

# Specific Ligand-Residue Interactions that Lead to Liver X Receptor Isoform Selectivity

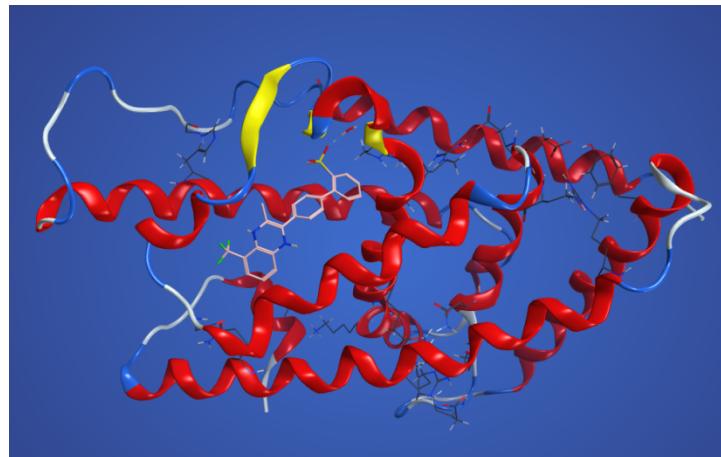
Susannah Davis and Kathryn Hardin

## Introduction

# Background

## Liver X Receptor (LXR)

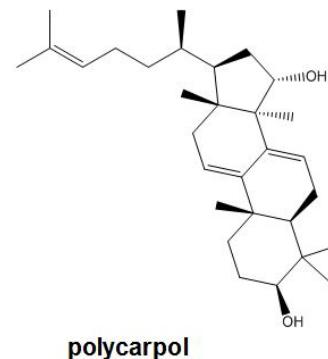
- Nuclear Receptor
  - Ligand Activated
  - Isoforms: Alpha and Beta



LXR $\beta$  Protein

# Functions

- Cholesterol and fatty acid metabolism
  - Glucose homeostasis
  - Inflammation
  - Neurological homeostasis



## Introduction

# Background

## Potential Applications

- Hormone-dependent cancer, atherosclerosis, and Alzheimer's disease

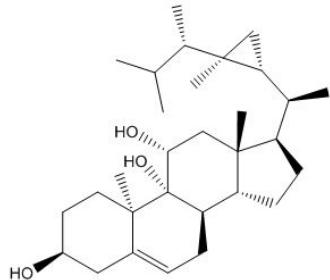
## LXR-623

- Beta selective
- First to human clinical trials
- Attacked central nervous system

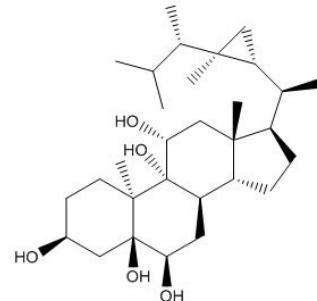
Isoform	Dominant Location	Effect on Cholesterol	Effect on Hepatic Triglyceride
Alpha	Liver, small intestine, macrophage	Lowers	Raises
Beta	Ubiquitous	Lowers	No effect

## Introduction

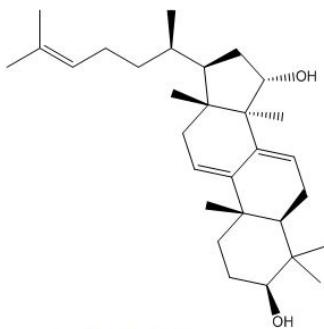
# 4 Ligands



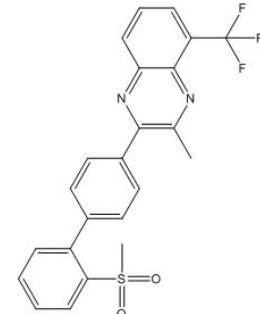
**gorgost-5-ene-3 $\beta$ ,9 $\alpha$ ,11 $\alpha$  -triol**  
Non-isoform selective



**gorgostane-3 $\beta$ ,9 $\alpha$ ,5 $\alpha$ , 6 $\beta$ , 11 $\alpha$ -tetrol**  
LXR $\alpha$  isoform selective



**polycarpol**  
LXR $\alpha$  isoform selective



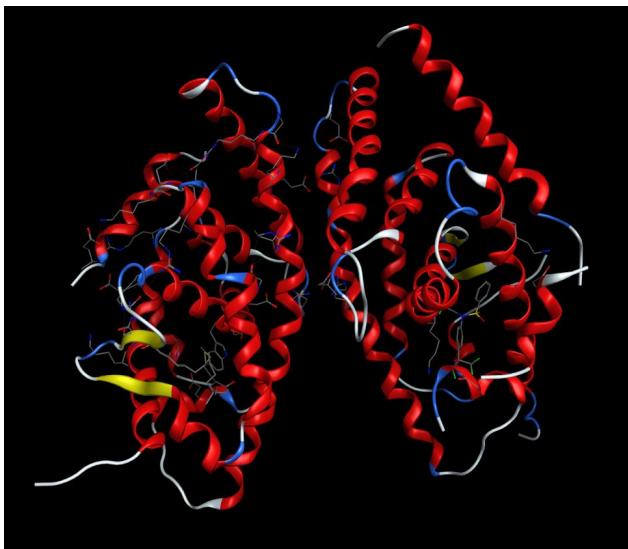
**wye-672**  
LXR $\beta$  isoform selective

