
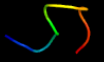







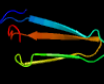









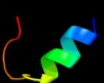




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0621 (-) _714205_715269
Date	Fri Jul 26 01:50:18 BST 2019
Unique Job ID	400bd0cb1f3c93f8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gb5B_	 Alignment		82.1	25	PDB header: hydrolase Chain: B: PDB Molecule: nadh pyrophosphatase; PDBTitle: crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
2	c3mhsE_	 Alignment		75.9	44	PDB header: hydrolase/transcription regulator/protei Chain: E: PDB Molecule: saga-associated factor 73; PDBTitle: structure of the saga ubp8/sgf11/sus1/sgf73 dub module bound to2 ubiquitin aldehyde
3	c2lo3A_	 Alignment		69.1	44	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 73; PDBTitle: solution structure of sgf73(59-102) zinc finger domain
4	c6o3pA_	 Alignment		66.1	55	PDB header: hydrolase Chain: A: PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
5	c4hcgA_	 Alignment		63.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: cupredoxin 1; PDBTitle: uncharacterized cupredoxin-like domain protein cupredoxin_1 with zinc2 bound from bacillus anthracis
6	d1wb9a4	 Alignment		57.2	18	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
7	c2kq9A_	 Alignment		53.4	31	PDB header: transcription Chain: A: PDB Molecule: dnak suppressor protein; PDBTitle: solution structure of dnak suppressor protein from agrobacterium2 tumefaciens c58. northeast structural genomics consortium target3 att12/ontario center for structural proteomics target atc0888
8	c4ijjA_	 Alignment		52.0	50	PDB header: hydrolase Chain: A: PDB Molecule: putative c4-type zinc finger protein, dksa/trar family; PDBTitle: structure of transcription factor dksa2 from pseudomonas aeruginosa
9	d1ewqa4	 Alignment		50.8	22	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
10	d1w7ab4	 Alignment		49.5	18	Fold: MutS N-terminal domain-like Superfamily: DNA repair protein MutS, domain I Family: DNA repair protein MutS, domain I
11	c3facE_	 Alignment		45.8	27	PDB header: unknown function Chain: E: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of rhodobacter sphaeroides protein2 rsp_2168. northeast structural genomics target rhr83.

12	c5opzB_	Alignment		45.6	28	PDB header: hydrolase Chain: B: PDB Molecule: chix; PDBTitle: crystal structure of serratia marcescens l-ala d-glu endopeptidase2 chix
13	c2l2dA_	Alignment		44.4	35	PDB header: hydrolase Chain: A: PDB Molecule: otu domain-containing protein 7a; PDBTitle: solution nmr structure of human uba-like domain of otud7a_11_83, nesg2 target ht6304a/ocsp target otud7a_11_83/sgc-toronto
14	c1tjlD_	Alignment		43.2	54	PDB header: transcription Chain: D: PDB Molecule: dnak suppressor protein; PDBTitle: crystal structure of transcription factor dksa from e. coli
15	c4l6tA_	Alignment		43.0	22	PDB header: hydrolase Chain: A: PDB Molecule: ecxa; PDBTitle: gm1 bound form of the ecx ab5 holotoxin
16	c2l2cqA_	Alignment		39.9	33	PDB header: metal binding protein Chain: A: PDB Molecule: putative toxin vapc6; PDBTitle: solution structure of the endonuclease nob1 from p.horikoshii
17	c2kgoA_	Alignment		39.5	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ybii; PDBTitle: solution nmr structure of zn finger protein ybil from escherichia2 coli. nesg target et107, ocsf target ec0402
18	c2rpiA_	Alignment		39.1	17	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease h; PDBTitle: the nmr structure of the submillisecond folding2 intermediate of the thermus thermophilus ribonuclease h
