To predict new TALe-DNA code by SPDVB

Group 10

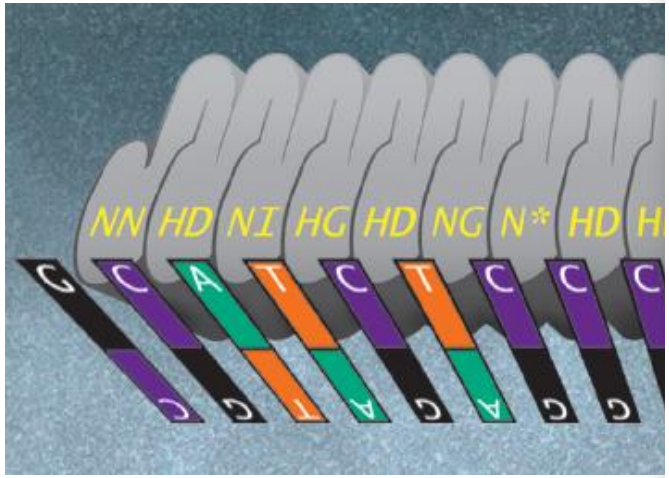
Members: 冷凤、梁芳、陆峰、王倩倩、叶延桢

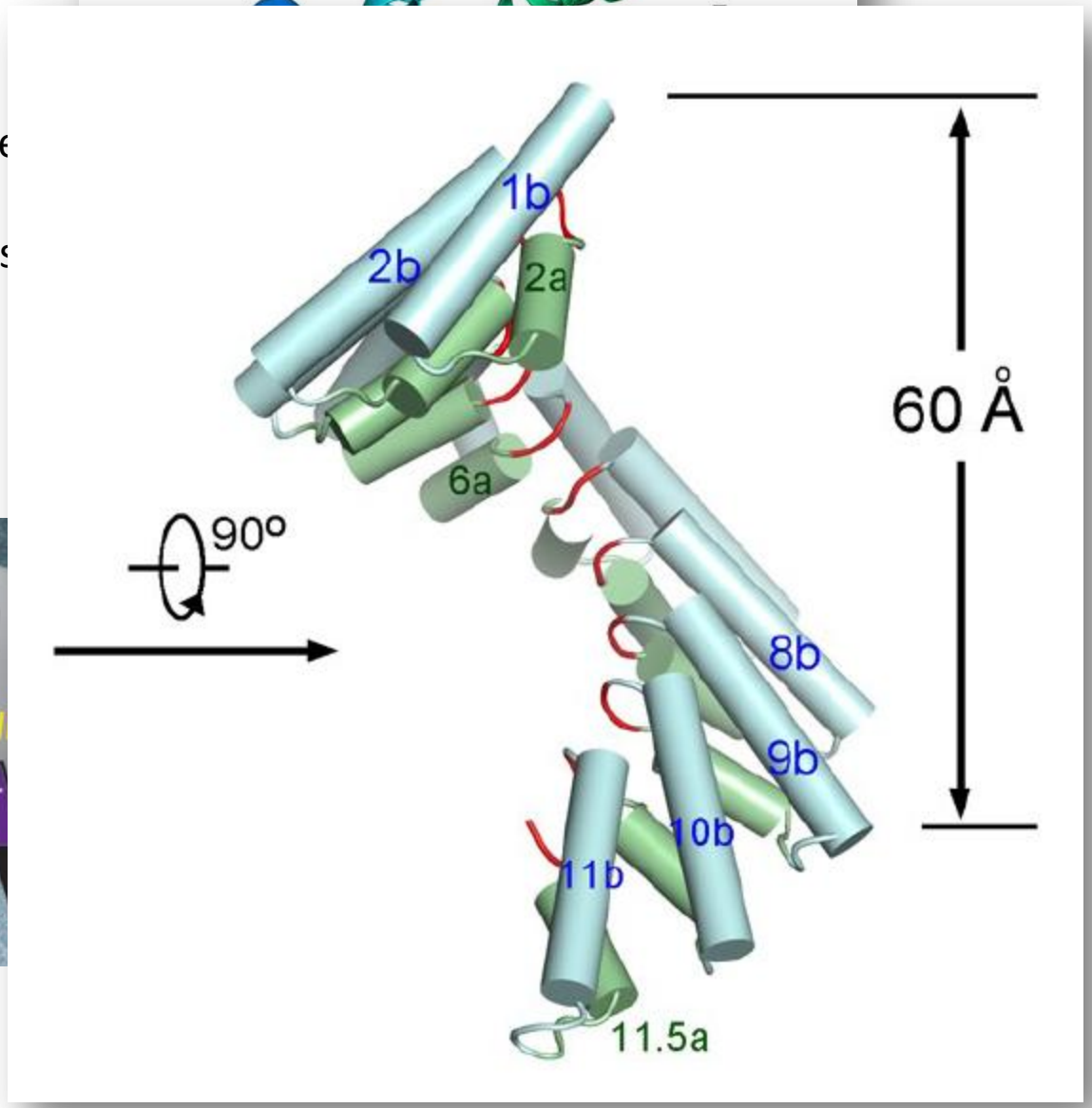
Outline

1\ what's TALe
2\ the history of TALe
3\ the issue we want to solve
To predict new code of TALe-DNA
4\ the method by which we solve the issue
