

Class11: Structural Bioinformatics

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```
db <- read.csv("Data Export Summary.csv", row.names=1)
head(db)
```

##	X.ray	NMR	EM	Multiple.methods	Neutron	Other	Total
## Protein (only)	142303	11804	5999	177	70	32	160385
## Protein/Oligosaccharide	8414	31	979	5	0	0	9429
## Protein/NA	7491	274	1986	3	0	0	9754
## Nucleic acid (only)	2368	1372	60	8	2	1	3811
## Other	149	31	3	0	0	0	183
## Oligosaccharide (only)	11	6	0	1	0	4	22

```
method.sums <- colSums(db)
method.sums
```

##	X.ray	NMR	EM	Multiple.methods
##	160736	13518	9027	194
##	Neutron	Other	Total	
##	72	37	183584	

#Q1.87.55% by X-ray and 4.92% by EM

```
round((method.sums/method.sums["Total"])*100,2)
```

##	X.ray	NMR	EM	Multiple.methods
##	87.55	7.36	4.92	0.11
##	Neutron	Other	Total	
##	0.04	0.02	100.00	

```
type.sums <- rowSums(db)
round((type.sums/method.sums["Total"])*100,2)
```

##	Protein (only)	Protein/Oligosaccharide	Protein/NA
##	174.73	10.27	10.63
##	Nucleic acid (only)	Other	Oligosaccharide (only)
##	4.15	0.20	0.02

```
round((db$Total/method.sums["Total"])*100,2)
```

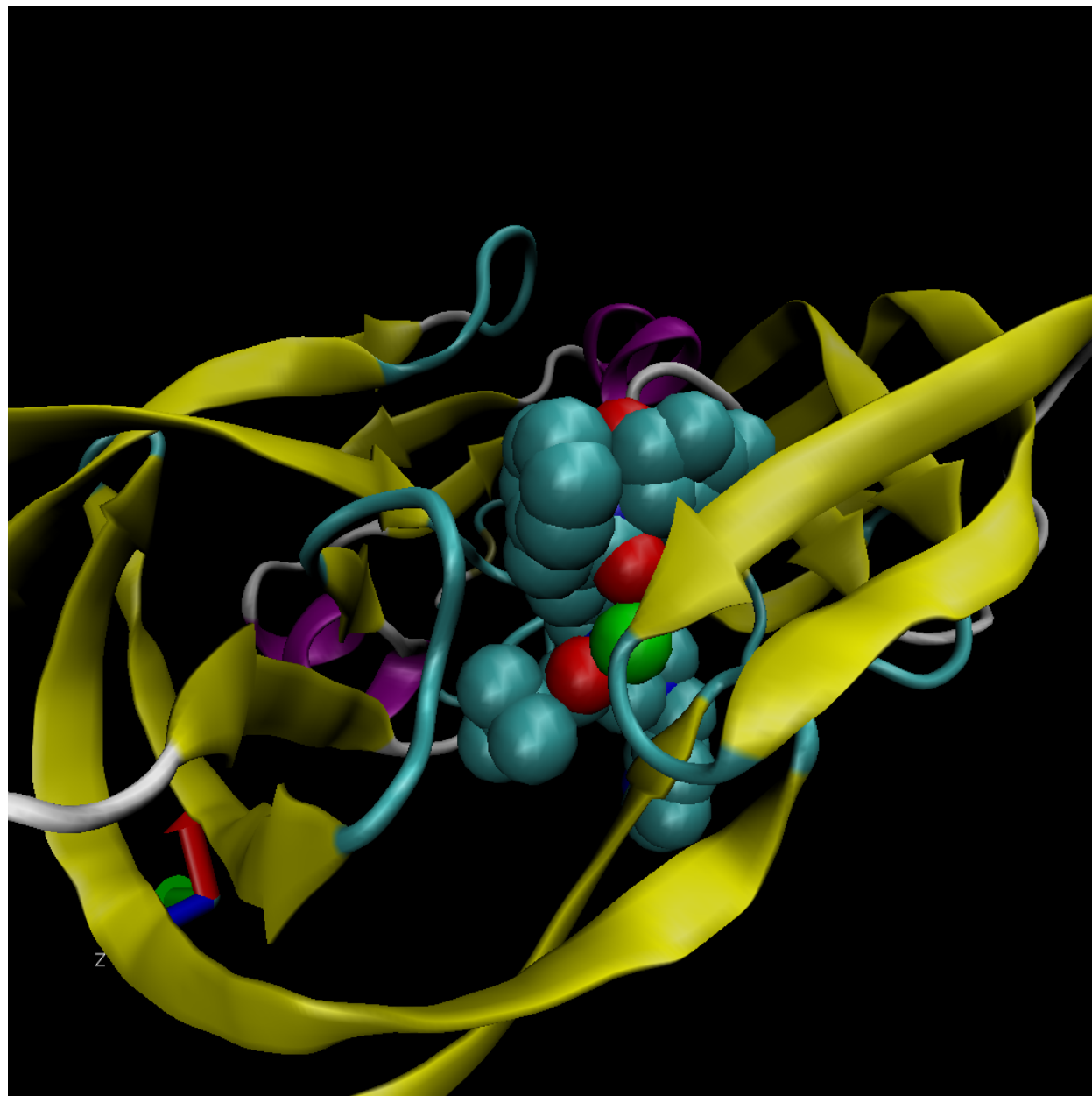
```
## [1] 87.36 5.14 5.31 2.08 0.10 0.01
```

87.36+5.14+5.31

[1] 97.81

#Q2: 87.36% of structures are protein only, 97.81% of structures contain proteins.

#Q3:1828 structures



#Q4: the hydrogen atoms are very small, and since no hydrogen atoms are shown, each water molecule will only show 1 atom which is the oxygen.

#Q5:the water molecule in MK1 ligand binding site is HOH308:0

#Q6: it is the alpha helix with loops on both of its ends