19	d1x4ka1	Alignment		39.1	32	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
20	d1x6ma_	Alignment		38.2	33	Fold: Mss4-like Superfamily: Mss4-like Family: Glutathione-dependent formaldehyde-activating enzyme, Gfa
21	c5w1sM_	Alignment	not modelled	37.9	33	PDB header: transferase Chain: M: PDB Molecule: protein trar; PDBTitle: x-ray crystal structure of escherichia coli rna polymerase and trar2 complex
22	c3cngC_	Alignment	not modelled	36.6	36	PDB header: hydrolase Chain: C: PDB Molecule: nudix hydrolase; PDBTitle: crystal structure of nudix hydrolase from nitrosomonas europaea
23	c3di4A_	Alignment	not modelled	36.0	20	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf1989; PDBTitle: crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
24	d1tyeb1	Alignment	not modelled	32.6	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Integrin domains Family: Integrin domains
25	c3mn8A_	Alignment	not modelled	32.2	10	PDB header: hydrolase Chain: A: PDB Molecule: lp15968p; PDBTitle: structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
26	c1jggA_	Alignment	not modelled	30.8	17	PDB header: hydrolase Chain: A: PDB Molecule: carboxypeptidase a; PDBTitle: crystal structure of the carboxypeptidase a from2 helioverpa armigera
27	d1lbya_	Alignment	not modelled	27.0	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
28	d1tjla2	Alignment	not modelled	26.8	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Prokaryotic DksA/TraR C4-type zinc finger
						Fold: Phosphorylase/hydrolase-like

29	d1obra_	Alignment	not modelled	26.2	8	Superfamily: Zn-dependent exopeptidases Family: Carboxypeptidase T
30	c2kdxA_	Alignment	not modelled	25.6	32	PDB header: metal-binding protein Chain: A: PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
31	c1ayeA_	Alignment	not modelled	25.3	17	PDB header: serine protease Chain: A: PDB Molecule: procarboxypeptidase a2; PDBTitle: human procarboxypeptidase a2
32	c2vo9C_	Alignment	not modelled	25.3	16	PDB header: hydrolase Chain: C: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: crystal structure of the enzymatically active domain of the listeria2 monocytogenes bacteriophage 500 endolysin ply500
33	d1xova1	Alignment	not modelled	24.7	33	Fold: SH3-like barrel Superfamily: Prokaryotic SH3-related domain Family: Ply C-terminal domain-like
34	c3nuzF_	Alignment	not modelled	24.4	44	PDB header: hydrolase Chain: F: PDB Molecule: putative acetyl xylan esterase; PDBTitle: crystal structure of a putative acetyl xylan esterase (bf1801) from2 bacteroides fragilis nctc 9343 at 2.30 a resolution
35	c6g8yA_	Alignment	not modelled	24.3	21	PDB header: protein binding Chain: A: PDB Molecule: acetylated cis-golgi protein, involved in er-to-golgi PDBTitle: crystal structures of the single pdz domains from grasp65 and their2 interaction with the golgin gm130
36	c1cpbA_	Alignment	not modelled	23.0	20	PDB header: hydrolase (c-terminal peptidase) Chain: A: PDB Molecule: carboxypeptidase b; PDBTitle: structure of carboxypeptidase b at 2.8 angstroms resolution
37	d1t2sa_	Alignment	not modelled	22.6	20	Fold: SH3-like barrel Superfamily: PAZ domain Family: PAZ domain
38	d1r6za1	Alignment	not modelled	22.4	15	Fold: SH3-like barrel Superfamily: PAZ domain Family: PAZ domain
39	c4ixjB_	Alignment	not modelled	21.9	29	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein (pilin); PDBTitle: the structure of pilj, a type iv pilin from clostridium difficile
40	d2v3ga1	Alignment	not modelled	21.8	16	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
