

1 A Discussion on the Pharmaceutical Terminology

2 In this work, we employ a comprehensive set of evaluation metrics—**Vina**, **QED**, **SA**, our pro-
3 posed **MRR**, the **Success Ratio**, and **QikProp**—to analyze different facets of molecular generation
4 performance. Following established practices, we use Vina scores to assess the 3D complementarity
5 between generated molecules and their target binding sites. Meanwhile, we evaluate broader
6 molecular properties using standard metrics (QED and SA), the domain-informed MRR, and physico-
7 chemical and pharmacokinetic descriptors from QikProp, which are widely used in computer-aided
8 drug design (CADD).

9 To clarify the key concepts underpinning our evaluation framework, we distinguish among **drug**
10 **potential**, **drug-likeness**, **molecular reasonability**, and **chemical validity**.

11 Previous studies have often focused too narrowly on geometric complementarity, overlooking other
12 essential requirements a drug-like molecule must fulfill. We introduce the term *drug potential* to
13 describe the overall suitability of a molecule as a drug candidate, encompassing not only binding
14 affinity but also synthetic accessibility, chemical stability, pharmacokinetics (absorption, distribution,
15 metabolism, and excretion), and safety. These properties are intrinsically determined by molecular
16 structure and collectively influence whether a molecule can reach its intended biological target and
17 survive the drug development process.

18 The term *drug-likeness* is widely used in medicinal chemistry to reflect the multidimensional suitabil-
19 ity of a molecule as a drug candidate. Drug discovery and development (DDD), however, are deeply
20 influenced by human expertise—including implicit preferences for molecular scaffolds and nuanced,
21 often tacit, domain knowledge that is difficult to formalize or quantify. As a result, even experienced
22 medicinal chemists struggle to define or approximate the true probability function $p(\text{drug})$, which
23 represents the likelihood that a molecule will become a viable therapeutic candidate. However, the
24 machine learning community often oversimplifies *drug-likeness* to metrics such as QED or Lipinski’s
25 Rule of Five, which capture only a narrow range of basic physicochemical properties. This simplifi-
26 cation overlooks critical factors such as oral bioavailability, metabolic stability, and toxicity risks
27 (e.g., hERG liability).

28 At a more fundamental level, a molecule must be *chemically valid*, meaning it adheres to basic
29 chemical rules such as proper valence and atom types. However, we observe that many model-
30 generated molecules—while technically valid—contain rare or unstable structural substructures that
31 would be flagged by human medicinal chemists. These structures are neither common nor practically
32 accessible and thus fall outside the bounds of what is typically accepted in pharmaceutical research.
33 Despite the central importance of this distinction, prior work has not proposed an effective metric to
34 differentiate between chemically plausible structures and those that are formally valid but unrealistic.
35 To fill this gap, we propose MRR, a rule-based metric that reflects medicinal chemistry heuristics. It
36 identifies implausible features such as unstable ring systems and uncommon conjugation patterns,
37 offering an interpretable and practical means of identifying unrealistic model outputs.

38 By explicitly defining these concepts and introducing MRR, we aim to guide molecular generation
39 efforts toward pharmaceutically meaningful directions, bridging the gap between computational
40 outputs and real-world drug development feasibility.

41 B Limitations

42 One limitation of CIDD is its dependence on pretrained LLMs, which may occasionally introduce
43 hallucinations in underexplored chemical regions.

44 C Detailed Prompts and Responses for LEDD

45 In this section, we present the detailed workflow of the CIDD framework, including the prompts and
46 example responses for each module.

47 Figure 1 illustrates the complete drug design pipeline. The Interaction Module first identifies key
48 fragments within the supporting molecule that interact with the protein pocket. This information is
49 then utilized by the Design Module, which devises strategies to replace uncommon or unfavorable
50 fragments while preserving crucial interactions. Once a new molecule is designed, the Evaluation

51 Phase within the Design Module assesses its viability. Finally, the Reflection Module analyzes the
 52 design process and outcomes, highlighting both strengths and areas for improvement.
 53 Figure 2 presents the prompt and example response for the Interaction Analysis Module.
 54 Figures 3 and 4 display the prompt and example response for the Design Module.
 55 Figures 5, 6, and 7 illustrate the prompt and example responses for the Reflection Module.
 56 Figures 8 and 9 show the prompt and example response for the Selection Module.

