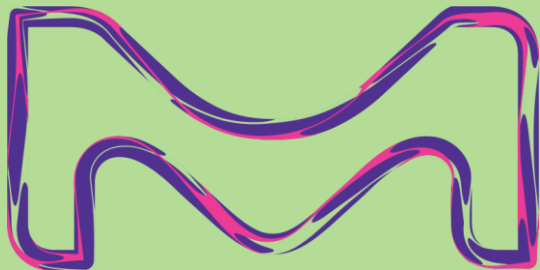


opportunities and challenges for free energy calculations in drug design

Christina Schindler
CompBioMed 2019



MERCK

Acknowledgements

MedChem Boston & Darmstadt

CompChem Boston & Darmstadt

- Theresa Johnson
- Alejandro Crespo
- Liwei Li
- Daniel Kuhn
- Jakub Gunera
- Paul Czodrowski
- Mireille Krier
- Jakub Gunera
- Hannah Baumann
- Robert Schulz
- Merveille Eguida

Schrödinger

- Daniel Cappel
- Thomas Steinbrecher
- Jörg Weiser
- Thijs Beuming
- Olivia Pierce

Digitize Merck team

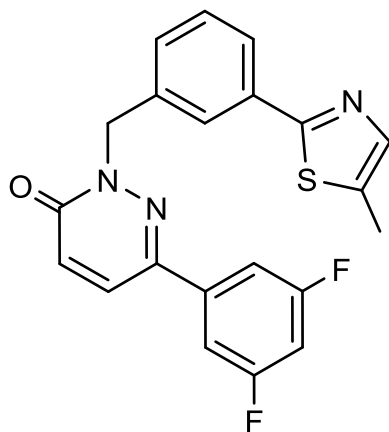
- Friedrich Rippmann
- Thomas Fürst

MSKCC

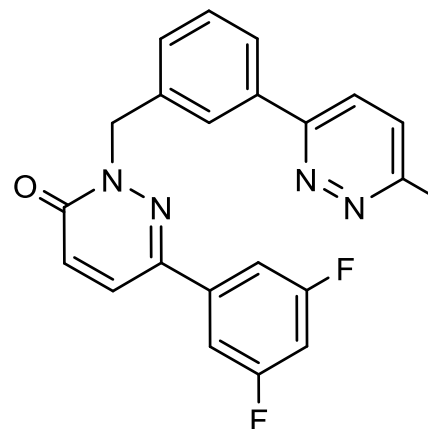
- Levi Naden
- John Chodera

Which compounds to synthesize next?

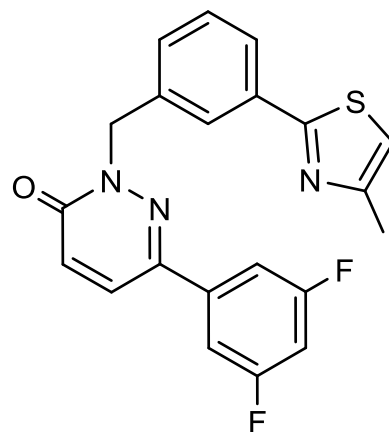
The holy grail of drug design: Prediction of binding constants



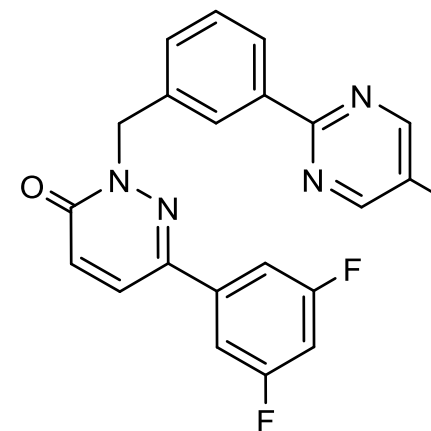
c-MET inhibitor CHEMBL3402750



c-MET inhibitor CHEMBL3402755



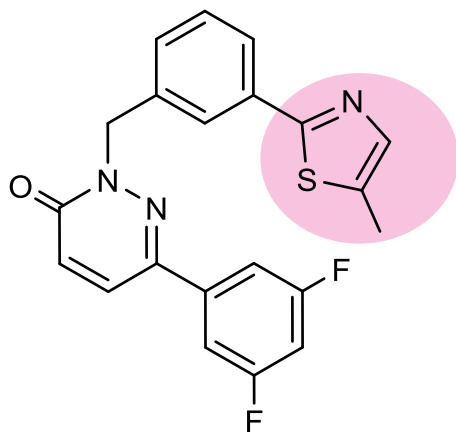
c-MET inhibitor CHEMBL3402751



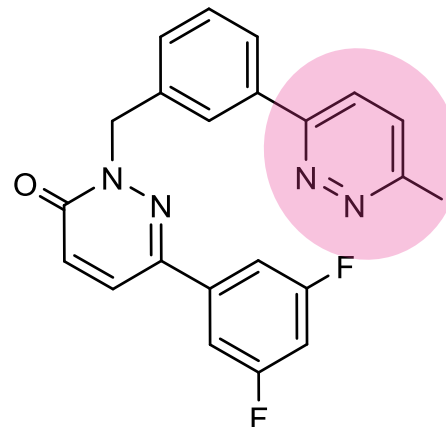
c-MET inhibitor CHEMBL3402754

Which compounds to synthesize next?

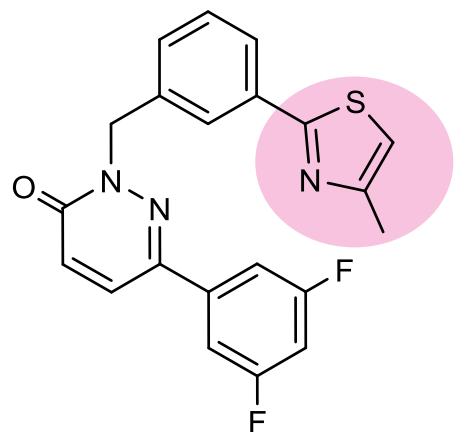
The holy grail of drug design: Prediction of binding constants



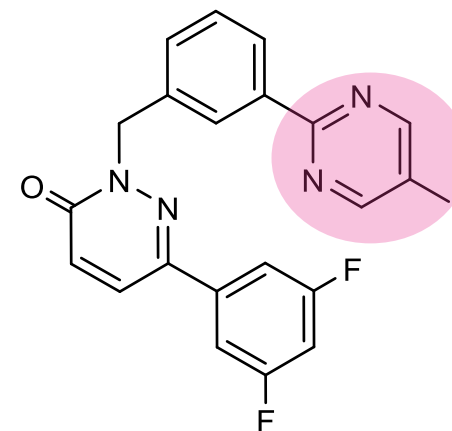
c-MET inhibitor CHEMBL3402750



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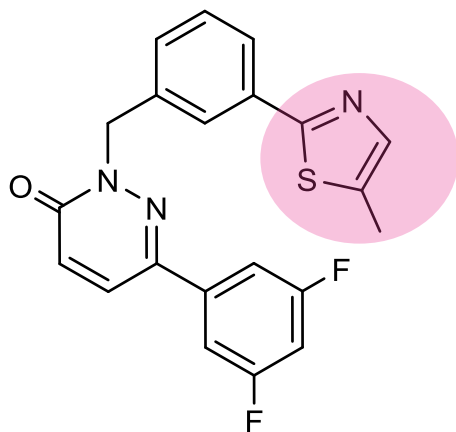
c-MET inhibitor CHEMBL3402751



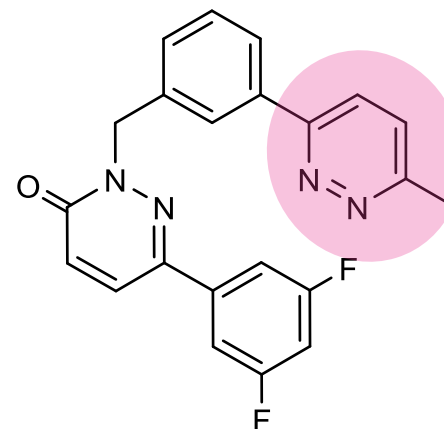
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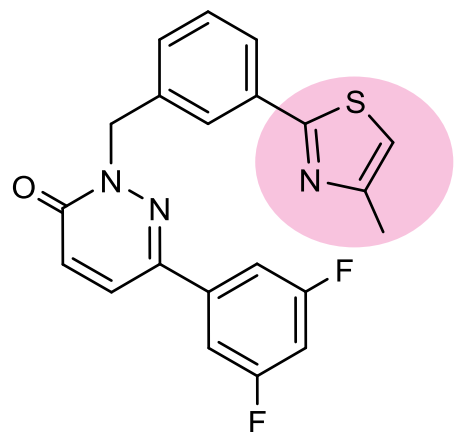
The holy grail of drug design: Prediction of binding constants



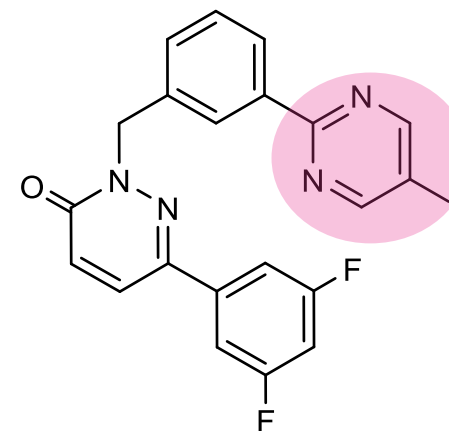
c-MET inhibitor CHEMBL3402750 (400 nM)



c-MET inhibitor CHEMBL3402755 (4200 nM)



c-MET inhibitor CHEMBL3402751 (2100 nM)



c-MET inhibitor CHEMBL3402754 (40 nM)

Finding promising molecules

Opportunities for FEP in drug discovery projects



Finding promising molecules

Opportunities for FEP in drug discovery projects

Focus on potent molecules by prioritizing ideas for synthesis



Finding promising molecules

Opportunities for FEP in drug discovery projects

Focus on potent molecules by prioritizing ideas for synthesis

Increase structural diversity and broadly explore chemical space with large libraries



Finding promising molecules

Opportunities for FEP in drug discovery projects

Focus on potent molecules by prioritizing ideas for synthesis

Increase structural diversity and broadly explore chemical space with large libraries

De-risk challenging synthesis e.g. for scaffold hops



Finding the right balance

Challenges for FEP in drug discovery projects



Finding the right balance

Challenges for FEP in drug discovery projects

Scientific:

Achieve sufficient
prediction accuracy
(<1.4 kcal/mol)



Finding the right balance

Challenges for FEP in drug discovery projects

Scientific:

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Technical:

Manage large-scale
computations on
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Finding the right balance

Challenges for FEP in drug discovery projects

Scientific:

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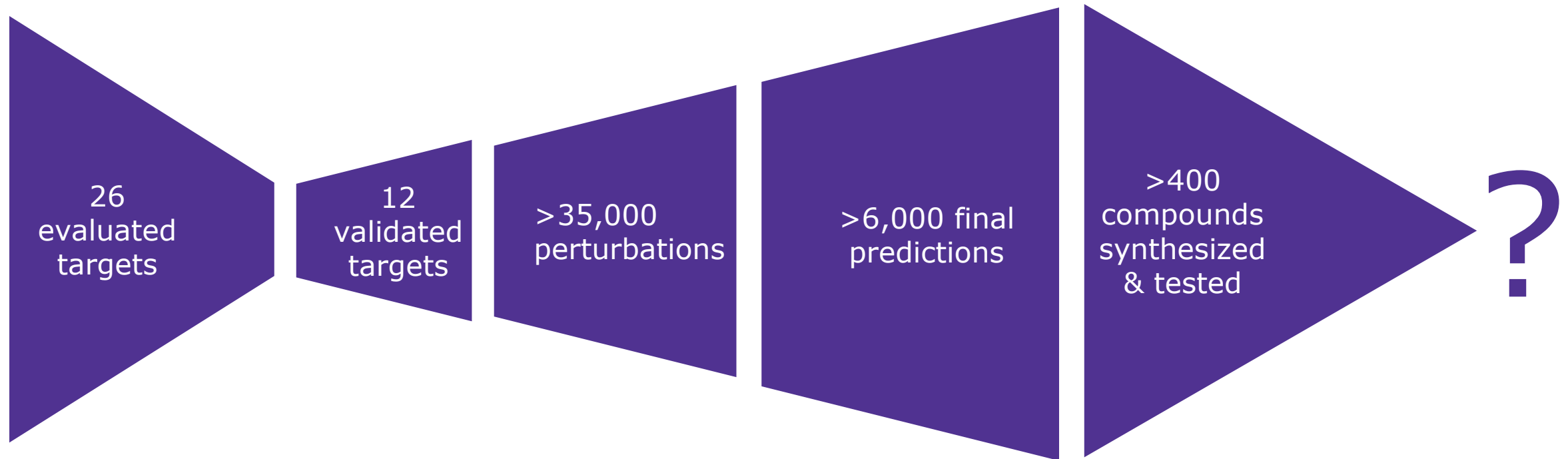
Manage large-scale computations on specialized hardware

Operational:
Communication, timing and impact in projects



Broad application across multiple targets and series

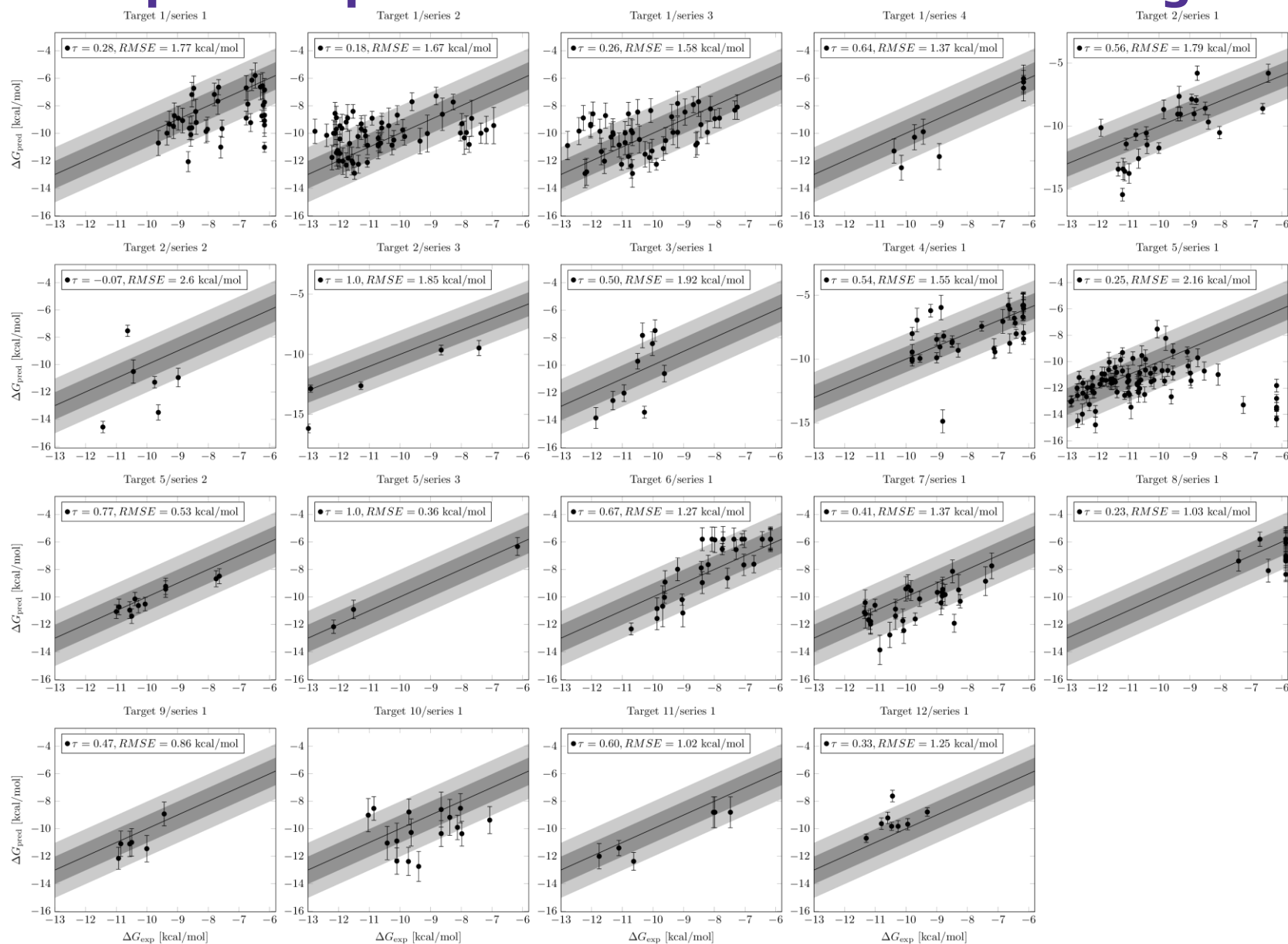
FEP+ in drug discovery at Merck KGaA, Darmstadt, Germany



- How does FEP perform?
- What are the learnings?
- What is the impact on projects?