41	d1fwxa1	Alignment	not modelled	21.6	19	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
42	c3r3pB_	Alignment	not modelled	20.7	10	PDB header: hydrolase Chain: B: PDB Molecule: mobile intron protein; PDBTitle: homing endonuclease i-bth0305i catalytic domain
43	d2bhga1	Alignment	not modelled	20.0	13	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
44	c2i5oA_	Alignment	not modelled	19.6	50	PDB header: transferase Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
45	c5t86A_	Alignment	not modelled	19.6	56	PDB header: toxin Chain: A: PDB Molecule: cdia toxin; PDBTitle: crystal structure of cdi complex from e. coli a0 34/86
46	c4b0sA_	Alignment	not modelled	19.4	17	PDB header: hydrolase Chain: A: PDB Molecule: deamidase-depupylase dop; PDBTitle: structure of the deamidase-depupylase dop of the prokaryotic2 ubiquitin-like modification pathway in complex with atp
47	d2vo9a1	Alignment	not modelled	19.4	15	Fold: Hedgehog/DD-peptidase Superfamily: Hedgehog/DD-peptidase Family: VanY-like
48	c5c4iB_	Alignment	not modelled	18.9	28	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
49	c3fcgB_	Alignment	not modelled	18.6	8	PDB header: membrane protein, protein transport Chain: B: PDB Molecule: f1 capsule-anchoring protein; PDBTitle: crystal structure analysis of the middle domain of the2 caf1a usher
50	c2mxzA_	Alignment	not modelled	17.7	13	PDB header: hydrolase Chain: A: PDB Molecule: l-alanyl-d-glutamate peptidase; PDBTitle: bacteriophage t5 l-alanyl-d-glutamate peptidase complex with zn2+2 (endo t5-zn2+)
51	d1jqga1	Alignment	not modelled	17.6	20	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases
52	c1psvA_	Alignment	not modelled	17.6	30	PDB header: designed peptide Chain: A: PDB Molecule: pda8d; PDBTitle: computationally designed peptide with a beta-beta-alpha2 fold selection, nmr, 32 structures
53	c2pziA_	Alignment	not modelled	17.5	58	PDB header: transferase Chain: A: PDB Molecule: probable serine/threonine-protein kinase pkng; PDBTitle: crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
54	c1pcaA_	Alignment	not modelled	17.4	13	PDB header: hydrolase(c-terminal peptidase) Chain: A: PDB Molecule: procarboxypeptidase a pcpa; PDBTitle: three dimensional structure of porcine pancreatic2 procarboxypeptidase a. a comparison of the a and b3 zymogens and their determinants for inhibition and4 activation

55	d2h6ma1	Alignment	not modelled	17.3	27	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
56	c2vb0A	Alignment	not modelled	17.3	27	PDB header: hydrolase Chain: A: PDB Molecule: polyprotein 3bcd; PDBTitle: crystal structure of coxsackievirus b3 proteinase 3c
57	c6cd2C	Alignment	not modelled	17.2	20	PDB header: membrane protein/chaperone Chain: C: PDB Molecule: outer membrane usher protein papc; PDBTitle: crystal structure of the papc usher bound to the chaperone-adhesin2 papd-papg
58	c2ddxA	Alignment	not modelled	17.2	24	PDB header: hydrolase Chain: A: PDB Molecule: beta-1,3-xylanase; PDBTitle: crystal structure of beta-1,3-xylanase from vibrio sp. ax-4
59	d1qnia1	Alignment	not modelled	16.5	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Nitrosocyanin
60	d1tdza3	Alignment	not modelled	16.5	32	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
61	c1yq2C	Alignment	not modelled	16.3	20	PDB header: hydrolase Chain: C: PDB Molecule: beta-galactosidase; PDBTitle: beta-galactosidase from arthrobacter sp. c2-2 (isozyme c2-2 2-1)
62	c3h0gl	Alignment	not modelled	16.1	20	PDB header: transcription Chain: I: PDB Molecule: dna-directed rna polymerase ii subunit rpb9; PDBTitle: rna polymerase ii from schizosaccharomyces pombe
