn9D	Alignment	not modelled	53.7	20	PDB header: hydrolase Chain: D: PDB Molecule: putative l-asparaginase; PDBTitle: structure of putative asparaginase encoded by escherichia coli ybik2 gene
41	c1k2xB	Alignment	not modelled	53.7	20	PDB header: hydrolase Chain: B: PDB Molecule: putative l-asparaginase; PDBTitle: crystal structure of putative asparaginase encoded by escherichia coli2 ybik gene
42	c2zalB	Alignment	not modelled	43.0	17	PDB header: hydrolase Chain: B: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of e. coli isoaspartyl aminopeptidase/l-asparaginase2 in complex with l-aspartate
43	d2fi0a1	Alignment	not modelled	41.1	15	Fold: SP0561-like Superfamily: SP0561-like Family: SP0561-like
44	c2gezF	Alignment	not modelled	40.8	17	PDB header: hydrolase Chain: F: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-independent plant asparaginase
45	c5InfA	Alignment	not modelled	39.7	8	PDB header: chaperone Chain: A: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: solution nmr structure of farnesylated pex19, c-terminal domain
46	c2w18D	Alignment	not modelled	38.4	8	PDB header: protein transport Chain: D: PDB Molecule: peroxisomal biogenesis factor 19; PDBTitle: x-ray crystal structure of pex19p
47	c5xugB	Alignment	not modelled	38.4	35	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-mannanase; PDBTitle: complex structure(rmman134a-m5).
48	c5jtsA	Alignment	not modelled	36.2	35	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,4-mannanase; PDBTitle: structure of a beta-1,4-mannanase, ssg134.
49	c3fpvC	Alignment	not modelled	34.5	18	PDB header: heme binding protein Chain: C: PDB Molecule: extracellular haem-binding protein; PDBTitle: crystal structure of hbps
50	c4pv3D	Alignment	not modelled	29.9	15	PDB header: hydrolase Chain: D: PDB Molecule: l-asparaginase beta subunit; PDBTitle: crystal structure of potassium-dependent plant-type l-asparaginase2 from phaseolus vulgaris in complex with na+ cations
51	c3ka5A	Alignment	not modelled	28.0	15	PDB header: chaperone Chain: A: PDB Molecule: ribosome-associated protein y (psrp-1); PDBTitle: crystal structure of ribosome-associated protein y (psrp-1)2 from clostridium acetobutylicum. northeast structural3 genomics consortium target id car123a
52	c2zuuA	Alignment	not modelled	27.1	30	PDB header: transferase Chain: A: PDB Molecule: lacto-n-biose phosphorylase; PDBTitle: crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
53	d1jq5a	Alignment	not modelled	26.3	23	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
54	c5loyD	Alignment	not modelled	26.1	18	PDB header: hydrolase Chain: D: PDB Molecule: designed anbu protein; PDBTitle: helical assembly of a designed anbu protein

55	c1udsA_	Alignment	not modelled	23.3	22	PDB header: transferase Chain: A; PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of the trna processing enzyme rnase ph r126a mutant2 from aquifex aeolicus
56	c3rf7A_	Alignment	not modelled	23.2	18	PDB header: oxidoreductase Chain: A; PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
57	c6d6rF_	Alignment	not modelled	22.9	26	PDB header: hydrolase Chain: F; PDB Molecule: exosome complex component mtr3; PDBTitle: human nuclear exosome-mtr4 rna complex - composite map after focused2 reconstruction
58	d1u5tb1	Alignment	not modelled	20.1	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
59	c3gxqB_	Alignment	not modelled	19.7	45	PDB header: dna binding protein/dna Chain: B; PDB Molecule: putative regulator of transfer genes arta; PDBTitle: structure of arta and dna complex
60	d1r6la1	Alignment	not modelled	19.0	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
61	c3hkmB_	Alignment	not modelled	18.8	21	PDB header: hydrolase Chain: B; PDB Molecule: os03g0854200 protein; PDBTitle: crystal structure of rice(oryza sativa) rrp46
62	c5nywT_	Alignment	not modelled	18.6	18	PDB header: unknown function Chain: T; PDB Molecule: proteasome subunit; PDBTitle: anbu (ancestral beta-subunit) from yersinia bercovieri
63	d2nn6f1	Alignment	not modelled	18.0	44	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
64	c4ifdC_	Alignment	not modelled	17.8	17	PDB header: hydrolase/rna Chain: C; PDB Molecule: exosome complex component rrp43; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
65	d2nn6a1	Alignment	not modelled	17.3	44	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
66	c3bt3B_	Alignment	not modelled	17.2	13	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: glyoxalase-related enzyme, arac type; PDBTitle: crystal structure of a glyoxalase-related enzyme from clostridium2 phytofermentans
67	d1udsA1	Alignment	not modelled	17.1	22	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
68	d2nn6e1	Alignment	not modelled	17.0	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
69	d2qalk1	Alignment	not modelled	16.5	17	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
70	c3h7hA_	Alignment	not modelled	16.0	27	PDB header: transcription Chain: A; PDB Molecule: transcription elongation factor spt4; PDBTitle: crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273)
