

# Class 09

## AUTHOR

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## The PDB database

```
library(readr)

stats <- read_csv("Data Export Summary.csv")
```

Rows: 6 Columns: 9  
 — Column specification —————  
 Delimiter: ","  
 chr (1): Molecular Type  
 dbl (4): Integrative, Multiple methods, Neutron, Other  
 num (4): X-ray, EM, NMR, Total

**i** Use `spec()` to retrieve the full column specification for this data.  
**i** Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

```
stats
```

Molecular Type	X-ray	EM	NMR	Integrative	Multiple methods	Neutron
<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1 Protein (only)	176378	20438	12709	342	221	83
2 Protein/Oligosacch..	10284	3396	34	8	11	1
3 Protein/NA	9007	5931	287	24	7	0
4 Nucleic acid (only)	3077	200	1554	2	15	3
5 Other	174	13	33	3	0	0
6 Oligosaccharide (o...	11	0	6	0	1	0

# i 2 more variables: Other <dbl>, Total <dbl>

Q1: What percentage of structures in the PDB are solved by X-Ray and Electron Microscopy.

```
Xray <- sum( stats$`X-ray` )
EM <- sum(stats$EM)
Total <- sum( stats$Total)

(Xray/Total)*100
```

[1] 81.43231

```
(EM/Total)*100
```

```
[1] 12.27148
```

```
((Xray+EM)/Total)*100
```

```
[1] 93.70379
```

Q2: What proportion of structures in the PDB are protein?

```
protein <- sum(stats[1, 2:(ncol(stats) - 1)])
```

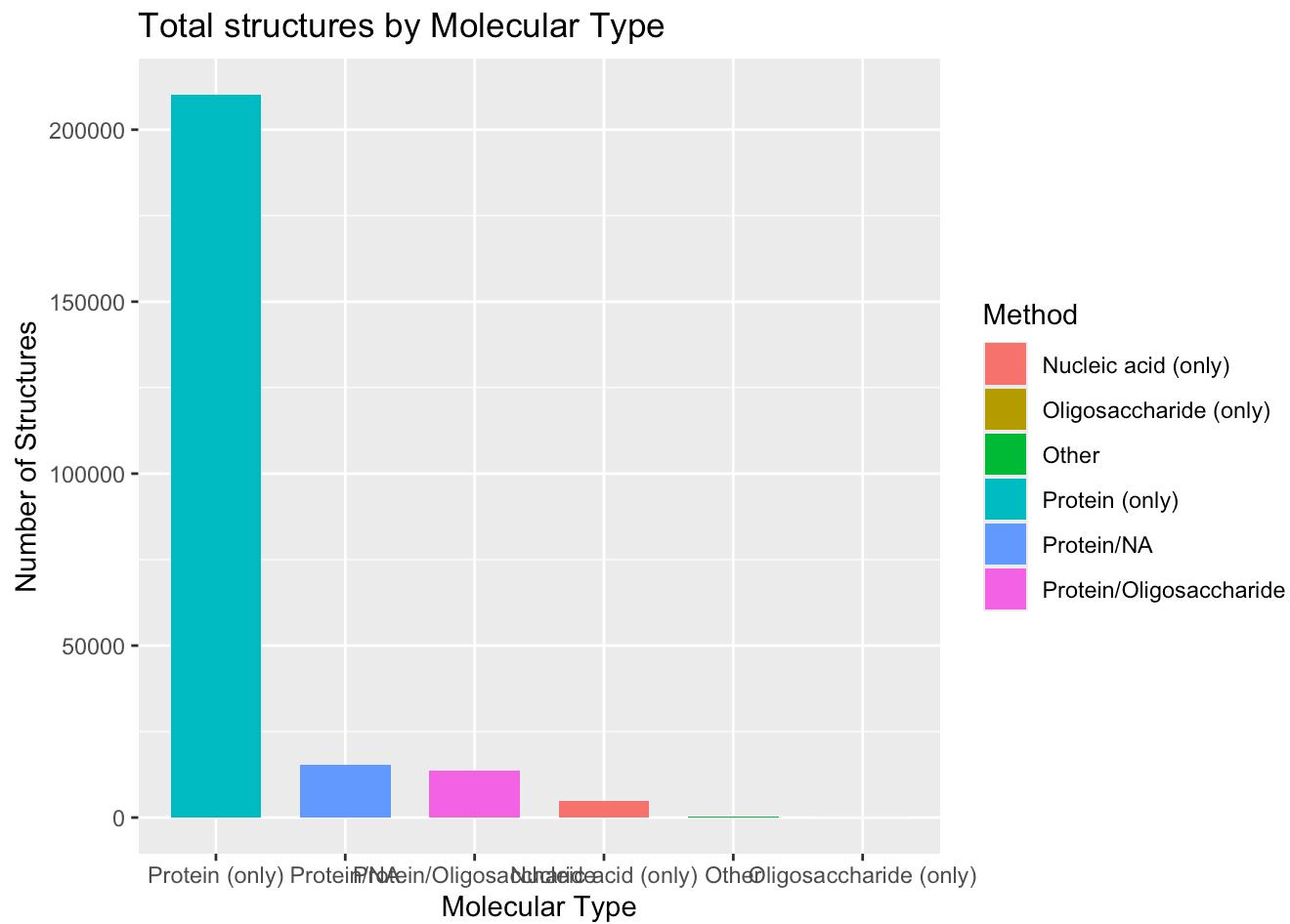
```
protein/Total
```

```
[1] 0.860465
```

