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Research Paper



Computer-aided drug repurposing for identification of potential therapeutic candidate for diabetes retinopathy

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Abstract

Diabetic Retinopathy (DR) is the leading cause of blindness in industrialized countries. Blood retinal barrier, polyol pathway, and protein kinase C activation pathway are the major pathways involved in DR. In this study, drug repurposing strategy using virtual screening to identify therapeutic candidates for treating DR was used. We selected six major proteins involved in three pathways in DR as potential targets through literature study: Vascular endothelial growth factor (VEGFR), Angiotensin-converting enzyme, TNF-a, Interleukin-1- β , Aldose reductase and Protein kinase C β . The pathogenesis study, connectivity map analysis, docking and interaction studies were conducted to elucidate the best-repurposed drugs for DR. Initial pathogenesis study of the six targets expounds inhibitory action of the proteins in the treatment of DR. Next, Connectivity Map analyses of these targets and the drugs explicate 66 drugs to be repurposed. Based on the docking and interaction studies, the best 19 drugs are proposed as the repurposing candidates for DR. After scrutiny, five drugs - Dovitinib, linifanib, regorafenib, sorafenib and brivanib-alaninate, which target VEGFR - a major target in blood retinal barrier pathway that is not involved in the treatment of diabetes and its related diseases - is proposed to be repurposed for the treatment of DR. To conclude, the study articulates that the Dovitinib, linifanib, regorafenib, sorafenib, and brivanib-alaninate drugs are appropriate to be repurposed for the treatment of DR. These drugs target the VEGFR pathway, which is one of the major pathways to be targeted for the early cure of DR. **Keywords:** Drug repurposing, diabetes retinopathy, BRB, docking and interaction study.

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I. Introduction

Diabetic retinopathy (DR) is still a prominent consequence of diabetes and the primary cause of blindness in adults around the world. Diabetes is a progressive disease that affects both Type I and Type II diabetics at any stage of the disease. Drug safety in diabetic retinopathy is a significant problem throughout the development of new medications. Thiazolidinediones, such as Rosiglitazone and Pioglitazone, are clinically available in India until 2010 [1]; hypoglycemic effects of Rosiglitazone were a success but had adverse effects like heart attack, sometimes leading to death, which led to the withdrawal of the drug [2]. Pioglitazone produced severe DME after two weeks of usage, with 10% of patients experiencing fluid retention, and the condition was shown to resolve following discontinuation [3]. Ten medications have been attempted for diabetic retinopathy in top pharmaceutical companies' current therapeutic research pipelines; just six medications survived the early stages of drug development (Phase I and II clinical trials), Phase III clinical trials, or post-market surveillance [4].

Laser has been used to treat DME for almost 30 years, however new research have called into consideration its significance in current pharmaceutical era. Most patients' eyesight improves with aggressive treatment, although many still do not reach reading and driving vision. New medications are required to supplement the achievements made by existing therapy. As a result, fresh methodologies are required for more rapidly producing newer diabetes medications with lesser safety hazards.

Several drugs have been approved to treat diabetic retinopathy. Currently, these drugs are injected into the eye through intravitreal injection [5,6]. Intravitreal aflibercept (Eylea) and ranibizumab are two more drugs utilised in clinical practise and clinical research (Lucentis). Eylea has a significantly longer lifespan. Bevacizumab (Avastin) is the least expensive and almost definitely as effective as the widely used Lucentis [7].

The existing treatments for DR/DME – laser photocoagulation and vitrectomy – only address the disease's advanced stages. Several biochemical mechanisms, including protein kinase $C-\beta$ activation, increased vascular endothelial growth factor production, oxidative stress, and accumulation of intracellular sorbitol and advanced glycosylation end products, may contribute to the vascular disruptions that characterize DR/DME[8].

Inhibiting these pathways provides the prospect of DR intervention at earlier, non-sight-threatening phases. Increased polyol pathway flux, increased advanced glycation end-products (AGE) formation, abnormal activation of signaling cascades such as activation of the protein kinase C (PKC) pathway, increased oxidative stress, increased hexosamine pathway flux, and peripheral nerve injury are some of the most researched mechanisms in diabetic retinopathy. Increased oxidative stress, inflammation, and vascular blockage are the end results of all of these processes [9, 10]. The collapse of the blood-retinal barrier (BRB) is a common early symptom of DR, and it can progress to macular edoema in later stages. VEGF, or vascular endothelial growth factor, is thought to play a role in the breakdown of BRB.



Fig 1: Processes and molecule involved in the pathogenesis of DR as potential drug targets.

The term "drug repurposing" refers to the discovery of new uses/targets for an approved or investigational medicine outside of its original medical indication [11]. The disease-centric approach, target-centric approach, and drug-centric approach are the three systematic approaches to medication repositioning. Disease-centric techniques uncover connections between old and emerging indications. A target-centric approach connects an unknown disease to a known target and its established treatment. Finally, a drug-centric approach links a well-known medication to a novel target and indication. A target centric approach is used to propose a new drug for the treatment of DR in this study, focusing on the targets in the BRB; Polyol pathway, Protein kinase C pathway, VEGFR Signaling, and the Blood-retinal barrier are the four major pathways selected. Aldose reductase (ALR2), vascular endothelial growth factor (VEGF), angiotensin-converting enzyme, protein kinase C (PKC), interleukin beta, and tumor necrosis factor-alpha (TNF-Alpha) are the six candidate proteins that are directly or indirectly involved in the four major pathways in diabetic retinopathy, and are elaborated in this study. The target centric approach explored here includes pathogenesis study, the connectivity map analysis, binding site analysis and docking, and interaction studies to acquire the drugs to be repurposed for the treatment of DR.

II. Materials and Methods

2.1. Mechanisms involved in DR and identification of targets

The Blood Retinal Barrier is a physiologic barrier that regulates ion, protein, and water transit into and out of the retina and is extremely tight and restrictive. Diabetic retinopathy and age-related macular degeneration (AMD), the two most common and important retinal disorders, are linked to changes in the BRB [12]. The other pathways considered are the polyol pathway, protein kinase c pathway, and VEGFR signaling. Aldose reductase (ALR2), vascular endothelial growth factor (VEGF), angiotensin-converting enzyme, protein kinase C (PKC), interleukin beta, and tumor necrosis factor (TNF) are the six major proteins in the primary pathways in the pathogenesis of DR are considered in this study.

Pathogenicity analysis of the targets elucidates the activity of the six targets. Connectivity Map analysis was conducted to obtain the FDA approved drugs for the selected targets and their present disease indication. The obtained significantly viable drugs were analyzed for binding site, docking, and interaction studies of the targets to elucidate the drugs to be repurposed for the treatment of DR. The overall workflow of the study is illustrated in Figure 2.



