

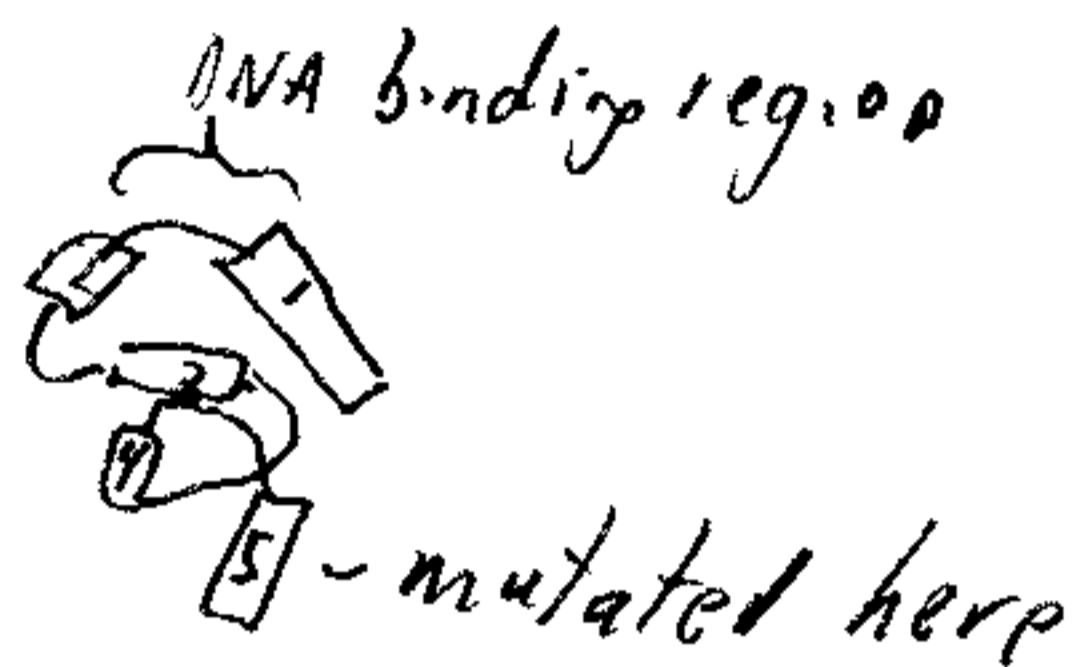
Hemoglobin structural evolution

- α -helices have pivoted in diff. globins

Site Directed Mutagenesis

λ Repressor

① cassette mutagenesis



② functional selection ...

- have λ R on plasmid which if λ x/1 provides resistance to superinfection

- assumption ... changes in 5 would affect DNA binding ~~by~~ affecting structure

③ results

two positions had restricted a.a.

- these were hydrophobic, buried a.a.

Hydrophobic Core

0 a.a. v. tightly packed

② 50 of 7 a.a. in core which are important

COMPOSITION	CONSTRAINT
VOLUME	"
STERIC	"

However

When assaying folding -- the mutants did fold
but didn't have binding.

AA → Structure

How can one tell if a particular aa sequence
will fold into known structures?

→ David Eisenberg -- coded each position by its
info. on environment