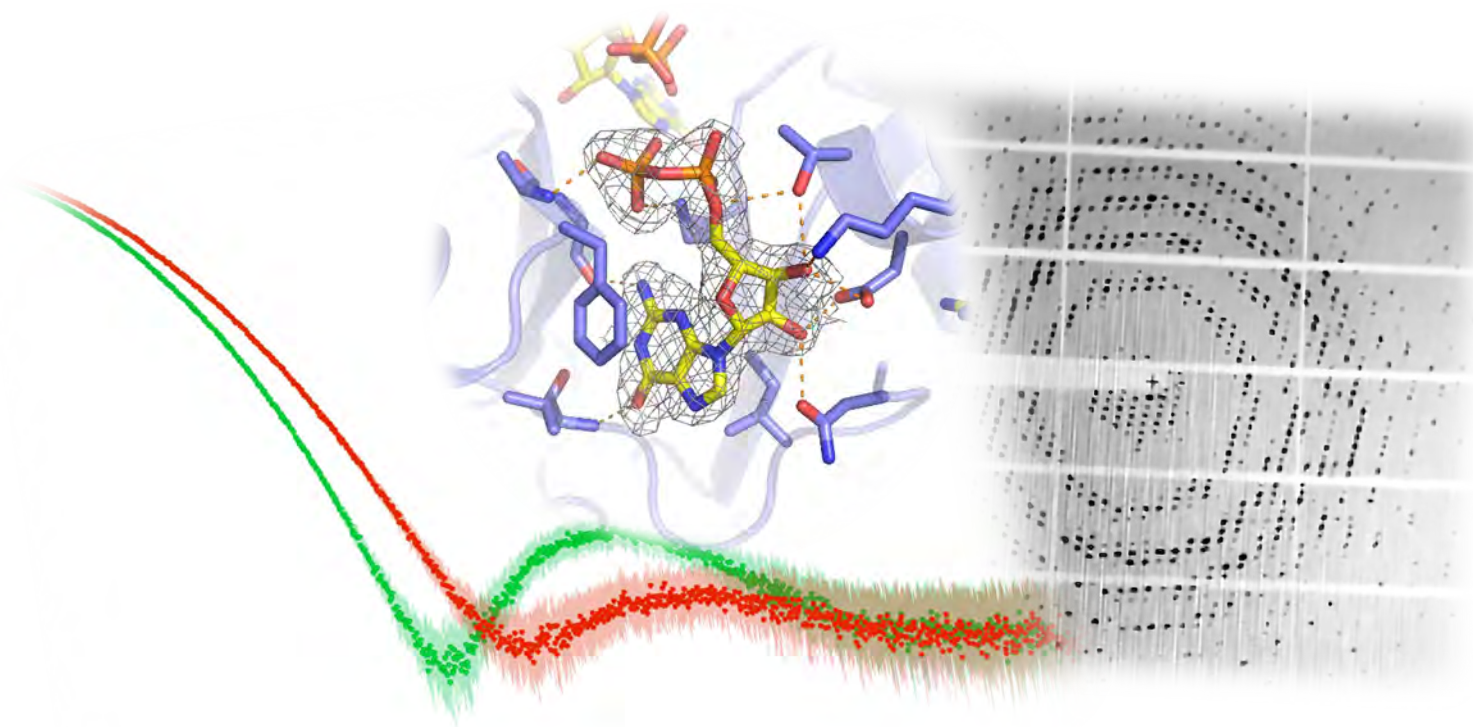


STRUCTURAL APPROACHES TO IDENTIFY NOVEL IMP DEHYDROGENASE INHIBITORS



Rubén Martínez-Buey
METABOLIC ENGINEERING GROUP



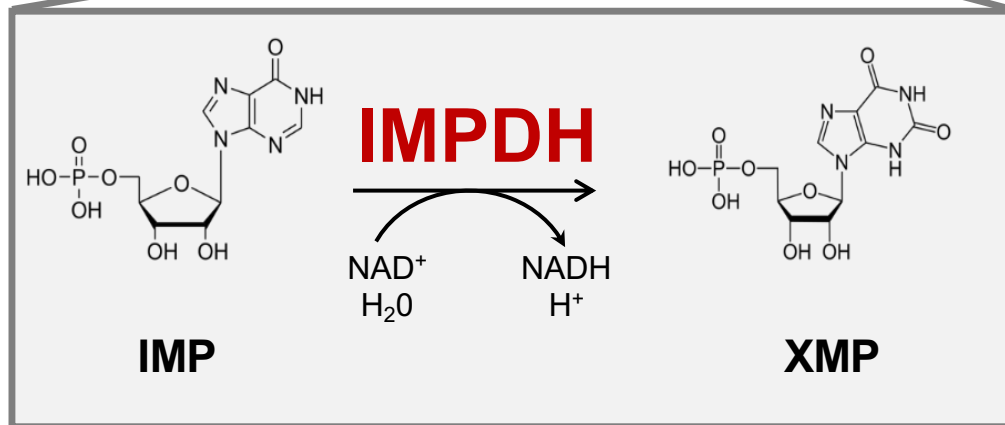
VNiVERSiDAD
DSALAMANCA

1st COMMITTED STEP IN GTP SYNTHESIS

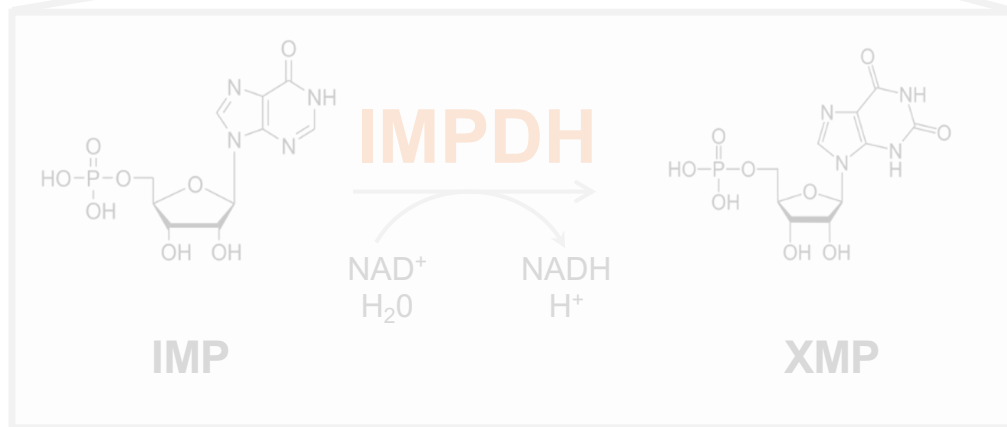
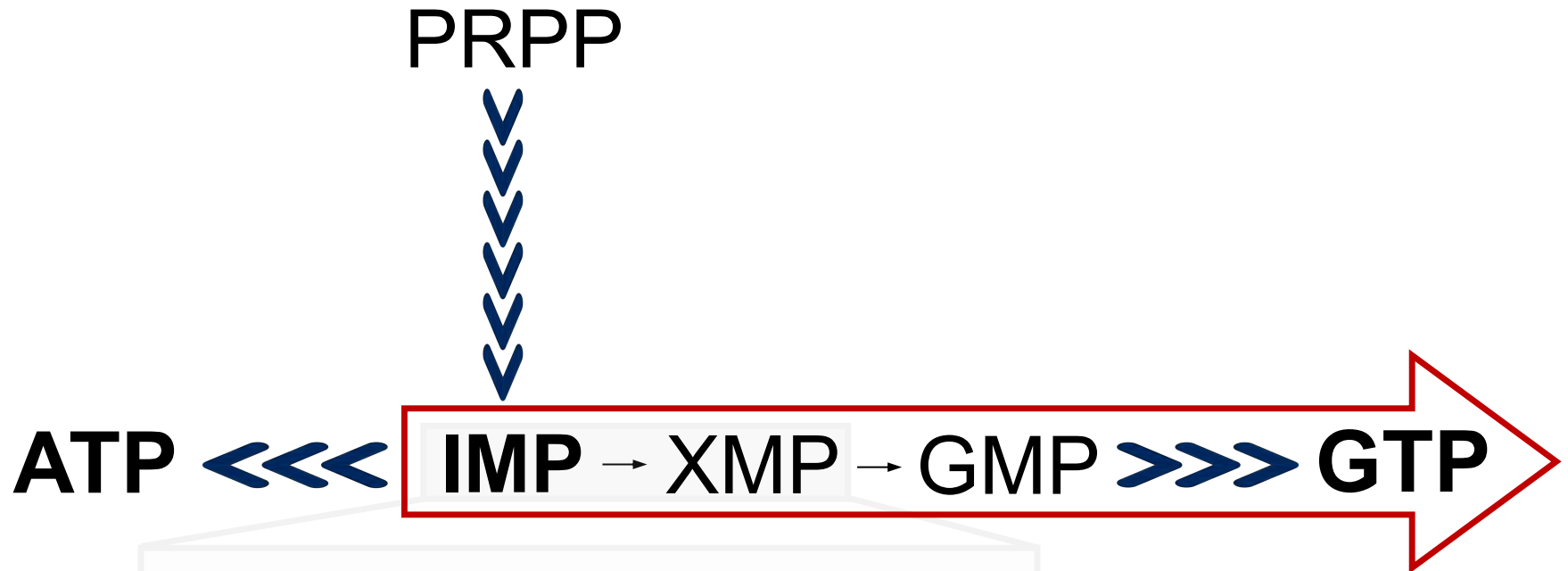
PRPP