Make a bar plot overview.

```
library(ggplot2)

ggplot(stats) +
  aes(x = reorder(`Molecular Type`, -Total), y = Total, fill = `Molecular Type`) +
  geom_col(width = 0.7) +
  labs(
    title = "Total structures by Molecular Type",
    x = "Molecular Type",
    y = "Number of Structures",
    fill = "Method")
```



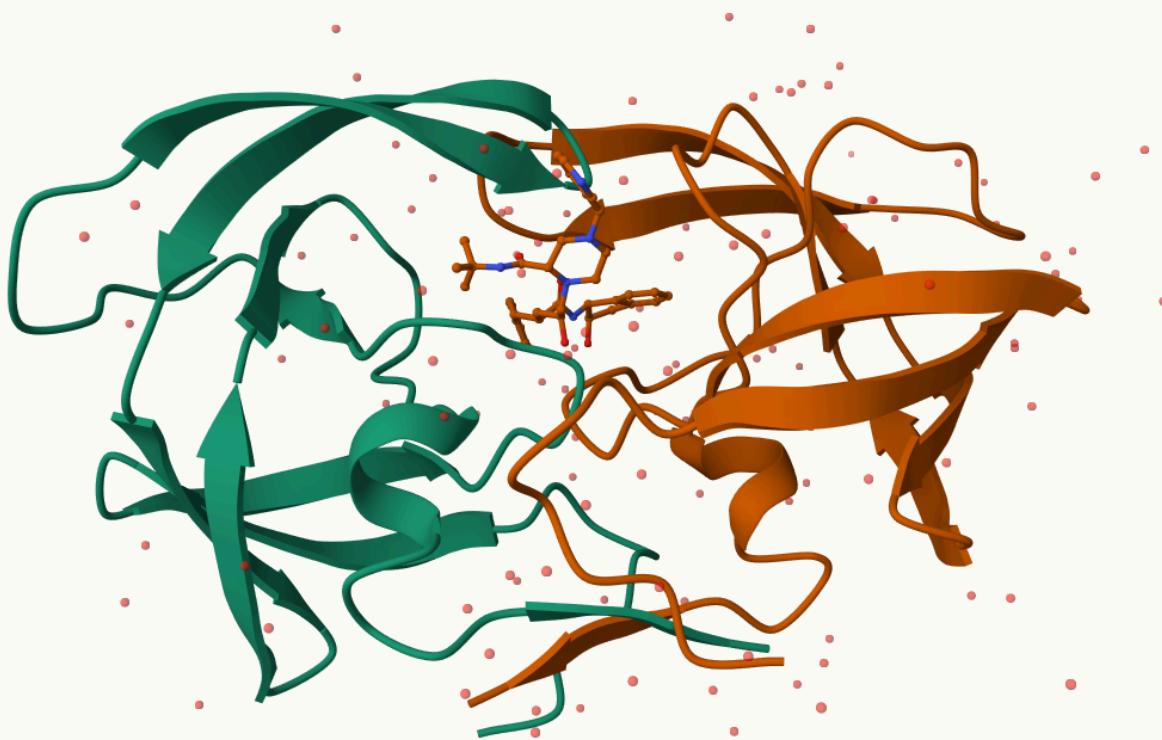
Q3: Type HIV in the PDB website search box on the home page and determine how many HIV-1 protease structures are in the current PDB?

