

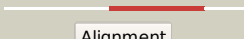
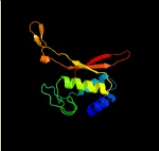
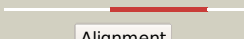








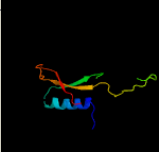









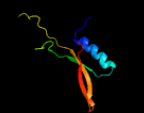









Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2569c_(-)_2893474_2894418
Date	Wed Aug 7 12:50:20 BST 2019
Unique Job ID	e66ebbf6f8699f7f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3lsrB_	 Alignment		100.0	21	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	25	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		99.8	21	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a tgase
4	d2q3za4	 Alignment		99.7	26	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
5	d2f4ma1	 Alignment		99.6	30	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
6	d1g0da4	 Alignment		99.6	30	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
7	d1vja4	 Alignment		99.6	34	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
8	d1ex0a4	 Alignment		99.6	36	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
9	c3kd4A_	 Alignment		99.4	11	PDB header: hydrolase Chain: A: PDB Molecule: putative protease; PDBTitle: crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
10	d1x3za1	 Alignment		99.3	27	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Transglutaminase core
11	c4u65F_	 Alignment		99.0	17	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

12	c3eswA	Alignment		98.9	25	PDB header: hydrolase Chain: A: PDB Molecule: peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine PDBTitle: complex of yeast pngase with glcnac2-iac.
13	c1l9mB	Alignment		98.8	26	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
14	c2qshA	Alignment		98.8	18	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
15	c1kv3F	Alignment		98.8	31	PDB header: transferase Chain: F: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: human tissue transglutaminase in gdp bound form
16	c1g0dA	Alignment		98.8	29	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of red sea bream transglutaminase
17	c1f13A	Alignment		98.8	34	PDB header: coagulation factor Chain: A: PDB Molecule: cellular coagulation factor xiii zymogen; PDBTitle: recombinant human cellular coagulation factor xiii
18	c4fgpB	Alignment		98.0	23	PDB header: hydrolase Chain: B: PDB Molecule: periplasmic protein; PDBTitle: legionella pneumophila lagp (egta-treated)
19	c2pfrB	Alignment		97.5	16	PDB header: transferase Chain: B: PDB Molecule: arylamine n-acetyltransferase 2; PDBTitle: human n-acetyltransferase 2
20	d1w4ta1	Alignment		97.3	15	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
21	d1e2ta	Alignment	not modelled	97.0	20	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
22	c2vfbA	Alignment	not modelled	97.0	21	PDB header: transferase Chain: A: PDB Molecule: arylamine n-acetyltransferase; PDBTitle: the structure of mycobacterium marinum arylamine n-2 acetyltransferase
23	c3lnbA	Alignment	not modelled	96.9	15	PDB header: transferase Chain: A: PDB Molecule: n-acetyltransferase family protein; PDBTitle: crystal structure analysis of arylamine n-acetyltransferase c from2 bacillus anthracis
24	c4guzA	Alignment	not modelled	96.8	24	PDB header: transferase Chain: A: PDB Molecule: probable arylamine n-acetyl transferase; PDBTitle: structure of the arylamine n-acetyltransferase from mycobacterium2 abscessus
25	c3d9wA	Alignment	not modelled	96.6	23	PDB header: transferase Chain: A: PDB Molecule: putative acetyltransferase; PDBTitle: crystal structure analysis of nocardia farcinica arylamine n-2 acetyltransferase
26	c4dmoB	Alignment	not modelled	96.5	13	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
27	d1w5ra1	Alignment	not modelled	96.4	15	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
28	d2bsza1	Alignment	not modelled	96.4	15	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase

29	d1kbla2	Alignment	not modelled	50.6	18	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
30	d2hlya1	Alignment	not modelled	47.5	17	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Atu2299-like
31	c2avxA	Alignment	not modelled	37.6	14	PDB header: transcription Chain: A: PDB Molecule: regulatory protein sdia; PDBTitle: solution structure of e coli sdia1-171
32	c6bjcC	Alignment	not modelled	36.8	15	PDB header: ligase Chain: C: PDB Molecule: serine-trna ligase; PDBTitle: crystal structure of cytoplasmic serine-trna ligase from naegleria2 fowleri in complex with amp
33	c3qo8A	Alignment	not modelled	31.8	16	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of seryl-trna synthetase from candida albicans
34	c3re2A	Alignment	not modelled	30.5	17	PDB header: unknown function Chain: A: PDB Molecule: predicted protein; PDBTitle: crystal structure of menin reveals the binding site for mixed lineage2 leukemia (ml) protein
35	c4gq6A	Alignment	not modelled	27.6	15	PDB header: transcription/transcription inhibitor Chain: A: PDB Molecule: menin; PDBTitle: human menin in complex with ml peptide
36	d1jvaa3	Alignment	not modelled	26.6	14	Fold: Homing endonuclease-like Superfamily: Homing endonucleases Family: Intein endonuclease
37	c2lzoA	Alignment	not modelled	26.0	43	PDB header: toxin Chain: A: PDB Molecule: ugtX; PDBTitle: spatial structure of pi-anmtX ugr 9a-1
38	c6h9xA	Alignment	not modelled	24.5	24	PDB header: ligase Chain: A: PDB Molecule: serine--trna ligase; PDBTitle: klebsiella pneumoniae seryl-trna synthetase in complex with the2 intermediate analog 5'-o-(n-(l-seryl)-sulfamoyl)adenosine
39	c3u88B	Alignment	not modelled	24.2	14	PDB header: transcription Chain: B: PDB Molecule: menin; PDBTitle: crystal structure of human menin in complex with ml1 and ledgf
40	c1sryB	Alignment	not modelled	24.0	18	PDB header: ligase(synthetase) Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: refined crystal structure of the seryl-trna synthetase from2 thermus thermophilus at 2.5 angstroms resolution
41	c6oteA	Alignment	not modelled	23.7	11	PDB header: ligase Chain: A: PDB Molecule: seryl-trna synthetase, cytoplasmic; PDBTitle: crystal structure of seryl-trna synthetase (serrs) from2 cryptosporidium parvum complexed with l-serylsulfamoyl adenosine
42	c5td8D	Alignment	not modelled	23.3	39	PDB header: replication Chain: D: PDB Molecule: kinetochore protein spc25; PDBTitle: crystal structure of an extended dwarf ndc80 complex
43	c5vglA	Alignment	not modelled	23.1	3	PDB header: isomerase Chain: A: PDB Molecule: lachrymatory-factor synthase; PDBTitle: crystal structure of lachrymatory factor synthase from allium cepa
44	d1vbga2	Alignment	not modelled	23.1	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
45	d1nyed	Alignment	not modelled	22.9	22	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
46	c3qp1A	Alignment	not modelled	22.9	10	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
47	c6d9nA	Alignment	not modelled	22.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein from2 elizabethkingia anophelis with crystallant-derived thiocyanate bound
48	c4mh4B	Alignment	not modelled	22.4	22	PDB header: protein binding Chain: B: PDB Molecule: osmc-like protein; PDBTitle: crystal structure of osmc-like protein from burkholderia cenocepacia2 j2315
49	c1vbaA	Alignment	not modelled	22.3	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate,orthophosphate dikinase; PDBTitle: pyruvate phosphate dikinase with bound mg-pep from maize
50	d1w7ja1	Alignment	not modelled	22.0	21	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
51	d2ftxa1	Alignment	not modelled	21.3	39	Fold: Kinetochore globular domain-like Superfamily: Kinetochore globular domain Family: Spc25-like
52	d1zyna2	Alignment	not modelled	21.2	25	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system
53	c2ml7A	Alignment	not modelled	20.9	27	PDB header: unknown function Chain: A: PDB Molecule: specific abundant protein 3; PDBTitle: ginsentides: characterization, structure and application of a new2 class of highly stable cystine knot peptides in ginseng
54	c3mwzA	Alignment	not modelled	20.5	13	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: sialostatin I2; PDBTitle: crystal structure of the selenomethionine derivative of the I2,47,2 100 m mutant of sialostatin I2 PDB header: hydrolase inhibitor