Prospective data for 19 chemical series available

Prospective performance varies between targets and series



N = 463

Average Kendall tau = 0.37

Average RMSE = 1.64 kcal/mol

Cohen's d for R2

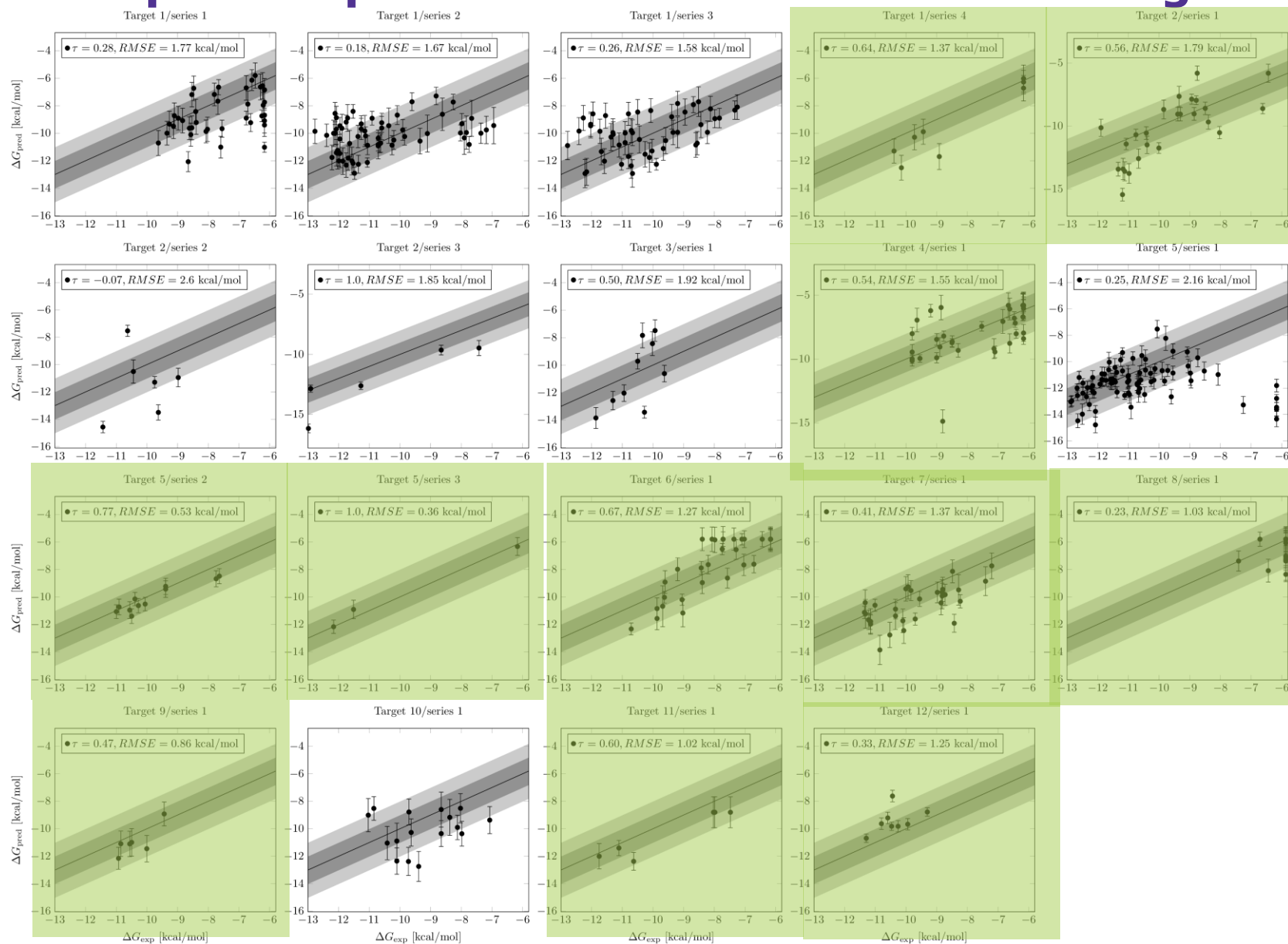
- Glide: 0.76
- Prime: 0.74

Challenges

- Predictions often not possible in certain parts of the molecule
- Transformation from short R-group to long, flexible chains
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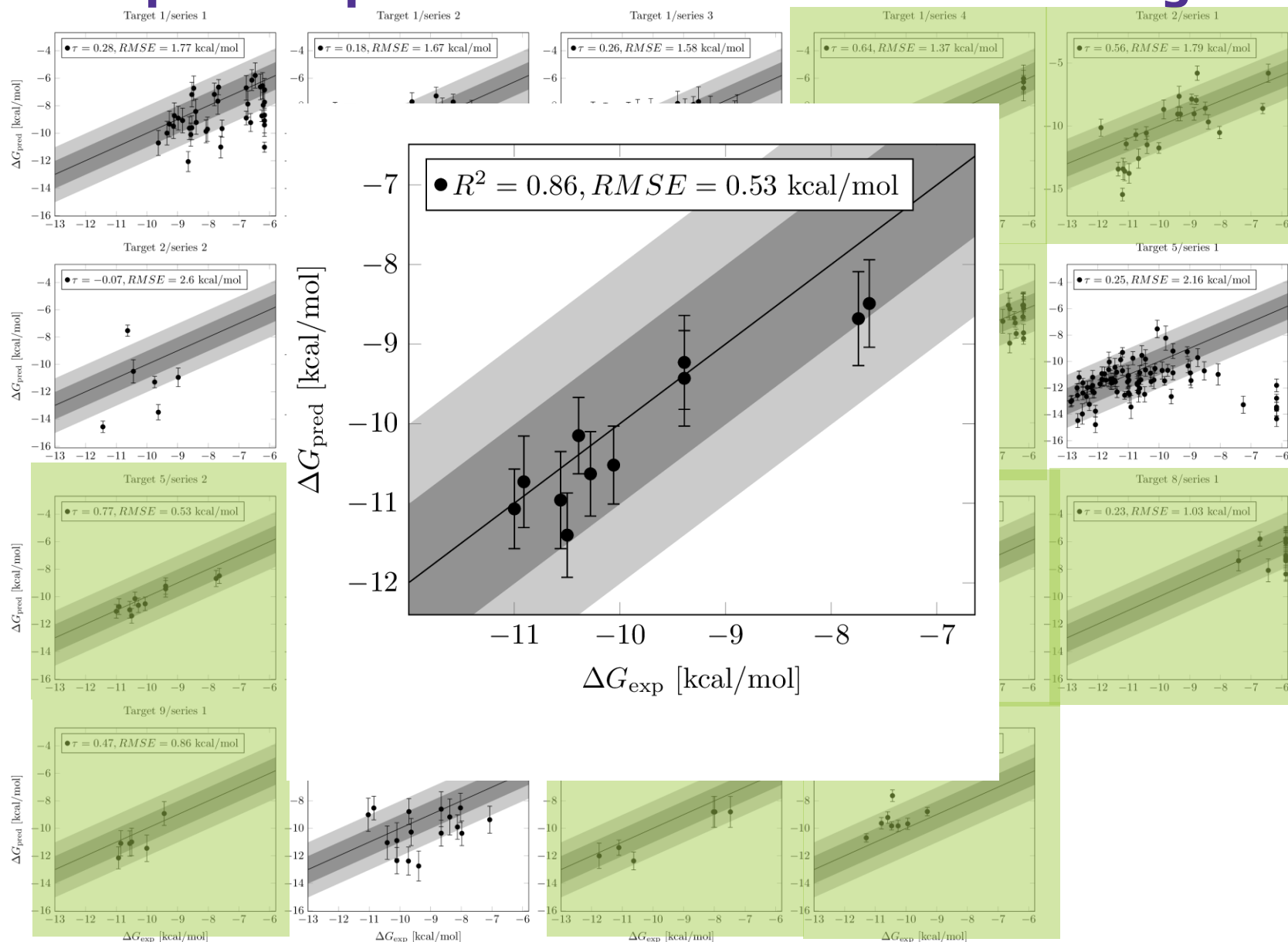
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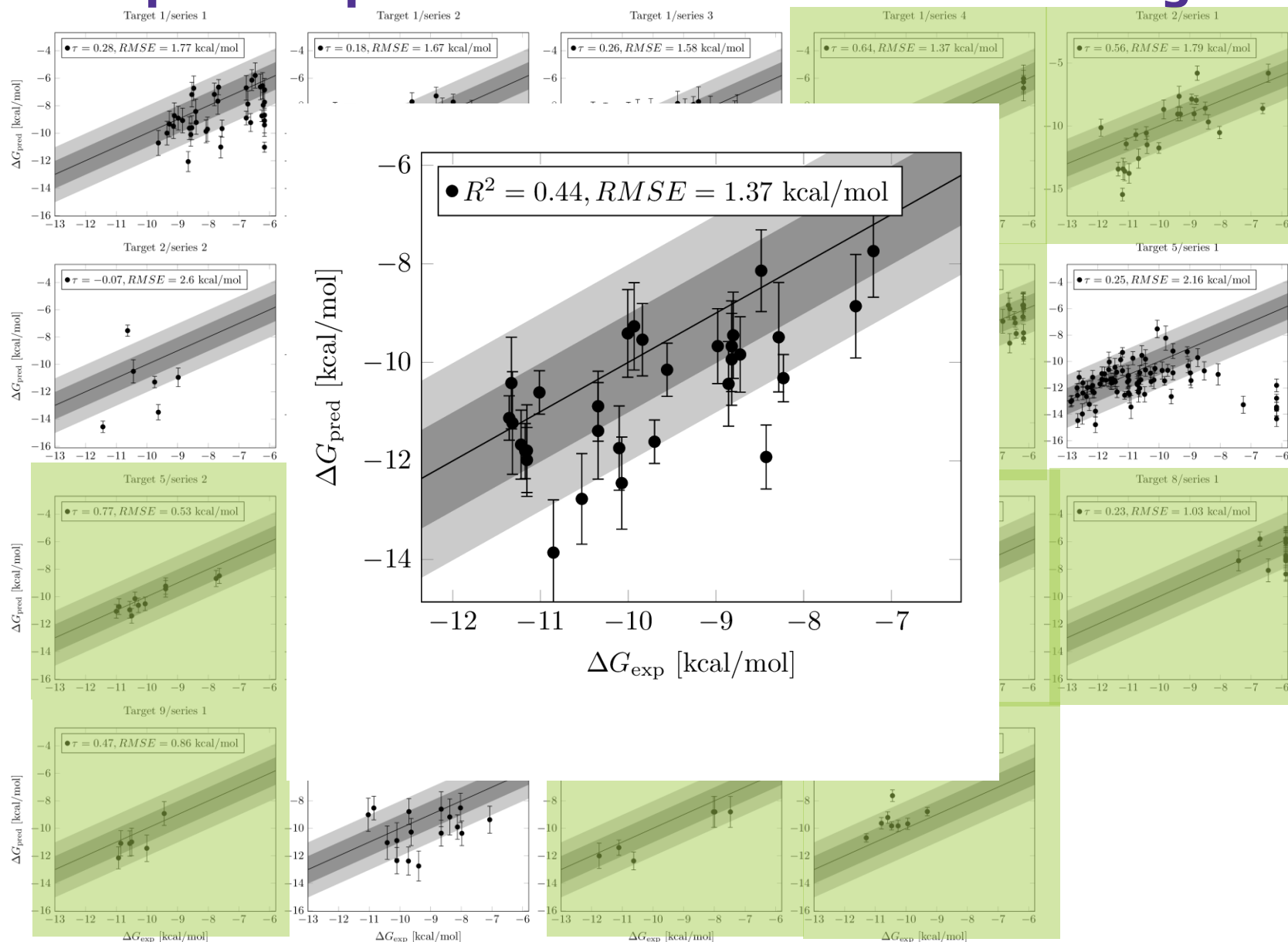
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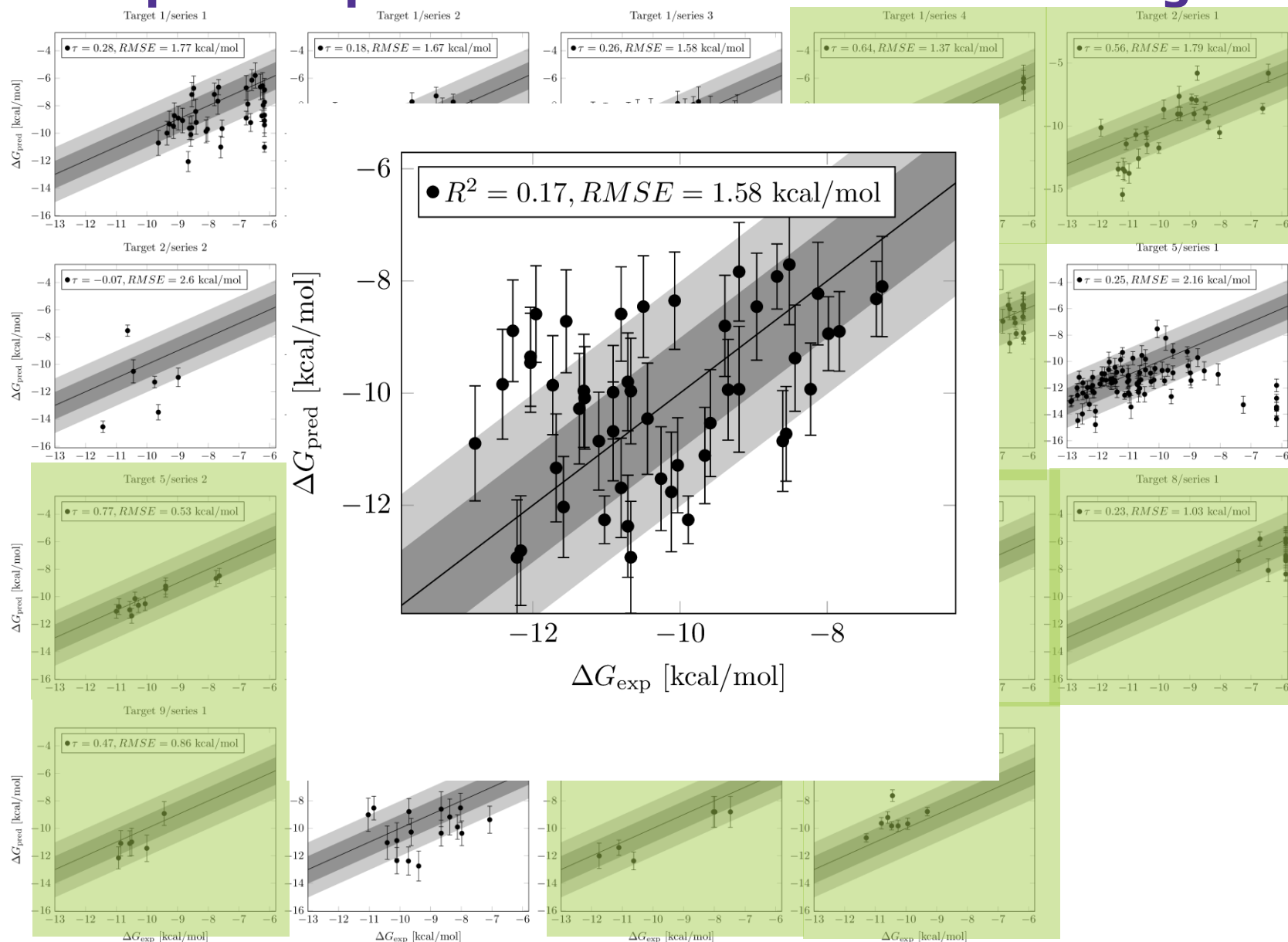
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264 ligands for eight pharmaceutically relevant targets

