

Protein-DNA Specificity Prediction

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Bradley lab

Program in Computational Biology

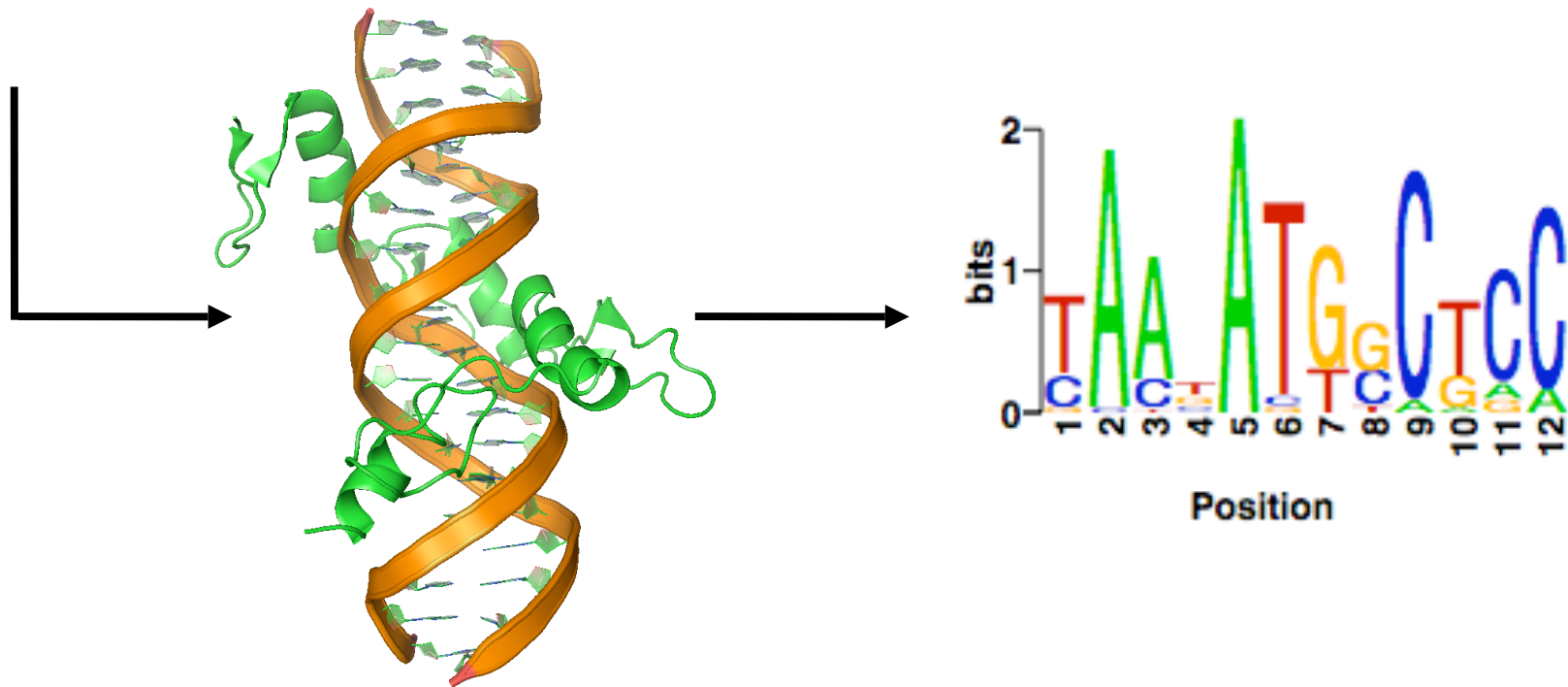
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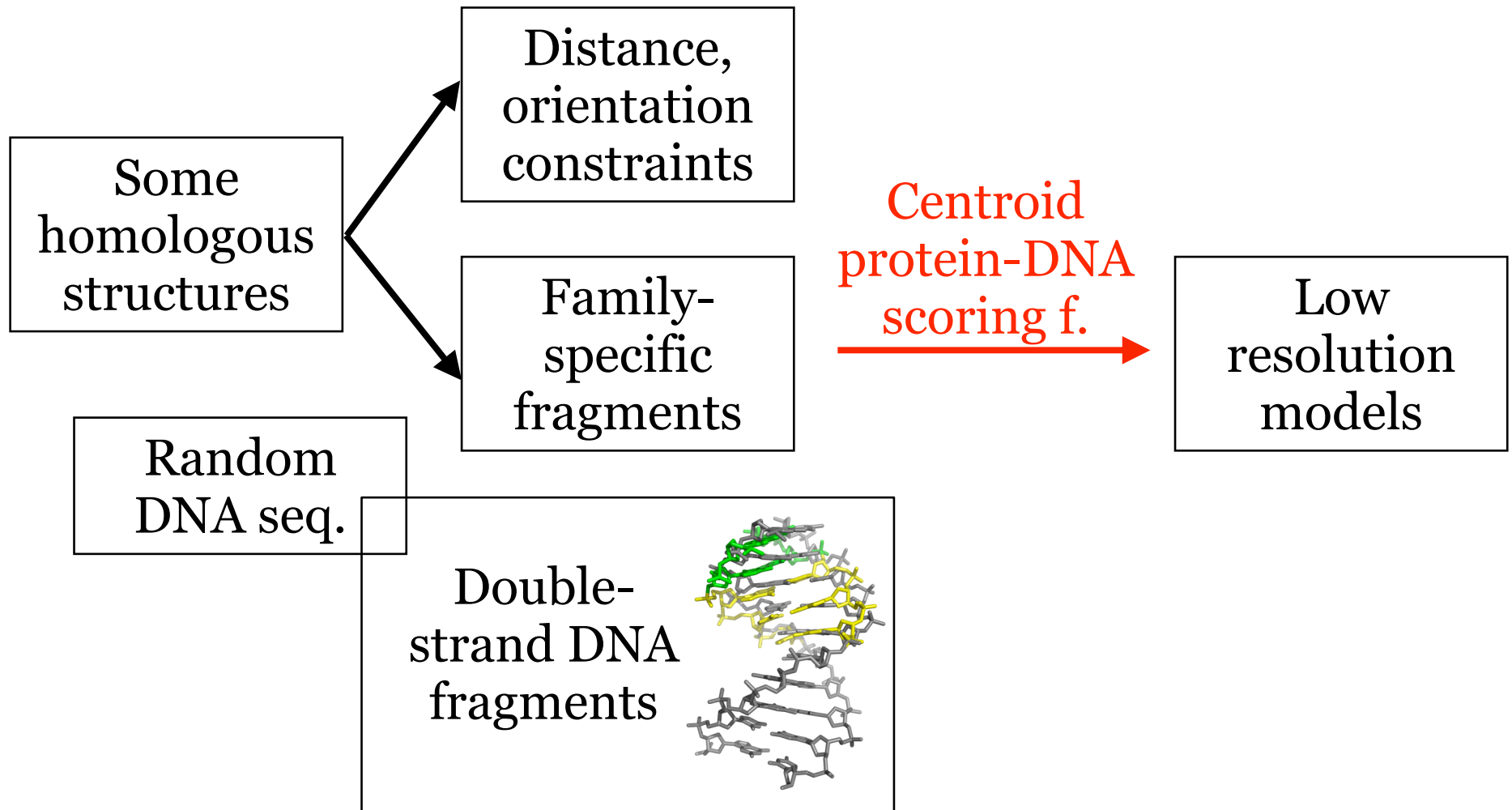
ROSETTACON 2009