There are currently 2,406 hits for HIV-1 protease structures

## Visualizing structure data

The Mol\* viewer is embedded in many bioinformatics website. The homepage is <https://molstar.org/>

I can insert any figure or image file using markdown format



The HIV-Pr dimer with bound inhibitor

## Bio3D package for structural bioinformatics

We can use the bio3d package to read and analyze biomolecular data in R

```
library(bio3d)  
  
hiv <- read.pdb("1hsg")
```

Note: Accessing on-line PDB file

```
hiv
```

Call: read.pdb(file = "1hsg")

Total Models#: 1  
Total Atoms#: 1686, XYZs#: 5058 Chains#: 2 (values: A B)

Protein Atoms#: 1514 (residues/Calpha atoms#: 198)

Nucleic acid Atoms#: 0 (residues/phosphate atoms#: 0)

Non-protein/nucleic Atoms#: 172 (residues: 128)

Non-protein/nucleic resid values: [ HOH (127), MK1 (1) ]

Protein sequence:

```
PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGGFIKVRQYD  
QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE  
ALLDTGADDTVLEEMSLPGRWKPKMIGGIGGGFIKVRQYDQILIEICGHKAIGTVLVGPTP  
VNIIGRNLLTQIGCTLNF
```

+ attr: atom, xyz, seqres, helix, sheet,  
calpha, remark, call

```
head(hiv$atom)
```

	type	eleno	elety	alt	resid	chain	resno	insert	x	y	z	o	b
1	ATOM	1	N	<NA>	PRO	A	1	<NA>	29.361	39.686	5.862	1	38.10
2	ATOM	2	CA	<NA>	PRO	A	1	<NA>	30.307	38.663	5.319	1	40.62
3	ATOM	3	C	<NA>	PRO	A	1	<NA>	29.760	38.071	4.022	1	42.64
4	ATOM	4	O	<NA>	PRO	A	1	<NA>	28.600	38.302	3.676	1	43.40
5	ATOM	5	CB	<NA>	PRO	A	1	<NA>	30.508	37.541	6.342	1	37.87
6	ATOM	6	CG	<NA>	PRO	A	1	<NA>	29.296	37.591	7.162	1	38.40
	segid	elesy	charge										
1	<NA>	N	<NA>										
2	<NA>	C	<NA>										
3	<NA>	C	<NA>										
4	<NA>	O	<NA>										
5	<NA>	C	<NA>										
6	<NA>	C	<NA>										

Let's get the sequence

```
pdbseq(hiv)
```

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
"P"	"Q"	"I"	"T"	"L"	"W"	"Q"	"R"	"P"	"L"	"V"	"T"	"I"	"K"	"I"	"G"	"G"	"Q"	"L"	"K"
21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
"E"	"A"	"L"	"L"	"D"	"T"	"G"	"A"	"D"	"D"	"T"	"V"	"L"	"E"	"E"	"M"	"S"	"L"	"P"	"G"
41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60
"R"	"W"	"K"	"P"	"K"	"M"	"I"	"G"	"G"	"I"	"G"	"G"	"F"	"I"	"K"	"V"	"R"	"Q"	"Y"	"D"
61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80
"Q"	"I"	"L"	"I"	"E"	"I"	"C"	"G"	"H"	"K"	"A"	"I"	"G"	"T"	"V"	"L"	"V"	"G"	"P"	"T"
81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	1
"P"	"V"	"N"	"I"	"I"	"G"	"R"	"N"	"L"	"L"	"T"	"Q"	"I"	"G"	"C"	"T"	"L"	"N"	"F"	"P"
2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
"Q"	"I"	"T"	"L"	"W"	"Q"	"R"	"P"	"L"	"V"	"T"	"I"	"K"	"I"	"G"	"G"	"Q"	"L"	"K"	"E"
22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41
"A"	"L"	"L"	"D"	"T"	"G"	"A"	"D"	"D"	"T"	"V"	"L"	"E"	"E"	"M"	"S"	"L"	"P"	"G"	"R"
42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61

```
"W" "K" "P" "K" "M" "I" "G" "G" "I" "G" "G" "F" "I" "K" "V" "R" "Q" "Y" "D" "Q"
 62  63  64  65  66  67  68  69  70  71  72  73  74  75  76  77  78  79  80  81
"I" "L" "I" "E" "I" "C" "G" "H" "K" "A" "I" "G" "T" "V" "L" "V" "G" "P" "T" "P"
 82  83  84  85  86  87  88  89  90  91  92  93  94  95  96  97  98  99
"V" "N" "I" "I" "G" "R" "N" "L" "L" "T" "Q" "I" "G" "C" "T" "L" "N" "F"
```

