

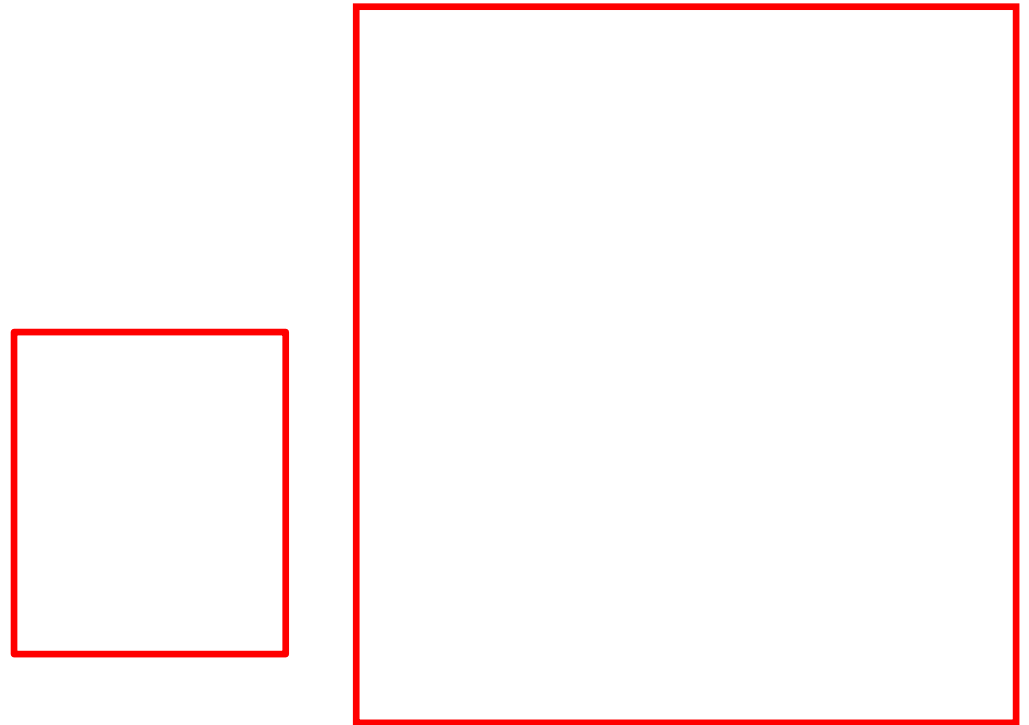


# Computational Design of the Structure and Sequence of a Protein-Binding Peptide

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# Protein-Peptide Interface Design – Target Complex



GoLoco (BLUE),  $G\alpha_{i1}$  (GREEN)  
(PDB ID=2OM2)

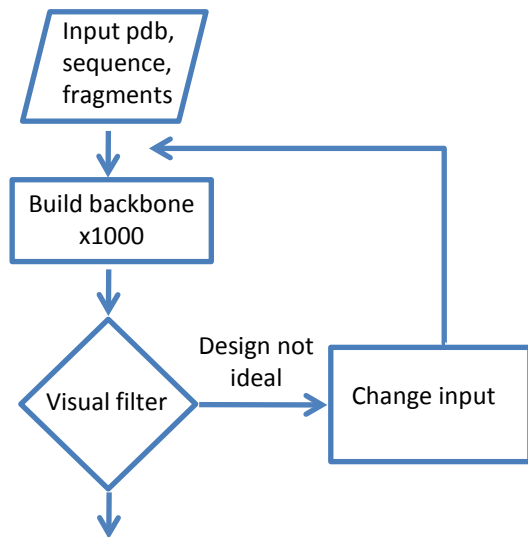
# Interface Design – Growing a Helix

GoLoco (BLUE)