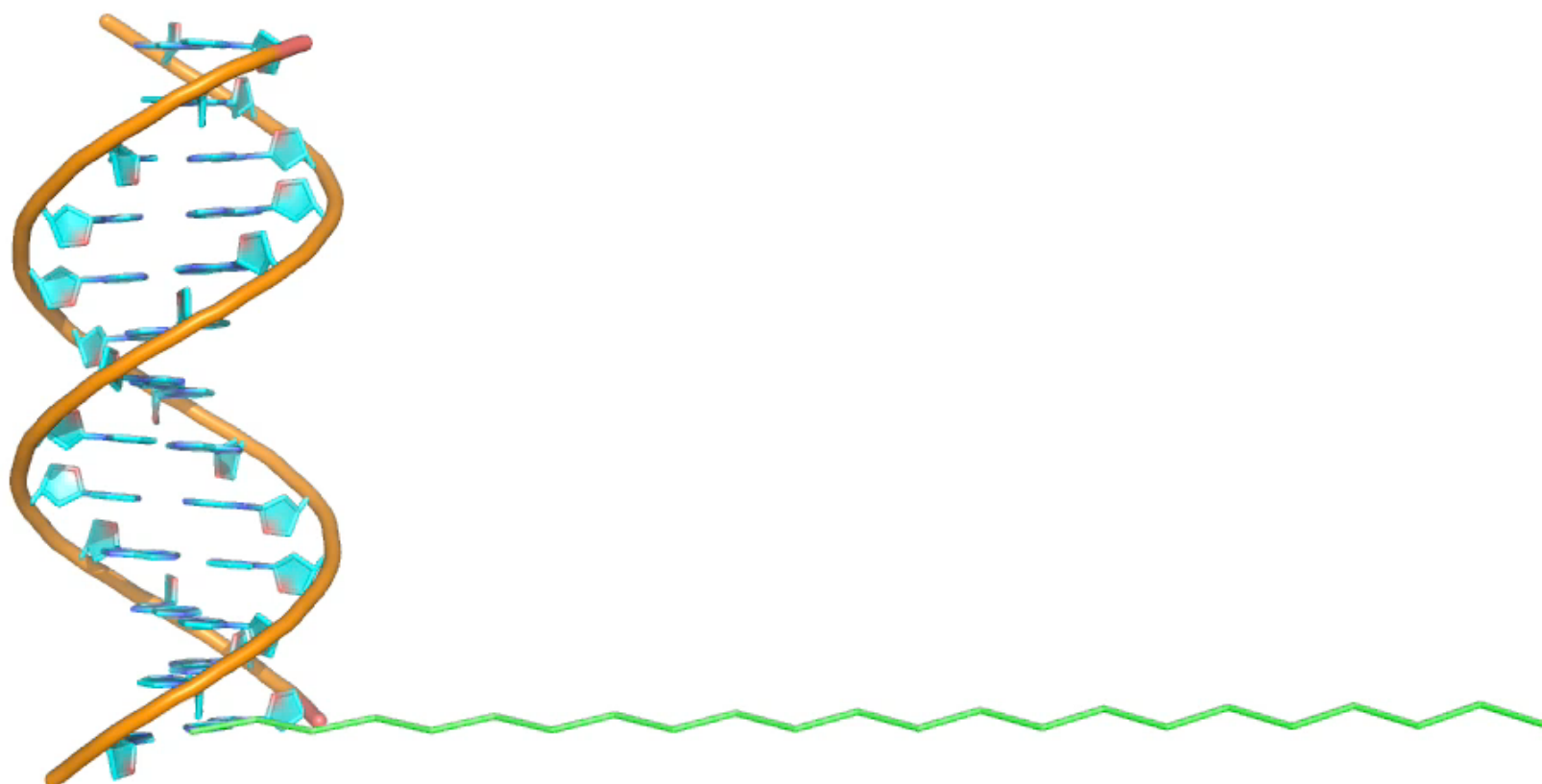
Goal: sequence → structure → specificity

```
>1ubd_C mol:protein length:124 PROTEIN (YY1 ZINC FINGER DOMAIN)  
MEPRTIACPHKGCTKMFRDNSAMRKHLHTHGPRVHVCAECGKAFVSSKLKRHQLVHTGE  
KPFQCTFEGCGKRFSLDFNLRTHVRIHTGDRPYVCPFDGCNKKFAQSTNLKSHILTHAKA  
KNNQ
```