## Structure Preparation

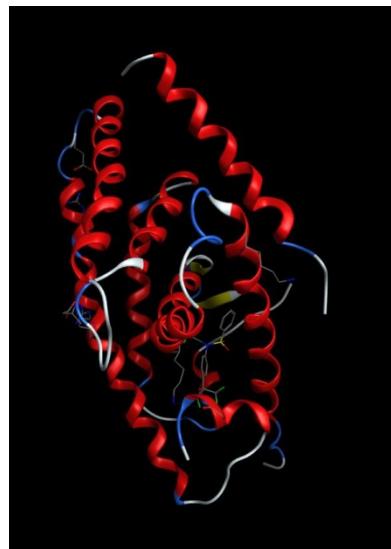
# Homology Model

	Tag	Chain	1	5	10
1UHL	1: 1UHL.A		GLU-MET-PRO-VAL-ASP-ARG-ILE-LEU-GLU-ALA-GLU-		
	2: 1UHL.B		MET-SER-PRO-GLU-GLN-LEU-GLY-MET-ILE-GLU-LYS-		
	3: 1UHL.C		HIS-LYS-ILE-LEU-HIS-ARG-LEU-LEU-GLN-ASP		
	4: 1UHL.D		HIS-LYS-ILE-LEU-HIS-ARG-LEU-LEU-GLN-ASP		
	5: 1UHL.A		MEI		
	6: 1UHL.B		444		
	7: 1UHL.A		HOH HOH HOH HOH HOH HOH HOH HOH HOH		
	8: 1UHL.B		HOH		

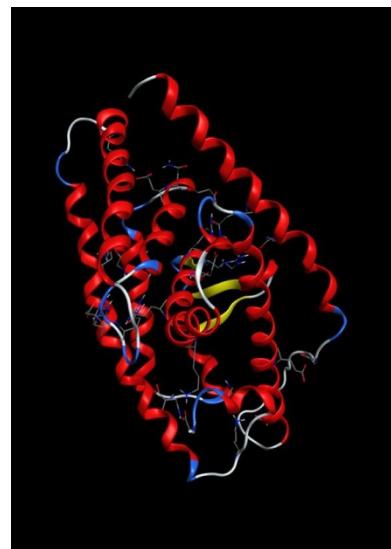
	Tag	Chain	1	5	10
1UHL	1: 1UHL.B		MET-SER-PRO-GLU-GLN-LEU-GLY-MET-ILE-GLU-LYS-		
	2: 1UHL.B		444		
	3: 1UHL.B		HOH		



