

# Class09

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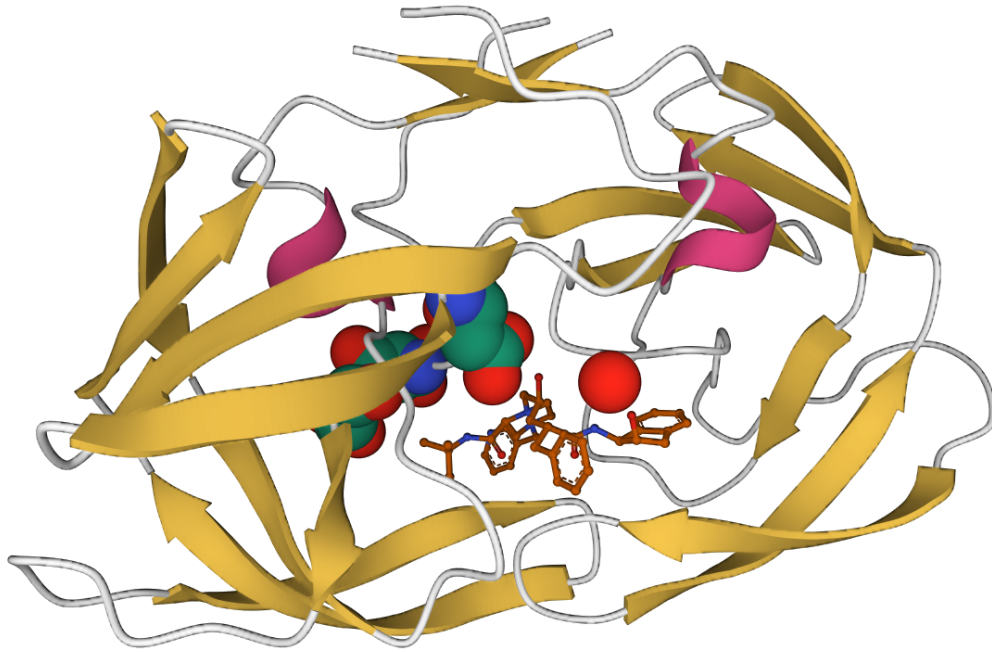
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## Protein Database

### section 1

skipped section 1 because the PDB statistics would not load on the website. The main point was that we saw mostly x ray crystallography and proteins in the database

## section 2 - Visualizing the HIV-1 protease structure



Q4: Water molecules normally have 3 atoms. Why do we see just one atom per water molecule in this structure?

Hydrogen is the smallest atom, and there is so much water surrounding the protein. The orange dots representing the oxygen of water that surround the protein are so small already, the way smaller hydrogens do not show up. They are too small and this also makes the image less messy.

Q5: There is a critical “conserved” water molecule in the binding site. Can you identify this water molecule? What residue number does this water molecule have

Yes, the water is in a spacefill model in the image above. It is water HOH 313.

Q6: Generate and save a figure clearly showing the two distinct chains of HIV-protease along with the ligand. You might also consider showing the catalytic residues ASP 25 in each chain and the critical water (we recommend “Ball & Stick” for these side-chains). Add this figure to your Quarto document.

image above. The ASP 25 residue and nearby ASP residues are in spacefill model as well as the conserved water.

Discussion Topic: Can you think of a way in which indinavir, or even larger ligands and substrates, could enter the binding site?

Q7: [Optional] As you have hopefully observed HIV protease is a homodimer (i.e. it is composed of two identical chains). With the aid of the graphic display can you identify secondary structure elements that are likely to only form in the dimer rather than the monomer?

There are some residues in the high 90s (i.e. THR96, Leu97, ASN98) that form beta sheets and there are additional beta sheets on the opposite side of the protein (AAs in the 40s). A Beta strand comes from each dimer, so I would expect that both of these strands are required to form the Beta sheet. If a dimer was missing I would expect these sheets would not form.

## Reading and working with Structures in R

The `bio3d` package for structural bioinformatics has lots of features for reading and working with biomolecular sequences and structures.

```
#load bio3d library
library(bio3d)
#read in HSV pdb file and save in pdb variable
pdb <- read.pdb("1hsg")
```

Note: Accessing on-line PDB file

```
pdb
```

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:
PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYD
QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE
```

```
ALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP
VNIIGRNLLTQIGCTLNF
```

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

```
#we can get attributes from pdb using $ feature
head(pdb$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>

Q7: How many amino acid residues are there in this pdb object?

128

Q8: Name one of the two non-protein residues?

water and MK1

Q9: How many protein chains are in this structure?

