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REPURPOSING OF ZAFIRLUKAST A LEUKOTRIENE RECEPTOR ANTAGONIST FOR TREATMENT OF PROTENURIA

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ABSTRACT

Proteinuria is associated with heart disease, chronic kidney disease (CKD), and increased mortality rates. It serves as a vital marker for renal failure. Due to the limited effectiveness of existing treatments like angiotensin receptor blockers (ARBs) and angiotensin-converting enzyme (ACE) inhibitors, there is a need for new therapeutic approaches. This study employs ligandbased virtual screening and molecular docking to explore the repurposing of medications for treating proteinuria. FILSPARI has been chosen as the primary ligand due to its specific renal effects, medicinal significance, and pharmacological profile. The outcomes show that leukotriene receptor antagonists, ARBs, and PDE5 inhibitors might occur excellent repurposed medicines for proteinuria. With regard to its excellent receptor binding and anti-inflammatory properties, zafirlukast particular demonstrated significant potential. To assess the therapeutic survival, extensive ADMET research and simulations involving mole must be done. This study widens up options into further preclinical and clinical validation of identified therapeutic candidates with valuable insights on unique kidneys protection techniques.

1.INTRODUCTION

The presence of a large quantity of protein in the urine, typically estimated at over 150 mg/day in adults, has been identified as proteinuria [1]. It generally suggests underlying renal diseases thus represents an important indication overall kidney health. [2] Clinically, proteinuria is related to serious risks that include coronary heart disease, chronic renal failure (CKD), and higher rates of mortality. [3] It is frequently assessed in patients with diabetes, hypertension, and other systemic disorders and is an important aspect of a check of renal function. [4]

Proteinuria includes an array of causes, which fall in three different groups: prerenal, renal, and post-renal.[5] Temporary proteinuria from concentrated urine may be related to normal pre-renal reasons, which include dehydration, fever, or rapid metabolism.[6] Intrinsic kidney diseases such as diabetic nephropathy, in which glomerular injury from hyperglycemia promotes protein excretion, are instance of renal causes.[7] Another symptom of glomerulonephritis, diseases resulting category of glomerular inflammation, is significant protein leakage.[8] Edema, significant proteinuria (>3.5)g/day), and hypoalbuminemia are additional manifestations of nephrotic syndrome. Post-renal causes included urinary tract infections or challenges that might lead to protein loss. [9]

Treating the underlying causes is the primary aim of proteinuria management. Angiotensin receptor blockers (ARBs) and angiotensin-converting enzyme (ACE)

inhibitors are two kinds of present medical treatments that are widely employed for minimizing proteinuria in diabetic nephropathy and hypertension. [10] These medicines might not always employment, nonetheless, which can have adverse reactions such renal impairment hyperkalaemia. For and treated autoimmune-related glomerulonephritis, corticosteroids and immunosuppressant are given; yet, there is a high chance of negative consequences. [11] Many patients still have persistent proteinuria in spite of these treatments, requiring for inquiry of substitute therapeutic agents. [12]

The lipoxygenase pathway turns arachidonic acid in bioactive lipids known leukotrienes. Cysteinyl leukotrienes (CysLTs) were some of those substances that are essential to renal physiology. [13] CysLT1 and CysLT2, the primary leukotriene receptors, induce physiologic effects such vasodilation, enhanced vascular permeability, and inflammatory cell chemotaxis. Zafirlukast in addition to leukotriene receptor antagonists (LTRAs) inhibit downstream chain reactions of signaling by stopping leukotrienes in binding to their respective receptors. Key factors in the etiology of kidney damage, like inflammation, vascular permeability, and fibrosis, are impacted with this antagonism connection. [14] Leukotrienes proteinuria and promote exacerbate inflammation glomerular in kidney disease, rendering LTRAs an ideal target fortherapeutic. [15]

Asthma medication is the main application in zafirlukast, a selective antagonist of the CysLT1 receptor. [16]

With plasma concentrations peak occurring within three hours, it has a favourable pharmacokinetic profile and is taken orally. decreases It bronchoconstriction and inflammation by preventing the action of leukotrienes by connecting to CysLT1 receptors. Its mechanism of action shows potential utility in renal conditions, but its original use in respiratory disease. In agreement with scientific studies, zafirlukast is a good asthma drug that enhances lung function and minimizes bronchial hyper activity. [17] In view of its success of managing inflammation and an allergy responses study of additional inflammatory conditions, including as kidney conditions, has increased. Studies on it has demonstrated that it is safe and acceptable, thus rendering it an acceptable choice for repurposing. [18]

