















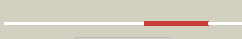







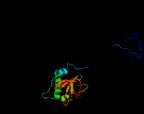

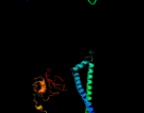






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2190c (-) _2452123_2453280
Date	Mon Aug 5 13:25:31 BST 2019
Unique Job ID	5a9d7358d24a8f46

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6biqA_</a>	 Alignment		100.0	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> clan ca, family c40, nlp/p60 superfamily cysteine <b>PDBTitle:</b> structure of nlp2 from trichomonas vaginalis
2	<a href="#">c2xivA_</a>	 Alignment		100.0	30	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical invasion protein; <b>PDBTitle:</b> structure of rv1477, hypothetical invasion protein of mycobacterium2 tuberculosis
3	<a href="#">c3pb1A_</a>	 Alignment		100.0	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> invasion protein; <b>PDBTitle:</b> structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
4	<a href="#">c2fg0B_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cog0791: cell wall-associated hydrolases (invasion- <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (npun_r0659) from nostoc punctiforme pcc 73102 at 1.793 a resolution
5	<a href="#">c3h41A_</a>	 Alignment		100.0	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60 family protein; <b>PDBTitle:</b> crystal structure of a nlp/p60 family protein (bce_2878) from2 bacillus cereus atcc 10987 at 1.79 a resolution
6	<a href="#">c4fdyA_</a>	 Alignment		100.0	27	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> similar to lipoprotein, nlp/p60 family; <b>PDBTitle:</b> crystal structure of a similar to lipoprotein, nlp/p60 family2 (sav0400) from staphylococcus aureus subsp. aureus mu50 at 2.23 a3 resolution
7	<a href="#">c3qt2A_</a>	 Alignment		100.0	35	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium paratuberculosis2 antigen map1272c
8	<a href="#">d2evra2</a>	 Alignment		100.0	29	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> NlpC/P60
9	<a href="#">c3nfpB_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dipeptidyl-peptidase vi; <b>PDBTitle:</b> crystal structure of a putative dipeptidyl-peptidase vi (bacova_00612)2 from bacteroides ovatus at 1.72 a resolution
10	<a href="#">c3i86A_</a>	 Alignment		100.0	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the p60 domain from m. avium subspecies2 paratuberculosis antigen map1204
11	<a href="#">c4hpeA_</a>	 Alignment		99.9	32	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell wall hydrolase tn916-like.ctn1-orf17; <b>PDBTitle:</b> crystal structure of a putative cell wall hydrolase (cd630_03720) from2 clostridium difficile 630 at 2.38 a resolution

12	<a href="#">c6b8cA</a>	Alignment		99.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> nlp/p60; <b>PDBTitle:</b> crystal structure of nlp/p60 domain of peptidoglycan hydrolase saga
13	<a href="#">c2k1gA</a>	Alignment		99.9	35	<b>PDB header:</b> lipoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> lipoprotein spr; <b>PDBTitle:</b> solution nmr structure of lipoprotein spr from escherichia coli k12.2 northeast structural genomics target er541-37-162
14	<a href="#">c4xcmB</a>	Alignment		99.9	28	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> cell wall-binding endopeptidase-related protein; <b>PDBTitle:</b> crystal structure of the putative nlp/p60 d,l endopeptidase from t.2 thermophilus
15	<a href="#">c3m1uB</a>	Alignment		99.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative gamma-d-glutamyl-l-diamino acid endopeptidase; <b>PDBTitle:</b> crystal structure of a putative gamma-d-glutamyl-l-diamino acid2 endopeptidase (dву_0896) from desulfovibrio vulgaris hildenborough at3 1.75 a resolution
16	<a href="#">c4cgkA</a>	Alignment		99.8	10	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> secreted 45 kda protein; <b>PDBTitle:</b> crystal structure of the essential protein pcsb from streptococcus2 pneumoniae
17	<a href="#">c2p1gA</a>	Alignment		99.1	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative xylanase; <b>PDBTitle:</b> crystal structure of a putative xylanase from bacteroides fragilis
18	<a href="#">c6ewyA</a>	Alignment		98.6	17	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> peptidoglycan endopeptidase ripa; <b>PDBTitle:</b> ripa peptidoglycan hydrolase (rv1477, mycobacterium tuberculosis) n-2 terminal domain