mutate the 13th AA, choose the appropriate conformation, compute the H bond, then choose steady conformation with highest H bond
5\ result and summary
6\ prospect

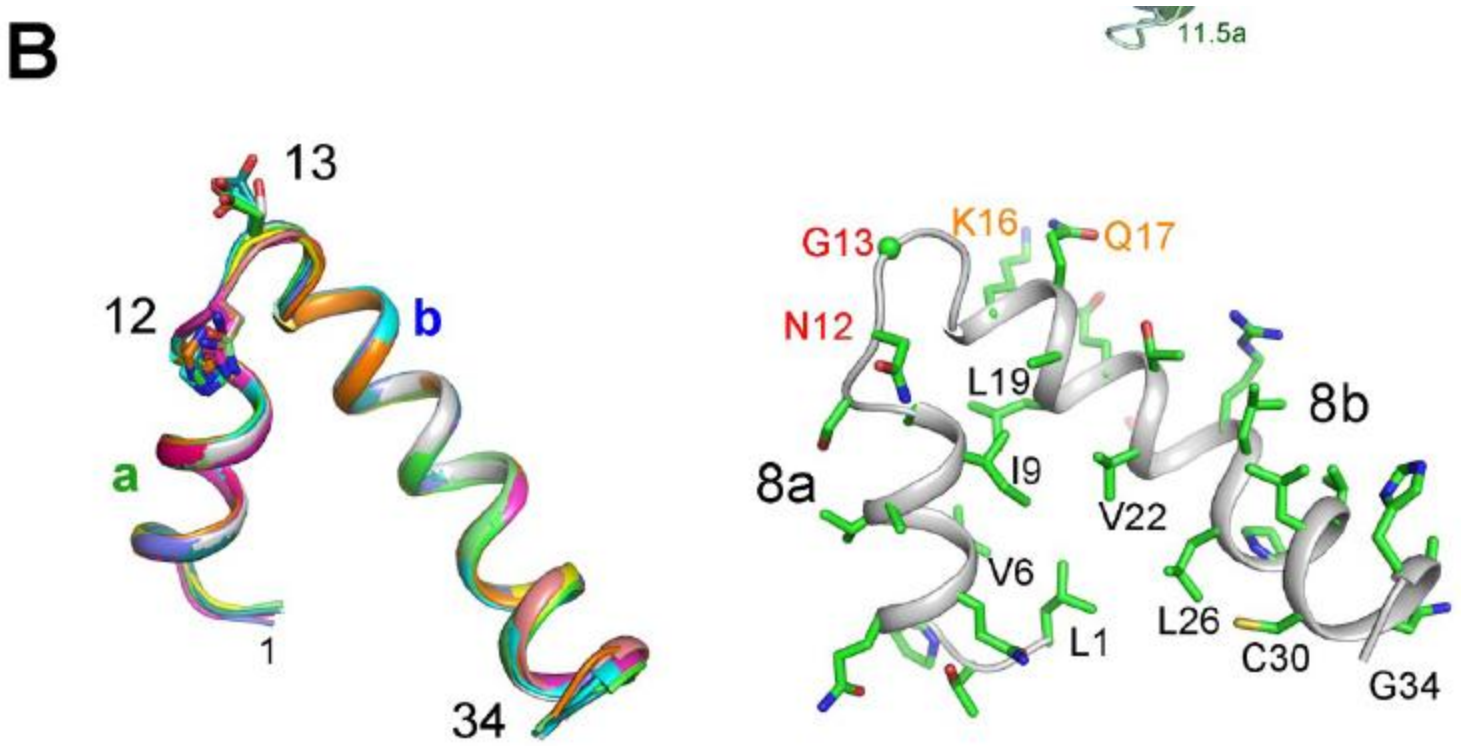
1\ what's TA

TAL effectors, secrete
bacteria,
recognize host DNA s
central domain
of tandem repeats.





