In-silico drug likeness predictions of novel 9-benzyl-6-(furan-2-yl)-2-(N,N dimethylamino)-9H-purine compound

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### **ABSTRACT:**

In silico studies, are increasing now-a-days, as through computer mechanics, screening of novel compounds based upon their physicochemical properties is important to reduce the cost of synthesizing novel medicinal compounds. In silico studies by network analysis and throughout screening helps to know and calculate biological activity of medicinal compounds. Novel 9-benzylpurine derivatives synthesized previously are used to study its structure and bioavailability radar, physicochemical properties, lipophilicity, solubility, pharmacokinetics, drug likeness and medicinal chemistry properties. These properties are calculated by use of Chem draw, open babel<sup>[16]</sup> and SwissADME software available freely. The novel 9-benzyl-6-(furan-2-yl) -2-(N,N dimethylamino)-9H-purine compound<sup>[17]</sup> shows good druglikeness properties to make it orally active.

YMER || ISSN : 0044-0477

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## **1. INTRODUCTION:**

Drug discovery is very time and money consuming process with low success rate. Despite advancements in new technology, drug discovery is very lengthy, difficult, expensive and inefficient process. A single entity takes 12-15 years with costs about US\$1.8 billion as per US FDA to bring it as drug in market. only 20% drug candidates reach clinical trials but only 1% in drug discovery, many new molecules don't reach target due to poor ADME and high toxicity. Poor bioavailability doesnot give threshold potential therapeutic effect while high toxicity makes compound unsuitable. This poor pharmacokinetics of drugs can be minimized by computational methods. So, drug development is a method of optimizing drug likeness to maximize safety, efficacy and pharmacokinetics. Pharmacokinetics of drugs helps to calculate drug's absorption, distribution, metabolism, excretion properties.<sup>[5]</sup>Lipinski rule of 5 helps in constituting a successful drug candidate. It states that orally active drug has one or more of the following properties i.e hydrogen bond acceptors less than 10, hydrogen bond donors less than 5, molecular mass less than 500 daltons and log P less than 5. More than 5 hydrogen bond donors and more than 10 hydrogen bond acceptors hinders permeability of drug across membrane bilayer.

### 2. MATERIALS AND METHODS:

- 2.1 Swiss ADME<sup>[1]</sup>
- 2.2 Structure and bioavailability radar: biovailability radar give the first glimpse of the drug-likeliness of the molecule in graphical view. By viewing it, a drug can be judge whether it is orally available bioactive or bioinactive. This bioavailability radar consists of 6 physicochemical properties like LIPO(Lipophlicity), SIZE, POLAR(Polarity),

INSOLU(Insolubility), INSATU(Insaturation), and FLEX(Flexibility). The exquisite range for each property are: LIPO, (XLOGP3 between -0.7 and + 5.0), SIZE (150-500 g/mol molecular weight), POLAR(TPSA between 20 and 130  $^{0}$ A, INSOLU(logS < 6), INSATU(Sp<sup>3</sup> hybridisation carbon fraction not less than 0.25, and FLEX (not more than 9 rotatable bonds)



The shaded portion represents exquisite range for each properties.

- 2.3 Physicochemical properties <sup>[4]</sup>: Physicochemical properties are the intrinsic physical and chemical characteristics of drugs that include molecular formula, molecular weight, no. of heavy and aromatic heavy atoms, Sp3 carbon fraction, number of hydrogen bond acceptor and donor, molar refractivity, total polar surface area.
- 2.4 Lipophilicity<sup>[18][19]</sup>: the overall quality of new drug candidate can by improved by lipophilicity. Lipophilicity is attributed with ADMET (Absorption, Distribution, Metabolism, Excretion and Toxicology) porperties of drugs. Improving ADMET properties will improve lipophicity that increases druglikeness and bioavailability.

Lipophilicity parameters calculated through swiss ADME are iLOGP,XLOGP3, WLOGP,MLOGP, SILICOS-IT, and consenus Log P.

Solubility: Solubility is important parameter to considered while administering drug as it greatly influenced absorption of drug in-vivo. Drugs intended for parenteral administration should be highly water solution to release maximum concentration of API. Two topological methods are available in SwissADME online plateform for predicting water solubility.

Pharmacokinetics<sup>[20]</sup>:

Drug likeness: Drug-likeness aims to predict whether drug is orally active or not with respect to its bioavailability. The SwissADME gives admittance to five different rule based approaches with variable ranges of properties which helps to identify drug likeness properties of drugs. These rule of five approaches helps in improving the quality of their proposed drug.