Heterodimer



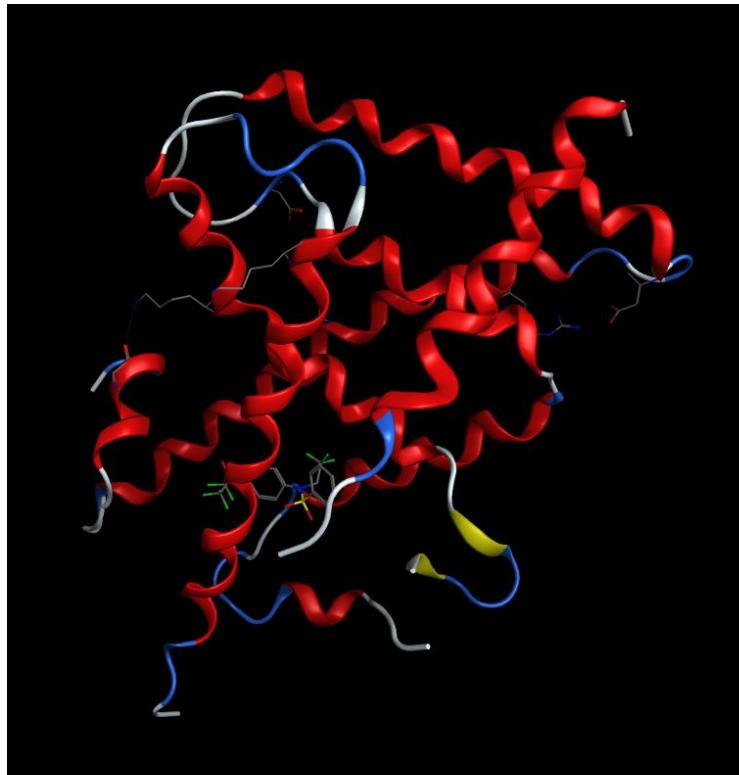
LXR $\alpha$



LXR $\alpha$  homology model

Structure Preparation

# Homology Model



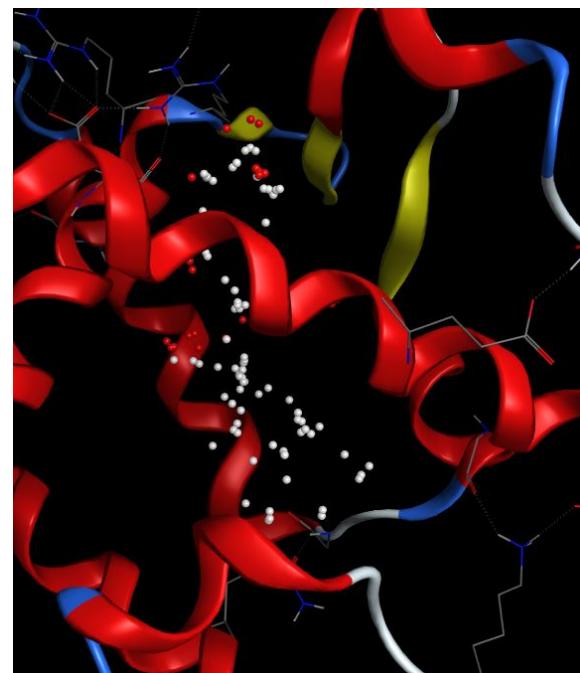
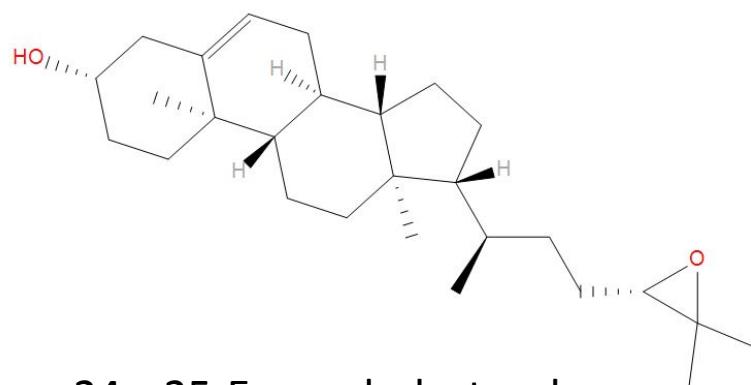
Before homology model



After homology model

Structure Preparation

# Ligand Replacement



## Docking

# Procedure

### Preparation

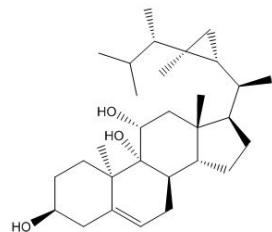
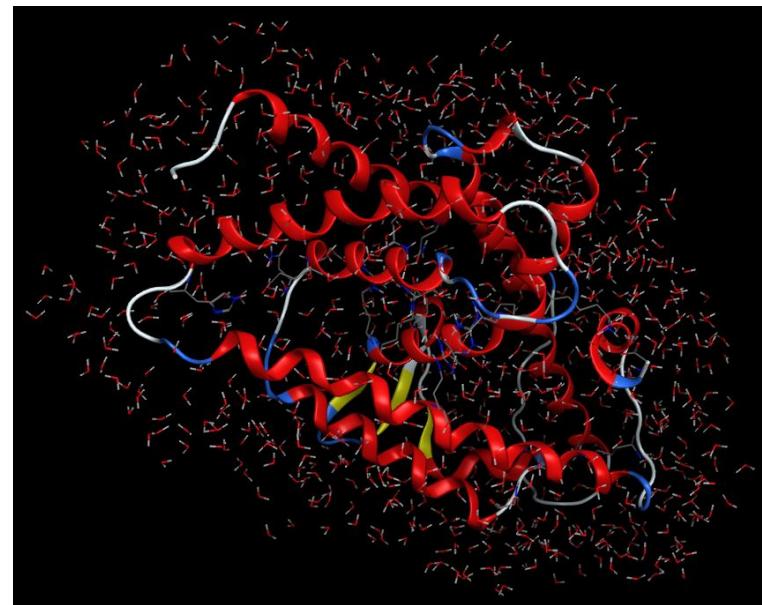
- Protonate
- Solvate

### Dock

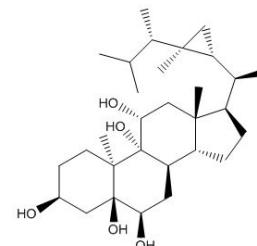
- Induced fit protocol
- Dummy atoms as the site
- Layer solvent of margin 4.0 Å

### Minimization

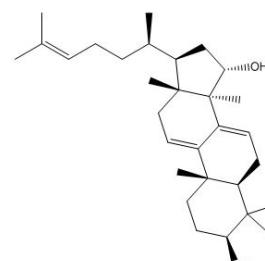
- Pose selection



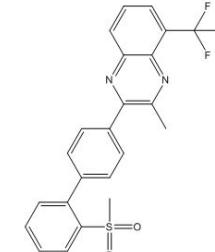
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Non-isoform selective



**gorgostane-3 $\beta$ ,9 $\alpha$ ,5 $\alpha$ , 6 $\beta$ , 11 $\alpha$ -tetrol**  
LXR $\alpha$  isoform selective



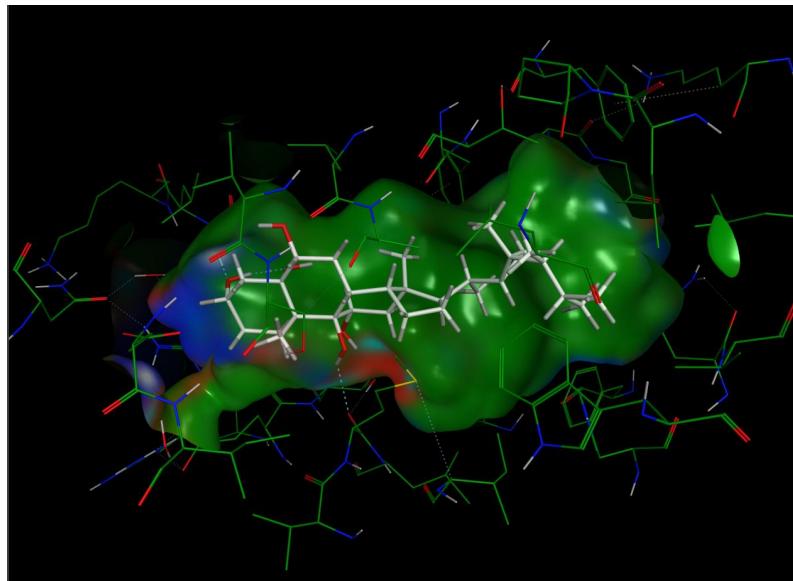
**polycarpol**  
LXR $\alpha$  isoform selective