Each repeat comprises 33-35
conserved amino acids and targets a specific
base pair
using two hypervariable residues (known as
RVD) at
positions 12 and 13.



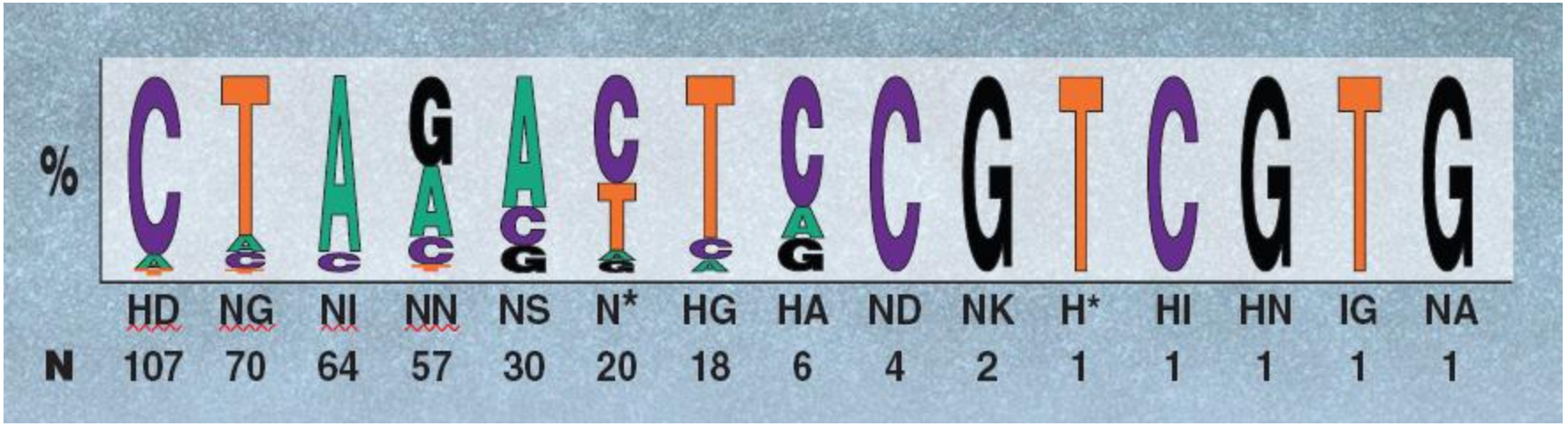
2\ the history of TALe

Found in plant pathogenic bacteria in the genus Xanthomonas in 1989