New benchmark for free energy calculations created

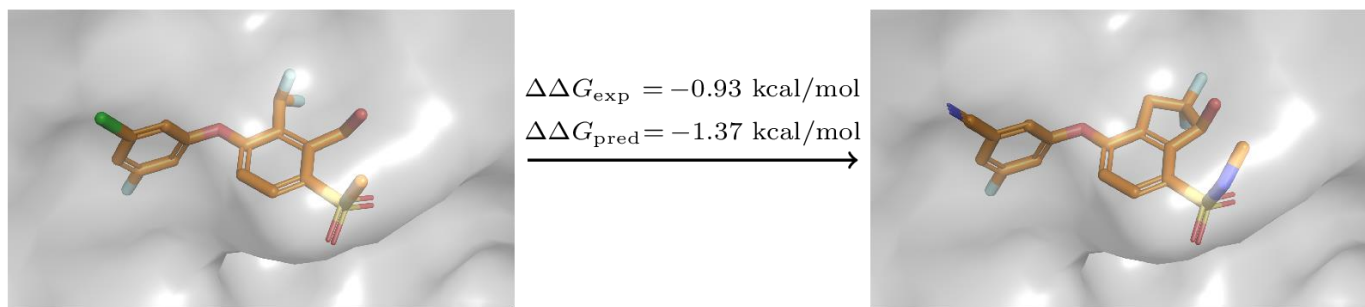
Recent ligand-target pairs collected from literature

Diverse chemical transformations representative of modifications in (early) compound optimization

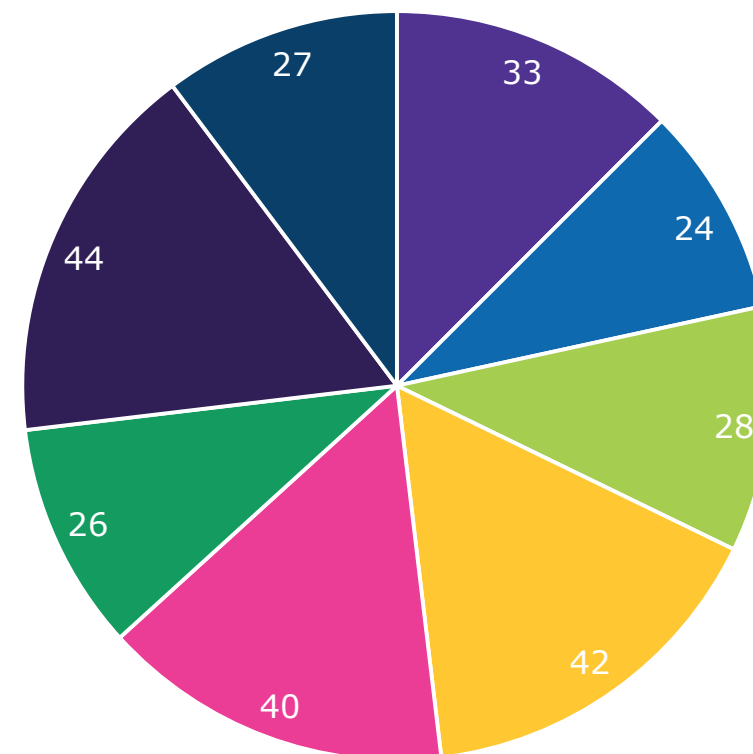
Challenging transformations to test methodological advances in FEP+: charge changes and ring openings

Available on github:

github.com/MCompChem/fep-benchmark



N = 264

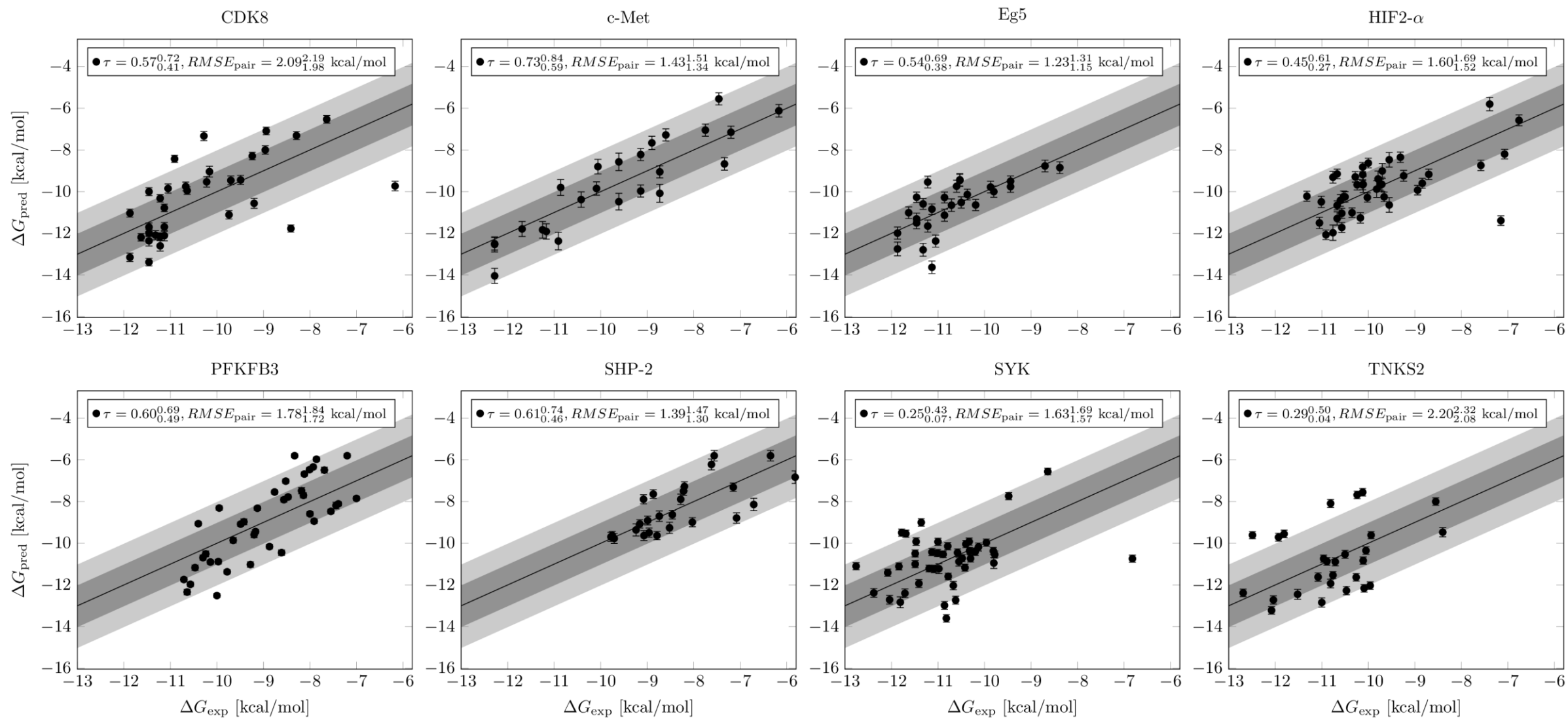


CDK8 c-MET Eg5 HIF2-alpha
PFKFB3 SHP2 SYK TNKS2

MERCK

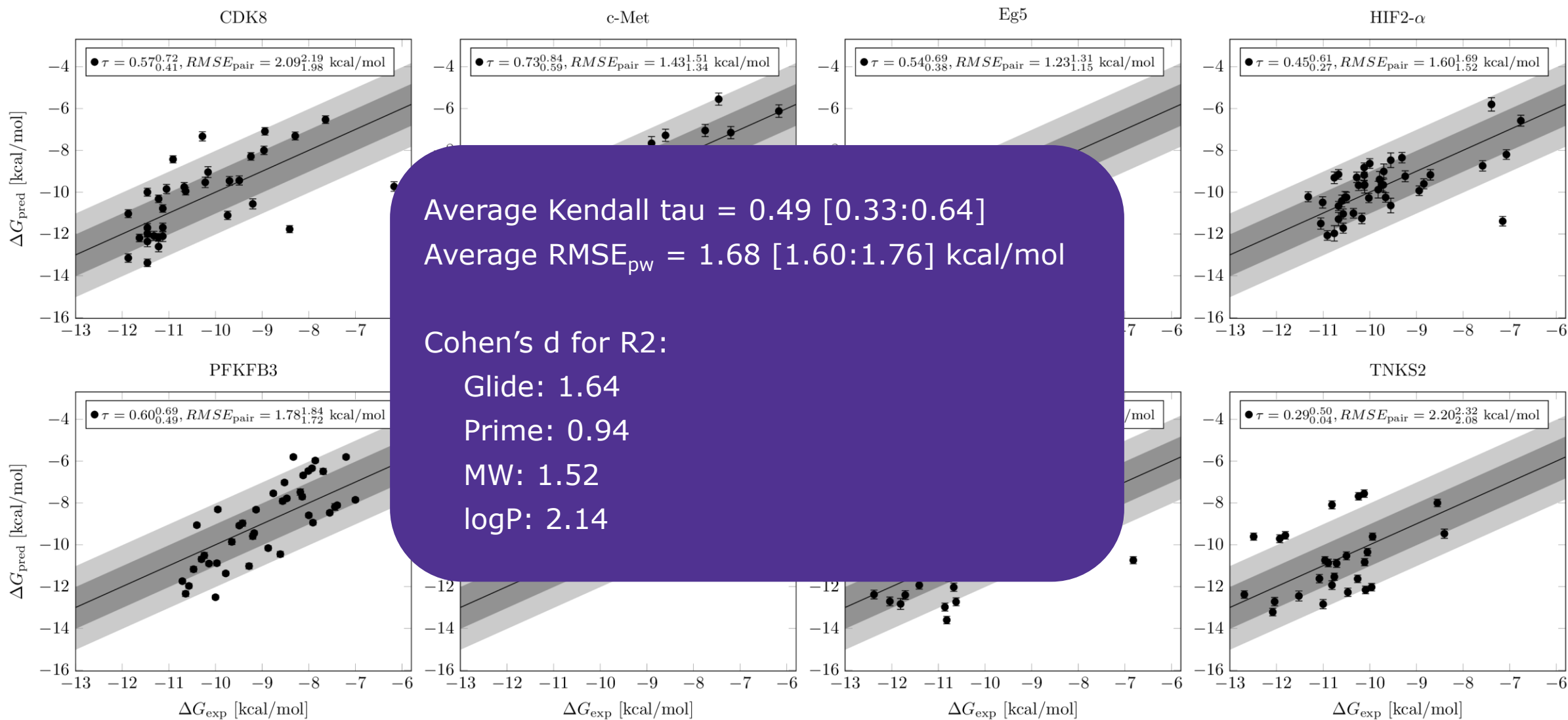
Large public benchmark with eight pharmaceutically relevant targets

Good performance on challenging data set



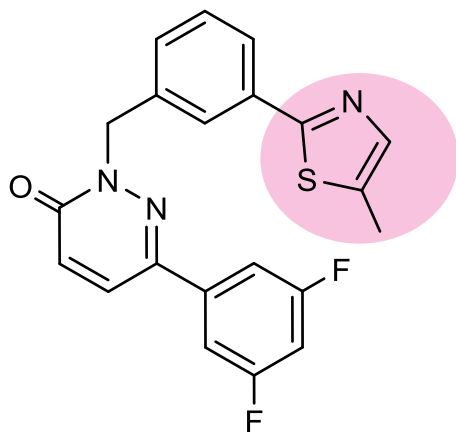
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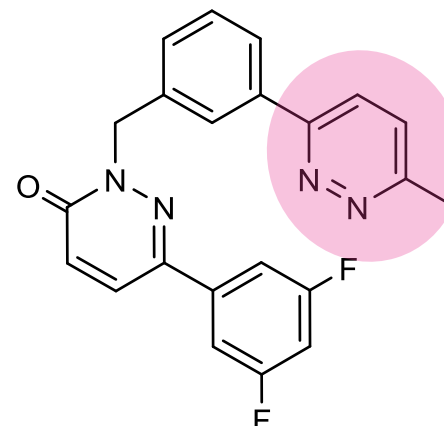


Which compounds to synthesize next?

