















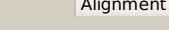
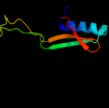
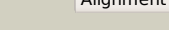

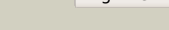
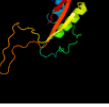


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0790c_(-)_884075_884803
Date	Fri Jul 26 01:50:37 BST 2019
Unique Job ID	9214ab8494f7895c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lsrB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: transglutaminase-like enzymes, putative cysteine protease; PDBTitle: the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
2	c6g49A_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of the periplasmic domain of tgpa from pseudomonas2 aeruginosa
3	c4xz7A_	 Alignment		99.9	21	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a tgase
4	c3kd4A_	 Alignment		99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: putative protease; PDBTitle: crystal structure of a putative protease (bdj_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
5	d2q3za4	 Alignment		99.7	21	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
6	d1g0da4	 Alignment		99.6	22	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
7	d2f4ma1	 Alignment		99.6	30	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
8	d1vjja4	 Alignment		99.6	23	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
9	d1ex0a4	 Alignment		99.5	27	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
10	d1x3za1	 Alignment		99.2	20	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
11	c1kv3F_	 Alignment		99.2	21	PDB header: transferase Chain: F: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: human tissue transglutaminase in gdp bound form

12	c1g0dA_	Alignment		99.1	22	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of red sea bream transglutaminase
13	c1f13A_	Alignment		99.1	28	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
14	c19mB_	Alignment		99.1	25	PDB header: transferase Chain: B: PDB Molecule: protein-glutamine glutamyltransferase e3; PDBTitle: three-dimensional structure of the human transglutaminase 32 enzyme: binding of calcium ions change structure for3 activation
15	c4u65F_	Alignment		99.0	16	PDB header: transferase/hydrolase Chain: F: PDB Molecule: putative cystine protease; PDBTitle: structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
16	c2qshA_	Alignment		98.9	12	PDB header: dna binding protein/dna Chain: A: PDB Molecule: dna repair protein rad4; PDBTitle: crystal structure of rad4-rad23 bound to a mismatch dna
17	c3eswA_	Alignment		98.9	19	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
18	c2pfrB_	Alignment		98.0	11	PDB header: transferase Chain: B: PDB Molecule: arylamine n-acetyltransferase 2; PDBTitle: human n-acetyltransferase 2
19	c4fgpB_	Alignment		98.0	13	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic protein; PDBTitle: legionella pneumophila lapg (egta-treated)
20	d1e2ta_	Alignment		97.9	12	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
21	d1w4ta1	Alignment	not modelled	97.8	12	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
22	c3lnbA_	Alignment	not modelled	97.8	11	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase family protein; PDBTitle: crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
23	c4guzA_	Alignment	not modelled	97.7	12	PDB header: transferase Chain: A: PDB Molecule: probable arylamine n-acetyl transferase; PDBTitle: structure of the arylamine n-acetyltransferase from mycobacterium2 abscessus
24	d2bsza1	Alignment	not modelled	97.6	10	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
25	c4dmoB_	Alignment	not modelled	97.6	9	PDB header: transferase Chain: B: PDB Molecule: n-hydroxyarylamine o-acetyltransferase; PDBTitle: crystal structure of the (baccr)nat3 arylamine n-acetyltransferase2 from bacillus cereus reveals a unique cys-his-glu catalytic triad
26	c2vfbA_	Alignment	not modelled	97.3	9	PDB header: transferase Chain: A: PDB Molecule: arylamine n-acetyltransferase; PDBTitle: the structure of mycobacterium marinum arylamine n-2 acetyltransferase
27	d1w5ra1	Alignment	not modelled	97.3	9	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
28	c3d9wA_	Alignment	not modelled	97.2	13	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure analysis of nocardia farcinica arylamine n-2 acetyltransferase