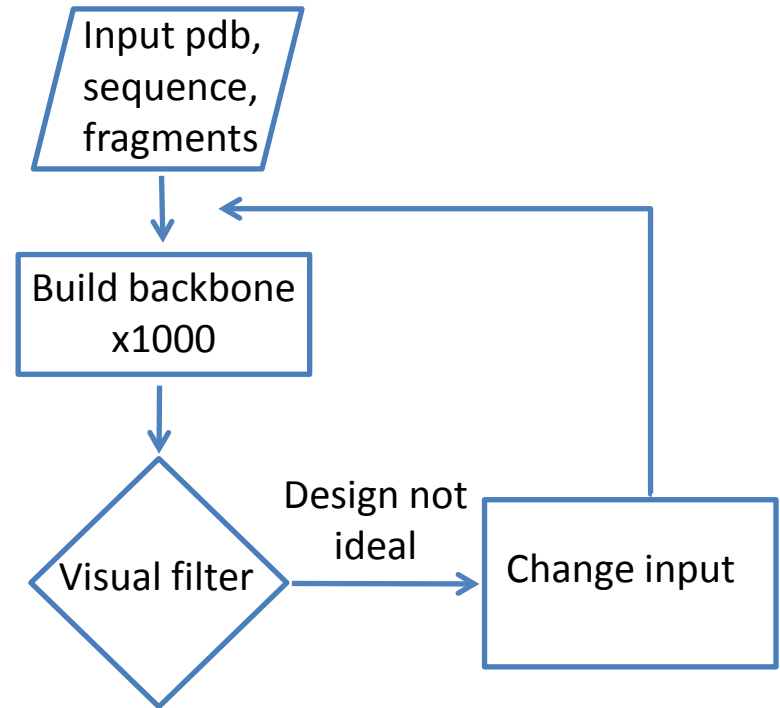
$G\alpha_{i1}$  (GREEN)