The anti-inflammatory effects zafirlukast constitute the idea behind its repurposing for proteinuria. By sustaining glomerular structure and function, reducing leukotrienes' action may help minimize proteinuria when their presence is critical to causing renal inflammation and damage. Zafirlukast can offer a novel therapeutic approach for patients with proteinuria by targeting the inflammatory pathways connected with kidney failure. [19]

This is increasing proof that proteinuria in a variety of kidney diseases is strongly correlated with elevated leukotriene levels. Studies has shown an association among higher levels of proteinuria in diabetic nephropathy with increased excretion of urine steroid hormones. In addition, leukotriene manufacturing decrease was shown in animal models to reduce inflammation and proteinuria in glomerulonephritis. [20]

2.MATERIALS AND METHODS

2.1 Ligand-Based Virtual Screening

The Drug Rep website is a powerful platform for drug repurposing that employs a ligand-based virtual screening approach. Researchers can evaluate ligand similarity using a wide range of molecular descriptors and fingerprints, drawing from an extensive database of FDA-approved drugs and molecular targets. One of the screening methods available on the platform is the Morgan Fingerprint, which effectively identifies compounds by encoding chemical substructures into a bit vector format. This particularly method is useful discovering chemically related compounds, as it captures both local and global physical Additionally, properties. the features molecular docking tools that allow for computational binding tests to validate the identified substances.

2.2 Selection of Filspari as a Ligand

The Drug Rep website is a powerful platform for drug repurposing that employs a ligand-based virtual screening approach. Researchers can evaluate ligand similarity using a wide range of molecular descriptors and fingerprints from an extensive database of FDA-approved drugs and molecular targetsOne of the screening methods offered on the platform is the Morgan Fingerprint, which accurately identifies compounds by converting chemical substructures into a bit vector format. This approach is beneficial uncovering chemically related compounds, as it encompasses both local

and global physical properties. Furthermore, the website includes molecular docking tools that enable computational binding tests to confirm the identified substances.

2.3 Docking studies

For molecular docking, we used Cb-Dock software to predict how ligands bind to their targets and their binding affinities. This intuitive docking tool combines several scoring functions and allows for flexible ligand docking, which accommodates changes in conformation during binding. To improve the study, we referenced the 5XPR approved drug library. This library includes a carefully curated selection of FDA-approved compounds from various drug classes and mechanisms of action. By docking Filspari against this library, we aimed to identify compounds with similar

binding profiles or therapeutic effects, which could uncover new applications for Filspari or related molecules (Table 1).

2.4 Data analysis

The results from screening and docking were checked based on certain rules, such as how well the compounds stick, their interaction profiles, and similarity scores. Compounds with lower binding energies were chosen first because they show stronger connections with the target. Interaction profiles, like hydrogen bonds and hydrophobic interactions, were looked at to check how stable the binding is. Also, compounds that looked a lot like Filspari were picked for more checks. Data work was done using tools like R and Python. Simple stats summed up what was found, and images like heat maps and scatter plots showed how compounds are related. The right stats tests made sure the data reading was clear and important (Figure 1).

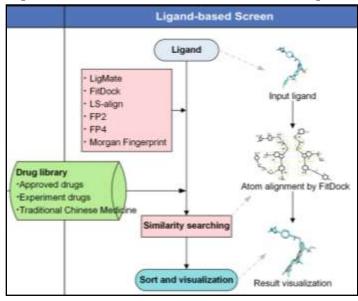


Figure 1: Schematic of ligand-based virtual screening, where input ligands are aligned using various algorithms and searched against diverse drug libraries, with results sorted and visualized.