Let's trim to chain A and just get it's sequence:

```
chainA<-trim.pdb(hiv, chain="A")
chainA.seq <-pdbseq(chainA)
```

Let's blast

```
blast <- blast.pdb(chainA.seq)
```

Searching ... please wait (updates every 5 seconds) RID = G55V7DB6014

.....  
Reporting 249 hits

```
head(blast$hit.tbl)
```

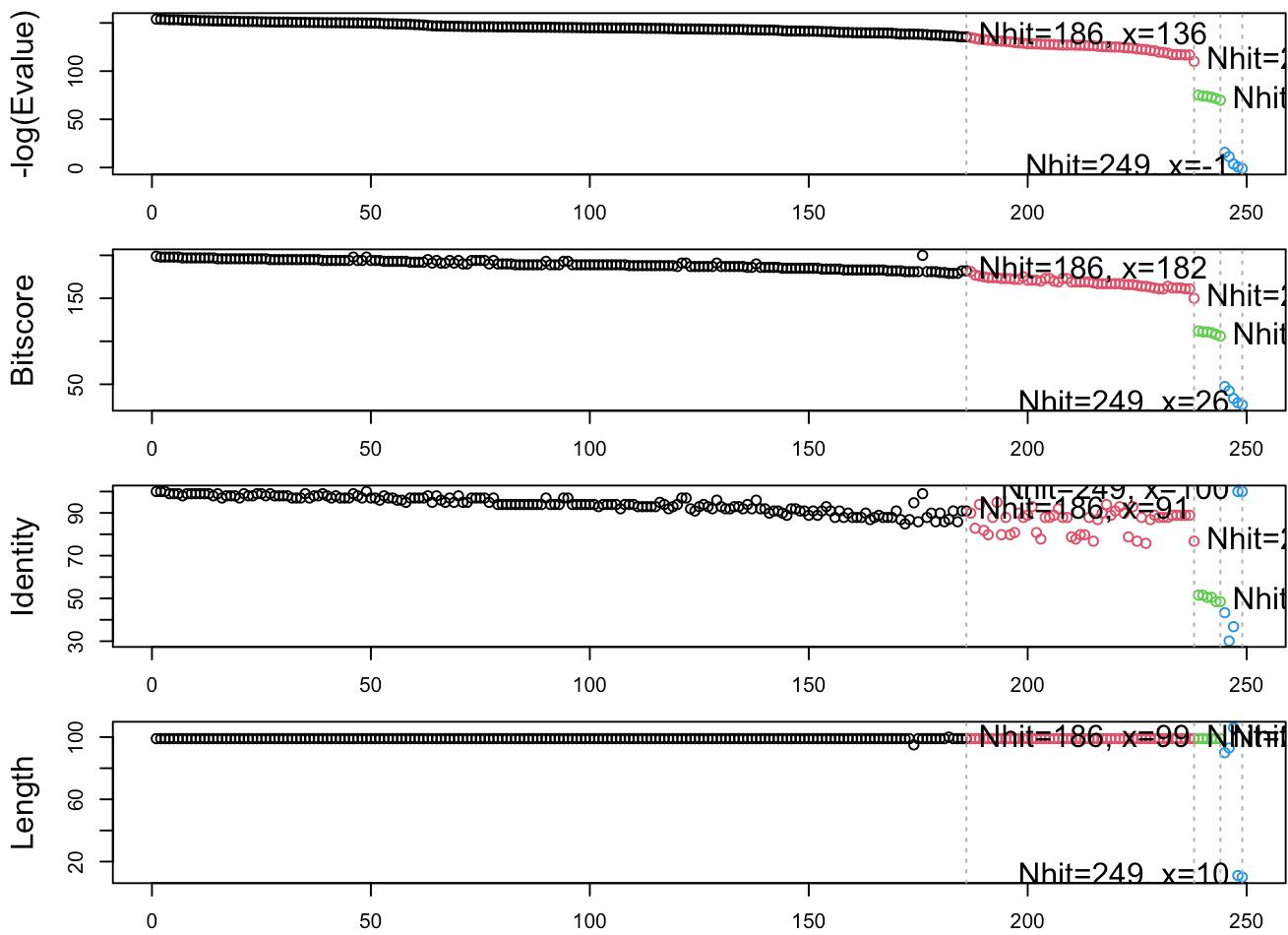
	queryid	subjectids	identity	alignmentlength	mismatches	gapopens	q.start		
1	Query_7131335	1W5V_A	100.00		99	0	0		
2	Query_7131335	2FDE_A	100.00		99	0	0		
3	Query_7131335	1AJV_A	100.00		99	0	0		
4	Query_7131335	2R38_A	98.99		99	1	0		
5	Query_7131335	2R3T_A	98.99		99	1	0		
6	Query_7131335	1HXB_A	98.99		99	1	0		
	q.end	s.start	s.end	evalue	bitscore	positives	mlog.evalue	pdb.id	acc
1	99	12	110	1.38e-67	199	100	153.9511	1W5V_A	1W5V_A
2	99	2	100	1.70e-67	198	100	153.7426	2FDE_A	2FDE_A
3	99	1	99	1.99e-67	198	100	153.5851	1AJV_A	1AJV_A
4	99	1	99	2.50e-67	198	100	153.3569	2R38_A	2R38_A
5	99	1	99	2.50e-67	198	100	153.3569	2R3T_A	2R3T_A
6	99	1	99	2.50e-67	198	100	153.3569	1HXB_A	1HXB_A