ATP <<< **IMP** → **XMP** → GMP >>> GTP



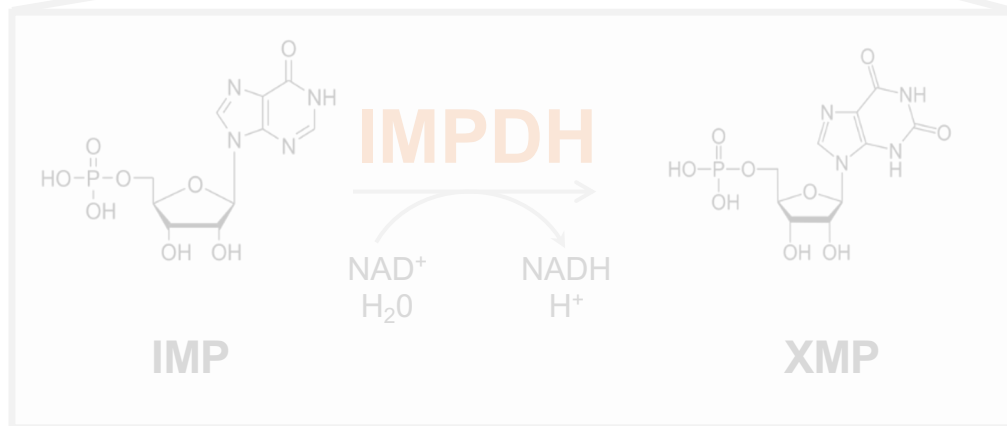
IMPDH CONTROLS GTP BIOSYNTHESIS



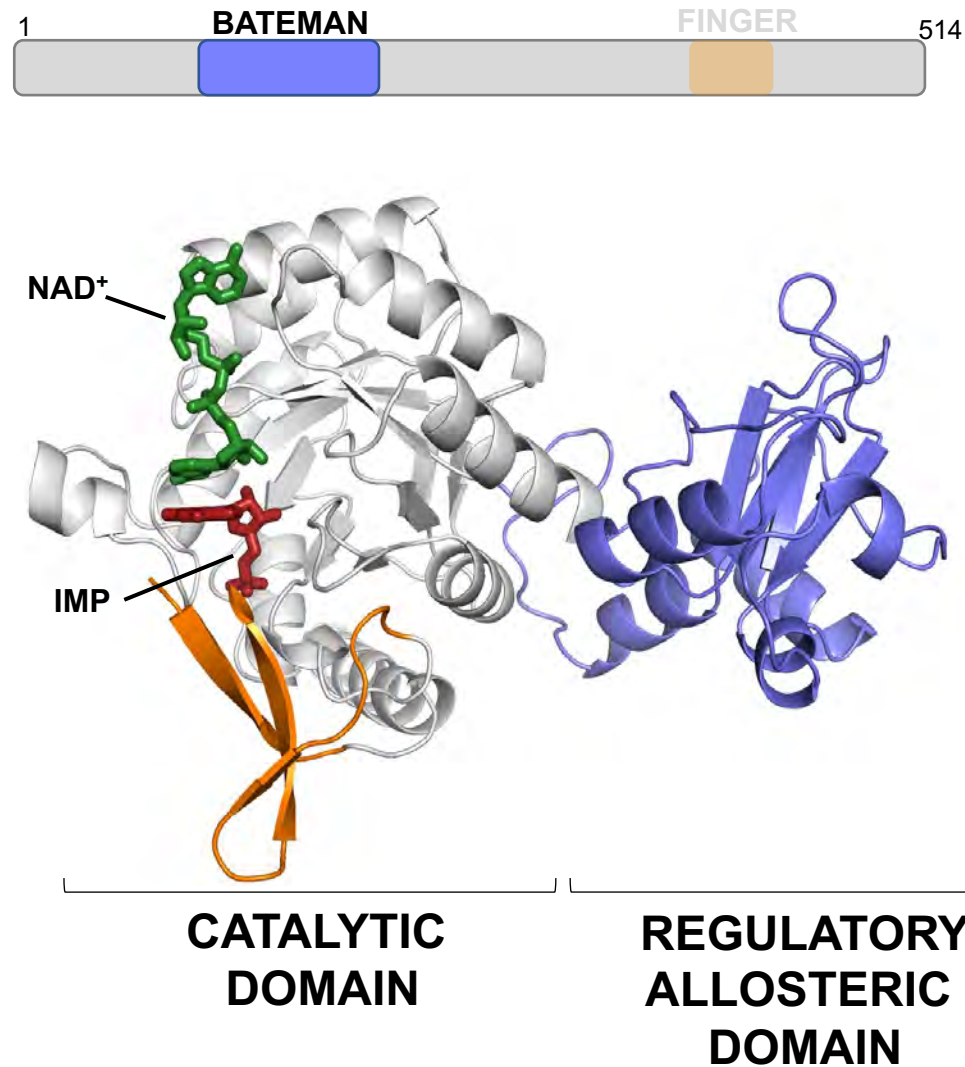
IMPDH IS A DRUG TARGET



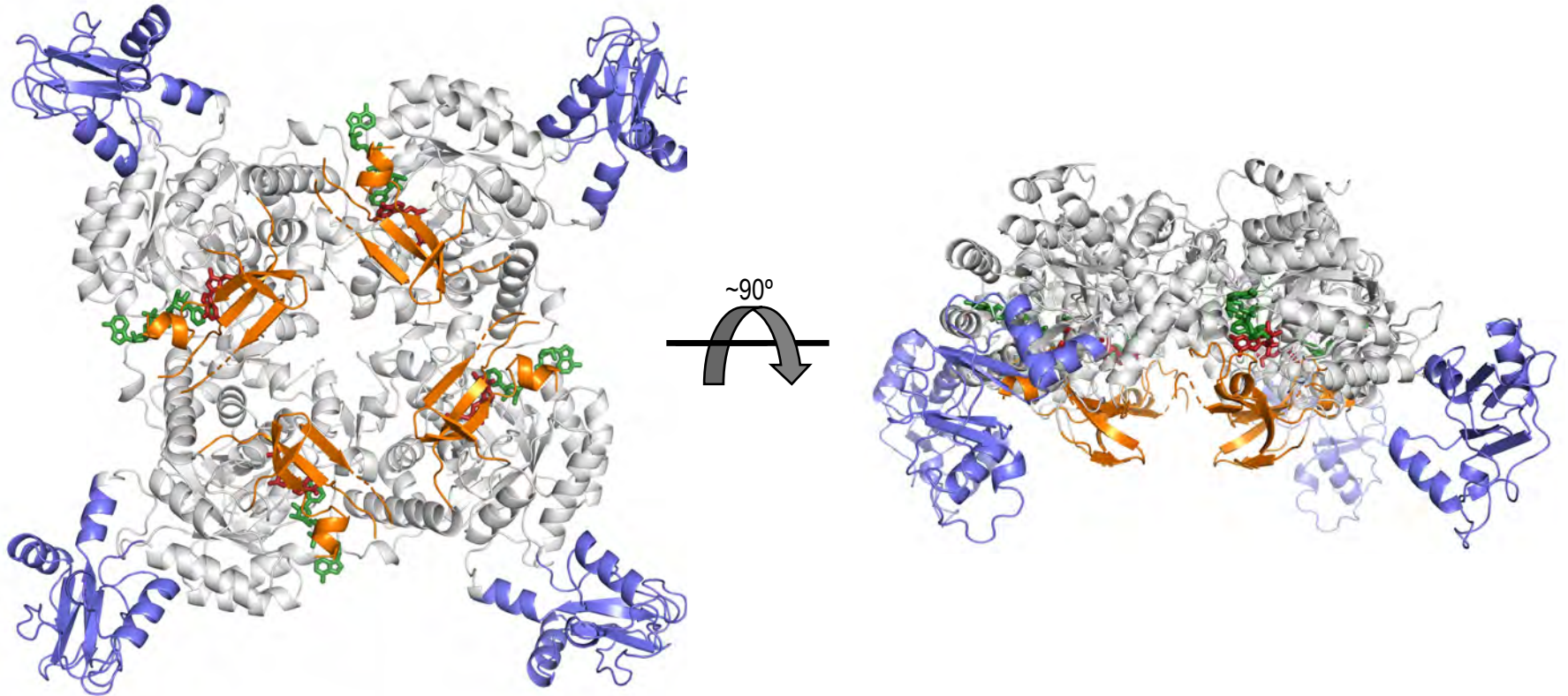
ATP <<< **IMP** → XMP → GMP >>> GTP



IMPDH MONOMERIC STRUCTURE



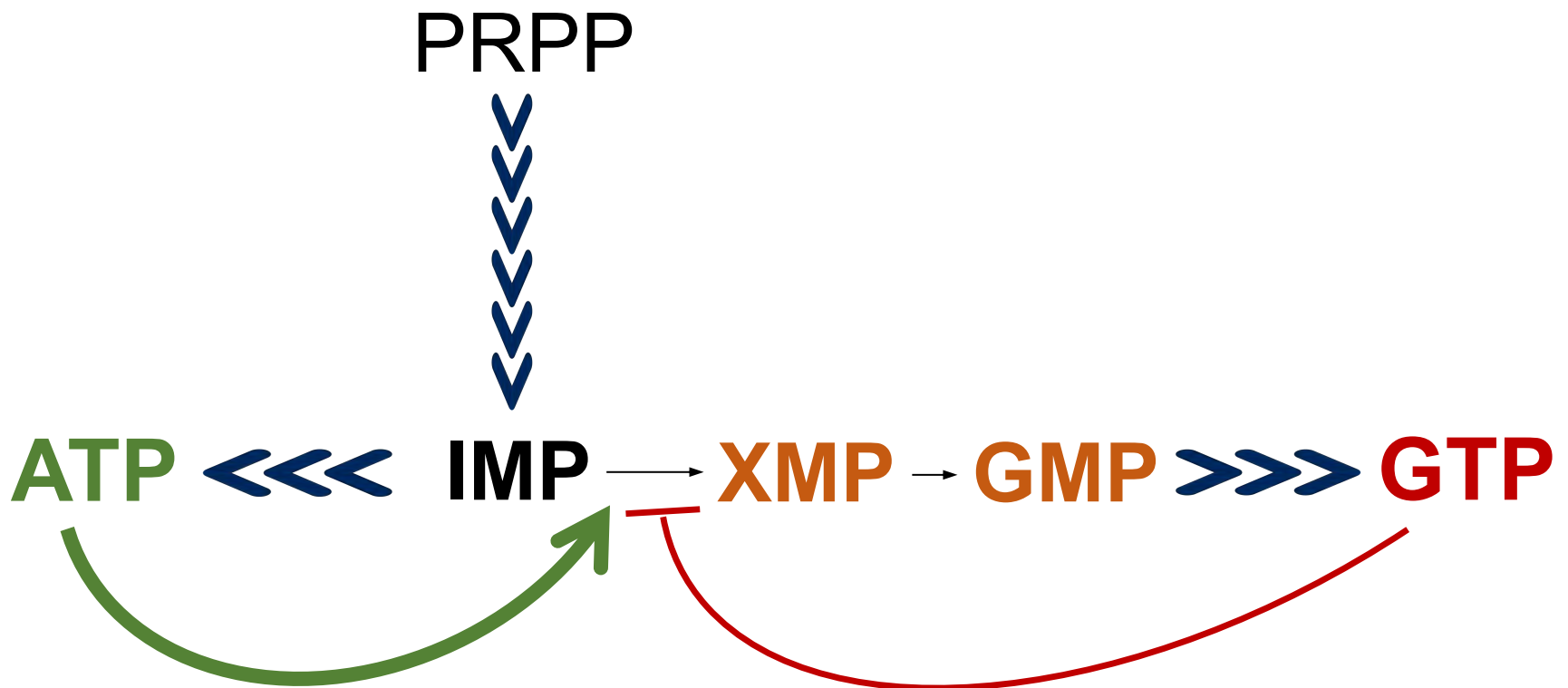
IMPDH FORMS TETRAMERS IN SOLUTION