2

```
#loading in another protein
adk <- read.pdb("6s36")
```

Note: Accessing on-line PDB file

PDB has ALT records, taking A only, rm.alt=TRUE

```
adk
```

```
Call: read.pdb(file = "6s36")
```

```
Total Models#: 1
```

```
Total Atoms#: 1898, XYZs#: 5694 Chains#: 1 (values: A)
```

```
Protein Atoms#: 1654 (residues/Calpha atoms#: 214)
```

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

```
Non-protein/nucleic Atoms#: 244 (residues: 244)
```

```
Non-protein/nucleic resid values: [ CL (3), HOH (238), MG (2), NA (1) ]
```

```
Protein sequence:
```

```
MRILLGAPGAGKGTQAQFIMEKYGIPQISTGDMRLRAAVKSGSELGKQAKDIMDAGKLV  
DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDKI  
VGRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG  
YYSKEAEAGNTKYAKVDGTPVAEVRADLEKILG
```

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

```
#attributes gets you all attributes
```

```
attributes(pdb)
```

```
$names
```

```
[1] "atom" "xyz" "seqres" "helix" "sheet" "calpha" "remark" "call"
```

```
$class
```

```
[1] "pdb" "sse"
```

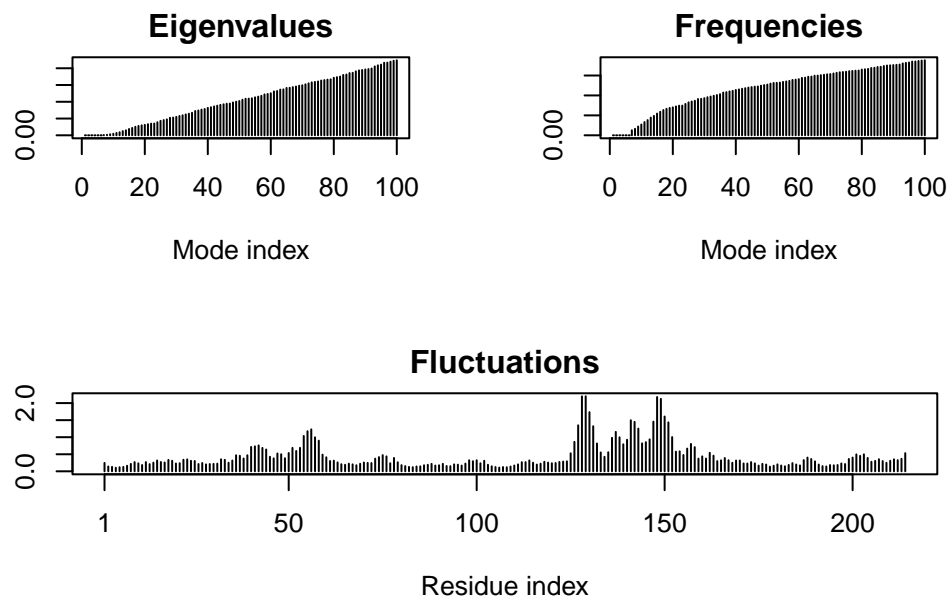
normal mode analysis (NMA) is a bioinformatics method for predicting functional motions.

```
m <- nma(adk)
```

```
Building Hessian... Done in 0.032 seconds.
```

```
Diagonalizing Hessian... Done in 0.322 seconds.
```

```
plot(m)
```



Make a “movei” of this thing moving!!

```
#make trajectory function  
mktrj(m,file="adk_nma.pdb")
```

## Comparative structure analysis of Adenylate Kinase

Install packages in the R console NOT your Rmd/Quarto file

```
install.packages("bio3d") install.packages("devtools") install.packages("BiocManager")
```

```
BiocManager::install("msa") devtools::install_bitbucket("Grantlab/bio3d-view")
```

Q10. Which of the packages above is found only on BioConductor and not CRAN?

BiocManager

Q11. Which of the above packages is not found on BioConductor or CRAN?:

the bickbucket package is from bickbucket, not CRAN or Bioconductor

Q12. True or False? Functions from the devtools package can be used to install packages from GitHub and BitBucket?

TRUE

```
game plan = get.seq() -> blast.pdb() -> get.pdb() -> PCA
```

```
#get sequence  
aa <- get.seq("lake_A")
```

Warning in get.seq("lake\_A"): Removing existing file: seqs.fasta

Fetching... Please wait. Done.

```
aa
```

```
      1      .      .      .      .      .      .      60  
pdb|1AKE|A  MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDMRLAAVKSSELGKQAKDIMDAGKLV  
      1      .      .      .      .      .      .      60  
  
     61      .      .      .      .      .      .      120  
pdb|1AKE|A  DELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRI  
     61      .      .      .      .      .      .      120  
  
    121      .      .      .      .      .      .      180  
pdb|1AKE|A  VGRRVHAPSGRVYHVKNPPKVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMTAPLIG  
    121      .      .      .      .      .      .      180  
  
    181      .      .      .      214  
pdb|1AKE|A  YYSKEAEAGNTKYAKVDGTPVAEVRADLEKILG  
    181      .      .      .      214
```

Call:

```
read.fasta(file = outfile)
```

Class:

```
fasta
```

Alignment dimensions:

```
1 sequence rows; 214 position columns (214 non-gap, 0 gap)
```

```
+ attr: id, ali, call
```

Q13. How many amino acids are in this sequence, i.e. how long is this sequence?