19	<a href="#">c6gaoC</a>	Alignment		98.5	8	<b>PDB header:</b> viral protein <b>Chain:</b> C: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail and body
20	<a href="#">c5cwsJ</a>	Alignment		98.5	10	<b>PDB header:</b> protein transport <b>Chain:</b> J: <b>PDB Molecule:</b> nucleoporin nup49; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
21	<a href="#">c3vkgA</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein motor domain
22	<a href="#">c3ojaB</a>	Alignment	not modelled	98.4	12	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> anopheles plasmodium-responsive leucine-rich repeat protein <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
23	<a href="#">c5ew5C</a>	Alignment	not modelled	98.3	7	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin-e9; <b>PDBTitle:</b> crystal structure of colicin e9 in complex with its immunity protein2 im9
24	<a href="#">c4iloA</a>	Alignment	not modelled	98.3	10	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> ct398; <b>PDBTitle:</b> 2.12a resolution structure of ct398 from chlamydia trachomatis
25	<a href="#">c4l1bB</a>	Alignment	not modelled	98.3	8	<b>PDB header:</b> signaling protein/transferase/inhibitor subunit alpha; <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha complexed with nish2 of p85alpha
26	<a href="#">c3na7A</a>	Alignment	not modelled	98.3	9	<b>PDB header:</b> gene regulation, chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> hp0958; <b>PDBTitle:</b> 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
27	<a href="#">c1bf5A</a>	Alignment	not modelled	98.2	7	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription 1- <b>PDBTitle:</b> tyrosine phosphorylated stat-1/dna complex
28	<a href="#">c3vkgB</a>	Alignment	not modelled	98.1	10	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of an mtbd truncation mutant of dynein

						motor domain
29	<a href="#">c6gapB_</a>	Alignment	not modelled	98.1	8	<b>PDB header:</b> viral protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t3d reovirus sigma1 coiled coil tail and body
30	<a href="#">c2efrB_</a>	Alignment	not modelled	98.0	14	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal tropomyosin fragment with n- and 2 c-terminal extensions of the leucine zipper at 1.8 angstroms3 resolution
31	<a href="#">c6o7xa_</a>	Alignment	not modelled	98.0	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a; <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3
32	<a href="#">c1bg1A_</a>	Alignment	not modelled	98.0	4	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> protein (transcription factor stat3b); <b>PDBTitle:</b> transcription factor stat3b/dna complex
33	<a href="#">c3ojaA_</a>	Alignment	not modelled	98.0	12	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> leucine-rich immune molecule 1; <b>PDBTitle:</b> crystal structure of lrim1/apl1c complex
34	<a href="#">c5xg2A_</a>	Alignment	not modelled	98.0	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc; <b>PDBTitle:</b> crystal structure of a coiled-coil segment (residues 345-468 and 694-2 814) of pyrococcus yayanosii smc
35	<a href="#">c6o7ua_</a>	Alignment	not modelled	98.0	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> <b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo
36	<a href="#">c5ijnF_</a>	Alignment	not modelled	97.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> nuclear pore complex protein nup54; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
37	<a href="#">c2kvtA_</a>	Alignment	not modelled	97.9	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> group xvi phospholipase a2; <b>PDBTitle:</b> solution structure of the h-rev107 n-terminal domain
38	<a href="#">c5j1iA_</a>	Alignment	not modelled	97.9	8	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> plectin; <b>PDBTitle:</b> structure of the spectrin repeats 7, 8, and 9 of the plakin domain of2 plectin
39	<a href="#">c3cwgA_</a>	Alignment	not modelled	97.8	5	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> unphosphorylated mouse stat3 core fragment
40	<a href="#">c4gkwB_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> spindle assembly abnormal protein 6; <b>PDBTitle:</b> crystal structure of the coiled-coil domain of c. elegans sas-6