Fig 2: Workflow of the current study elucidating step-by-step process in drug repositioning.

2.2. Pathogenesis study:

To gather acquaintance on the pathogenesis of the six diabetic retinopathy targets OMIM (http://www.omim.org) and a literature search (PubMed) was used. Pathogenesis study of each target protein was performed for predicting the impact of the drug on the course of the disease phenotype. Function, chromosomal location and its phenotypic relation of each target protein and their diseases were studied.

2.3. Connectivity Map analysis:

The Therapeutic Target Database (TTD version 4.3.02) and Clue.io (https://clue.io/) were used for the connectivity analyses. The Connectivity map elucidates the connection of the targets and the drugs projects. The clue repurposing tool elaborates the clinical phase of the drugs for each target and the current disease indication of the drug. The Connectivity Map dataset comprises 1.3M L1000 profiles and the tools for analyses. A total of 27,927 perturbagens have been profiled to produce 476,251 expression signatures. Target proteins are analyzed for their respective drugs that can be repurposed. The Therapeutic Target Database contains information on 236 targets of 20667 drugs at approved, under clinical trial, and in experimental stages; TTD can be used to assess the feasibility of drug projects with diabetes retinopathy risk proteins [13]. In this study, drug projects with Diabetic Retinopathy risk proteins are studied based on the following information – target, current disease indication, drug name, drug progress stage, and drug action mode. The drugs at the stages of approved or under clinical trials were included in the subsequent studies. To emphasize the most promising drugs to be repurposed in diabetes retinopathy therapy, targets/drugs in Phases I and II were excluded.

2.4. Binding site analysis of the target proteins:

Binding site analysis was accomplished using the 3DLigandSite [14] and cofactor tools [15]. 3DLigandSite tool localizes the ligand binding in the protein. *Cofactor tool* is a structure, sequence, and protein-

protein interaction (PPI) based method for biological function annotation of protein molecules. Key binding site amino acids were identified for all the six targets; the binding pocket with all the binding amino acids was targeted in the docking scrutiny.

2.5. Docking and Interaction analysis:

Docking was done using AutoDock Vina in PyRx software [16], an online software for molecular graphics, modeling and simulation. Molecular docking is a structure-based drug design approach to identify the essential amino acid interactions between the selected protein and generated ligands with low energy conformation. Target proteins and the FDA-approved drugs were obtained from the Protein data bank (PDB) (https://www.rcsb.org/) and PubChem. Interaction analysis was done using PyMol [17]. Vascular endothelial growth factor (VEGF) -1vpf, Angiotensin-converting enzyme (ACE) – 2xy9, Tumor necrosis factor-alpha (TNF-a) – 1tnf, Interleukin-1 beta (il-1b) – 1t4q, Aldose reductase -3v36 and Protein kinase c beta -3pfq were obtained from PDB for further study. Interactions were calculated based on binding energy and number of polar bonds.

III. Results and Discussion:

3.1. Literature search and retrieval of DR related protein targets:

Our literature search revealed six target proteins involved in three major pathways that are considered as the potential targets for DR in this study. The selected target proteins, their corresponding pathways, and functions are elucidated in Table 1.

Table 1. DK targets, its pathways, and function					
S. No	Target	Pathway	Function		
1	Vascular endothelial growth factor receptor (VEGFR)	Blood retinal barrier	Pathological angiogenesis [18]		
2	Angiotensin-converting enzyme	The renin-angiotensin system (RAS)	Help relax your veins and arteries to lower your blood pressure [19]		
3	Tumor necrosis factor a	Blood retinal barrier	Promotes apoptosis and the loss of retinal microvascular cells.[20]		
4	Interleukin-1- β (il-1 β)	Blood retinal barrier	IL-1β accelerates apoptosis of retinal capillary cells [21]		
5	Aldose reductase	Polyol pathway	Contribute to the BRB breakdown in diabetes [22]		
6	Protein kinase C β	Protein Kinase C (PKC) Pathway	<i>PKC</i> - β inhibition could prevent BRB breakdown in <i>diabetic</i> <i>retinopathy</i> [23]		

Table 1. DR targets, its pathways, and function

3.2. Pathogenesis study:

Each of the above selected targets was studied for its pathogenesis against DR using OMIM and literature. Pathogenesis study confers the therapeutic potential of all the six targets against DR. The mode of action of each target was retrieved from OMIM and literature, and is shown in Table 2.

	^	
S.	Target	Mode of Action
NO	-	
1	Vascular endothelial growth factor receptor(VEGFR)	Inhibition of VEGF suppresses retinal neovascularization and increased retinal vascular permeability [24]
2	Angiotensin-converting enzyme	Angiotensin-converting enzyme inhibitor (ACE-I) can prevent the destruction of blood- retina barrier (BRB) and retard progression of the disease to PDR.1[25,26,27,28]
3	Tumor necrosis factor α	TNF α is involved in the breakdown of the blood retinal barrier in later stages of DR.[29]
4	Interleukin-1 β (il-1b)	IL-1 β has an important role in retinal microglia activation and proliferation under diabetes, limiting IL-1 β -triggered inflammatory processes may provide a new therapeutic strategy to prevent the progression of diabetic retinopathy.[30]
5	Aldose reductase	Increased aldose reductase activity contributes to retinal oxidative stress and retinal damage, inhibiting which will help in avoiding retinal damage. [31]
6	Protein kinase c β	PKC activation induces VEGF expression causing retinal neovascularization and vascular permeability [32,33]

Table 2: The protein targets and their biological mode of action

3.3. Binding site analysis of the target proteins:

The binding site analysis elucidates the particular sites for drugs to bind, thereby either inhibiting or activating the process or the protein itself. Pathogenesis studies suggest that inhibition of the target proteins was deemed to support diabetes retinopathy therapy. Literature study also elucidated that the binding sites are the inhibitory sites of the targets. Active sites of the respective targets are shown in below Table 3.