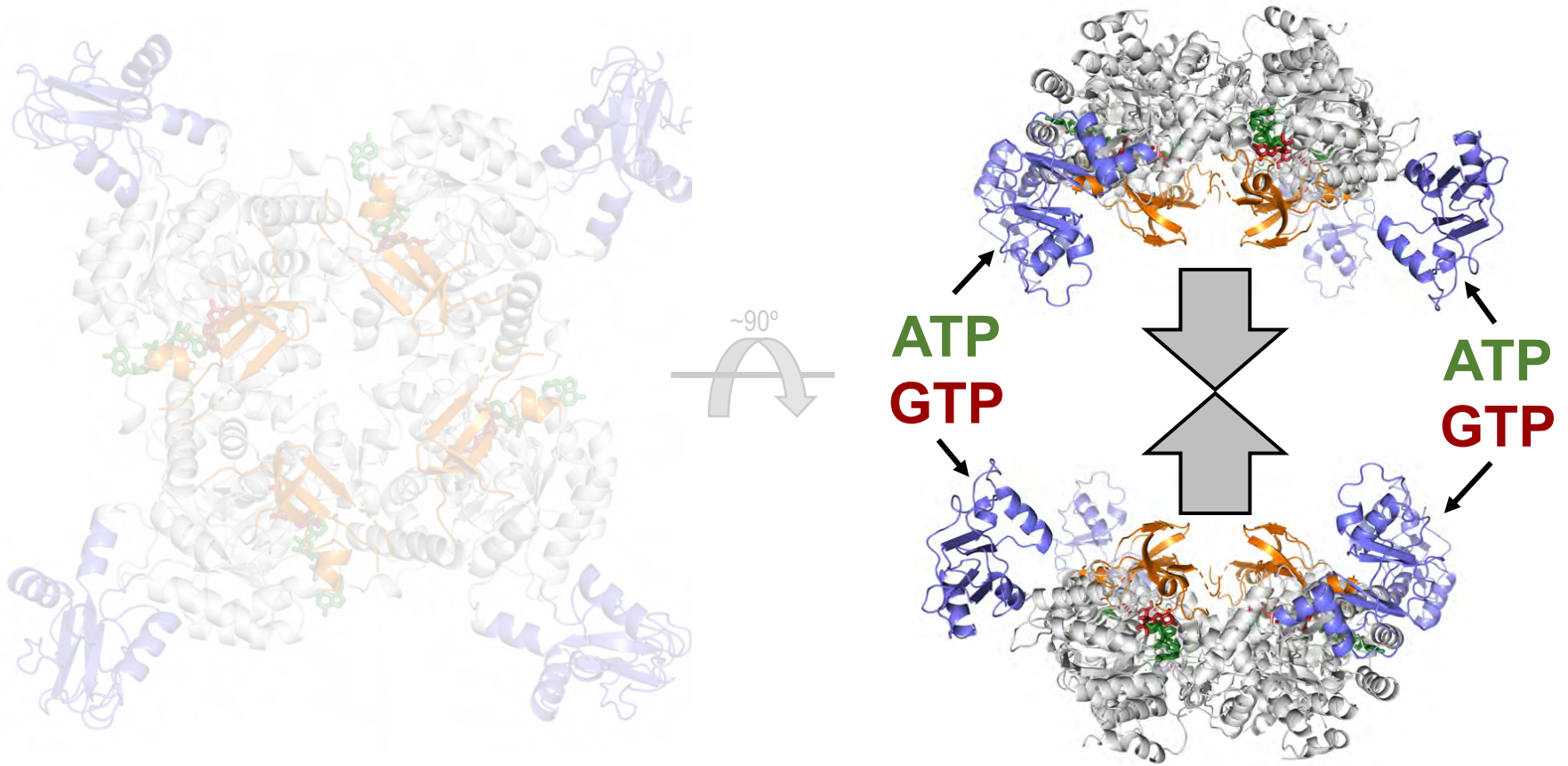


**HOW IS IMPDH
REGULATED?**

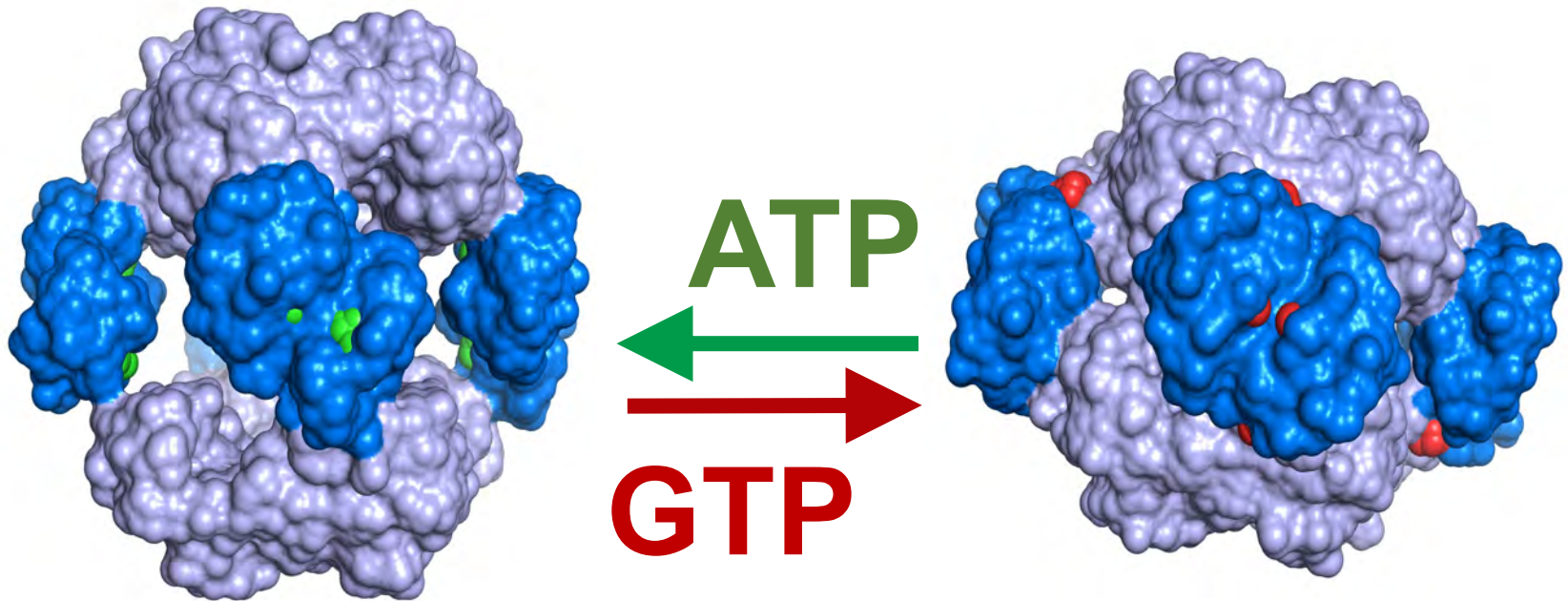
ATP & GTP ARE ALLOSTERIC MODULATORS



ATP & GTP INDUCE OCTAMERS



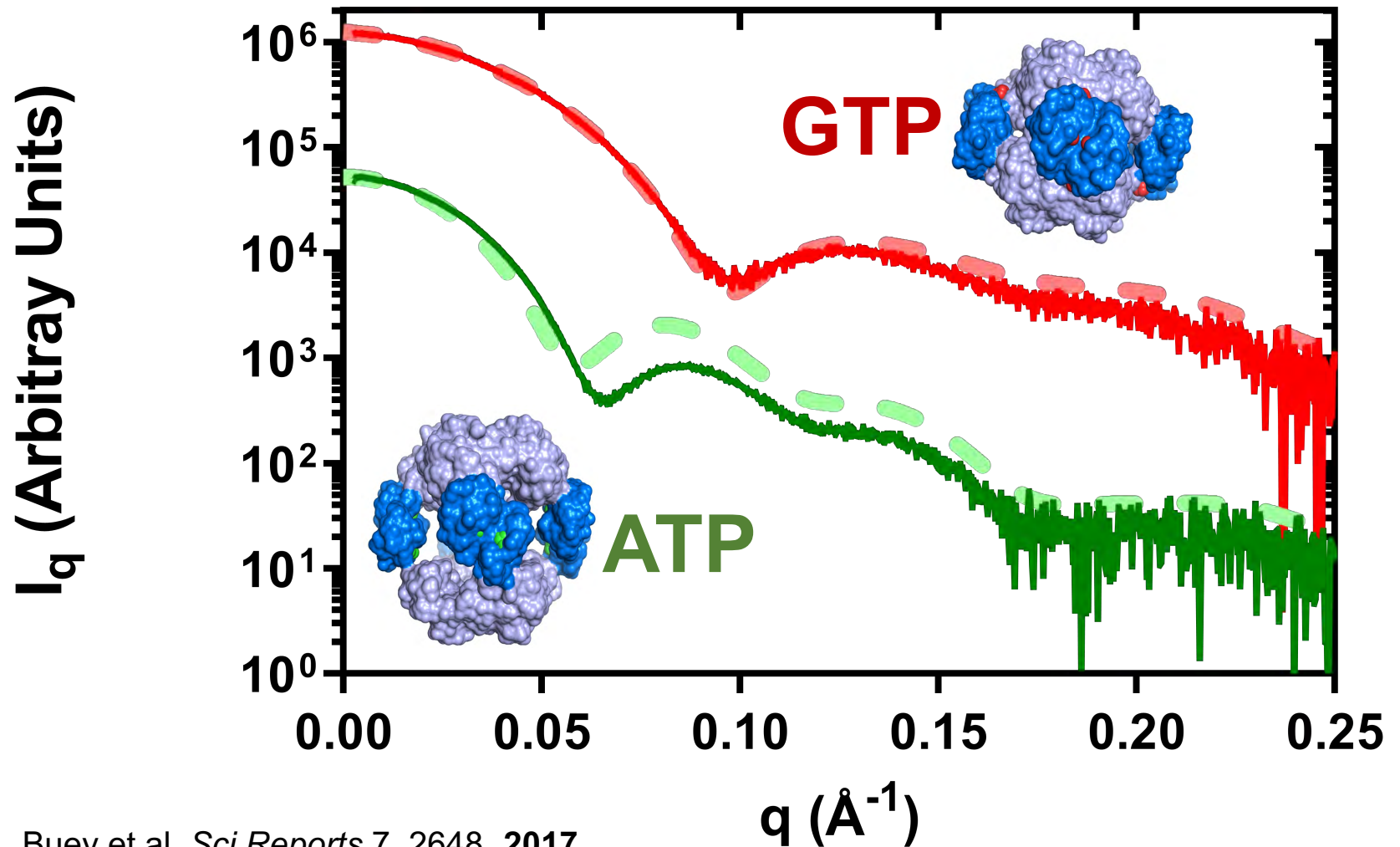
CONFORMATIONAL SWITCH



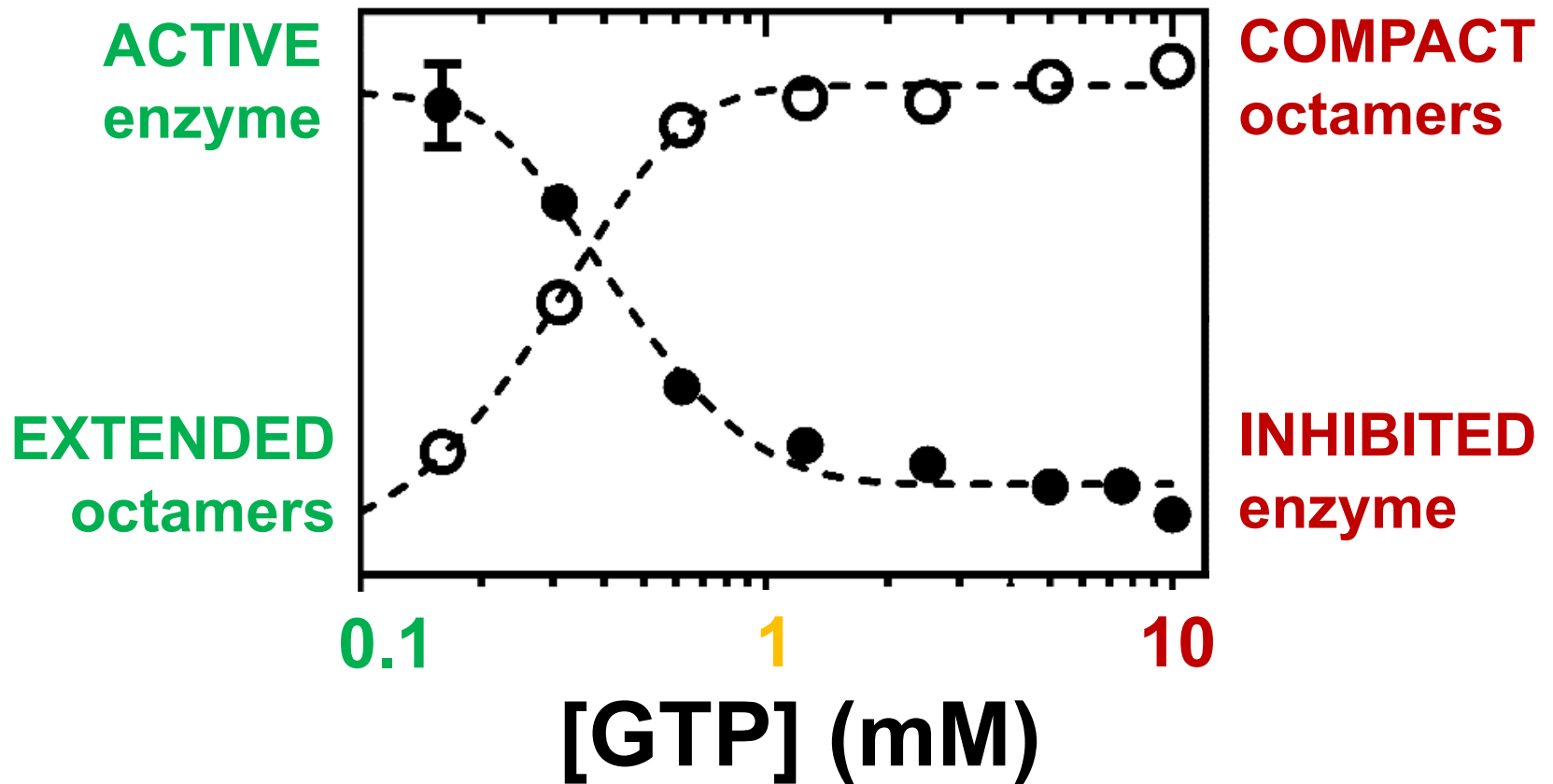
PDB-ID **4Z87**; Buey et al. *Nat Commun* 6, 8923. **2015**