Currently, developed to be applied in gene know out

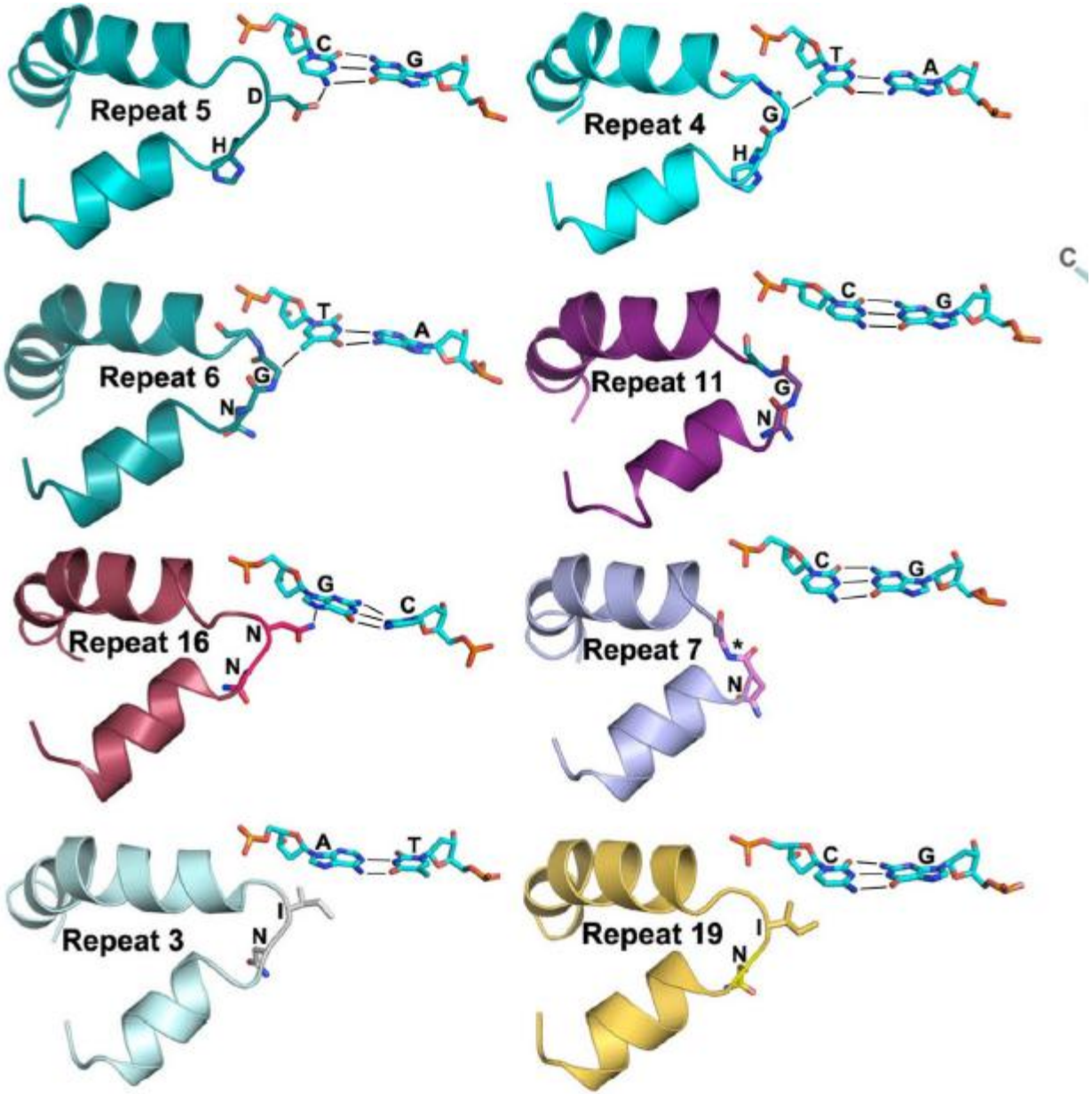
3\ the issue we want to solve

TALe targets a specific base pair
using two hypervariable residues (known as RVD) at positions 12 and 13.



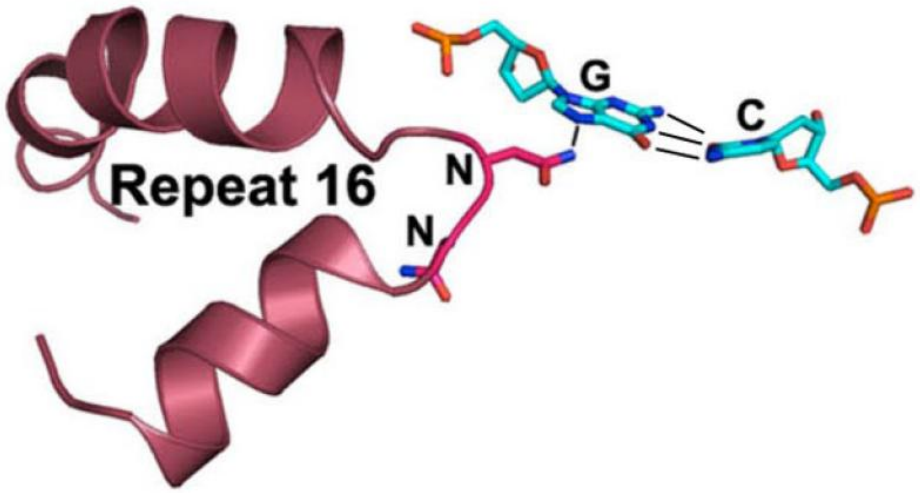
The code right now we can use in engineering:

C: HD
T: NG
A: NI
G: NN



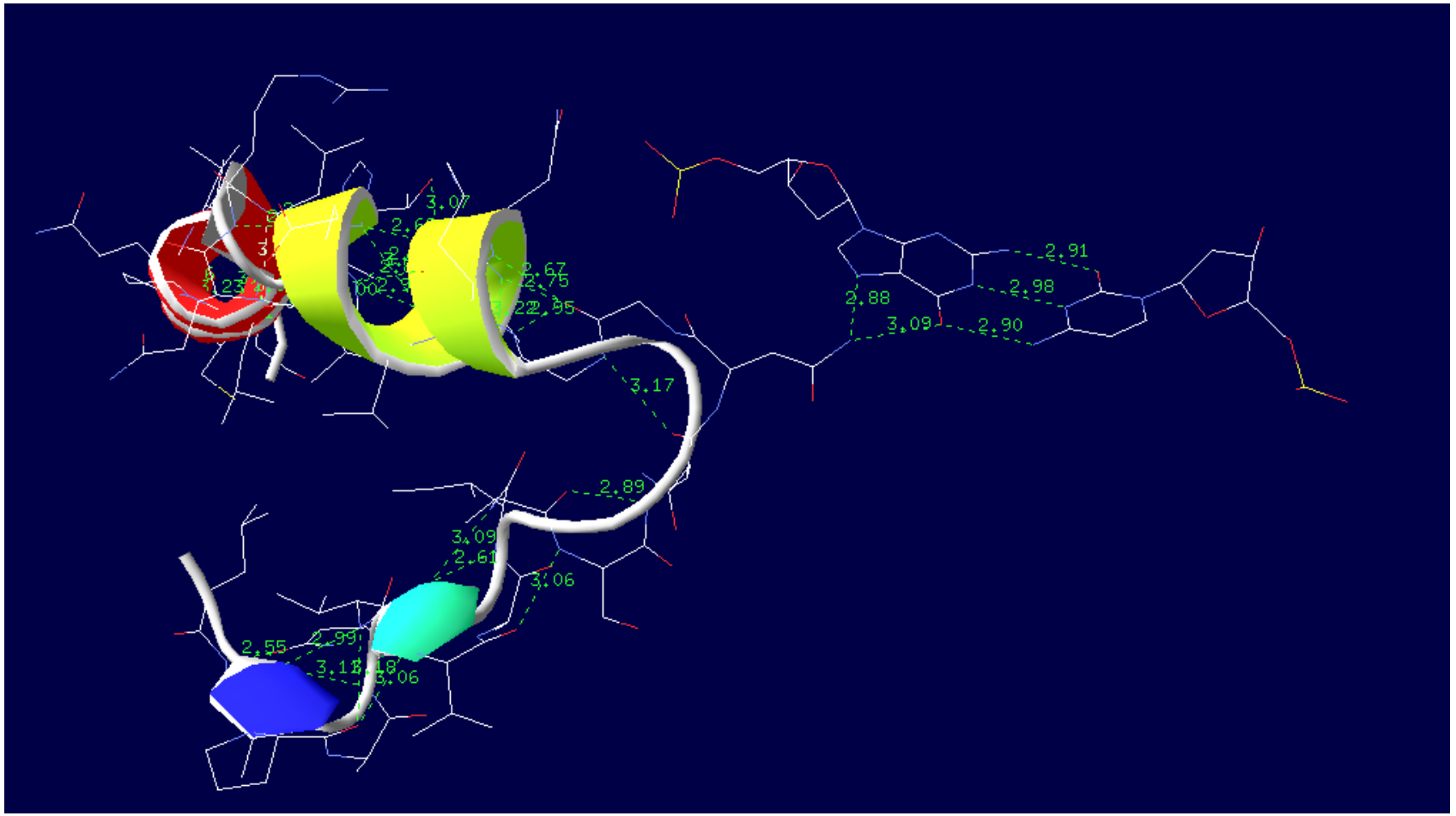
The problem is : NN recognizes G base with low efficiency

How to improve it ? or is there new code for G with high efficiency?