63	c3dgvB	Alignment	not modelled	15.8	13	PDB header: hydrolase Chain: B: PDB Molecule: carboxypeptidase b2; PDBTitle: crystal structure of thrombin activatable fibrinolysis inhibitor2 (tafi)
64	c5jysA	Alignment	not modelled	15.7	25	PDB header: transport protein Chain: A: PDB Molecule: protein pry1; PDBTitle: pry1 cap domain
65	c2qv5C	Alignment	not modelled	15.4	75	PDB header: cell cycle Chain: C: PDB Molecule: sfi1p; PDBTitle: crystal structure of sfi1p/cdc31p complex
66	c2aanA	Alignment	not modelled	15.4	21	PDB header: electron transport Chain: A: PDB Molecule: auracyanin a; PDBTitle: auracyanin a: a "blue" copper protein from the green thermophilic2 photosynthetic bacterium, chloroflexus aurantiacus
67	d5mdha1	Alignment	not modelled	15.3	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
68	c3lm3A	Alignment	not modelled	15.3	69	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative glycoside hydrolase/deacetylase2 (bdi_3119) from parabacteroides distasonis at 1.44 a resolution
69	c4n0oC	Alignment	not modelled	15.2	39	PDB header: hydrolase/dna Chain: C: PDB Molecule: replicase polyprotein 1ab; PDBTitle: complex structure of arterivirus nonstructural protein 10 (helicase)2 with dna
70	d1b4ub	Alignment	not modelled	14.9	8	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
71	d1nsaa1	Alignment	not modelled	14.5	21	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Pancreatic carboxypeptidases
72	d1weqa	Alignment	not modelled	14.4	38	Fold: FYVE/PHD zinc finger Superfamily: FYVE/PHD zinc finger Family: PHD domain
73	c6cnbR	Alignment	not modelled	14.4	20	PDB header: transcription/dna Chain: R: PDB Molecule: transcription factor iiib 70 kda subunit,tata-box-binding PDBTitle: yeast rna polymerase iii initial transcribing complex
74	c2wweA	Alignment	not modelled	14.2	19	PDB header: transferase Chain: A: PDB Molecule: phosphoinositide-3-kinase, class 2, gamma polypeptide; PDBTitle: crystal structure of the phox homology domain of human2 phosphoinositide-3-kinase-c2-gamma
75	d1x68a2	Alignment	not modelled	14.2	32	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
76	c3i7mA	Alignment	not modelled	14.2	16	PDB header: hydrolase Chain: A: PDB Molecule: xaa-pro dipeptidase; PDBTitle: n-terminal domain of xaa-pro dipeptidase from lactobacillus brevis.
77	c3nswA	Alignment	not modelled	13.9	24	PDB header: immune system Chain: A: PDB Molecule: excretory-secretory protein 2; PDBTitle: crystal structure of ancylostoma ceylanicum excretory-secretory2 protein 2
78	c4fr9A	Alignment	not modelled	13.7	27	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a blip-like protein (bf1215) from bacteroides2 fragilis nctc 9343 at 1.20 a resolution
79	c5kzxA	Alignment	not modelled	13.7	20	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal alpha-glucosidase; PDBTitle: crystal structure of human gaa
80	d1tuga1	Alignment	not modelled	13.6	16	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
						PDB header: ligase

81	c5hj0C_	Alignment	not modelled	13.5	50	Chain: C; PDB Molecule: kinetochore protein mis18; PDBTitle: crystal structure of mis18 'yippee-like' domain
82	c3topA_	Alignment	not modelled	13.5	24	PDB header: hydrolase/hydrolase inhibitor Chain: A; PDB Molecule: maltase-glucoamylase, intestinal; PDBTitle: crystal structure of the c-terminal subunit of human maltase-2 glucoamylase in complex with acarbose
83	c2boaB_	Alignment	not modelled	13.4	20	PDB header: hydrolase Chain: B; PDB Molecule: carboxypeptidase a4; PDBTitle: human procarboxypeptidase a4.