3.RESULT AND DISCUSSION

3.1 Result of ligand based repurposing

Table 1: Justification for selecting FILSPARI as primary ligand for designing new agent targeting kidney failure

Justification	Details			
Mechanistic Insights	Influences renal pathways, particularly in glomerular filtration and			
Mechanistic hisights	tubular reabsorption.			
Pharmacological Profile	Well-characterized pharmacokinetics and pharmacodynamics support			
T Harmacological T Tome	understanding of dosing, side effects, and drug interactions.			
Target Specificity	Selectively binds to renal receptors, allowing targeted therapeutic			
rarget specificity	strategies with minimal off-target effects.			
Clinical Evidence	Existing clinical data supports efficacy in managing renal conditions,			
Cililical Evidence	aiding in the development of new agents.			
Potential for Novel	Can serve as a template for designing derivatives or formulations to			
Formulations	enhance renal protective effects or mitigate proteinuria.			
Addressing Unmet	Addresses the significant need for effective therapies targeting			
Needs	proteinuria in various kidney diseases.			

3.2 Result of ligand based screening using the DrugRep platform

Table 2: Binding score and target interaction of various compound

Sr.n	Compoun	Name	Scor	Sr.n	Compoun	Name	Scor
О	ds	Name	e	O	ds	Name	e
1 DB01029	Irbesartan	0.47	11	DB00706	Tamsulosin	0.25	
1	1 DB01029	nvesarian	9	11	DD00700	Tarrisulosiri	5
2 DB01251	DB01251	Gliquidone	0.27	12	DB12500	Fedratinib	0.25
	2 DB01231		6	12			1
3 DB00678	Losartan	0.27	13	3 DB04855	Dronedaro	0.25	
		2	13		ne	1	
4 DB00932	Tipranavir	0.26	14	DB11591	Bilastine	0.24	
		9				9	
7	5 DB06267	Udenafil	0.26	15	DB00203	Sildenafil	0.24
			4				9
6	DB00549	19 Zafirlukast	0.26	16	DB00275	Olmesartan	0.24
6 DD00549	Zamiukasi	3	10	DD00273	OfficeSartaff	7	
8	DB08822	Azilsartanmedoxo	0.26	17	DB00912	Repaglinide	0.24
		mil	3				7
9	DB08439	Parecoxib	0.26	18	DB00216	Eletriptan	0.24

			3				7
10 DB00862	Vardenafil	0.25	19	DB01623	Thiothixene	0.24	
		9	19			4	
DB00690	Flurazepam	0.25	20	DB09063	Ceritinib	0.24	
		8				3	

Table 2 shows how well different drugs can stick to a certain protein. Lower scores mean they stick better. Irbesartan (DB01029) got the best score, 0.479, which shows it sticks very well. This makes sense because it helps with high blood pressure and kidney issues. Other drugs like Losartan (DB00678) and Olmesartan (DB00275), which are also for blood pressure, had good scores too. Gliquidone (DB01251), for diabetes, and Tipranavir (DB00932), for HIV, had okay scores, suggesting they might work on those diseases in the body. Frequent exercise has many benefits for the body

including better heart health and lower risk of many diseases. A study by Nystoriak et al. in 2018 found that regular exercise is linked to lower rates of heart-related deaths and fewer heart diseases. Exercise helps manage or change many risk factors for heart disease like high blood pressure and high cholesterol levels. Also, both aerobic and strength training can cause changes in the body that improve blood vessel and metabolic health, helping to prevent diseases.

3.3 Docking studies and validation process result:

Table 3: Validation metrics from PDB-REDO

Validation Metrics	Original	PDB-REDO			
Crystallographic refinement					
R	0.2646	0.2646			
R-free	0.3085	0.3104			
Bond length RMS Z-score	0.217	0.541			
Bond angle RMS Z-score	0.517	0.652			
Model quality raw scores percentiles					
Ramachandran plot normality	20	18			
Rotamer normality	2	5			
Coarse packing	45	41			
Fine packing	42	60			
Bump severity	17	42			
Hydrogen bond satisfaction	86	86			

The update checks from PDB-REDO show that some parts of the structure got better, while the overall quality of the crystal work stayed the same. The main score didn't change, it's still 0.2646. But a secondary score went up just a little, from 0.3085 to

0.3104, which means the minor changes made did not mess up the model. When looking at how the bonds are set up, the scores went up a bit for both bond lengths (from 0.217 to 0.541) and bond angles (from 0.517 to 0.652). This suggests that there are

small steps away from the perfect setup, which might be a balance to fit the model better. The overall scores for quality show different results; the score for how the model's shapes fit a known good pattern went down a bit from 20 to 18, but the score for how the side pieces turn improved from 2 to 5, showing better side placements. The general packing score went down from 45 to 41, but the detailed packing got a lot better, going from 42 to 60, showing that the pieces in the model are set up better now. The bump severity score, which tells us

about clashing, went from 17 to 42, possibly due to trying to optimize the model. Hydrogen bond content stays the same at 86, showing that the model's network of hydrogen bonds is kept well. Overall, PDB-REDO improves the shape and packing of side chains but also slightly raises steric clashes and changes in bond shapes. This calls for more checks to make sure that the updated model still fits with what happens in real life (Table 3).

