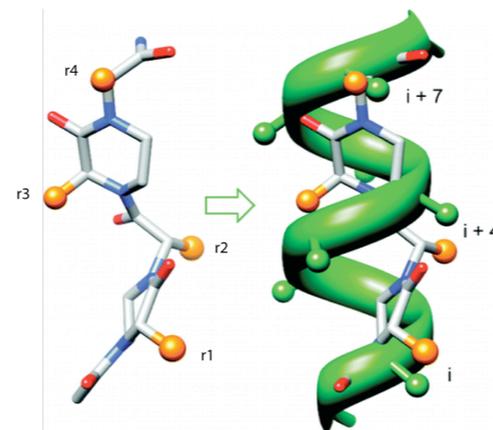


Rational design of protein inhibitors using Oligooxopiperazines (OOPs)

RosettaCon 2012
Kevin Drew
Tuesday, July 31, 2012



Tosovska, P., 2010

Outline

- **Motivation and Background**
 - helical mimetics
 - MDM2 - P53 protein interface
 - OOPs
- **Inhibitor Design**
 - Design Protocol
 - Designs
 - Binding Mode
 - Scaffold Library

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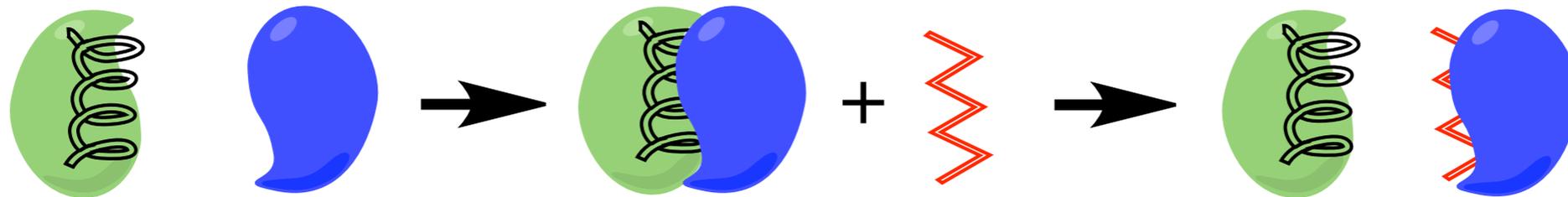
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Inhibitor Design - Goal

Rationally design a molecule to disrupt a specific protein interaction

- screening is expensive and laborious
- small molecules do not span full interaction interface
- use natural interface as starting point



Inhibitor Design - Goal

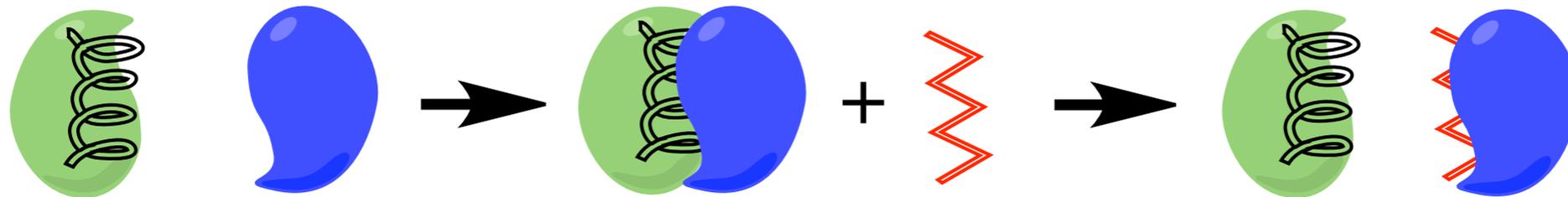
Rationally design a molecule to disrupt a specific protein interaction

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Wadman Nature Biotechnology (2012)

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Inhibitor Design - Goal

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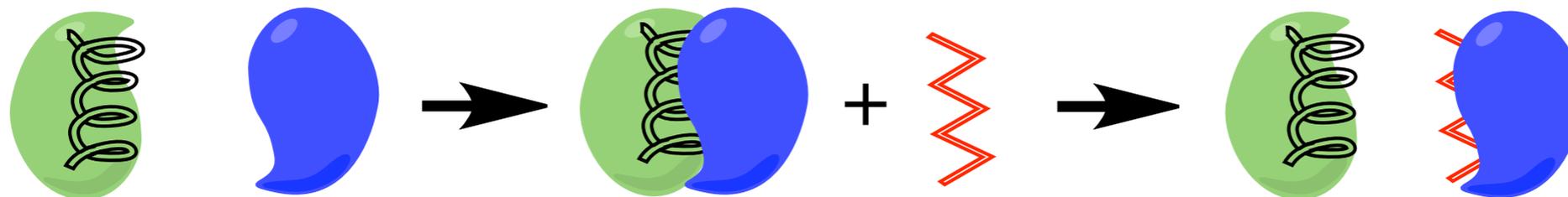
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- ~300 - 1000 Å² protein - small molecule interactions vs ~1500 - 3000 Å² protein protein interactions
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Inhibitor Design - Goal

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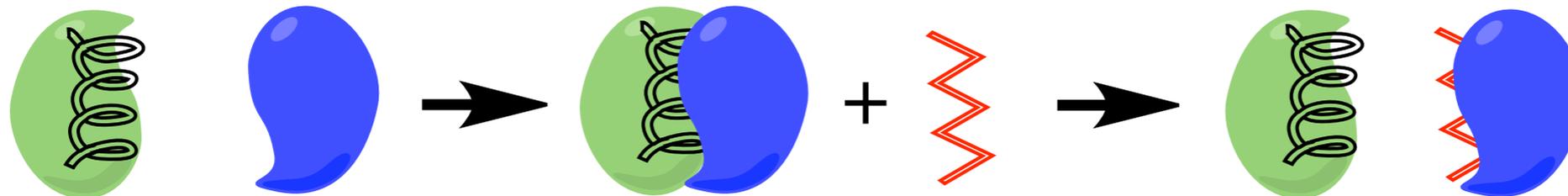
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Wells & McClendon Nature (2007)

- use natural interface as starting point

- mimic hotspot residues on a stable proteolytic resistant scaffold

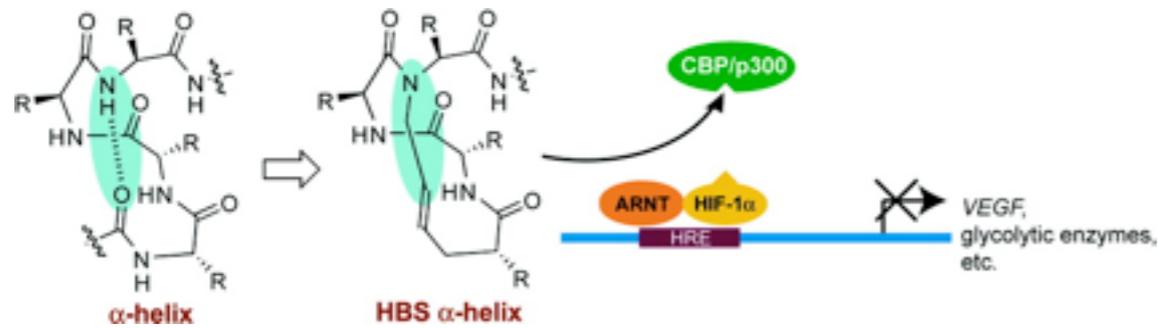


Inhibitor Design - Background

Helical mimetic successes

Hydrogen bond surrogate -

inhibits Hypoxia Inducible Factor 1 / coactivator interaction



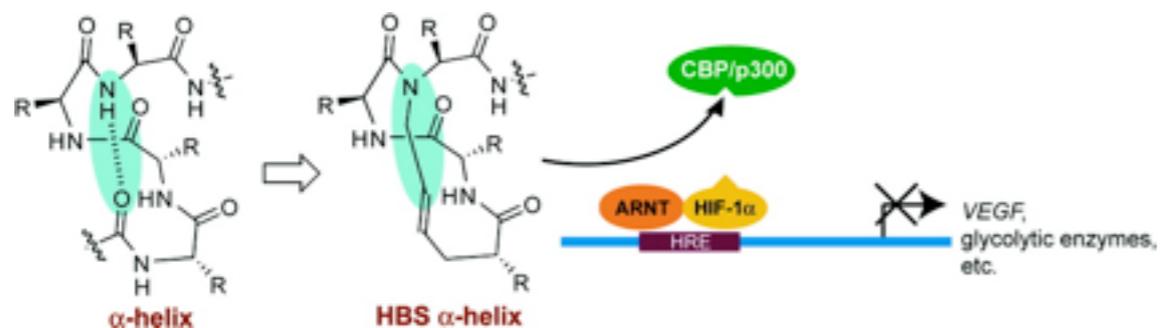
Henchey et al JACS 2010

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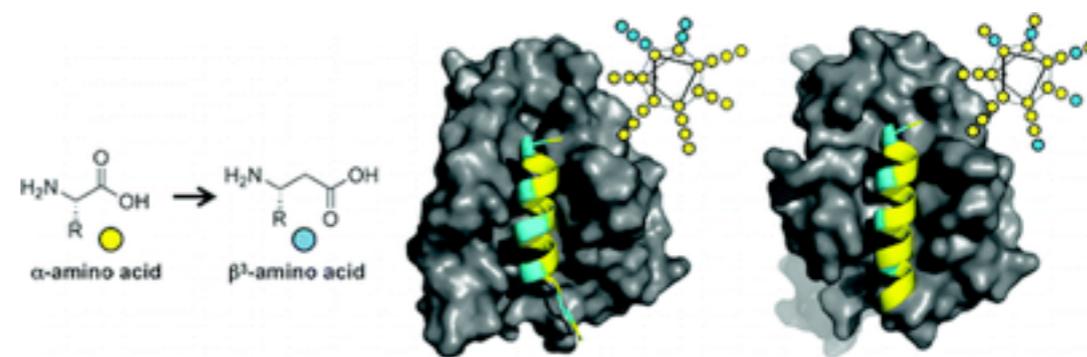
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Henchey et al JACS 2010

Alpha-beta peptides -

binds bcl2 family (anti-apoptotic protein)



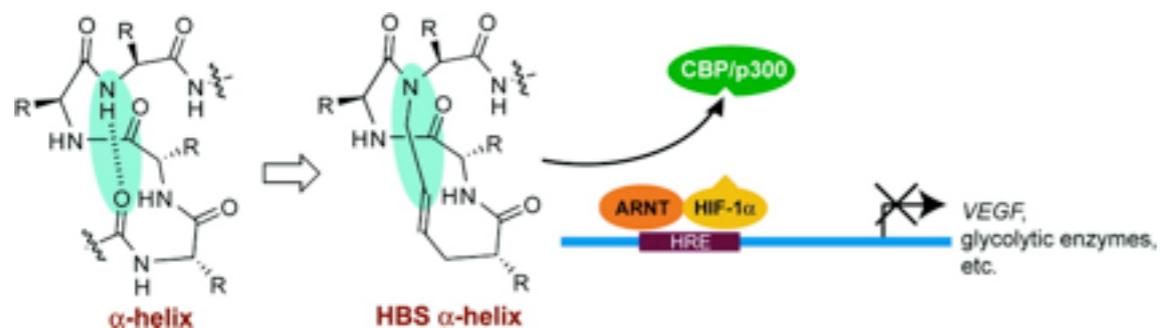
Boersma et al JACS 2011

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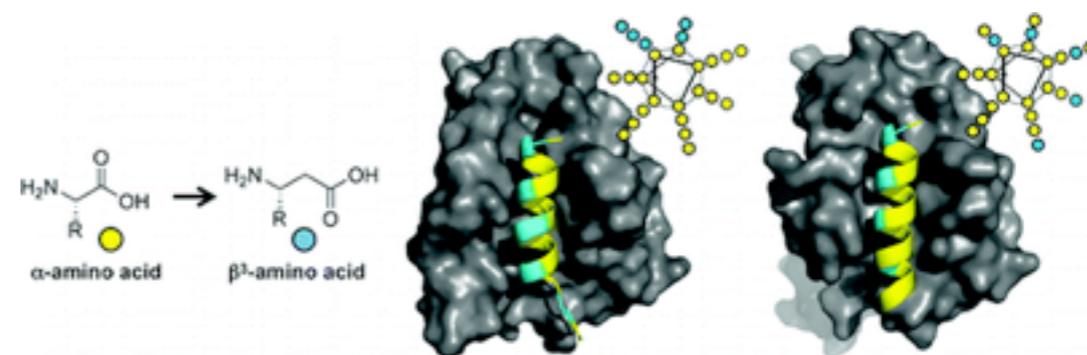
inhibits Hypoxia Inducible Factor 1 / coactivator interaction



Henchey et al JACS 2010

Alpha-beta peptides -

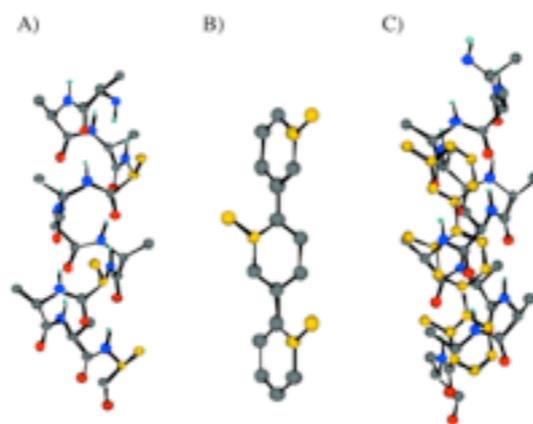
binds bcl2 family (anti-apoptotic protein)



Boersma et al JACS 2011

Terphenyl -

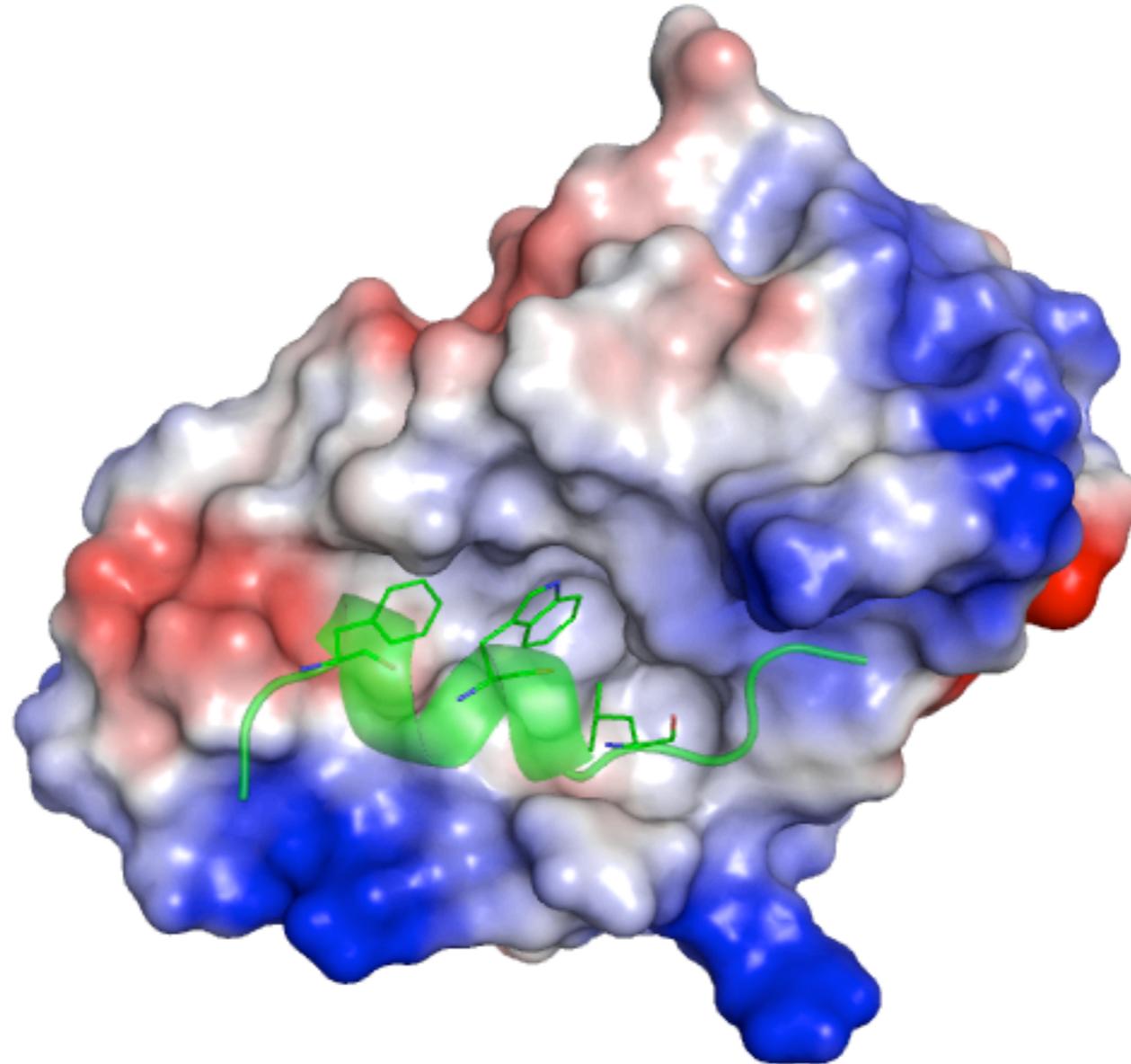
disruption of gp41 oligomerization



Ernst et al ACIE 2002

Inhibitor Design - Model System

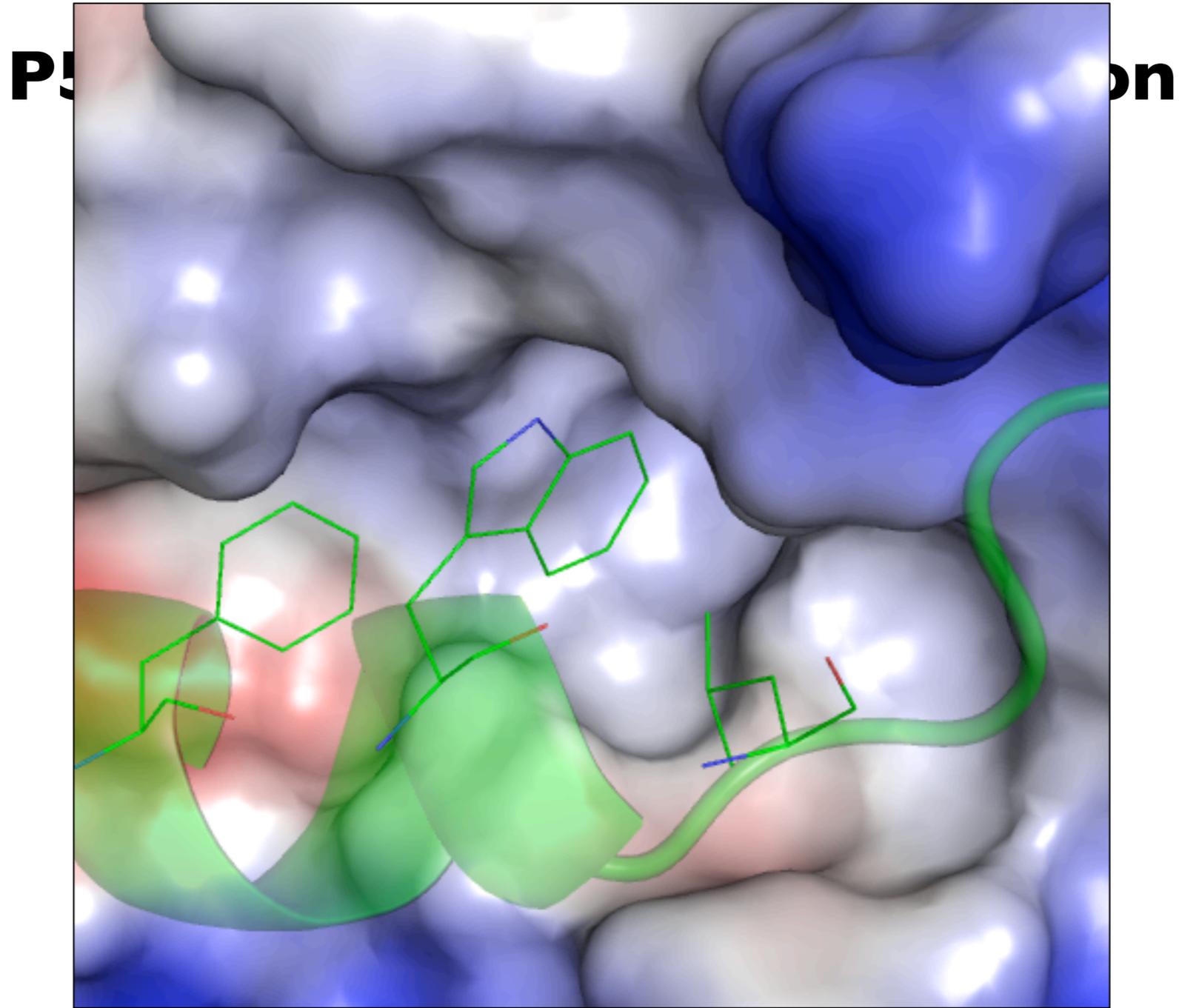
P53 - MDM2 Protein Interaction



P53 transactivating domain (green) bound to MDM2 (electrostatic)
pdbid: 1YCR. (Kussie et al. Science 1996)

Side chains important for binding shown in lines.