PDB-ID **5MCP**; Buey et al. *Sci Reports* 7, 2648. **2017**

CONFORMATIONAL SWITCH BY SAXS



THE CONFORMATIONAL SWITCH CONTROLS ENZYME ACTIVITY





HOW IS IMPDH REGULATED?

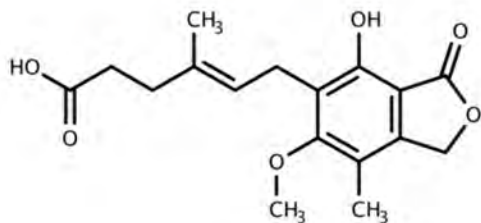


IMPDH IS A DRUG TARGET

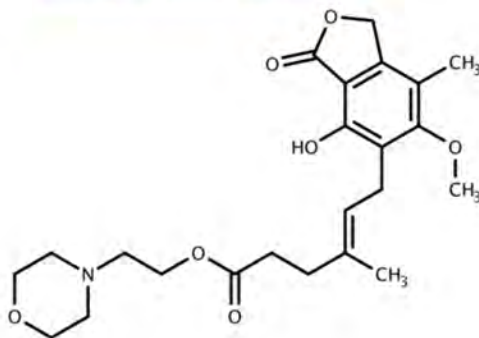


ALL KNOWN IMPDH INHIBITORS ARE ORTHOSTERIC

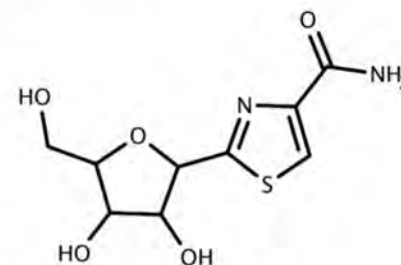
Mycophenolic Acid (MPA)



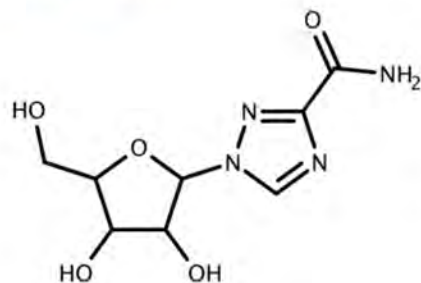
Mycophenolate Mofetil (MMF)



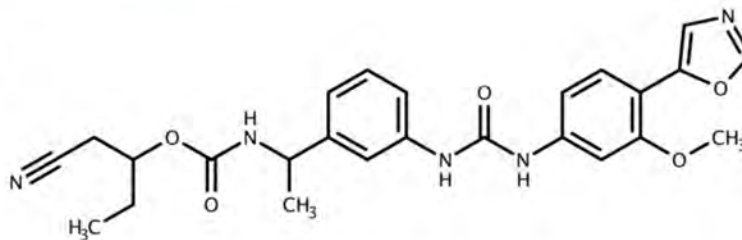
Tiazofurin



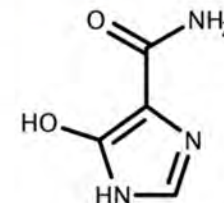
Ribavirin



VX-944



FF-10501





**CAN WE OBTAIN
ALLOSTERIC IMPDH
INHIBITORS ?**

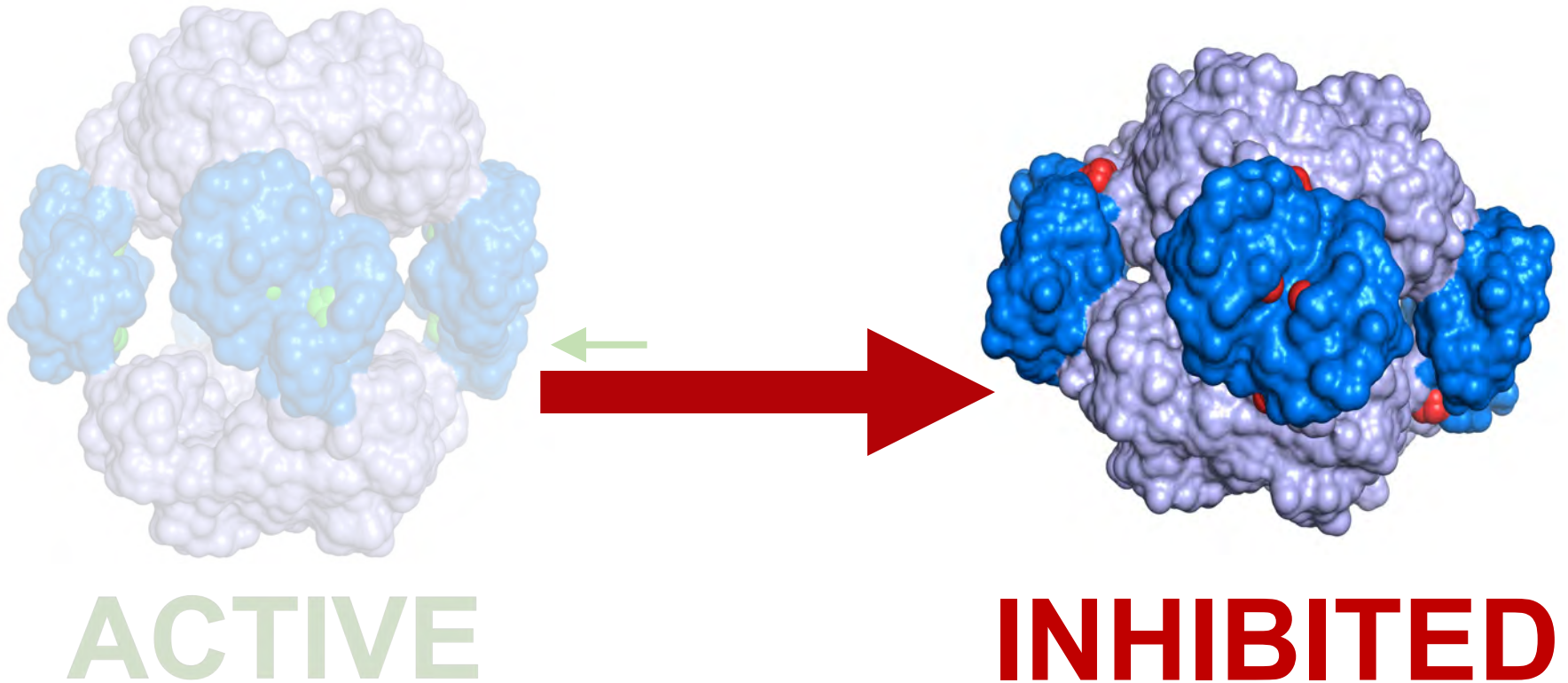
BENEFITS OF ALLOSTERIC INHIBITORS



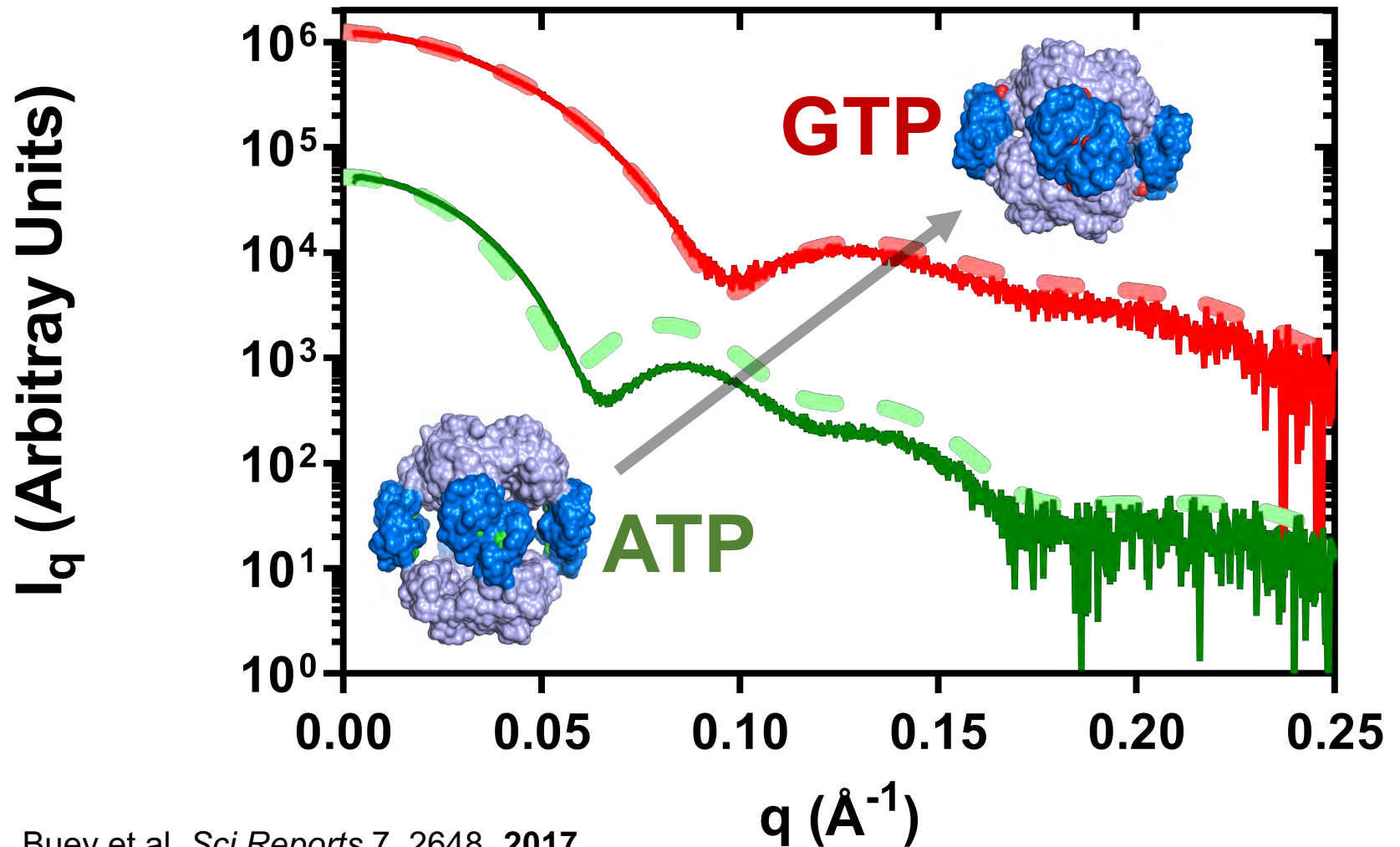
BENEFITS OF ALLOSTERIC INHIBITORS



WHAT ARE WE SEARCHING FOR?