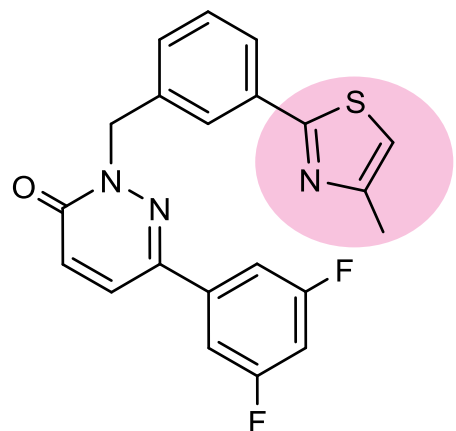
The holy grail of drug design: Prediction of binding constants



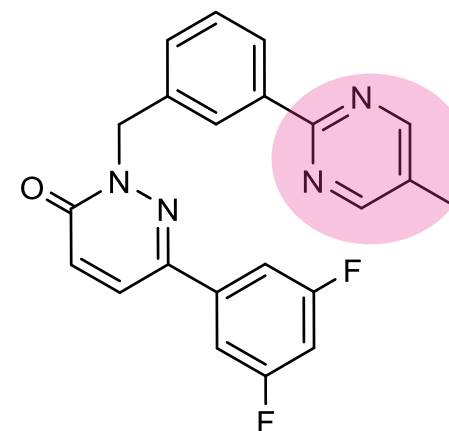
c-MET inhibitor CHEMBL3402750



c-MET inhibitor CHEMBL3402755



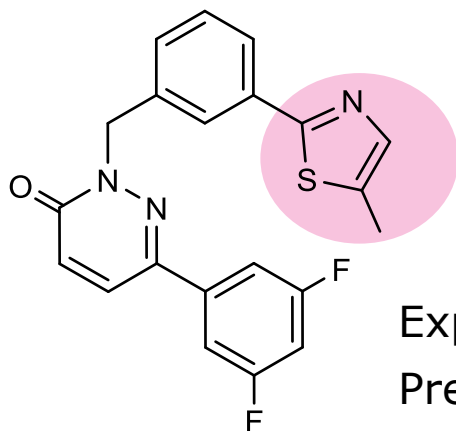
c-MET inhibitor CHEMBL3402751



c-MET inhibitor CHEMBL3402754

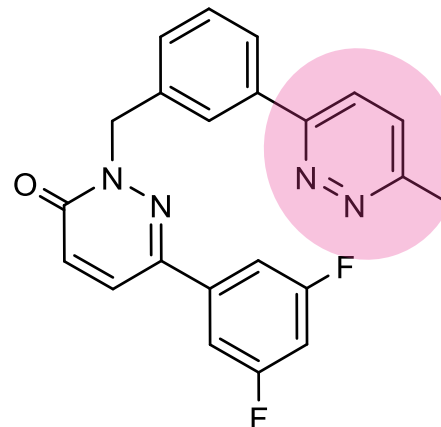
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The holy grail of drug design: Prediction of binding constants



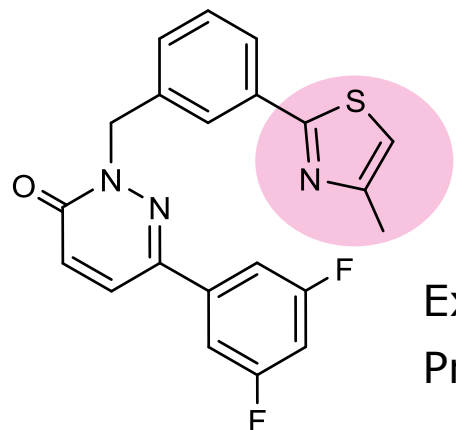
Exp. IC₅₀ = 400 nM
Pred. IC₅₀ = 232 nM

c-MET inhibitor CHEMBL3402750



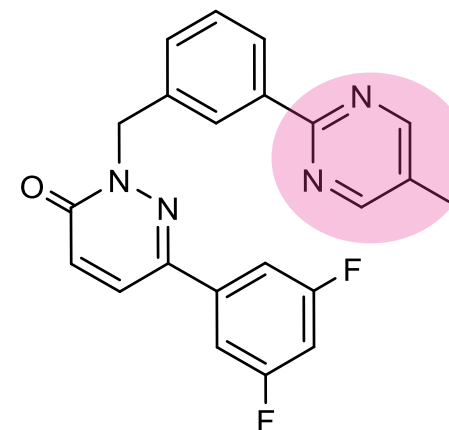
Exp. IC₅₀ = 4200 nM
Pred. IC₅₀ = 441 nM

c-MET inhibitor CHEMBL3402755



Exp. IC₅₀ = 2100 nM
Pred. IC₅₀ = 5020 nM

c-MET inhibitor CHEMBL3402751



Exp. IC₅₀ = 40 nM
Pred. IC₅₀ = 60 nM

c-MET inhibitor CHEMBL3402754

We can predict binding affinity with good accuracy...

...but how to best use it?

Use cases for FEP in projects

Prioritize synthesis proposals & focus on promising molecules

22 compounds synthesized and tested

		Experimental Affinity	
		< 100 nM	> 100 nM
Predicted Affinity	< 100 nM	1	11
	> 100 nM		10

Scenario:

Continuous evaluation of synthesis proposals and prioritization with FEP

Benefit:

Save synthesis resources spent on inactive molecules

Problems:

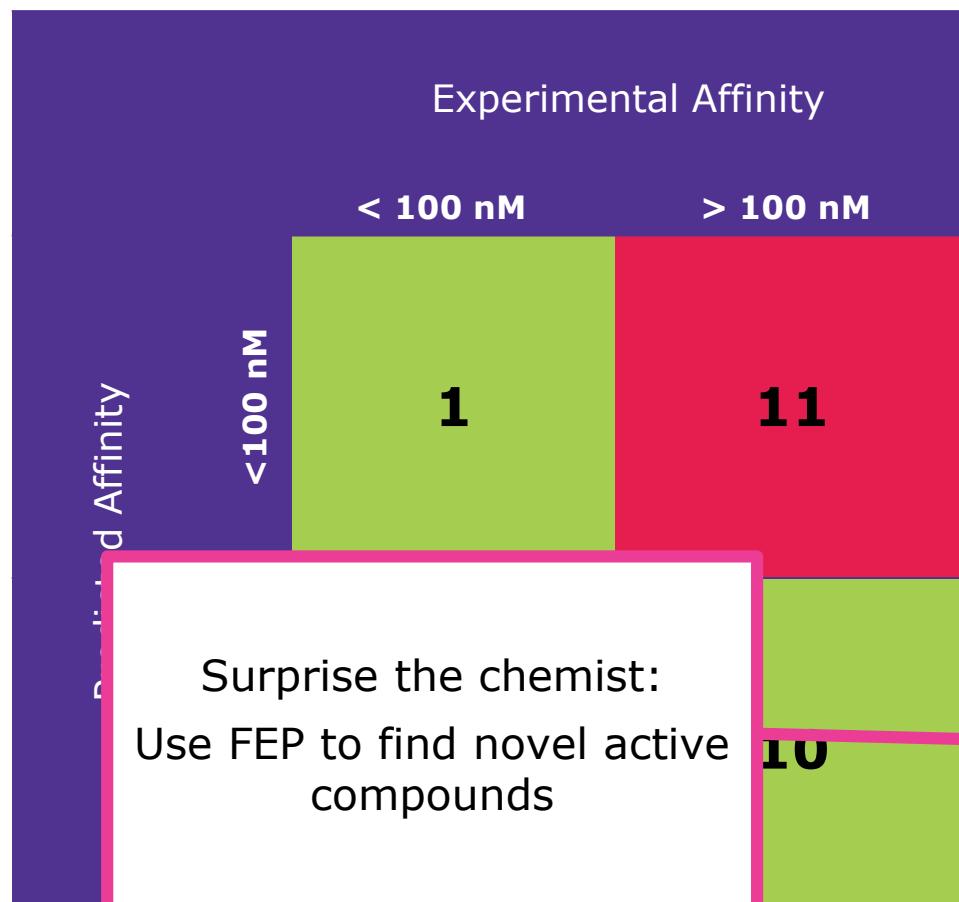
- Number of compounds proposed often not much larger than compounds synthesized
- Chemists don't want to wait for FEP predictions
- After 6 months, nobody will remember the bad molecules that were not made

→ Project impact limited

Use cases for FEP in projects

Prioritize synthesis proposals & focus on promising molecules

22 compounds synthesized and tested



Surprise the chemist:
Use FEP to find novel active
compounds

Scenario:

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Problems:

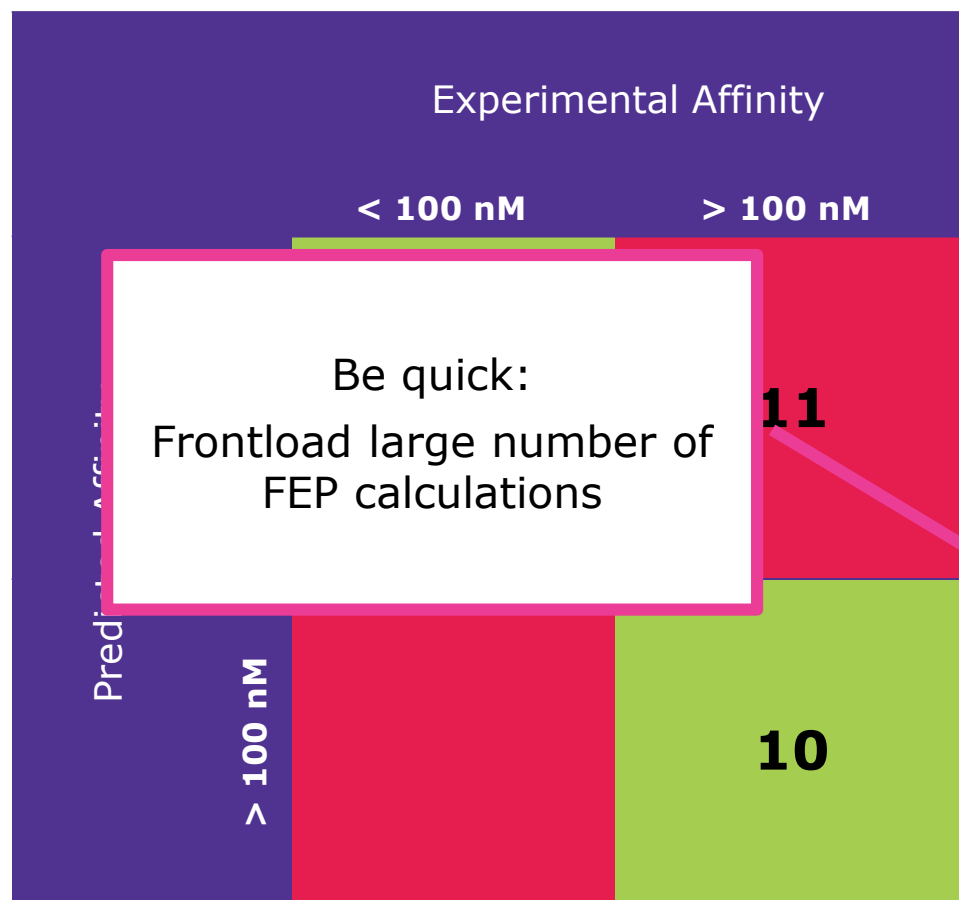
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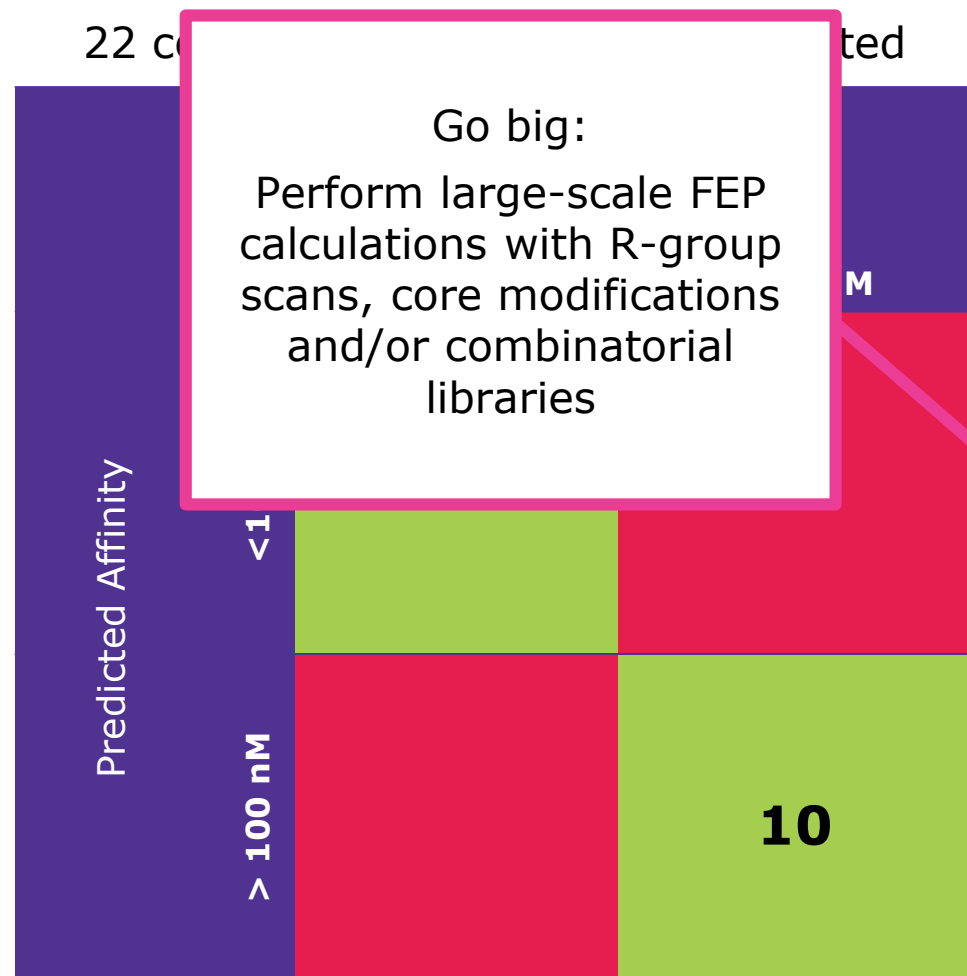
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Chemical space exploration with FEP