214

```
#blast search  
b <- blast.pdb(aa)
```

Searching ... please wait (updates every 5 seconds) RID = NKEYGDC4016

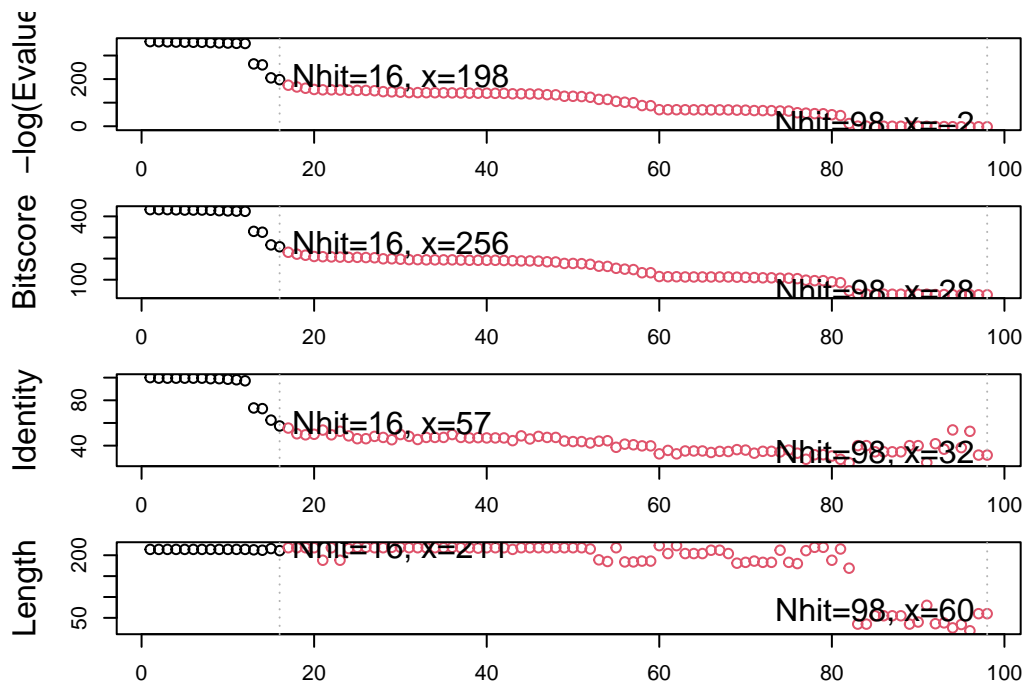
.....

Reporting 98 hits

```
#plot a summary of the search results  
hits <- plot(b)
```

```
* Possible cutoff values: 197 -3  
    Yielding Nhits: 16 98
```

```
* Chosen cutoff value of: 197  
    Yielding Nhits: 16
```





```
#list out the top hits
head(hits$pdb.id)
```

```
[1] "1AKE_A" "4X8M_A" "6S36_A" "6RZE_A" "4X8H_A" "3HPR_A"
```

```
#annotate collected pdb structures gathered from hits from BLAST
pdb.annotate(hits$pdb.id)
```

	structureId	chainId	macromoleculeType	chainLength	experimentalTechnique
1AKE_A	1AKE	A	Protein	214	X-ray
4X8M_A	4X8M	A	Protein	214	X-ray
6S36_A	6S36	A	Protein	214	X-ray
6RZE_A	6RZE	A	Protein	214	X-ray
4X8H_A	4X8H	A	Protein	214	X-ray
3HPR_A	3HPR	A	Protein	214	X-ray
1E4V_A	1E4V	A	Protein	214	X-ray
5EJE_A	5EJE	A	Protein	214	X-ray
1E4Y_A	1E4Y	A	Protein	214	X-ray
3X2S_A	3X2S	A	Protein	214	X-ray
6HAP_A	6HAP	A	Protein	214	X-ray
6HAM_A	6HAM	A	Protein	214	X-ray
4K46_A	4K46	A	Protein	214	X-ray
4NP6_A	4NP6	A	Protein	217	X-ray
3GMT_A	3GMT	A	Protein	230	X-ray
4PZL_A	4PZL	A	Protein	242	X-ray
	resolution	scopDomain	pfam		
1AKE_A	2.000	Adenylate kinase	Adenylate kinase, active site lid (ADK_lid)		
4X8M_A	2.600	<NA>	Adenylate kinase, active site lid (ADK_lid)		
6S36_A	1.600	<NA>	Adenylate kinase, active site lid (ADK_lid)		
6RZE_A	1.690	<NA>	Adenylate kinase, active site lid (ADK_lid)		
4X8H_A	2.500	<NA>	Adenylate kinase, active site lid (ADK_lid)		
3HPR_A	2.000	<NA>	Adenylate kinase, active site lid (ADK_lid)		
1E4V_A	1.850	Adenylate kinase	Adenylate kinase, active site lid (ADK_lid)		
5EJE_A	1.900	<NA>	Adenylate kinase, active site lid (ADK_lid)		
1E4Y_A	1.850	Adenylate kinase	Adenylate kinase, active site lid (ADK_lid)		
3X2S_A	2.800	<NA>	Adenylate kinase, active site lid (ADK_lid)		
6HAP_A	2.700	<NA>	Adenylate kinase, active site lid (ADK_lid)		
6HAM_A	2.550	<NA>	Adenylate kinase, active site lid (ADK_lid)		
4K46_A	2.010	<NA>	Adenylate kinase, active site lid (ADK_lid)		
4NP6_A	2.004	<NA>	Adenylate kinase, active site lid (ADK_lid)		