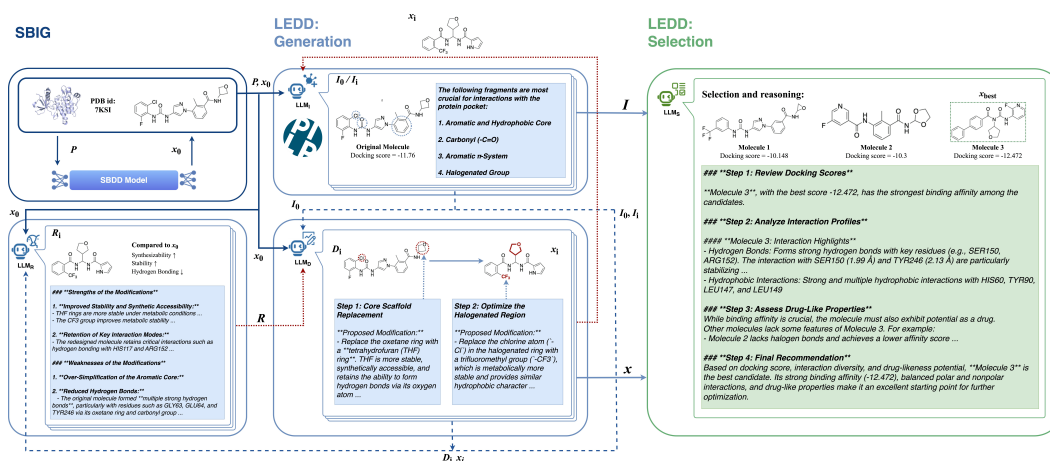


Figure 1: Workflow of CIDD framework

Interaction analysis

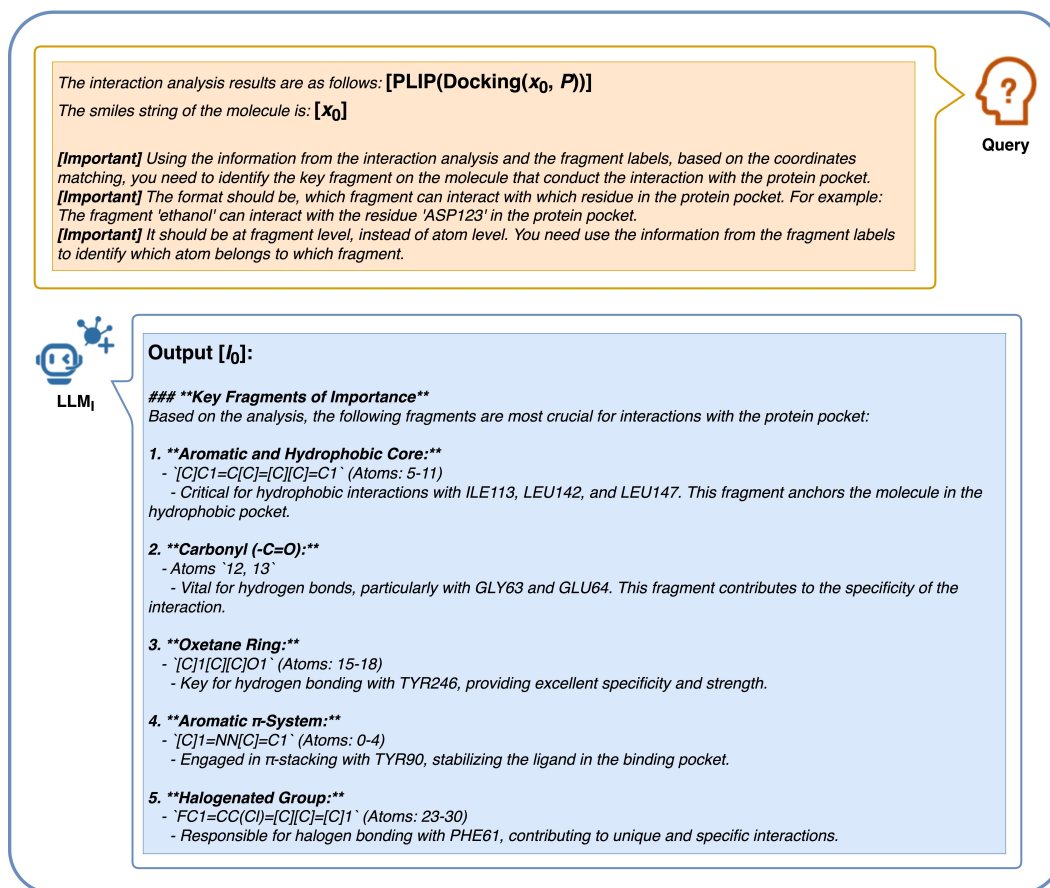


Figure 2: Interaction analysis module

Design - Part 1

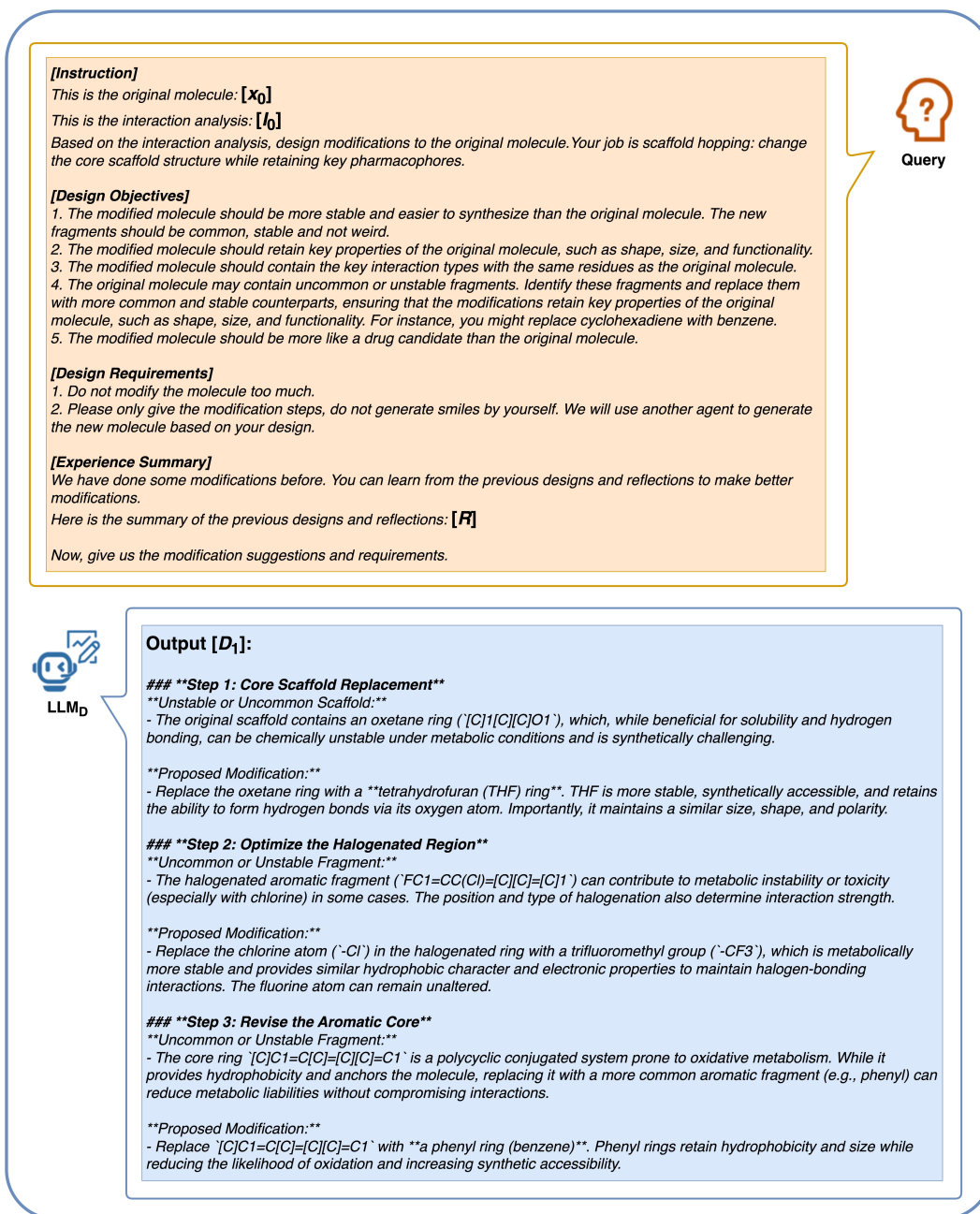


Figure 3: Design Module

Design - Part 2

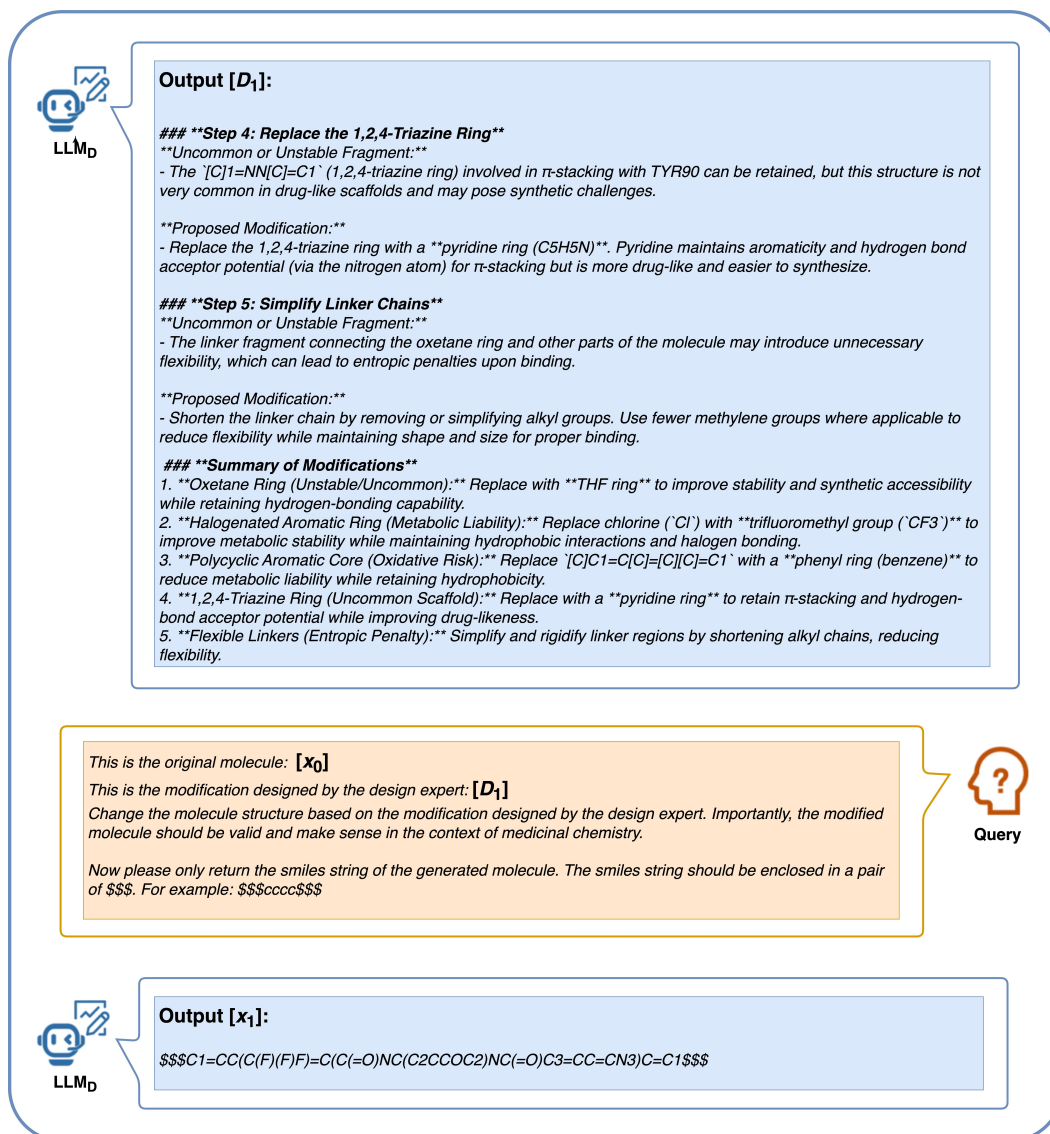


Figure 4: Design Module

Reflection - Part 1

[Instruction]

=====

This is the original molecule structure: **[x₀]**

This is the interaction analysis of this molecule and the protein pocket: **[I₀]**

=====

This is the modification design generated by you: **[D₁]**

This is the molecule structure designed based on your modification: **[x₁]**

This is the interaction analysis generated by interaction export agent: **[I₁]**

=====


Previously, we asked you to modify a molecule to get a new molecule that binds better to the protein pocket. We analyzed the binding of the new molecule to the protein pocket and put it together with the binding before the modification for comparison.

Based on these analyses, you need to reflect on the previous modification and provide feedback on the design. Besides, we hope you can find out which fragments inside the structure of these two molecules are useful for binding to the protein pocket.


=====

Please use critical thinking to analyze, pointing out both the good and the bad points. Your reflection is:

=====



Query



LLMR

Output [R₁]:

****Strengths of the Modifications****

- **Improved Stability and Synthetic Accessibility:****
 - Replacing the ****oxetane ring**** with a ****tetrahydrofuran (THF) ring**** is a commendable adjustment. THF rings are more stable under metabolic conditions, while retaining key hydrogen-bonding interactions and similar steric bulk. This was a sensible change that aligns well with drug-likeness principles.
 - Removing the ****chlorine atom**** in favor of a ****trifluoromethyl (CF₃) group**** was another thoughtful modification. The CF₃ group improves metabolic stability and reduces potential toxicity from reactive halogens, while maintaining the original hydrophobicity and shape.
- **Retention of Key Interaction Modes:****
 - The redesigned molecule retains critical interactions such as hydrogen bonding with HIS117 and ARG152, hydrophobic interactions with HIS60, LEU147, and PHE188, and π -stacking with TYR90. These interactions are crucial for binding affinity and ensure the molecule continues to engage the protein pocket effectively.
 - The ****pyridine ring**** (replacing the less common 1,2,4-triazine ring) aligns better with drug-likeness rules while maintaining hydrogen bonding and hydrophobic capabilities. This substitution strengthens the molecule's pharmacokinetic prospects.
- **Refinement of Scaffolds and Simplification:****
 - Simplifying the polycyclic aromatic core into a ****benzene ring**** was a reasonable modification to reduce oxidation-prone elements. This ensures the molecule is more stable and synthetically tractable without losing significant hydrophobic interactions.

****Weaknesses of the Modifications****

- **Reduction in Docking Score:****
 - The docking score decreased from **** -11.76 (original molecule) **** to **** -9.215 (modified molecule) ****, indicating a clear drop in binding affinity. While the modified molecule retains key interactions, some critical binding contributions were inadvertently weakened during redesign. The TEF reduction suggests a loss of key complementary contacts between the ligand and protein pocket.
- **Over-Simplification of the Aromatic Core:****
 - Replacing the conjugated aromatic system (**** '[C]C1=C[C]=C[C][C]=C1 '****) with a simple ****benzene ring**** reduced the hydrophobic surface area and π -electron system available for interactions. Consequently, hydrophobic interactions with residues like TYR90, ILE113, and LEU142 were diminished, and the molecule lost some of its ability to stabilize key π -interactions within the pocket.
- **Unutilized Potential of the Trifluoromethyl Group:****
 - While the trifluoromethyl (CF₃) group improved metabolic stability, it did not directly contribute to binding interactions within the protein pocket. This functional group occupies space but does not engage with any specific residues, effectively adding to molecular weight without enhancing binding. A better-placed or functionally active replacement could have yielded greater interaction strength.

Figure 5: Reflection Module

Reflection - Part 2



Output [R₁]:

4. **Reduced Hydrogen Bonds:**

- The original molecule formed **multiple strong hydrogen bonds**, particularly with residues such as GLY63, GLU64, and TYR246 via its oxetane ring and carbonyl group. These hydrogen bonds were either weakened or lost in the redesign, with new hydrogen bonds (forming with HIS117 and ARG152) failing to fully compensate for this depletion.

5. **Flexibility in the THF Ring:**

- While the THF ring is more stable than the oxetane ring, it likely introduces greater flexibility due to its sp³-hybridized carbons. This flexibility may lead to entropic penalties upon binding, making the molecule less efficient in achieving a preorganized, bioactive conformation.

6. **Over-Reliance on Hydrophobic Interactions:**

- Similar to the original molecule, the modified structure still relies heavily on **hydrophobic interactions** for binding (e.g., HIS60, TYR90, LEU147). Hydrophobic interactions are less specific than polar or ionic interactions, which are critical for selectivity and affinity. By not introducing additional polar groups, the redesign missed an opportunity to improve overall binding specificity.

Comparison of Binding Fragments

Original Molecule:

1. **Oxetane Ring (Lost in the Redesign):**

- Forms key hydrogen bonds with TYR246 in the binding pocket, contributing significantly to specific and strong ligand binding. Its removal weakened overall binding affinity.

2. **Conjugated Hydrophobic Core ('[C]C1=C[C]=[C][C]=C1'):**

- Provides extensive hydrophobic and π -stacking interactions with residues such as ILE113, LEU142, and TYR90. Replacing this rich aromatic structure with a benzene ring reduced the hydrophobic and π -electron contribution to binding.

3. **Halogenated Aromatic Ring ('FC1=CC(CI)=C[C]=[C]1'):**

- Engages the protein via halogen bonding with PHE61, adding specificity to binding interactions. Replacing chlorine with CF₃ abolished some halogen bonds, weakening protein-ligand complementarity.

Modified Molecule:

1. **THF Ring (Introduced):**

- Retains the ability to form hydrogen bonds (e.g., with ARG152). However, its introduction has caused greater flexibility and entropic penalties that may offset its stabilizing contributions.

2. **Trifluoromethyl Group (CF₃, Introduced):**

- Metabolically stable and hydrophobic but does not directly interact with the protein. Its placement on the aromatic ring adds molecular weight but no functional enhancement to binding.

3. **Pyridine Ring (Introduced):**


- Maintains hydrogen-bonding with HIS117 and interacts hydrophobically with HIS60, performing well as a replacement for 1,2,4-triazine. Though not as inherently diverse in interaction opportunities as its predecessor, it improves the drug-likeness of the molecule.

4. **Benzene Ring (Simplified):**

- While it retains some hydrophobic interaction capability, this fragment no longer engages residues like TYR90 or PHE188 as robustly as the original conjugated aromatic system. This reduced binding affinity.