41	<a href="#">c6fnE_</a>	Alignment	not modelled	97.8	8	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> e3 ubiquitin/isp15 ligase trim25; <b>PDBTitle:</b> crystal structure of the human trim25 coiled-coil and pryspry domains
42	<a href="#">c5cwsE_</a>	Alignment	not modelled	97.8	15	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> nucleoporin nup57; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
43	<a href="#">c1ciiA_</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> transmembrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia; <b>PDBTitle:</b> colicin ia
44	<a href="#">c6gajA_</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer capsid protein sigma-1; <b>PDBTitle:</b> crystal structure of the t1l reovirus sigma1 coiled coil tail (iodide)
45	<a href="#">c4rh7A_</a>	Alignment	not modelled	97.7	15	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> green fluorescent protein/cytoplasmic dynein 2 heavy chain <b>PDBTitle:</b> crystal structure of human cytoplasmic dynein 2 motor domain in2 complex with adp.vi
46	<a href="#">c5dfzD_</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 30; <b>PDBTitle:</b> structure of vps34 complex ii from s. cerevisiae.
47	<a href="#">c5goxB_</a>	Alignment	not modelled	97.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dna repair protein rad50; <b>PDBTitle:</b> eukaryotic rad50 functions as a rod-shaped dimer
48	<a href="#">c1jchC_</a>	Alignment	not modelled	97.6	13	<b>PDB header:</b> ribosome inhibitor, hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> colicin e3; <b>PDBTitle:</b> crystal structure of colicin e3 in complex with its immunity protein
49	<a href="#">c2lktA_</a>	Alignment	not modelled	97.6	31	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> retinoic acid receptor responder protein 3; <b>PDBTitle:</b> solution structure of n-terminal domain of human tig3 in 2 m urea
50	<a href="#">c5cwsC_</a>	Alignment	not modelled	97.6	9	<b>PDB header:</b> protein transport <b>Chain:</b> C: <b>PDB Molecule:</b> nucleoporin nsp1; <b>PDBTitle:</b> crystal structure of the intact chaetomium thermophilum nsp1-nup49-2 nup57 channel nucleoporin heterotrimer bound to its nic96 nuclear3 pore complex attachment site
51	<a href="#">c2oevA_</a>	Alignment	not modelled	97.6	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death 6-interacting protein; <b>PDBTitle:</b> crystal structure of alix/aip1
52	<a href="#">c4xa3A_</a>	Alignment	not modelled	97.5	12	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> gp7-myh7(1361-1425)-eb1 chimera protein; <b>PDBTitle:</b> crystal structure of the coiled-coil surrounding skip 2 of myh7
						<b>PDB header:</b> motor protein <b>Chain:</b> X: <b>PDB Molecule:</b> bicd family-like cargo adapter 1,bicd

53	<a href="#">c6f1tX</a>	Alignment	not modelled	97.5	7	family-like cargo <b>PDBTitle:</b> cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
54	<a href="#">c2d3eD</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> contractile protein <b>Chain:</b> D: <b>PDB Molecule:</b> general control protein gcn4 and tropomyosin 1 alpha chain; <b>PDBTitle:</b> crystal structure of the c-terminal fragment of rabbit skeletal alpha-2 tropomyosin
55	<a href="#">c2i1kA</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> cell adhesion, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> moesin; <b>PDBTitle:</b> moesin from spodoptera frugiperda reveals the coiled-coil domain at2 3.0 angstrom resolution
56	<a href="#">c6f1tx</a>	Alignment	not modelled	97.5	7	<b>PDB header:</b> motor protein <b>Chain:</b> X: <b>PDB Molecule:</b> bicd family-like cargo adapter 1,bicd family-like cargo <b>PDBTitle:</b> cryo-em structure of two dynein tail domains bound to dynactin and2 bicdr1
57	<a href="#">c1yv1B</a>	Alignment	not modelled	97.5	6	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription <b>PDBTitle:</b> structure of unphosphorylated stat1
58	<a href="#">c3o0zD</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> rho-associated protein kinase 1; <b>PDBTitle:</b> crystal structure of a coiled-coil domain from human rock i
59	<a href="#">c5t1qB</a>	Alignment	not modelled	97.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> n-acetylmuramoyl-l-alanine amidase domain-containing <b>PDBTitle:</b> 2.15 angstrom crystal structure of n-acetylmuramoyl-l-alanine amidase2 from staphylococcus aureus.