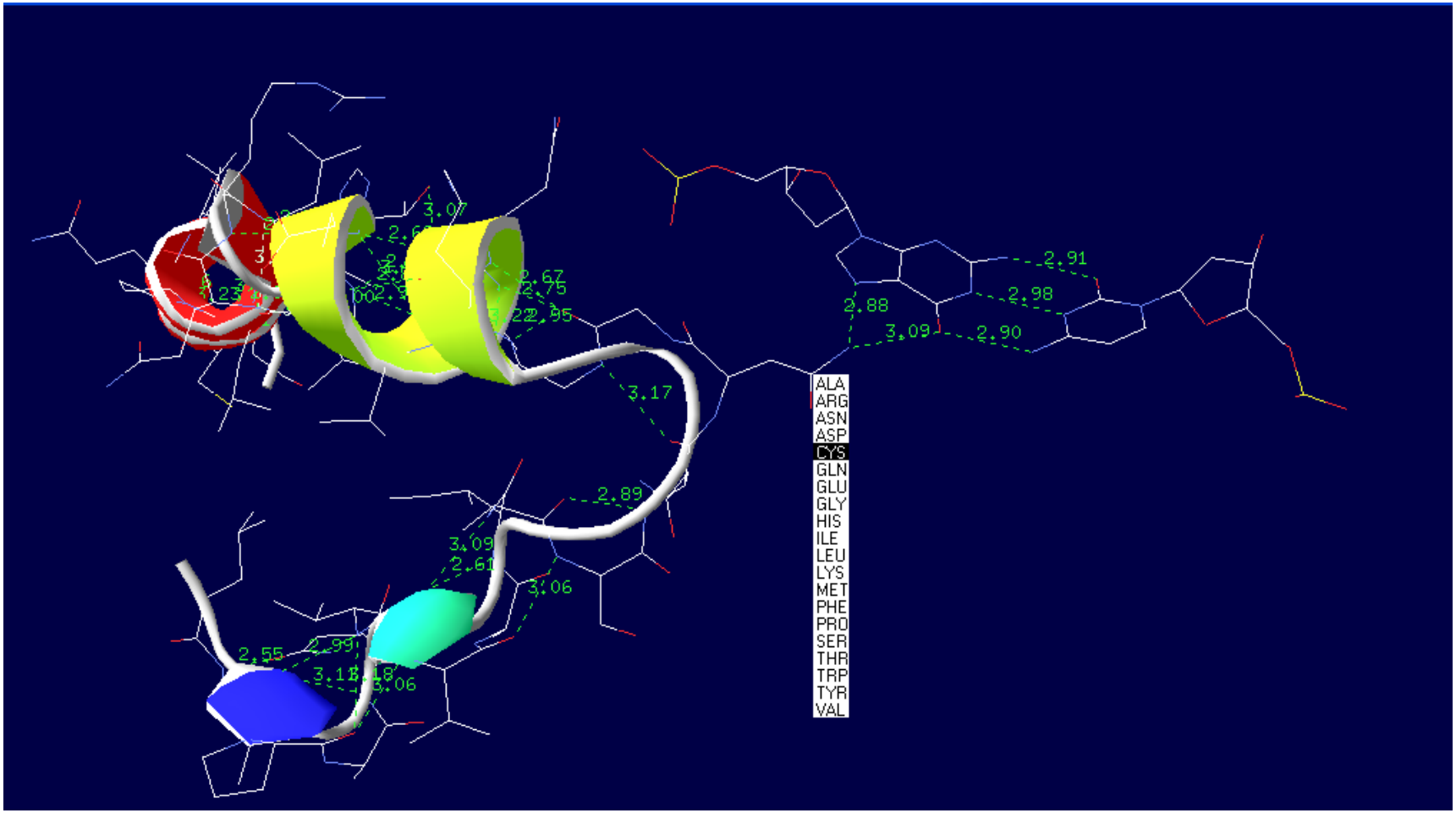


4\ the method by which we solve the issue

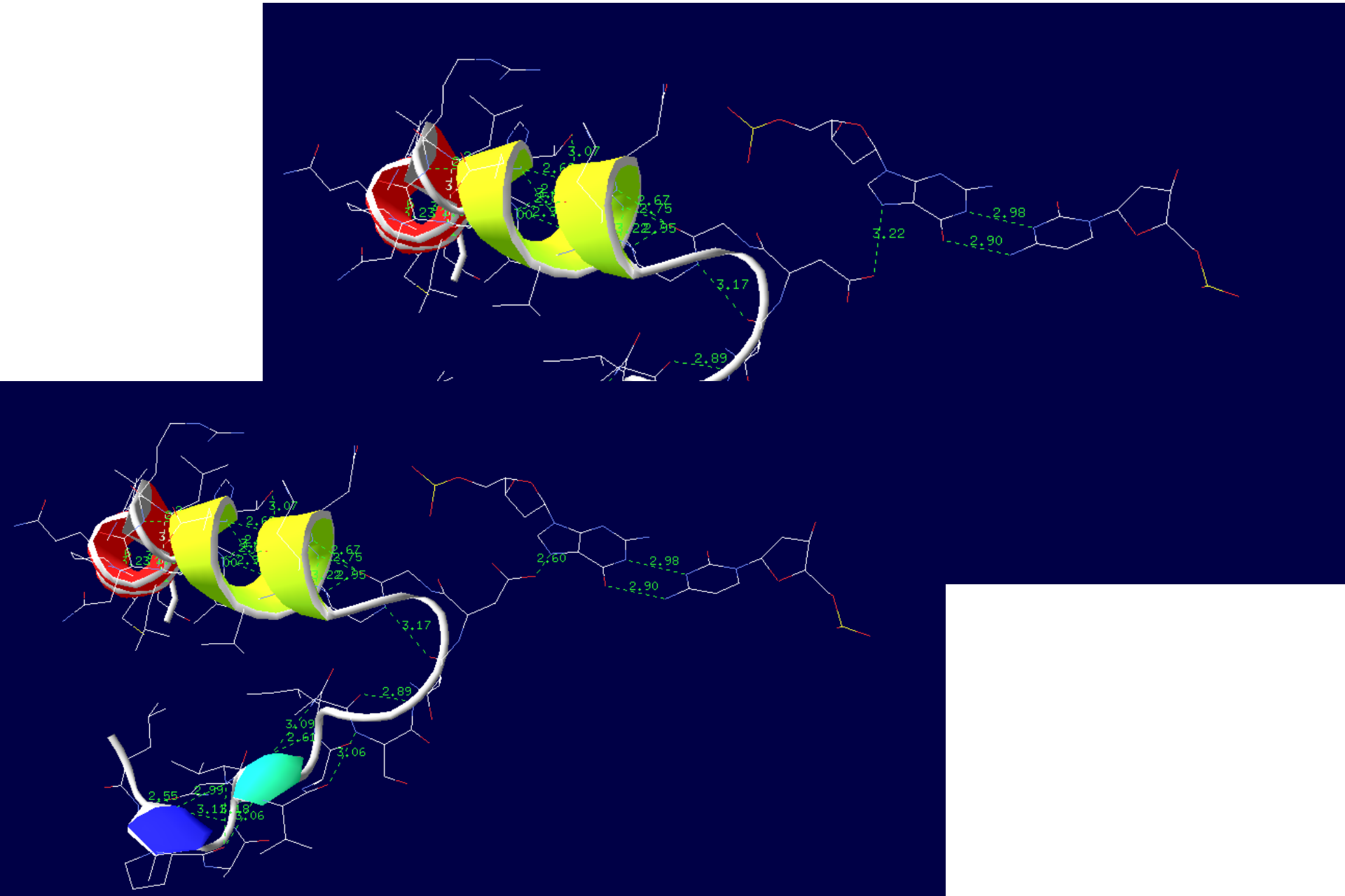
Use SPDBV
1\ extract the TALe unit and its GC pairs
2\ as to the possible 400(20*20) assembles, we fix the 12^{th} AA as N. We mutate the 13^{th} AA one by one.
3\ when we mutate the AA, we compute the H bond and their distance.
4\ we record the distance and the possible number of H bond.
5\ compared with the data together, we choose the strongest H bond without steric hindrance conformation as the predicted code.