Inhibitor Design - Model System

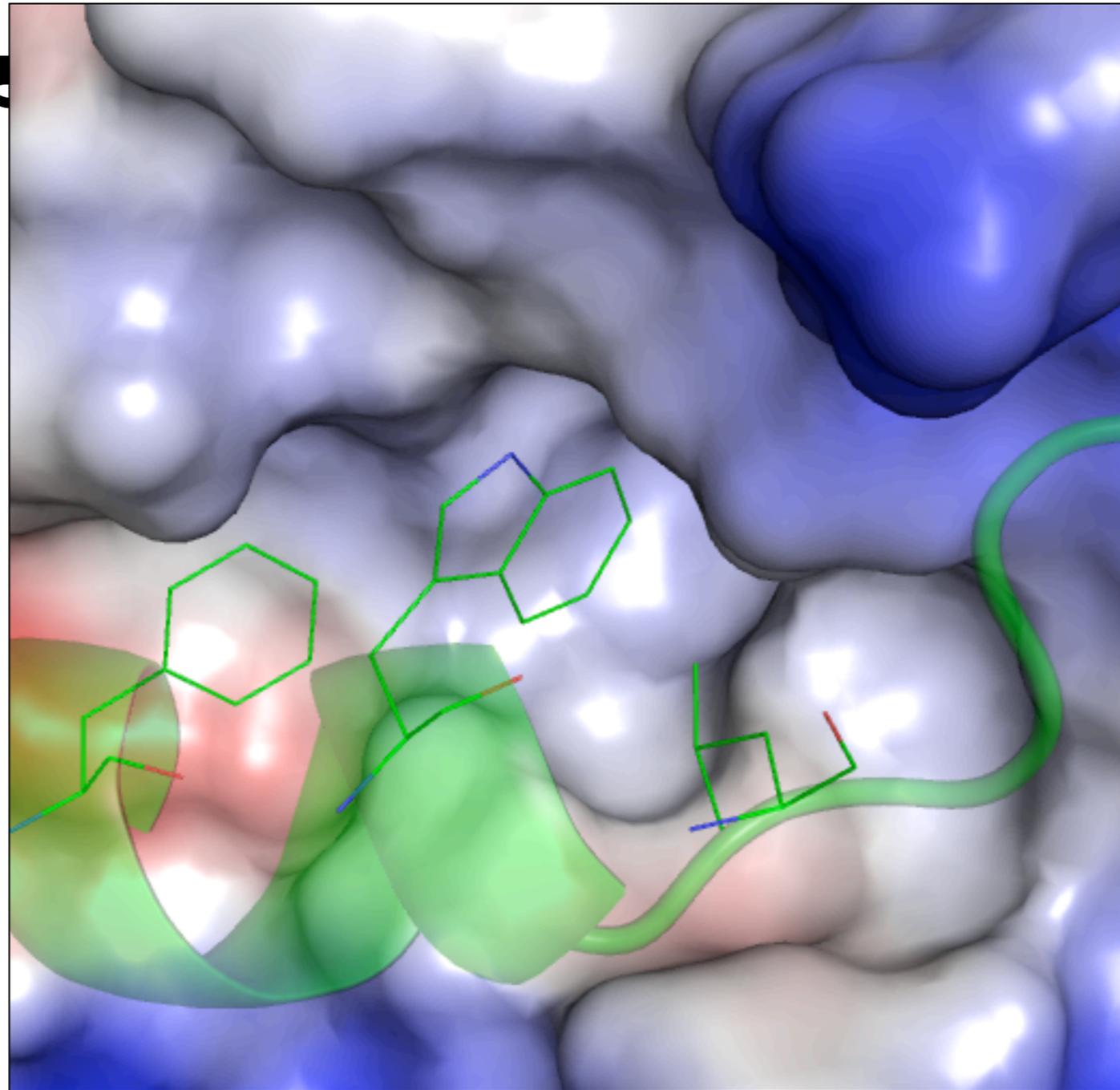


P53 transactivating domain (green) bound to MDM2 (electrostatic)
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Inhibitor Design - Model System

Nutlins - small molecules known to disrupt interaction, $\sim 140\text{nM IC}_{50}$

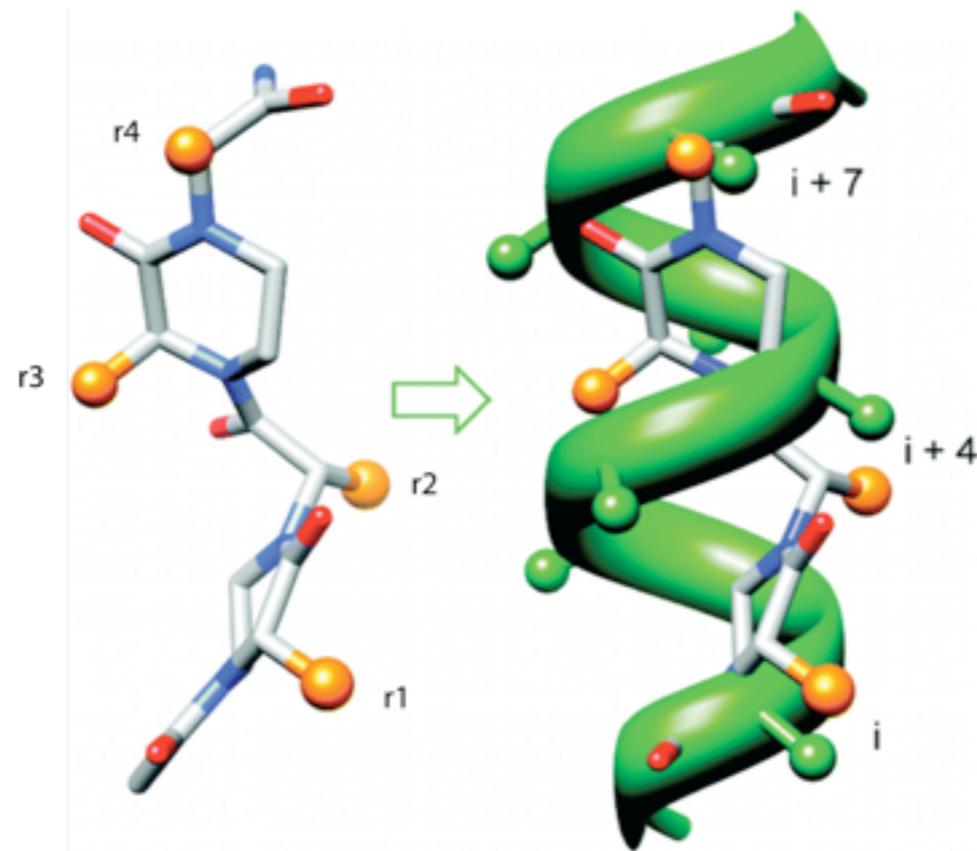


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Inhibitor Design - Scaffold

Oligooxopiperazines (OOPs)

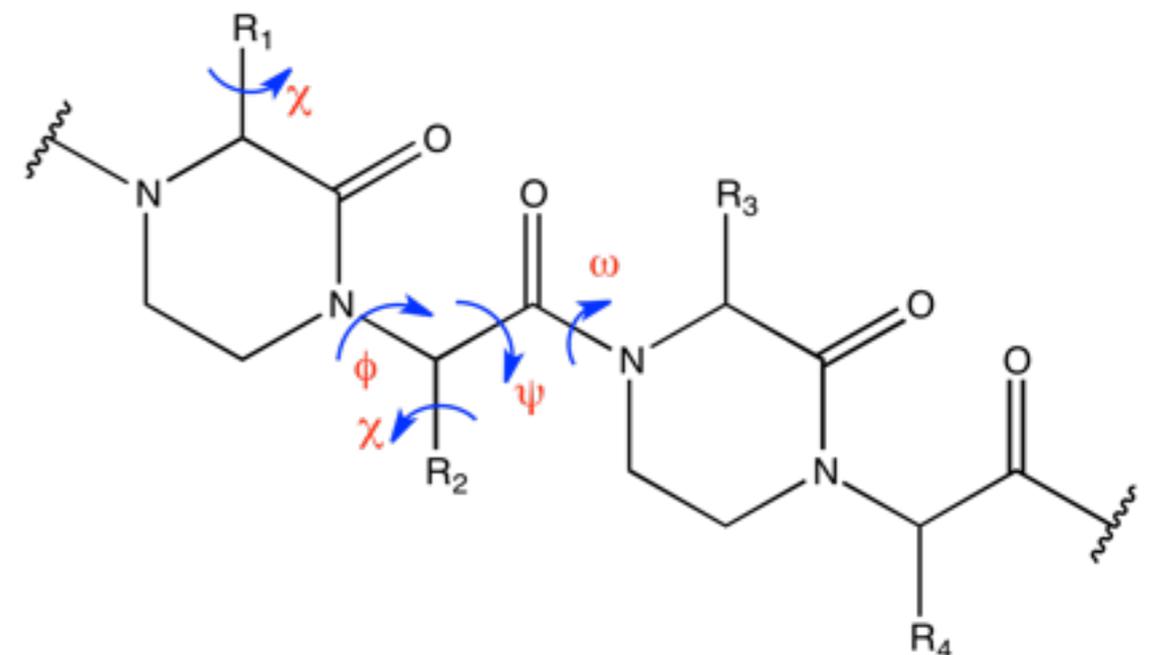


Tosovska, P. 2010

Mimics i , $i+4$ and $i+7$ residues of helix

Peptide backbone with C-C bond

Easy to synthesize (solid phase)



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OOP quantum characterization

How does Rosetta energy function compare?

OOP quantum characterization

How does Rosetta energy function compare?

Quantum Calculations

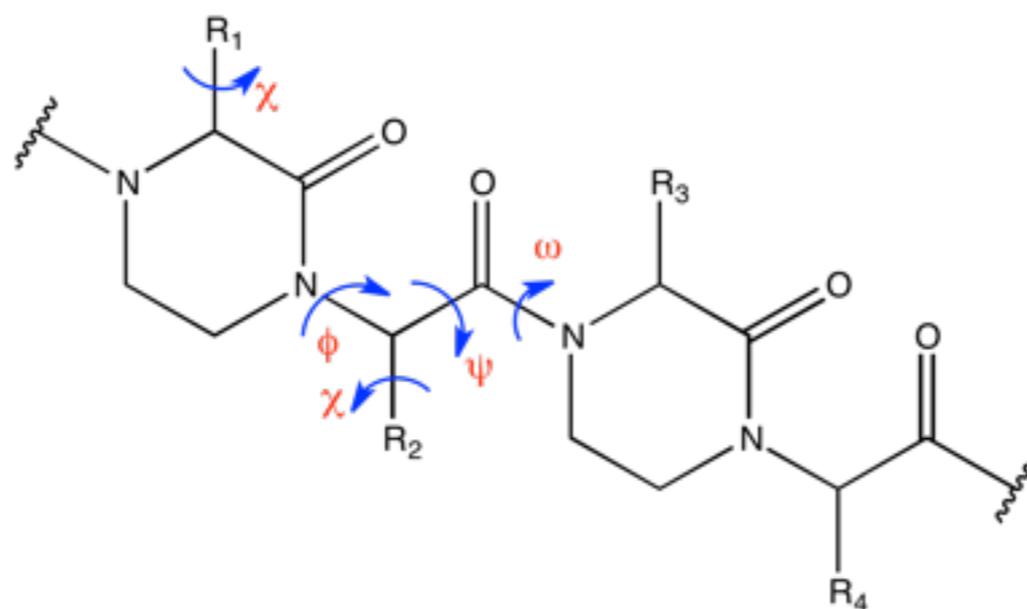
Approach - Gaussian QM Software

Rotate each bond 360° (increment 15°)

Hartree-Fock optimization

B3LYP 6-31G(d) energy calculation

MP2 6-31G(d) energy calculation



OOP quantum characterization

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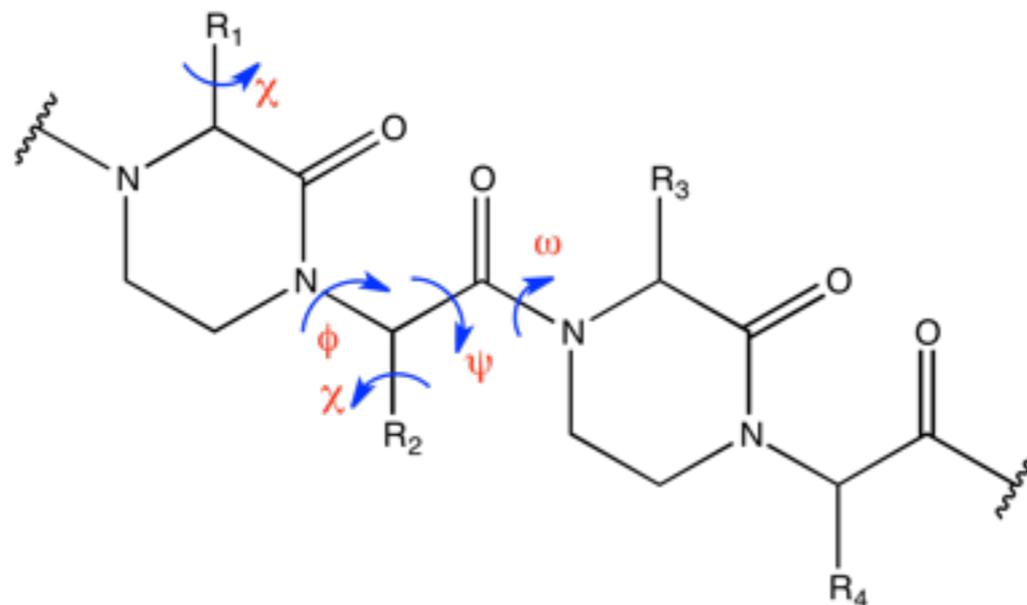
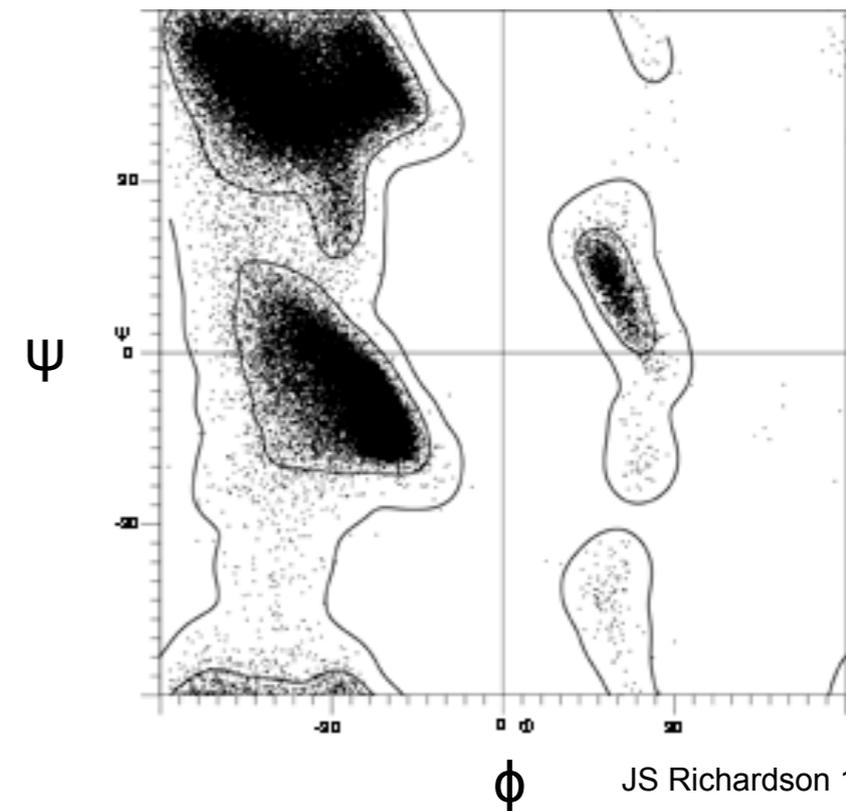
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Ramachandran Map



OOP quantum characterization

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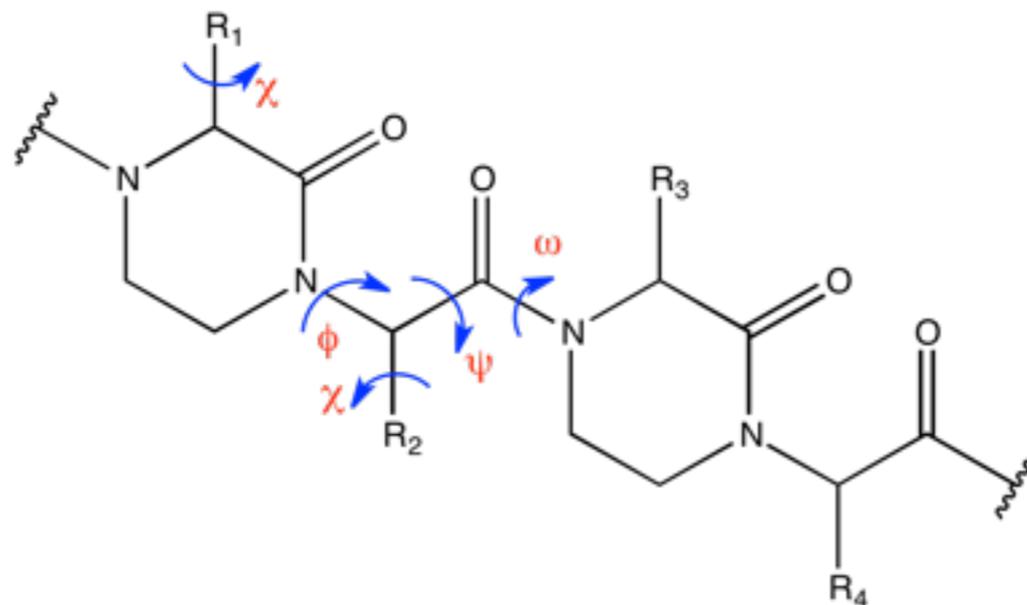
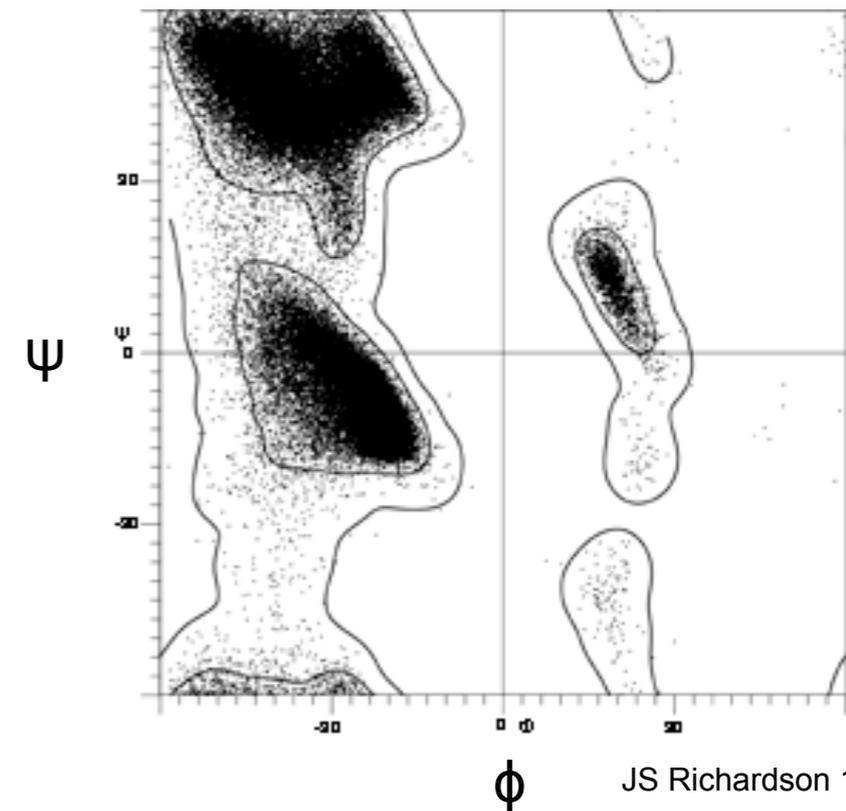
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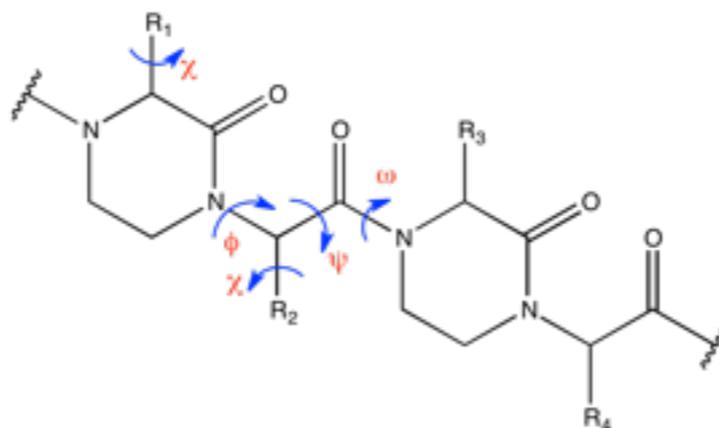
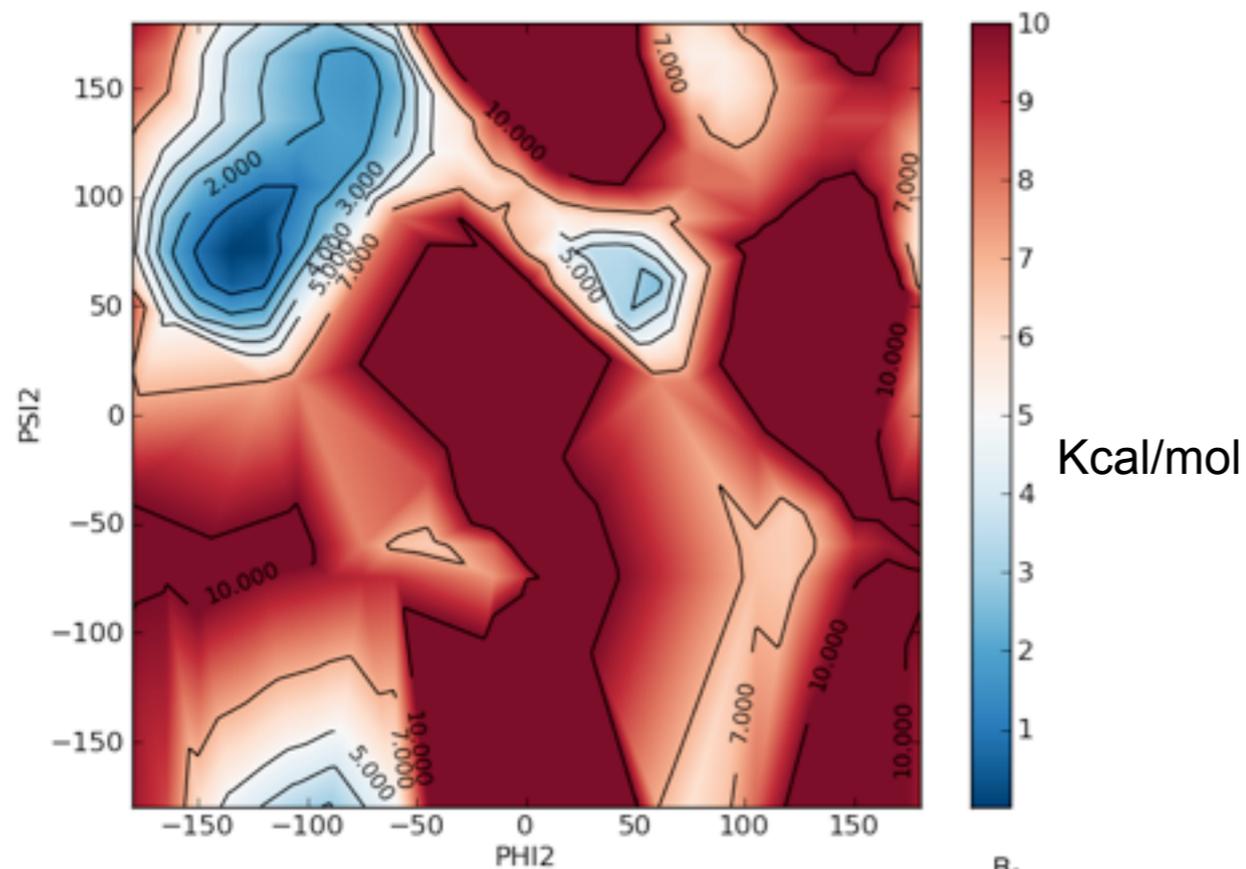
Quantum vs Rosetta: Phi/Psi energy comparison