GoLoco with Modeled Helix

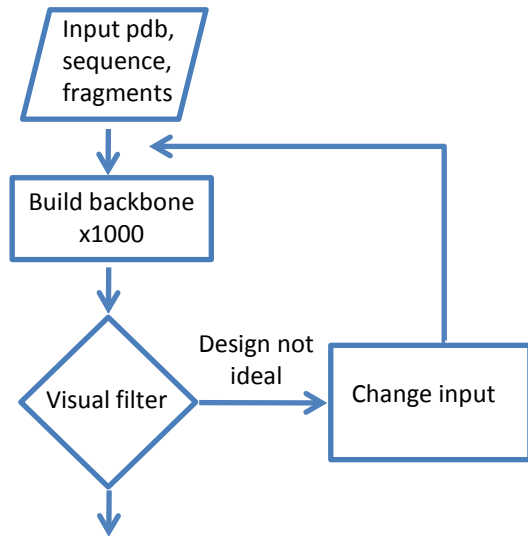
Design Backbone



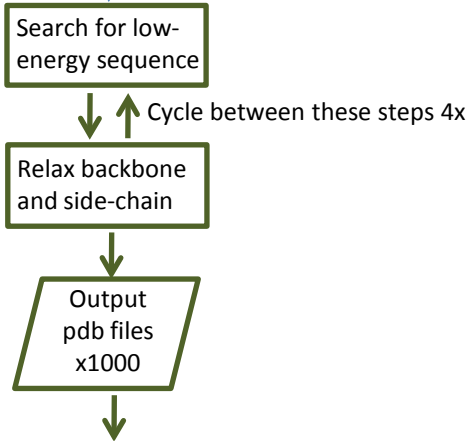
# Backbone Design



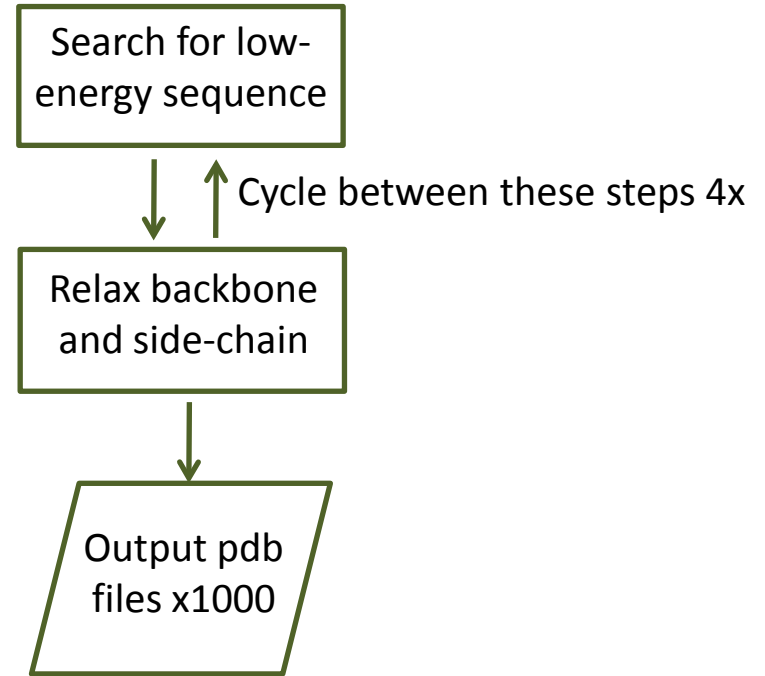
Design Backbone



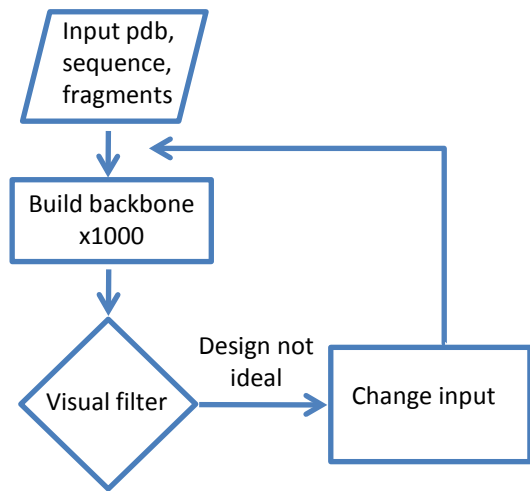
Design Sequence



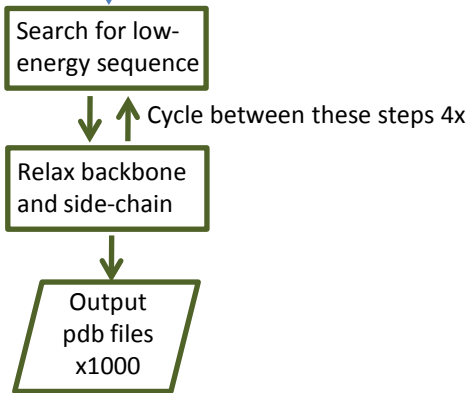
# Sequence Design



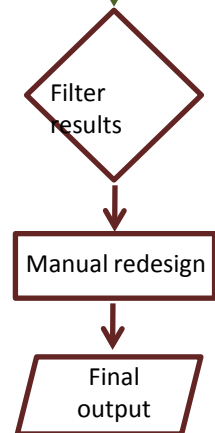
Design Backbone



Design Sequence



Select best designs

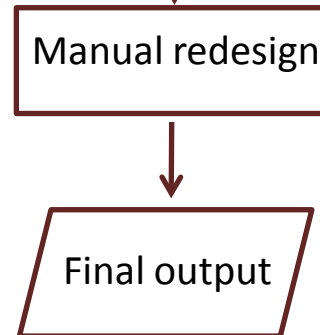


## Selecting designs for characterization

(C)



(D)



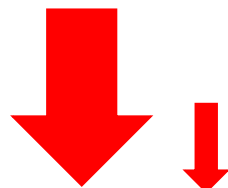
(C) Filters: See next slides

(D) Manual redesign: solvent-exposed side-chains were changed to enhance solubility

# Selecting Designs for Experimental Characterization

- Filter – remove designs with unsatisfied hydrogen bond partners
- Sort
  - First sort by “Score” ( $\Delta G$ )
  - Second sort by  $SASA_{\text{pack}}$