3.07
2.67
2.95
3.17
2.89
3.09
2.61
3.06
2.55
2.99
3.06
2.91
2.98
2.88
3.09
2.90

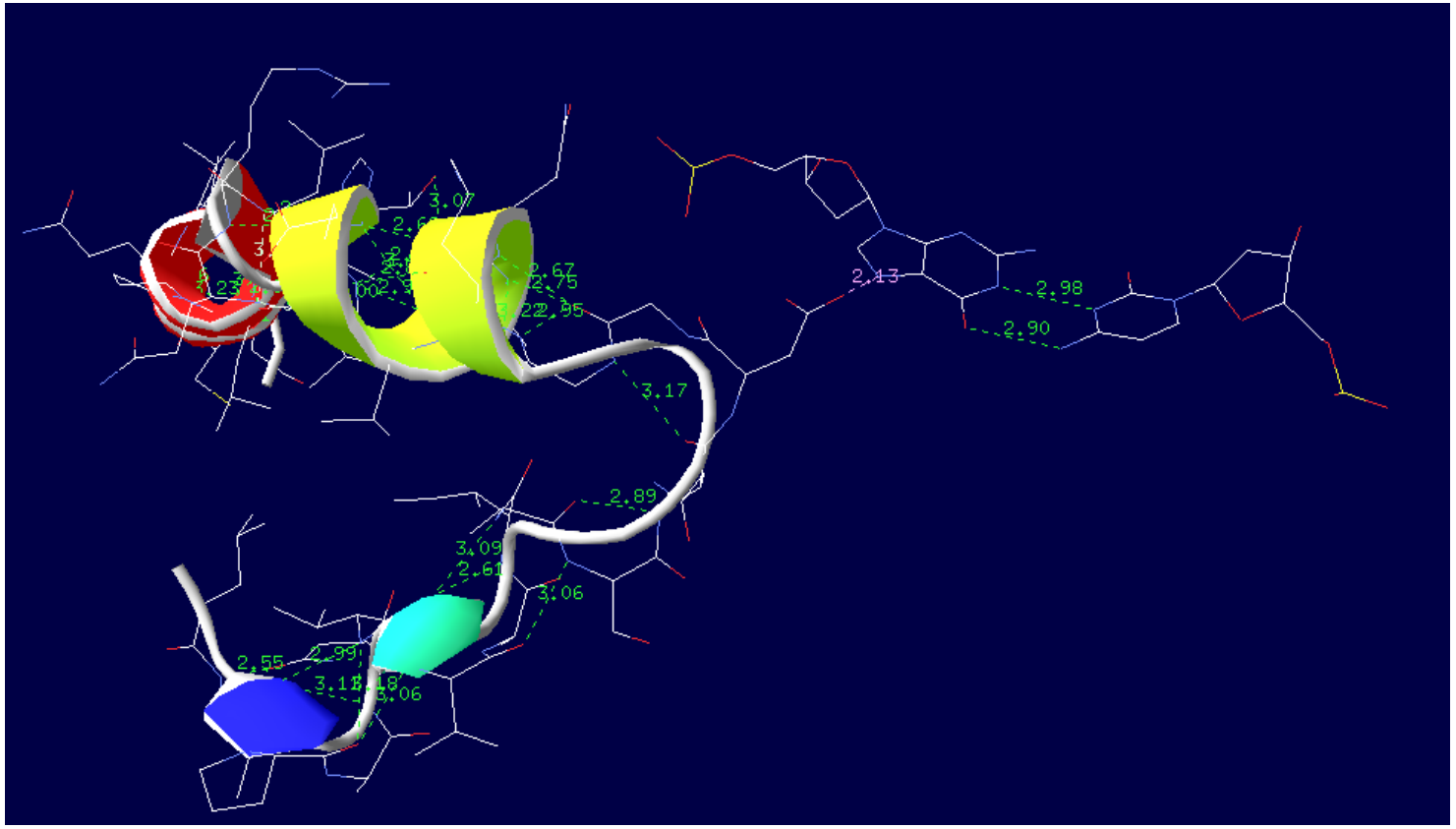
Mutated


3.07
2.67
2.75
2.95
3.17
2.89
3.09
2.61
3.06
2.55
2.99
3.18
3.06
2.91
2.98
2.88
3.09
2.90
ALA
ARG
ASN
ASP
CYS
GLN
GLU
GLY
HIS
ILE
LEU
LYS
MET
PHE
PRO
SER
THR
TRP
TYR
VAL

Mutated to Asp, see the new H bond



Avoide steric hindrance



We try 20 kinds of AA to fit the G

13th	A	T	C	G
GLN(E)	0	0	0	0
GLU(Q)	0	0	0	0
GLY(G)	0	0	0	0
HIS(H)	2 3.21；3.24	0	1 2.53	1 3.21
ILE(I)	0	0	0	0

	A	T	C	G
Asn(L)	0	0	0	0
Asn(K)	0	0	0	0
Asn(M)	2.68/2.67	2.68/2.67	2.68/2.67	2.68/2.67
Asn(F)	0	0	0	0
Asn(P)	0	0	0	0

aa group	nucleotide			
	A	T	G	C
Ala(A)	–	–	–	–
Arg(R)	3.33	0	2.48	空间位阻
Asp(D)	2.58；3.48	空间位阻	2.6	2.55
Asn(N)	–	空间位阻	2.88；3.09	–
Cys(C)	3.15	空间位阻	3.15	3.44

To ensure the specificity of TALe to G base, we also checked the AA we tested corresponded with other bases: A T C

The data is updating..

5\ result and summary

- The most possible code we predicted for G base is :

6\ prospect

The younger but stronger brother of ZFN

- As we know, ZFN has been used in gene knock out for decades.
- TALe will replace it?
- The technology , biological issue