Prioritizing promising compounds from a large library

Jakub Gunera



IC₅₀ = 92 nM

Chemical space exploration with FEP

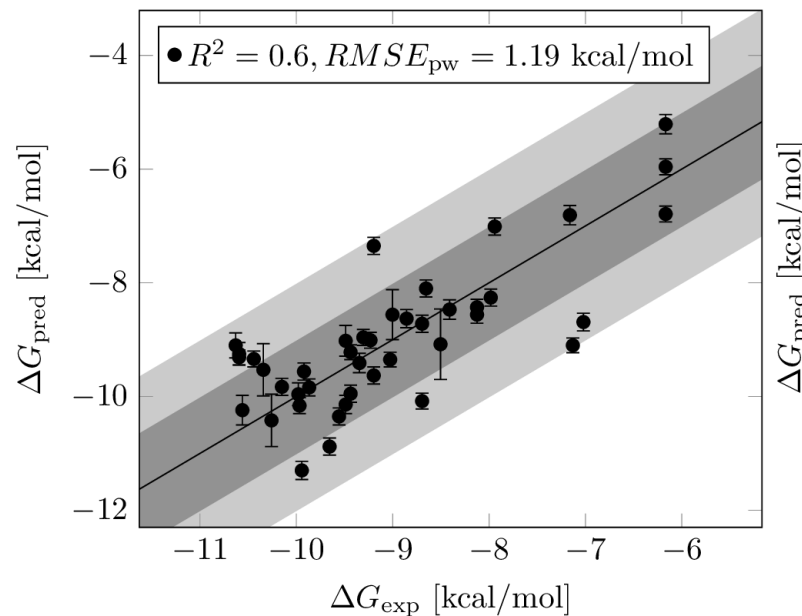
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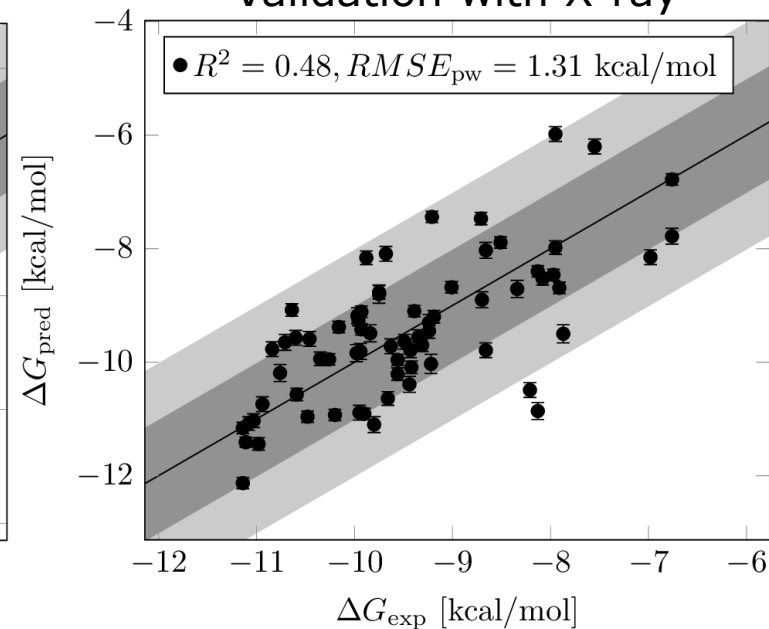


IC50 = 92 nM

Validation with docking pose



Validation with X-ray



Chemical space exploration with FEP

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variation of R-groups

Library constructed from
commercially available
building blocks
15,600 cpds

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Filtering by properties and
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307 cpds

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FEP

20 cpds selected
Synthesis on-going

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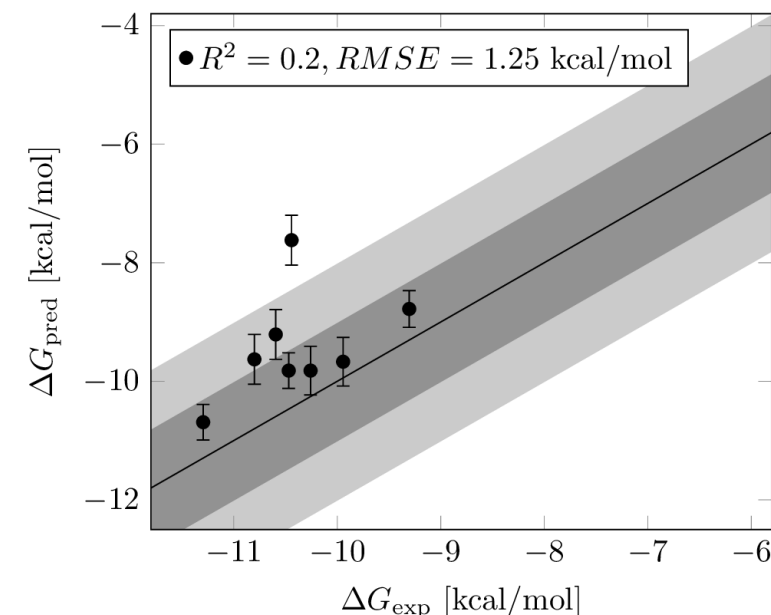


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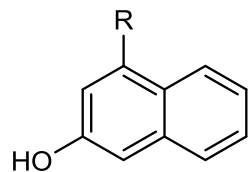
Prospective



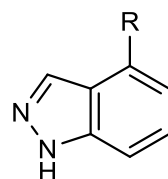
Library scanning with covalent FEP

Replacement for unwanted R-group needed

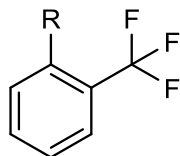
Known SAR



IC50 = 15 nM

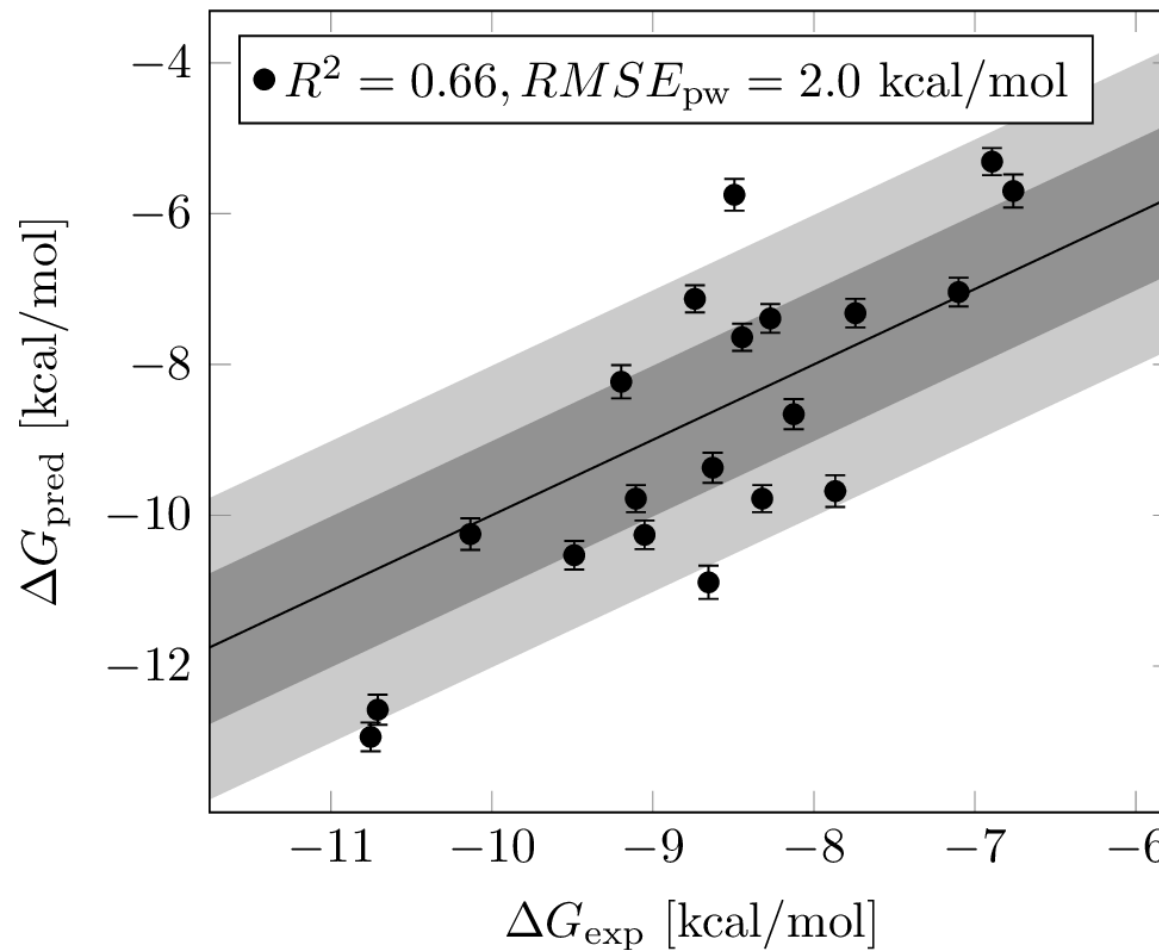


IC50 = 230 nM



IC50 = 2000 nM

FEP validation study



Library scanning with covalent FEP

Successful replacement of unwanted R-group

Library constructed
from available building
blocks



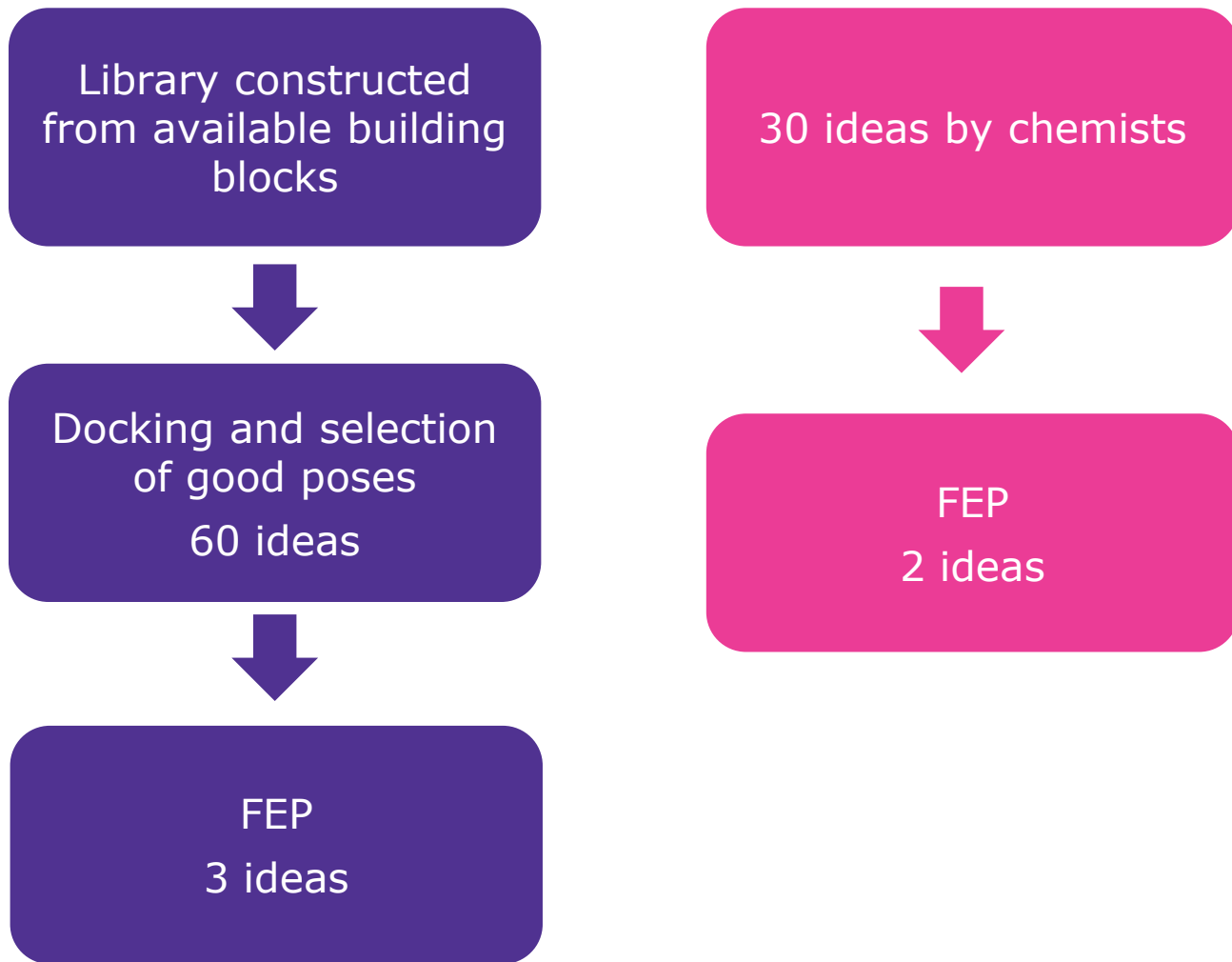
Docking and selection
of good poses
60 ideas