29	d1yuaa2	Alignment	not modelled	57.1	18	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Prokaryotic DNA topoisomerase I, a C-terminal fragment
30	c1ezaA	Alignment	not modelled	48.5	17	PDB header: phosphotransferase Chain: A: PDB Molecule: enzyme i; PDBTitle: amino terminal domain of enzyme i from escherichia coli nmr,2 restrained regularized mean structure
31	c5woyA	Alignment	not modelled	47.3	14	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: nmr solution structure of enzyme i (neit) protein using two 4d-spectra
32	c1yuaA	Alignment	not modelled	44.6	17	PDB header: dna binding protein Chain: A: PDB Molecule: topoisomerase i; PDBTitle: c-terminal domain of escherichia coli topoisomerase i
33	c6h8mB	Alignment	not modelled	41.7	21	PDB header: hydrolase Chain: B: PDB Molecule: neurotrypsin; PDBTitle: crystal structure of the third srcr domain of murine neurotrypsin.
34	c2jopA	Alignment	not modelled	40.0	21	PDB header: immune system Chain: A: PDB Molecule: t-cell surface glycoprotein cd5; PDBTitle: solution structure of the n-terminal extracellular domain2 of the lymphocyte receptor cd5 (cd5 domain 1)
35	d1kbla2	Alignment	not modelled	36.6	18	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
36	c4ruIA	Alignment	not modelled	33.9	25	PDB header: isomerase/dna Chain: A: PDB Molecule: dna topoisomerase 1; PDBTitle: crystal structure of full-length e.coli topoisomerase i in complex2 with ssdna
37	d1h6za2	Alignment	not modelled	33.6	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
38	c3nrIB	Alignment	not modelled	33.1	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein rumgna_01417; PDBTitle: crystal structure of protein rumgna_01417 from ruminococcus gnavus,2 northeast structural genomics consortium target ugr76
39	c2ottY	Alignment	not modelled	30.8	15	PDB header: immune system Chain: Y: PDB Molecule: t-cell surface glycoprotein cd5; PDBTitle: crystal structure of cd5_diii
40	c3chgB	Alignment	not modelled	29.8	8	PDB header: ligand binding protein Chain: B: PDB Molecule: glycine betaine-binding protein; PDBTitle: the compatible solute-binding protein opuac from bacillus2 subtilis in complex with dmsa
41	d1ou8a	Alignment	not modelled	26.5	14	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
42	c1vbaA	Alignment	not modelled	25.6	13	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
43	c3jsyA	Alignment	not modelled	25.2	32	PDB header: ribosomal protein Chain: A: PDB Molecule: acidic ribosomal protein p0 homolog; PDBTitle: n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
44	d1zszc1	Alignment	not modelled	24.4	14	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
45	d1ou9a	Alignment	not modelled	23.4	14	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
46	c6cgaA	Alignment	not modelled	22.3	13	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
47	c2a5wC	Alignment	not modelled	22.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: sulfite reductase, desulfoviridin-type subunit gamma PDBTitle: crystal structure of the oxidized gamma-subunit of the dissimilatory2 sulfite reductase (dsrc) from archaeoglobus fulgidus
48	c3j21k	Alignment	not modelled	22.1	18	PDB header: ribosome Chain: K: PDB Molecule: 50s ribosomal protein l14e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
49	d1j0aa	Alignment	not modelled	22.0	17	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
50	c3a56B	Alignment	not modelled	20.9	12	PDB header: hydrolase Chain: B: PDB Molecule: protein-glutaminase; PDBTitle: crystal structure of pro- protein-glutaminase
51	c4nwbA	Alignment	not modelled	20.9	17	PDB header: unknown function Chain: A: PDB Molecule: mrna turnover protein 4; PDBTitle: crystal structure of mrt4
52	c5t1oB	Alignment	not modelled	20.5	27	PDB header: transferase Chain: B: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase ptsp; PDBTitle: solution-state nmr and saxs structural ensemble of npr (1-85) in2 complex with ein-ntr (170-424)
53	d1zyma2	Alignment	not modelled	20.3	25	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system

54	d1yfnal	Alignment	not modelled	19.6	14	Fold: SspB-like Superfamily: SspB-like Family: Stringent starvation protein B, SspB
55	d1p5ja	Alignment	not modelled	19.6	25	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
56	c1p5jA	Alignment	not modelled	19.6	25	PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
57	c2hwgA	Alignment	not modelled	19.5	20	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of phosphorylated enzyme i of the phosphoenolpyruvate:sugar2 phosphotransferase system
58	c1yx3A	Alignment	not modelled	19.3	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrc; PDBTitle: nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
59	c1kblA	Alignment	not modelled	18.5	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
60	c3izcs	Alignment	not modelled	17.9	53	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein rpl20 (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
61	c2rkbE	Alignment	not modelled	17.4	25	PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
62	d3be7a1	Alignment	not modelled	15.9	11	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Zn-dependent arginine carboxypeptidase-like
63	c3iz5s	Alignment	not modelled	15.9	18	PDB header: ribosome Chain: S: PDB Molecule: 60s ribosomal protein l18a (l18ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
64	c6ei1A	Alignment	not modelled	15.6	21	PDB header: hydrolase Chain: A: PDB Molecule: zinc finger with ufm1-specific peptidase domain protein; PDBTitle: crystal structure of the covalent complex between deubiquitinase zufsp2 (zup1) and ubiquitin-pa
65	c2hroA	Alignment	not modelled	15.4	23	PDB header: transferase Chain: A: PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: structure of the full-length enzyme i of the pts system from2 staphylococcus carnosus
66	d1vbga2	Alignment	not modelled	15.3	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
67	c5xa2B	Alignment	not modelled	15.2	13	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrylase from planctomyces2 limnophila
68	d1wkva1	Alignment	not modelled	14.9	25	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
69	c3qp1A	Alignment	not modelled	14.6	13	PDB header: transcription Chain: A: PDB Molecule: cvir transcriptional regulator; PDBTitle: crystal structure of cvir ligand-binding domain bound to the native2 ligand c6-hsl
70	c5xenB	Alignment	not modelled	14.3	12	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of a hydrogen sulfide-producing enzyme (fn1220) from2 fusobacterium nucleatum in complex with l-serine-plp schiff base
71	c3j3bq	Alignment	not modelled	13.8	26	PDB header: ribosome Chain: Q: PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the human 60s ribosomal proteins
72	c5b3kA	Alignment	not modelled	13.8	24	PDB header: electron transport Chain: A: PDB Molecule: uncharacterized protein pa3435; PDBTitle: c101a mutant of flavodoxin from pseudomonas aeruginosa
73	c5ybwA	Alignment	not modelled	13.7	12	PDB header: isomerase Chain: A: PDB Molecule: aspartate racemase; PDBTitle: crystal structure of pyridoxal 5'-phosphate-dependent aspartate2 racemase
74	c4d8tC	Alignment	not modelled	13.7	12	PDB header: lyase Chain: C: PDB Molecule: d-cysteine desulfhydrase; PDBTitle: crystal structure of d-cysteine desulfhydrase from salmonella2 typhimurium at 2.2 a resolution
75	d1jvaa3	Alignment	not modelled	13.6	19	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
76	c4hubG	Alignment	not modelled	13.4	37	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l10e; PDBTitle: the re-refined crystal structure of the haloarcula marismortui large2 ribosomal subunit at 2.4 angstrom resolution: more complete structure3 of the l7/l12 and l1 stalk, l5 and lx proteins
77	c2gn0A	Alignment	not modelled	13.1	9	PDB header: lyase Chain: A: PDB Molecule: threonine dehydratase catabolic; PDBTitle: crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)