Figure 6: Reflection Module

Reflection - Part 3



LLM_R

Output [R₁]:

**Key Fragments Retained or Lost for Binding**

****Critical Retained Fragments:****

1. ****Pyridine Ring**** for π -stacking and hydrogen bonding with TYR90 and HIS117.
2. ****Hydrogen Bonding Carbonyl Group**** interacting with HIS117 and ARG152.

****Critical Fragments Lost:****

1. ****Oxetane Ring**** contributed unusually strong hydrogen bonds to TYR246, which were lost in the redesign.
2. ****Conjugated Hydrophobic Core**** ensured multisite hydrophobic interactions and π -stacking with residues like LEU142 and TYR90.
3. ****Halogenated Aromatic Ring**** provided halogen bonds with PHE61, contributing unique specificity lost in the redesign.

**Suggestions for Improvement**

1. ****Reintroduce Hydrogen Bonding Groups:****
 - Add back polar fragments (e.g., hydroxyl, amide groups) to increase hydrogen-bonding capacity with residues like TYR246, GLY63, and GLU64.
2. ****Revisit the Aromatic Core:****
 - Instead of oversimplifying the hydrophobic core to benzene, consider a polycyclic aromatic or heterocyclic system to balance hydrophobicity and metabolic stability.
3. ****Optimize Trifluoromethyl Group Placement:****
 - Move or replace the CF₃ group with a fragment that directly engages residues in the protein pocket (e.g., a difluorophenyl or hydrophilic substituent).
4. ****Rigidify the THF Ring:****
 - Lock the THF ring into a constrained system (e.g., fused bicyclic rings) to reduce flexibility and entropic penalties.

**Conclusion**

The modifications resulted in a molecule that is synthetically and metabolically improved but less effective in binding to the protein pocket, as indicated by the diminished docking score. While retaining important interactions, the redesign lost too many advantageous fragments (e.g., oxetane, conjugated aromatic core). Future optimizations should aim to restore lost interactions, improve hydrogen bonding, and balance hydrophobicity with polar contacts for stronger and more specific binding.

Figure 7: Reflection Module

Selection - Part 1

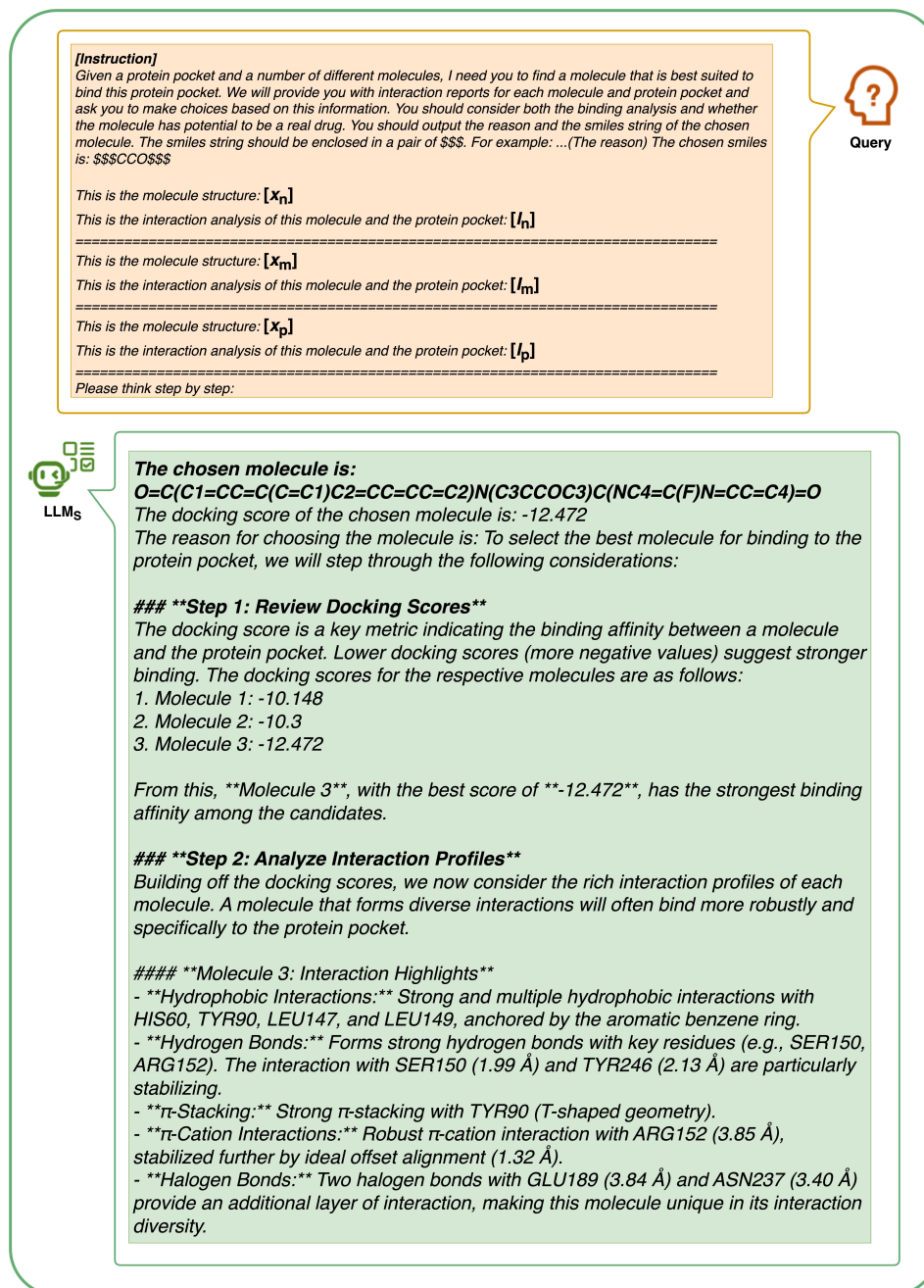



Figure 8: Selection Module



****Key Strengths:****

- The interaction diversity and strength of Molecule 3 far surpass other molecules, leveraging hydrophobic forces, hydrogen bonding, π -stacking, π -cation interactions, and halogen bonding.
- The molecule effectively anchors itself to both polar and nonpolar regions, ensuring specificity for the protein pocket.

**Step 3: Assess Drug-Like Properties**

While binding affinity is crucial, the molecule must also exhibit potential as a drug. Properties relevant to drug-likeness include:

- ****Hydrophobic Components:**** Ensure solubility and stability for membrane diffusion.
- ****Hydrogen Bonding Groups:**** Contribute to specificity and bioactivity.
- ****Halogen Incorporation:**** Enhances membrane permeability and metabolic stability.
- ****Compact, Non-Bulky Structure:**** Ensures the molecule fits within the protein pocket without steric clashes.

For Molecule 3:

- The combination of aromatic rings, amide groups, and fluorine atoms supports balanced hydrophobic and polar properties, increasing stability and bioavailability.
- The inclusion of halogens enhances drug-likeness further.

Other molecules lack some features of Molecule 3. For example:

- Molecule 2 lacks halogen bonds and achieves a lower affinity score.
- Molecule 1 have good binding but lack the breadth of interactions seen with Molecule 3.

**Step 4: Final Recommendation**

Based on docking score, interaction diversity, and drug-likeness potential, ****Molecule 3**** is the best candidate. Its strong binding affinity (-12.472), balanced polar and nonpolar interactions, and drug-like properties make it an excellent starting point for further optimization.

**Chosen Molecule**

****Reason:**** Molecule 3 exhibits the highest docking score, with diverse interaction types (hydrophobic, hydrogen bonding, π -stacking, π -cation, and halogen bonding) that secure it in critical regions of the protein pocket. Additionally, it offers promising drug-like features such as halogen incorporation and a well-optimized molecular structure.

****Selected SMILES String:****

\$\$\$O=C(C1=CC=C(C=C1)C2=CC=CC=C2)N(C3CCOC3)C(NC4=C(F)N=CC=C4)=O\$\$\$

Figure 9: Selection Module

57 D Algorithm for MRR and AUR

58 The complete calculation process for assessing the reasonability of a molecule is outlined in Algo-
 59 rithm 1.

Algorithm 1: Evaluation of Molecular Reasonability

Input: Molecule object (*mol*)

Output: Molecular Reasonability (*MRR*) and Atom Unreasonable Ratio (*AUR*)

Step 1: Detect Carbonyl and Imine Group Carbons

Initialize an empty list for *carbonyl/imine carbons*.

foreach *bond* in *mol* **do**

if *bond* is double and one atom is carbon, the other is oxygen or nitrogen **then**
 Record the carbon atom in *carbonyl/imine groups*.

Step 2: Identification of Ring Systems

Identify all ring structures and their corresponding atom indices within *mol*.

Calculate the number of atoms in each ring.

foreach *ring* in the molecule **do**

if the ring shares one or more atoms with another ring **then**
 Group the connected rings into a single *ring system*.

Step 3: Evaluation of Molecular Reasonability

Exclude any atoms previously identified as part of carbonyl or imine groups.

Classify the remaining carbon atoms in each ring system as follows:

- *sp² hybridized*: Aromatic or unsaturated carbons.
- *Non-sp² hybridized*: Saturated carbons.

foreach *ring system* in the ring systems **do**

if the ring system contains multiple rings and all carbon atoms are non-*sp²* **then**
 Mark the molecule as unreasonable.
 Add the atoms to the unreasonable atom list.

foreach *ring system* in the remaining ring systems **do**

foreach *ring* in the ring system **do**

if all carbon atoms within the ring are consistent in hybridization (either all *sp²* or all non-*sp²*) **then**
 Mark the ring as reasonable.
 else
 Add the ring to the remaining ring list.

while the remaining ring list is not empty **do**

foreach *ring* in the remaining ring list **do**

 Exclude atoms that have already been classified as reasonable.
 if all remaining carbon atoms are consistent in hybridization (either all *sp²* or all non-*sp²*) **then**
 Mark the ring as reasonable.

if no new reasonable rings are identified **then**

 Mark the molecule as unreasonable.
 Add the carbon atoms in the remaining rings to the unreasonable atom list.
 Exit the loop.

Calculate *AUR* as the ratio of unreasonable atom count to the total ring atom count.

Return *MRR* and *AUR*.

E QikProp properties

The full set of properties used for the QikProp pass ratio analysis is presented in Table 1.

The QikProp filter applied in the main text incorporates a comprehensive range of criteria provided by QikProp, including "#stars", "#amine", "#amidine", "#acid", "#amide", "#rotor", "#rtvFG", "mol_MW", "dipole", "SASA", "FOSA", "FISA", "PISA", "WPSA", "volume", "donorHB", "acceptHB", "dip²/V", "ACxDN-5/SA", "glob", "QPpolrz", "QPlogPC16", "QPlogPoct", "QPlogPw", "QPlogPo/w", "QPlogS", "CIQPlogS", "QPPCaco", "QPlogBB", "QPPMDCK", "QPlogKp", "IP(eV)", "EA(eV)", "#metab", "QPlogKhsa", "PercentHumanOralAbsorption", "SAFluorine", "SAamideO", "PSA", "#NandO", and "RuleOfThree".