OOP characterization

Quantum vs Rosetta: Phi/Psi energy comparison

Quantum

B3LYP SOLV 6-31G(d)

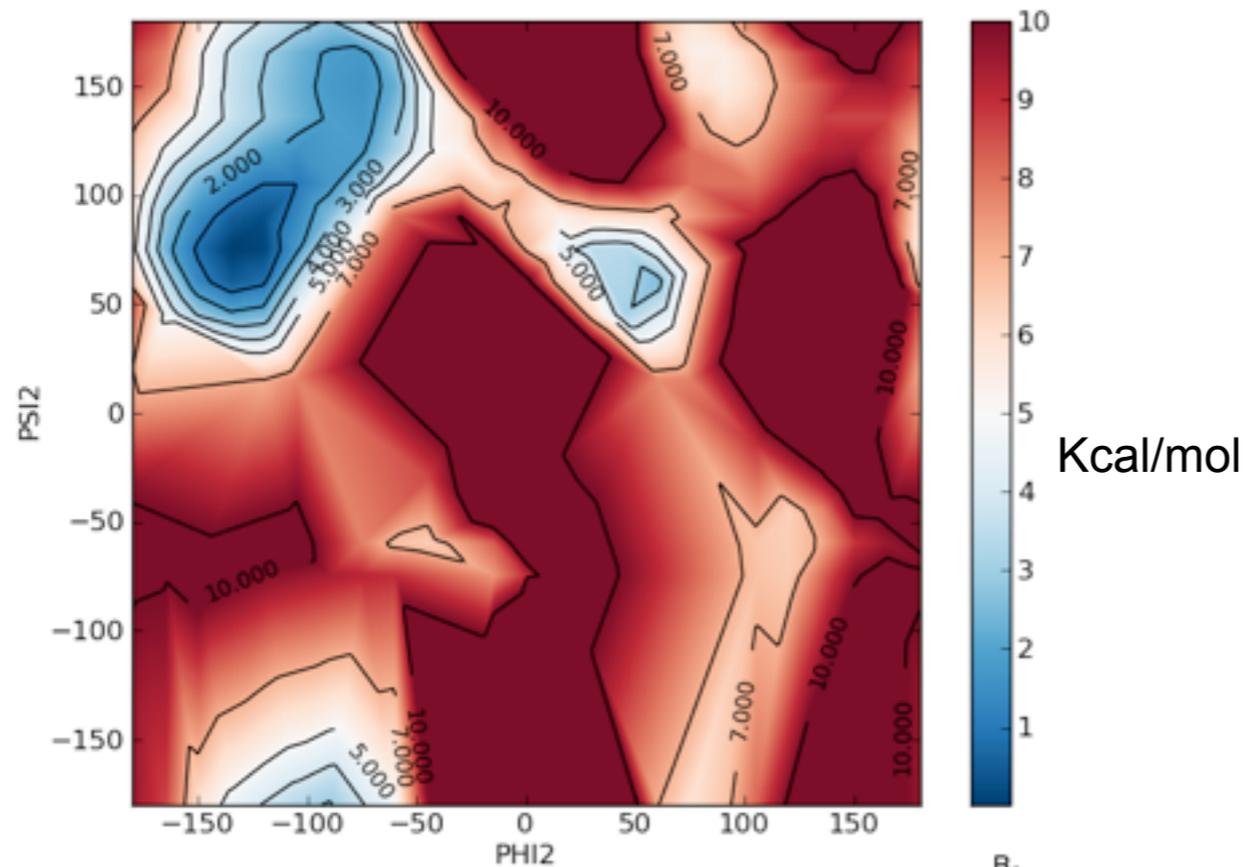


OOP characterization

Quantum vs Rosetta: Phi/Psi energy comparison

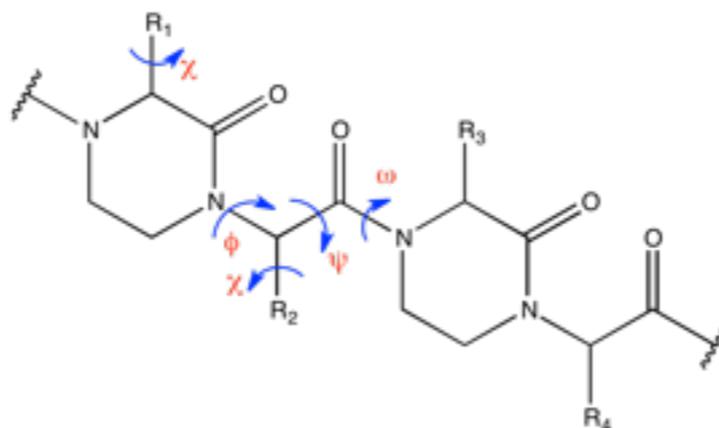
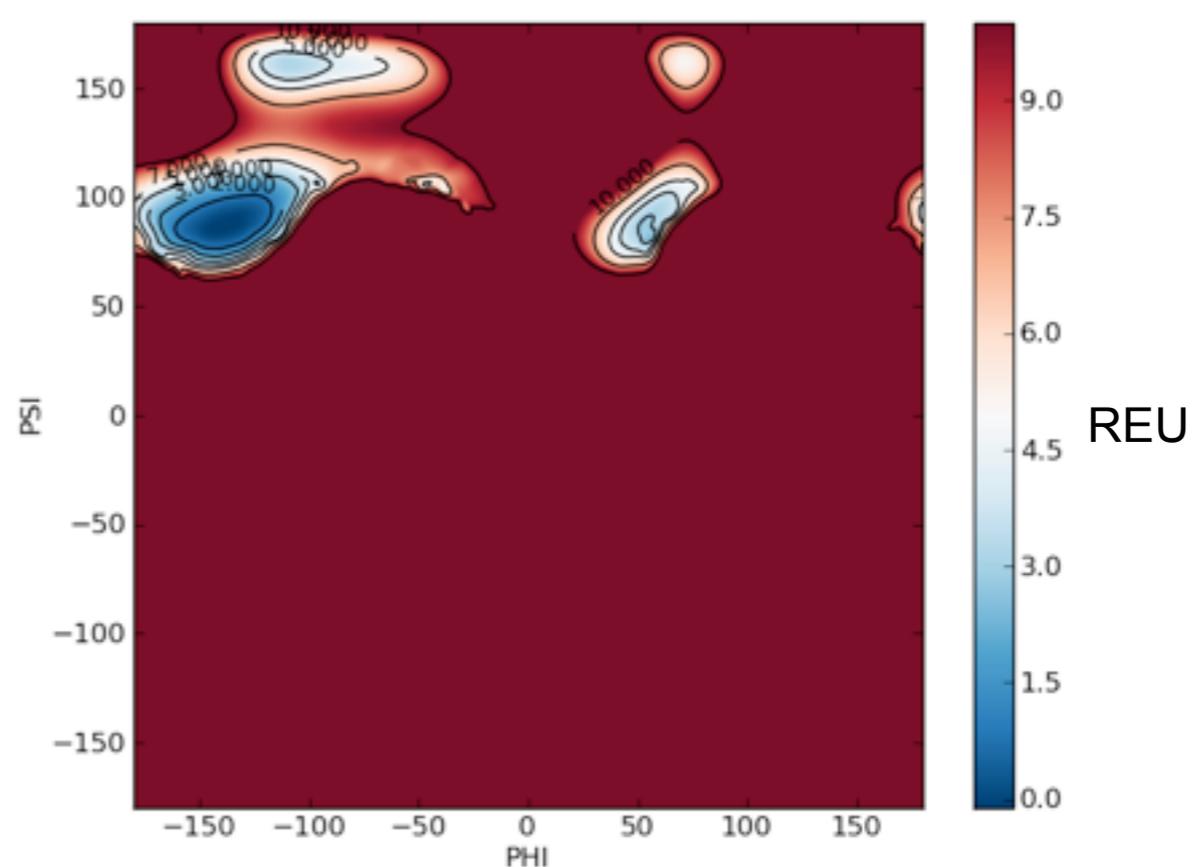
Quantum

B3LYP SOLV 6-31G(d)



Rosetta

MM: Lennard-Jones potential, Lazaridius Karplus solvation, Hbond, reference energy

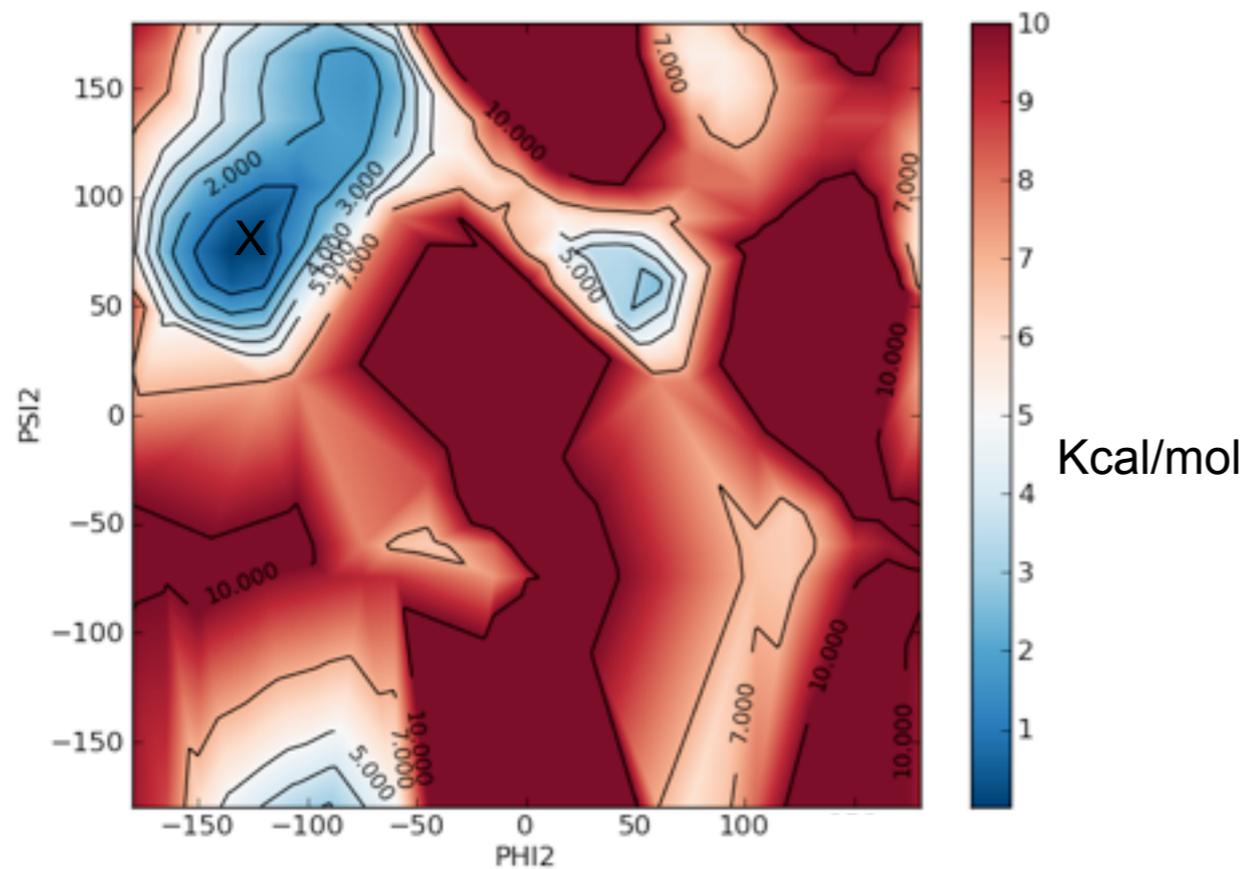


OOP characterization

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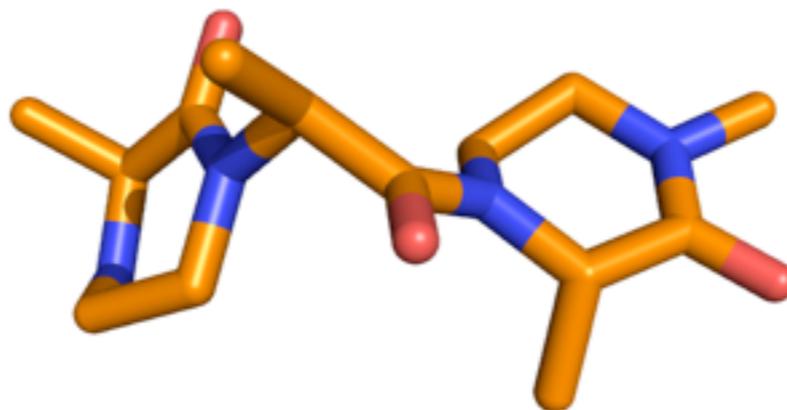
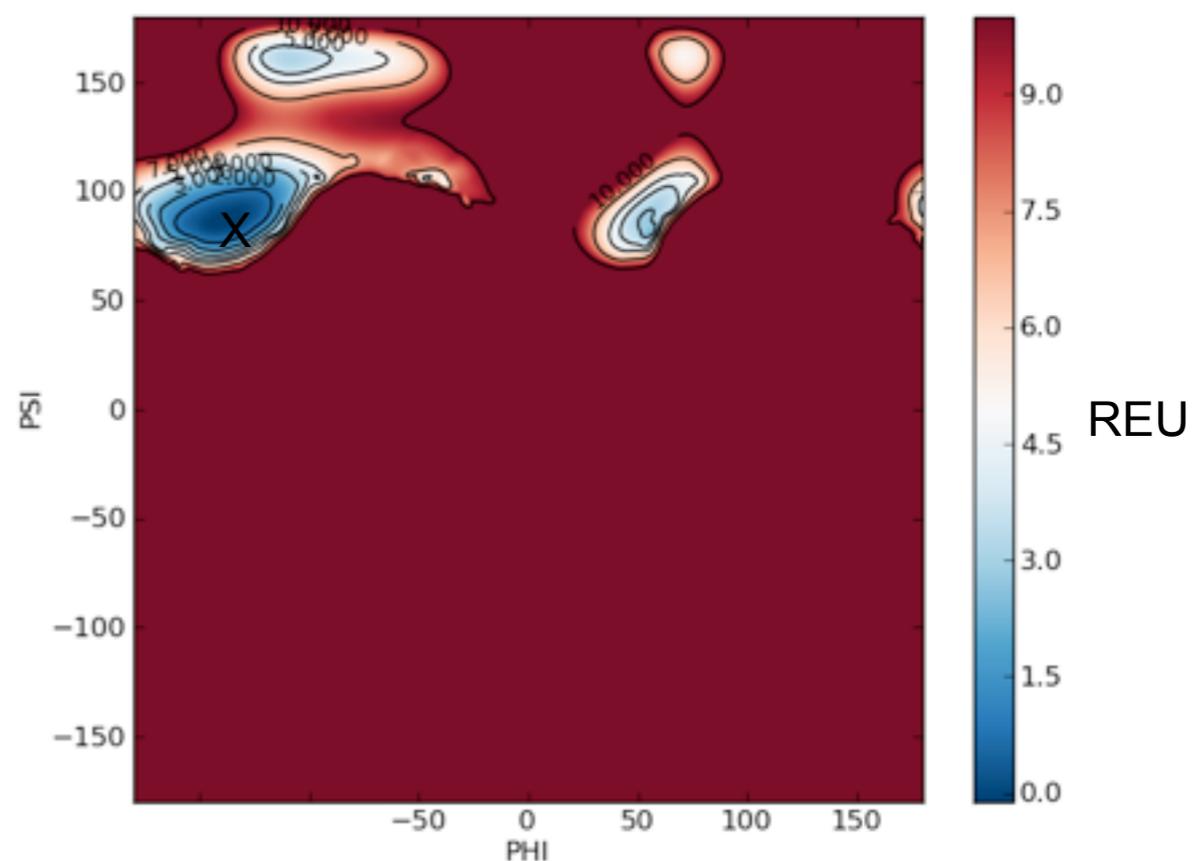
Quantum