Plot a quick overview of blast results

```
hits <- plot(blast)
```

```
* Possible cutoff values: 135 110 69 -2
Yielding Nhits: 186 238 244 249

* Chosen cutoff value of: 69
Yielding Nhits: 244
```



```
hits$pdb.id
```

```
[1] "1W5V_A" "2FDE_A" "1AJV_A" "2R38_A" "2R3T_A" "1HXB_A" "1BV9_A" "1AAQ_A"
[9] "1AXA_A" "1HVS_A" "1ZP8_A" "2QHC_A" "1A8G_A" "204L_A" "5C0K_A" "1TCX_A"
[17] "2Z54_A" "1D4S_A" "1BV7_A" "1BWA_A" "1A9M_A" "2FLE_A" "10DY_A" "1GNN_A"
[25] "1GNM_A" "5YRS_B" "1HEF_E" "10DX_A" "4QGT_A" "1BVE_A" "2AZ8_A" "1A30_A"
[33] "6DH6_A" "6DH0_A" "2I4D_A" "600S_A" "1RL8_A" "5YRS_A" "1ZSF_A" "2Q64_A"
[41] "6DH3_A" "2NPH_A" "2Q63_A" "1LZQ_A" "1FB7_A" "1G6L_A" "1HIV_A" "600U_A"
[49] "1HVC_A" "2I4V_A" "2AZ9_A" "600T_A" "2P3B_B" "5KAO_A" "2WL0_A" "60PT_A"
[57] "1IZI_A" "1MRX_A" "2PYM_A" "2PYN_A" "1DMP_A" "4K4P_A" "1LV1_A" "1AID_A"
[65] "1LV1_A" "1ZBG_A" "3TKG_A" "1HVC_A" "5Y0K_A" "1G6L_A" "1FGC_C" "3K4V_A"
[73] "3KT5_A" "3KT5_A" "4QLH_A" "4QLH_A" "2F3K_A" "4Q5M_A" "2A0C_A" "3B80_A"
[81] "3VF5_A" "2AVQ_A" "1DW6_C" "1KZK_A" "2HS1_A" "1K6C_A" "1MTB_A" "4Q1X_A"
[89] "4Q1W_A" "4Q5M_A" "3D1X_A" "2AVM_A" "3PWM_A" "3KT2_A" "3KT2_A" "1SDV_A"
[97] "3JWV_A" "30Y4_A" "1A94_A" "2HS2_A" "4EJ8_A" "2FGU_A" "2AVV_A" "3JW2_A"
[105] "3BVA_A" "1FFF_C" "3S43_B" "2NXD_A" "1FG6_C" "1EBK_C" "4Q1Y_A" "3EL4_A"
[113] "1F7A_A" "1K2B_A" "2FGV_A" "1Z8C_A" "2G69_A" "3EL9_A" "30XV_A" "1BDR_A"
[121] "3N3I_A" "3N3I_A" "30XW_A" "3S43_A" "3EM3_A" "3CYW_A" "5KQX_A" "2B60_A"
[129] "7D0Z_A" "1K2C_A" "1MT7_A" "3EM4_A" "4QJ9_A" "1BDL_A" "3LZS_A" "5T84_A"
[137] "4DQB_A" "7D0Z_A" "4QJ2_A" "3LZV_A" "1SGU_A" "2FXE_A" "1BDQ_A" "3U71_A"
[145] "2R5P_A" "40BD_A" "7MAS_A" "3IX0_A" "3D3T_A" "5Y0J_A" "3LZU_A" "4NJS_A"
[153] "3EKP_A" "1B6J_A" "3EKQ_A" "2RKF_A" "1C6X_A" "7MAR_A" "4DQF_A" "1RPI_A"
[161] "3OU1_B" "3PJ6_A" "2P3A_A" "60GQ_A" "30Q7_A" "5KR1_A" "30QD_A" "4RVI_A"
```

```
[169] "30QA_A" "1B6K_A" "30UD_B" "6MK9_A" "3S09_A" "1Q9P_A" "6I45_A" "7SEP_A"
[177] "4NJT_A" "3BXR_A" "4Y0A_A" "4DQC_A" "2FDD_A" "2RKG_A" "4DQH_A" "2P3C_A"
[185] "4EP2_A" "4EP2_A" "4EQ0_A" "4NPT_A" "60PU_A" "4NPU_A" "3U7S_A" "3HAW_A"
[193] "2AZB_A" "3TTP_A" "3HBO_A" "3GGU_A" "7N6T_A" "60PV_A" "4EQ0_A" "60PX_A"
[201] "204N_A" "5T2E_A" "3UCB_A" "3KA2_A" "3FSM_A" "60PW_A" "2AZC_A" "3FSM_A"
[209] "3HL0_A" "2P3D_A" "3T3C_A" "7MYP_A" "6054_X" "60PY_A" "4Z4X_A" "60PZ_A"
[217] "2JE4_A" "1DAZ_C" "7MAP_A" "7MAQ_A" "1K1U_A" "2B7Z_A" "3MWS_A" "1K1T_A"
[225] "8DCH_A" "3I2L_A" "6P9A_A" "2FXD_A" "2J9J_A" "3DCK_A" "2J9J_B" "3NXE_A"
[233] "2040_A" "2040_A" "3NXE_A" "3KA2_A" "3HL0_A" "5B18_A" "1SIP_A" "2SAM_A"
[241] "1AZ5_A" "1SIV_A" "1HII_A" "1IVP_A"
```