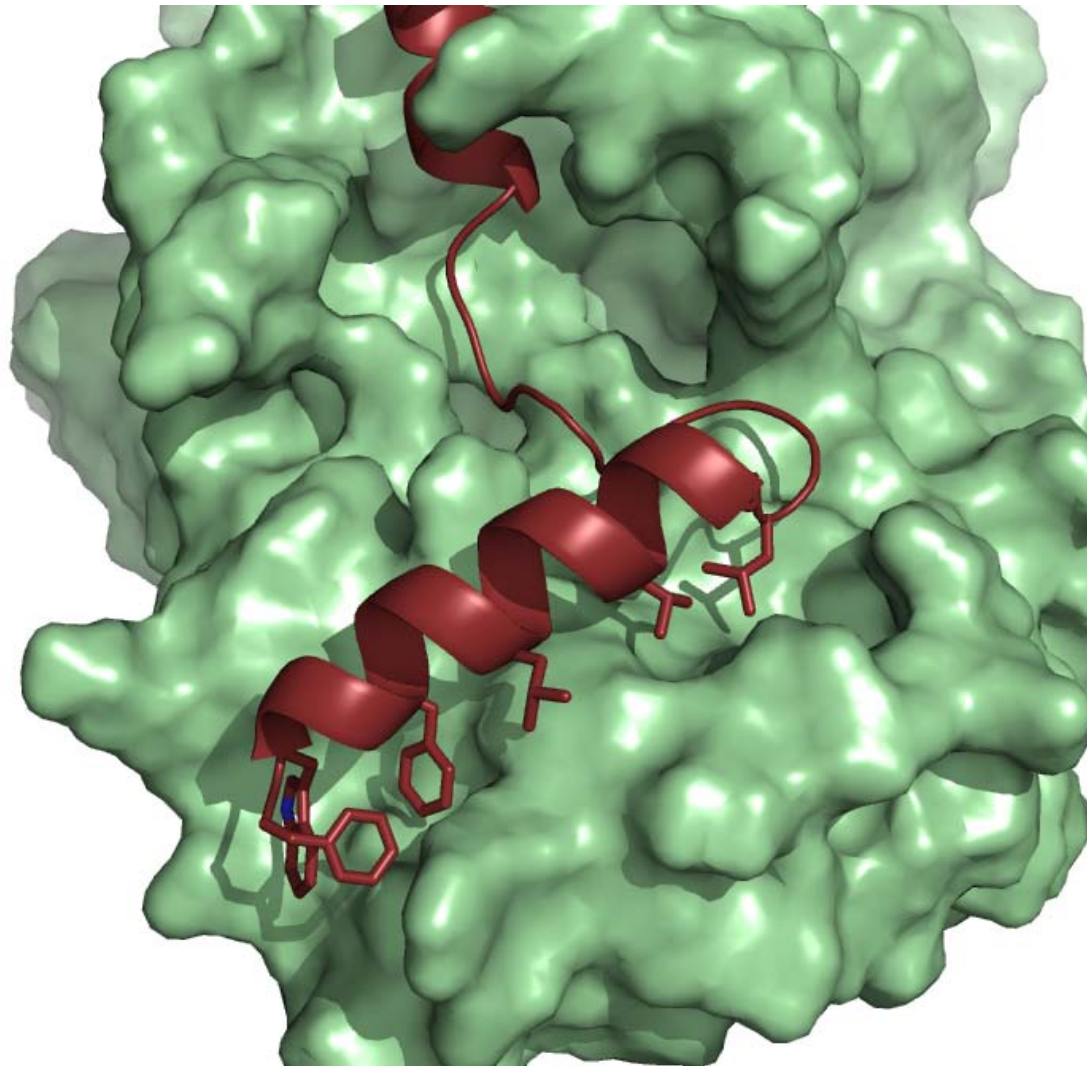
# Sorted Results - Selecting Designs for Experimental Characterization