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Rosetta

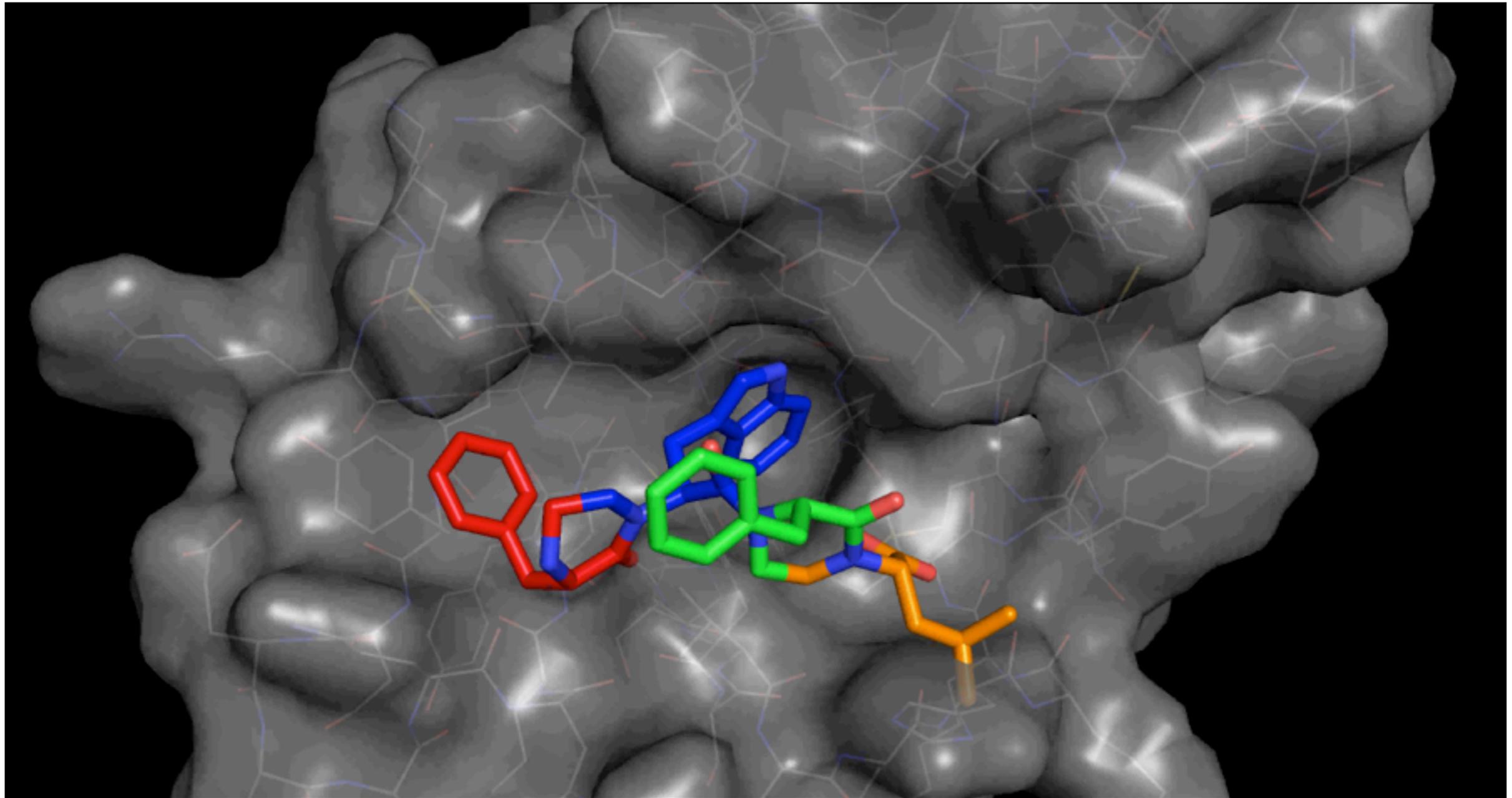
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Design Movie

1st pos	2nd pos	4th pos
dimethyl-PHE	hydroxy-phenylglycine	dehydro-LEU
3methyl-PHE	phenylglycine	fluoro-LEU
4methyl-PHE		
naphthyl-alanine		

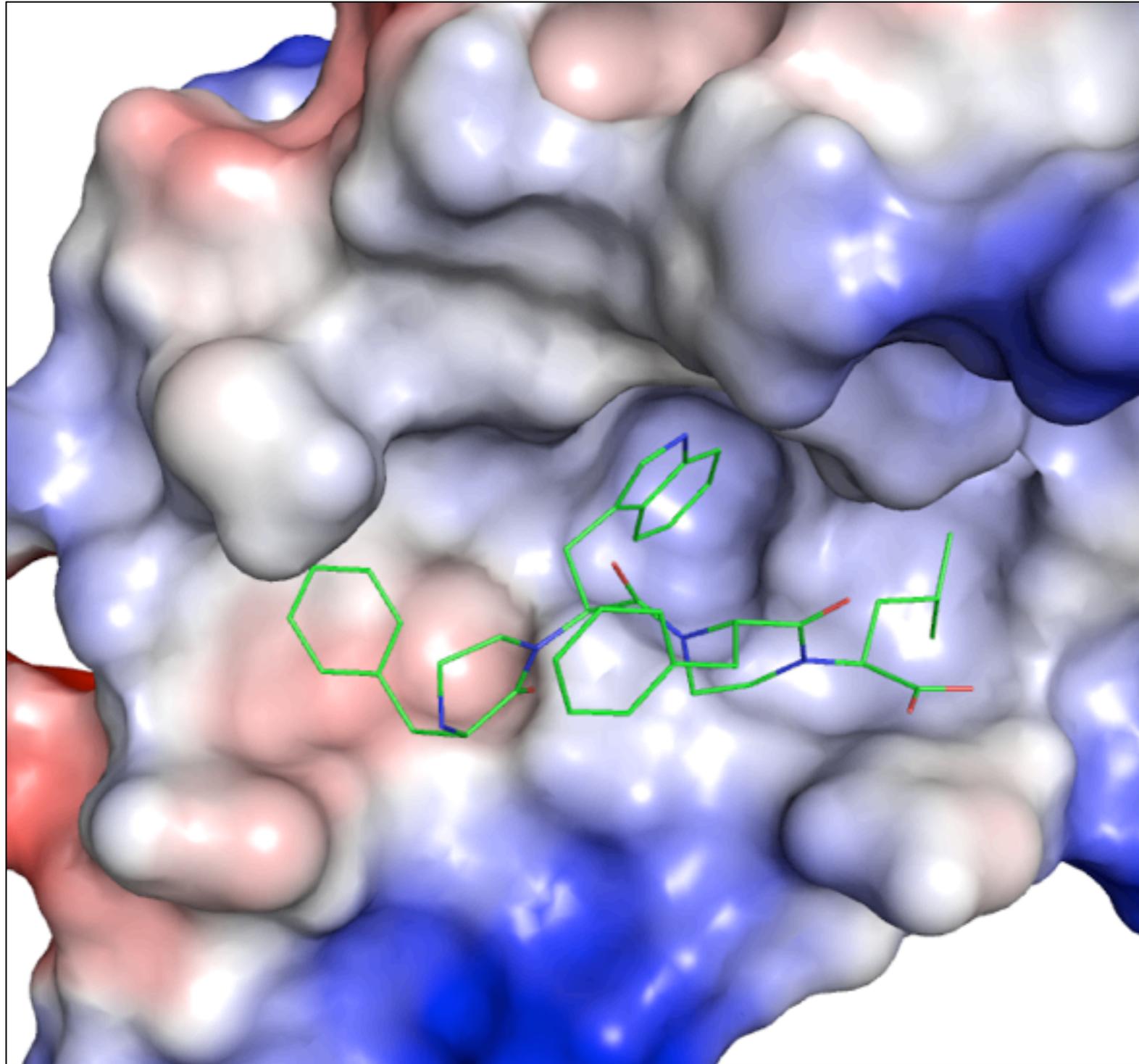
Design Movie



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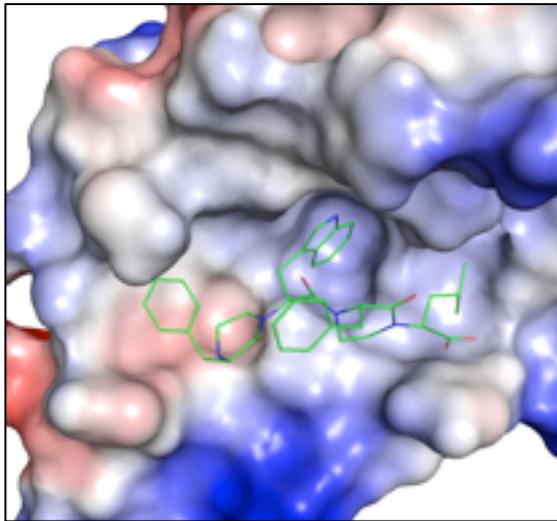
OOP Design

OOP Design

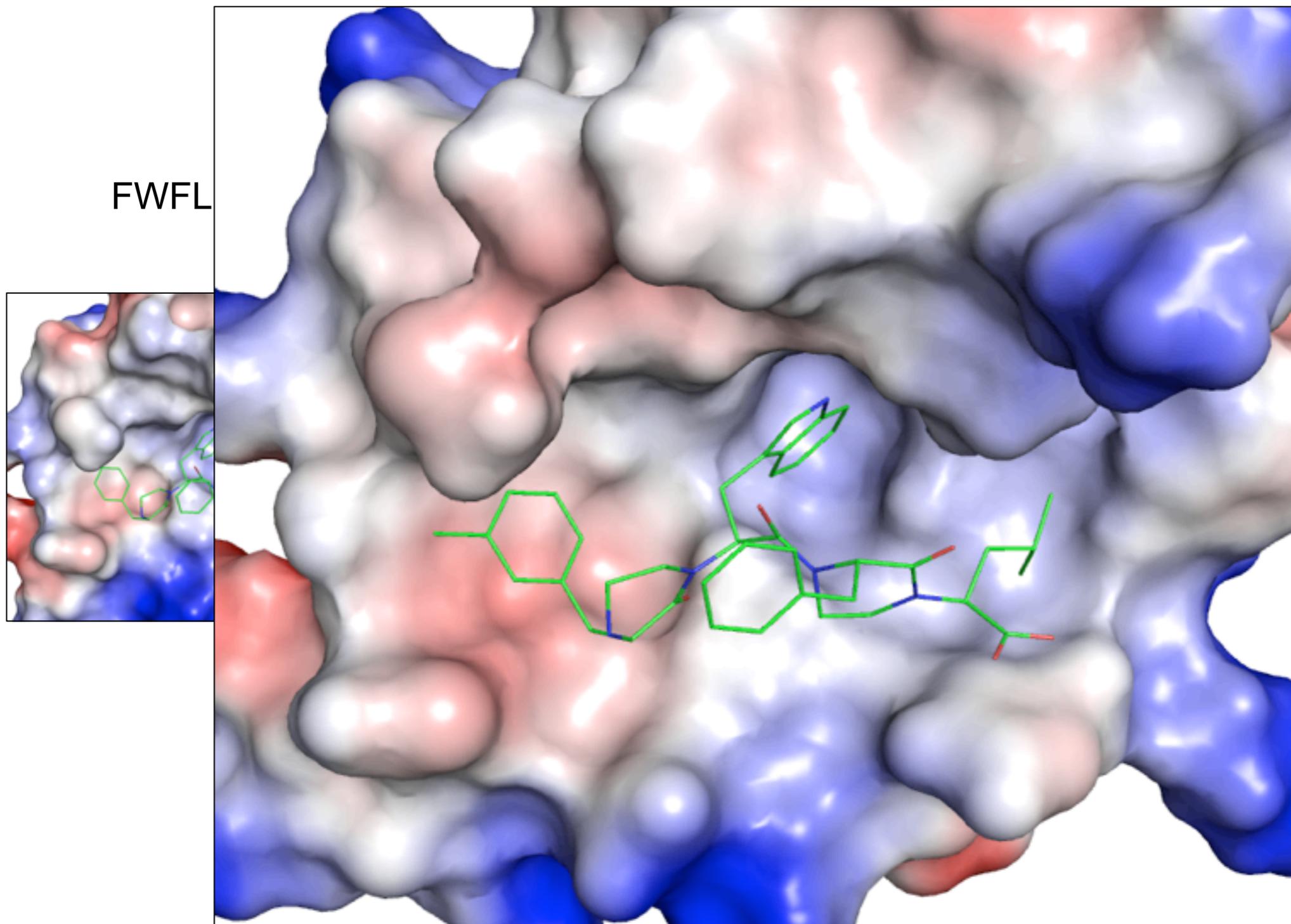


OOP Design

FWFL

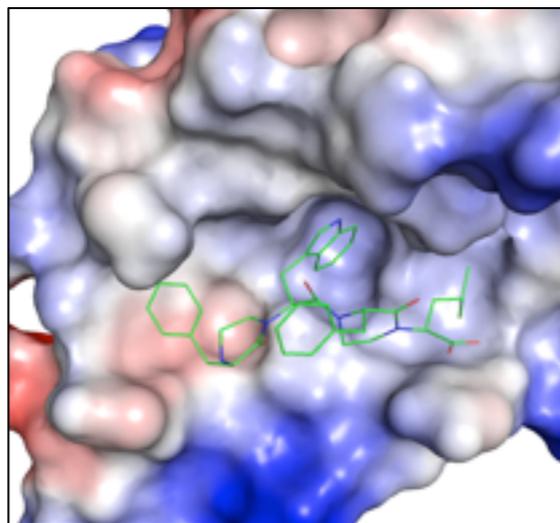


OOP Design

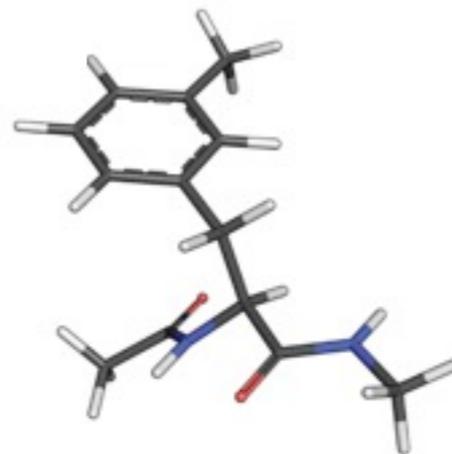
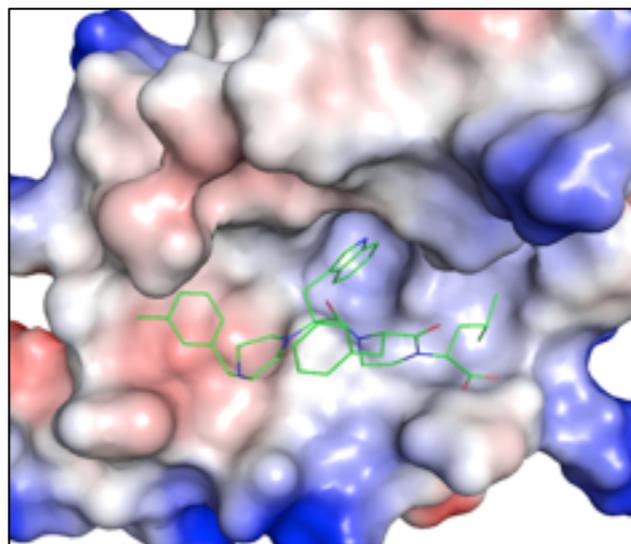


OOP Design

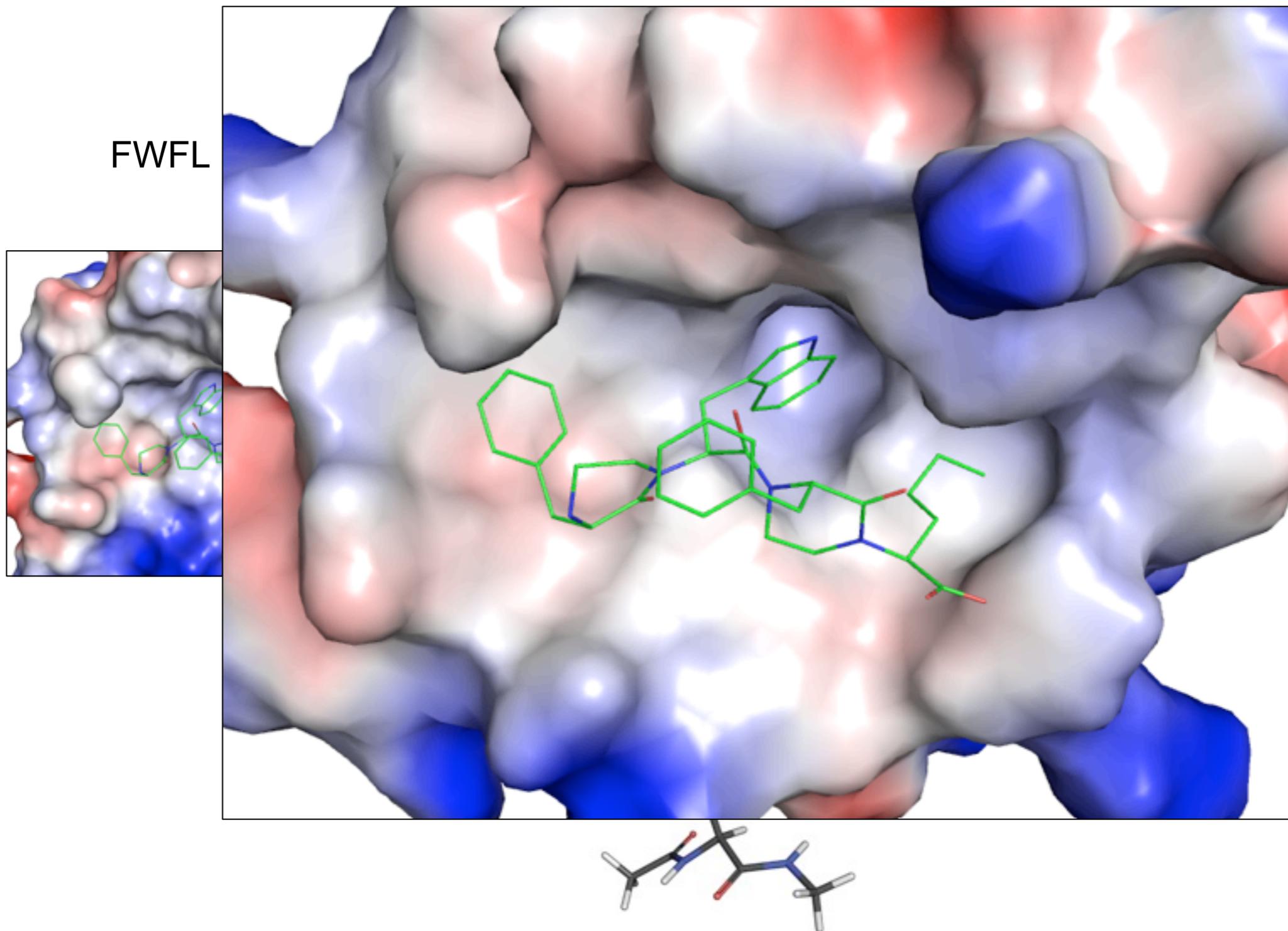
FWFL



[3-methyl-PHE] WFL

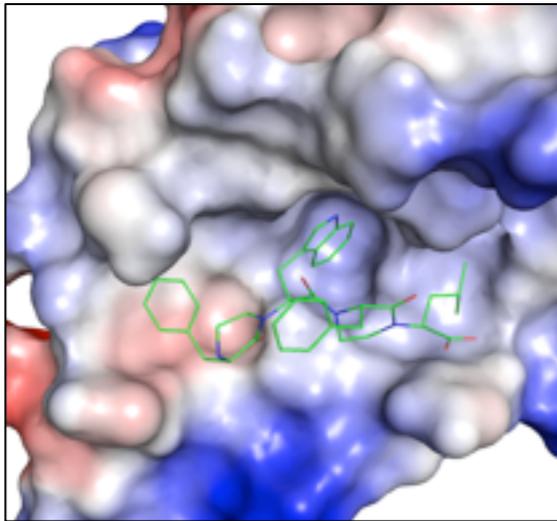


OOP Design

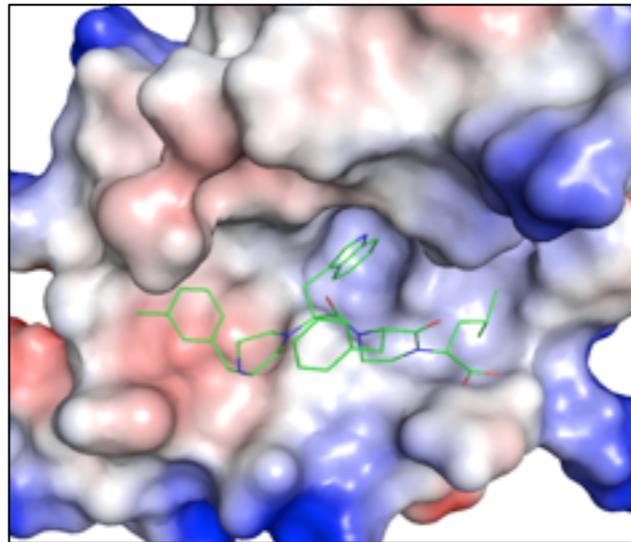


OOP Design

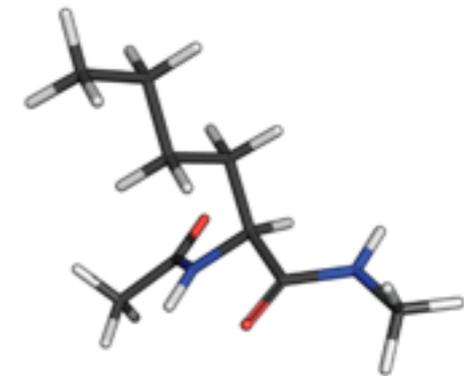
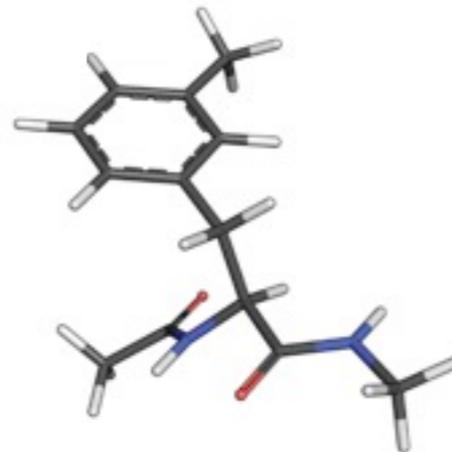
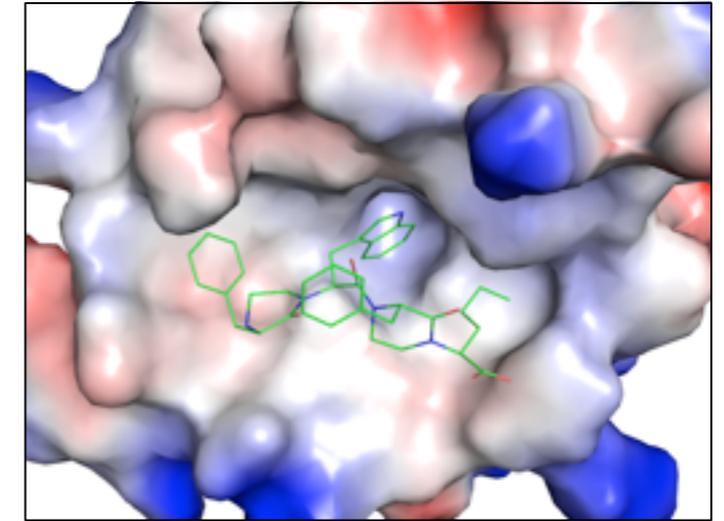
FWFL