	Table 5:	The protein targets and their binding site animo acids
SNo	Target	Binding SITES
	0	
1	Waaaalan andathalial	DDO21 MET40 DDOC2 CLUCC LEUCC LUCO2 DDO21 CLUCE ACNO2 LVCO4 CVC57 CLU20
1	vascular endotheliai	PRO21 ME148 PRO03 GLU00 LEU00 HIS92 PRO21 GLU05 ASN93 L1594 C1557 GLU30
	growth factor (VEGF)	PRO46 GLU66 SER50 ASN68
2	Angiotensin-converting	HIS353 GLU345 HIS353 GLU384 GLN69 ASN374 ILE73 ASN33 THR302 GLU37 THR38
	enzyme	ASP307 ARG309 ASP13 ARG14 GLN281 ASP357 LEU358 PRO359, SER517
3	Tumor necrosis factor α	THR77, GLU35, GLU116, LEU29, PHE144, ALA145, GLU146, ASP45, ASP140, TYR141,
		VAL17, HIS73, VAL74, GLN102
4	Interleukin-1 β (il-1b)	VAL19, MET20, SER21, LEU31, ASP35, GLU37, GLN38, GLN39, THR137, GLY140,
		GLN141, ASP142, SER13, LYS109, SER70, VAL72, GLN81, GLU64, ARG98
5	Aldose reductase	GLY39 THR40 TRP41 LYS42 ASP64 TYR69 LYS98 HIS131 TRP111 SER180 ASN181
		GLN204 TYR230 SER231 PRO232 LEU233 GLY234 SER235 PRO236 ASP237 LEU249
		ALA266 ILE281 PRO236 ASP237 LEU249 ALA266 ILE281 PRO282 LYS283 SER284
		VAL285 THR286 ARG289 GLU292 ASN293 CVS319 SER302
6	Protein kinase c ß	ALASTO I VS372 THD405 META21 CIUT7 TVD123 VALA24 ASD471 ASN424
U	i iotem kinase e p	ALAJ/0, L155/2, 1110402, ME1421, GL04//, 111123, VAL424, ASF4/1, ASIN424,
		ME14/4, ALA484, ASP483

Table 3: The protein targets and their binding site amino acids

3.4. The Connectivity Map analysis:

Initial CMap analysis results for the selected six targets elucidate 66 drugs that can be repurposed for the treatment of DR. The number of active drugs for each target are as follows: Vascular endothelial growth factor (VEGF) – 26 drugs, Angiotensin-converting enzyme (ACE) – 20 drugs, Tumor necrosis factor α (TNF-a) – 2 drugs, Interleukin-1- β (il-1b) – 2 drugs, Aldose reductase – 6 drugs, and Protein kinase C β – 10 drugs (Table 4).

Table 4: The targets and their res	pective drugs obtained fo	r repurposing in the treatme	ent of the DR
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S.No	Protein	No. of Drugs	Drugs
1	VEGFR	26	Dovitinib, Sorafenib, Linifanib, Regorafenib, Brivanib-alaninate, KI-8751, MGCD-
			265, Nintedanib, Lenvatinib, Cabozantinib, DMH4, Pazopanib, Motesanib,
			ZM323881, Anlotinib, Axitinib, Fruquintinib, Semaxanib, KRN 633, Orantinib, PD-
			173074, Brivanib, Sunitinib, SU4312, SKLB1002 and SAR131675 (CID_71295845)
2	TNF-α	2	Thalidomide and Ligustilide
3	Interleukin-1-	2	Diacerein and Bergenin
	β		
4	Angiotensin-	20	Deserpidine, Cilazapril, Delapril, Quinaprilat, Ramipril, Imidapril, Benazepril,
	converting		Fosinoprilat, Benazepril, Enalapril, Quinapril, Temocapril, Fosinopril(monopril),
	enzyme		Lisinopril, Moexipril, Enalaprilat, Nicainoprol, Captopril, Captopril and Deserpidine
5	Aldose	6	Imirestat, Hyperin, Alrestatin, EBPC, Ranirestat, Cinnamaldehyde, Fidarestat,
	reductase		Epalrestat, Sorbinil and Ponalrestat (statil).
6	ΡΚС-β	10	Enzastaurin, Bisindolylmaleimide-IX, Myricitrin, CGP-53353, Dequalinium, Ingenol,
	-		GF109203X, Ingenol-mebutate, Aurothioglucose and Ethylenediaminetetraacetic-acid.

Further, repurposing analysis using Clue repurposing tool indicated that among the 66 drugs, 10 drugs have antidiabetic information and 17 drugs show diabetes-related disease information. 39 of the total drugs did show any anti-diabetic information in CMap. Among the 66 drugs based on the best docking score and number of polar interactions, 19 drugs are proposed for repurposing in the treatment of DR. (Supplementary Table 1).







Fig 3: The above figure (a, c, e, g, i, and k) explains the biological process and mode of action of all the targets. The box plots in the figure (b, d, f, h, j, and l) shows the clinical phase and purity of the drugs obtained for each target.

3.5. Interaction and Docking Analysis:

Docking and interaction studies of the six targets and 66 drugs were performed. Based on the RMSD, and Binding affinity of the drug with the targets, the final top 19 drugs were considered for further analyses (Table 5). Each of the targets for their interaction with the drugs is discussed in detail below:

i) Vascular endothelial growth factor receptor (VEGFR): VEGFR is studied for its interaction with 26 drugs, and the best five drugs were considered for further analyses. The drugs Dovitinib, sorafenib, linifanib, regorafenib and Brivanib - alaninate with binding affinities of -9.3, -9.1, -8.7, -8.6 and -8.3 kcal/mol were studied for the interaction. Dovitinib interacts with LEU32(2 bonds) and GLU30 with a polar bond length of 2.2 and 2.3 A^o (Fig 4(a)), Sorafenib interacts with ASP63, CYS61(2 bonds), SER50, and GLY59 with a polar bond length of 2.2, 2.5, 2.1, 2.8, and 2.6 A^o respectively (Fig 4(b)), while Linifanib interacts with LEU66(2 bonds), LEU32, ASP63 and GLY59(2 bonds) with a polar bond length of 2.5, 2.6, 2.7, 2.0, 2.3 and 2.9 A^o (Fig 4(c)). Regorafenib interacts with GLY59, ASP63(2 bonds), and CYS61with a polar bond length of 2.8, 2.6, 2.7, 2.0 2.3 and 2.9 A^o (Fig 4(d)), whereas Brivanib-alaninate interacts with LEU66, CYS612(2 bonds), CYS68, and GLU30(2 bonds) with a polar bond length of 2.3, 2.0, 2.3, 2.5, 2.4, and 2.7 A^o (Fig 4(e)) (Supplementary Table 2).

ii) TNF-a: The TNF-a is studied for two drugs – Thalidomide and Ligustilide, with a binding affinity of -8.4 and -5.9 kcal/mol. Thalidomide is studied based on binding affinity and polar interactions. Thalidomide interacts with GLN102(2 bonds), ARG103, and GLN102(2 bonds) with a polar bond length of 2.2, 2.3, 2.6, 3.5 and 2.2 A^{\circ} respectively (Fig 4(f)) (Supplementary Table 2).