FEP
3 ideas

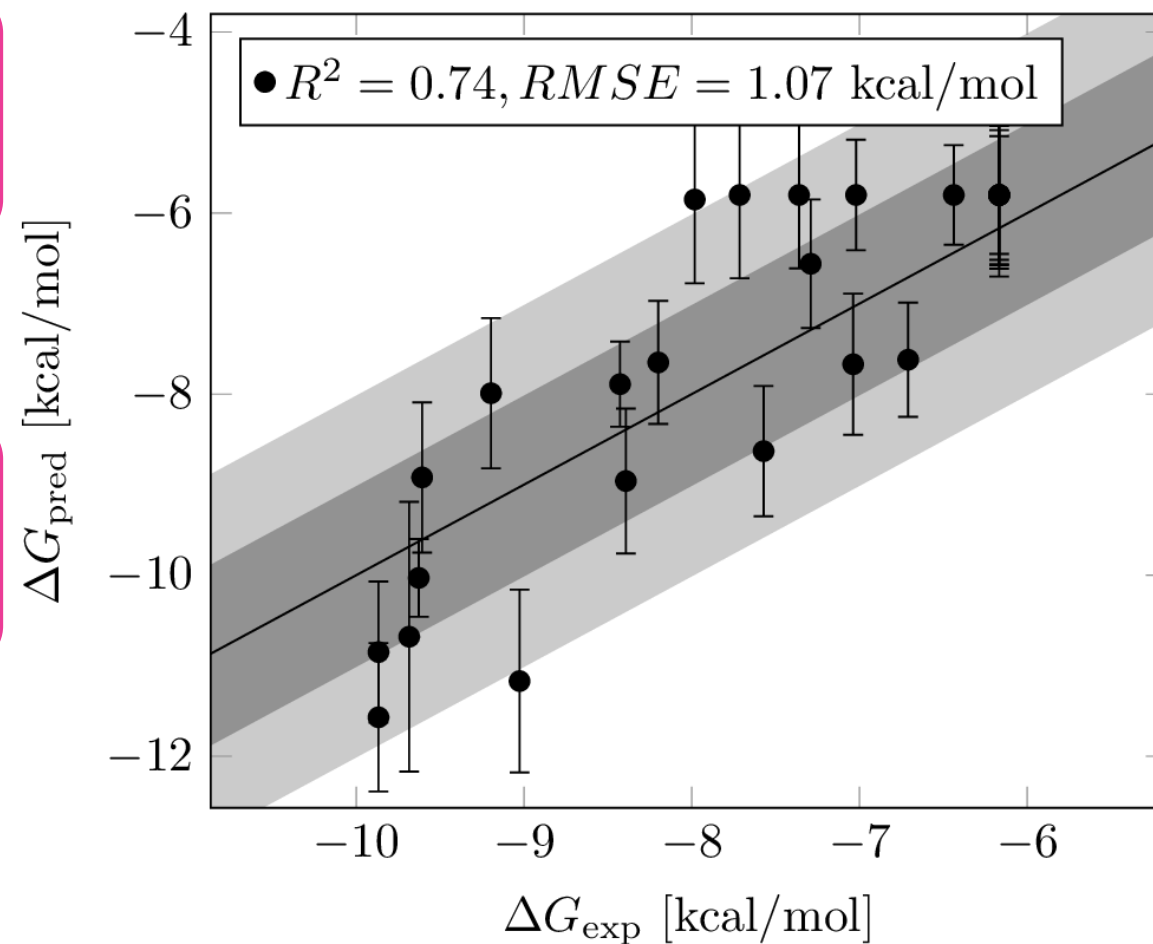
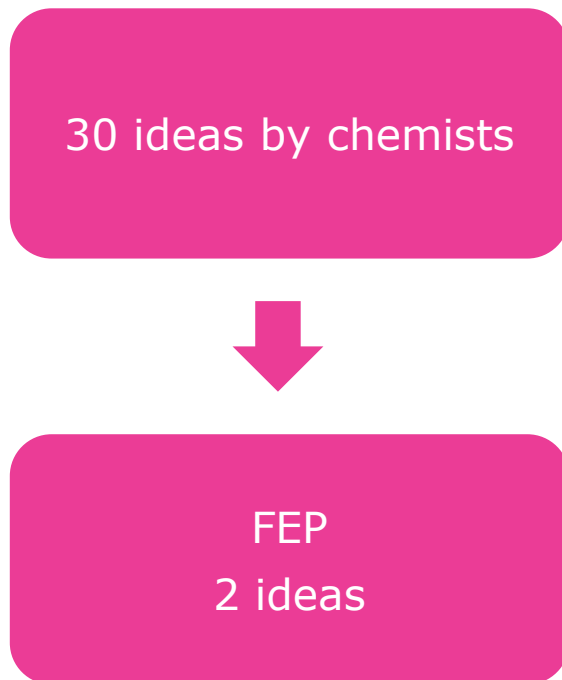
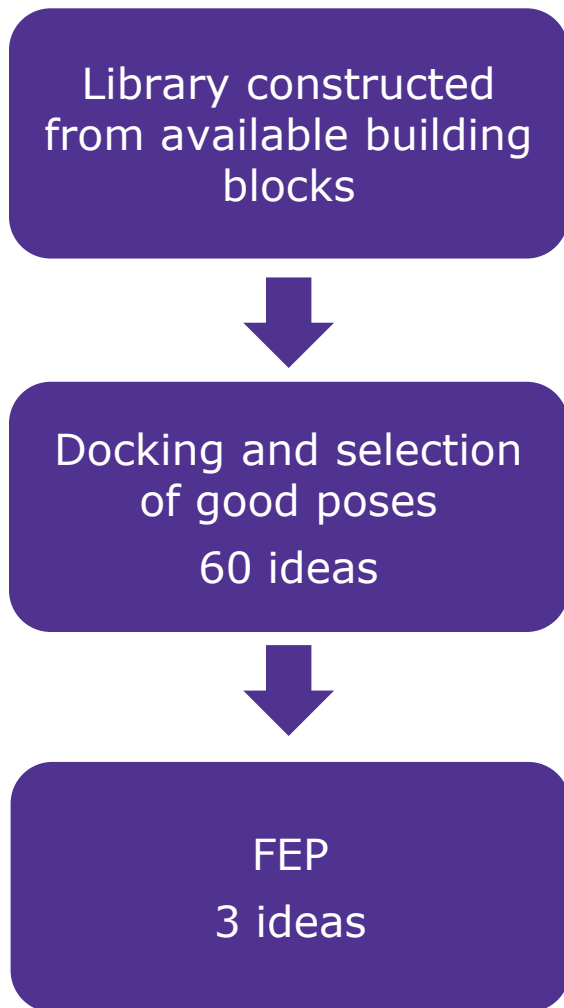
Library scanning with covalent FEP

Successful replacement of unwanted R-group



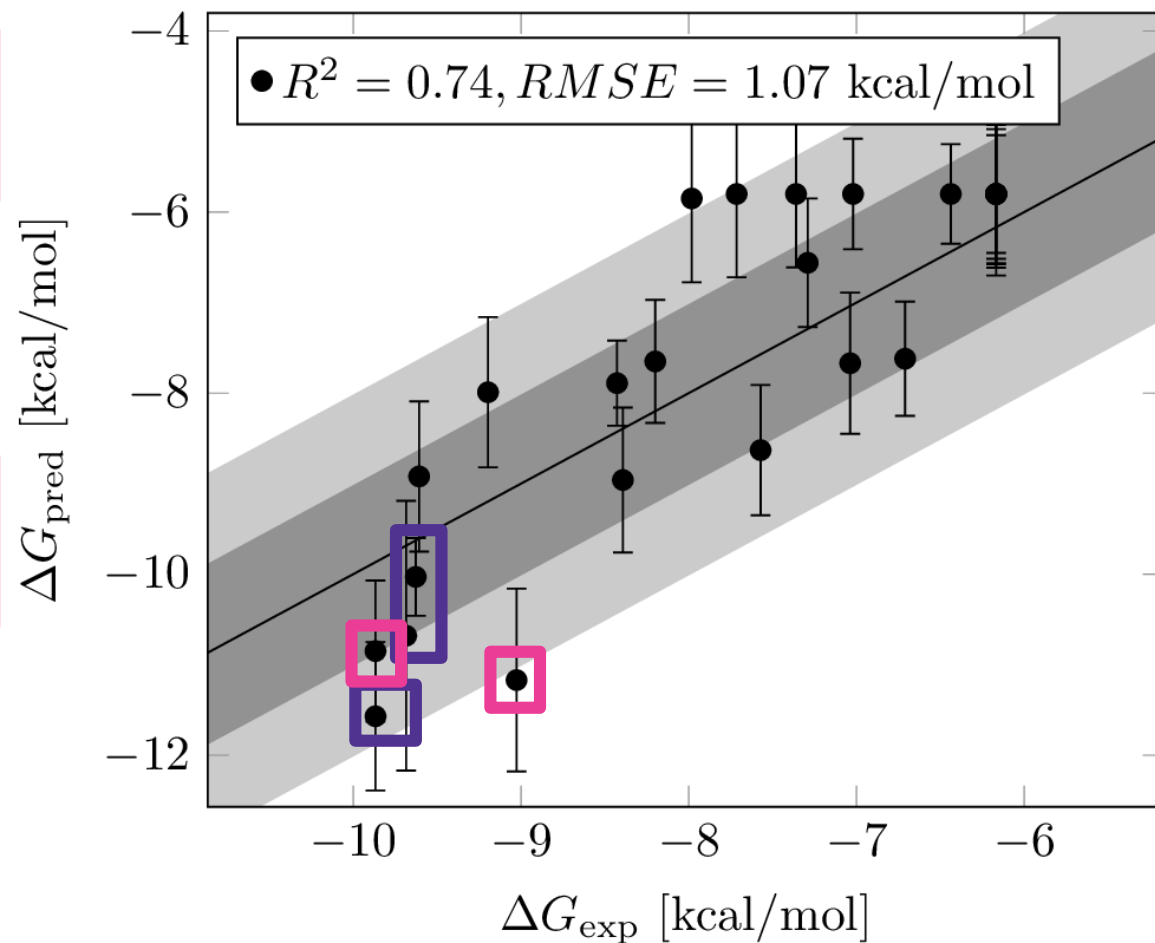
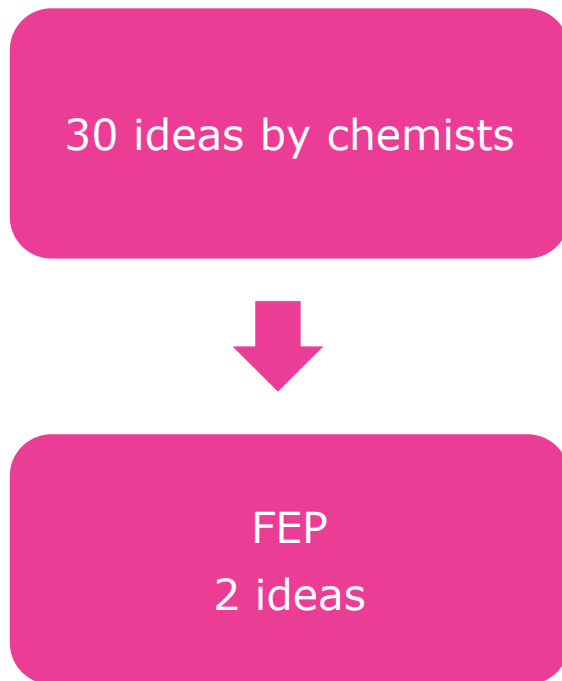
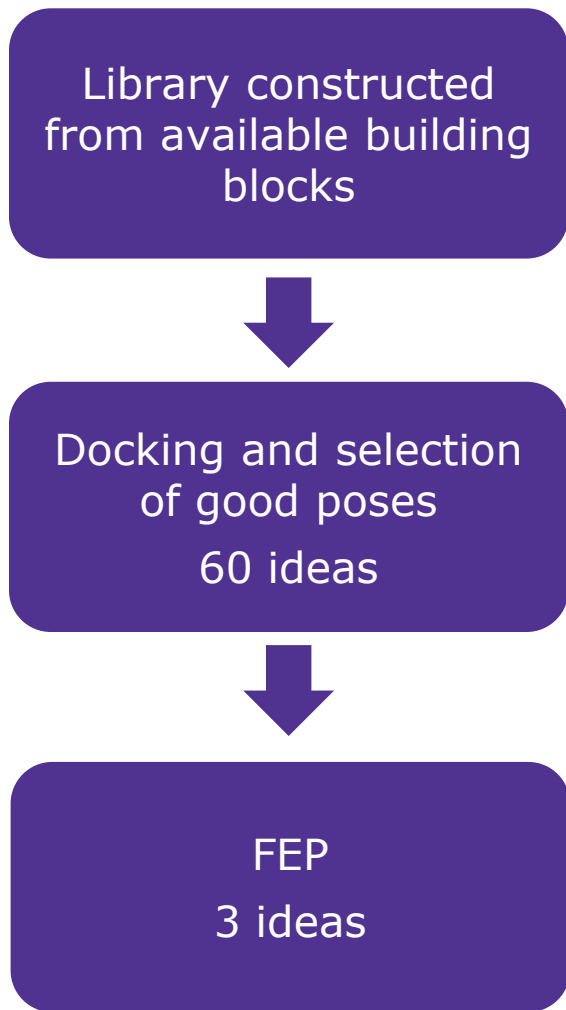
Library scanning with covalent FEP

Successful replacement of unwanted R-group



Library scanning with covalent FEP

Successful replacement of unwanted R-group



Library scanning with covalent FEP

Successful replacement of unwanted R-group

Library constructed from available building blocks



Docking and selection of good poses
60 ideas

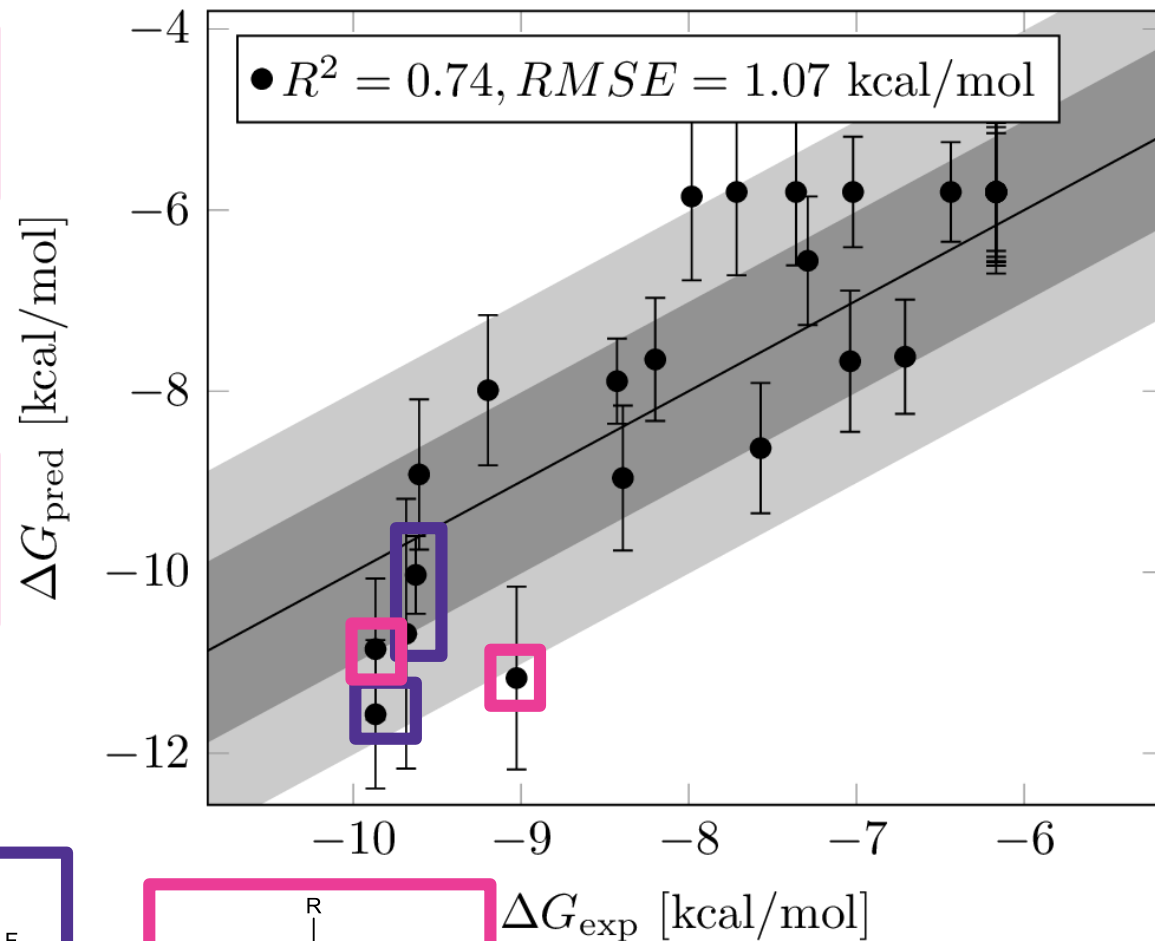
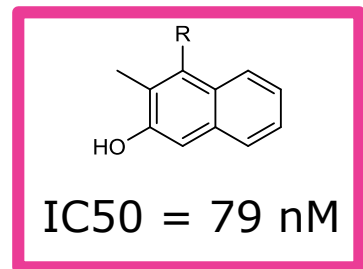
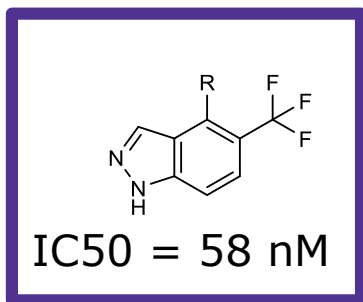