Table 1: QikProp Properties and Descriptors

Property or Descriptor	Description	Range or Recommended Values
Molecule name	The molecule’s identifier derived from the title line in the input structure file. If no title is provided, the file name is used.	
#stars	Count of descriptors or properties falling outside the 95% range for known drugs. A higher count indicates reduced drug-likeness.	0 – 5
#amine	Total non-conjugated amine groups present in the molecule.	0 – 1
#amidine	Number of amidine or guanidine functional groups in the structure.	0
#acid	Quantity of carboxylic acid groups in the molecule.	0 – 1
#amide	Count of non-conjugated amide groups.	0 – 1
#rotor	Number of rotatable bonds that are neither trivial nor sterically hindered.	0 – 15
#rtvFG	Total reactive functional groups present in the molecule, potentially affecting stability or toxicity.	0 – 2
mol_MW	Molecular weight of the compound.	130.0 – 725.0
Dipole	Calculated dipole moment of the molecule in Debye units.	1.0 – 12.5
SASA	Solvent-accessible surface area (SASA) in square angstroms, measured with a probe of 1.4 Å radius.	300.0 – 1000.0
FOSA	Hydrophobic part of the SASA, representing saturated carbon and attached hydrogen atoms.	0.0 – 750.0
FISA	Hydrophilic fraction of the SASA, encompassing polar atoms like nitrogen and oxygen.	7.0 – 330.0
PISA	SASA component attributable to π -systems.	0.0 – 450.0
WPSA	Weakly polar component of the SASA, including atoms like halogens, phosphorus, and sulfur.	0.0 – 175.0
Volume	Total solvent-accessible volume in cubic angstroms, determined with a 1.4 Å radius probe.	500.0 – 2000.0
donorHB	Estimated number of hydrogen bonds donated to water in solution.	0.0 – 6.0
acceptHB	Estimated number of hydrogen bonds accepted from water.	2.0 – 20.0
Dip ² /V	Dipole moment squared divided by molecular volume, a key factor in solvation energy.	0.0 – 0.13
ACxDN ^(0.5) /SA	Cohesive interaction index in solids based on molecular properties.	0.0 – 0.05
glob	Descriptor measuring how close the shape of a molecule is to a sphere.	0.75 – 0.95
QPpolarz	Predicted molecular polarizability in cubic angstroms.	13.0 – 70.0
QPlogPC16	Predicted partition coefficient between hexadecane and gas phases.	4.0 – 18.0
QPlogPoct	Predicted partition coefficient between octanol and gas phases.	8.0 – 35.0
QPlogPw	Predicted partition coefficient between water and gas phases.	4.0 – 45.0
QPlogPo/w	Predicted partition coefficient between octanol and water phases.	-2.0 – 6.5
QPlogS	Predicted solubility of the molecule in water (log S, in mol/L).	-6.5 – 0.5
CIQPlogS	Conformation-independent prediction of water solubility (log S).	-6.5 – 0.5
QPPCaco	Predicted permeability through Caco-2 cells, in nm/s.	<25 poor, >500 great
QPlogBB	Predicted partition coefficient for brain/blood.	-3.0 – 1.2
QPPMDCK	Predicted permeability through MDCK cells, in nm/s.	<25 poor, >500 great
QPlogKp	Predicted skin permeability (log Kp).	-8.0 – -1.0
IP(eV)	Ionization potential calculated using PM3.	7.9 – 10.5
EA(eV)	Electron affinity calculated using PM3.	-0.9 – 1.7
#metab	Predicted number of possible metabolic reactions.	1 – 8
QPlogKhsa	Predicted binding affinity to human serum albumin.	-1.5 – 1.5
HumanOralAbsorption	Qualitative assessment of oral absorption: 1 (low), 2 (medium), or 3 (high).	
PercentHumanOralAbsorption	Quantitative prediction of oral absorption percentage.	>80% high, <25% poor
SAFluorine	Solvent-accessible fluorine surface area.	0.0 – 100.0
SAamideO	Solvent-accessible surface area of amide oxygen atoms.	0.0 – 35.0
PSA	Polar surface area, calculated for nitrogen, oxygen, and carbonyl groups.	7.0 – 200.0
#NandO	Total count of nitrogen and oxygen atoms.	2 – 15
RuleOfFive	Number of Lipinski’s Rule of Five violations.	Max 4
RuleOfThree	Number of Jorgensen’s Rule of Three violations.	Max 3
#ringatoms	Count of atoms within molecular rings.	
#in34	Number of atoms in 3- or 4-membered rings.	
#in56	Number of atoms in 5- or 6-membered rings.	
#noncon	Number of ring atoms unable to form conjugated aromatic systems.	
#nonHtm	Count of heavy (non-hydrogen) atoms in the structure.	
Jm	Predicted maximum transdermal transport rate ($\mu\text{g cm}^{-2} \text{hr}^{-1}$).	

70 F Computing Resource

71 In this work, we primarily utilize pretrained 3D generative models and large language model (LLM)
 72 APIs to conduct our experiments. The 3D model sampling is performed using a single NVIDIA A100
 73 GPU. For the LLM component, we rely on API-based access provided by the service provider, which
 74 requires no local computational resources.

75 G More Experiment Results

76 Based on the different criteria presented in Table 1, we provide additional pass ratio results in Table 2.
 77 Filter 1 is identical to the QikProp filter used in the main text.
 78 Filter 2 removes some non-essential properties and focuses on well-defined physicochemical proper-
 79 ties, including "#rtvFG", "QPlogS", "QPlogPo/w", "mol_MW", "dipole", "SASA", "FOSA", "FISA",
 80 "IP(eV)", "EA(eV)", "#metab", "PercentHumanOralAbsorption", and "PSA".

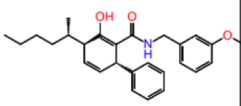
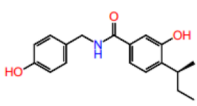
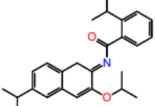
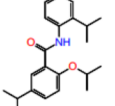
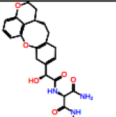
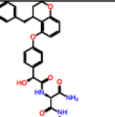
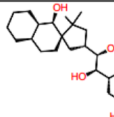
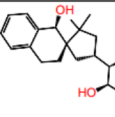
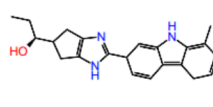
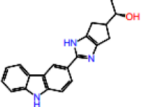
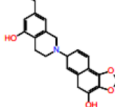
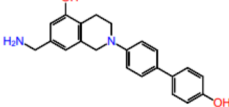
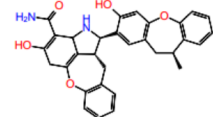
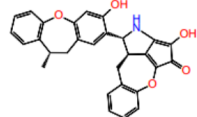
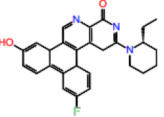
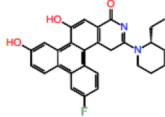
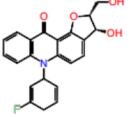
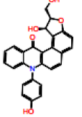
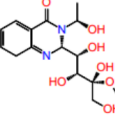
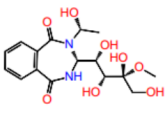
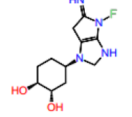
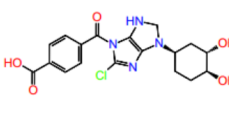
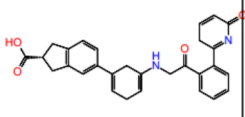
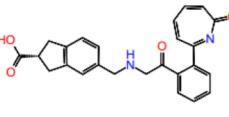
81 Filter 3 assesses molecular compliance with the "RuleOfFive" criterion. However, instead of allowing
 82 up to four violations as typically recommended, this filter adopts a stricter definition, considering
 83 only molecules that fully comply (i.e., setting the maximum allowable violations to zero).

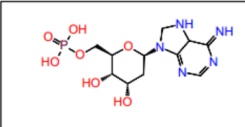
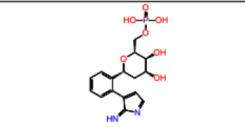
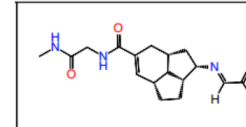
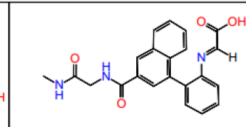
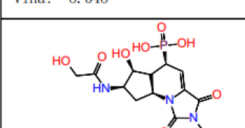
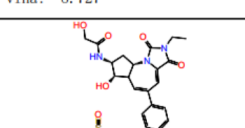
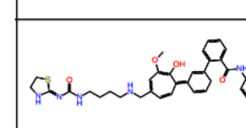
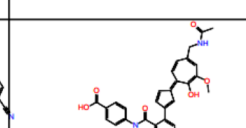
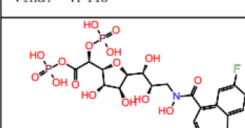
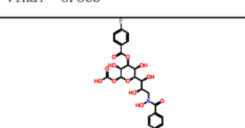
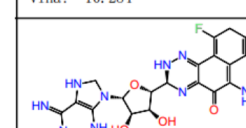
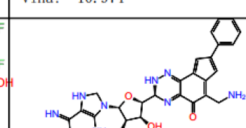
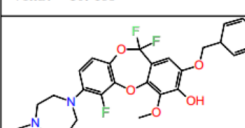
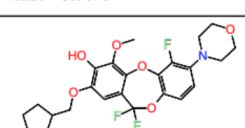
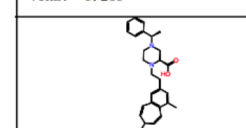
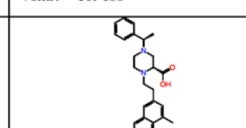
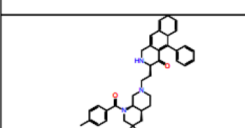
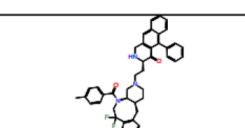
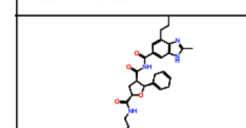
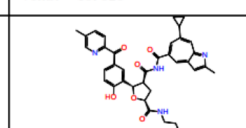
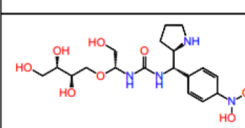
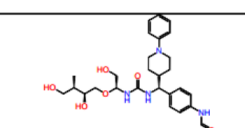
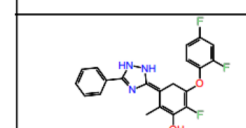
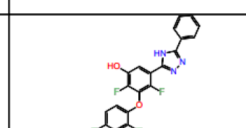
Table 2: QikProp results for different methods with and without CIDD

Method	Filter 1	Filter 2	Filter 3
Pocket2Mol			
Original	29.58%	51.52%	89.58%
CIDD	56.97%	75.64%	92.24%
TargetDiff			
Original	26.32%	48.20%	69.47%
CIDD	53.37%	75.60%	81.85%
DecompDiff			
Original	29.04%	53.96%	55.14%
CIDD	37.54%	68.48%	65.64%
MolCRAFT			
Original	22.37%	43.52%	66.45%
CIDD	35.22%	63.23%	74.09%

84 H More cases

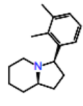
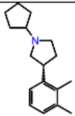
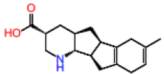
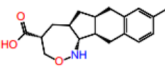
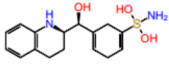
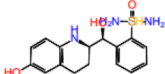
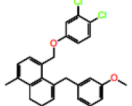
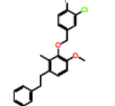
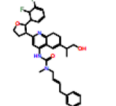
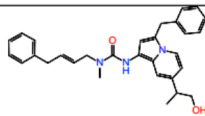
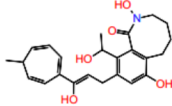
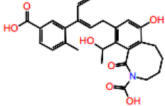
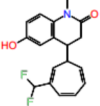
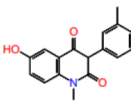
85 More generated molecules from CIDD are presented below. For each case, we display the initial
 86 supporting molecule derived from 3D-SBDD models alongside the final designed molecules produced
 87 by CIDD.