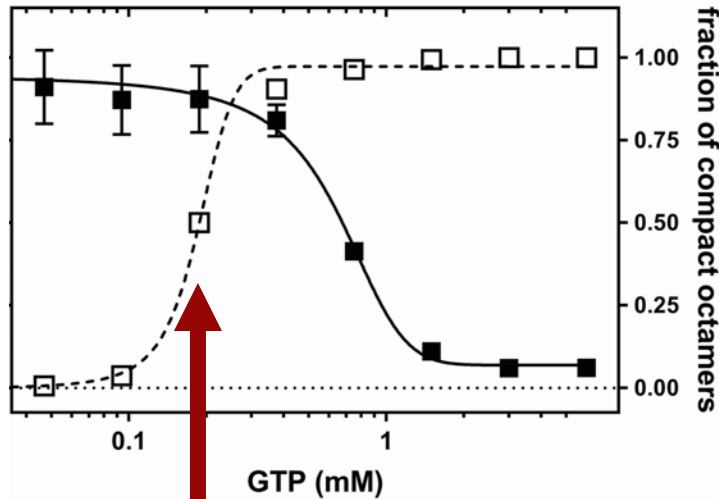


IMPDH CONFORMATIONS BY SAXS

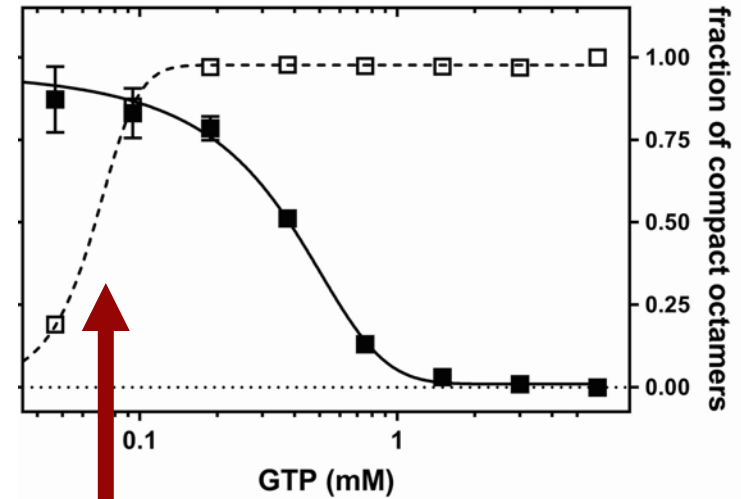


CONFORMATION SHIFTS AT SUB-INHIBITORY CONCENTRATIONS

human IMDPH1 + ATP



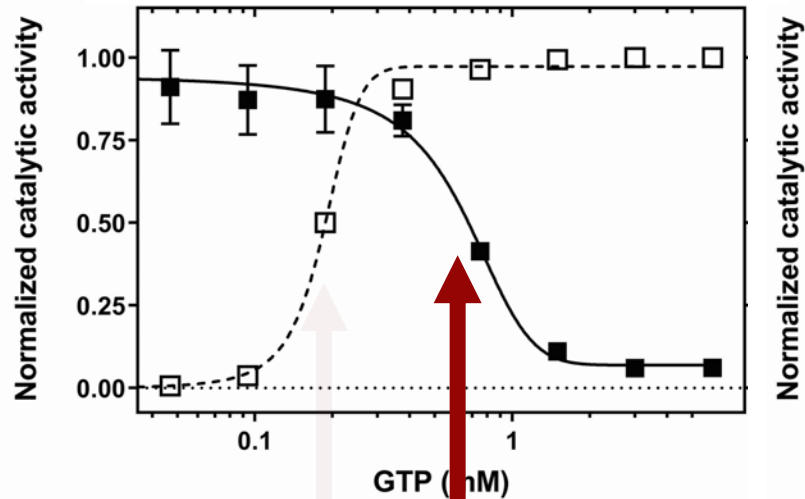
human IMDPH2 + ATP



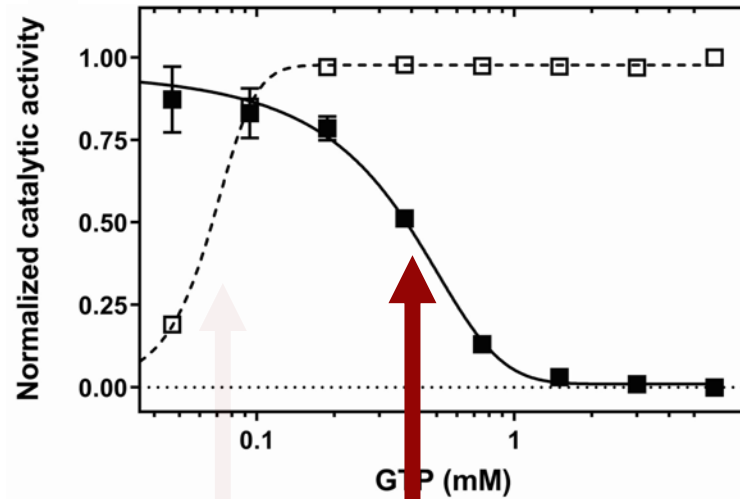
$K_{1/2}$ octamer compaction

CONFORMATION SHIFTS AT SUB-INHIBITORY CONCENTRATIONS

human IMDPH1 + ATP



human IMDPH2 + ATP



$K_{1/2}$ catalytic activity inhibition

SAXS IS MORE SENSITIVE THAN FUNCTIONAL ASSAYS

**SAXS
SCREENING**



CONFORMATIONAL CHANGE

**ACTIVITY
INHIBITION
SCREENING**



ACTIVITY INHIBITION

[INHIBITOR]