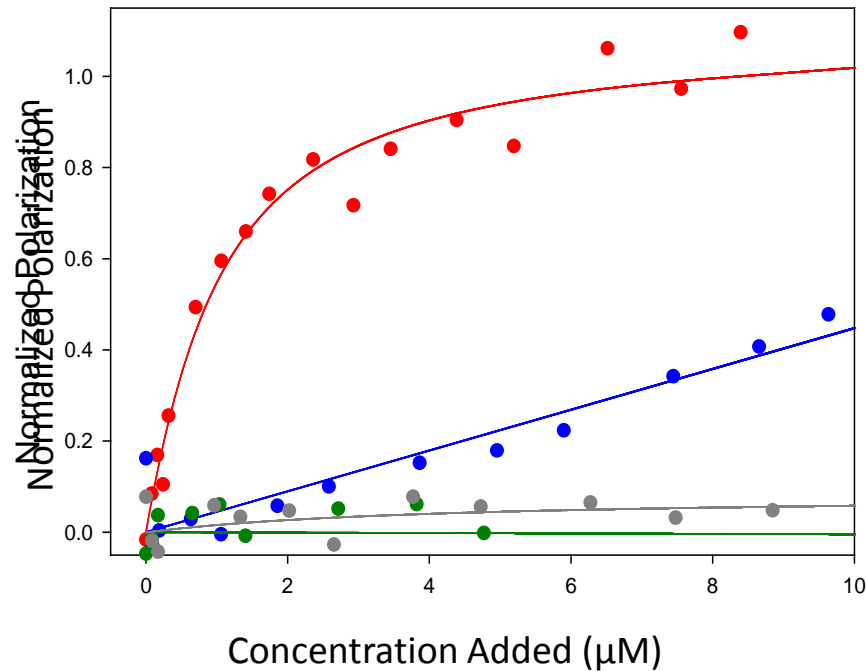
	LJ <sub>atr</sub>	LJ <sub>rep</sub>	Sol	Hb	Elec	Tot.	SASA <sub>pack</sub>	BBHb <sub>UNS</sub>	SCHB <sub>UNS</sub>	Design #
1	-88.9	7.1	43.8	-9.9	-4.1	-52.8	-0.7702	1	4	0273
2	-91.3	9.7	44.6	-11	-3.9	-52.7	-0.0853	1	4	0441
3	-89.2	7.6	44.6	-10.4	-4.4	-52.6	-0.7939	1	2	0845
4	-87.4	6.8	43.1	-10	-4.4	-52.6	-0.0397	1	3	0988
5	-88	8.8	42.4	-9.6	-5	-52.3	-0.1033	1	2	0216
6	-88.3	8.9	43.3	-11	-4.1	-52	-0.7602	1	4	0951
7	-88	9.3	43.5	-10.6	-5.4	-52	-0.2395	1	3	0480
8	-87.8	7	43.9	-9.9	-4.3	-52	-0.1541	1	3	0450
9	-88.8	7.6	43.7	-9.9	-3.8	-52	-0.0796	1	2	0620
10	-87.3	7.7	44.7	-11.3	-4.9	-51.9	-0.8178	1	3	0763



# Model Structure of $G\alpha_{i1}$ – GoLoco helix



# Characterization of 4 Best Designs



GoLoco 496 **D**I**E**G**L**V**E**L**L**N**R**V**Q**S**S**G**A**H**D****Q**R**G**L**L**R**K**E**D**L**V**L**P**E**F**L**Q**<sub>531</sub>