Supporting molecule	CIDD output	Supporting molecule	CIDD output
 title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -7.824	 title: IDHP_HUMAN_40_452_0 : Reasonable vina: -10.106	 title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -7.941	 title: IDHP_HUMAN_40_452_0 : Reasonable vina: -9.66
 title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -9.415	 title: NOS1_HUMAN_302_723_0 : Reasonable vina: -10.098	 title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -8.054	 title: NOS1_HUMAN_302_723_0 : Reasonable vina: -8.432
 title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -10.069	 title: NOS1_HUMAN_302_723_0 : Reasonable vina: -10.22	 title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -9.287	 title: NOS1_HUMAN_302_723_0 : Reasonable vina: -9.6
 title: ABL2_HUMAN_274_551_0 : Unreasonable vina: -10.007	 title: ABL2_HUMAN_274_551_0 : Reasonable vina: -10.946	 title: ABL2_HUMAN_274_551_0 : Unreasonable vina: -9.916	 title: ABL2_HUMAN_274_551_0 : Reasonable vina: -10.509
 title: AK1BA_HUMAN_1_316_0 : Unreasonable vina: -10.421	 title: AK1BA_HUMAN_1_316_0 : Reasonable vina: -10.778	 title: NQO1_HUMAN_2_274_0 : Unreasonable vina: -8.37	 title: NQO1_HUMAN_2_274_0 : Reasonable vina: -9.24
 title: NQO1_HUMAN_2_274_0 : Unreasonable vina: -7.951	 title: NQO1_HUMAN_2_274_0 : Reasonable vina: -9.51	 title: PHP_SULSO_1_314_0 : Unreasonable vina: -11.034	 title: PHP_SULSO_1_314_0 : Reasonable vina: -11.397

Supporting molecule	CIDD output	Supporting molecule	CIDD output
 <p>title: PHKG1_RABIT_6_296_ATPsite_0 : Unreasonable vina: -8.548</p>	 <p>title: PHKG1_RABIT_6_296_ATPsite_0 : Reasonable vina: -8.727</p>	 <p>title: BGL07_ORYSJ_25_504_0 : Unreasonable vina: -8.041</p>	 <p>title: BGL07_ORYSJ_25_504_0 : Reasonable vina: -9.949</p>
 <p>title: CD38_HUMAN_44_300_0 : Unreasonable vina: -7.443</p>	 <p>title: CD38_HUMAN_44_300_0 : Reasonable vina: -8.863</p>	 <p>title: TNKS2_HUMAN_948_1162_0 : Unreasonable vina: -10.284</p>	 <p>title: TNKS2_HUMAN_948_1162_0 : Reasonable vina: -10.974</p>
 <p>title: P2Y12_HUMAN_1_342_0 : Unreasonable vina: -10.463</p>	 <p>title: P2Y12_HUMAN_1_342_0 : Reasonable vina: -10.674</p>	 <p>title: HMD_METJA_1_358_0 : Unreasonable vina: -9.259</p>	 <p>title: HMD_METJA_1_358_0 : Reasonable vina: -10.458</p>
 <p>title: SQHC_ALIAD_1_631_0 : Unreasonable vina: -14.278</p>	 <p>title: SQHC_ALIAD_1_631_0 : Reasonable vina: -17.408</p>	 <p>title: SQHC_ALIAD_1_631_0 : Unreasonable vina: -13.626</p>	 <p>title: SQHC_ALIAD_1_631_0 : Reasonable vina: -13.825</p>
 <p>title: BGAT_HUMAN_63_353_0 : Unreasonable vina: -7.891</p>	 <p>title: BGAT_HUMAN_63_353_0 : Reasonable vina: -9.201</p>	 <p>title: CHIB_SERMA_1_499_0 : Unreasonable vina: -10.676</p>	 <p>title: CHIB_SERMA_1_499_0 : Reasonable vina: -13.113</p>
 <p>title: CHIB_SERMA_1_499_0 : Unreasonable vina: -7.115</p>	 <p>title: CHIB_SERMA_1_499_0 : Reasonable vina: -8.719</p>	 <p>title: NRIH4_HUMAN_258_486_0 : Unreasonable vina: -10.038</p>	 <p>title: NRIH4_HUMAN_258_486_0 : Reasonable vina: -11.021</p>

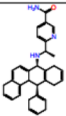
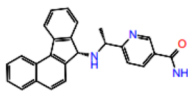
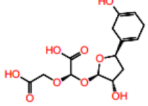
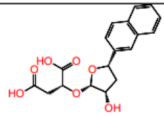
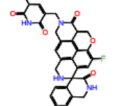
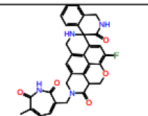
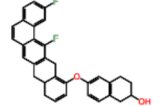
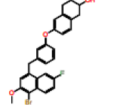
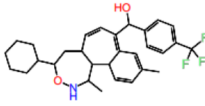
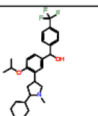
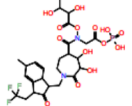
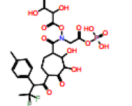
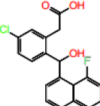
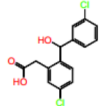
Supporting molecule

CIDD output

	
title: SDIA_ECOLI_1_171_0 : Unreasonable vina: -11.019	title: SDIA_ECOLI_1_171_0 : Reasonable vina: -11.294
	
title: GSTP1_HUMAN_2_210_0 : Unreasonable vina: -7.591	title: GSTP1_HUMAN_2_210_0 : Reasonable vina: -8.725
	
title: HDHA_ECOLI_1_255_0 : Unreasonable vina: -8.5	title: HDHA_ECOLI_1_255_0 : Reasonable vina: -8.515
	
title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -8.176	title: IDHP_HUMAN_40_452_0 : Reasonable vina: -10.774
	
title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -7.605	title: IDHP_HUMAN_40_452_0 : Reasonable vina: -11.661
	
title: AK1B_HUMAN_1_316_0 : Unreasonable vina: -9.845	title: AK1B_HUMAN_1_316_0 : Reasonable vina: -9.981
	
title: OLIAC_CANSA_1_101_0 : Unreasonable vina: -7.631	title: OLIAC_CANSA_1_101_0 : Reasonable vina: -8.866

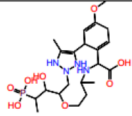
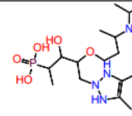
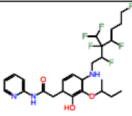
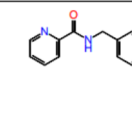
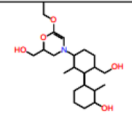
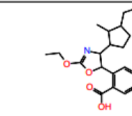
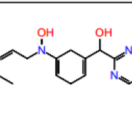
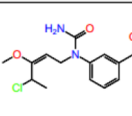
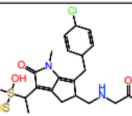
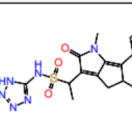
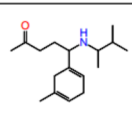
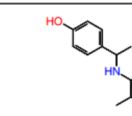
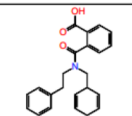
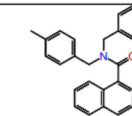
Supporting molecule

CIDD output

	
title: SDIA_ECOLI_1_171_0 : Unreasonable vina: -8.52	title: SDIA_ECOLI_1_171_0 : Reasonable vina: -13.937
	
title: HDHA_ECOLI_1_255_0 : Unreasonable vina: -7.709	title: HDHA_ECOLI_1_255_0 : Reasonable vina: -8.778
	
title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -11.943	title: NOS1_HUMAN_302_723_0 : Reasonable vina: -12.979
	
title: NR1H4_HUMAN_258_486_0 : Unreasonable vina: -6.824	title: NR1H4_HUMAN_258_486_0 : Reasonable vina: -8.578
	
title: CPXB_BACMB_2_464_0 : Unreasonable vina: -9.607	title: CPXB_BACMB_2_464_0 : Reasonable vina: -10.132
	
title: P2Y12_HUMAN_1_342_0 : Unreasonable vina: -7.75	title: P2Y12_HUMAN_1_342_0 : Reasonable vina: -16.253
	
title: SIR3_HUMAN_117_398_0 : Unreasonable vina: -8.238	title: SIR3_HUMAN_117_398_0 : Reasonable vina: -8.331

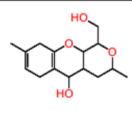
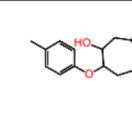
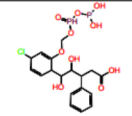
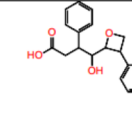
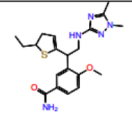
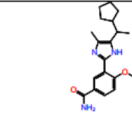
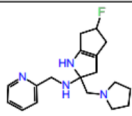
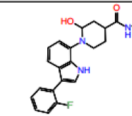
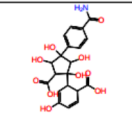
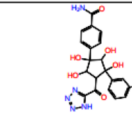
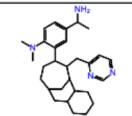
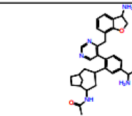
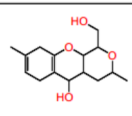
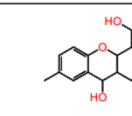
Supporting molecule

CIDD output

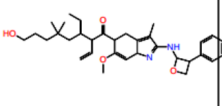
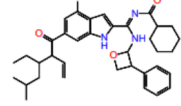
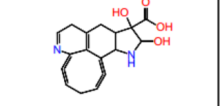
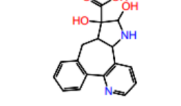
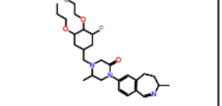
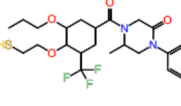
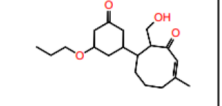
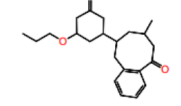
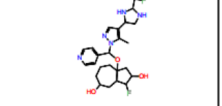
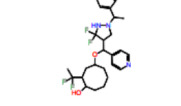
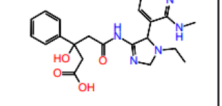
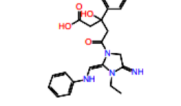
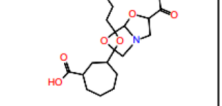
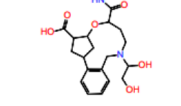
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 title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -7.796	 title: IDHP_HUMAN_40_452_0 : Reasonable vina: -11.383
 title: AKT1_HUMAN_1_137_0 : Unreasonable vina: -8.605	 title: AKT1_HUMAN_1_137_0 : Reasonable vina: -9.926
 title: HMD_METJA_1_358_0 : Unreasonable vina: -7.825	 title: HMD_METJA_1_358_0 : Reasonable vina: -8.55
 title: SIR3_HUMAN_117_398_0 : Unreasonable vina: -7.93	 title: SIR3_HUMAN_117_398_0 : Reasonable vina: -10.435
 title: DYRK2_HUMAN_145_550_0 : Unreasonable vina: -7.961	 title: DYRK2_HUMAN_145_550_0 : Reasonable vina: -8.399
 title: DIDH_RAT_1_319_0 : Unreasonable vina: -9.165	 title: DIDH_RAT_1_319_0 : Reasonable vina: -10.631