60	<a href="#">c1c1qA</a>	Alignment	not modelled	97.4	11	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> tropomyosin; <b>PDBTitle:</b> crystal structure of tropomyosin at 7 angstroms resolution in the2 spermium-induced crystal form
61	<a href="#">c6mi3A</a>	Alignment	not modelled	97.4	13	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kb essential modulator,nf-kappa-b essential modulator, <b>PDBTitle:</b> structure of nemo(51-112) with n- and c-terminal coiled-coil adaptors.
62	<a href="#">c3hizB</a>	Alignment	not modelled	97.4	8	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha h1047r mutant in complex with nish2 of2 p85alpha
63	<a href="#">c5y06A</a>	Alignment	not modelled	97.3	9	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> msmeg_4306; <b>PDBTitle:</b> structural characterization of msmeg_4306 from mycobacterium smegmatis
64	<a href="#">c6ogdB</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> toxin <b>Chain:</b> B: <b>PDB Molecule:</b> toxin subunit yena2; <b>PDBTitle:</b> cryo-em structure of yentca in its prepore state
65	<a href="#">c4a7fB</a>	Alignment	not modelled	97.3	10	<b>PDB header:</b> structural protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> tropomyosin 1 alpha; <b>PDBTitle:</b> structure of the actin-tropomyosin-myosin complex (rigor atm 3)
66	<a href="#">c3kw0D</a>	Alignment	not modelled	97.3	33	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> cysteine peptidase; <b>PDBTitle:</b> crystal structure of cysteine peptidase (np_982244.1) from bacillus2 cereus atcc 10987 at 2.50 a resolution
67	<a href="#">c5nmoA</a>	Alignment	not modelled	97.3	9	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein smc,chromosome partition <b>PDBTitle:</b> structure of the bacillus subtilis smc joint domain
68	<a href="#">c5gasN</a>	Alignment	not modelled	97.3	9	<b>PDB header:</b> hydrolase <b>Chain:</b> N: <b>PDB Molecule:</b> archaeal/vacuolar-type h+-atpase subunit i; <b>PDBTitle:</b> thermus thermophilus v/a-atpase, conformation 2
69	<a href="#">c5voxb</a>	Alignment	not modelled	97.3	8	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> v-type proton atpase subunit b; <b>PDBTitle:</b> yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)
70	<a href="#">c2v71A</a>	Alignment	not modelled	97.2	16	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear distribution protein nude-like 1; <b>PDBTitle:</b> coiled-coil region of nudel
71	<a href="#">c1ei3E</a>	Alignment	not modelled	97.2	7	<b>PDB header:</b> blood clotting <b>Chain:</b> E: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
72	<a href="#">c1ei3C</a>	Alignment	not modelled	97.2	7	<b>PDB header:</b> blood clotting <b>Chain:</b> C: <b>PDB Molecule:</b> fibrinogen; <b>PDBTitle:</b> crystal structure of native chicken fibrinogen
73	<a href="#">c4cg4D</a>	Alignment	not modelled	97.2	9	<b>PDB header:</b> actin-binding protein <b>Chain:</b> D: <b>PDB Molecule:</b> pyrin; <b>PDBTitle:</b> crystal structure of the chs-b30.2 domains of trim20