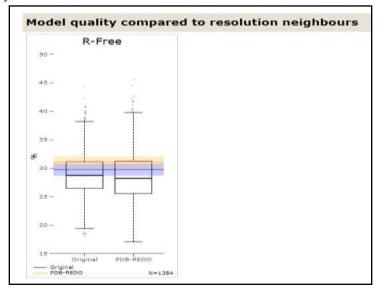


Figure 2: Comparison of R-Free Values between Original and PDB-REDO Models

The box plot shows the R-free values for the original and PDB-REDO models compared to other similar structures (N=1384). The middle R-free values for both models are close, with a small rise in PDB-REDO. The middle 50% of values show some differences for both, with PDB-REDO having a bit less spread, showing it's more consistent in its adjustments (Figure 2). The end points show that both models have

some unusual values, but the overall spread is within normal limits. The colored bands (blue for the original and orange for PDB-REDO) show how these values stack up against similar ones. The close R-free values suggest that PDB-REDO hasn't greatly changed the refinement quality, but just tweaked some structure details while keeping overall accuracy similar.

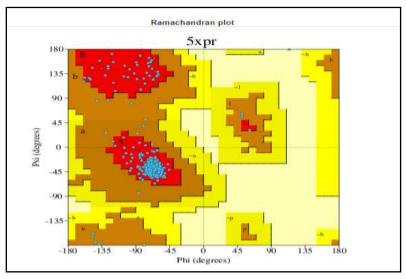


Figure 3: Ramachandran Plot Analysis of 5XPR

The Ramachandran plot for the 5XPR structure shows the spread of ϕ (phi) and ψ (psi) angle twists of the protein backbone, with different areas showing allowed, favored, and outlier shapes. The red and brown areas show the most okay and allowed shapes, while the yellow areas show less okay or not allowed spots (Figure 3). Most of the blue dots (which stand for single parts) group within the red and brown areas, showing that the backbone

shape fits well with shapes that work well with space. But, a few parts show up in not allowed areas, pointing out possible structural stress or mistakes in the model. These outliers might need more fix-up or check-up to make sure of structural soundness. On the whole, the plot hints that the 5XPR model has mostly good backbone form, with a small count of parts possibly needing more work to make better.

3.4 Docking result:

Table 4: Binding Affinity Analysis of Drugbank Compound to Target pocket: Identification of Potential Drug Candidates

Sr. No	Compound	Pocket	Score	Sr. No	Compound	Pocket	Score
1	Irbesartan	C1	-8.3	11	Tamsulosin	C2	-6.7
2	Gliquidone	C2	-8.7	12	Fedratinib	C1	-8.7
3	Losartan	C1	-7.6	13	Dronedarone	C2	-6.3
4	Tipranavir	C1	-8.6	14	Bilastine	C1	-8.4
5	Udenafil	C2	-7.6	15	Sildenafil	C2	-8.2
6	Zafirlukast	C1	-9.8	16	Olmesartan	C1	-7.8
7	Azilsartanmedoxomil	C1	-9.6	17	Repaglinide	C1	-8.0
8	Parecoxib	C1	-7.9	18	Eletriptan	C4	-7.7
9	Vardenafil	C1	-8.0	19	Thiothixene	C1	-8.6
10	Flurazepam	C2	-7.3	20	Ceritinib	C1	-8.2

The docking study looks at how well different compounds bind to various spots, with lower scores showing stronger bonds. Among the compounds, Zafirlukast (-9.8, C1) and Azilsartanmedoxomil (-9.6, C1) have the highest binding strengths, showing strong ties with the target protein. Other compounds like Tipranavir (-8.6, C1), Bilastine (-8.4, C1), Ceritinib (-8.2, C1), and Sildenafil (-8.2, C2) also show good binding ability. Interestingly, Fedratinib (-8.7, C1) and Gliquidone (-8.7, C2) show strong affinities in different spots, indicating they

prefer multiple binding sites. Tamsulosin (-6.7, C2) and Dronedarone (-6.3, C2) show the weakest bindings, suggesting less stability compared to other compounds. The spread of compounds across different pockets (C1, C2, and C4) shows variation in how ligands interact with the structure. The compounds that stick strongly, especially those in C1, could be good options to look at for reusing as drugs. The compounds that don't score as high might need changes or different ways of targeting (Table 4).