# 3. RESULT:

Physicochemical Properties (Table 1)							
Formula	C18H17N5O						
Molecular weight	319.36 g/mol						
Num. heavy atoms	24						
Num. aromatic heavy atoms	20						
Fraction Csp3	0.17						
Num. rotatable bonds	4						

Num. H-bond acco	eptors		4			
Lipophilicity (Table 2)						
Log P <sub>o/w</sub> (iLOGP)	[3]	3.03				
Log P <sub>o/w</sub> (XLOGP	3) [4]	2.87				
Log P <sub>o/w</sub> (WLOGH	<b>P</b> )	3.20				
Log P <sub>o/w</sub> (MLOGF	<b>)</b> <sup>[5]</sup>	1.72				
Log P <sub>o/w</sub> (SILICO	S-IT)	2.30				
Consensus Log Po	/w	2.62				
Wate	ble 3)					
$\log S (\text{ESOL})^{[6]}$	-3.98					
Solubility	3.34e-02	02 mg/ml ; 1.05e-04 mol/l				
Class	Soluble	2				
$Log S (Ali)^{[7]}$	-3.79					
Solubility	5.19e-02	02 mg/ml ; 1.63e-04 mol/l				
Class	Soluble					
Log S (SILICOS-	-6.08					
IT)	0.00					
Solubility	2.63e-04	4 mg/ml	; 8.24e-07 mol/l			
Class	Poorly s	soluble				

Pharmacokinetics (Table 4)					
GI absorption		High			
BBB permeant		Yes			
P-gp substrate		No			
CYP1A2 inhibito	r	Yes			
CYP2C19 inhibit	or	Yes			
CYP2C9 inhibitor	r	Yes			
CYP2D6 inhibito	r	Yes			
CYP3A4 inhibito	r	Yes			
Log $K_p$ (skin		-6.21 cm/s			
permeation)					
Dru	gliken	ess (Table 5)			
Lipinski	Yes;	0 violation			
Ghose <sup>[8]</sup>	Yes				
Veber <sup>[9]</sup>	Yes				
Egan <sup>[10]</sup>	Yes				
Muegge <sup>[11]</sup>	Yes				
Bioavailability <sup>[12]</sup>	0.55				
Medicin	al Che	emistry ( Table 6)			
PAINS <sup>[13]</sup>	0 aler	t			
1	1				

Leadlikeness <sup>[15]</sup>	Yes
Synthetic accessibility	3.11

# Swiss Target Prediction :

Target	Comm	Uniprot	ChEMBL	Target Class	Probability*	Known
	on	ID	ID			actives
	name					( <b>3D/2D</b> )
Adenosine A1	ADORA	P30542	CHEMB	Family A G	0.50042790	564
receptor	1		L226	protein-	394	/298
				coupled		
				receptor		
Adenosine A2a	ADOR	P29274	CHEMB	Family A G	0.50042790	625
receptor	A2A		L251	protein-	394	/337
				coupled		
				receptor		
Adenosin	ADOR	P29275	CHEMB	Family A G	0.104671941	238 /
e A2b	A2B		L255	protein-	128	135
receptor				coupled		
				receptor		
Adenosi	ADOR	PODM	CHEMB	Family A G	0.104671941	298 /

ne A3	A3	<b>S</b> 8	L256	protein-	128	167
receptor				coupled		
				receptor		
GABA-A	GAB	P284	CHEMB	Ligand-gated	0.104671941	53 / 0
receptor;	RB3	72	L209412	ionchannel	128	
alpha-	GAB	P349	0			
3/beta-3/	RA3	03				
gamma-2	GAB	P185				
	RG2	07				
GABA-A	GAB	P284	CHEMB	Ligand-gated	0.104671941	49 / 0
receptor;	RB3	72	L209412	ionchannel	128	
alpha-	GAB	P185	1			
1/beta-3/	RG2	07				
gamma-2	GAB	P148				
	RA1	67				
GABA-A	GAB	P284	CHEMB	Ligand-gated	0.104671941	57/0
receptor;	RB3	72	L209412	ionchannel	128	
alpha-	GAB	P185	2			
5/beta-3/	RG2	07				
gamma-2	GAB	P316				
	RA5	44				
GABA-A	GAB	P478	CHEMB	Ligand-gated	0.104671941	55/0
receptor;	RA2	69	L209413	ionchannel	128	