iii) Interleukin-1- β : Interleukin-1- β is studied for the interaction with two drugs, both were considered for further analyses. The drugs Diacerein and Bergenin with binding affinities of -6.3 and -6.2 kcal/mol were studied for the interaction. Diacerein interacts with LYS109, ASP145, SER13, THR144, ASP142, GLN126, and GLY140 with a polar bond length of 2.1, 3.0, 2.6, 1.9, 2.7, 2.8 and 2.3 A^{\circ} respectively (Fig 4(g)) while Bergenin interacts with ASN7, SER43, TYR68, LYS65, and GLU64 with a polar bond length of 2.2, 2.4, 2.5, 2.3 and 2.6 A^{\circ} (Fig 4(h)) (Supplementary Table 2).

iv) Angiotensin-converting enzyme: The Angiotensin-converting enzyme is studied for the interaction with 20 drugs and the best five drugs are considered for further analysis. The Drugs Deserpidine, Cilazapril, Delapril,

Quinaprilat, and Ramipril are studied for the interaction with binding affinities of -9.6, -8.7, -8.7, -8.6, and -8.3 kcal/mol respectively. Deserpidine interacts with TYR135, SER517, and TRP220 with a polar bond length of 2.4, 2.3, and 2.6 A^{\circ} respectively (Fig 4(i)). The Cilazapril interacts with HIS513, LYS511, GLN281, and HIS353(2 bonds) with a polar bond length of 2.1, 2.1, 2.5, 2.6, and 2.6 A^{\circ} respectively (Fig 4(j)). Delapril interacts with THR302 and ASN374 with a polar bond length of 2.7 and 2.9 A^{\circ} respectively (Fig 4(k)). The Quinaprilat interacts with THR282(2 bonds) and LYS454(2 bonds) with a polar bond length of 2.7, 2.6, 2.3, and 2.2 A^{\circ} respectively (Fig 4(I)), while Ramipril interacts with THR282 and ASN277 with a polar bond length of 2.6 and 2.4 A^{\circ} (Fig 4(m)) (Supplementary Table 2).

v) Aldose reductase: Aldose reductase is studied for the interaction with six drugs, and the best three drugs are considered for further analysis. The Drugs imirestat, Hyperin, and Alrestatin are studied for the interaction with the binding affinities of -9.1, -8.3, and -7.8 kcal/mol respectively. Imirestat interacts with SER302(2 bonds) with a polar bond length of 2.4 and 2.3 A \circ (Fig 4(n)). The Hyperin interacts with TRP20(2), HIS110, TRP111, LEU301, and GLN49 with polar bond lengths of 1.8, 2.6, 2.2, 1.9, 2.3 and 2.2 A \circ respectively (Fig 4(o)) (Supplementary Table 2).

vi) Protein kinase C β : Protein kinase C is studied for the interaction with 10 drugs, and the best five drugs were considered for further analyses. The Drugs Enzastaurin, Bisindolylmaleimide-IX, Myricitrin, CGP-53353, and Dequalinium were studied for their interactions, with the binding affinities of -10.5, -9.7, -9.7, -9.5, and -9 kcal/mol respectively. Enzastaurin interacts with GLU477, SER477, SER476, ASN424, TYR123, and GLN128 with a polar bond length of 2.1, 2.1, 2.2, 3.3, 2.4 and 2.4 A° respectively (Fig 4(p)). Bisindolylmaleimide-IX was observed to interact with SER476, ASN424, TYR123, TYR422(2 bonds), and GLN128 with a polar bond length of 2.1, 2.2, 3.5, 2.5, 2.3 and 2.5 A° respectively (Fig 4(q)). Myricitrin interacts with TYR123, SER476, TYR422, LEU367, LYS141, and ARG142 with a polar bond length of 2.4, 2.5, 2.2, 2.6, 2.2, 2.7 and 2.2 A° respectively (Fig 4(r)). CGP-53353 interacts with GLU477, SER476, ASP475, TYR422, and GLU421 with a polar bond length of 2.5, 2.5, 2.6, 2.4 and 3.3 A° respectively (Fig 4(s)) (Supplementary Table 2).



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Fig 4: The top 19 drugs to be repurposed and their docked poses showing the polar interaction of the drug and protein.

21N0	Protein	Drug	RMSD(A)	Binding energy(kcal/mol)	No. of H bonds	Amino acids involved
1	VEGFR	Dovitinib	0.96	-9.3	3	LEU32(2 bonds), GLU30
		Sorafenib	0.50	-9.1	5	ASP63, CYS61(2 bonds), SER50, GLY59
		Linifanib	0.67	-8.7	6	LEU66(2 bonds), LEU32, ASP63, GLY59(2 bonds)
		Regorafenib	0.89	-8.6	4	GLY59, ASP63(2 bonds), CYS61
		Brivanib-alaninate	0.54	-8.3	6	LEU66, CYS612(2 bonds), CYS68, GLU30(2 bonds)
2	TNF-α	Thalidomide	1.87	-8.4	5	GLN102(2 bonds), ARG103, GLN102(2 bonds)
3	Interleukin- 1-β	Diacerein	1.45	-6.3	7	LYS109, ASP145, SER13, THR144, ASP142, GLN126, GLY140
		Bergenin	0.56	-6.2	5	ASN7, SER43, TYR68, LYS65, GLU64
4	Angiotensin- converting enzyme	Deserpidine	0.87	-9.6	3	TYR135 SER517 TRP220
		Cilazapril	1.28	-8.7	5	HIS513 LYS511 GLN281 HIS353(2 bonds)
		Delapril	1.85	-8.7	2	THR302 ASN374
		Quinaprilat	0.67	-8.6	4	THR282(2 bonds), LYS454(2 bonds)
		Ramipril	0.45	-8.3	2	THR282 ASN277
5	Aldose reductase	Imirestat	0.67	-9.1	2	SER302(2 bonds)
		Hyperin	0.65	-8.3	6	TRP20(2 bonds), HIS110, TRP111, LEU301, GLN49
6	РКС В	Enzastaurin	1.54	-10.5	6	GLU477, SER477, SER476, ASN424, TYR123, GLN128
		Bisindolylmaleimide- IX	1.21	-9.7	6	SER476 ASN424 TYR123 TYR422(2 bonds) GLN128
		Myricitrin	0.98	-9.7	6	TYR123, SER476, TYR422, LEU367, LYS141, ARG142
		CGP-53353	0.78	-9.5	5	GLU477, SER476, ASP475, TYR422, GLU421
		Dequalinium	0.65	-9	2	GLU477, GLU421

Table 5: The interaction studies of the six targets and their respective drugs.