3GMT_A	2.100	<NA> Adenylate kinase, active site lid (ADK_lid)
4PZL_A	2.100	<NA> Adenylate kinase, active site lid (ADK_lid)
	ligandId	
1AKE_A	AP5	
4X8M_A	<NA>	
6S36_A	CL (3),NA,MG (2)	
6RZE_A	NA (3),CL (2)	
4X8H_A	<NA>	
3HPR_A	AP5	
1E4V_A	AP5	
5EJE_A	AP5,CO	
1E4Y_A	AP5	
3X2S_A	JPY (2),AP5,MG	
6HAP_A	AP5	
6HAM_A	AP5	
4K46_A	ADP,AMP,PO4	
4NP6_A	<NA>	
3GMT_A	SO4 (2)	
4PZL_A	CA,FMT,GOL	

	ligandName
1AKE_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE
4X8M_A	<NA>
6S36_A	CHLORIDE ION (3),SODIUM ION,MAGNESIUM ION (2)
6RZE_A	SODIUM ION (3),CHLORIDE ION (2)
4X8H_A	<NA>
3HPR_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE
1E4V_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE
5EJE_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE,COBALT (II) ION
1E4Y_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE
3X2S_A	N-(pyren-1-ylmethyl)acetamide (2),BIS(ADENOSINE)-5'-PENTAPHOSPHATE,MAGNESIUM ION
6HAP_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE
6HAM_A	BIS(ADENOSINE)-5'-PENTAPHOSPHATE
4K46_A	ADENOSINE-5'-DIPHOSPHATE,ADENOSINE MONOPHOSPHATE,PHOSPHATE ION
4NP6_A	<NA>
3GMT_A	SULFATE ION (2)
4PZL_A	CALCIUM ION,FORMIC ACID,GLYCEROL

	source
1AKE_A	Escherichia coli
4X8M_A	Escherichia coli
6S36_A	Escherichia coli
6RZE_A	Escherichia coli
4X8H_A	Escherichia coli
3HPR_A	Escherichia coli K-12

1E4V_A	Escherichia coli
5EJE_A	Escherichia coli 0139:H28 str. E24377A
1E4Y_A	Escherichia coli
3X2S_A	Escherichia coli str. K-12 substr. MDS42
6HAP_A	Escherichia coli 0139:H28 str. E24377A
6HAM_A	Escherichia coli K-12
4K46_A	Photobacterium profundum
4NP6_A	Vibrio cholerae 01 biovar El Tor str. N16961
3GMT_A	Burkholderia pseudomallei 1710b
4PZL_A	Francisella tularensis subsp. tularensis SCHU S4

1AKE\_A STRUCTURE OF THE COMPLEX BETWEEN ADENYLATE KINASE FROM ESCHERICHIA COLI AND THE INHIBIT

4X8M\_A  
6S36\_A  
6RZE\_A  
4X8H\_A  
3HPR\_A  
1E4V\_A  
5EJE\_A  
1E4Y\_A  
3X2S\_A  
6HAP\_A  
6HAM\_A  
4K46\_A  
4NP6\_A  
3GMT\_A  
4PZL\_A