Low resolution phase





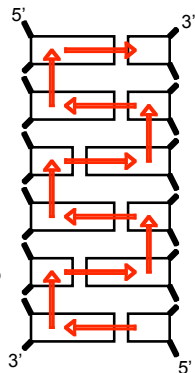
High resolution phase

All atom refinement,
w/ simultaneous sampling
of DNA sequence

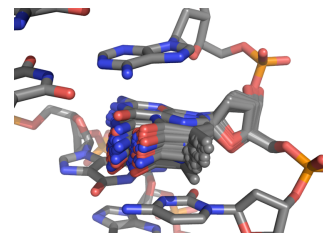
Low
resolution
models

High
resolution
models

DNA base-
centric
kinematics

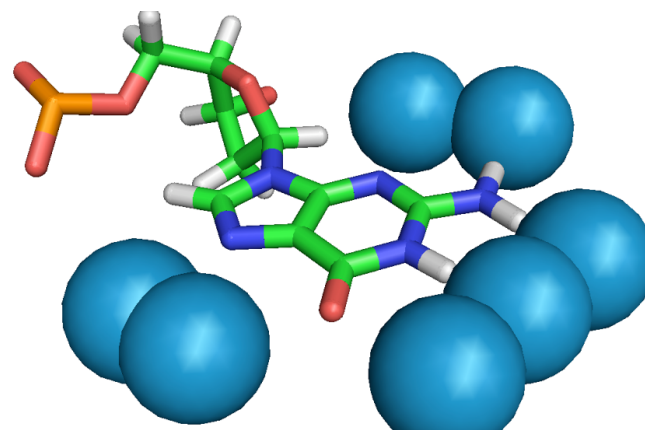


DNA “rotamers”



Full-atom score function

- Explicit electrostatic (hack_elec)
- LK orientation-dependent
- Base-step ref energy



Decoys to specificity

energy DNA

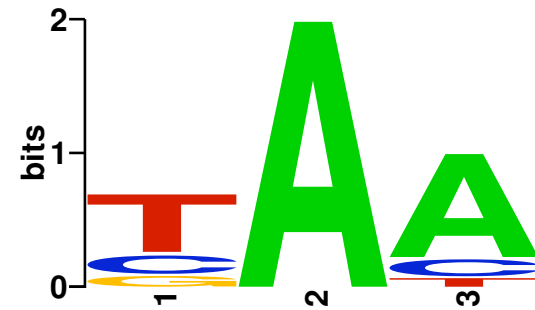
-212.866 aca
 -211.624 gaa
 -211.259 taa
 -209.915 tac
 -209.865 taa
 -209.282 taa
 -209.112 gaa
 -208.631 ccc
 -208.593 gac
 -208.281 gta
 -208.204 caa
 -208.058 caa

[1ubdC, F4]