IV. Discussion:

Diabetes retinopathy is a major complication in diabetes. The treatment being mostly only in the later stages, we have identified, in this study, six targets and possible 66 drugs to be repurposed for early treatment of DR. The drugs in Phase I and II are excluded from the study to avoid unwanted biological misperception.

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Breakdown of the Blood Retinal Barrier (BRB) is an early event in DR, leading to macular edema in more advanced stages of the pathology. Vascular endothelial growth factor (VEGF) is considered a major factor in the breakdown of BRB. This study includes VEGFR, interleukin-1- β and TNF- α of the blood retinal barrier cascade among the six targets identified, and concentrates on the targets in the BRB - Polyol pathway and protein kinase C activation. The BRB breakdown being the early event in DR, focusing on three targets simultaneously in this cascade would perhaps help in the early treatment of the disease. The possible impact of 66 drugs with diabetes and the related diseases was studied. Clue repurposing analysis further showed 10 drugs to have anti-diabetic information. 17 drugs were shown to demonstrate diabetes-related disease information in Cmap scrutiny. A total of 39 drugs did not show any anti-diabetic information in CMap. Based on the drug target interactions, which complement the role of crucial binding residues (that were earlier defined), thereby inhibiting the targets and used in the DR therapy. The targets and the best drugs are given below: **VEGFR** – Dovitinib, sorafenib, linifanib, regorafenib, and Brivanib – alaninate, **TNF-** α – thalidomide, **Interleukin-1-** β – Diacerein and Bergenin, Angiotensin-converting enzyme - Deserpidine, Cilazapril, Delapril, Quinaprilat and Ramipril, Aldose reductase – imirestat and Hyperin and Protein kinase C β – Enzastaurin, Bisindolylmaleimide-IX, Myricitrin, CGP-53353, and Dequalinium. As given in 3.3 and 3.4, all the 6 targets are conferred with connectivity repurposing analysis, docking, and interaction study results.

VEGFR: The connectivity repurposing analyses show 70% of the VEGFR inhibitor drugs with 85–100% purity. Purity is defined as the compatibility of the drug in the treatment of specific diseases. The graph (Fig 3(a)) shows the percent of drugs in the different clinical phases. It was crucial to consider the drugs in Phase III, preclinical, and launched categories, hence, for fruitful results, drugs in Phases I and II are ignored. A list of 26 drugs was obtained, among which 14 drugs showed a score >95 (Fig. 3(b)) and is shown effective in the VEGFR inhibition. The score shows enrichment in the process, the VEGFR inhibitor. Dovitinib, Linifanib, and Sorafenib show lower binding energy values for VEGFR compared to regorafenib and Brivanib-Alaninate, as presented in Table 5. The RMSD value of Dovitinib, Linifanib, Sorafenib, regorafenib and Brivanib-Alaninate of 0.96, 0.05, 0.67, 0.89 and 0.54 A^o (Table 5). The reference RMSD value (<1) shows all five drugs to be finest bound to the protein (Table 5).

TNF-a: The connectivity map analysis elucidates score in the range of 76.10–89.19 (Fig 3(c)) as CCK receptor antagonist, TGF β receptor inhibitor, which is a major progression in diabetic patients. 100% of angiotensin-converting enzyme inhibitor drugs fall into 85–100% purity Approximately 90% of the drugs are launched in the market; 10% of the drugs in Phases I and II are ignored in this study. (Fig 3(d)). Reference RMSD of Thalidomide are 1.87 A^o, which fall into the reference range, indicating that thalidomide inhibits the TNF- α protein more than 50%.

Interleukin-1- β : The drugs show an enrichment score between 76.10–89.19 as Na-K-Cl transporter inhibitor, which is a major process in inflammatory diseases. (Fig 3(e)). The purity of the ace inhibitor drugs obtained is around 80–100%. The connectivity repurposing analysis illustrates that 90% of the drugs are at preclinical phase, and only 10% of the drugs are launched in the market, whereas 10% of the drugs are withdrawn. (Fig 3(f)). The RMSD of Diacerein and Bergenin are 1.45 and 0.56 A^o, respectively. The values show that both the drugs have good binding ability and show more than 50% interleukin-1- β inhibition.

Angiotensin-converting enzyme: The drugs show a score in the range of 99.10-92.19 (Fig 3(g)) as a dihydrofolate inhibitor, a major process in vitamin absorption that is impaired in diabetic patients. 70% of angiotensin-converting enzyme inhibitor drugs fall into 85-100% purity. The 90% of the drugs are launched in the market, 10% of the drugs in Phase I and II are ignored in this study (Fig 3(h)). The RMSD of Deserpidine, Cilazapril, Delapril, Quinaprilat, and Ramipril are 0.87, 1.28, 1.85, 0.67 and 0.45 A° respectively (Table 5). Based on the RMSD and the binding energy values, Cilazapril and Quinaprilat were observed to show better binding and inhibition compared to other drugs obtained. Overall, all the best five drugs fall into the reference value and so they can be proposed for the best leads.

Aldose reductase: The drugs show a score between 92.84–98.30 as a sigma receptor antagonist, Na-K-Cl transporter inhibitor, which is a responsible for major microvascular inflammation process. (Fig 3(i)). 90% of aldose reductase inhibitor drugs fall into 85–100% purity. 80% of the drugs are in the preclinical and Phase III stage. Approximately 20% of the drugs are already launched in the market. (Fig 3(j)). The drugs Imirestat and Hyperin show reference RMSD values (<1) of 0.67 and 0.65 A^{\diamond}, which indicate that the binding is appropriate.

Protein kinase C \beta: The drugs show a score between 92.43–97.31 as SRC inhibitor and EGFR inhibitor, which is a major TNF- α inhibition process. (Fig 3(k)). 90% of aldose reductase inhibitor drugs fall into 85–100% purity. Around 20% of the drugs are launched in the market, 30% of the drugs in Phases II and III are ignored in this study (Fig 3(1)). The RMSD are 1.54, 1.21, 0.98, 0.78, and 0.65 A^o for Enzastaurin, Bisindolylmaleimide-IX, Myricitrin, CGP-53353 and Dequalinium, respectively (Table 5). Inclusively, all the best five drugs fall into the reference value, hence can be proposed for the best leads.

In summary, drug repositioning provides a powerful tool to find novel indications for marketed drugs and clinical candidates of complex human diseases, such as diabetic retinopathy. By analyzing connectivity of the drug to the target, mapping diabetes retinopathy related proteins to drug projects (TTD and Clue.io), and inputting pathogenesis knowledge, **19 drugs** are proposed to be repurposed with a potential indication for diabetic retinopathy treatment.