FEP
3 ideas

30 ideas by chemists

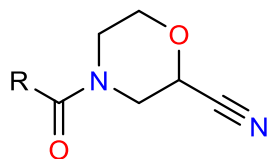


FEP
2 ideas



Discovery of new chemical starting points with FEP

From fragment to hit: Proof-of-principle for in silico optimization

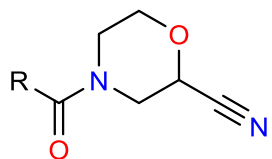


SPR KDss = 300 μ M

LE = 0.25

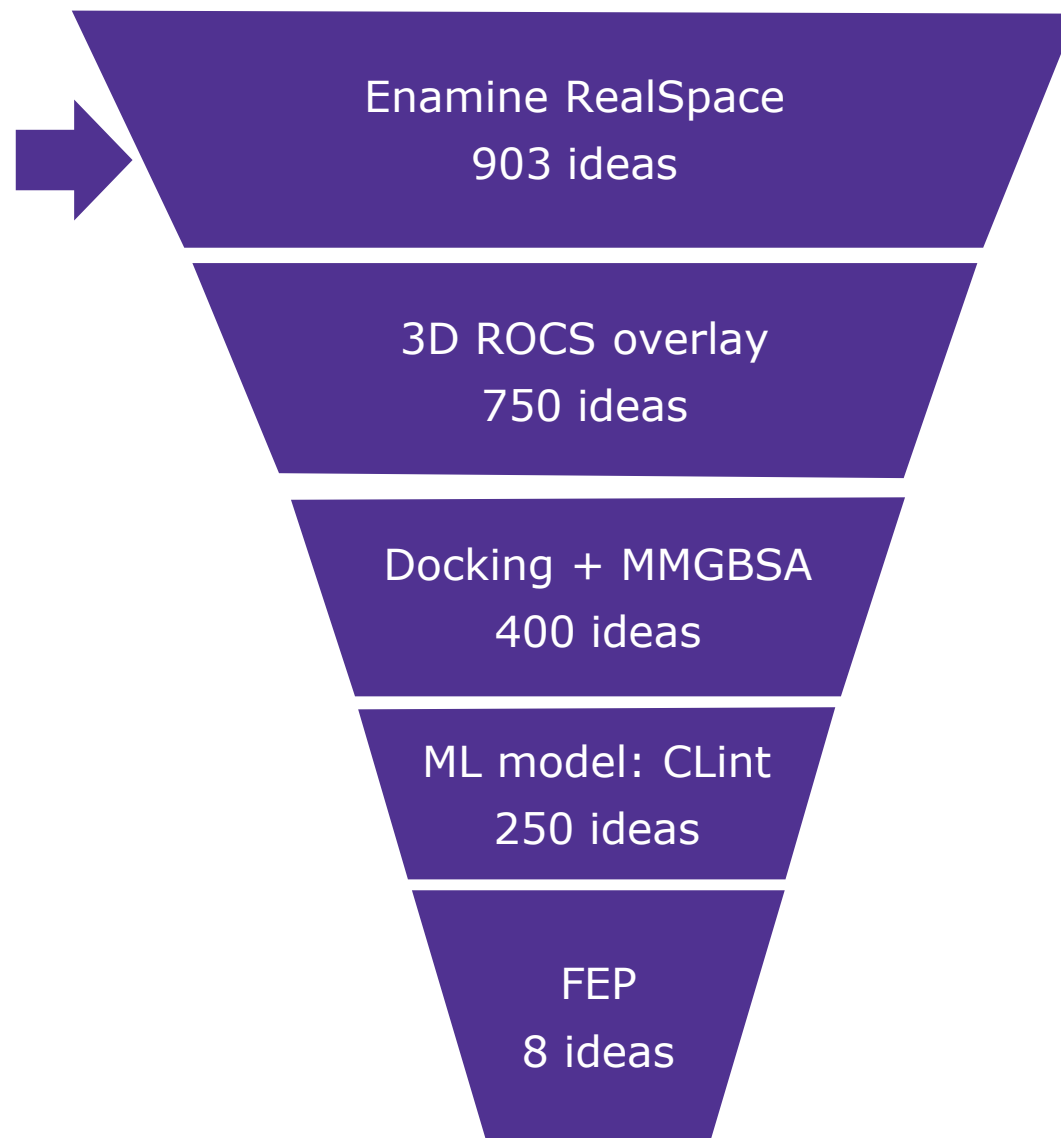
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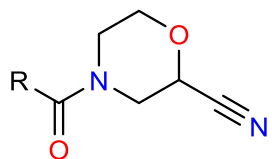
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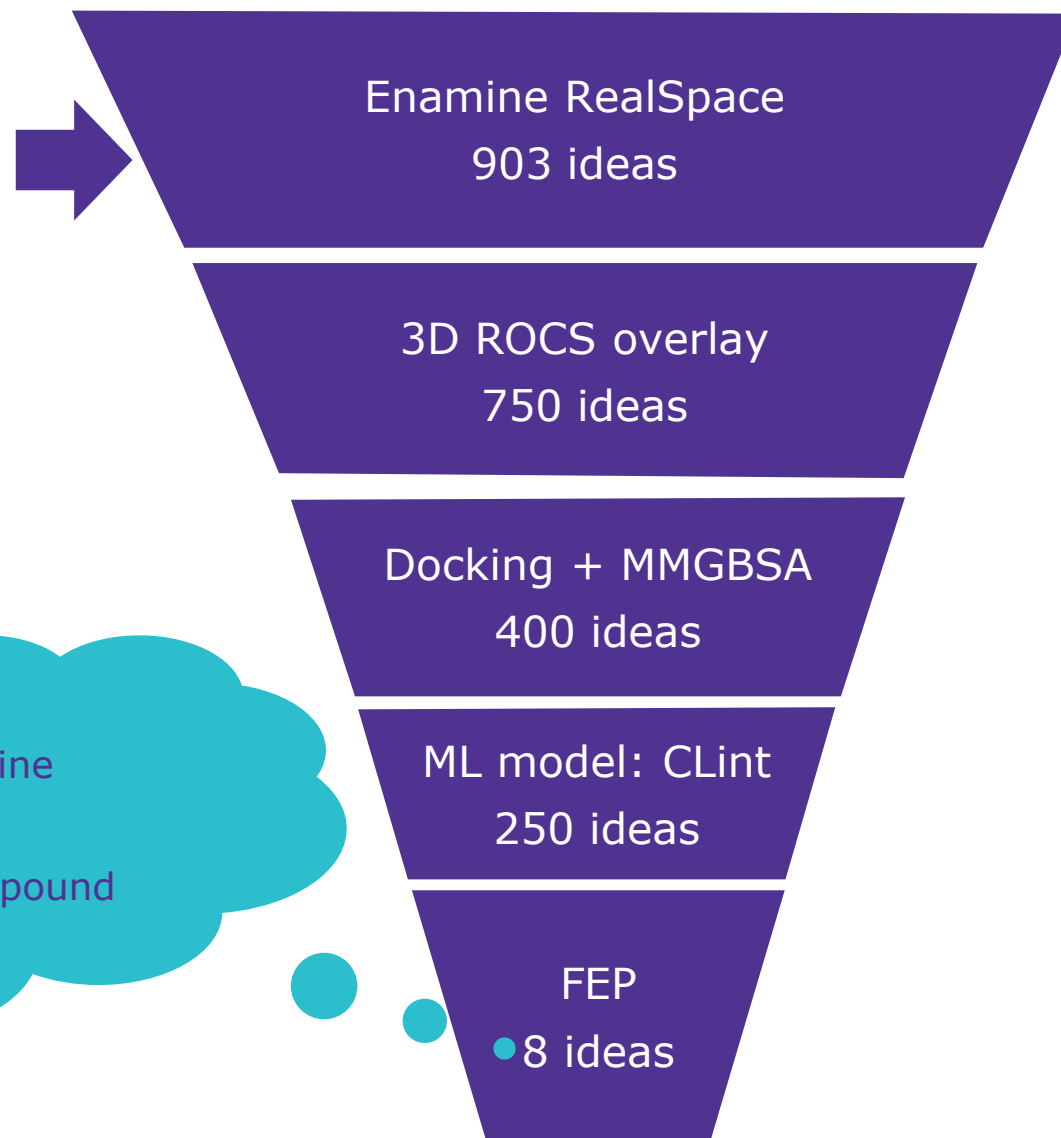
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From fragment to hit: Proof-of-principle for in silico optimization



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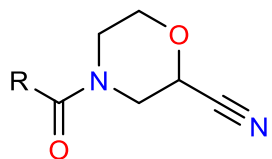


Synthesis at Enamine

- 4 weeks
- < 100 EUR per compound

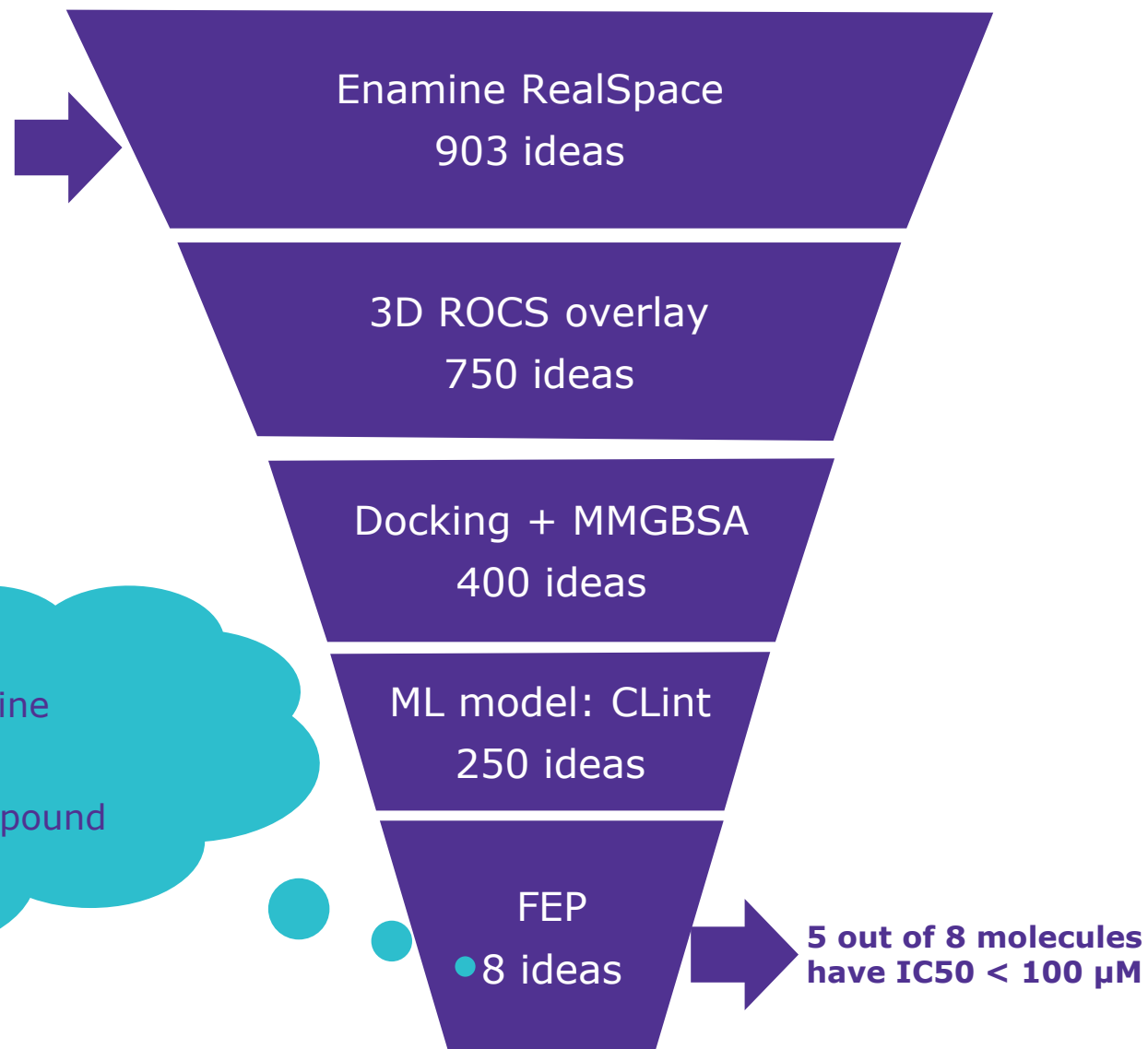
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SPR KDss = 300 μ M

LE = 0.25

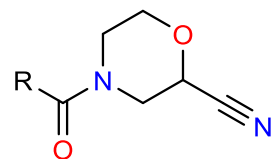


Synthesis at Enamine

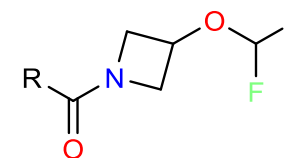
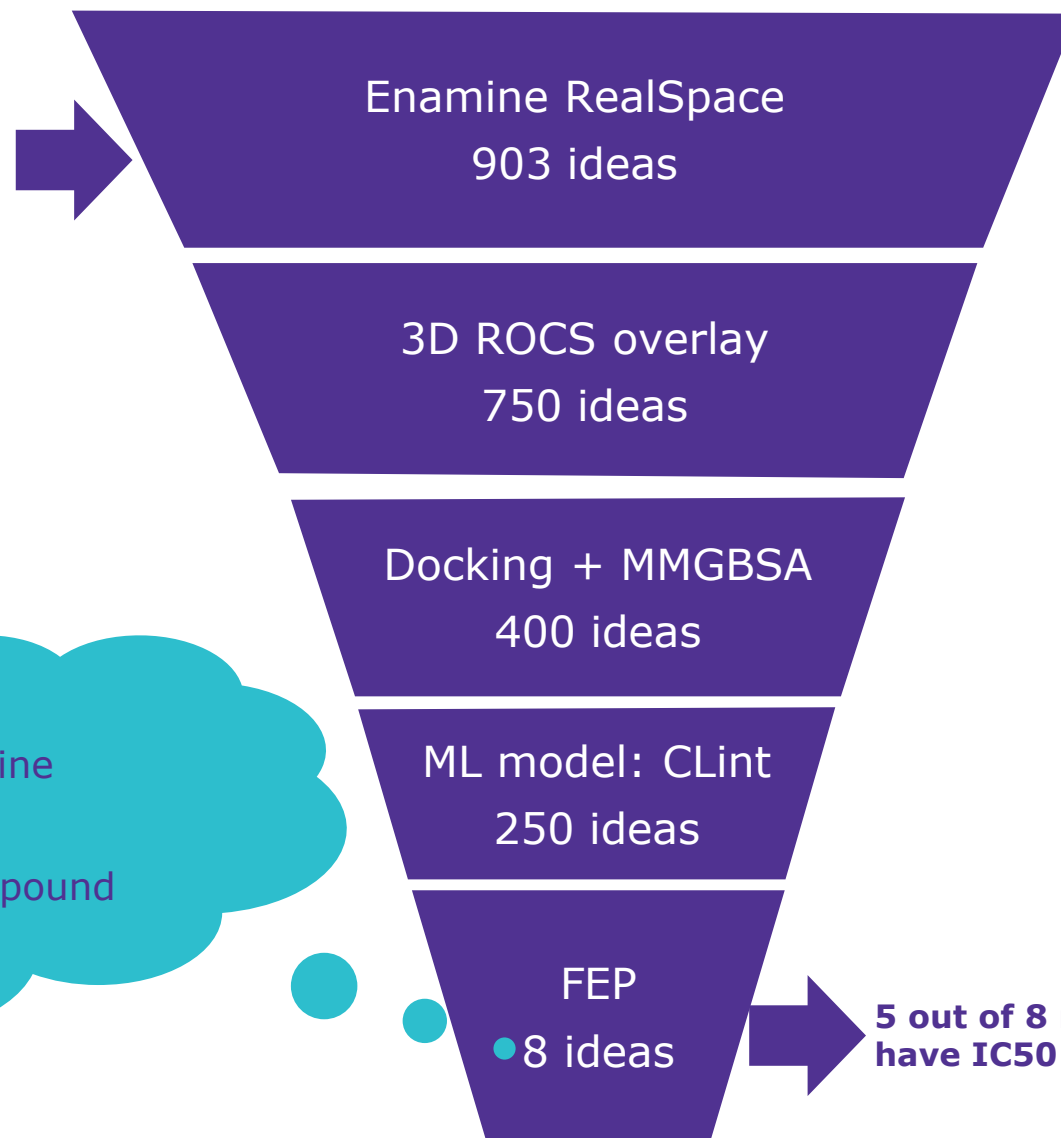
- 4 weeks
- < 100 EUR per compound