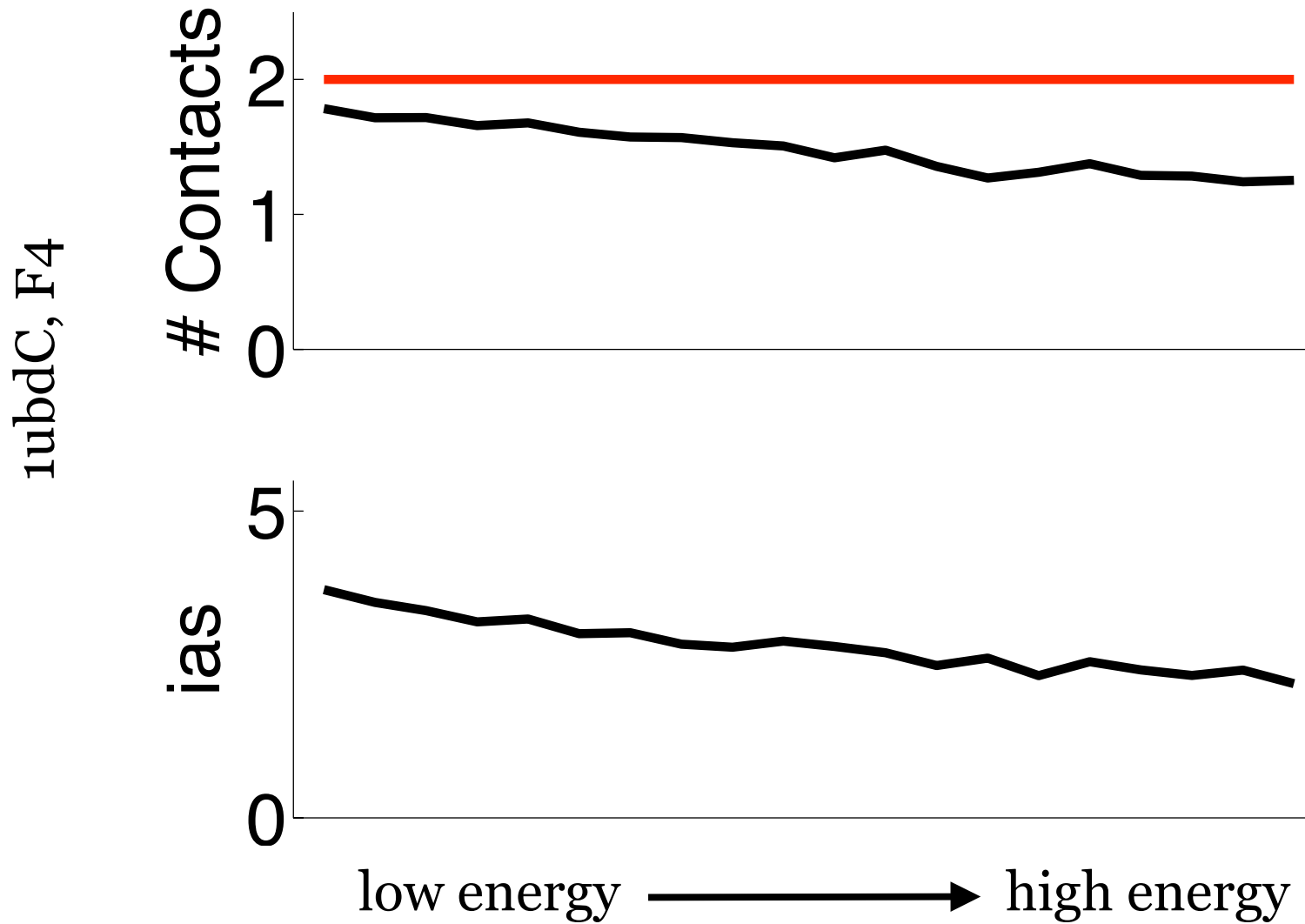
DNA #

taa 259
 caa 139
 tac 90
 gaa 89
 tat 51

A 0, 628, 487
C 139, 0, 90
G 89, 0, 0
T 400, 0, 51

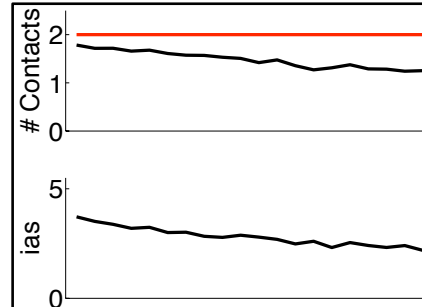


Results: structure prediction



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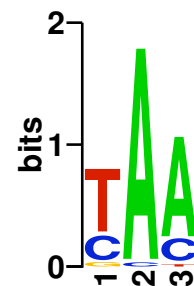
Full protocol



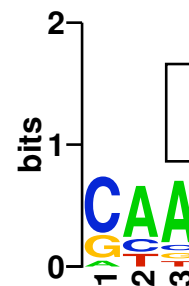
1ubdC, F4

	repack	sc-mcm	high res.
1aayA, F1			
2drpA, F1			

Results: single ZF specificity prediction



Predicted



Experimental

1ubdC, F4

	Position	Position	Position
	repack	sc-mcm	high res.
1aayA, F1			
2drpA, F1			

Results: multi-ZF specificity prediction

	Predicted	Experimental
YY1 [1ubdC]	bits Position	bits Position
Egr1 [1aayA]	bits Position	bits Position
TTK [2drpA]	bits Position	bits Position

Summary

- Structure-based prediction of DNA binding specificity, using family info
- Works well for C₂H₂ ZFs
 - more families to follow

Acknowledgements

- Phil Bradley, Bradley lab
- FHCRC

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