55	c5o46A_	Alignment	not modelled	20.4	38	Chain: A; PDB Molecule: iristatin; PDBTitle: crystal structure of iristatin, a secreted salivary cystatin from the2 hard tick ixodes ricinus
56	c3iz5s_	Alignment	not modelled	18.5	4	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
57	c4nwbA_	Alignment	not modelled	18.4	19	PDB header: unknown function Chain: A; PDB Molecule: mrna turnover protein 4; PDBTitle: crystal structure of mrt4
58	c3jsyA_	Alignment	not modelled	17.7	11	PDB header: ribosomal protein Chain: A; PDB Molecule: acidic ribosomal protein p0 homolog; PDBTitle: n-terminal fragment of ribosomal protein l10 from methanococcus2 jannaschii
59	c3lssA_	Alignment	not modelled	16.8	14	PDB header: ligase Chain: A; PDB Molecule: seryl-trna synthetase; PDBTitle: trypanosoma brucei seryl-trna synthetase in complex with atp
60	c1x4rA_	Alignment	not modelled	16.6	6	PDB header: apoptosis Chain: A; PDB Molecule: parp14 protein; PDBTitle: solution structure of wwe domain in parp14 protein
61	c5woyA_	Alignment	not modelled	16.4	12	PDB header: transferase Chain: A; PDB Molecule: phosphoenolpyruvate-protein phosphotransferase; PDBTitle: nmr solution structure of enzyme i (neit) protein using two 4d-spectra
62	c2dq0A_	Alignment	not modelled	16.1	16	PDB header: ligase Chain: A; PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of seryl-trna synthetase from pyrococcus2 horikoshii complexed with a seryl-adenylate analog
63	d2d7va1	Alignment	not modelled	15.7	11	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
64	c3idwA_	Alignment	not modelled	15.5	32	PDB header: endocytosis Chain: A; PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
65	d1uspa_	Alignment	not modelled	15.3	17	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
66	d1n2fa_	Alignment	not modelled	15.3	14	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
67	d2pn2a1	Alignment	not modelled	15.2	9	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
68	c6ei1A_	Alignment	not modelled	15.1	13	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
69	c3sztB_	Alignment	not modelled	15.0	17	PDB header: transcription Chain: B; PDB Molecule: quorum-sensing control repressor; PDBTitle: quorum sensing control repressor, qscr, bound to n-3-oxo-dodecanoyl-l-2 homoserine lactone
70	c2ql8A_	Alignment	not modelled	15.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: putative redox protein; PDBTitle: crystal structure of a putative redox protein (lsei_0423) from2 lactobacillus casei atcc 334 at 1.50 a resolution
71	c3j21k_	Alignment	not modelled	14.7	13	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)
72	d1h59b_	Alignment	not modelled	14.6	24	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Growth factor receptor domain Family: Growth factor receptor domain
73	c6ak0A_	Alignment	not modelled	14.2	50	PDB header: unknown function Chain: A; PDB Molecule: cys-leu-gly-val-gly-ser-cys-val-asp-phe-ala-gly-cys-gly- PDBTitle: solution nmr structure of a new lasso peptide specialicin
74	c4nozA_	Alignment	not modelled	14.1	14	PDB header: protein binding Chain: A; PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein from2 burkholderia cenocepacia
75	c3j3bq_	Alignment	not modelled	14.0	18	PDB header: ribosome Chain: Q; PDB Molecule: 60s ribosomal protein l18; PDBTitle: structure of the human 60s ribosomal proteins
76	d1qwia_	Alignment	not modelled	13.8	20	Fold: OsmC-like Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
77	c1ezaA_	Alignment	not modelled	13.5	14	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
78	c2j0wA_	Alignment	not modelled	13.2	20	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	c5t1oB_	Alignment	not modelled	13.1	19	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)
80	d1h6za2	Alignment	not modelled	13.1	25	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain

81	c1kblA	Alignment	not modelled	13.1	18	PDB header: transferase Chain: A: PDB Molecule: pyruvate phosphate dikinase; PDBTitle: pyruvate phosphate dikinase
82	c6cggA	Alignment	not modelled	13.1	8	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: threonine synthase from bacillus subtilis atcc 6633 with plp and plp-2 ala
83	c2hroA	Alignment	not modelled	12.9	17	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
84	c3npdA	Alignment	not modelled	12.9	30	PDB header: unknown function Chain: A: PDB Molecule: putative secreted protein; PDBTitle: crystal structure of a putative secreted protein (pa3611) from2 pseudomonas aeruginosa at 1.60 a resolution
85	c5mjrA	Alignment	not modelled	12.4	16	PDB header: photosynthesis Chain: A: PDB Molecule: protein thf1; PDBTitle: structure of psb29 at 1.55a
86	c2kiIA	Alignment	not modelled	12.2	7	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: nmr structure of the h103g mutant so2144 h-nox domain from2 shewanella oneidensis in the fe(ii)co ligation state
87	c4hubG	Alignment	not modelled	12.1	24	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
88	c6girA	Alignment	not modelled	12.0	16	PDB header: cytosolic protein Chain: A: PDB Molecule: serine--trna ligase, cytoplasmic; PDBTitle: arabidopsis thaliana cytosolic seryl-trna synthetase
89	c1rpcA	Alignment	not modelled	12.0	50	PDB header: replication inhibitor Chain: A: PDB Molecule: tricyclic peptide rp 71955; PDBTitle: solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
90	c2uv0G	Alignment	not modelled	11.7	16	PDB header: transcription Chain: G: PDB Molecule: transcriptional activator protein lasr; PDBTitle: structure of the p. aeruginosa lasr ligand-binding domain bound to its2 autoinducer
91	c1rpbA	Alignment	not modelled	11.6	50	PDB header: replication inhibitor Chain: A: PDB Molecule: tricyclic peptide rp 71955; PDBTitle: solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
92	c3izcs	Alignment	not modelled	11.5	23	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
93	c2bjoA	Alignment	not modelled	11.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: organic hydroperoxide resistance protein ohrb; PDBTitle: crystal structure of the organic hydroperoxide resistance2 protein ohrb of bacillus subtilis
94	c5ancC	Alignment	not modelled	10.9	14	PDB header: translation Chain: C: PDB Molecule: 60s acidic ribosomal protein p0; PDBTitle: mechanism of eif6 release from the nascent 60s ribosomal subunit
95	c4xz6A	Alignment	not modelled	10.2	14	PDB header: transport protein Chain: A: PDB Molecule: glycine betaine/proline abc transporter, periplasmic PDBTitle: tmox in complex with tmao
96	d1u2ca1	Alignment	not modelled	10.2	43	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cadherin-like Family: Dystroglycan, N-terminal domain
97	c1wleB	Alignment	not modelled	10.1	20	PDB header: ligase Chain: B: PDB Molecule: seryl-trna synthetase; PDBTitle: crystal structure of mammalian mitochondrial seryl-trna2 synthetase complexed with seryl-adenylate
98	c6mjnC	Alignment	not modelled	9.6	14	PDB header: oxidoreductase Chain: C: PDB Molecule: organic hydroperoxide resistance protein; PDBTitle: crystal structure of an organic hydroperoxide resistance protein osmc,2 predicted redox protein, regulator of sulfide bond formation from3 legionella pneumophila
99	d1p5ja	Alignment	not modelled	9.6	19	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