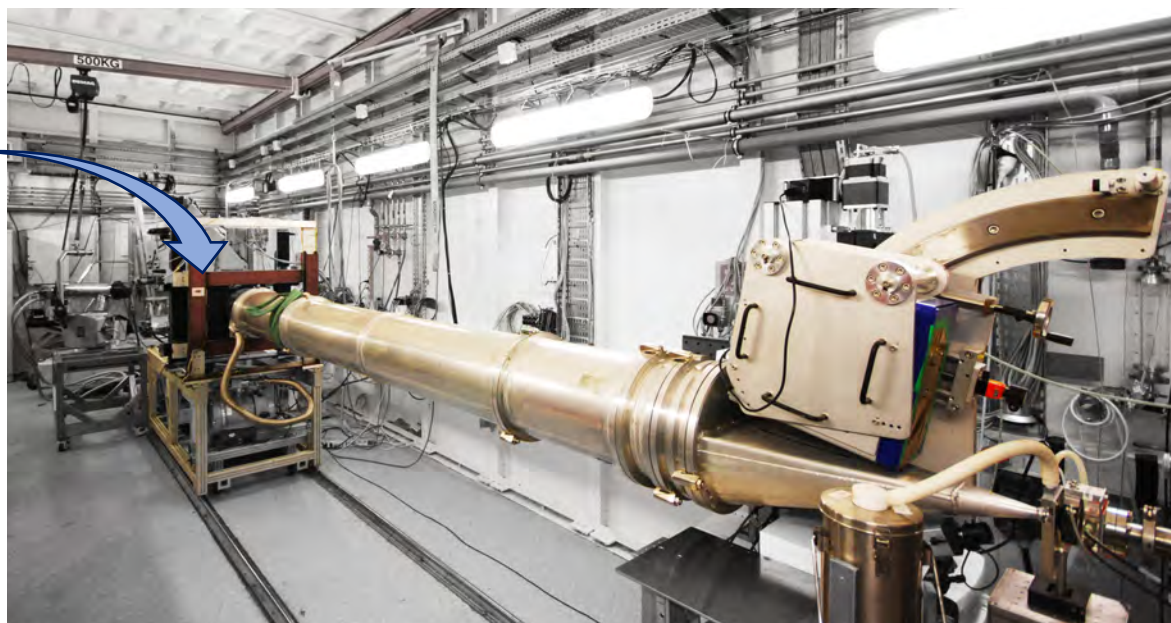


**SAXS AS A PRIMARY
SCREENING METHOD?**

IDENTIFYING ALLOSTERIC INHIBITORS BY HT-SAXS

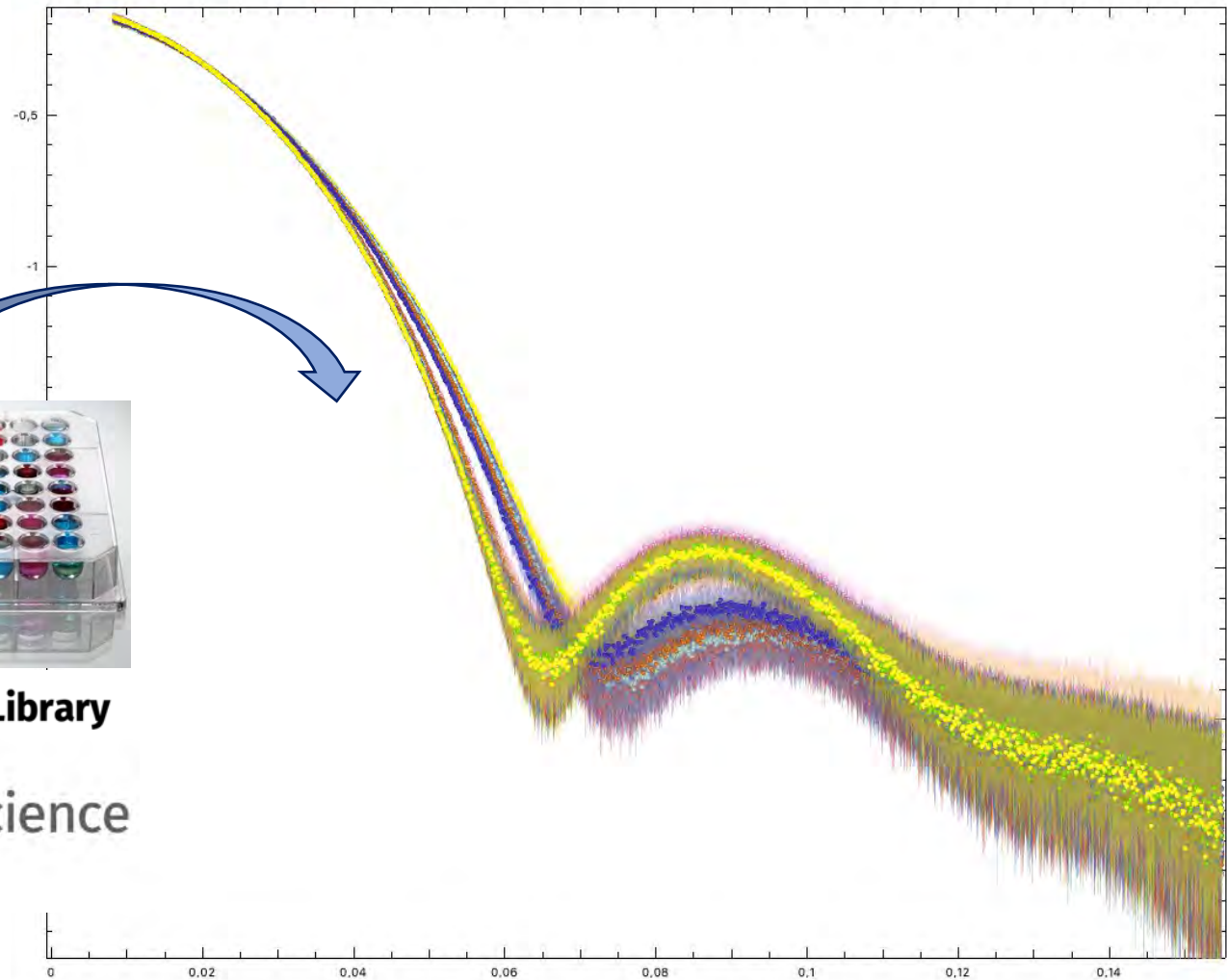


Guanosine Nucleotide Library



B21 BEAMLIN @  **diamond**

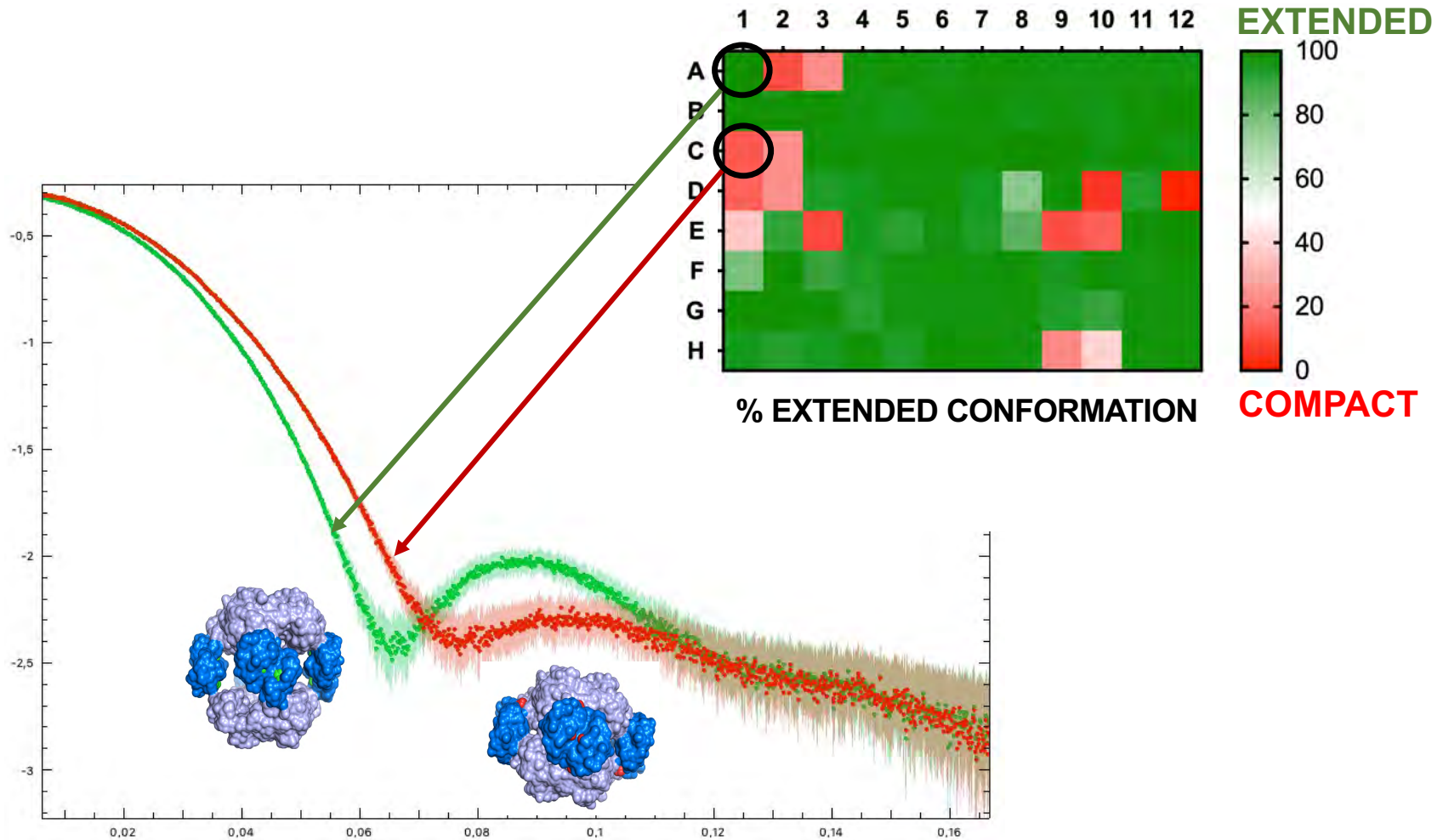
SCATTERING PROFILES



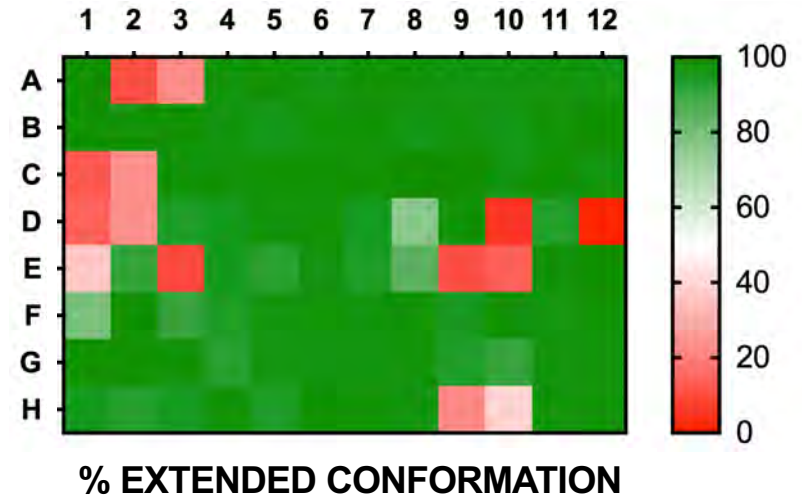
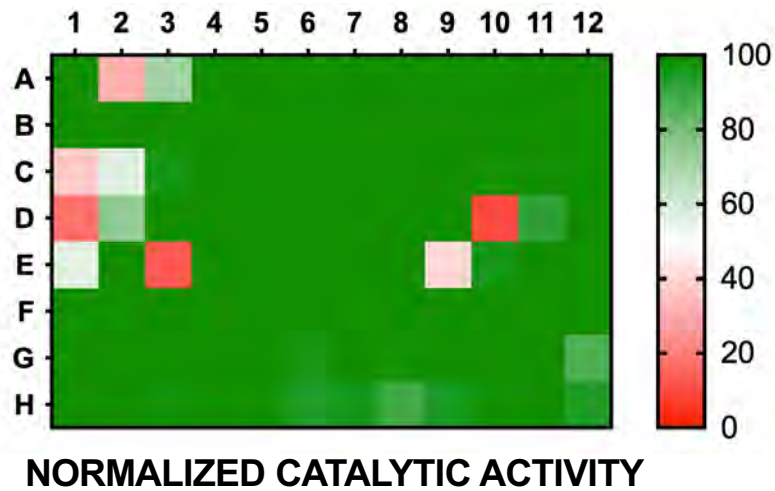
Guanosine Nucleotide Library



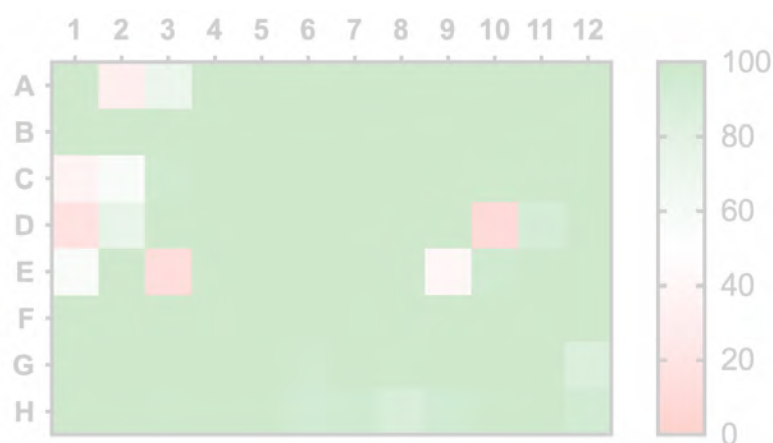
EXTENDED vs COMPACT OCTAMERS



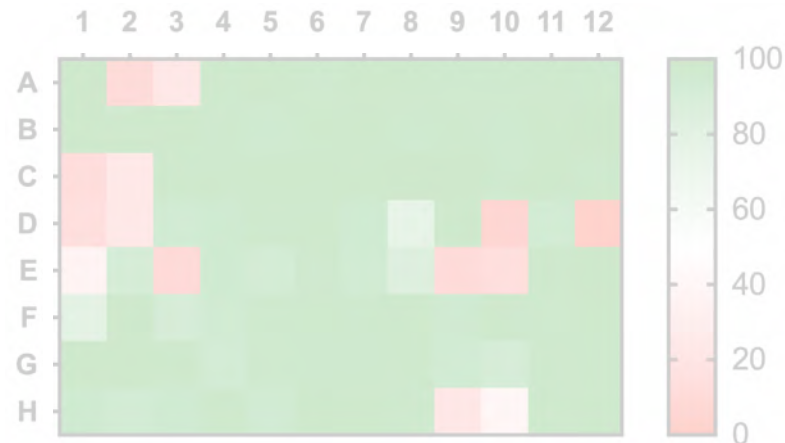
FUNCTIONAL vs STRUCTURAL ASSAY









FUNCTIONAL vs STRUCTURAL ASSAY



NORMALIZED CATALYTIC ACTIVITY




% EXTENDED CONFORMATION

ACTIVITY INHIBITION		SAXS	
Sensitivity	 10 hits (≥ 50% inhibition)	 15 hits (≥ 50% inhibition)	
[Protein]	 ~ 100 μg	 ~ 8 mg	
Time	 ~ 30 min	 ~ 3 h 20 min	

BIO-SAXS BEAMLINE OPTIMIZATION

washing the sample cell
requires ~70% of the
experimental time!

ACTIVITY INHIBITION		SAXS	
Sensitivity	10 hits ($\geq 50\%$ inhibition)		15 hits ($\geq 50\%$ inhibition)
[Protein]	~ 100 μg		~ 8 mg
Time	~ 30 min		~ 3 h 20 min



SCREENING LARGE CHEMICAL LIBRARIES USING SAXS?