74	<a href="#">c2lrjA</a>	Alignment	not modelled	97.2	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> staphyloxanthin biosynthesis protein, putative; <b>PDBTitle:</b> nmr solution structure of staphyloxanthin biosynthesis protein
75	<a href="#">c3ghgl</a>	Alignment	not modelled	97.2	10	<b>PDB header:</b> blood clotting <b>Chain:</b> I: <b>PDB Molecule:</b> fibrinogen gamma chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
76	<a href="#">c4a55B</a>	Alignment	not modelled	97.1	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> crystal structure of p110alpha in complex with ish2 of p85alpha and2 the inhibitor pik-108
77	<a href="#">c3hnwB</a>	Alignment	not modelled	97.1	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a basic coiled-coil protein of unknown

						function2 from eubacterium eligens atcc 27750
78	<a href="#">c2k3aA</a>	Alignment	not modelled	97.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> chap domain protein; <b>PDBTitle:</b> nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11
79	<a href="#">c1deqO</a>	Alignment	not modelled	97.1	4	<b>PDB header:</b> blood clotting <b>Chain:</b> O: <b>PDB Molecule:</b> fibrinogen (beta chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
80	<a href="#">c3ghgK</a>	Alignment	not modelled	97.0	3	<b>PDB header:</b> blood clotting <b>Chain:</b> K: <b>PDB Molecule:</b> fibrinogen beta chain; <b>PDBTitle:</b> crystal structure of human fibrinogen
81	<a href="#">c5oenB</a>	Alignment	not modelled	97.0	5	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> signal transducer and activator of transcription; <b>PDBTitle:</b> crystal structure of stat2 in complex with irf9
82	<a href="#">c5wjbA</a>	Alignment	not modelled	97.0	13	<b>PDB header:</b> actin/dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> capsid assembly scaffolding protein,myosin-7; <b>PDBTitle:</b> crystal structure of amino acids 1733-1797 of human beta cardiac2 myosin fused to gp7
83	<a href="#">c5nnvD</a>	Alignment	not modelled	97.0	7	<b>PDB header:</b> cell cycle <b>Chain:</b> D: <b>PDB Molecule:</b> chromosome partition protein smc,chromosome partition <b>PDBTitle:</b> structure of a bacillus subtilis smc coiled coil middle fragment
84	<a href="#">c3q8tB</a>	Alignment	not modelled	97.0	7	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> beclin-1; <b>PDBTitle:</b> crystal structure of the coiled coil domain of beclin 1, an essential2 autophagy protein
85	<a href="#">c1y4cA</a>	Alignment	not modelled	97.0	12	<b>PDB header:</b> de novo protein <b>Chain:</b> A: <b>PDB Molecule:</b> maltose binding protein fused with designed <b>PDBTitle:</b> designed helical protein fusion mbp
86	<a href="#">c1f5nA</a>	Alignment	not modelled	96.9	6	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> interferon-induced guanylate-binding protein 1; <b>PDBTitle:</b> human guanylate binding protein-1 in complex with the gtp analogue,2 gmppnp.