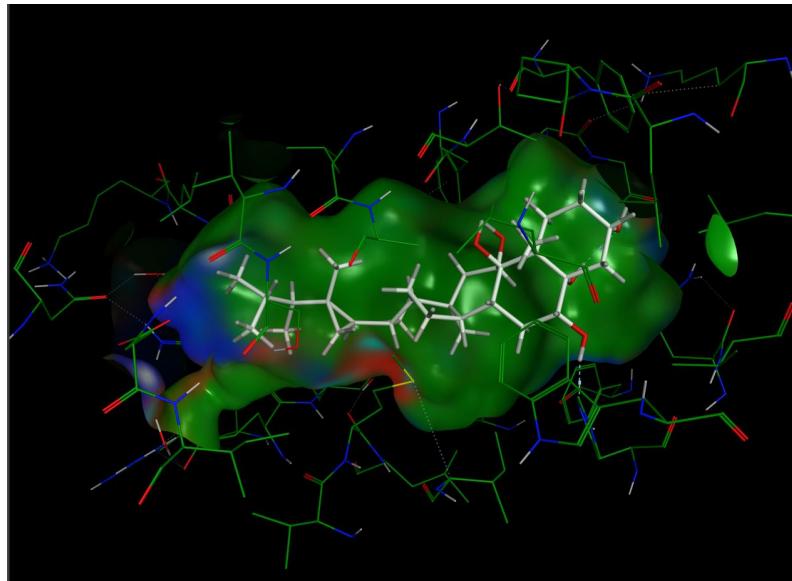
**wye-672**  
LXR $\beta$  isoform selective