84	c1wygA_	Alignment	not modelled	12.8	26	PDB header: oxidoreductase Chain: A; PDB Molecule: xanthine dehydrogenase/oxidase; PDBTitle: crystal structure of a rat xanthine dehydrogenase triple mutant2 (c535a, c992r and c1324s)
85	c1loiA_	Alignment	not modelled	12.8	63	PDB header: hydrolase Chain: A; PDB Molecule: cyclic 3',5'-amp specific phosphodiesterase rd1; PDBTitle: n-terminal splice region of rat c-amp phosphodiesterase,2 nmr, 7 structures
86	c3skqA_	Alignment	not modelled	12.7	33	PDB header: metal transport Chain: A; PDB Molecule: mitochondrial distribution and morphology protein 38; PDBTitle: mdm38 is a 14-3-3-like receptor and associates with the protein2 synthesis machinery at the inner mitochondrial membrane
87	c1opmA_	Alignment	not modelled	12.5	18	PDB header: oxidoreductase Chain: A; PDB Molecule: protein (peptidylglycine alpha-hydroxylating PDBTitle: oxidized (cu2+) peptidylglycine alpha-hydroxylating monooxygenase2 (phm) with bound substrate
88	d1nvpd2	Alignment	not modelled	12.4	60	Fold: Transcription factor IIA (TFIIA), beta-barrel domain Superfamily: Transcription factor IIA (TFIIA), beta-barrel domain Family: Transcription factor IIA (TFIIA), beta-barrel domain
89	c4f2eA_	Alignment	not modelled	12.4	6	PDB header: metal transport Chain: A; PDB Molecule: cupa; PDBTitle: crystal structure of the streptococcus pneumoniae d39 copper chaperone2 cupa with cu(i)
90	c2lfvA_	Alignment	not modelled	12.3	35	PDB header: cell cycle Chain: A; PDB Molecule: protein damx; PDBTitle: solution structure of the spor domain from e. coli damx
91	c5a3aA_	Alignment	not modelled	12.3	26	PDB header: transferase Chain: A; PDB Molecule: sir2 family protein; PDBTitle: crystal structure of the adp-ribosylating sirtuin (sirtm)2 from streptococcus pyogenes (apo form)
92	c1h8lA_	Alignment	not modelled	12.2	13	PDB header: carboxypeptidase Chain: A; PDB Molecule: carboxypeptidase gp180 residues 503-882; PDBTitle: duck carboxypeptidase d domain ii in complex with gemsa
93	c3osyA_	Alignment	not modelled	12.1	27	PDB header: hydrolase Chain: A; PDB Molecule: 3c protease; PDBTitle: human enterovirus 71 3c protease
94	d1ee8a3	Alignment	not modelled	12.1	26	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
95	d2j0151	Alignment	not modelled	12.0	11	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein L32p
96	d1dxwa_	Alignment	not modelled	12.0	63	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral proteases
97	c2l0dA_	Alignment	not modelled	11.8	9	PDB header: cell adhesion Chain: A; PDB Molecule: cell surface protein; PDBTitle: solution nmr structure of putative cell surface protein ma_4588 (272-2 376 domain) from methanosarcina acetivorans, northeast structural3 genomics consortium target mvr254a
98	c2rpwX_	Alignment	not modelled	11.7	57	PDB header: transport protein Chain: X; PDB Molecule: 25 meric peptide from v-type proton atpase PDBTitle: structure of a peptide derived from h+-v-atpase subunit a
99	c5i1tA_	Alignment	not modelled	11.7	18	PDB header: hydrolase Chain: A; PDB Molecule: stage ii sporulation protein d; PDBTitle: 2.6 angstrom resolution crystal structure of stage ii sporulation2 protein d (spoid) from clostridium difficile in complex with3 triacetylchitotriose