71	c2qntA_	Alignment	not modelled	15.9	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein atu1872; PDBTitle: crystal structure of protein of unknown function from agrobacterium2 tumefaciens str. c58
72	c5lbdB_	Alignment	not modelled	15.9	7	PDB header: hydrolase Chain: B; PDB Molecule: copper-transporting atpase paa1, chloroplastic; PDBTitle: crystal structure of the n-domain of hma6, a copper-transporting p-2 type atpase
73	d2ccaa1	Alignment	not modelled	15.9	15	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
74	c3k2tA_	Alignment	not modelled	15.6	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: lmo2511 protein; PDBTitle: crystal structure of lmo2511 protein from listeria2 monocytogenes, northeast structural genomics consortium3 target lkr84a
75	c3b4tC_	Alignment	not modelled	15.4	26	PDB header: transferase Chain: C; PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of mycobacterium tuberculosis rnase ph, the2 mycobacterium tuberculosis structural genomics consortium target3 rv1340
76	d1u2ka_	Alignment	not modelled	15.4	12	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: Catalase-peroxidase KatG
77	c4ifdE_	Alignment	not modelled	15.3	0	PDB header: hydrolase/rna Chain: E; PDB Molecule: exosome complex component rrp42; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna
78	c3t5xB_	Alignment	not modelled	15.3	25	PDB header: transcription Chain: B; PDB Molecule: 26s proteasome complex subunit dss1; PDBTitle: pcid2:dss1 structure
79	d1huwa_	Alignment	not modelled	15.2	12	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines
80	c4n04B_	Alignment	not modelled	15.2	12	PDB header: oxidoreductase Chain: B; PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase;

						PDBTitle: the crystal structure of glyoxalase / bleomycin resistance protein2 from catenulispora acidiphila dsm 44928
81	c2nn6A_	Alignment	not modelled	15.0	44	PDB header: hydrolase/transferase Chain: A: PDB Molecule: polymyositis/scleroderma autoantigen 1; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
82	d2nn6d1	Alignment	not modelled	14.8	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
83	d2ba0g1	Alignment	not modelled	14.4	44	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
84	c5o19A_	Alignment	not modelled	14.4	13	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor, mitochondrial; PDBTitle: structure of human mitochondrial transcription elongation factor2 (tefm) n-terminal domain
85	c2qz5A_	Alignment	not modelled	14.1	16	PDB header: signaling protein, lipid binding protein Chain: A: PDB Molecule: axin interactor, dorsalization associated PDBTitle: crystal structure of the c-terminal domain of aida
86	c5yvmA_	Alignment	not modelled	13.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
87	c2zkqk_	Alignment	not modelled	13.8	9	PDB header: ribosomal protein/rna Chain: K: PDB Molecule: PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
88	c2wnrB_	Alignment	not modelled	13.0	26	PDB header: hydrolase Chain: B: PDB Molecule: probable exosome complex exonuclease 1; PDBTitle: the structure of methanothermobacter thermautotrophicus2 exosome core assembly
89	c2f4nA_	Alignment	not modelled	12.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein mj1651; PDBTitle: crystal structure of protein mj1651 from methanococcus2 jannaschii dsm 2661, pfam duf62
90	d2uubk1	Alignment	not modelled	12.9	13	Fold: Ribonuclease H-like motif Superfamily: Translational machinery components Family: Ribosomal protein L18 and S11
91	c2nn6F_	Alignment	not modelled	12.8	44	PDB header: hydrolase/transferase Chain: F: PDB Molecule: exosome component 6; PDBTitle: structure of the human rna exosome composed of rrp41, rrp45,2 rrp46, rrp43, mtr3, rrp42, csl4, rrp4, and rrp40
92	c2wp8B_	Alignment	not modelled	12.6	11	PDB header: hydrolase Chain: B: PDB Molecule: exosome complex component ski6; PDBTitle: yeast rrp44 nuclease
93	c3itwA_	Alignment	not modelled	11.7	16	PDB header: peptide binding protein Chain: A: PDB Molecule: protein tiox; PDBTitle: crystal structure of tiox from micromonospora sp. ml1
94	d2i09a2	Alignment	not modelled	11.0	33	Fold: DeoB insert domain-like Superfamily: DeoB insert domain-like Family: DeoB insert domain-like
95	d1oysa1	Alignment	not modelled	10.9	17	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
96	d2je6a1	Alignment	not modelled	10.8	33	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: Ribonuclease PH domain 1-like
97	c3dd6A_	Alignment	not modelled	10.7	17	PDB header: transferase Chain: A: PDB Molecule: ribonuclease ph; PDBTitle: crystal structure of rph, an exoribonuclease from bacillus anthracis2 at 1.7 a resolution
98	c2br2G_	Alignment	not modelled	10.7	33	PDB header: hydrolase Chain: G: PDB Molecule: exosome complex exonuclease 2; PDBTitle: rnase ph core of the archaeal exosome
99	c2kmvA_	Alignment	not modelled	10.7	9	PDB header: hydrolase Chain: A: PDB Molecule: copper-transporting atpase 1; PDBTitle: solution structure of the nucleotide binding domain of the2 human menkes protein in the atp-free form