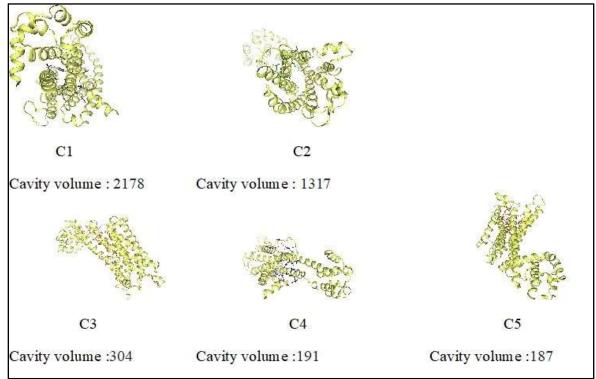


Figure 4: Visualisation of Five Binding Pocket (Curpocket Id C1-C5) On Target Protein

The picture (Figure 4) shows five protein shapes (C1–C5) with spaces inside them ranging from 187 cubic Å to 2178 cubic Å. C1, with the biggest space (2178 cubic Å), suggests it can bind with larger things or be flexible in interactions. C2 (1317 cubic Å) has a medium space, showing it can bind with things of moderate size. C3 (304 cubic

Å), C4 (191 cubic Å), and C5 (187 cubic Å) have smaller spaces, which means they bind with smaller, more specific things. These space sizes are important to know for seeing how proteins interact with other molecules, and can help in creating drugs where different-sized molecules may target these spaces for health benefits.

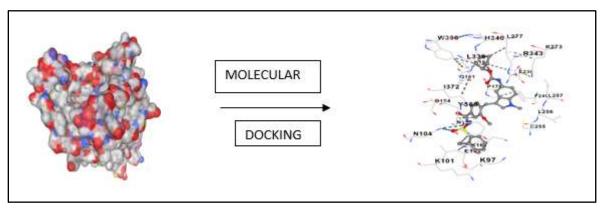


Figure 5: Molecular docking of Zafirlukast with Endothelian receptor

The picture (Figure 5) shows zafirlukast connecting with a cell receptor in 3D. On the left is the shape of the receptor, and on the right are the specific ways zafirlukast sticks to receptor parts. Molecular docking guesses how zafirlukast fits in the receptor's active spot, showing important links like hydrogen bonds. This helps understand how the drug sticks to the receptor and helps in making better drugs for treatment.

4 CONCLUSION

This study looked into new ways to find old drugs that could treat protein leaks in urine and kidney issues. FILSPARI was chosen as the main drug based on its known role in kidney functions, its well-understood drug actions, and how well it works in treating kidney conditions. Screening with the DrugRep tool showed that drugs like Irbesartan. Losartan, and Olmesartan (which all block angiotensin receptors), PDE5 blockers (like Sildenafil Vardenafil), reducing and drugs inflammation Zafirlukast (like and Parecoxib) are good options to consider using again for these health problems.

Docking studies gave deeper understanding of how well these compounds attach to proteins. Zafirlukast (-9.8 kcal/mol) and

Azilsartanmedoxomil (-9.6 kcal/mol) showed the strongest attachment, suggesting they could be good for treating kidney problems. We found five different binding spots (C1-C5) showing different ways ligands can attach. C1 (2178 ų) turned out to be the best spot for drug binding because it has the largest space and can fit different ligands well.

Structural checks with PDB-REDO confirm that the docking models are reliable, showing better side-chain shapes and closer atomic fits. However, small clashes and slight bond shape errors were seen. Analysis with a Ramachandran plot shows that the 5XPR model is mostly good, with most of its parts in the best shapes.

This research gives a strong reason to do more tests, both before and in clinics, on high-binding ligands, especially Zafirlukast and Azilsartanmedoxomil, for treating protein leaks in urine and kidney issues. Future work should look at molecule action over time and test drug profiles to back up these results and find new ways to help protect kidneys.

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