Diabetes retinopathy is an inflammatory disease. Bergenin (Interleukin-1-beta) and Hyperin (aldose reductase inhibitor) are currently being used in the treatment of inflammatory diseases. Two of the major drugs Imirestat (aldose reductase inhibitor) and Thalidomide (TNF-Alpha) are revealed to be used in diabetes. Aldose reductase inhibitor is involved in the polyol pathway, which is one of the major pathways in DR. Cilazapril, Delapril, Deserpidine, Quinaprilat, and Ramipril are used in the treatment of hypertension, targeting ACE protein. Among the six targets, the targets in the BRB are more significant since they target early cure of DR. BRB disruption being the major milestone in the development of DR, the VEGFR (Dovitinib, Linifanib, Regorafenib, Sorafenib, and Brivanib-Alaninate), TNF-alpha (Thalidomide) and Interleukin-1-beta (Bergenin and Diacerein) are the targets, and their respective drugs to be considered for treatment of DR. Therefore, concentrating on VEGFR, TNF- α , and Interleukin-1- β and their eight respective drugs will create a potential possibility of early treatment of DR. Dovitinib, linifanib, regorafenib, sorafenib, and brivanib-alaninate are the drugs that are not involved in the treatment of diabetes and diabetes related diseases. The drugs which do not have any information related to diabetes but target the major target sites in DR can be proposed to be repurposed for the treatment of DR. All the five drugs target VEGFR, which is a major target in the BRB. Preclinical or clinical trials may be initiated to establish the efficacy of these repositioned drugs for diabetic retinopathy treatment.

V. Conclusion:

Drug repurposing is an effective strategy to treat new diseases caused by infectious agents that spread rapidly. In this paper, the drug repurposing strategy was applied using virtual screening to identify better and early therapeutic options for Diabetes retinopathy. By analyzing connectivity of the drug and the target, mapping diabetes retinopathy related proteins to drug projects, and inputting pathogenesis knowledge, **19 drugs** are proposed to be repurposed with a potential for diabetic retinopathy treatment. Preclinical or clinical trials might be initiated to establish the efficacy of these repositioned drugs for diabetic retinopathy treatment. From the analysis, we can suggest that early detection and treatment is a better way to treat DR. Targets in the BRB can be considered for the treatment of DR. The total of **8 drugs**; VEGFR-Dovitinib, sorafenib, linifanib, regorafenib, Brivanib-alaninate, TNF- α -thalidomide, Interleukin-1- β -Diacerein, and Bergenin can be considered for further study to treat DR. Among the eight drugs, Dovitinib, Linifanib, Regorafenib, Sorafenib, and Brivanib-<u>A</u>laninate are not involved in the treatment of diabetes and diabetes related diseases, but target the major target sites in the BRB. To conclude, the above **five drugs** are appropriate to be repurposed for the treatment of DR. Summarizing, by creating an approach that reasonably selects drugs based on their described mode of action and repurposing already available drugs, the coming years would see increasing prospects in rapid increase in the repertoire of drugs available to treat Diabetic Retinopathy in its early stages.

Supporting Information:

Supplementary table 1: The CMap analysis of the 6 targets and 66 drugs, their mode of action and current indication for treating Diabetic retinopathy are shown in this table.

Supplementary table 2: The table shows the interaction of the targets with the drugs and the polar bonds are also explicated. The lower the binding affinity and higher the polar bonds, it is a virtuous drug for the disease.

Declarations:

Conflict of Interest:

Authors declare that there is no conflict of interests.

Ethical Approval:

This article does not contain any studies with human participants.

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Computer-aided drug repurposing for identification of potential therapeutic candidate for diabetes retinopathy

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				Action
Drug name	Current drug indication	Stage	Target	mode
Anlotinib	Thyroid cancer	Launched	VEGFR	Inhibitor
Axitinib	Renal cell carcinoma (RCC)	Launched	VEGFR	Inhibitor
Brivanib	Metastatic colorectal cancer	Phase 3	VEGFR	Inhibitor
Brivanib-alaninate	Coronavirus Disease 2019(Phase 3)	Phase 3	VEGFR	Inhibitor
Cabozantinib	Medullary thyroid cancer (MTC)	Launched	VEGFR	Inhibitor
Cediranib	Breast cancer	Phase 3	VEGFR	Inhibitor
DMH4	Lymphoma	Preclinical	VEGFR	Inhibitor
Dovitinib	Non-small-cell lung cancer	Phase 3	VEGFR	Inhibitor
Elemene	Breast cancer	Phase 3	VEGFR	Inhibitor
Fruquintinib	Colorectal cancer	Launched	VEGFR	Inhibitor
KI-8751	Cancer	Preclinical	VEGFR	Inhibitor
KRN-633	Cancer	Preclinical	VEGFR	Inhibitor
Lenvatinib	Thyroid cancer	Launched	VEGFR	Inhibitor
Linifanib	Mammary cancer	Phase 3	VEGER	Inhibitor
MGCD-265	Colorectal cancer	Preclinical	VEGER	Inhibitor
Motesanib	Thyroid cancer	Phase 3	VEGER	Inhibitor
Nintedanib	Idiopathic pulmonary fibrosis (IPF)	Launched	VEGER	Inhibitor
Orantinib	Diabetes complications	Phase 3	VEGER	Inhibitor
ofunitino	Renal cell carcinoma (RCC) soft	T huse 5	(Hork	minortor
Pazonanih	tissue sarcoma (STS)	Launched	VEGER	Inhibitor
PD-173074	Cancer	Preclinical	VEGER	Inhibitor
10 1100/1	Colorectal cancer gastrointestinal	Treemieur	(Hork	minortor
Regorafenib	stromal tumors (GIST)	Launched	VEGER	Inhibitor
SAR131675	Breast cancer	Preclinical	VEGER	Inhibitor
Semayanih	Renal cell carcinoma	Phase 3	VEGER	Inhibitor
SKI B1002	Cancer	Preclinical	VEGER	Inhibitor
SILLETOOL	Renal cell carcinoma (RCC)	Treemieur	(Hork	minortor
	thyroid cancer, hepatocellular			
Sorafenib	carcinoma (HCC)	Launched	VEGER	Inhibitor
	gastrointestinal stromal tumors			
	(GIST), renal cell carcinoma			
	(RCC), neuroendocrine tumors of			
Sunitinib	pancreatic origin (PNET)	Launched	VEGFR	Inhibitor
SU4312	Cancer	Preclinical	VEGFR	Inhibitor
TG-100572	Age-related macular degeneration	Preclinical	VEGFR	Inhibitor
Tiyozanib	Renal cell carcinoma (RCC)	Launched	VEGFR	Inhibitor
Vandetanib	Medullary thyroid cancer (MTC)	Launched	VEGFR	Inhibitor
Vatalanib	Cancer	Phase 3	VEGFR	Inhibitor
XL647	Cancer	Phase 3	VEGFR	Inhibitor
ZM-306416	Myocardial infarction	Preclinical	VEGFR	Inhibitor
ZM-323881	Gastrointestinal stromal tumors	Preclinical	VEGER	Inhibitor
			angiotensin converting	
Alacepril	Hypertension	Launched	enzyme inhibitor	Inhibitor
			angiotensin converting	
Benazepril	Hypertension	Launched	enzyme inhibitor	Inhibitor
	Hypertension congestive heart			
	failure, myocardial infarction.			
	diabetes mellitus, diabetic		angiotensin converting	
Captopril	nephropathy	Launched	enzyme inhibitor	Inhibitor
	Hypertension, congestive heart		angiotensin converting	
Cilazapril	failure	Launched	enzyme inhibitor	Inhibitor
•			angiotensin converting	
Delapril	Hypertension	Launched	enzyme inhibitor	Inhibitor
· ·		1	angiotensin converting	
Deserpidine	Hypertension	Launched	enzyme inhibitor	Inhibitor
· ·	Hypertension, congestive heart	1	- ·	1
	failure, left ventricular systolic		angiotensin converting	1
Enalapril	dysfunction (LVSD)	Launched	enzyme inhibitor	Inhibitor
			angiotensin converting	
Enalaprilat	Hypertension	Launched	enzyme inhibitor	Inhibitor