Docking

# Pose Selection



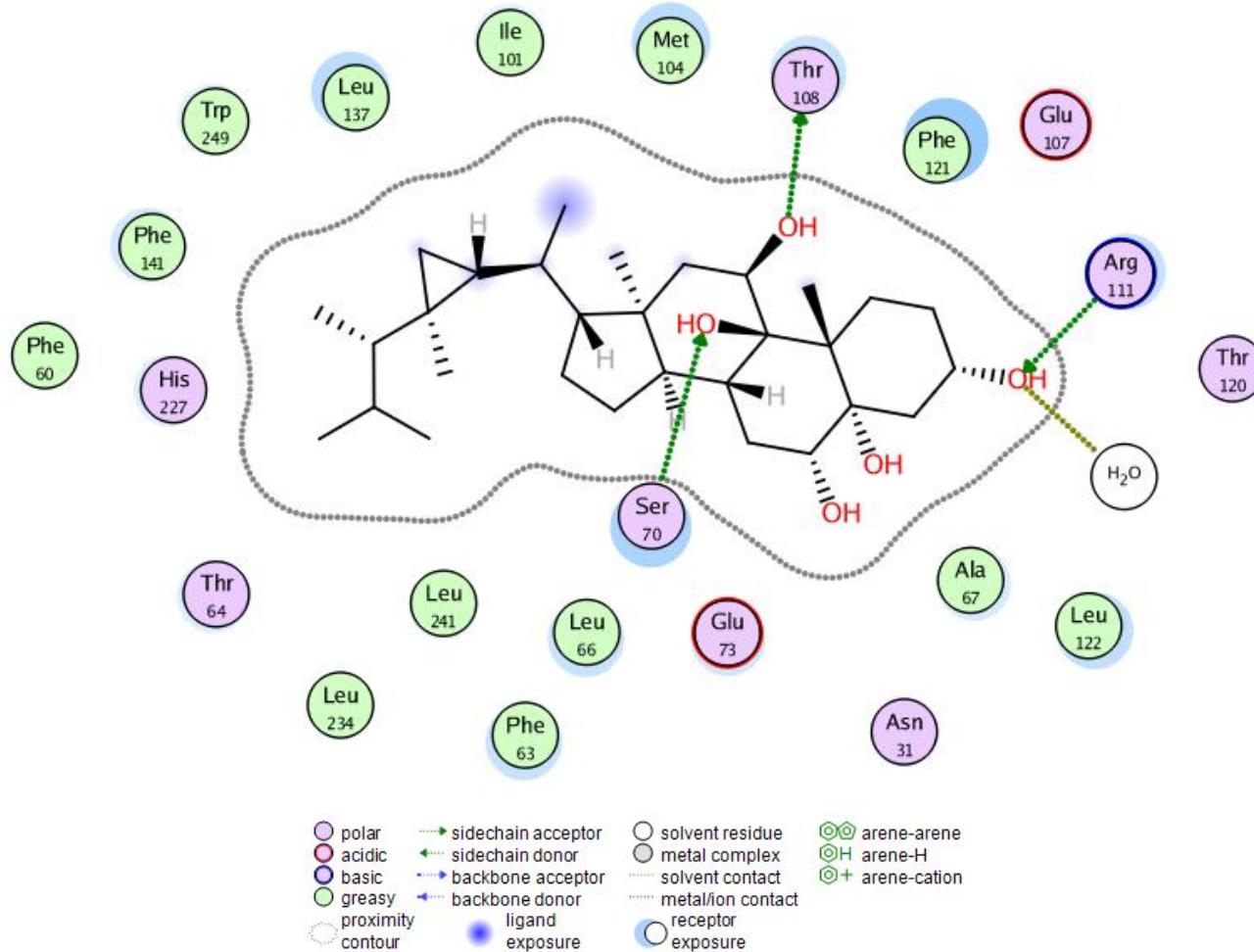
Correct



Incorrect

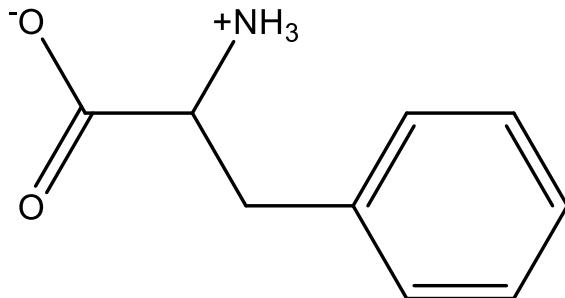
# Glycine Scan

# Ligand Interactions

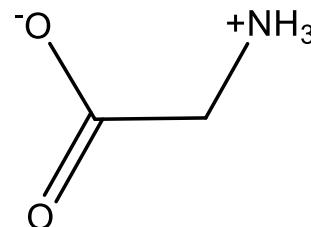


## Glycine Scan

# Procedure



Phe - phenylalanine

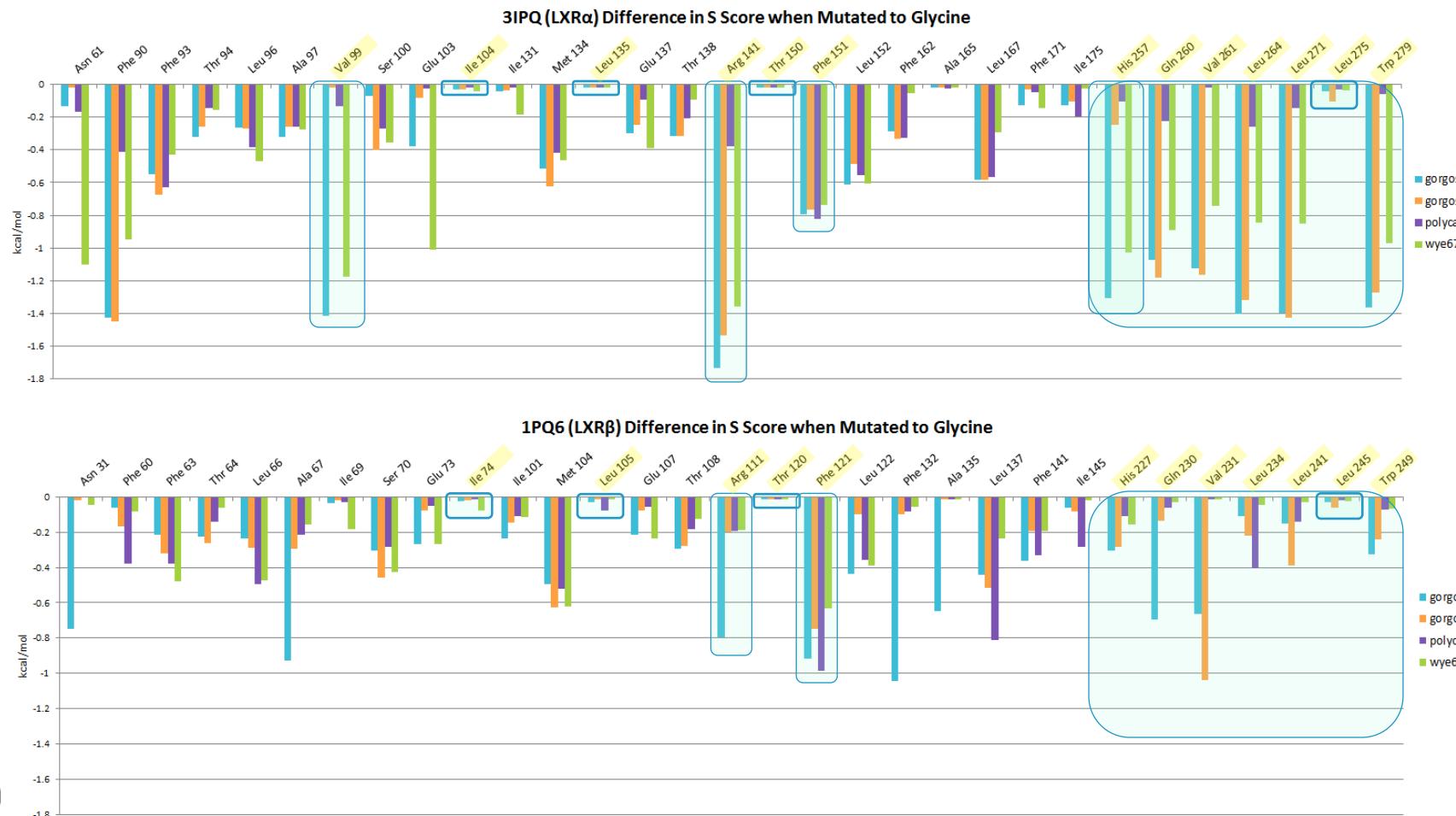


Gly - Glycine

Ligand	Base S score	Thr 150	Arg 141
Gorgost-5	-13.019	-13.019	-11.286
Gorgostane	-12.561	-12.556	-11.028
Polycarpol	-10.937	-10.931	-10.558
Wye-672	-11.159	-11.156	-9.801