[3-methyl-PHE] WFL

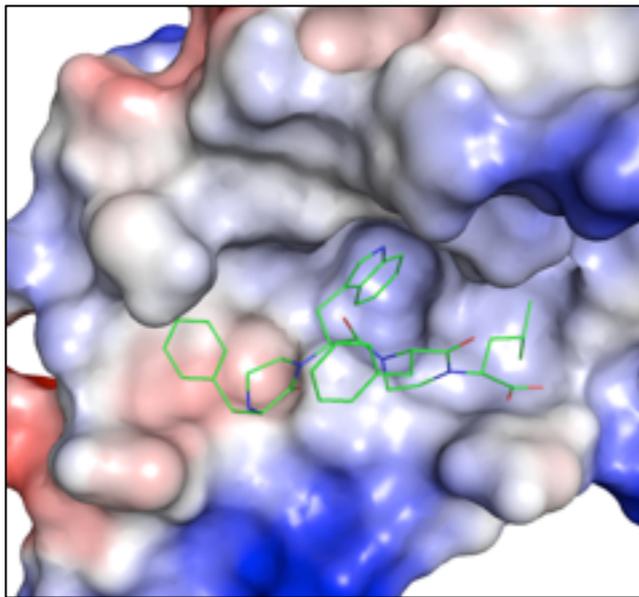


FWF Norleucine

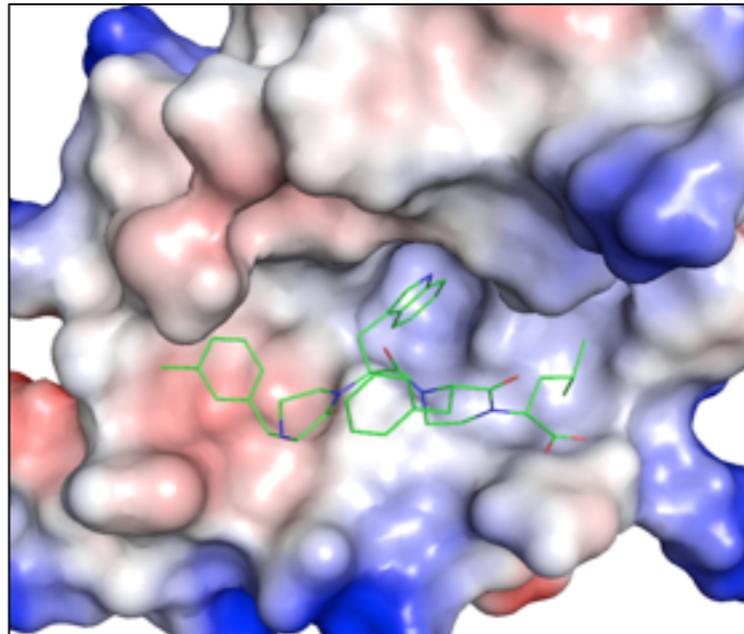


OOP Design

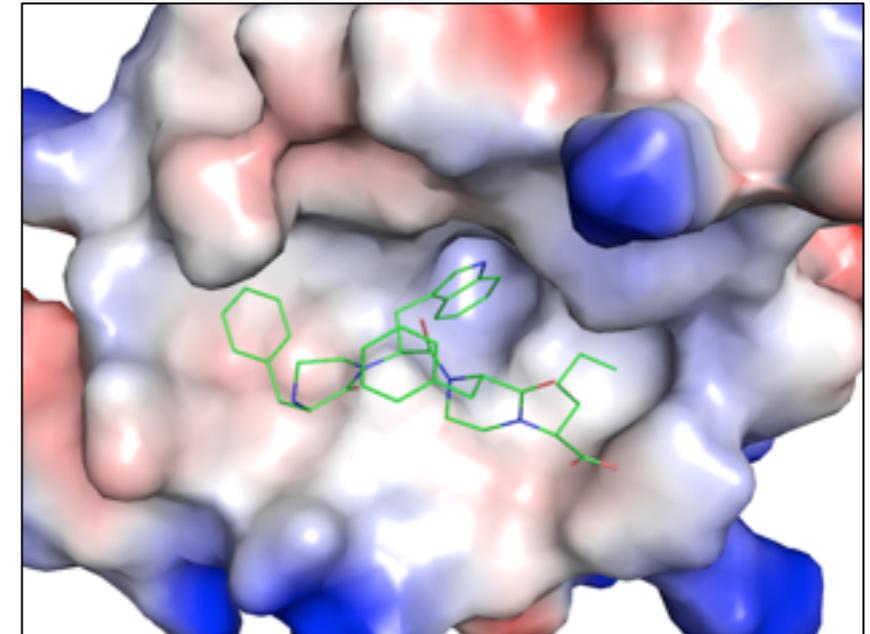
FWFL



[3-methyl-PHE] WFL

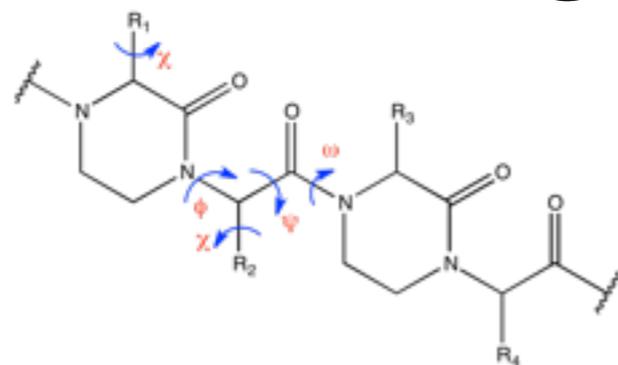


FWF Norleucine

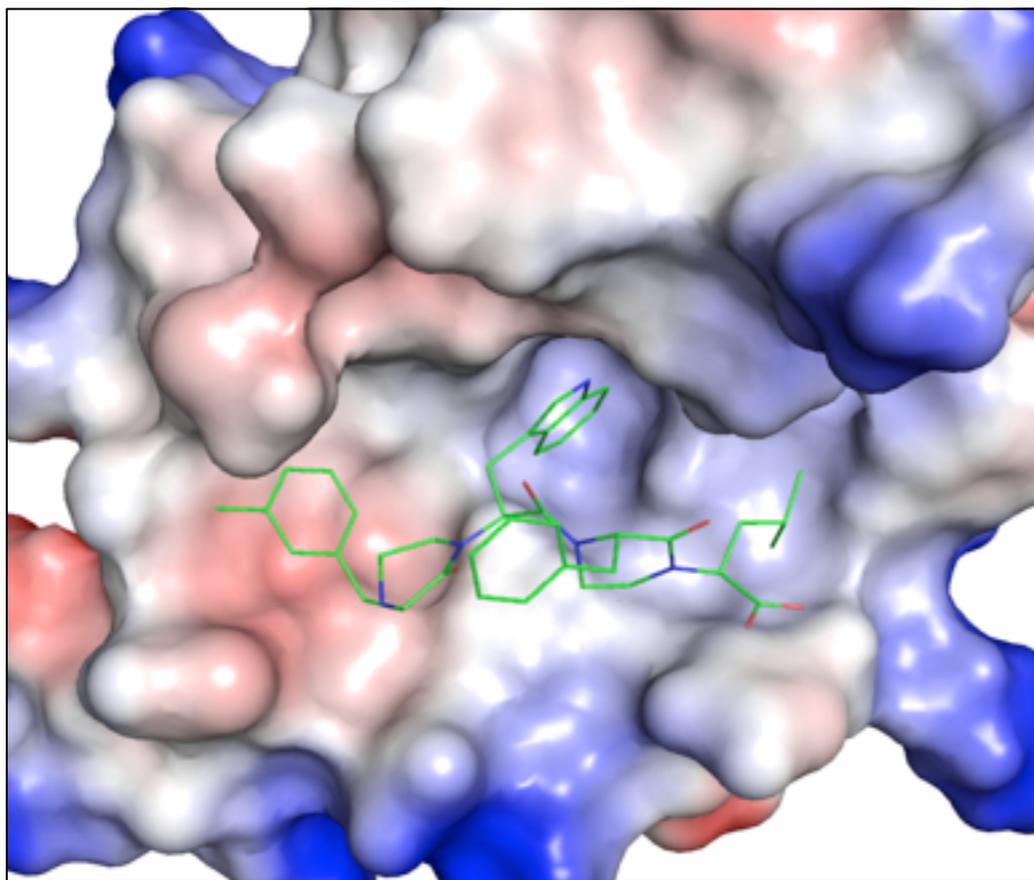


Metric	FWFL	[3-methyl-PHE]WFL	FWF Norleucine
K_d	6.9 μM Bullock (Arora Lab)	pending	pending

OOP Binding Mode

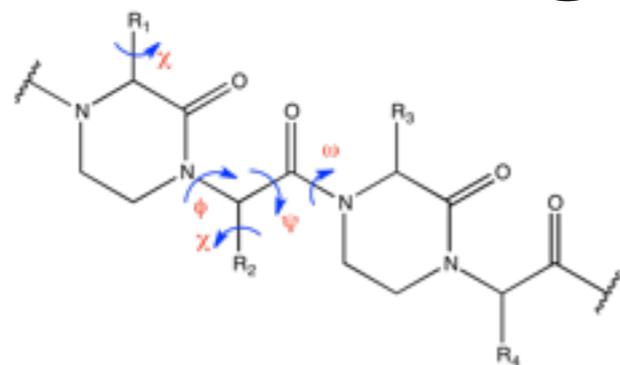


Omega Trans or Cis?

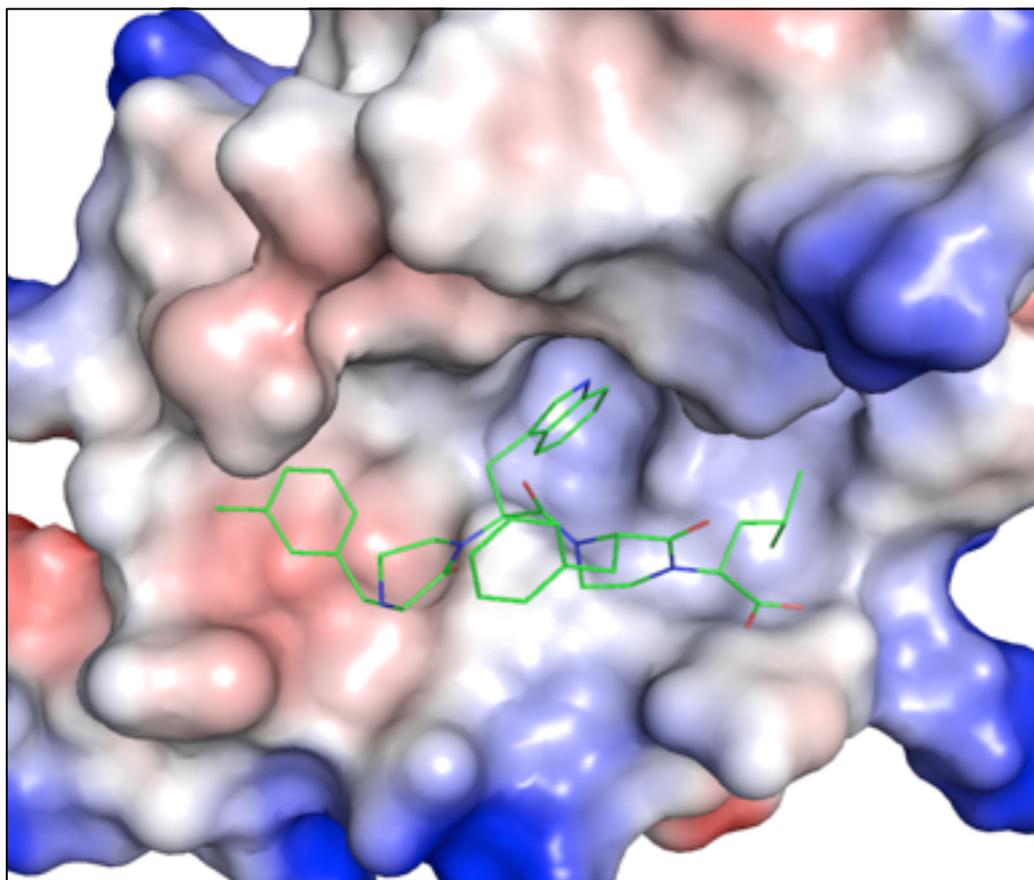


Trans

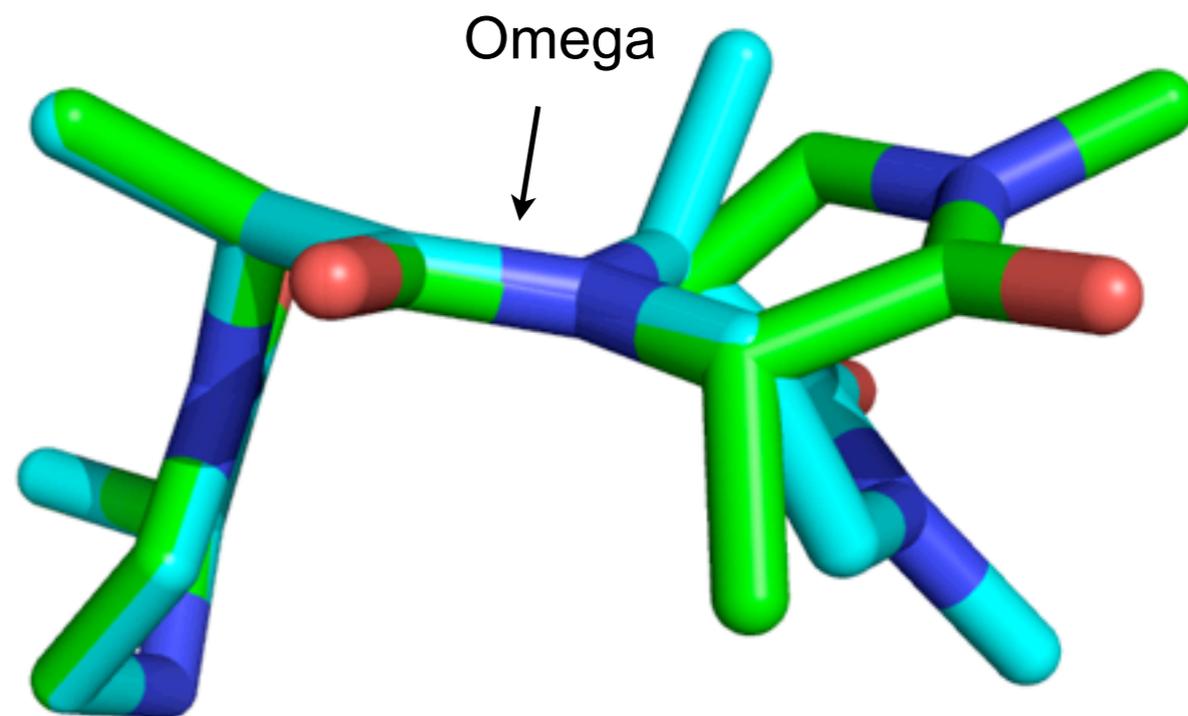
OOP Binding Mode



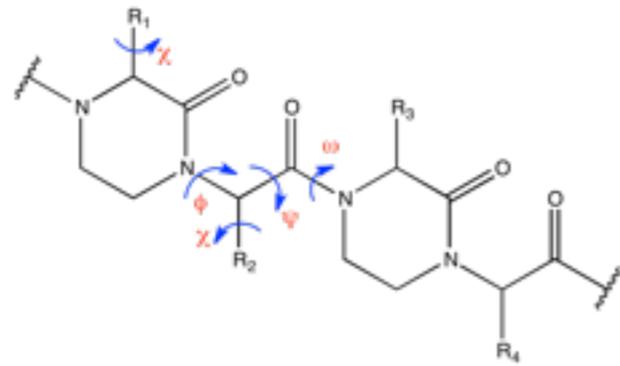
Omega Trans or Cis?



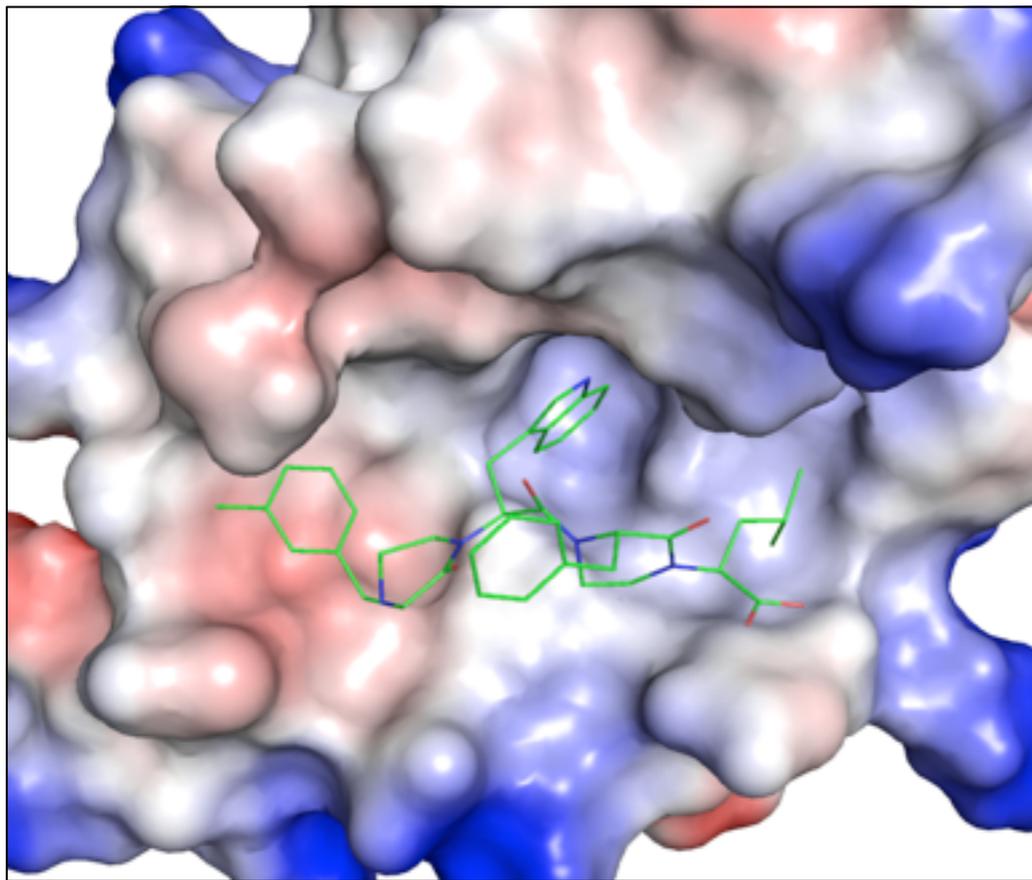
Trans



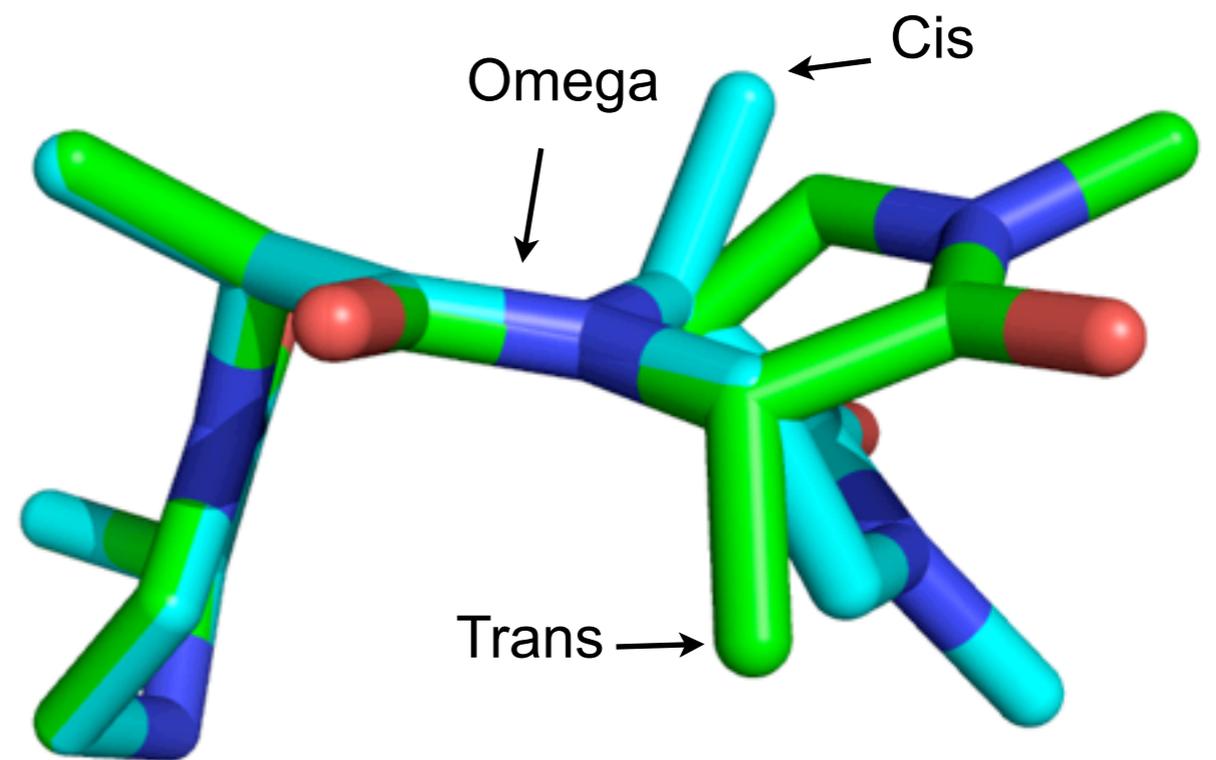
OOP Binding Mode



Omega Trans or Cis?