78	c2j0wA_	Alignment	not modelled	12.6	28	PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
79	c2f4qA_	Alignment	not modelled	12.5	32	PDB header: isomerase Chain: A: PDB Molecule: type i topoisomerase, putative; PDBTitle: crystal structure of deinococcus radiodurans topoisomerase ib
80	c2d1fA_	Alignment	not modelled	11.9	20	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
81	d1fcja_	Alignment	not modelled	11.9	8	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
82	c2m3dA_	Alignment	not modelled	11.7	21	PDB header: hydrolase Chain: A: PDB Molecule: nucleolar rna helicase 2; PDBTitle: nmr structure of the guct domain from human dead box polypeptide 21
83	c4airB_	Alignment	not modelled	11.7	17	PDB header: transferase Chain: B: PDB Molecule: cysteine synthase; PDBTitle: leishmania major cysteine synthase
84	d1tyza_	Alignment	not modelled	11.6	8	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
85	c2ct6A_	Alignment	not modelled	11.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sh3 domain-binding glutamic acid-rich-like PDBTitle: solution structure of the sh3 domain-binding glutamic acid-2 rich-like protein 2
86	c2zsjB_	Alignment	not modelled	11.3	24	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
87	d2e29a1	Alignment	not modelled	11.3	15	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: GUCT domain
88	d1f2da_	Alignment	not modelled	11.1	13	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
89	c5cvcB_	Alignment	not modelled	11.1	21	PDB header: isomerase Chain: B: PDB Molecule: serine racemase; PDBTitle: structure of maize serine racemase
90	c4aecB_	Alignment	not modelled	11.0	4	PDB header: lyase Chain: B: PDB Molecule: cysteine synthase, mitochondrial; PDBTitle: crystal structure of the arabidopsis thaliana o-acetylserine-(thiol)-2 lyase c
91	c5c3uA_	Alignment	not modelled	9.8	20	PDB header: lyase Chain: A: PDB Molecule: l-serine ammonia-lyase; PDBTitle: crystal structure of a fungal l-serine ammonia-lyase from rhizomucor2 miehei
92	d1tdja1	Alignment	not modelled	9.8	25	Fold: Tryptophan synthase beta subunit-like PLP-dependent enzymes Superfamily: Tryptophan synthase beta subunit-like PLP-dependent enzymes Family: Tryptophan synthase beta subunit-like PLP-dependent enzymes
93	c4ql4A_	Alignment	not modelled	9.7	0	PDB header: lyase Chain: A: PDB Molecule: o-acetylserine lyase; PDBTitle: crystal structure of o-acetylserine sulphydrylase from bacillus2 anthracis
94	d1by2a_	Alignment	not modelled	9.6	14	Fold: SrcR-like Superfamily: SrcR-like Family: Scavenger receptor cysteine-rich (SrcR) domain
95	c4xvzB_	Alignment	not modelled	9.5	22	PDB header: transferase Chain: B: PDB Molecule: mycinamicin iii 3'-o-methyltransferase; PDBTitle: mycf mycinamicin iii 3'-o-methyltransferase in complex with mg
96	c5fbtA_	Alignment	not modelled	9.5	18	PDB header: transferase/antibiotic Chain: A: PDB Molecule: phosphoenolpyruvate synthase; PDBTitle: crystal structure of rifampin phosphotransferase rph-1m from listeria2 monocytogenes in complex with rifampin
97	c1x1qA_	Alignment	not modelled	9.5	8	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
98	d1h59b_	Alignment	not modelled	9.3	19	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
99	c5ancC_	Alignment	not modelled	9.3	12	PDB header: translation Chain: C: PDB Molecule: 60s acidic ribosomal protein p0; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit