

# Class10: Structural Bioinformatics (pt.1)

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## The PDB database

The [Protein Data Bank \(PDB\)](#) is the main repository of biomolecular structure data. Let's see what is in it:

```
stats <- read.csv("/Users/eloisesimpson/Documents/BIMM143/Class10_structure/pdbstats26.csv",
stats
```

	X.ray	EM	NMR	Integrative	Multiple.methods	Neutron
Protein (only)	178795	21825	12773	343	226	84
Protein/Oligosaccharide	10363	3564	34	8	11	1
Protein/NA	9106	6335	287	24	7	0
Nucleic acid (only)	3132	221	1566	3	15	3
Other	175	25	33	4	0	0
Oligosaccharide (only)	11	0	6	0	1	0
	Other	Total				
Protein (only)	32	214078				
Protein/Oligosaccharide	0	13981				
Protein/NA	0	15759				
Nucleic acid (only)	1	4941				
Other	0	237				
Oligosaccharide (only)	4	22				

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

```
n.sums <- colSums(stats)
n <- n.sums/n.sums["Total"]
round(n, digits=2)
```

	X.ray	EM	NMR	Integrative
	0.81	0.13	0.06	0.00
Multiple.methods		Neutron	Other	Total
	0.00	0.00	0.00	1.00

What is the total number of entries in the PDB?

```
n.sums["Total"]
```

Total
249018

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

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?

## Using Molstar

We can use the main [Molstar viewer online](#):

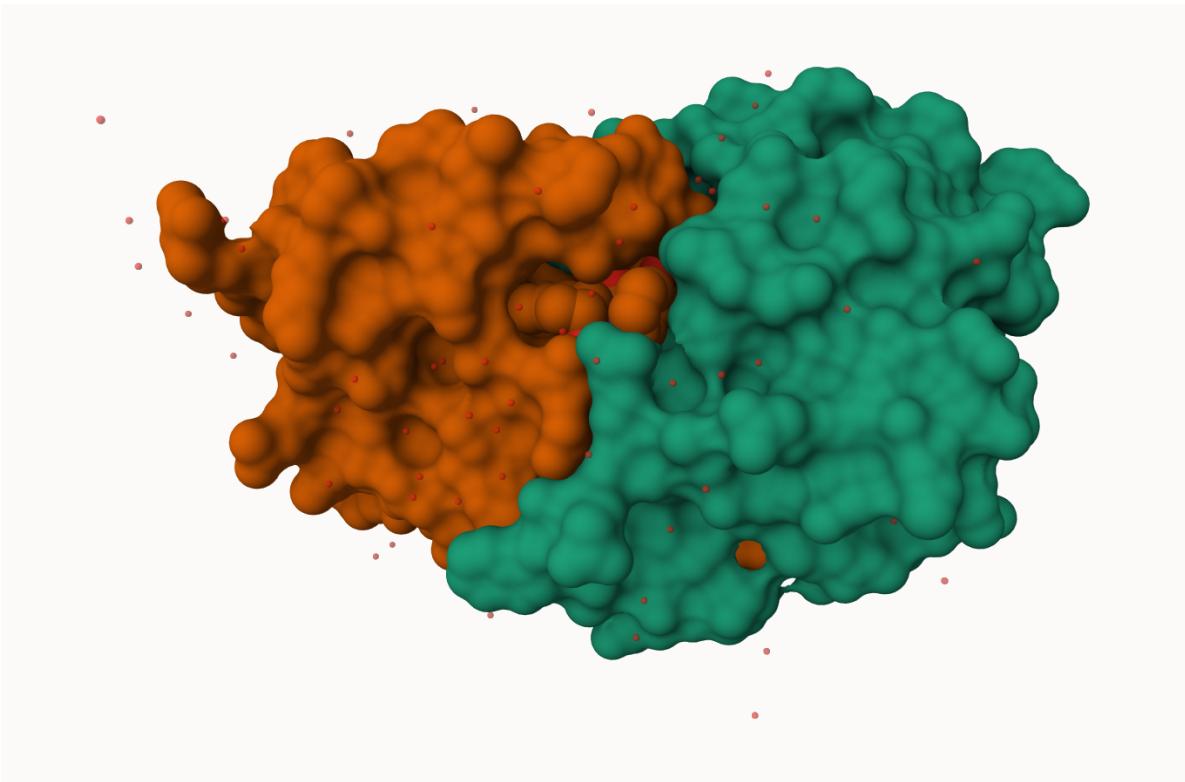
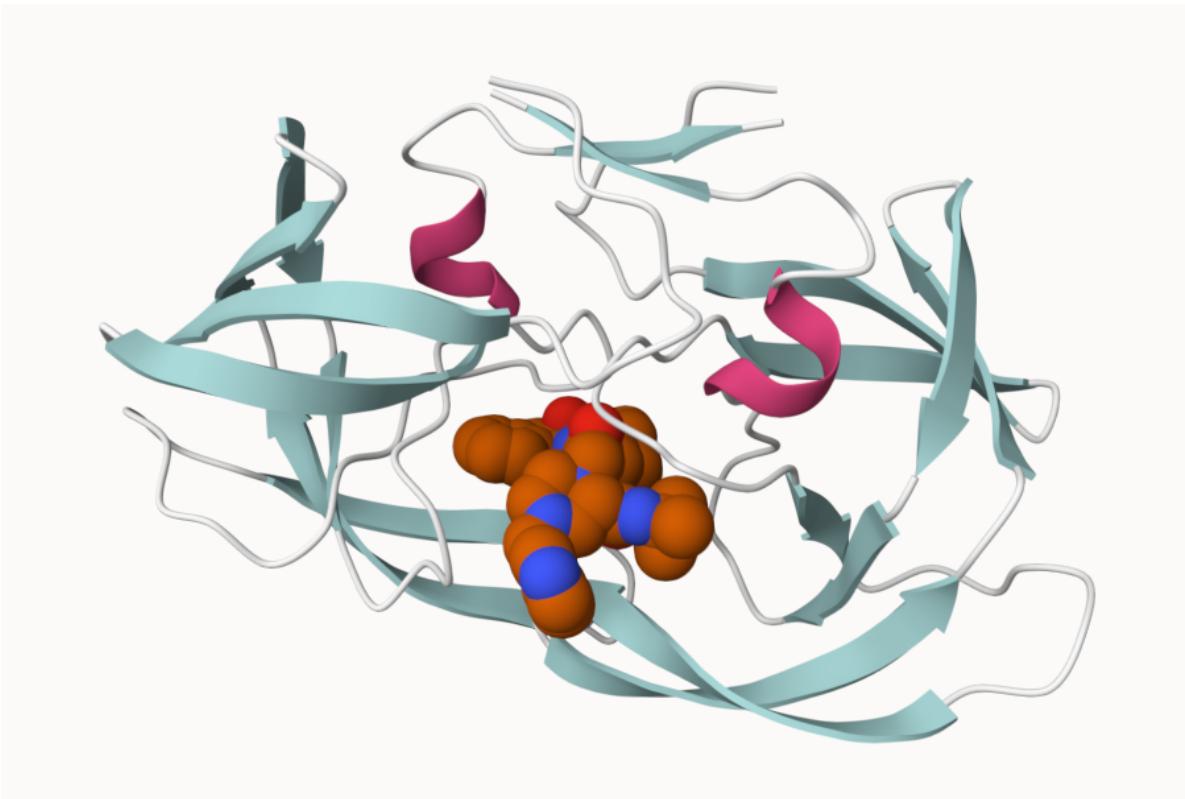


Figure 1: First view of HIV-Pr dimer with bound inhibitor

Q. Generate and insert an image of the HIV-Pr cartoon colored by secondary structure, showing the inhibitor (ligand) in spacefill.



>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. all important active site water molecule as spacefill



```
## The Bio3D package for structural bioinformatics
```

```
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:
```

```

PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPCKMIGGIGGFIKVRQYD
QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFPQITLWQRPLVTIKIGGQLKE
ALLDTGADDTVLEEMSLPGRWPCKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP
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>										

```
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 try out the new **bio3dview** package that is not yet on CRAN. We can use the **remotes** package to install any R package from GitHub.

## Quick viewing of PDBs

```

library("bio3dview")
#view.pdb(hiv)

sele <- atom.select(hiv, resno = 25)
#view.pdb(hiv, backgroundColor = "pink")
#           highlight = sele
#           highlight.style = "spacefill"

```

## Prediction of Protein dynamics

adenylate kinase: used to control relative proportions of nucleotides.

```
adk <- read.pdb("6s36")
```

```

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

```

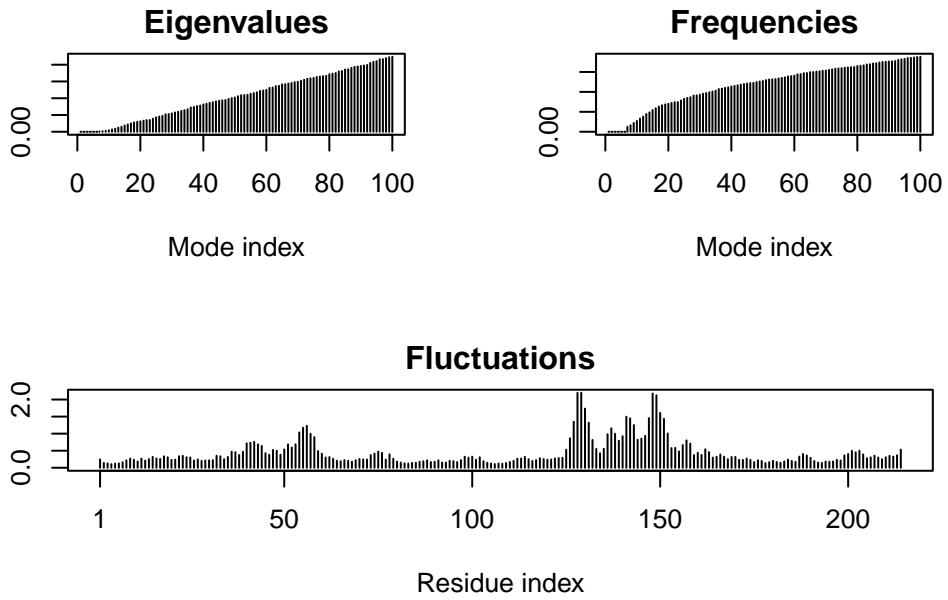
```
m <- nma(adk)
```

```

Building Hessian...      Done in 0.01 seconds.
Diagonalizing Hessian... Done in 0.036 seconds.

```

```
plot(m)
```



Write out our results as a wee trajectory movie:

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

```
#view.nma(m)
```