REDUCING SAXS EXPERIMENTAL TIME



Fragment libraries



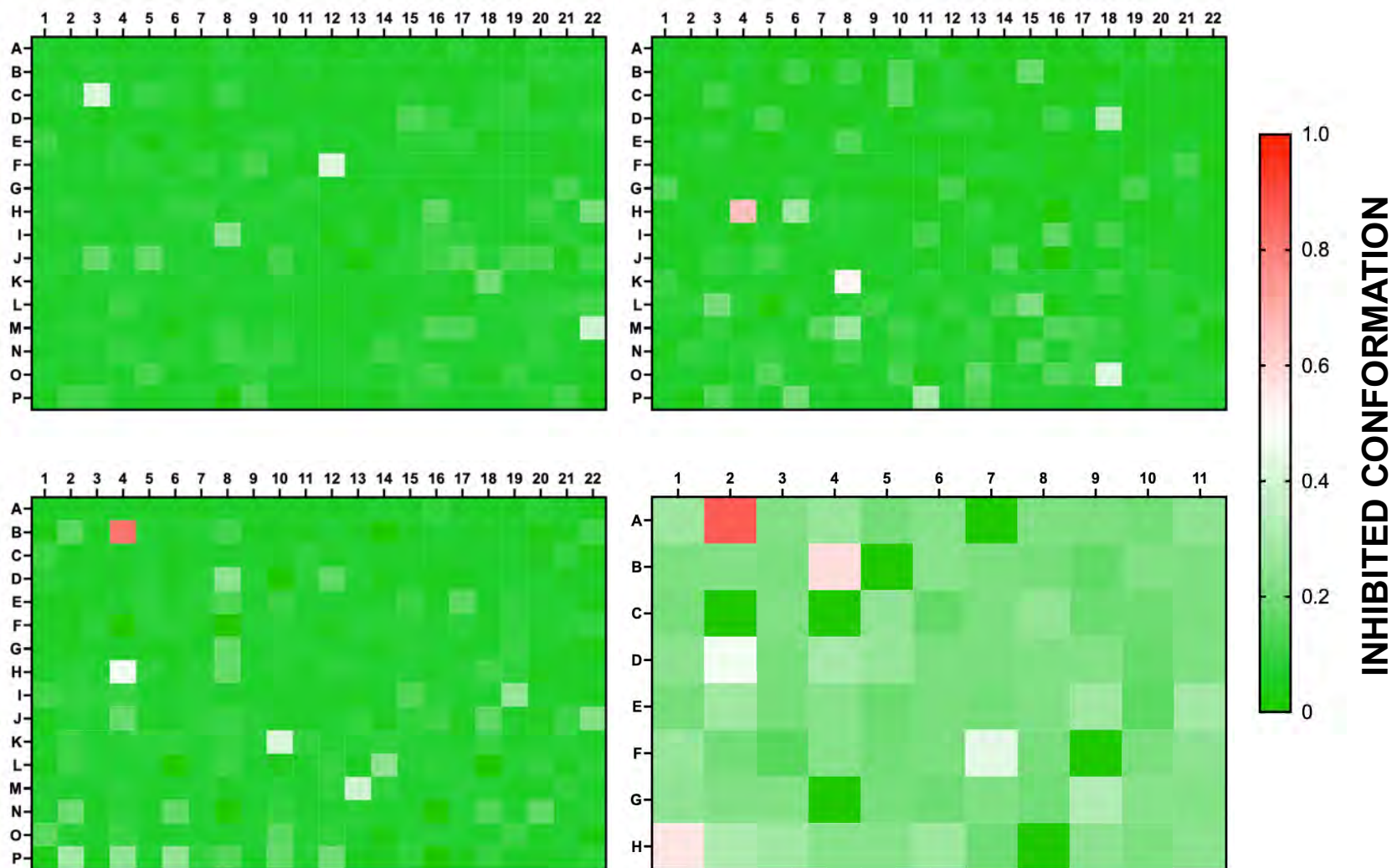
**MAXIMIZE
CHEMICAL
SPACE**

**REDUCE
SAMPLE
COUNT**



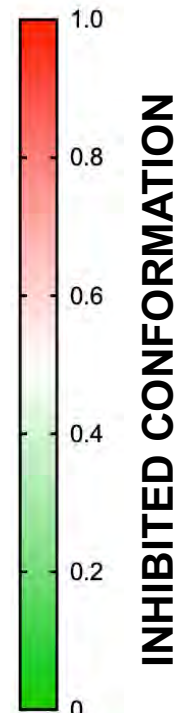
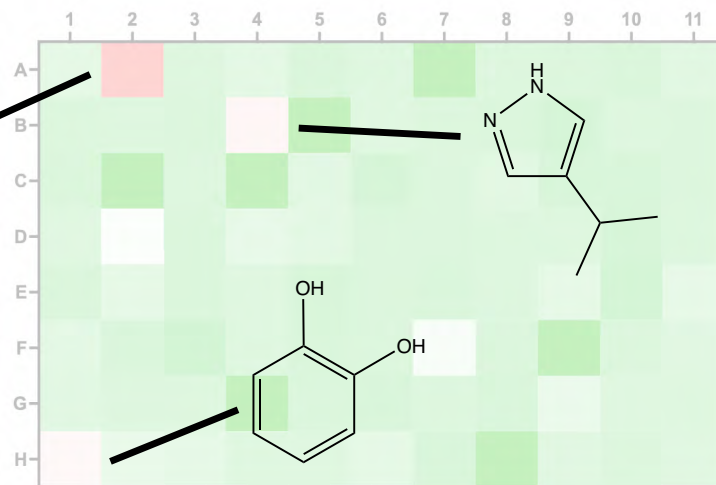
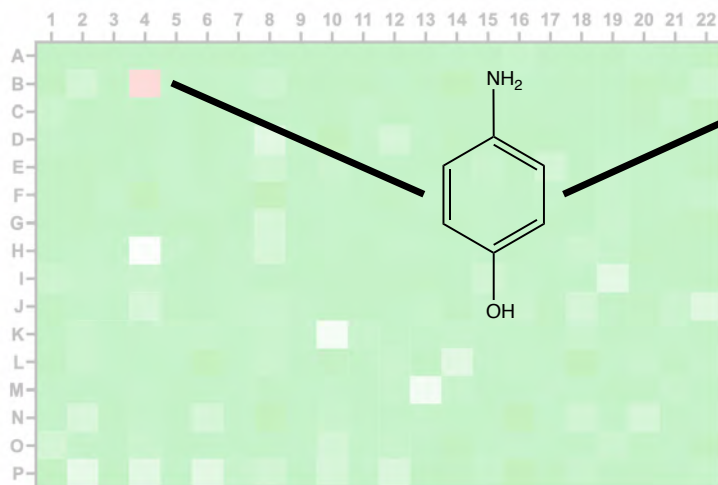
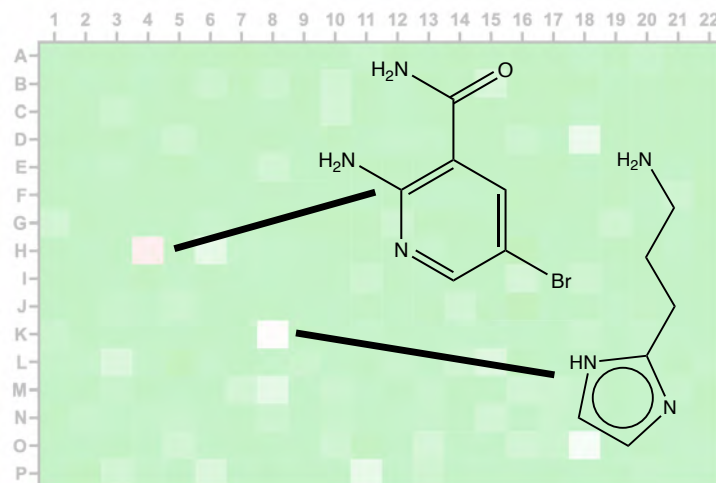
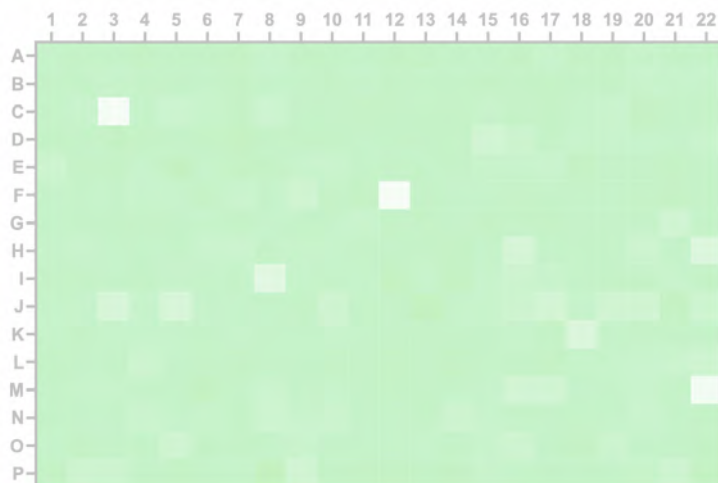
Compound pooling

EU-OPENSOURCE FRAGMENT LIBRARY

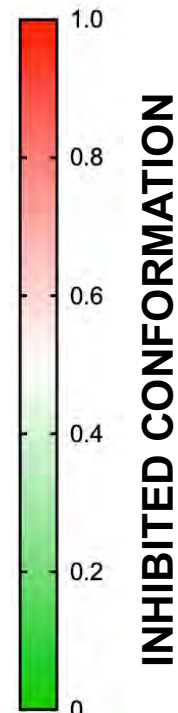
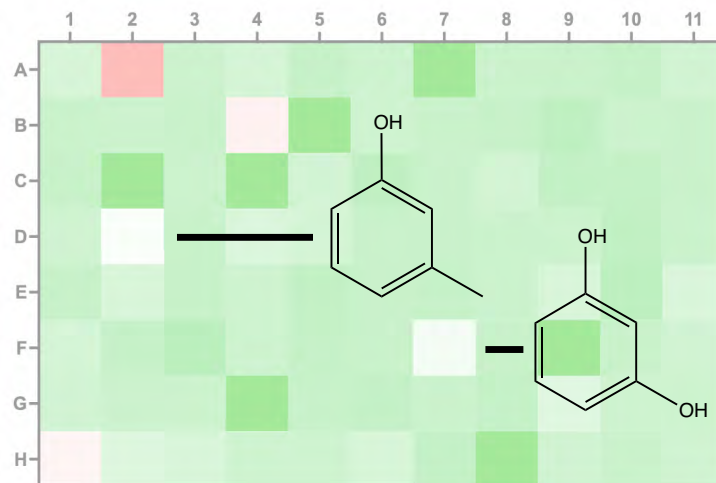
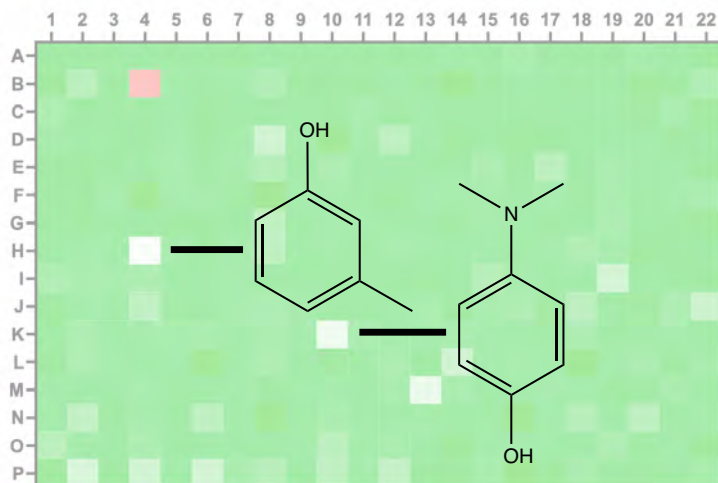
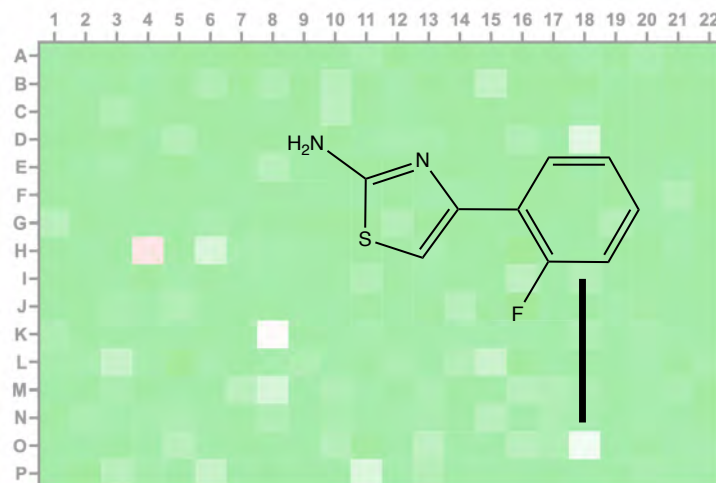
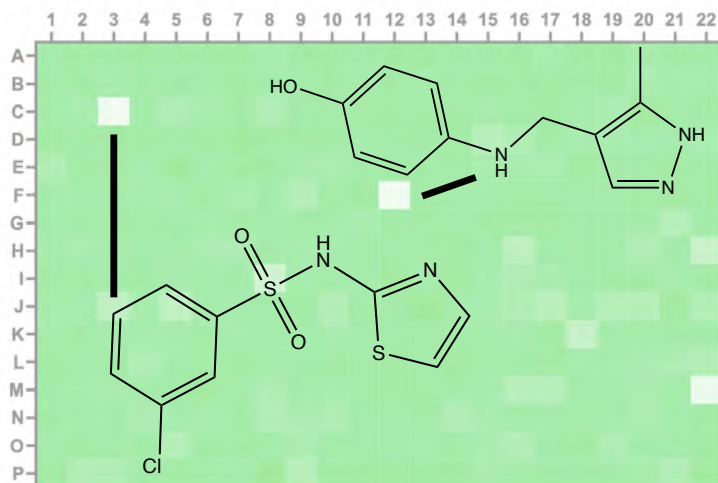