Supporting molecule

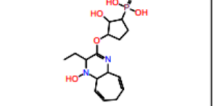
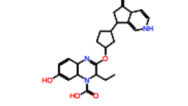
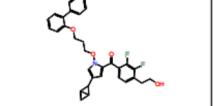
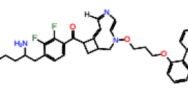
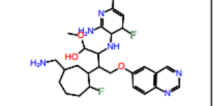
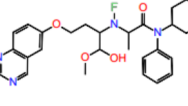
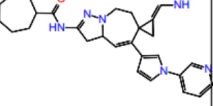
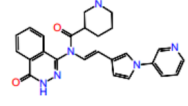
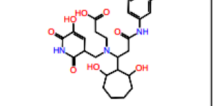
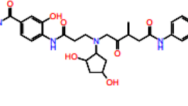
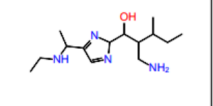
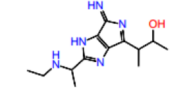
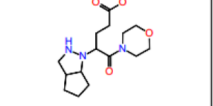
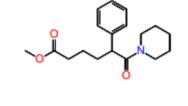
CIDD output

 title: DIDH_RAT_1_319_0 : Unreasonable vina: -8.26	 title: DIDH_RAT_1_319_0 : Reasonable vina: -8.722
 title: COAA_MYCTU_1_312_0 : Unreasonable vina: -7.572	 title: COAA_MYCTU_1_312_0 : Reasonable vina: -9.731
 title: M3K14_HUMAN_321_678_0 : Unreasonable vina: -7.453	 title: M3K14_HUMAN_321_678_0 : Reasonable vina: -9.209
 title: CHIB1_ASPPM_39_433_0 : Unreasonable vina: -8.054	 title: CHIB1_ASPPM_39_433_0 : Reasonable vina: -10.096
 title: SIR3_HUMAN_117_398_0 : Unreasonable vina: -6.991	 title: SIR3_HUMAN_117_398_0 : Reasonable vina: -10.758
 title: NOS3_HUMAN_65_480_0 : Unreasonable vina: -9.583	 title: NOS3_HUMAN_65_480_0 : Reasonable vina: -10.652
 title: DIDH_RAT_1_319_0 : Unreasonable vina: -8.503	 title: DIDH_RAT_1_319_0 : Reasonable vina: -8.895

Supporting molecule CIDD output

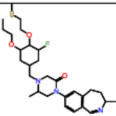
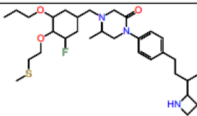
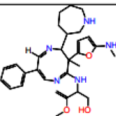
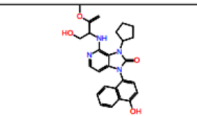
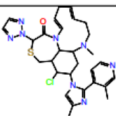
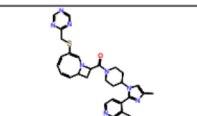
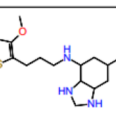
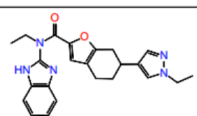
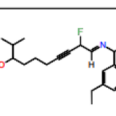
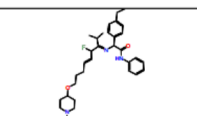
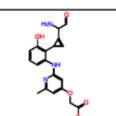
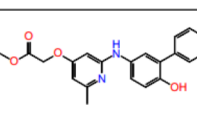
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 title: F16P1_HUMAN_1_338_0 : Unreasonable vina: -8.173	 title: F16P1_HUMAN_1_338_0 : Reasonable vina: -8.633
 title: CAT_ECOLX_1_219_0 : Unreasonable vina: -9.838	 title: CAT_ECOLX_1_219_0 : Reasonable vina: -10.164
 title: DFPA_LOLVU_2_314_0 : Unreasonable vina: -7.208	 title: DFPA_LOLVU_2_314_0 : Reasonable vina: -8.581
 title: QPCT_HUMAN_33_361_0 : Unreasonable vina: -8.178	 title: QPCT_HUMAN_33_361_0 : Reasonable vina: -9.527
 title: KS6A3_HUMAN_41_357_0 : Unreasonable vina: -8.242	 title: KS6A3_HUMAN_41_357_0 : Reasonable vina: -8.738
 title: AROE_THET8_1_263_0 : Unreasonable vina: -8.741	 title: AROE_THET8_1_263_0 : Reasonable vina: -8.794

Supporting molecule CIDD output

 title: GRK4_HUMAN_1_578_0 : Unreasonable vina: -7.158	 title: GRK4_HUMAN_1_578_0 : Reasonable vina: -8.93
 title: CPXB_BACMB_2_464_0 : Unreasonable vina: -10.201	 title: CPXB_BACMB_2_464_0 : Reasonable vina: -11.121
 title: BSD_ASPTTE_1_130_0 : Unreasonable vina: -7.492	 title: BSD_ASPTTE_1_130_0 : Reasonable vina: -8.786
 title: RGI_RAUSE_1_513_0 : Unreasonable vina: -10.06	 title: RGI_RAUSE_1_513_0 : Reasonable vina: -11.978
 title: QPCT_HUMAN_33_361_0 : Unreasonable vina: -7.531	 title: QPCT_HUMAN_33_361_0 : Reasonable vina: -8.356
 title: GUX1_HYPJE_18_451_0 : Unreasonable vina: -7.25	 title: GUX1_HYPJE_18_451_0 : Reasonable vina: -8.375
 title: UPPS_ECOLI_1_253_0 : Unreasonable vina: -7.288	 title: UPPS_ECOLI_1_253_0 : Reasonable vina: -8.315

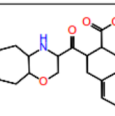
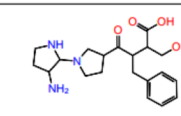
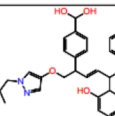
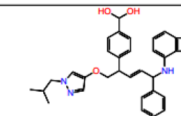
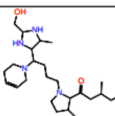
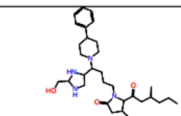
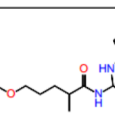
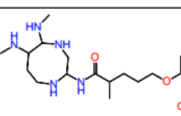
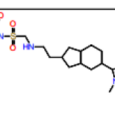
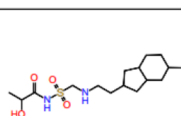
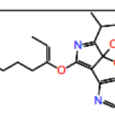
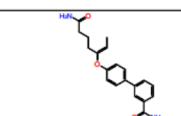
Supporting molecule

CIDD output

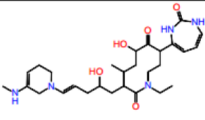
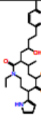
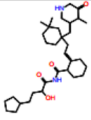
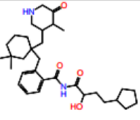
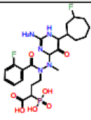
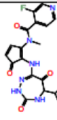
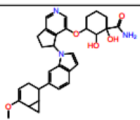
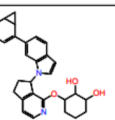
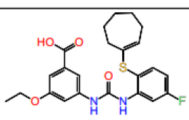
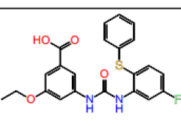
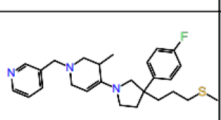
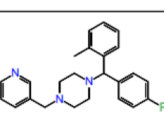
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 title: NOS2_HUMAN_78_505_0 : Unreasonable vina: -10.504	 title: NOS2_HUMAN_78_505_0 : Reasonable vina: -11.006
 title: BTRN_BACCI_2_250_0 : Unreasonable vina: -4.306	 title: BTRN_BACCI_2_250_0 : Reasonable vina: -11.729
 title: ACE_HUMAN_650_1230_0 : Unreasonable vina: -9.498	 title: ACE_HUMAN_650_1230_0 : Reasonable vina: -10.987
 title: AKT1_HUMAN_1_137_0 : Unreasonable vina: -11.185	 title: AKT1_HUMAN_1_137_0 : Reasonable vina: -11.293
 title: BAPA_SPHXN_30_402_0 : Unreasonable vina: -7.681	 title: BAPA_SPHXN_30_402_0 : Reasonable vina: -8.683

Supporting molecule

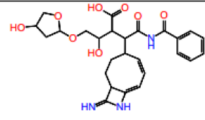
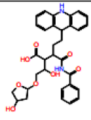
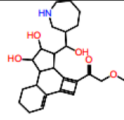
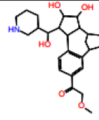
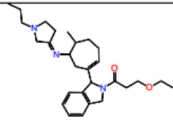
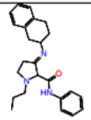
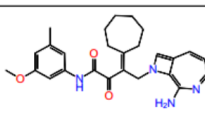
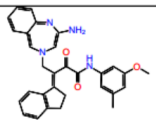
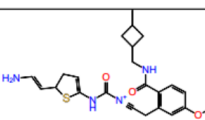
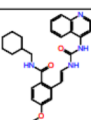
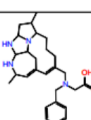
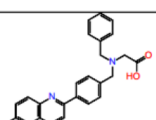
CIDD output

 title: ATS5_HUMAN_262_480_0 : Unreasonable vina: -8.133	 title: ATS5_HUMAN_262_480_0 : Reasonable vina: -8.863
 title: NOS2_HUMAN_78_505_0 : Unreasonable vina: -10.76	 title: NOS2_HUMAN_78_505_0 : Reasonable vina: -12.037
 title: ACE_HUMAN_650_1230_0 : Unreasonable vina: -8.564	 title: ACE_HUMAN_650_1230_0 : Reasonable vina: -10.503
 title: ACE_HUMAN_650_1230_0 : Unreasonable vina: -8.69	 title: ACE_HUMAN_650_1230_0 : Reasonable vina: -8.905
 title: TBK1_HUMAN_1_303_0 : Unreasonable vina: -7.693	 title: TBK1_HUMAN_1_303_0 : Reasonable vina: -8.868
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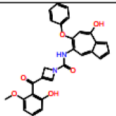
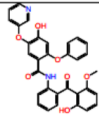
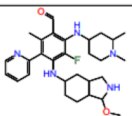
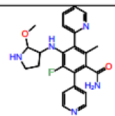
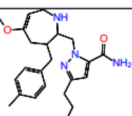
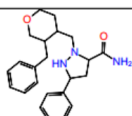
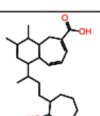
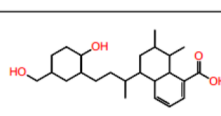
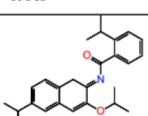
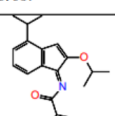
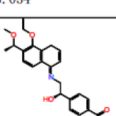
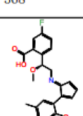
Supporting molecule CIDD output