	Hypertension, congestive heart		angiotensin converting	
Fosinopril	failure	Launched	enzyme inhibitor	Inhibitor
P 1 1	TT / ·	T 1 1	angiotensin converting	T 1 11 12
Fosinoprilat	Hypertension	Launched	enzyme inhibitor	Inhibitor
Insidentil	Hypertension, congestive heart	Lounshad	angiotensin converting	Inhibitor
inidaprii	Humortonsion, congostive baart	Launched	enzyme minotor	minutor
Lisinopril	failure diabetes mellitus	Launched	angiotensin converting	Inhibitor
Lisinopin	fanule, diabetes menitus	Launcheu	angiotensin converting	minoitoi
Moexinril	Hypertension	Launched	enzyme inhibitor	Inhibitor
Moexipiii		Launened	angiotensin converting	minontor
Nicainoprol	Antiarrhythmic drug	Preclinical	enzyme inhibitor	Inhibitor
	Hypertension, myocardial			
	infarction, coronary artery disease		angiotensin converting	
Perindopril	(CAD)	Launched	enzyme inhibitor	Inhibitor
	Hypertension, congestive heart		angiotensin converting	
Quinapril	failure, angioedema	Launched	enzyme inhibitor	Inhibitor
			angiotensin converting	
Quinaprilat	Hypertension, angioedema	Launched	enzyme inhibitor	Inhibitor
			angiotensin converting	
Ramipril	Hypertension	Launched	enzyme inhibitor	Inhibitor
	Hypertension, congestive heart			
	failure, diabetic nephropathy,		angiotensin converting	
Temocapril	coronary artery disease (CAD)	Launched	enzyme inhibitor	Inhibitor
m 11 1	Hypertension, myocardial		angiotensin converting	.
Trandolapril	infarction	Launched	enzyme inhibitor	Inhibitor
Vol tra	Matabalia diagonag	Drealiniaal	angiotensin converting	Inhibitor
val-tyr	Metabolic diseases	Preclimical		Infilibitor
Zofenonril calcium	Hypertension	Launched	angiotensin converting	Inhibitor
AurothioglucoSe	Typertension	Launcheu		minoitoi
Automogiaeose	Rheumatoid arthritis	Launched	PKC inhibitor	Inhibitor
Bisindolylmaleimide-IX	Thrombocytopenia	Launened		minortor
Districtory interesting of the	momooeytopenia	Preclinical	PKC inhibitor	Inhibitor
CGP-53353	Hereditary hemorrhagic		EGFR inhibitor, PKC	
	telangiectasia	Preclinical	inhibitor	Inhibitor
Dequalinium	Solid tumour/cancer	Launched	PKC inhibitor	Inhibitor
Enzastaurin	Metastatic colorectal cancer			
		Phase 3	PKC inhibitor	Inhibitor
Ethylenediaminetetraacetic-acid	Coronavirus Disease 2019(Phase 3)			
		Launched	PKC inhibitor	Inhibitor
GF109203X	Idiopathic pulmonary fibrosis	Preclinical	PKC inhibitor	Inhibitor
Ingenol	Non-small-cell lung cancer	Launched	PKC activator	Inhibitor
	Psoriasis vulgaris; Diabetic macular			
Ingenol-mebutate	edema;	Launched	PKC activator	Inhibitor
	Solid tumour/cancer (phase2)		FLT3 inhibitor, KIT	
Midostaurin		Launched	inhibitor, PKC inhibitor	Inhibitor
Myricitrin	Solid tumour/cancer (phase3)	Preclinical	PKC inhibitor	Inhibitor
PD-40/824	Cancer	Preclinical	PKC inhibitor	Inhibitor
Ruboxistaurin	Metabolic Disease	Phase 3	PKC inhibitor	Inhibitor
Vitamin E	Inflommatory discossos	Lounabad	DE OXIDATION INNIDITOR,	Inhibitor
v Italiiiii-E	Easial inflamation	Droolinical	r KC IIIIII0110f	Inhibitor
A Importation	Facial IIIIanananon diabatia	Preclinical	protein kinase activator	Inhibitor
Allestatin	diabetic	Preclimical	aldose reductase inhibitor	Infilibitor
Cinnamaldehyde		Dreclinical	TPPV agonist	Inhibitor
EBPC		Preclinical	aldose reductase inhibitor	Inhibitor
Epile	nenhrology	Launched	aldose reductase inhibitor	Inhibitor
Fidarestat	Diabetes complication	Phase 3	aldose reductase inhibitor	Inhibitor
Hyperin	Vascular inflammatory diseases	Preclinical	aldose reductase inhibitor	Inhibitor
Imirestat	Diabetes	Preclinical	aldose reductase inhibitor	Inhibitor
Ranirestat	Diabetic neuropathy	Phase 3	aldose reductase inhibitor	Inhibitor
Sorbinil	Diabetic cataract	Phase 3	aldose reductase inhibitor	Inhibitor
Statil	Diabetes complication	Preclinical	aldose reductase inhibitor	Inhibitor
Bergenin	Inflammatory diseases	Preclinical	Interleukin1beta	Inhibitor
Diacerein	osteoarthritis	Launched	Interleukin1beta	Inhibitor
Ligustilide	-	Preclinical	TNF-Aplha	Inhibitor
Thalidomide	Type 2 diabetes and cancer	Launched	TNF-Aplha	Inhibitor
			1 · · · · · · · · · · · · · · · · · · ·	

Computer-aided drug repurposing for identification of potential therapeutic candidate for diabetes retinopathy

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Supplementary table 2 : The table shows the interaction of the targets with the drugs and the polar bonds are also explicated. The lower the binding affinity and higher the polar bonds, it is a virtuous drug for the disease.