~ 42 HOURS @ B21  diamond

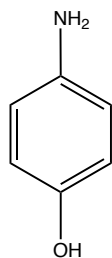
INHIBITED CONFORMATION $\geq 50\%$



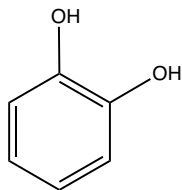
50% \geq INHIBITED CONFORMATION \geq 40%



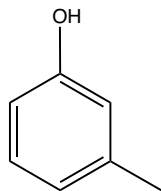
2 MAJORITARY FRAGMENT CHEMOTYPES



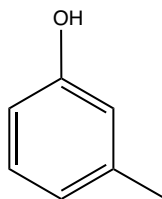
(87%)



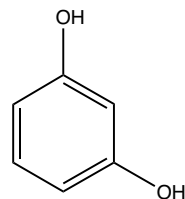
(56%)



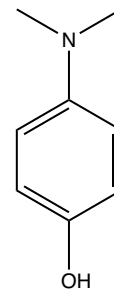
(47%)



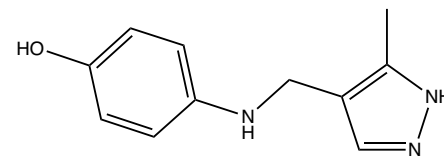
(47%)



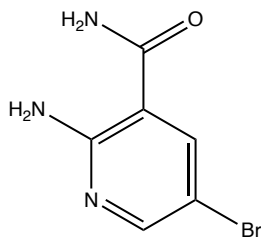
(44%)



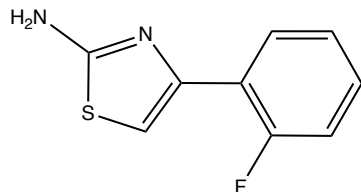
(41%)



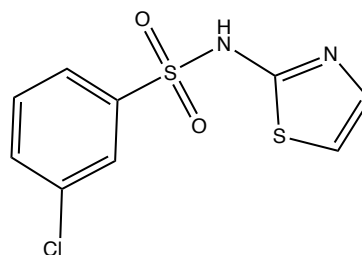
(41%)



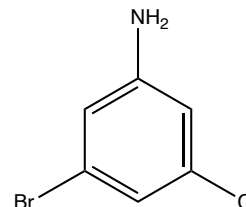
(65%)



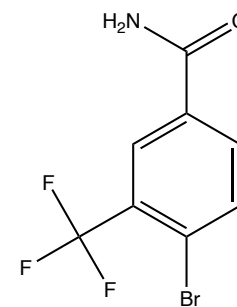
(42%)



(41%)

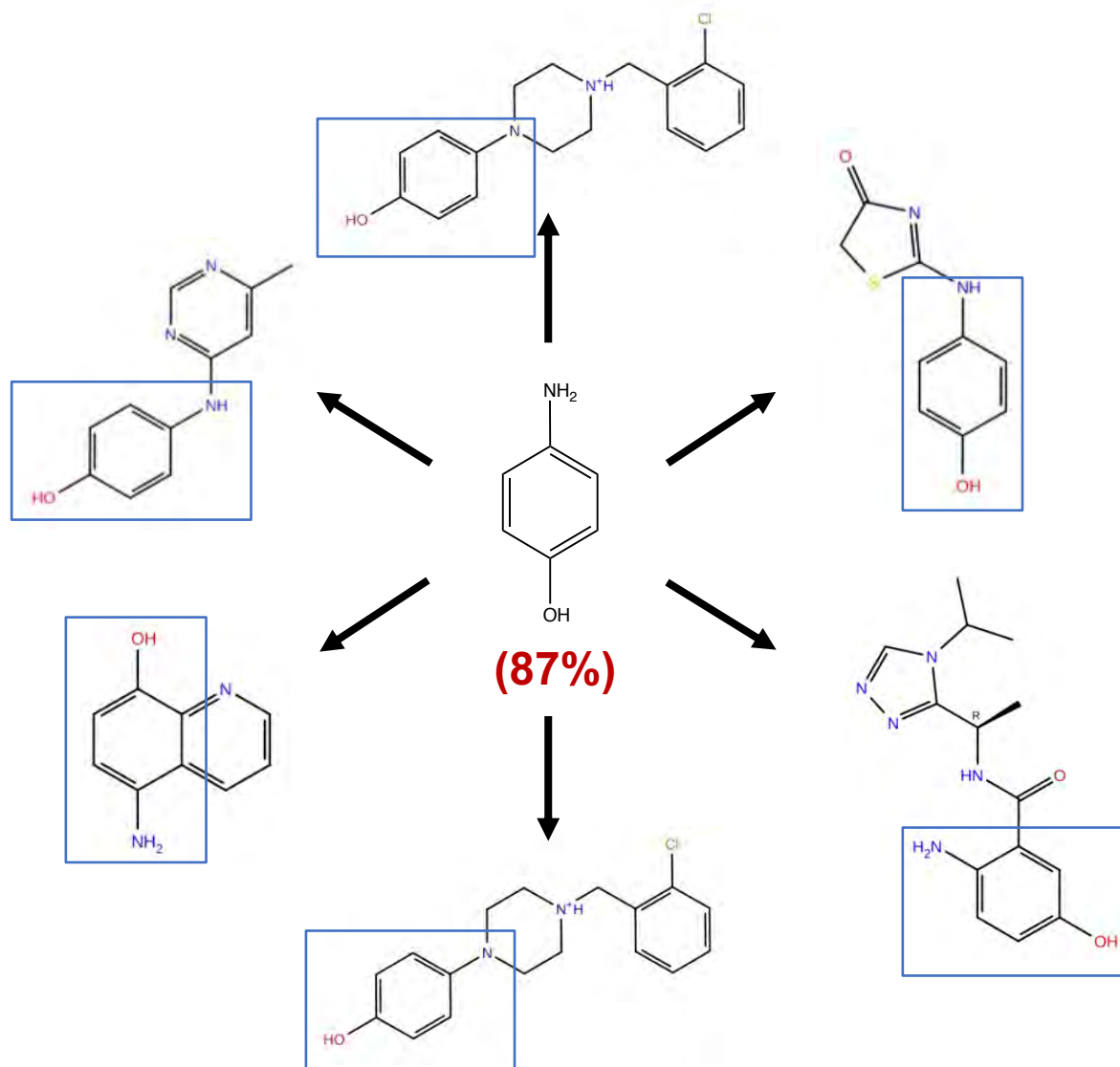


(38%)

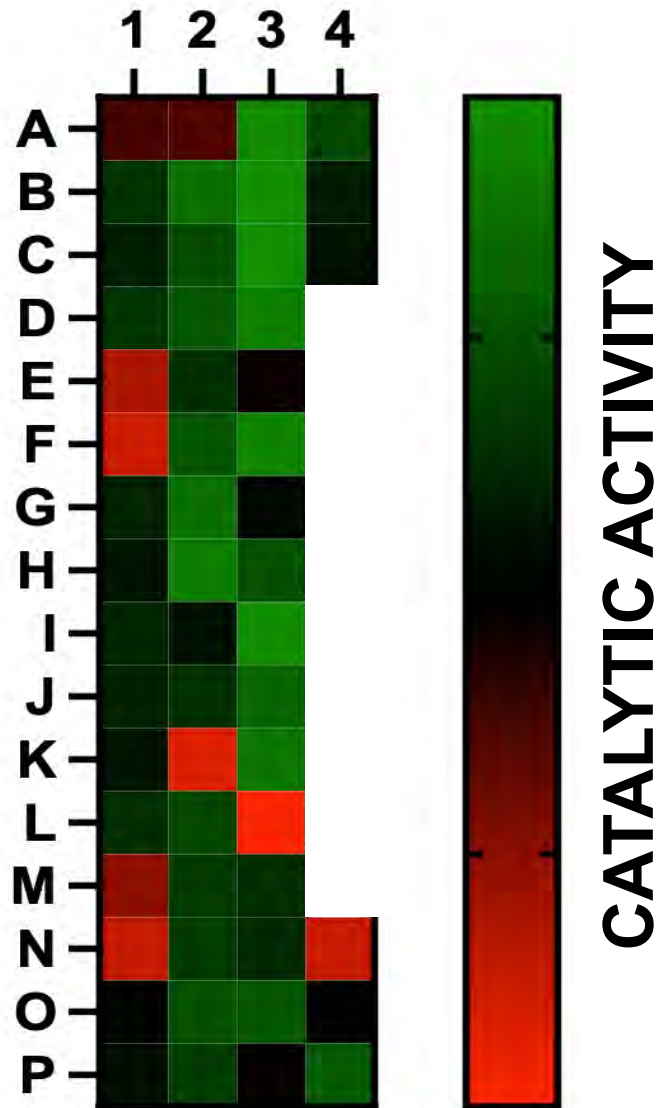


(32%)

ENHANCED SUB-STRUCTURE SEARCH IN THE EU-OPENSOURCE LIBRARY



EFFECT ON CATALYTIC ACTIVITY



in progress...

COLLABORATORS



NATE COWIESON



ANA MARTÍNEZ



**VNiVERSiDAD
D SALAMANCA**

RAFAEL PELÁEZ