 <p>title: PHKG1_RABIT_6_296_ATPsite_0 : Unreasonable vina: -8.922</p>	 <p>title: PHKG1_RABIT_6_296_ATPsite_0 : Reasonable vina: -9.205</p>
 <p>title: RGI_RAUSE_1_513_0 : Unreasonable vina: -10.484</p>	 <p>title: RGI_RAUSE_1_513_0 : Reasonable vina: -11.024</p>
 <p>title: CD38_HUMAN_44_300_0 : Unreasonable vina: -8.72</p>	 <p>title: CD38_HUMAN_44_300_0 : Reasonable vina: -9.327</p>
 <p>title: XANLY_BACGL_26_777_0 : Unreasonable vina: -9.053</p>	 <p>title: XANLY_BACGL_26_777_0 : Reasonable vina: -9.483</p>
 <p>title: PPIA_HUMAN_1_165_0 : Unreasonable vina: -8.023</p>	 <p>title: PPIA_HUMAN_1_165_0 : Reasonable vina: -8.605</p>
 <p>title: SQHC_ALIAD_1_631_0 : Unreasonable vina: -11.51</p>	 <p>title: SQHC_ALIAD_1_631_0 : Reasonable vina: -14.292</p>

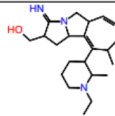
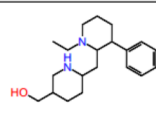
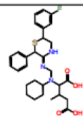
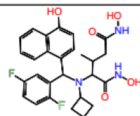
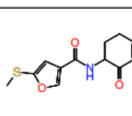
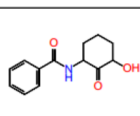
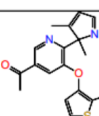
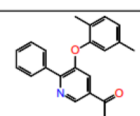
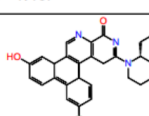
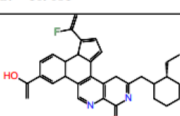
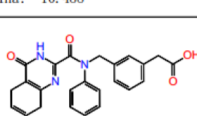
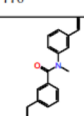
Supporting molecule CIDD output

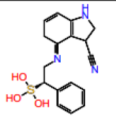
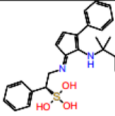
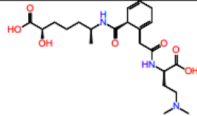
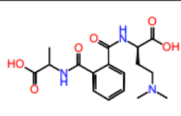
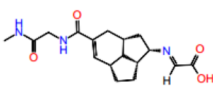
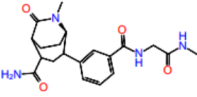

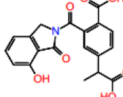
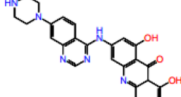
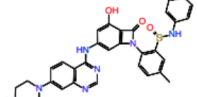
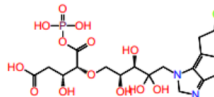
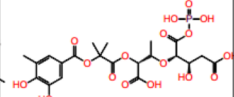
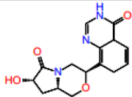
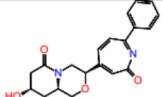
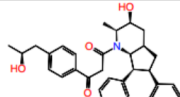
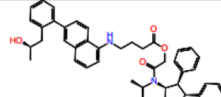
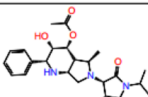
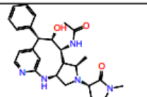



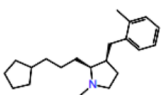


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 <p>title: DPP2_HUMAN_27_492_0 : Unreasonable vina: -9.855</p>	 <p>title: DPP2_HUMAN_27_492_0 : Reasonable vina: -11.224</p>
 <p>title: PTGIS_HUMAN_20_500_0 : Unreasonable vina: -8.318</p>	 <p>title: PTGIS_HUMAN_20_500_0 : Reasonable vina: -9.448</p>
 <p>title: PPIA_HUMAN_1_165_0 : Unreasonable vina: -8.777</p>	 <p>title: PPIA_HUMAN_1_165_0 : Reasonable vina: -10.083</p>
 <p>title: HMD_METJA_1_358_0 : Unreasonable vina: -8.349</p>	 <p>title: HMD_METJA_1_358_0 : Reasonable vina: -9.593</p>
 <p>title: KS6A3_HUMAN_41_357_0 : Unreasonable vina: -8.967</p>	 <p>title: KS6A3_HUMAN_41_357_0 : Reasonable vina: -11.101</p>

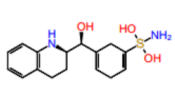
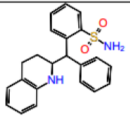
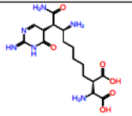
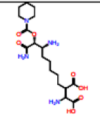
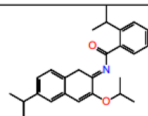
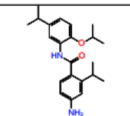
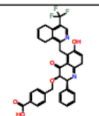
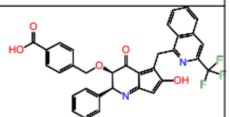
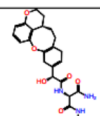
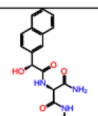
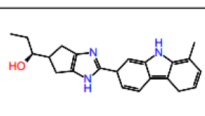
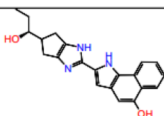
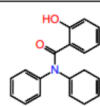
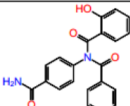
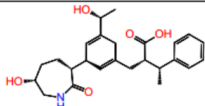
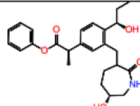
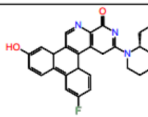
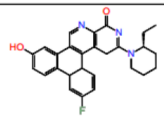
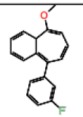
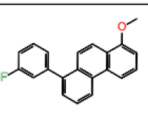
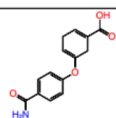
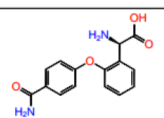
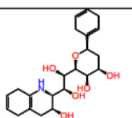
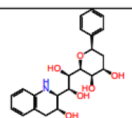
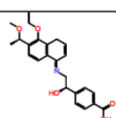
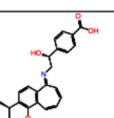
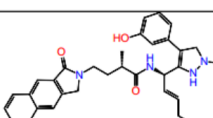
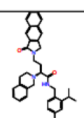
Supporting molecule CIDD output

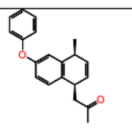
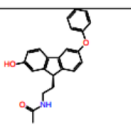
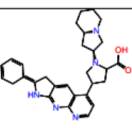
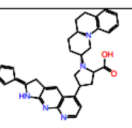
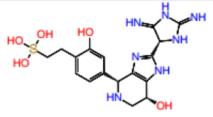
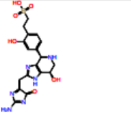
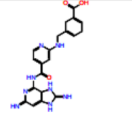
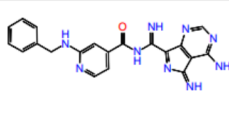
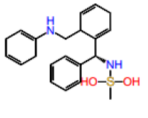
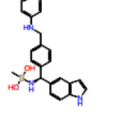
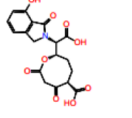
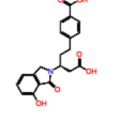
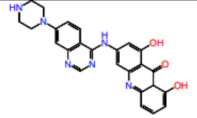
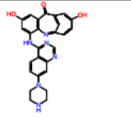
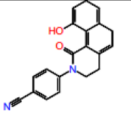
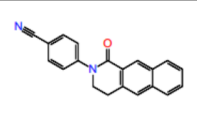
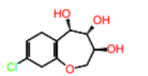
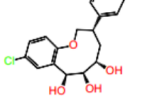
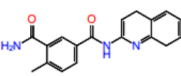
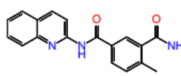
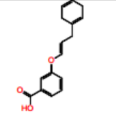
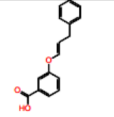
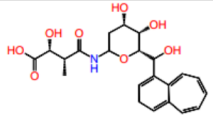
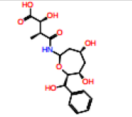
	
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title: NR1H4_HUMAN_258_486_0 : Unreasonable vina: -3.528	title: NR1H4_HUMAN_258_486_0 : Reasonable vina: -14.043
	
title: SDIA_ECOLI_1_171_0 : Unreasonable vina: -10.997	title: SDIA_ECOLI_1_171_0 : Reasonable vina: -13.15
	
title: HDHA_ECOLI_1_255_0 : Unreasonable vina: -9.845	title: HDHA_ECOLI_1_255_0 : Reasonable vina: -9.957
	
title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -8.034	title: IDHP_HUMAN_40_452_0 : Reasonable vina: -10.368
	
title: AKT1_HUMAN_1_137_0 : Unreasonable vina: -10.124	title: AKT1_HUMAN_1_137_0 : Reasonable vina: -10.13

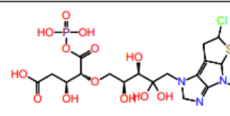
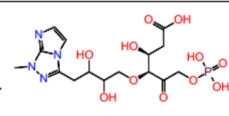
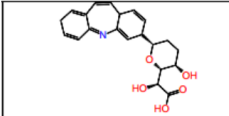
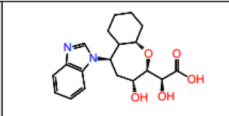
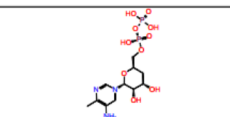
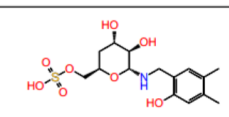
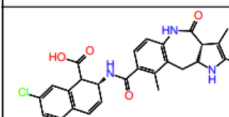
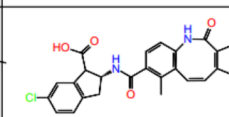
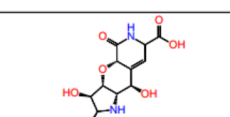
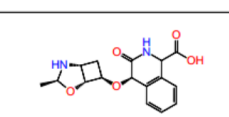
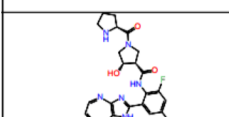
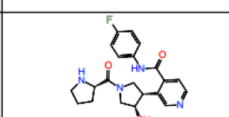
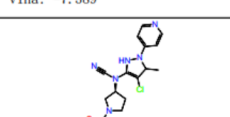
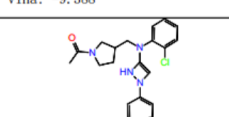
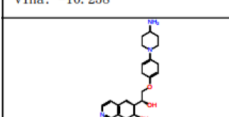
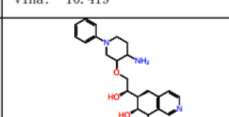
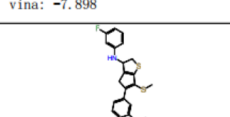
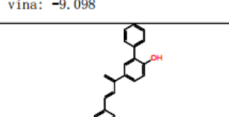
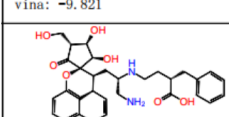
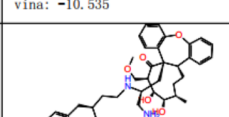
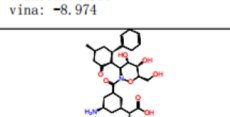
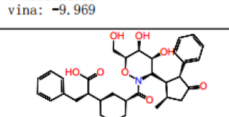
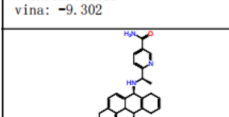
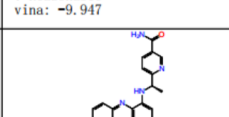
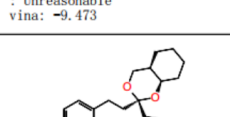
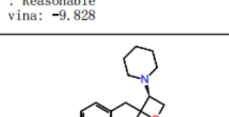
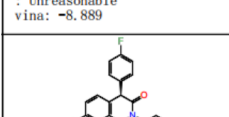
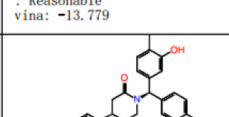
Supporting molecule CIDD output