## Prediction of functional motions

We can run a Normal Mode Analysis (NMA) to predict large scale motions/flexibility/dynamics of any biomolecule that we can read into R.

Let's look at ADK chain A only!

```
adk <- read.pdb("1ake")
```

Note: Accessing on-line PDB file  
 PDB has ALT records, taking A only, rm.alt=TRUE

```
adk_A <- trim.pdb(adk, chain="A")
adk_A
```

Call: trim.pdb(pdb = adk, chain = "A")

Total Models#: 1  
 Total Atoms#: 1954, XYZs#: 5862 Chains#: 1 (values: A)

Protein Atoms#: 1656 (residues/Calpha atoms#: 214)  
 Nucleic acid Atoms#: 0 (residues/phosphate atoms#: 0)

Non-protein/nucleic Atoms#: 298 (residues: 242)  
 Non-protein/nucleic resid values: [ AP5 (1), HOH (241) ]

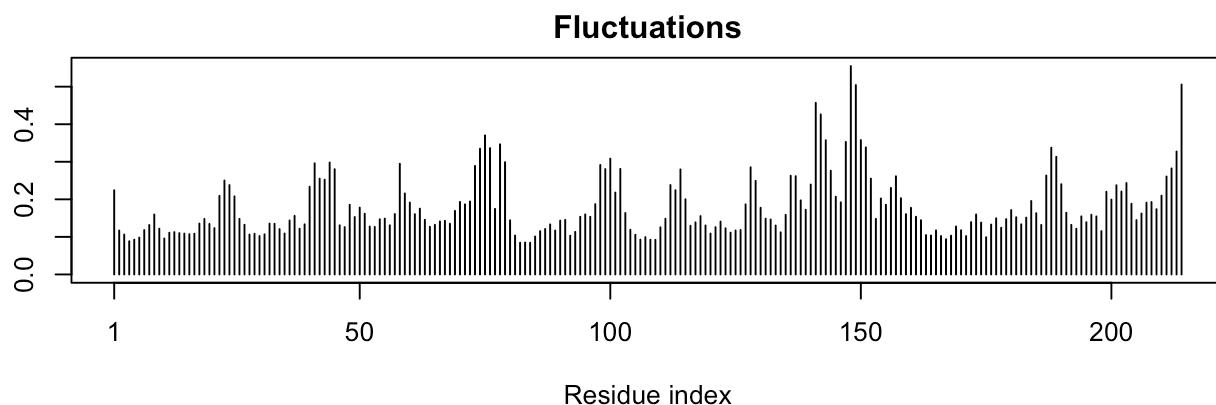
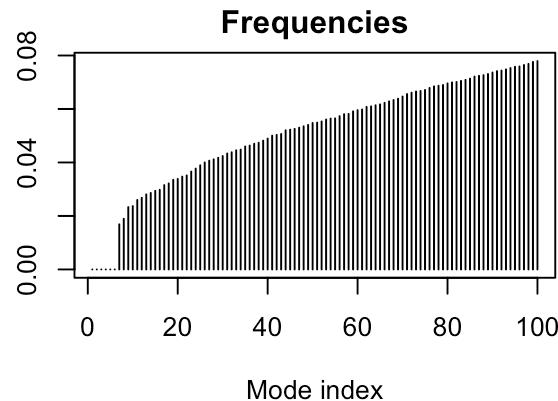
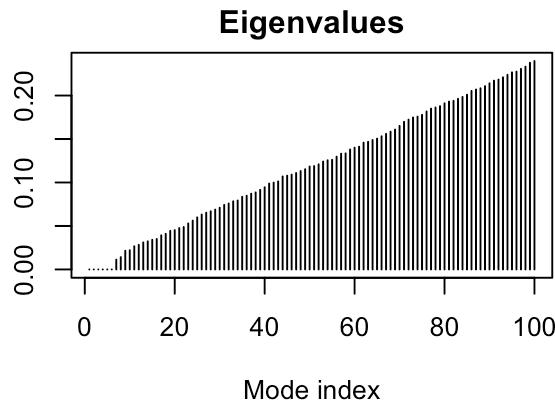
Protein sequence:  
 MRIILLGAPGAGKGQTQAQFIMEKYGIPQISTGDMRAAVKSGSELGKQAKDIMDAGKLVT  
 DELVIALVKERIAQEDCRNGFLLDGFPRTRIPQADAMKEAGINVVDYVLEFDVPDELIVDRI  
 VGRRVHAPSGRVYHVKNPPKVEGKDDVTGEELTRKDDQEETVRKRLVEYHQMTAPLIG  
 YYSKAEAGNTKYAKVDTKPVAEVRADLEKILG

```
+ attr: atom, helix, sheet, seqres, xyz,
       calpha, call
```

```
m <- nma(adk_A)
```

Building Hessian... Done in 0.008 seconds.  
 Diagonalizing Hessian... Done in 0.171 seconds.

```
plot(m)
```



Let's write out a "trajectory" of predicted motion

```
mktrj(m, file="adk_nma.pdb")
```

## Play with 3D viewing in R

We can use the new **bio3dview** package, which is not yet on CRAN, to render interactive 3D views in R and HTML quarto output reports.

To install from Github we can use the **pak** package.

```
library(bio3dview)
#view.pdb(adk)
```