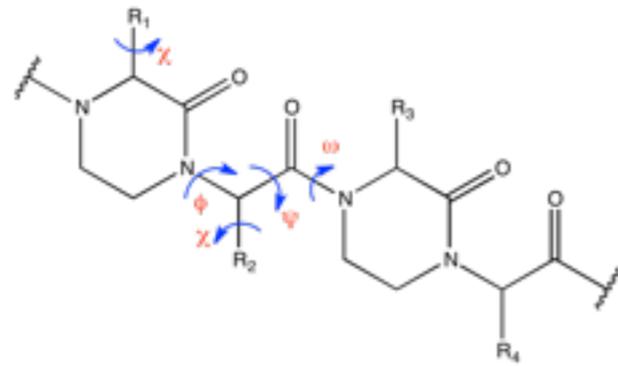


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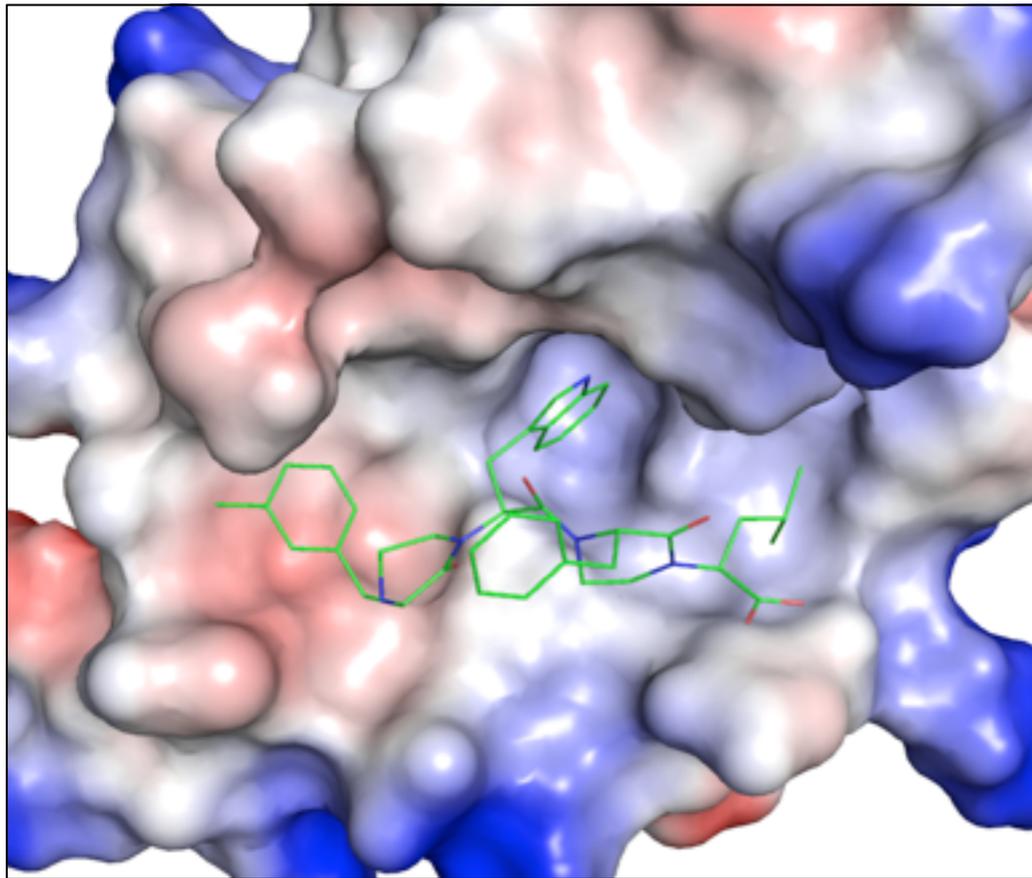
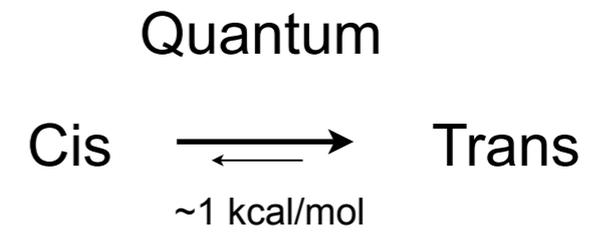


Trans →

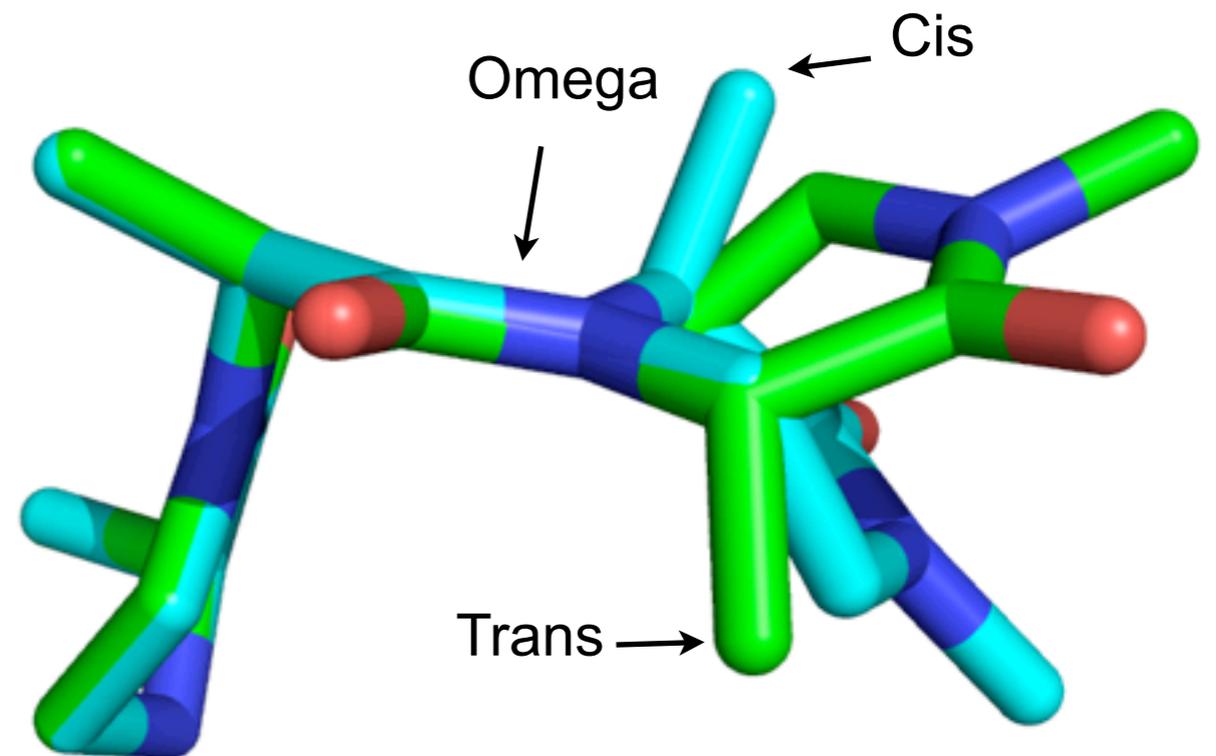
OOP Binding Mode



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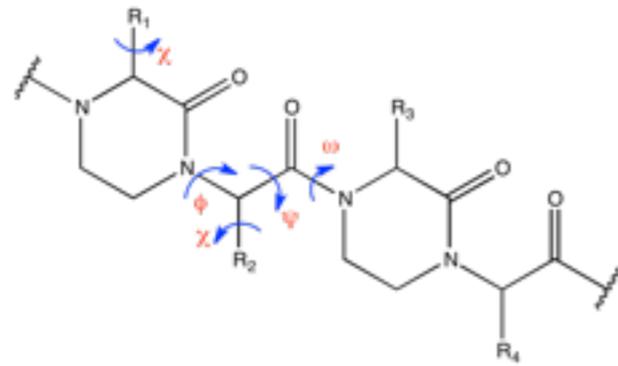


Trans

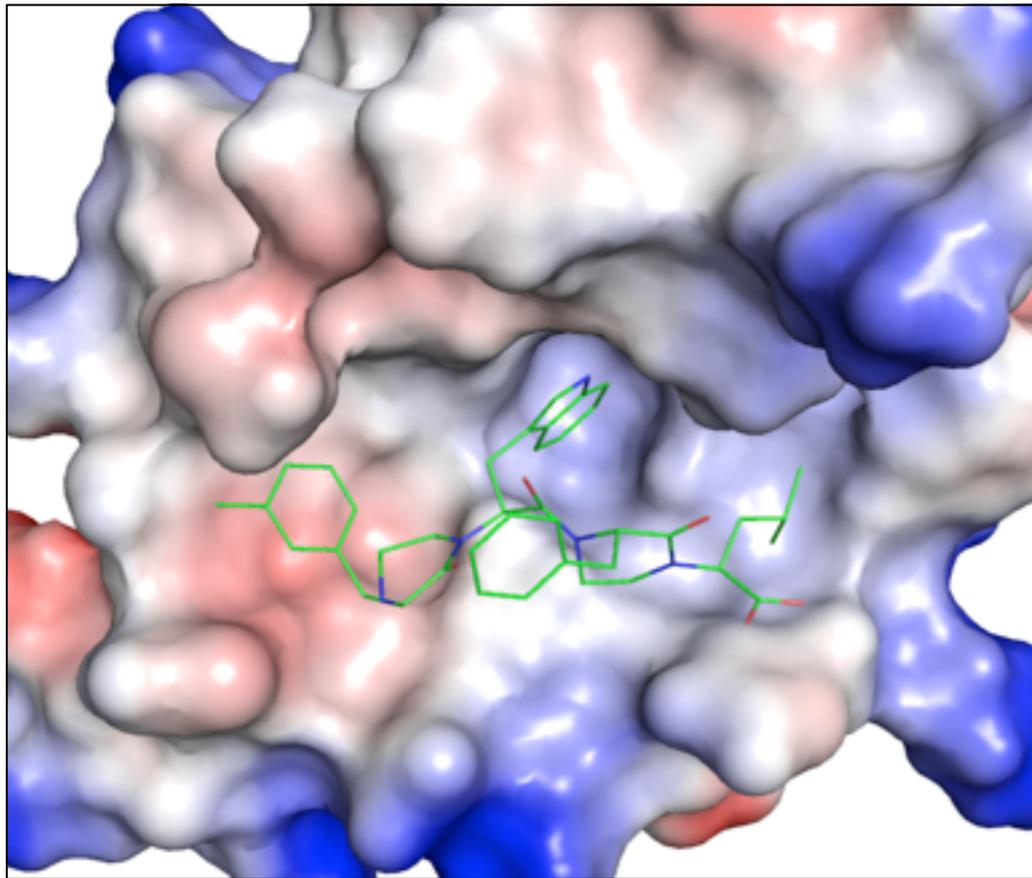
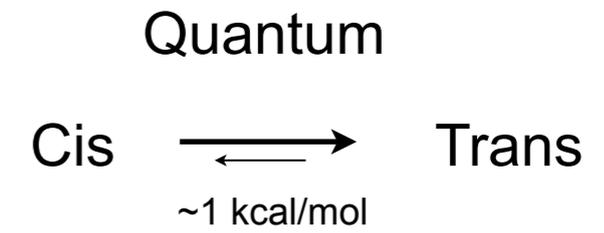


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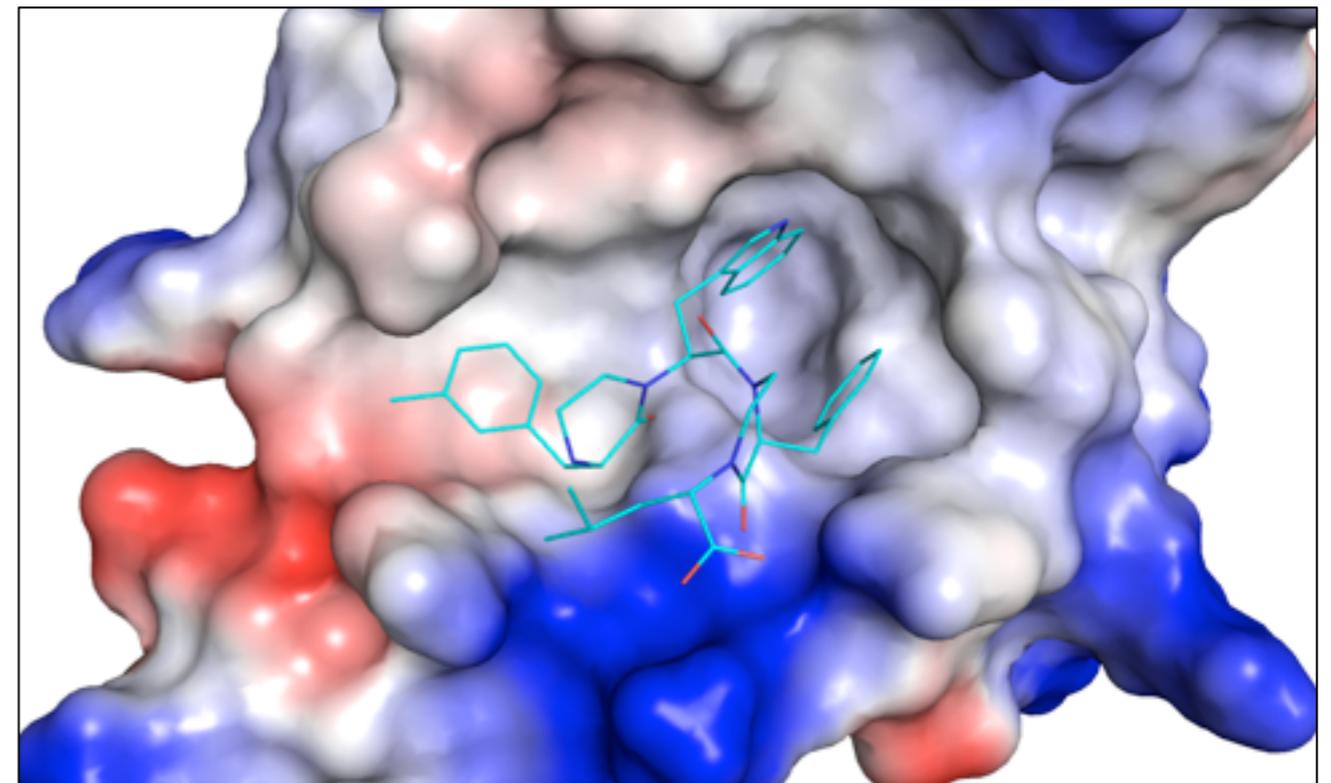
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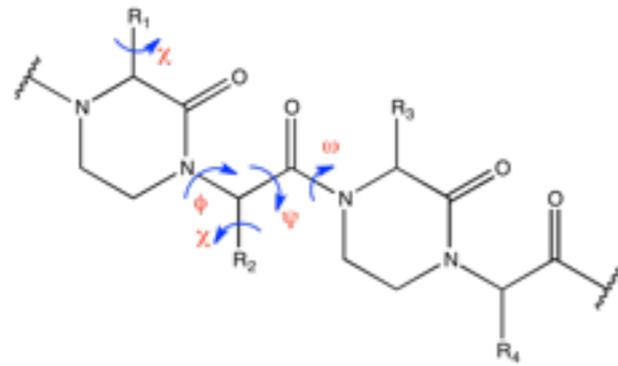


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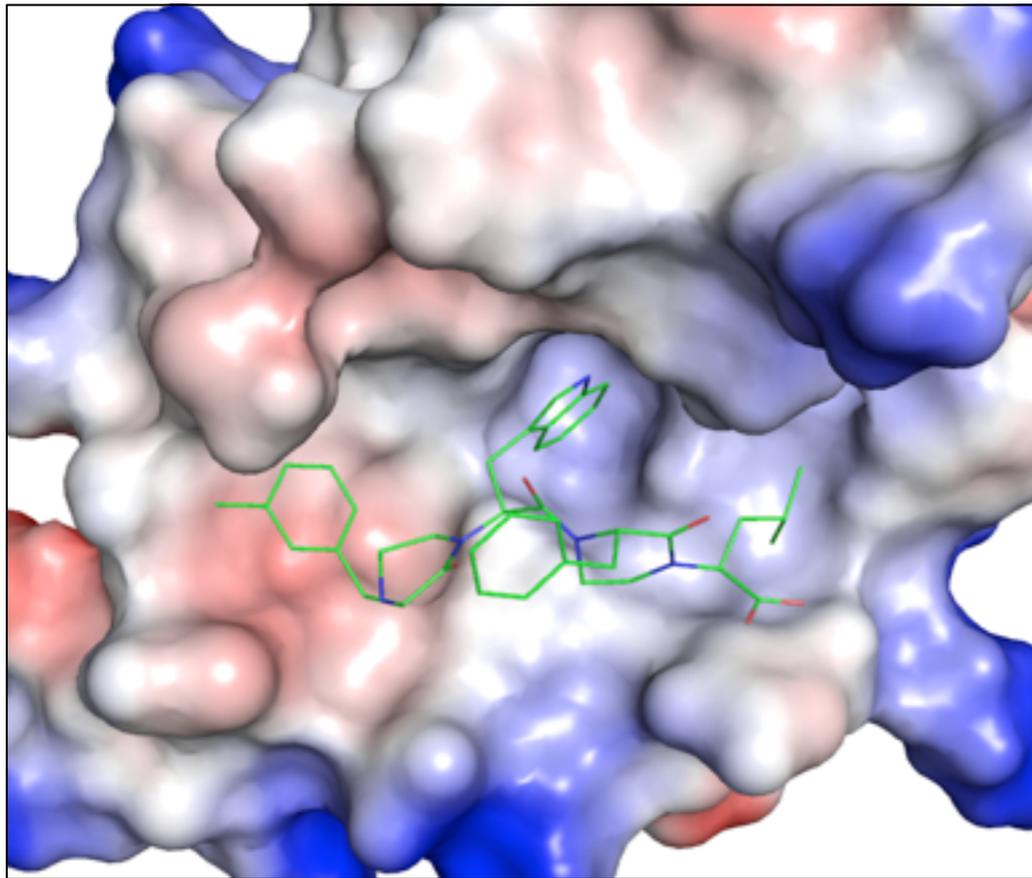
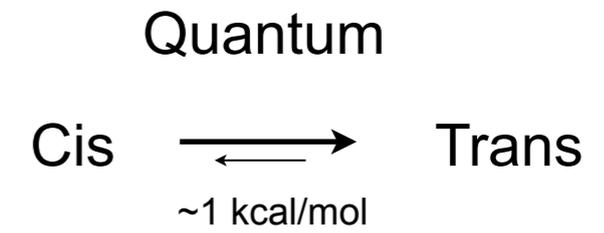


Cis

OOP Binding Mode

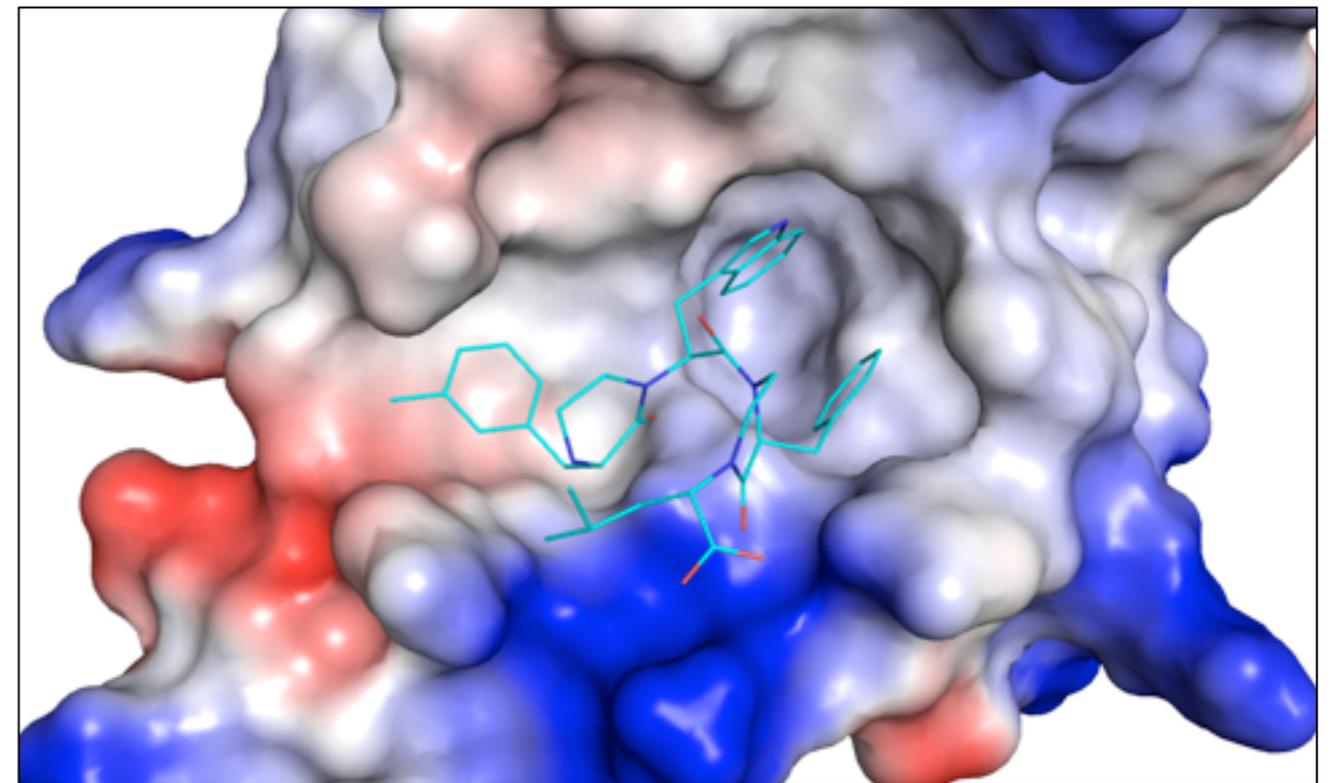


Omega Trans or Cis?