SNo	Target	Drug	Binding Affinity	Polar bonds with bond length below 1 A	Interacting amino acid residues
1	VEGFR(26)	Dovitinib	-9.3	3	LEU32(2), GLU30
		Sorafenib	-9.1	5	ASP63, CYS61(2), SER50, GLY59
		Linifanib	-8.7	6	LEU66(2), LEU32, ASP63, GLY59(2)
		Regorafenib	-8.6	4	GLY59, ASP63(2), CYS61
		Brivanib-alaninate	-8.3	6	LEU66, CYS612(2), CYS68, GLU30(2)
		KI-8751	-8.3	3	LYS107, GLY59, ASP63
		MGCD-265	-8.3	3	LEU66, GLY59, LEU32
		Nintedanib	-8.2	4	GLY59, GLU30, LEU32(2)
		Lenvatinib	-8	3	LEU32(2), LEU66
		Cabozantinib	-7.9	3	SER50, GLY59, THR31
		DMH4	-7.8	2	ASP63, CYS61
		Pazopanib	-7.8	4	ASP34(2), CYS61(2)
		Motesanib	-7.7	3	SER50, LEU66, ASP63
		ZM323881	-7.5	4	GLU30(2), LEU32, GLY59
		Anlotinib	-7.4	4	LEU32.THR31. CYS57.CYS61
		Axitinib	-7.4	3	ASN62, CYS61, ASP63
		Fruquintinib	-7.3	4	LEU32, GLU30, CYS57, GLY59
		Semaxanib	-7.2	3	ASN62(2) PHE47
		KRN-633	-7.1	3	CYS68 CYS61 LEU32
		Orantinih	-7.1	4	CYS61(2) ASP34 CYS68
		PD-173074	-7.1	3	I EU32 ASP34 CYS57
		Brivanih	-7	5	Thr31 Glu30(2) Leu32 CY857
		Sunitinib	-6.9	5	ASP34 CYS57 GLY59 CYS61(2)
		SU4312	-6.9	2	CYS61(2)
		SKI B1002	-6.6	3	GLU30(2) CY857
		SAR131675	0.0	5	ASP34 SER50(3) CVS61
		(CID 71295845)	-6.4	7	I EU66 L EU32
2	TNF-α	Thalidomide	-8.4	5	GLN102(2), ARG103, GLN102(2)
-	1111 00	Ligustilide	-5.9	3	GLN102(2), PRO100
3	Interleukin -ß	Diacerein	-6.3	7	LYS109, ASP145, SER13, THR144.
-	P				ASP142, GLN126, GLY140
		Bergenin	-6.2	5	ASN7, SER43, TYR68, LYS65, GLU64
4	Angiotensin	Deserpidine	-9.6	3	TYR135 SER517 TRP220
	converting	Cilazapril	-8.7	5	HIS513 LYS511 GLN281 HIS353(2)
	enzyme(20)	Delapril	-8.7	2	THR302 ASN374
		Ouinaprilat	-8.6	4	THR282(2), LYS454(2)
		Ramipril	-8.3	2	THR282 ASN277
		Imidapril		<i>.</i>	ASN277(2), THR282(2), LYS454,
		L	-8.2	6	GLU376
		Benazepril	-8.1	3	GLU384 HIS383 HIS353
		Fosinoprilat	-8.1		
		Benazepril	-8.1	3	GLU384 HIS383 HIS353
		Enalapril	-8	1	THR302
		Ouinapril	-8	4	ASN66, ASP358, TYR394, HIS410
		Temocapril	-8	3	ASN70, SER355, ASP358
		Fosinopril(monopril)	-7.9	3	ASN277 HIS353 ALA354
		Lisinopril	-7.9	5	ASP288, ASN285(2), GLU376, LEU375
		Moexipril	-7.8	4	ALA356 HIS387 TYR360 ASN66
		Enalaprilat	-7.4	4	LYS454 THR282 ASN277(2)
		Nicainoprol	-6.8	3	ASP453 SER284 MET299
		Captopril	-5.8	4	HIS513 LYS511 GLN281 HIS353
		Captopril	-5.8	4	HIS513 LYS511 GLN281 HIS353
		Deserpidine	-9.6	3	TYR135 SER517 TRP220
5	Aldose	Imirestat	-9.1	2	SER302(2)
5	reductase(6)	Hyperin	2.1		TRP20(2), HIS110 TRP111 LEU301
			-8.3	6	GLN49

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Computer-allocating reput posing for identification of potential inerapeatic cumulate for .	Computer-aided drug	repurposing for	identification of potentia	al therapeutic cand	idate for
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		Alrestatin	-7.8	2	HIS110 TRP111
		EBPC	-7.2	3	TRP20 TRP111 HIS110
		Ranirestat	-7	4	GLU314, ARG296(3)
		Ponalrestat(statil)	-6.9	2	ARG40 LEU15
		Cinnamaldehyde	-6.8	2	ASN160, HIS110
		Fidarestat	-6.8	4	SER2 LEU15 ARG40 GLY38
		Epalrestat	-6.6	5	GLN49 TYR48 LYS21 SER22 TRP20
		Sorbinil	-6.3	4	GLU314, LYS194, GLU193, ASN292
6	РКС-β(10)	Enzastaurin	-10.5	6	GLU477, SER477, SER476, ASN424, TYR123, GLN128
		Bisindolylmaleimide- IX	-9.7	6	SER476 ASN424 TYR123 TYR422(2) GLN128
		Myricitrin	-9.7	6	TYR123, SER476, TYR422, LEU367, LYS141, ARG142
		CGP-53353	-9.5	5	GLU477, SER476, ASP475, TYR422, GLU421
		Dequalinium	-9		GLU477, GLU421
		Ingenol	-8.6	3	ASP470 ASP427, GLY426
		GF109203X	-7.5	3	ASN471, ASP470, ASP427
		Ingenol-mebutate	-7	2	LYS371
		Aurothioglucose	-6.1	5	ARG415, LYS375, ASP414(2), ASP376
		Ethylenediaminetetraac etic-acid	-5.5	7	GLU421, GLN405(2), LYS481, ASN481, ASN424, SER476