# Glycine Scan

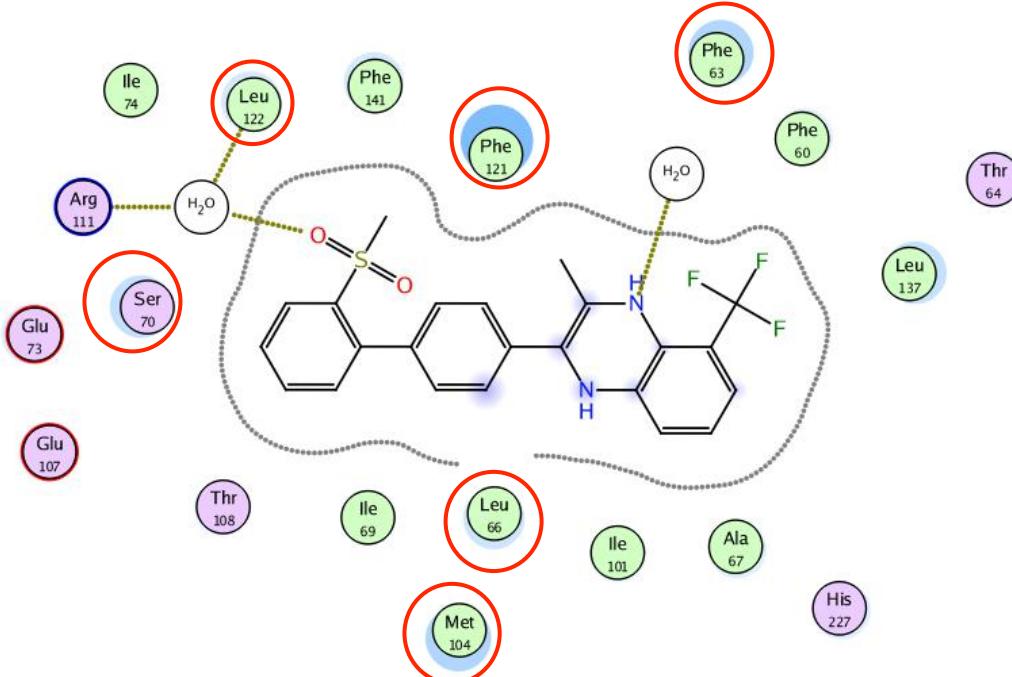
# Results



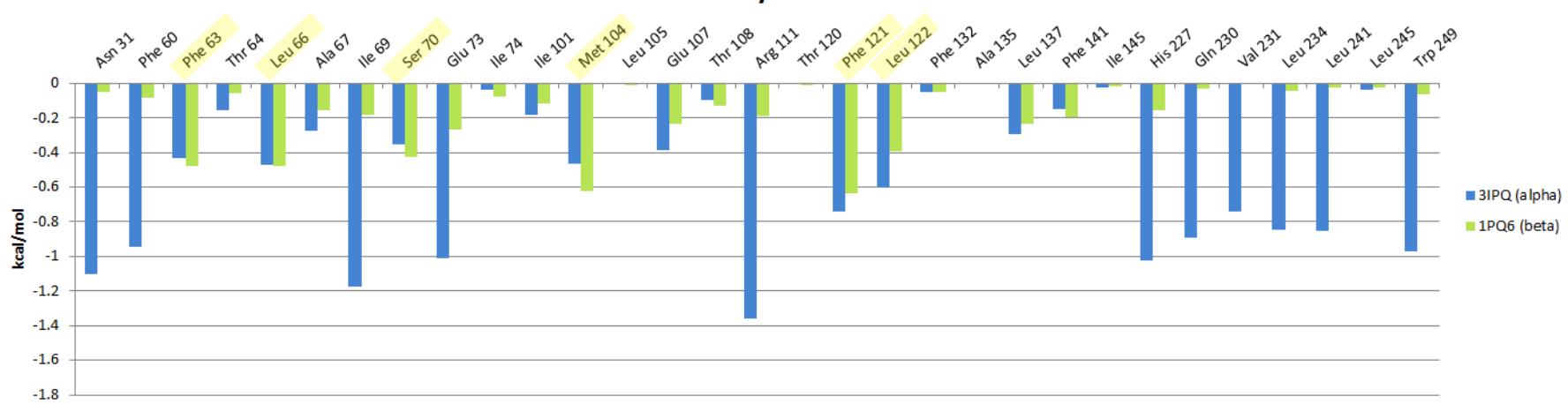
# Glycine Scan

# Results

Amino Acid	Difference
Phe 121	-0.6341
Met 104	-0.62322
Phe 63	-0.47719
Leu 66	-0.47576
Ser 70	-0.4263
Leu 122	-0.39017