	
title: DYRK2_HUMAN_145_550_0 : Unreasonable vina: -6.725	title: DYRK2_HUMAN_145_550_0 : Reasonable vina: -9.337
	
title: BACE2_HUMAN_76_460_0 : Unreasonable vina: -9.145	title: BACE2_HUMAN_76_460_0 : Reasonable vina: -9.806
	
title: TRAR_RHIRD_1_234_0 : Unreasonable vina: -8.935	title: TRAR_RHIRD_1_234_0 : Reasonable vina: -12.018
	
title: UPPS_ECOLI_1_253_0 : Unreasonable vina: -7.717	title: UPPS_ECOLI_1_253_0 : Reasonable vina: -10.031
	
title: ABL2_HUMAN_274_551_0 : Unreasonable vina: -10.488	title: ABL2_HUMAN_274_551_0 : Reasonable vina: -10.776
	
title: : Unreasonable vina: -10.487	title: : Reasonable vina: -10.893

Supporting molecule	CIDD output	Supporting molecule	CIDD output
 <p>title: MURA_ECOLI_1_419_catalytic_0 : Unreasonable vina: -8.295</p>	 <p>title: MURA_ECOLI_1_419_catalytic_0 : Reasonable vina: -9.241</p>	 <p>title: BGL07_ORYSJ_25_504_0 : Unreasonable vina: -8.187</p>	 <p>title: BGL07_ORYSJ_25_504_0 : Reasonable vina: -8.434</p>
 <p>title: BGL07_ORYSJ_25_504_0 : Unreasonable vina: -8.028</p>	 <p>title: BGL07_ORYSJ_25_504_0 : Reasonable vina: -9.632</p>	 <p>title: PAC_ECOLX_27_846_0 : Unreasonable vina: -8.228</p>	 <p>title: PAC_ECOLX_27_846_0 : Reasonable vina: -8.313</p>
 <p>title: PAC_ECOLX_27_846_0 : Unreasonable vina: -9.538</p>	 <p>title: PAC_ECOLX_27_846_0 : Reasonable vina: -10.042</p>	 <p>title: P2Y12_HUMAN_1_342_0 : Unreasonable vina: -8.514</p>	 <p>title: P2Y12_HUMAN_1_342_0 : Reasonable vina: -8.942</p>
 <p>title: EXG1_CANAL_41_438_0 : Unreasonable vina: -9.965</p>	 <p>title: EXG1_CANAL_41_438_0 : Reasonable vina: -10.569</p>	 <p>title: FKB1A_HUMAN_2_108_0 : Unreasonable vina: -7.899</p>	 <p>title: FKB1A_HUMAN_2_108_0 : Reasonable vina: -8.786</p>
 <p>title: CHIB_SERMA_1_499_0 : Unreasonable vina: -9.972</p>	 <p>title: CHIB_SERMA_1_499_0 : Reasonable vina: -10.354</p>	 <p>title: KS6A3_HUMAN_41_357_0 : Unreasonable vina: -7.827</p>	 <p>title: KS6A3_HUMAN_41_357_0 : Reasonable vina: -8.545</p>
 <p>title: SDIA_ECOLI_1_171_0 : Unreasonable vina: -10.933</p>	 <p>title: SDIA_ECOLI_1_171_0 : Reasonable vina: -11.339</p>	 <p>title: GUX1_HYPJE_18_451_0 : Unreasonable vina: -10.767</p>	 <p>title: GUX1_HYPJE_18_451_0 : Reasonable vina: -12.3</p>

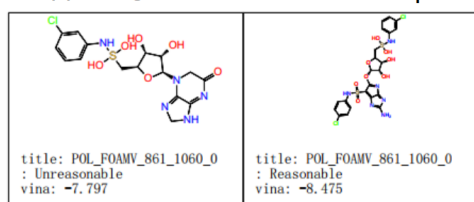
Supporting molecule	CIDD output	Supporting molecule	CIDD output
 title: HDHA_ECOLI_1_255_0 : Unreasonable vina: -8.511	 title: HDHA_ECOLI_1_255_0 : Reasonable vina: -9.995	 title: ODBB_THET8_1_324_0 : Unreasonable vina: -9.002	 title: ODBB_THET8_1_324_0 : Reasonable vina: -9.322
 title: IDHP_HUMAN_40_452_0 : Unreasonable vina: -8.039	 title: IDHP_HUMAN_40_452_0 : Reasonable vina: -9.819	 title: CPXB_BACMB_2_464_0 : Unreasonable vina: -9.196	 title: CPXB_BACMB_2_464_0 : Reasonable vina: -12.034
 title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -9.495	 title: NOS1_HUMAN_302_723_0 : Reasonable vina: -9.579	 title: NOS1_HUMAN_302_723_0 : Unreasonable vina: -10.062	 title: NOS1_HUMAN_302_723_0 : Reasonable vina: -10.305
 title: CAT_ECOLX_1_219_0 : Unreasonable vina: -9.2	 title: CAT_ECOLX_1_219_0 : Reasonable vina: -13.057	 title: BSD_ASPTE_1_130_0 : Unreasonable vina: -8.807	 title: BSD_ASPTE_1_130_0 : Reasonable vina: -9.501
 title: ABL2_HUMAN_274_551_0 : Unreasonable vina: -10.702	 title: ABL2_HUMAN_274_551_0 : Reasonable vina: -11.583	 title: NQO1_HUMAN_2_274_0 : Unreasonable vina: -9.262	 title: NQO1_HUMAN_2_274_0 : Reasonable vina: -10.424
 title: BTRN_BACCI_2_250_0 : Unreasonable vina: -8.786	 title: BTRN_BACCI_2_250_0 : Reasonable vina: -8.951	 title: NAGZ_VIBCH_1_330_0 : Unreasonable vina: -7.206	 title: NAGZ_VIBCH_1_330_0 : Reasonable vina: -8.307
 title: AKT1_HUMAN_1_137_0 : Unreasonable vina: -10.1	 title: AKT1_HUMAN_1_137_0 : Reasonable vina: -11.478	 title: AKT1_HUMAN_1_137_0 : Unreasonable vina: -12.405	 title: AKT1_HUMAN_1_137_0 : Reasonable vina: -13.048

Supporting molecule	CIDD output	Supporting molecule	CIDD output
 title: PA21B_PIG_23_146_0 : Unreasonable vina: -8.391	 title: PA21B_PIG_23_146_0 : Reasonable vina: -10.029	 title: PHKG1_RABIT_6_296_ATPsite_0 : Unreasonable vina: -10.937	 title: PHKG1_RABIT_6_296_ATPsite_0 : Reasonable vina: -13.466
 title: M3K14_HUMAN_321_678_0 : Unreasonable vina: -8.948	 title: M3K14_HUMAN_321_678_0 : Reasonable vina: -9.001	 title: M3K14_HUMAN_321_678_0 : Unreasonable vina: -9.44	 title: M3K14_HUMAN_321_678_0 : Reasonable vina: -8.899
 title: PTGIS_HUMAN_20_500_0 : Unreasonable vina: -7.955	 title: PTGIS_HUMAN_20_500_0 : Reasonable vina: -9.193	 title: PAC_ECOLX_27_846_0 : Unreasonable vina: -7.907	 title: PAC_ECOLX_27_846_0 : Reasonable vina: -8.704
 title: PAC_ECOLX_27_846_0 : Unreasonable vina: -9.272	 title: PAC_ECOLX_27_846_0 : Reasonable vina: -9.421	 title: TNKS2_HUMAN_948_1162_0 : Unreasonable vina: -10.215	 title: TNKS2_HUMAN_948_1162_0 : Reasonable vina: -12.537
 title: XANLY_BACGL_26_777_0 : Unreasonable vina: -6.991	 title: XANLY_BACGL_26_777_0 : Reasonable vina: -8.994	 title: PPIA_HUMAN_1_165_0 : Unreasonable vina: -9.243	 title: PPIA_HUMAN_1_165_0 : Reasonable vina: -9.435
 title: PPIA_HUMAN_1_165_0 : Unreasonable vina: -7.765	 title: PPIA_HUMAN_1_165_0 : Reasonable vina: -8.447	 title: P2Y12_HUMAN_1_342_0 : Unreasonable vina: -8.744	 title: P2Y12_HUMAN_1_342_0 : Reasonable vina: -10.352

Supporting molecule	CIDD output	Supporting molecule	CIDD output
 <p>title: P2Y12_HUMAN_1_342_0 : Unreasonable vina: -8.31</p>	 <p>title: P2Y12_HUMAN_1_342_0 : Reasonable vina: -9.509</p>	 <p>title: EXG1_CANAL_41_438_0 : Unreasonable vina: -10.072</p>	 <p>title: EXG1_CANAL_41_438_0 : Reasonable vina: -10.17</p>
 <p>title: MENE_BACSU_2_486_0 : Unreasonable vina: -8.029</p>	 <p>title: MENE_BACSU_2_486_0 : Reasonable vina: -8.629</p>	 <p>title: SQHC_ALIAD_1_631_0 : Unreasonable vina: -9.519</p>	 <p>title: SQHC_ALIAD_1_631_0 : Reasonable vina: -12.291</p>
 <p>title: CHIB_SERMA_1_499_0 : Unreasonable vina: -7.389</p>	 <p>title: CHIB_SERMA_1_499_0 : Reasonable vina: -9.388</p>	 <p>title: SIR3_HUMAN_117_398_0 : Unreasonable vina: -10.258</p>	 <p>title: SIR3_HUMAN_117_398_0 : Reasonable vina: -10.419</p>
 <p>title: DYRK2_HUMAN_145_550_0 : Unreasonable vina: -7.898</p>	 <p>title: DYRK2_HUMAN_145_550_0 : Reasonable vina: -9.098</p>	 <p>title: NOS3_HUMAN_65_480_0 : Unreasonable vina: -9.821</p>	 <p>title: NOS3_HUMAN_65_480_0 : Reasonable vina: -10.535</p>
 <p>title: NR1H4_HUMAN_258_486_0 : Unreasonable vina: -8.974</p>	 <p>title: NR1H4_HUMAN_258_486_0 : Reasonable vina: -9.969</p>	 <p>title: BACE2_HUMAN_76_460_0 : Unreasonable vina: -9.302</p>	 <p>title: BACE2_HUMAN_76_460_0 : Reasonable vina: -9.947</p>
 <p>title: BACE2_HUMAN_76_460_0 : Unreasonable vina: -9.473</p>	 <p>title: BACE2_HUMAN_76_460_0 : Reasonable vina: -9.828</p>	 <p>title: SDIA_ECOLI_1_171_0 : Unreasonable vina: -8.889</p>	 <p>title: SDIA_ECOLI_1_171_0 : Reasonable vina: -13.779</p>
 <p>title: TRAR_RHIRD_1_234_0 : Unreasonable vina: -10.182</p>	 <p>title: TRAR_RHIRD_1_234_0 : Reasonable vina: -13.112</p>	 <p>title: TRAR_RHIRD_1_234_0 : Unreasonable vina: -9.69</p>	 <p>title: TRAR_RHIRD_1_234_0 : Reasonable vina: -15.856</p>

Supporting molecule

CIDD output



Supporting molecule

CIDD output