alpha-	GAB	P284	0			
2/beta-3/	RB3	72				
gamma-2	GAB	P185				
	RG2	07				
Phosphodiestera	PDE5A	O7607	CHEMB	Phosphodieste	0.104671941	173 / 0
se 5A		4	L1827	rase	128	
GABA	GABR	P31644	CHEMB	Ligand-gated	0.104671941	133 / 0
receptor	A5		L5112	ionchannel	128	
alpha-5						
subunit						
Metabotropic	GRM5	P41594	CHEMB	Family C G	0.104671941	213 / 0
glutamate			L3227	protein-	128	
receptor 5 (by				coupled		
homology)				receptor		
Serine/threoni	PLK1	P53350	CHEMB	Kinase	0.104671941	44 / 0
ne- protein			L3024		128	
kinase PLK1						
Butyrylcholinest	BCHE	P06276	CHEMB	Hydrolase	0.104671941	64 / 0
erase			L1914		128	
Estrogen	ESR2	Q9273	CHEMB	Nuclear	0.104671941	52/0
receptorbeta		1	L242	receptor	128	
Acetylcholineste	ACHE	P22303	CHEMB	Hydrolase	0.104671941	102 / 0

rase			L220		128	
Serine/threo	AURK	Q96GD	CHEMB	Kinase	0.104671941	178 / 0
nine-protein	В	4	L2185		128	
kinase						
Aurora-B						
Glycogen	GSK3B	P49841	CHEMB	Kinase	0.104671941	273 / 0
synthase			L262		128	
kinase-3 beta						
Serine/threo	AURK	O1496	CHEMB	Kinase	0.104671941	321 / 0
nine-protein	А	5	L4722		128	
kinase						
Aurora-A						
Arachidonate 5-	ALOX	P09917	CHEMB	Oxidoreducta	0.104671941	93 / 0
lipoxygenase	5		L215	se	128	
Cathepsin K	CTSK	P43235	CHEMB	Protease	0.104671941	214 / 0
			L268		128	
Cathepsin S	CTSS	P25774	CHEMB	Protease	0.104671941	235 / 0
			L2954		128	
Cathepsin (V	CTSV	O6091	CHEMB	Protease	0.104671941	35 / 0
and K) (by		1	L3272		128	
homology)						
Prostanoid	PTGER	P43115	CHEMB	Family A G	0.104671941	162 / 0

EP3	3	L3710	protein-	128	
receptor			coupled		
			receptor		

## 4. DISCUSSION:

The most important step in drug designing is find out whether the synthesized novel moiety is orally active or not. So, for carrying out ADMET studies, SwissADME web tool is used describes disposition of drug compound in the body. SwissADME online plateform helps for computation of physicochemical, pharmacokinetic, drug-like and related parameters. 9-benzyl-6-(furan-2-yl) -2-(N,N dimethylamino)-9H-purine follows lipinski's rule of five with 0 violation (Table 5) that makes this moiety clinically effective. In Swiss target prediction, this novel 9-benzylpurine makes good binding with adenosine receptors that belongs to target class Family A G protein- coupled receptor. Both A<sub>1</sub> receptors and A<sub>2A</sub> play roles in the heart, regulating myocardial oxygen consumption and coronary blood flow while A<sub>2A</sub> receptor also has broader anti-inflammatory effects throughout the body. Also, these receptors are responsible for the regulating the release of various neurotransmitters like dopamine and glutamate. Adenosine A<sub>2B</sub> and A<sub>3</sub> receptors are located mainly peripherally and are involved in processes such as inflammation and immune responses.

 $A_1$  receptors binding probability 0.50042790394,  $A_{2A}$  has 0.50042790394,  $A_{2B}$  has 0.104671941128 and  $A_3$  has 0.104671941128.

## 5. CONCLUSION:

ADMET in-silico studies provides an invaluable method in lead identification and optimization. In this study, novel 9-benzyl-6-(furan-2-yl) -2-(N,N dimethylamino)-9H-purine, shows antimalarial agents were designed. ADMET in-silico studies of this 9-benzylpurine derivatives showed good pharmacokinetic profile that makes it orally active and less toxic. This novel 9benzylpurine derivative has good pharmacological adenosine receptors binding and also can be used as leadlikeness (Table 6)

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GRAPHS:



Graph 1: Physicochemical Properties of 9-benzylpurine derivatives



Graph 2: Lipophilicity of 9-benzylpurine derivatives



Graph 3: water solubility

Pharmacokinetics											
High	Yes	No	Yes	Yes	Yes	Yes	Yes	-6.21 cm/s			
Gl absorption	BBB permeant	P-gp substrate	CYP1A2 inhibitor	CYP2C19 inhibitor	CYP2C9 inhibitor	CYP2D6 inhibitor	CYP3A4 inhibitor	Log Kp (skin permeation)			
						Series1		ac			

Graph 4: Pharmacokinetics



Graph 5: Drug likeness