Cryst

The crys

	citation	rObserved	rFree
1AKE_A	Muller, C.W., et al. J Mol Biol (1992)	0.19600	NA
4X8M_A	Kovermann, M., et al. Nat Commun (2015)	0.24910	0.30890
6S36_A	Rogne, P., et al. Biochemistry (2019)	0.16320	0.23560
6RZE_A	Rogne, P., et al. Biochemistry (2019)	0.18650	0.23500
4X8H_A	Kovermann, M., et al. Nat Commun (2015)	0.19610	0.28950
3HPR_A	Schrank, T.P., et al. Proc Natl Acad Sci U S A (2009)	0.21000	0.24320
1E4V_A	Muller, C.W., et al. Proteins (1993)	0.19600	NA
5EJE_A	Kovermann, M., et al. Proc Natl Acad Sci U S A (2017)	0.18890	0.23580
1E4Y_A	Muller, C.W., et al. Proteins (1993)	0.17800	NA
3X2S_A	Fujii, A., et al. Bioconjug Chem (2015)	0.20700	0.25600
6HAP_A	Kantaev, R., et al. J Phys Chem B (2018)	0.22630	0.27760
6HAM_A	Kantaev, R., et al. J Phys Chem B (2018)	0.20511	0.24325
4K46_A	Cho, Y.-J., et al. To be published	0.17000	0.22290
4NP6_A	Kim, Y., et al. To be published	0.18800	0.22200
3GMT_A	Buchko, G.W., et al. Biochem Biophys Res Commun (2010)	0.23800	0.29500



Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
1E4V.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
5EJE.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
1E4Y.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
3X2S.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
6HAP.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
6HAM.pdb.gz exists. Skipping download

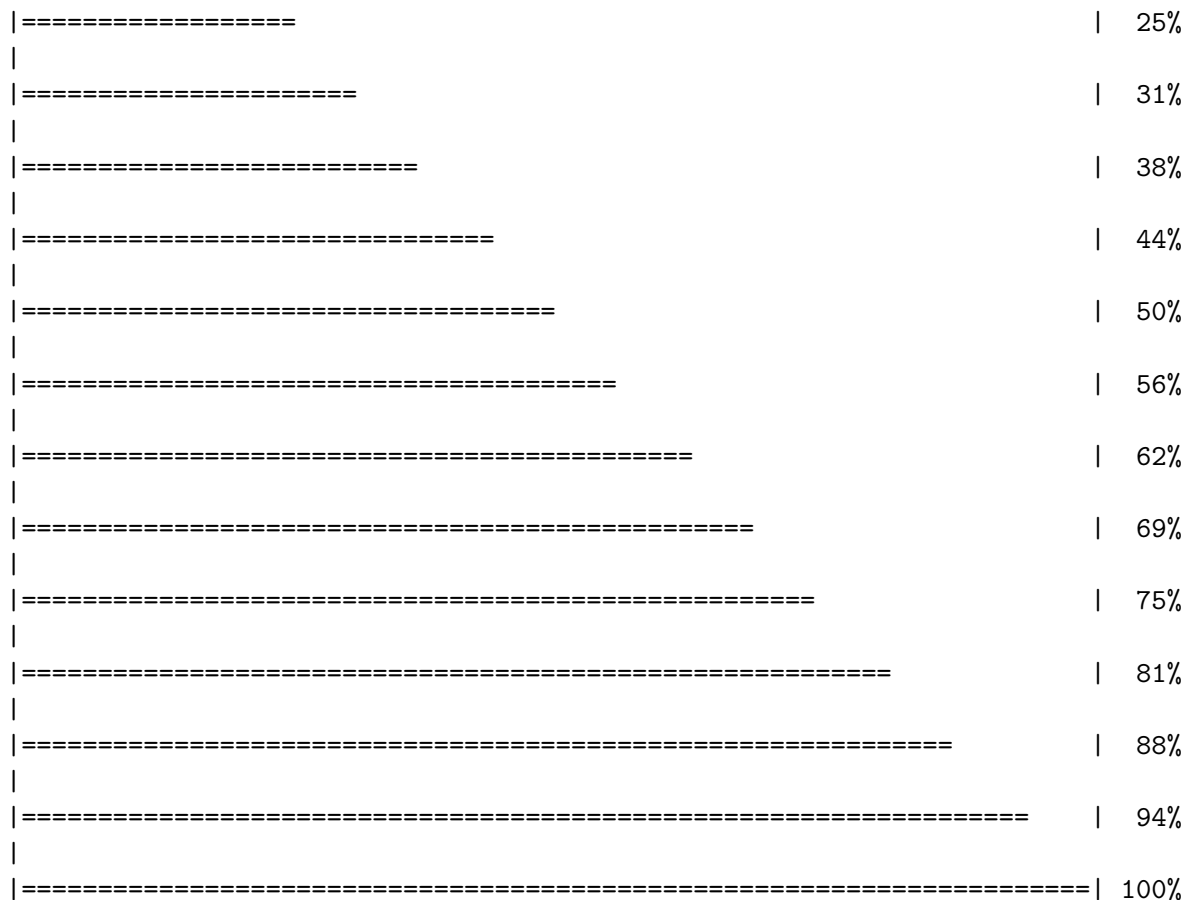
Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
4K46.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
4NP6.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
3GMT.pdb.gz exists. Skipping download

Warning in get.pdb(hits\$pdb.id, path = "pdbs", split = TRUE, gzip = TRUE): pdbs/  
4PZL.pdb.gz exists. Skipping download

	0%
====	6%
=====	12%
=====	19%



Viewing all these structures looks like a hot mess! We need to try something else...  
we will align and superimpose these structures.

```
pdbs <- pdbaln(files, fit = TRUE, exefile="msa")
```

Reading PDB files:

```
pdbs/split_chain/1AKE_A.pdb
pdbs/split_chain/4X8M_A.pdb
pdbs/split_chain/6S36_A.pdb
pdbs/split_chain/6RZE_A.pdb
pdbs/split_chain/4X8H_A.pdb
pdbs/split_chain/3HPR_A.pdb
pdbs/split_chain/1E4V_A.pdb
pdbs/split_chain/5EJE_A.pdb
pdbs/split_chain/1E4Y_A.pdb
```

```

pdb/split_chain/3X2S_A.pdb
pdb/split_chain/6HAP_A.pdb
pdb/split_chain/6HAM_A.pdb
pdb/split_chain/4K46_A.pdb
pdb/split_chain/4NP6_A.pdb
pdb/split_chain/3GMT_A.pdb
pdb/split_chain/4PZL_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
..    PDB has ALT records, taking A only, rm.alt=TRUE
.    PDB has ALT records, taking A only, rm.alt=TRUE
..    PDB has ALT records, taking A only, rm.alt=TRUE
..    PDB has ALT records, taking A only, rm.alt=TRUE
....    PDB has ALT records, taking A only, rm.alt=TRUE
.    PDB has ALT records, taking A only, rm.alt=TRUE
....

```

#### Extracting sequences

```

pdb/seq: 1    name: pdb/split_chain/1AKE_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 2    name: pdb/split_chain/4X8M_A.pdb
pdb/seq: 3    name: pdb/split_chain/6S36_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 4    name: pdb/split_chain/6RZE_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 5    name: pdb/split_chain/4X8H_A.pdb
pdb/seq: 6    name: pdb/split_chain/3HPR_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 7    name: pdb/split_chain/1E4V_A.pdb
pdb/seq: 8    name: pdb/split_chain/5EJE_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 9    name: pdb/split_chain/1E4Y_A.pdb
pdb/seq: 10   name: pdb/split_chain/3X2S_A.pdb
pdb/seq: 11   name: pdb/split_chain/6HAP_A.pdb
pdb/seq: 12   name: pdb/split_chain/6HAM_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 13   name: pdb/split_chain/4K46_A.pdb
    PDB has ALT records, taking A only, rm.alt=TRUE
pdb/seq: 14   name: pdb/split_chain/4NP6_A.pdb
pdb/seq: 15   name: pdb/split_chain/3GMT_A.pdb
pdb/seq: 16   name: pdb/split_chain/4PZL_A.pdb

```

```

1                                     .                .                40
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPVAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGALVAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMEKYGIPQIS
-----MRIILLGAPGAGKGTQAQFIMAKFGIPQIS
-----NAMRIILLGAPGAGKGTQAQFIMEKFVIPQIS
-----MRLILLGAPGAGKGTQANFIKEKFVIPQIS
TENLYFQSNAMRIILLGAPGAGKGTQAKIIEQKYNIAHIS
          **~*****      *****      *   *^ *   **
1           .               .               .                               40

41           .               .               .                               80
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDACKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDCGKLVTDELVLIALVKE
TGDMMLRAAVKSGSELGKQAKDIMDAGKLVTDELVLIALVRE
TGDMMLRAAIKSGSELGKQAKDIMDAGKLVTDEIIIALVKE
TGDMMLRAAIKAGTELKGQAKSVIDAGQLVSDDIILGLVKE
TGDMMLRAAIKAGTELKGQAKAVIDAGQLVSDDIILGLIKE
TGDMMLRAAVKAGTPLGVVEAKTYMDEGKLVPDSLIIIGLVKE
TGMIRETIKSGSALGQELKKVLDAGELVSDEFIIVKVD
****~*    ~* *~ **      *   ~*      ** *    ^^ ~~~~
41           .               .               .                               80
```