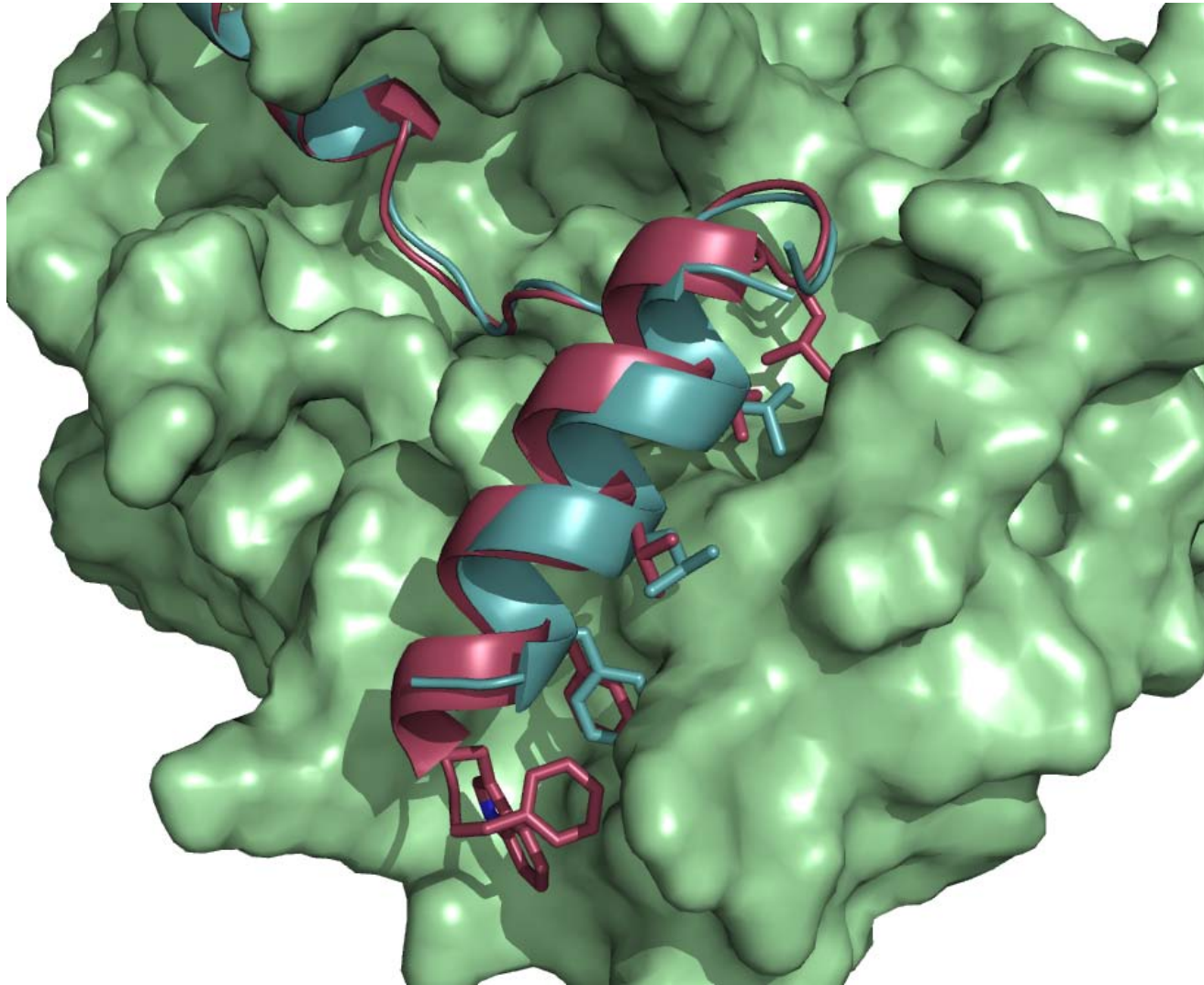
GL<sub>helix</sub>-1 496 **D**I**E**G**L**V**E**L**L**N**R**V**Q**S**S**G**A**H**D****Q**R**G**L**L**I**L****Q**R**L**E**E**D**F**R**K**W**L**R**M**L**R**<sub>536</sub>

GL<sub>helix</sub>-2 496 **D**I**E**G**L**V**E**L**L**N**R**V**Q**S**S**G**A**H**D****Q**R**G**L**S**E**W****Q**R**F**W**R**R**W**L**E**W**L**I**Y**L**F**<sub>536</sub>

GL<sub>helix</sub>-3 496 **D**I**E**G**L**V**E**L**L**N**R**V**Q**S**S**G**A**H**D****Q**R**S**L**L**R**Q**E**E**M**Q**R**A**I**R**D**F**A**K**W**F**<sub>535</sub>

GL<sub>helix</sub>-4 496 **D**I**E**G**L**V**E**L**L**N**R**V**Q**S**S**G**A**H**D****Q**R**G**L**L**S**N**E**E**V**F**R**A**L**R**D**F**D**R**W**F**<sub>535</sub>

# $G\alpha_{i1}$ -GL<sub>helix</sub>-4 : Crystal Structure with Design Structure



# Acknowledgements

- Brian Kuhlman
- Glenn Butterfoss
- Carrie Purbeck
- David Siderovski
- Dustin Bosch
- Mischa Machius