Discovery of new chemical starting points with FEP

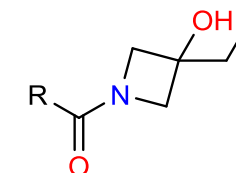
From fragment to hit: Proof-of-principle for in silico optimization



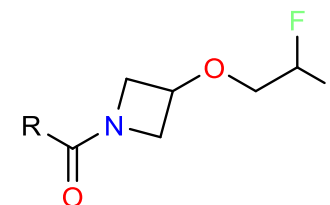
SPR KDss = 300 μ M
LE = 0.25



Top 1 in FEP
IC50 = 1.2 μ M
ITC KD = 1 μ M
LE = 0.41



IC50 = 24 μ M



IC50 = 47 μ M

5 out of 8 molecules
have IC50 < 100 μ M

Synthesis at Enamine

- 4 weeks
- < 100 EUR per compound

Summary

- Large-scale prospective benchmarking demonstrated that accuracy of 1.6 kcal/mol can be obtained for diverse and challenging targets in an industry setting
- Large new public benchmark for free energy calculations created
- Accuracy on benchmark is in line with prospective results from in-house projects
- Recommended use case: large library scanning with FEP
- Successful in-silico optimization of fragment to hit

FEP has become a mainstay in computational chemistry support at Merck KGaA, Darmstadt, Germany

FEP benchmark available on github:

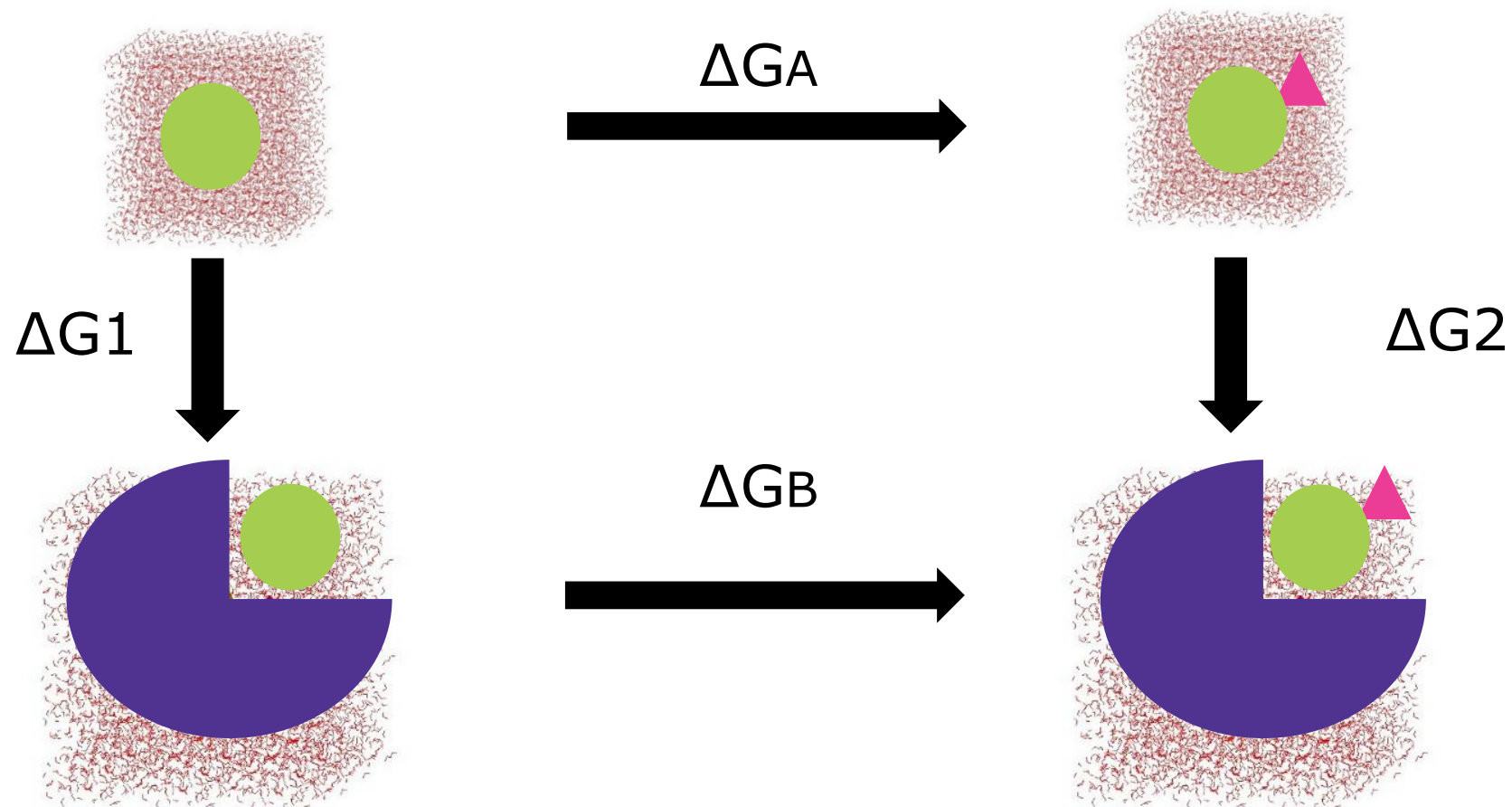
github.com/MCompChem/fep-benchmark



MERCK

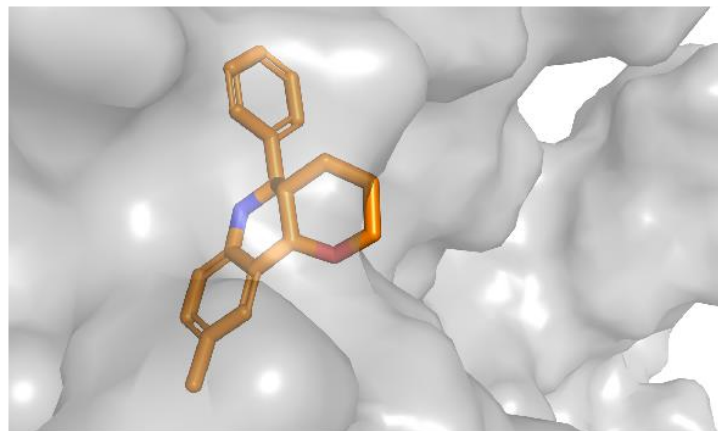
Free energy perturbation (FEP)

A physics-based method for computing binding affinity differences with molecular dynamics simulations



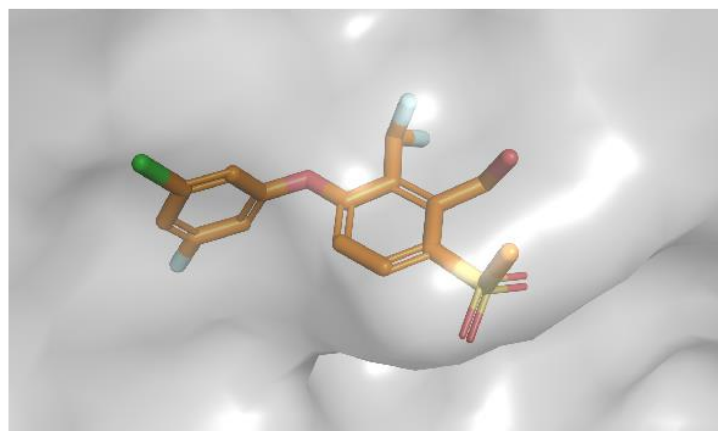
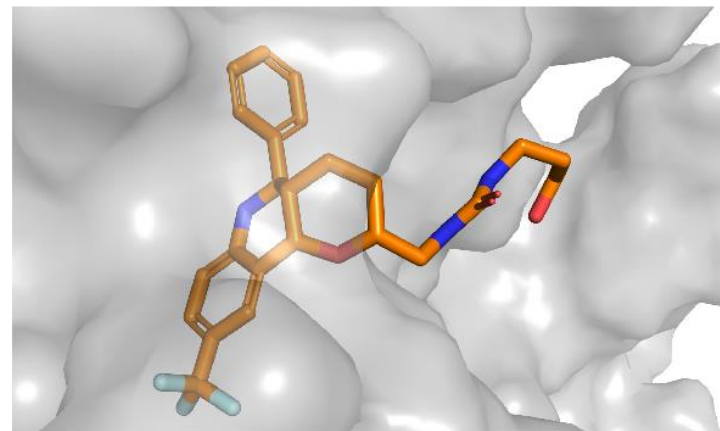
$$\Delta\Delta G = \Delta G_1 - \Delta G_2 = \Delta G_B - \Delta G_A$$

264 ligands for eight pharmaceutically relevant targets
New benchmark for free energy calculations created



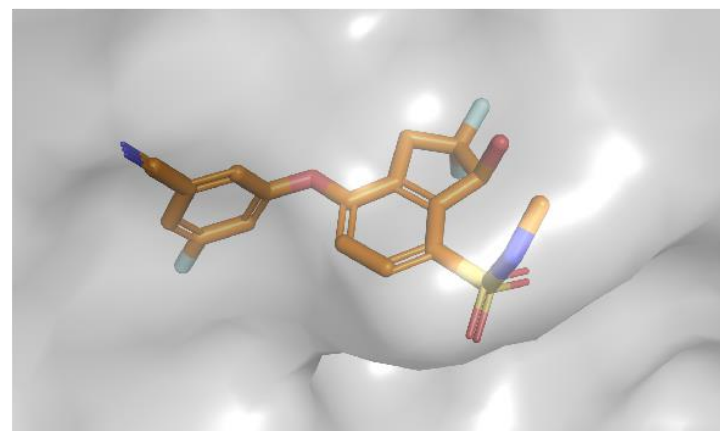
$$\Delta\Delta G_{\text{exp}} = -2.16 \text{ kcal/mol}$$

$$\Delta\Delta G_{\text{pred}} = -2.36 \text{ kcal/mol}$$



$$\Delta\Delta G_{\text{exp}} = -0.93 \text{ kcal/mol}$$

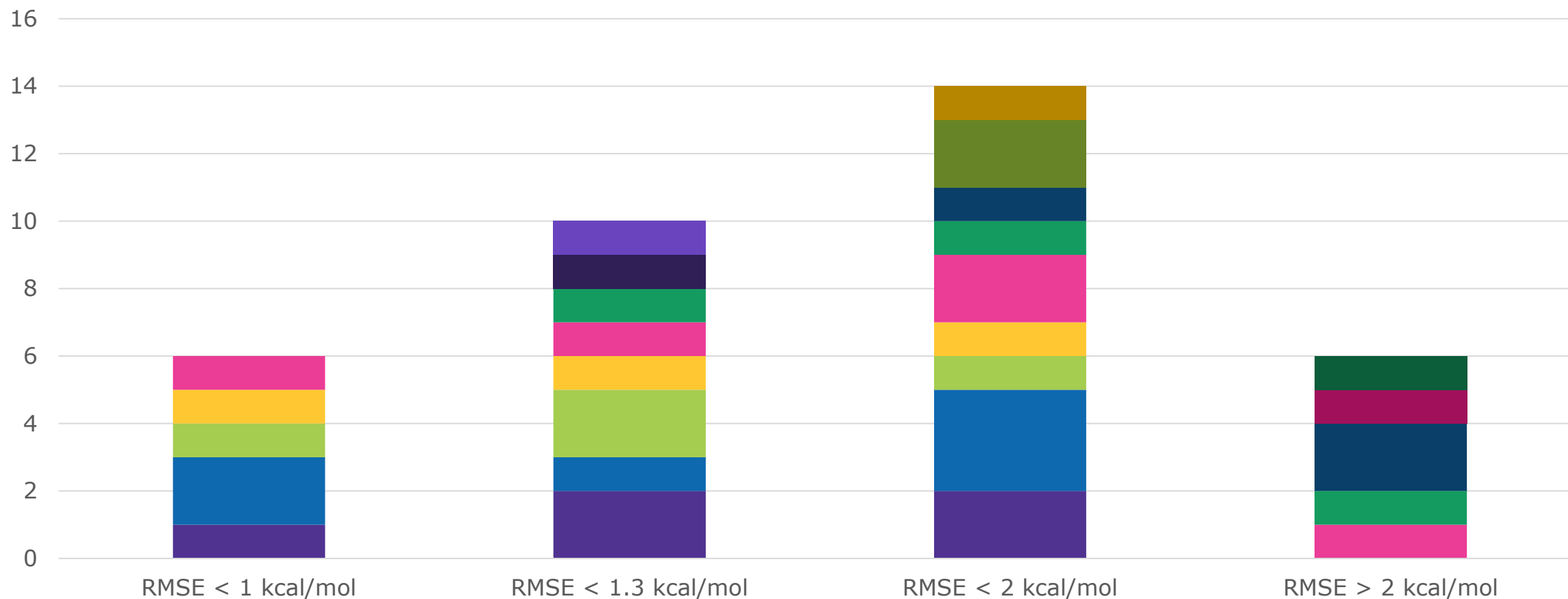
$$\Delta\Delta G_{\text{pred}} = -1.37 \text{ kcal/mol}$$



Desired accuracy below 1 kcal/mol

Validation results vary across targets and (sub-)series

FEP validation studies



Pushing the technology to the edge

Observed limitations in FEP calculations (qualitative)

- Predictions often not possible in certain parts of the molecule (indicated by validation study)
- Difficulty in predicting solvent accessible R-groups (often overestimated)
- Transformation from short R-group to long, flexible chains
- Transformation from aromatic to aliphatic ring → improvement in OPLS3e
- Changes in net charge and charge distribution
- Substituted aliphatic rings → improvement with new torsion fitting feature in release 19-3