	81	.	.	.	120
[Truncated_Name:1] 1AKE_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:2] 4X8M_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:3] 6S36_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:4] 6RZE_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:5] 4X8H_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:6] 3HPR_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:7] 1E4V_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:8] 5EJE_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:9] 1E4Y_A.pdb	RIAQEDCRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:10] 3X2S_A.pdb	RIAQEDSRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:11] 6HAP_A.pdb	RICQEDSRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:12] 6HAM_A.pdb	RICQEDSRNGFLLDGFPR	TIPQADAMKEAGINVDYV	LEFD		
[Truncated_Name:13] 4K46_A.pdb	RIAQDDCAKGFLLDGFPR	TIPQADGLKEVGVVVDYV	IEFD		
[Truncated_Name:14] 4NP6_A.pdb	RIAQADCEKGFLLDGFPR	TIPQADGLKEMGINVDYV	IEFD		
[Truncated_Name:15] 3GMT_A.pdb	RLKEADCANGYLFDFGPR	TIAQADAMKEAGVAIDYV	LEID		
[Truncated_Name:16] 4PZL_A.pdb	RISKNCNNGFLLDGVPR	TIPQAQELDKLGVNIDYV	IEVD		
	*~	*	*~* ** ***** **	^	*~ ^**~* *
	81	.	.	.	120
	121	.	.	.	160
[Truncated_Name:1] 1AKE_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:2] 4X8M_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:3] 6S36_A.pdb	VPDELIVDKIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:4] 6RZE_A.pdb	VPDELIVDAIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:5] 4X8H_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:6] 3HPR_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	GTG		
[Truncated_Name:7] 1E4V_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:8] 5EJE_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:9] 1E4Y_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:10] 3X2S_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:11] 6HAP_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:12] 6HAM_A.pdb	VPDELIVDRIVGRRVHAP	SGRVYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:13] 4K46_A.pdb	VADSVIVERMAGRRAHLA	SGRTYHNVYNPPKVEGKDD	VDTG		
[Truncated_Name:14] 4NP6_A.pdb	VADDVIVERMAGRRAHLA	PSGRTYHVVYNPPKVEGKDD	VDTG		
[Truncated_Name:15] 3GMT_A.pdb	VPFSEIIERMSGRRTHPA	SGRTYHVKNPPKVEGKDD	VDTG		
[Truncated_Name:16] 4PZL_A.pdb	VADNLLIERITGRRIHPA	SGRTYHTKFNPPKVADKDD	VDTG		
	*	^^^ ^	*** *	*** **	^***** *** **
	121	.	.	.	160
	161	.	.	.	200
[Truncated_Name:1] 1AKE_A.pdb	EELTTRKDDQEETVRKRL	VEYHQMTAPLIGYYSKEAEAGN			
[Truncated_Name:2] 4X8M_A.pdb	EELTTRKDDQEETVRKRL	VEWHQMTAPLIGYYSKEAEAGN			

[Truncated_Name:3] 6S36_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:4] 6RZE_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:5] 4X8H_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:6] 3HPR_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:7] 1E4V_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:8] 5EJE_A.pdb	EELTTRKDDQEECVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:9] 1E4Y_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:10] 3X2S_A.pdb	EELTTRKDDQEETVRKRLCEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:11] 6HAP_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:12] 6HAM_A.pdb	EELTTRKDDQEETVRKRLVEYHQM	TAPLIGYYSKEAEAGN
[Truncated_Name:13] 4K46_A.pdb	EDLVIREDDKEETVLARLGVYHNQ	TAPLIAYYGKEAEAGN
[Truncated_Name:14] 4NP6_A.pdb	EDLVIREDDKEETVRARLNVYHTQ	TAPLIEYYGKEAAAGK
[Truncated_Name:15] 3GMT_A.pdb	EPLVQRDDKEETVKKRLDVYEAQ	TKPLITYYGDWARRGA
[Truncated_Name:16] 4PZL_A.pdb	EPLITRTDDNEDTVKQRLSVYHAQ	TAKLIDFYRNFSSNT
	* * * * *	^ * * * ^
	161	200
	201	227
[Truncated_Name:1] 1AKE_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:2] 4X8M_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:3] 6S36_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:4] 6RZE_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:5] 4X8H_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:6] 3HPR_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:7] 1E4V_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:8] 5EJE_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:9] 1E4Y_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:10] 3X2S_A.pdb	T--KYAKVDG	TKPVAEVRADLEKILG-
[Truncated_Name:11] 6HAP_A.pdb	T--KYAKVDG	TKPVCEVRADLEKILG-
[Truncated_Name:12] 6HAM_A.pdb	T--KYAKVDG	TKPVCEVRADLEKILG-
[Truncated_Name:13] 4K46_A.pdb	T--QYLKFDG	TKAVAEVSAELEKALA-
[Truncated_Name:14] 4NP6_A.pdb	T--QYLKFDG	TKQVSEVSADIAKALA-
[Truncated_Name:15] 3GMT_A.pdb	E-----	NGLKAPA-----YRKISG-
[Truncated_Name:16] 4PZL_A.pdb	KIPKYIKINGDQAVEKVSQDIFDQLNK	
	*	
	201	227

Call:

```
pdbaln(files = files, fit = TRUE, exefile = "msa")
```

Class:

```
pdb, fasta
```

Alignment dimensions:

16 sequence rows; 227 position columns (204 non-gap, 23 gap)