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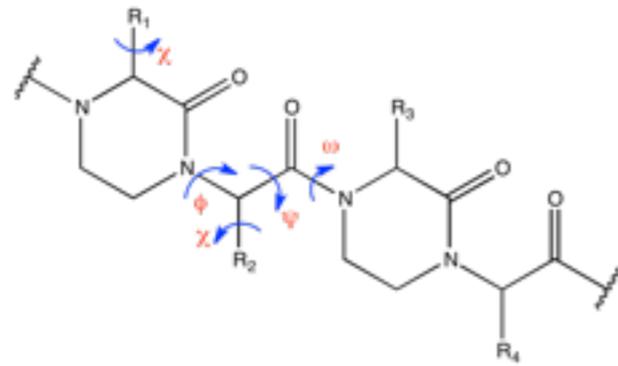
Energy Complex (REU) = -31.264



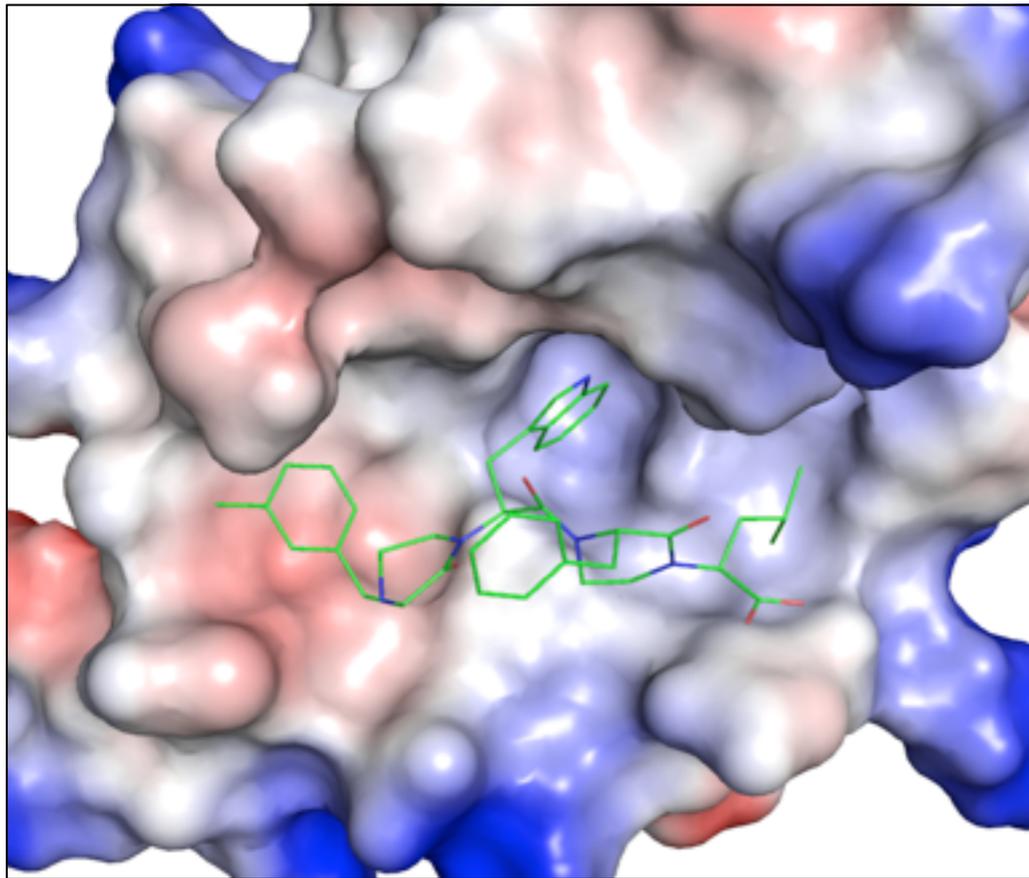
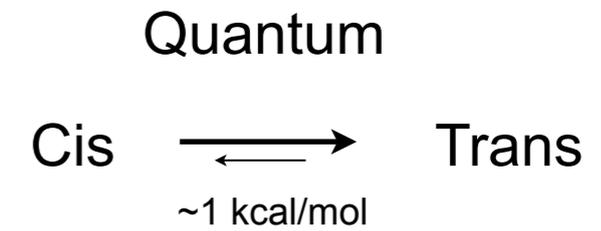
Cis

Energy Complex (REU) = -32.493

OOP Binding Mode

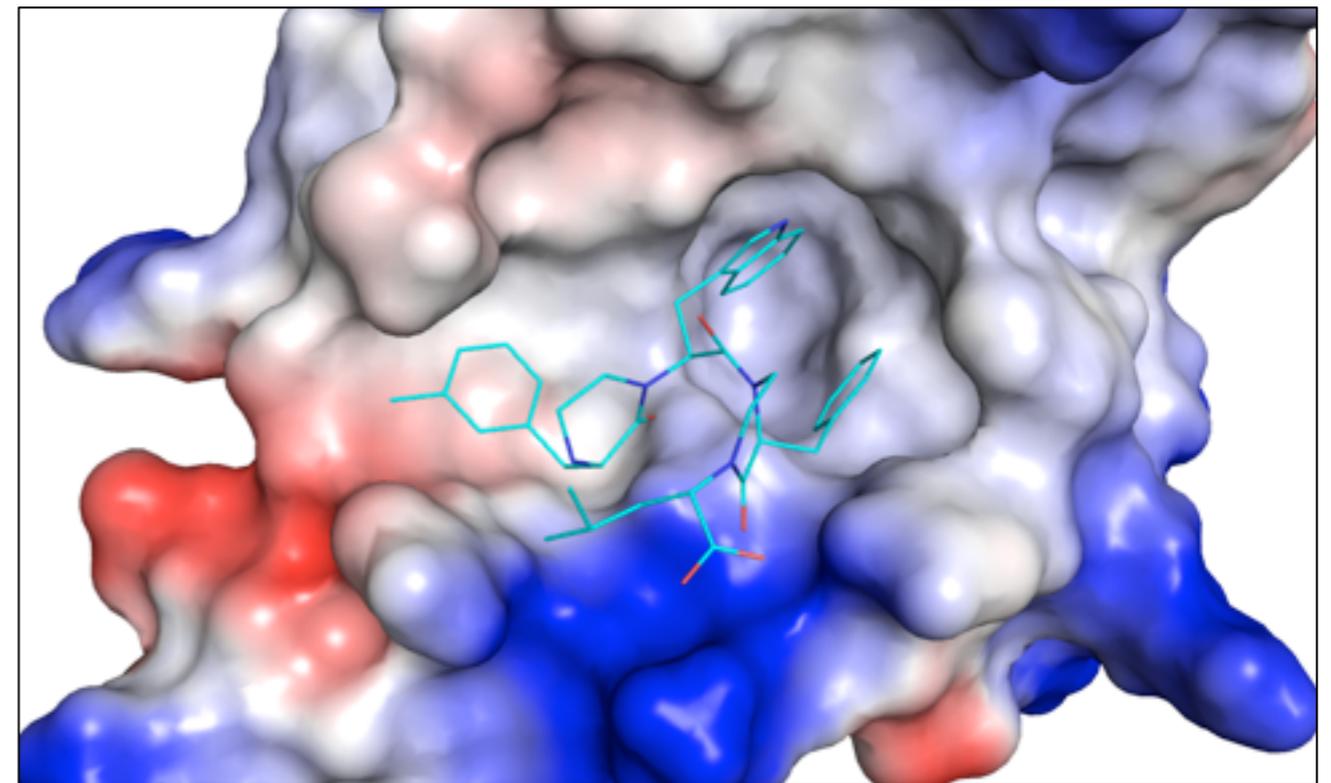


Omega Trans or Cis?



Trans

Energy Complex (REU) = -31.264



Cis

Energy Complex (REU) = -32.493

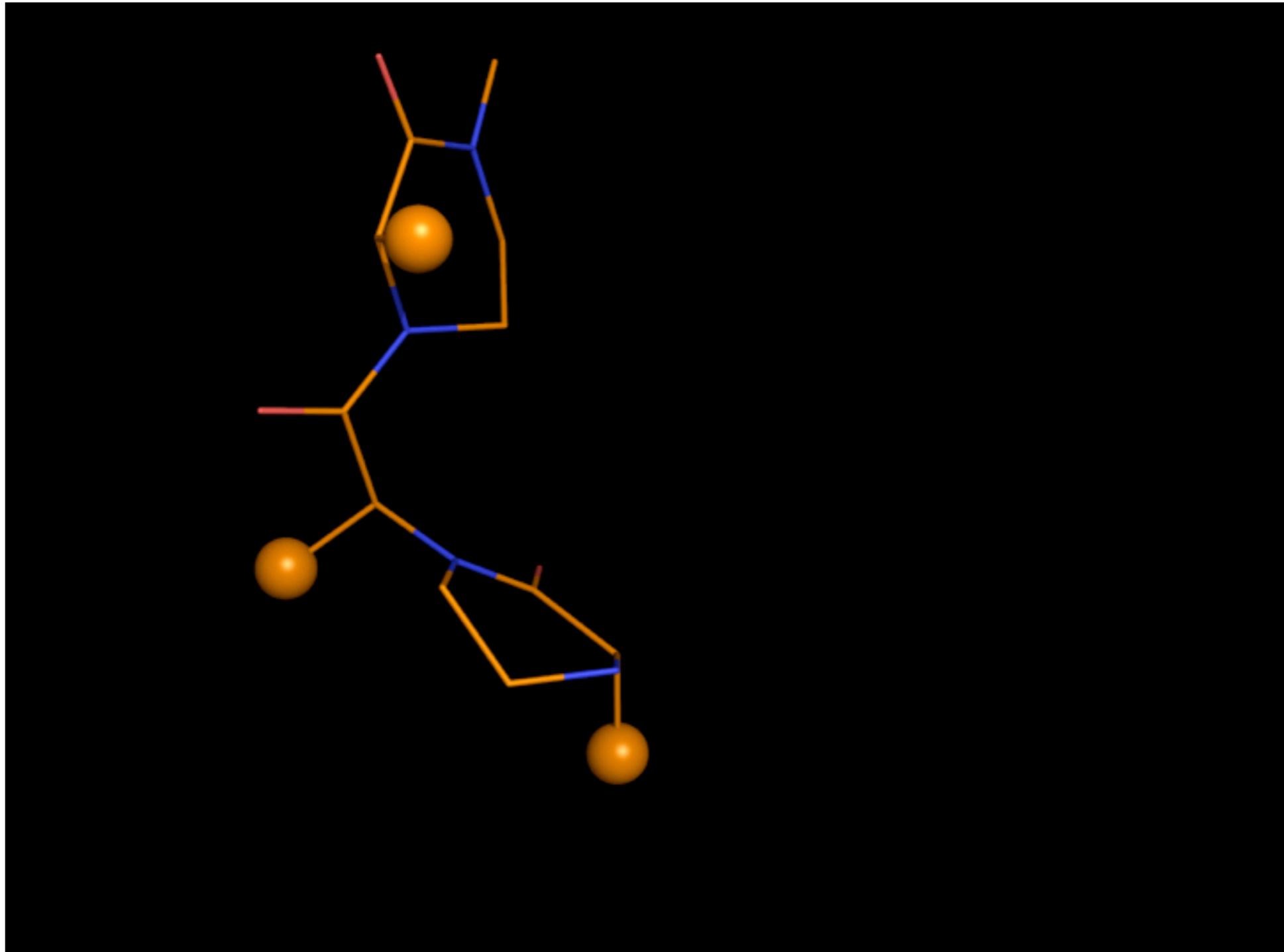
Cis orientation explains experiment:

FWFL K_d = **6.9 μ M**

FWKL K_d > **200 μ M**

Increasing Versatility of OOPs

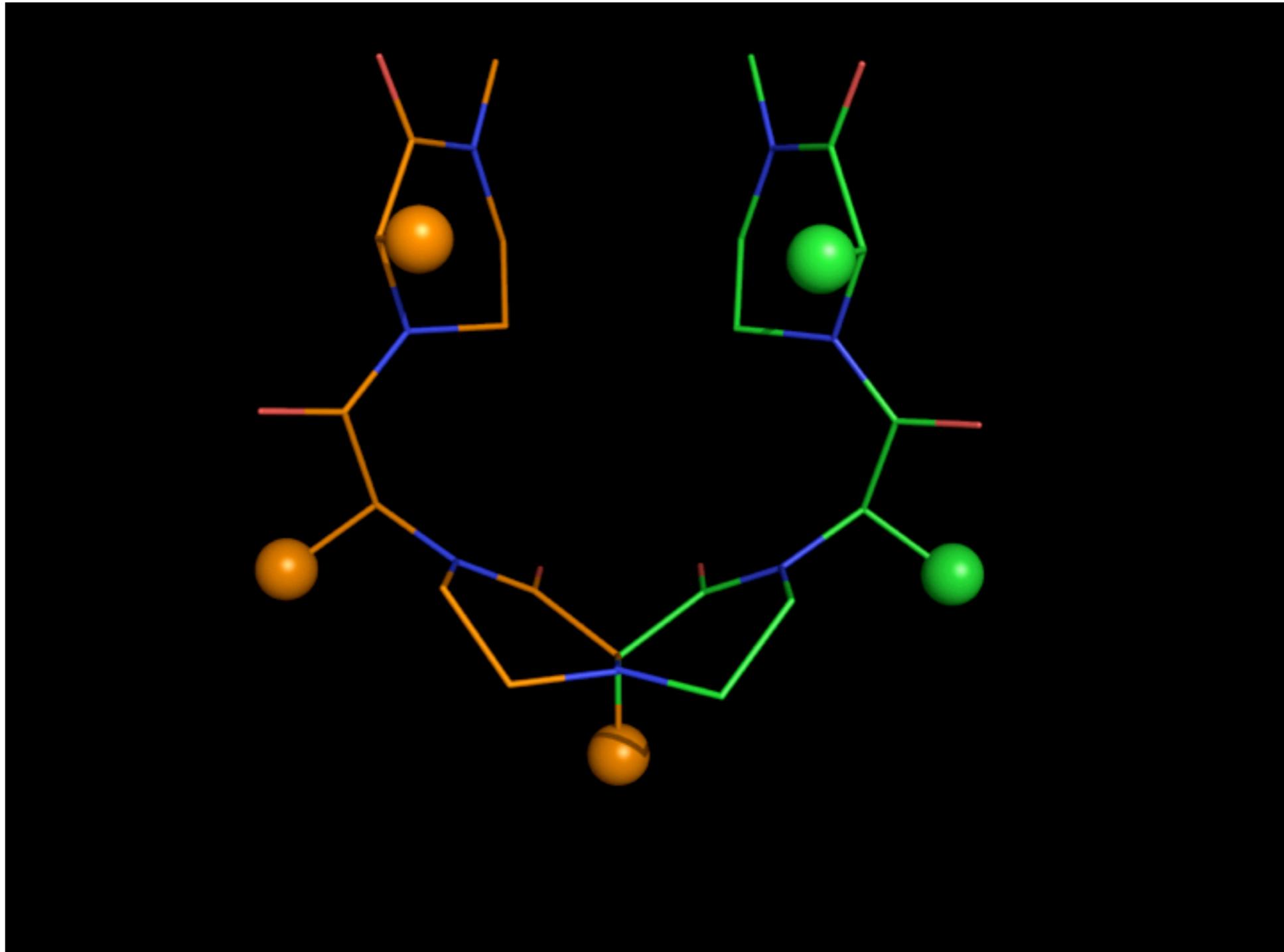
LLL



Increasing Versatility of OOPs

LLL

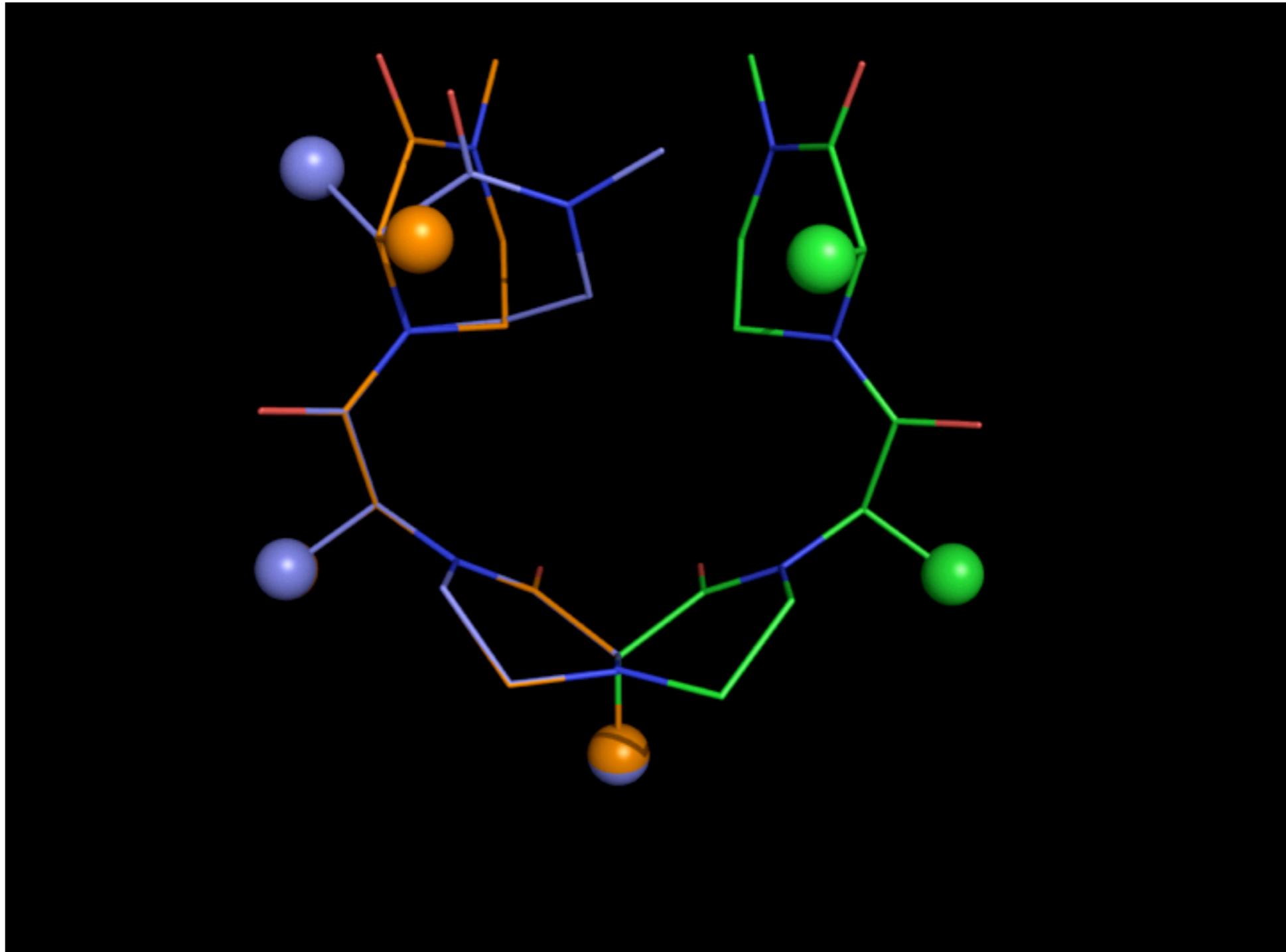
DDD



Increasing Versatility of OOPs

LLL

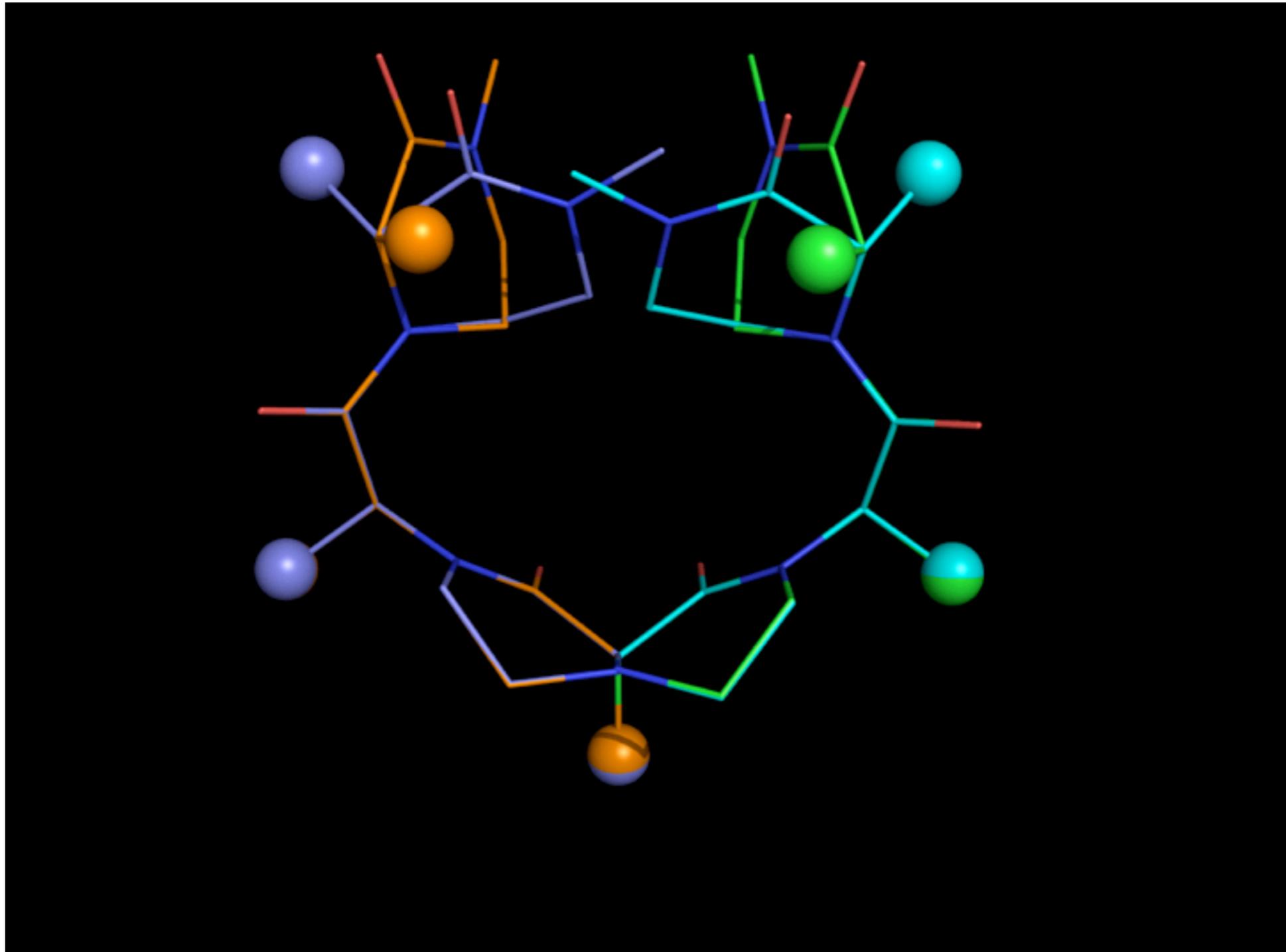
LLD



Increasing Versatility of OOPs

LLL

LLD

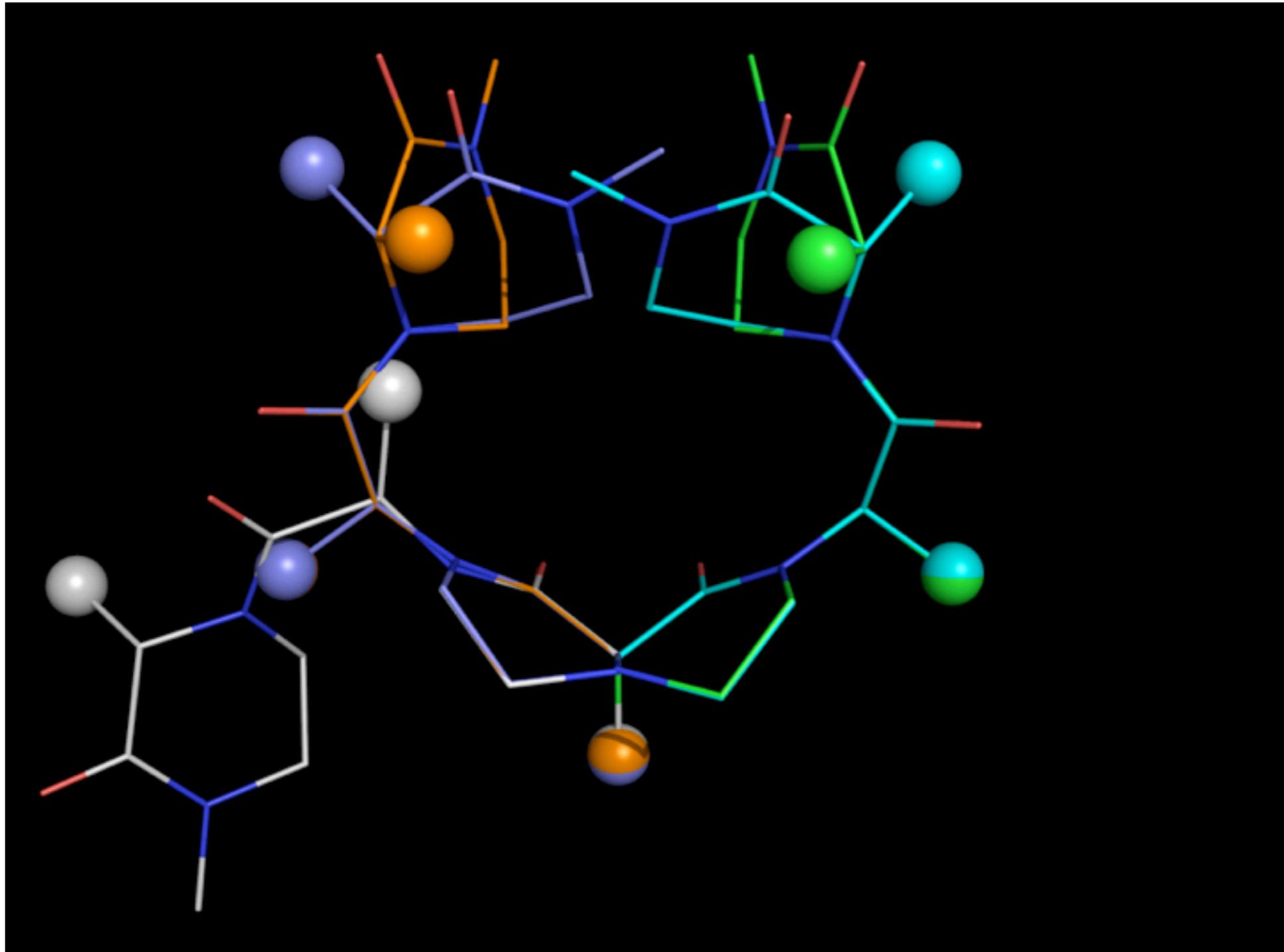


DDD

DDL

Increasing Versatility of OOPs

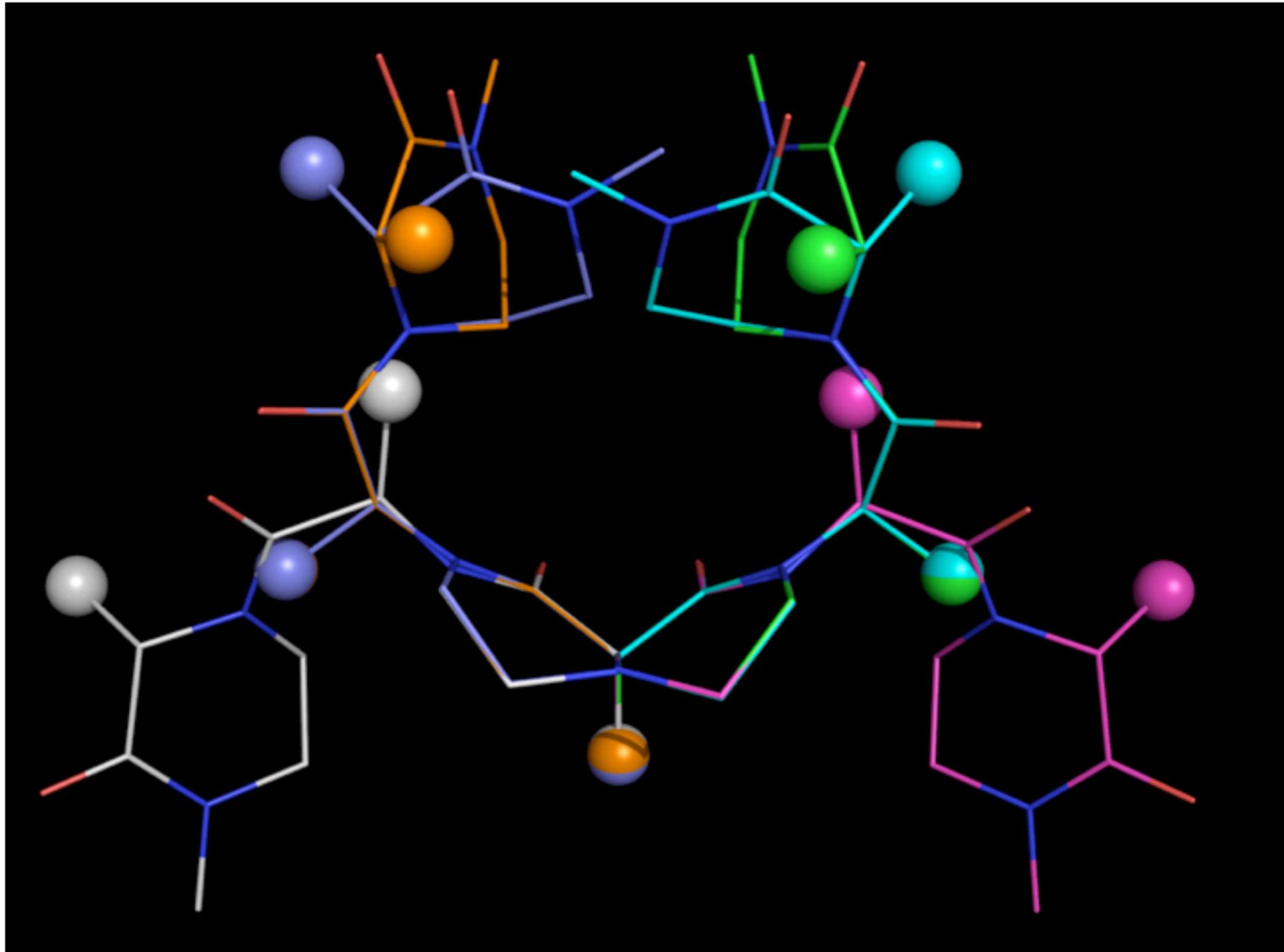
LLL
LLD
LDL



DDD
DDL

Increasing Versatility of OOPs

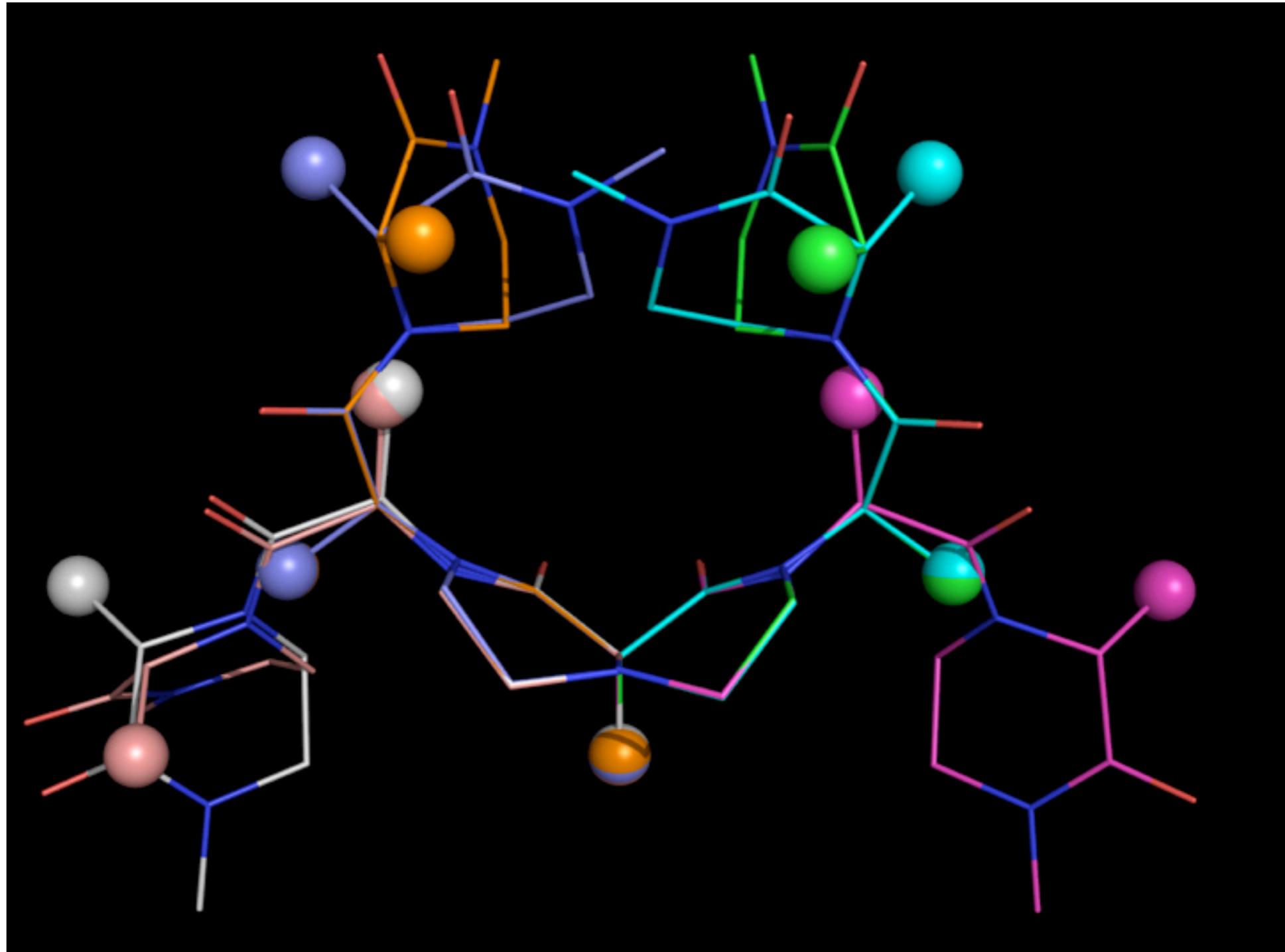
LLL
LLD
LDL



DDD
DDL
DLD

Increasing Versatility of OOPs

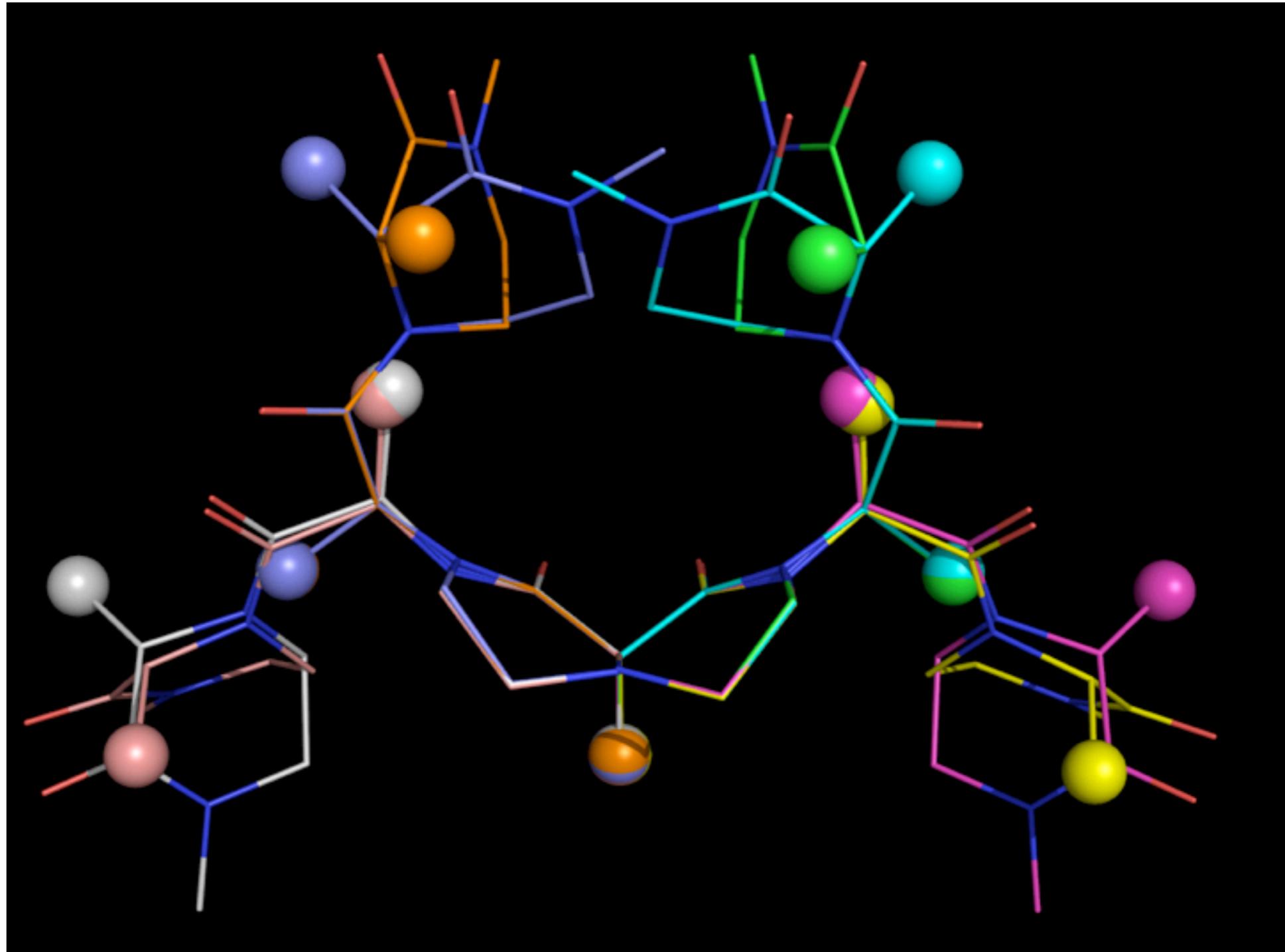
LLL
LLD
LDL
LDD



DDD
DDL
DLD

Increasing Versatility of OOPs

LLL
LLD
LDL
LDD



DDD
DDL
DLD
DLL

Acknowledgements

Rosetta- Commons

Arora Lab

Brooke Bullock*

Bonneau Lab

P. Douglas Renfrew*
Glenn Butterfoss*
Alex Greenfield
Aviv Madar
Chris Poultney
Duncan Penfold Brown
Leif Halvorsen
Kieran Mace
Noah Youngs
Christoph Hafemeister
Evan Baugh
Tim Craven
Abba Leffler
Patrick Winters (former)

Funding

DOD
DOE
NSF
NYU SOM NIH Training Grant Fellowship

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Alex Morozov (Rutgers Physics)
Christine Vogel (NYU Biology)
Jane Carlton (NYU Parasitology)
Paramjit Arora (NYU Chemistry)
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