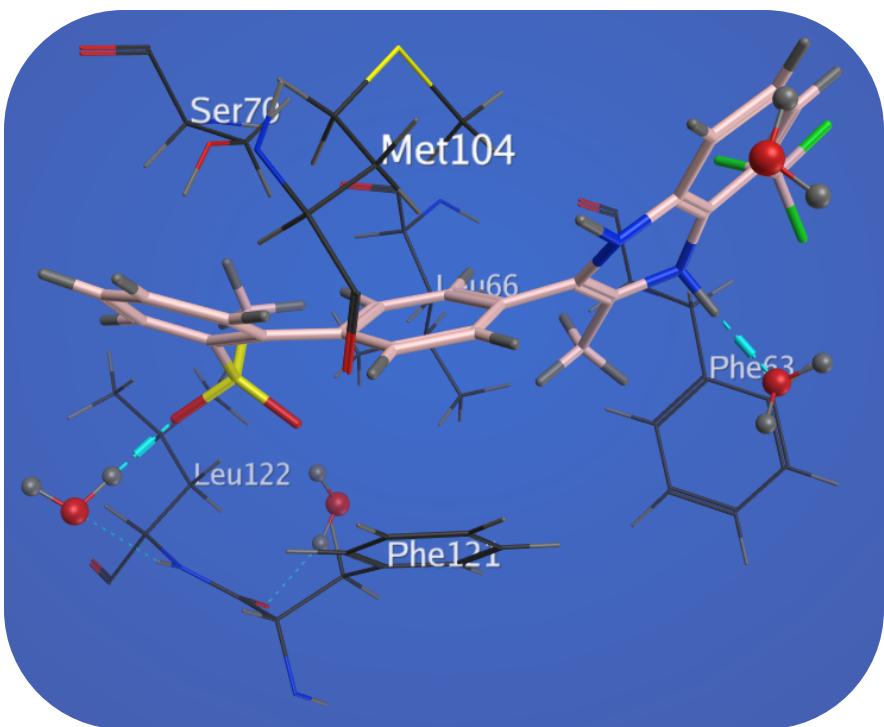


Wye-672



## Scaffold Replacement

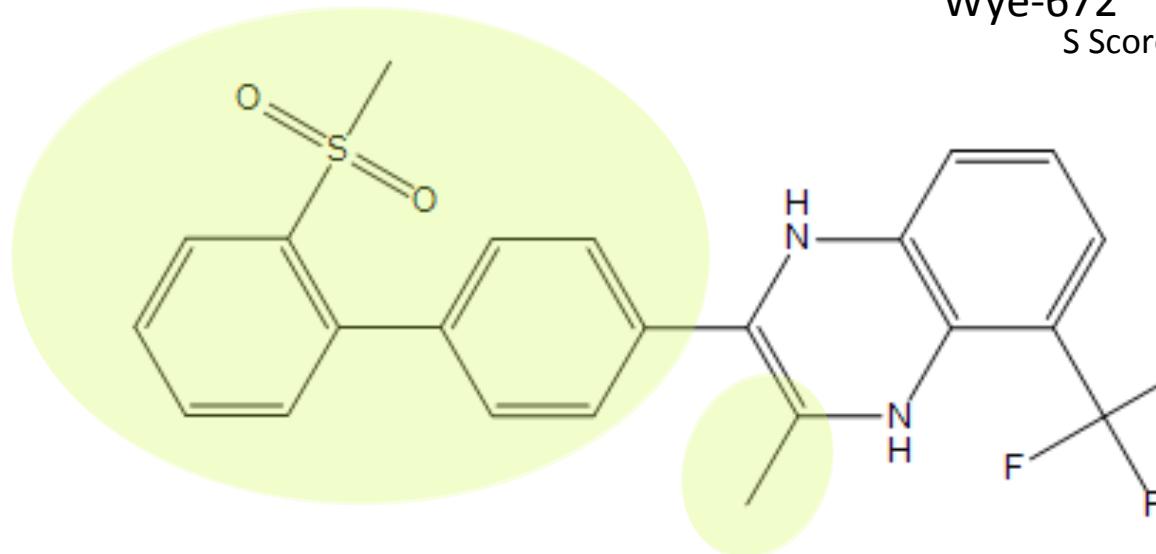
# Features of Wye-672



Amino Acid	Interaction
Phe 121	pi-pi
Met 104	hydrophobic
Phe 63	pi-methyl; hydrophobic
Leu 66	hydrophobic
Ser 70	pi-OH
Leu 122	H-bond bridged by H <sub>2</sub> O

## Scaffold Replacement

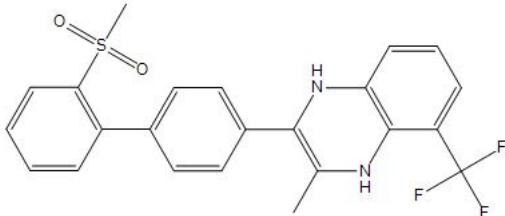
# Procedure



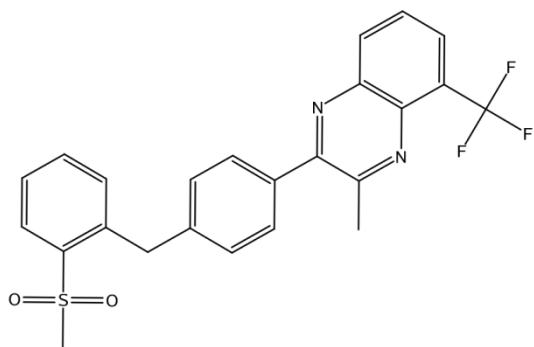
Results	m_46	m_10	m_5
S score (kcal/mol)			