87	<a href="#">c5nugB</a>	Alignment	not modelled	96.9	17	<b>PDB header:</b> motor protein <b>Chain:</b> B: <b>PDB Molecule:</b> cytoplasmic dynein 1 heavy chain 1; <b>PDBTitle:</b> motor domains from human cytoplasmic dynein-1 in the phi-particle2 conformation
88	<a href="#">c6ec0A</a>	Alignment	not modelled	96.9	6	<b>PDB header:</b> protein fibril <b>Chain:</b> A: <b>PDB Molecule:</b> keratin 1; <b>PDBTitle:</b> crystal structure of the wild-type heterocomplex between coil 1b2 domains of human intermediate filament proteins keratin 1 (krt1) and3 keratin 10 (krt10)
89	<a href="#">c6h2xA</a>	Alignment	not modelled	96.9	10	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> chromosome partition protein mukb,chromosome partition <b>PDBTitle:</b> mukb coiled-coil elbow from e. coli
90	<a href="#">c3dtpA</a>	Alignment	not modelled	96.8	14	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain chimera of smooth and cardiac muscle; <b>PDBTitle:</b> tarantula heavy meromyosin obtained by flexible docking to tarantula2 muscle thick filament cryo-em 3d-map
91	<a href="#">c6a9pD</a>	Alignment	not modelled	96.8	11	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> glial fibrillary acidic protein; <b>PDBTitle:</b> crystal structure of the human glial fibrillary acidic protein 1b2 domain
92	<a href="#">c3l9oA</a>	Alignment	not modelled	96.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dob1; <b>PDBTitle:</b> crystal structure of mtr4, a co-factor of the nuclear exosome
93	<a href="#">c3vkhA</a>	Alignment	not modelled	96.7	15	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> dynein heavy chain, cytoplasmic; <b>PDBTitle:</b> x-ray structure of a functional full-length dynein motor domain
94	<a href="#">c4lI8E</a>	Alignment	not modelled	96.7	8	<b>PDB header:</b> motor protein/transport protein <b>Chain:</b> E: <b>PDB Molecule:</b> swi5-dependent ho expression protein 3; <b>PDBTitle:</b> complex of carboxy terminal domain of myo4p and she3p middle fragment
95	<a href="#">c6e2jB</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> protein fibril <b>Chain:</b> B: <b>PDB Molecule:</b> keratin, type i cytoskeletal 10; <b>PDBTitle:</b> crystal structure of the heterocomplex between human keratin 1 coil 1b2 containing s233l mutation and wild-type human keratin 10 coil 1b
96	<a href="#">c2fxmB</a>	Alignment	not modelled	96.6	9	<b>PDB header:</b> contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> myosin heavy chain, cardiac muscle beta isoform; <b>PDBTitle:</b> structure of the human beta-myosin s2 fragment
97	<a href="#">c4hzba</a>	Alignment	not modelled	96.6	28	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cytoplasmic protein; <b>PDBTitle:</b> crystal structure of the type vi semet effector-immunity complex tae3-2 tai3 from ralstonia pickettii
98	<a href="#">c3wuqA</a>	Alignment	not modelled	96.6	10	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic dynein 1 heavy chain 1; <b>PDBTitle:</b> structure of the entire stalk region of the dynein motor domain
99	<a href="#">c2v1yB</a>	Alignment	not modelled	96.5	9	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> structure of a phosphoinositide 3-kinase alpha adaptor-2 binding domain (abd) in a complex with the ish2 domain3 from p85 alpha
100	<a href="#">c3u59C</a>	Alignment	not modelled	96.5	8	<b>PDB header:</b> contractile protein <b>Chain:</b> C: <b>PDB Molecule:</b> tropomyosin beta chain; <b>PDBTitle:</b> n-terminal 98-aa fragment of smooth muscle tropomyosin beta

101	<a href="#">c2b9cA_</a>	Alignment	not modelled	96.5	9	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> striated-muscle alpha tropomyosin; <b>PDBTitle:</b> structure of tropomyosin's mid-region: bending and binding sites for 2 actin
102	<a href="#">c6djlE_</a>	Alignment	not modelled	96.4	9	<b>PDB header:</b> signaling protein/protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> sh3 domain-binding protein 5; <b>PDBTitle:</b> crystal structure of the rab11 gef sh3bp5 bound to nucleotide free2 rab11a