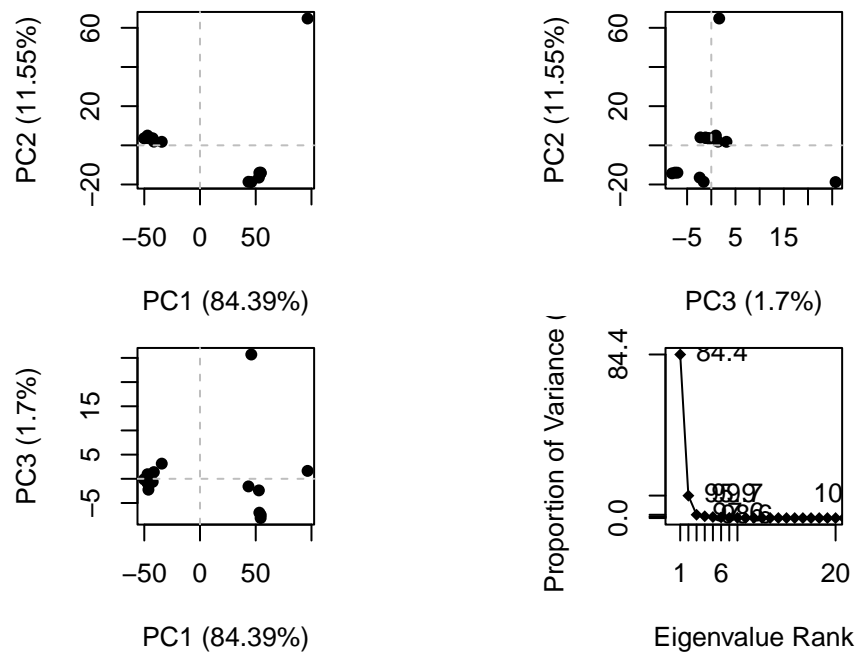
+ attr: xyz, resno, b, chain, id, ali, resid, sse, call

## PCA to the RESCUE

```
#perform PCA
pc.xray <- pca(pdbx)

#plot(pdbx)
#figure margins too large so I am not running this block

#plot my PCA results
plot(pc.xray)
```



```
#this PCA is of the coordinates of the atoms
```

let's make a movie!

```
mktrj(pc.xray,pc=1, file="pc_1.pdb")
```

## Normal Mode Analysis

```
modes <- nma(pdb)
```

### Details of Scheduled Calculation:

```
... 16 input structures
... storing 606 eigenvectors for each structure
... dimension of x$U.subspace: ( 612x606x16 )
... coordinate superposition prior to NM calculation
... aligned eigenvectors (gap containing positions removed)
... estimated memory usage of final 'eNMA' object: 45.4 Mb
```

	0%
====	6%
=====	12%
=====	19%
=====	25%
=====	31%
=====	38%
=====	44%
=====	50%
=====	56%
=====	62%
=====	69%
=====	75%

```

=====| 81%
|
=====| 88%
|
=====| 94%
|
=====| 100%

```

```

# Calculate RMSD
rd <- rmsd(pdb)

```

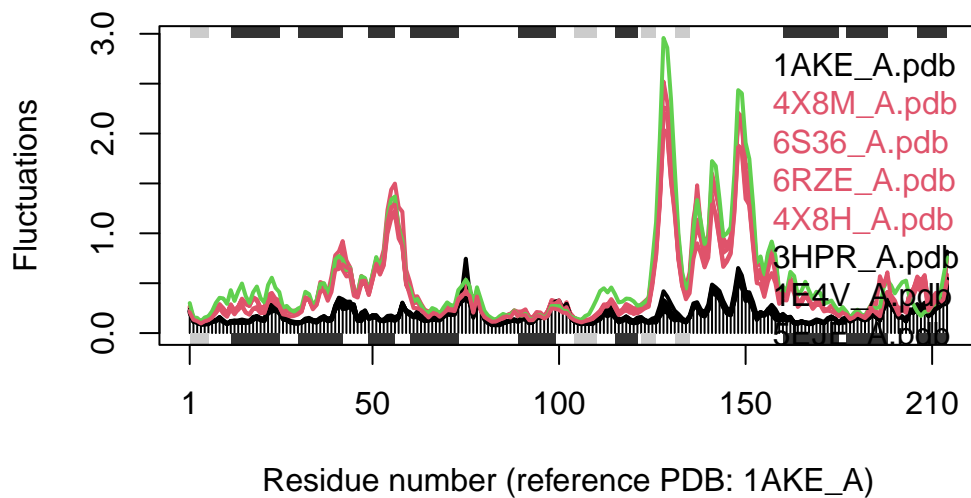
Warning in rmsd(pdb): No indices provided, using the 204 non NA positions

```

# Structure-based clustering
hc.rd <- hclust(dist(rd))
grps.rd <- cutree(hc.rd, k=3)
#plot nma
plot(modes,pdb,col=grps.rd)

```

Extracting SSE from pdb\$sse attribute



Q14. What do you note about this plot? Are the black and colored lines similar or different? Where do you think they differ most and why?

The black and colored lines are different. The colored lines have more fluctuation. This graph is kind of like we are looking at the movie of the structure moving. They differ most at the flexible regions I expect, because these are regions that conformationally change for ligand binding, etc.