## Scaffold Replacement

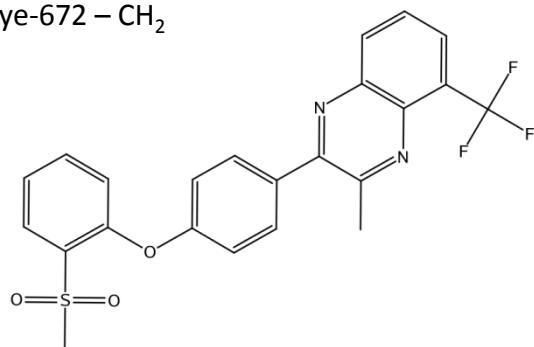
# Alterations for Synthesis



Wye-672 – no change



Wye-672 - CH<sub>2</sub>

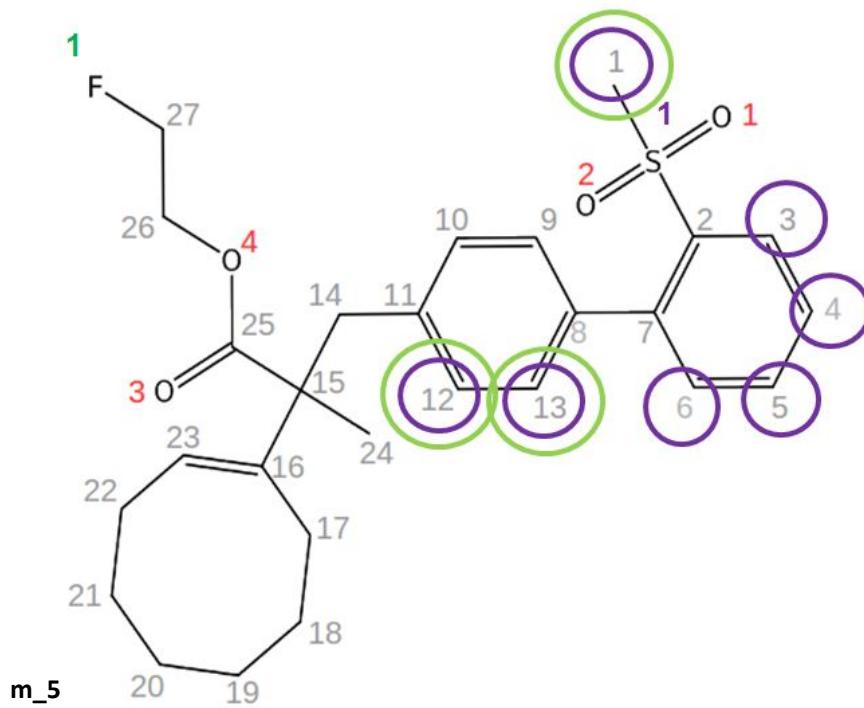
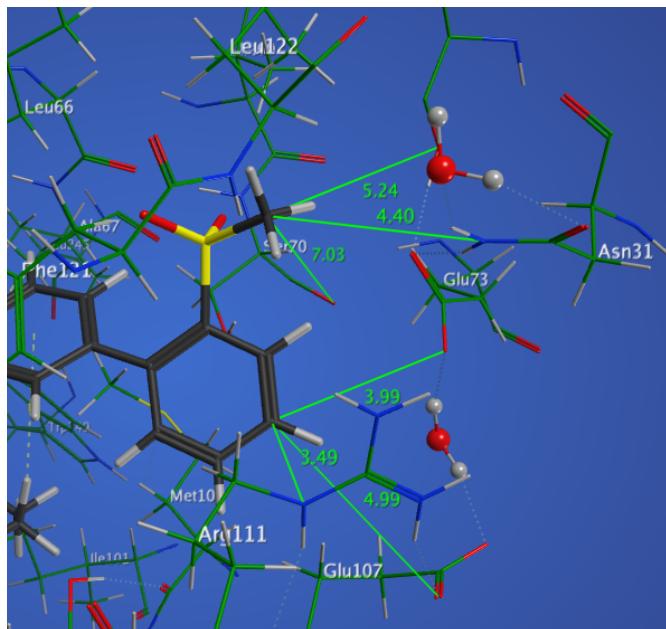


Wye-672 - O

Ligand	Original S score (kcal/mol)	-CH <sub>2</sub> S score (kcal/mol)	-O S score (kcal/mol)
wye-672	-9.974	-10.357	-10.333
m_10	-11.621	-12.418	-11.798
m_5	-11.210	-11.962	-11.543
m_46	-11.836	-11.661	-11.497
m_21	-10.022	-10.702	-10.426

## Scaffold Replacement

# Substituent Groups



# Possible Substituents

- **Greasy** – methyl
  - **Polar** – hydroxyl, amine

## Conclusion

# Future Work

- Evaluate scaffold replacement results for viability as LXR $\beta$  selective ligands using YASARA (Yet Another Scientific Artificial Reality Application).
- Perform glycine scanning and scaffold replacement using other beta selective ligands.
- Corroborate results by repeating procedure with alternate starting crystal structures for LXR $\alpha$  and LXR $\beta$ .
- Perform molecular dynamics simulation to obtain snapshots for further analysis.
- Synthesize developed structures

# Acknowledgement

- Dr. Riley and Dr. Sridhar
- National Science Foundation
  - EPSCoR Cooperative Agreement No. EPS-1003897
- National Institute of Health
  - AREA program (1R15GM113193)
- Xavier Chemistry Department

## References

1. Viennois E, Mouzat K, Dufour J, Morel L, Lobaccaro JM, Baron S. Selective liver X receptor modulators (SLIMs): what use in human health? *Mol Cell Endocrinol.* 2011;351(2):129-41.
2. Matsuda, Takayuki, Ayumu Okuda, Yuichiro Watanabe, Tohru Miura, Hidefumi Ozawa, Ayako Tosaka, Koichi Yamazaki, Yuki Yamaguchi, Sayaka Kurobuchi, Minoru Koura, and Kimiyuki Shibuya. "Design and Discovery of 2-oxochromene Derivatives as Liver X Receptor  $\beta$ -selective Agonists." *Bioorganic & Medicinal Chemistry Letters* 25.6 (2015): 1274-278. Web.