103	<a href="#">c4zryA_</a>	Alignment	not modelled	96.4	6	<b>PDB header:</b> protein fibril <b>Chain:</b> A: <b>PDB Molecule:</b> keratin, type i cytoskeletal 10; <b>PDBTitle:</b> crystal structure of the heterocomplex between coil 2b domains of 2 human intermediate filament proteins keratin 1 (krt1) and keratin 103 (krt10)
104	<a href="#">c3ol1A_</a>	Alignment	not modelled	96.4	9	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> vimentin; <b>PDBTitle:</b> crystal structure of vimentin (fragment 144-251) from homo sapiens, 2 northeast structural genomics consortium target hr4796b
105	<a href="#">c5ijnT_</a>	Alignment	not modelled	96.4	10	<b>PDB header:</b> transport protein <b>Chain:</b> T: <b>PDB Molecule:</b> nuclear pore glycoprotein p62; <b>PDBTitle:</b> composite structure of the inner ring of the human nuclear pore2 complex (32 copies of nup205)
106	<a href="#">c1deqF_</a>	Alignment	not modelled	96.3	6	<b>PDB header:</b> blood clotting <b>Chain:</b> F: <b>PDB Molecule:</b> fibrinogen (gamma chain); <b>PDBTitle:</b> the crystal structure of modified bovine fibrinogen (at ~42 angstrom resolution)
107	<a href="#">c5udmA_</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phage-associated cell wall hydrolase; <b>PDBTitle:</b> phage-associated cell wall hydrolase plypy from streptococcus2 pyogenes, space group p6522
108	<a href="#">c4olkB_</a>	Alignment	not modelled	96.2	14	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> endolysin; <b>PDBTitle:</b> the chap domain of lysgh15
109	<a href="#">c5oi7A_</a>	Alignment	not modelled	96.2	8	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> centrosomal protein of 85 kda; <b>PDBTitle:</b> human cep85 - coiled coil domain 4
110	<a href="#">c4rsiB_</a>	Alignment	not modelled	96.1	5	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> structural maintenance of chromosomes protein 4; <b>PDBTitle:</b> yeast smc2-smc4 hinge domain with extended coiled coils
111	<a href="#">c6ianA_</a>	Alignment	not modelled	96.0	9	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> intraflagellar transport protein 74; <b>PDBTitle:</b> t. brucei ift22/74/81 gtp-bound crystal structure
112	<a href="#">c3ipkA_</a>	Alignment	not modelled	95.9	20	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> agi/ii; <b>PDBTitle:</b> crystal structure of a3vp1 of agi/ii of streptococcus mutans
113	<a href="#">c3jbhA_</a>	Alignment	not modelled	95.8	15	<b>PDB header:</b> contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> myosin 2 heavy chain striated muscle; <b>PDBTitle:</b> two heavy meromyosin interacting-heads motifs flexible docked into 2 tarantula thick filament 3d-map allows in depth study of intra- and 3 intermolecular interactions
114	<a href="#">c2gl2B_</a>	Alignment	not modelled	95.8	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> adhesion a; <b>PDBTitle:</b> crystal structure of the tetra mutant (t66g,r67g,f68g,y69g) of 2 bacterial adhesin fada
115	<a href="#">c5bu8A_</a>	Alignment	not modelled	95.8	13	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna stabilization protein; <b>PDBTitle:</b> hk620 tail needle crystallized at ph 7.5 and derivatized with xenon
116	<a href="#">d2if6a1</a>	Alignment	not modelled	95.8	24	<b>Fold:</b> Cysteine proteinases <b>Superfamily:</b> Cysteine proteinases <b>Family:</b> Yiix-like
117	<a href="#">c3g67A_</a>	Alignment	not modelled	95.7	8	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> methyl-accepting chemotaxis protein; <b>PDBTitle:</b> crystal structure of a soluble chemoreceptor from thermotoga2 maritima
118	<a href="#">c2ocyB_</a>	Alignment	not modelled	95.7	9	<b>PDB header:</b> endocytosis/exocytosis <b>Chain:</b> B: <b>PDB Molecule:</b> rab guanine nucleotide exchange factor sec2; <b>PDBTitle:</b> complex of the guanine exchange factor sec2p and the rab gtpase sec4p
119	<a href="#">c3wolB_</a>	Alignment	not modelled	95.6	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> dipeptidyl aminopeptidase bii; <b>PDBTitle:</b> crystal structure of the dap bii dipeptide complex i
120	<a href="#">c2rd0B_</a>	Alignment	not modelled	95.6	7	<b>PDB header:</b> transferase/oncoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> phosphatidylinositol 3-kinase regulatory subunit alpha; <b>PDBTitle:</b> structure of a human p110alpha/p85alpha complex