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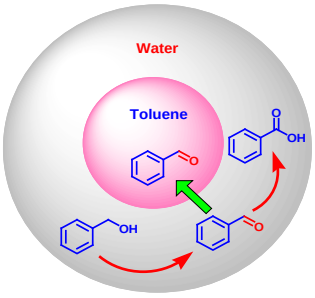
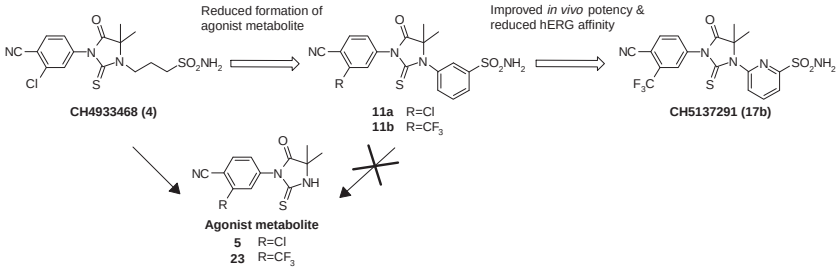
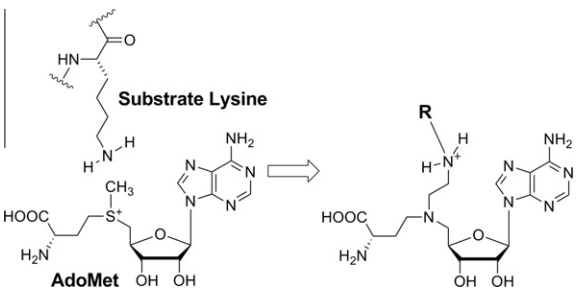
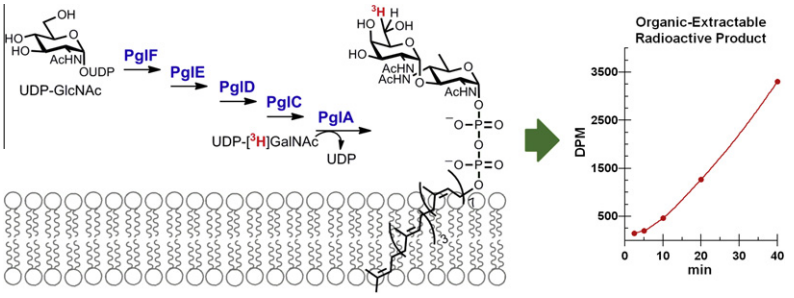
Contents

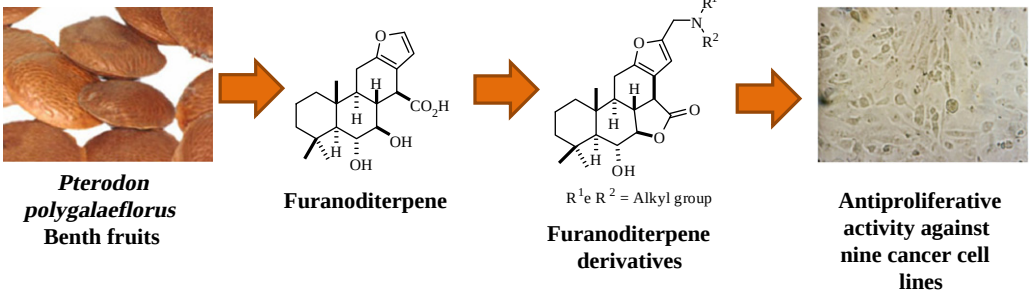
ARTICLES

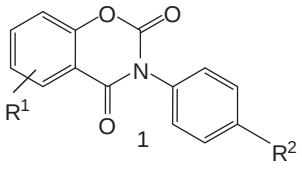




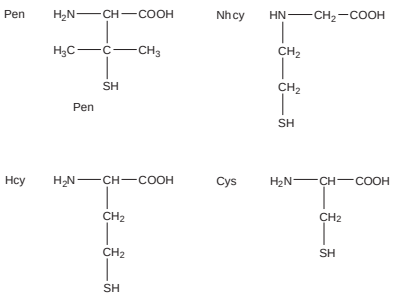


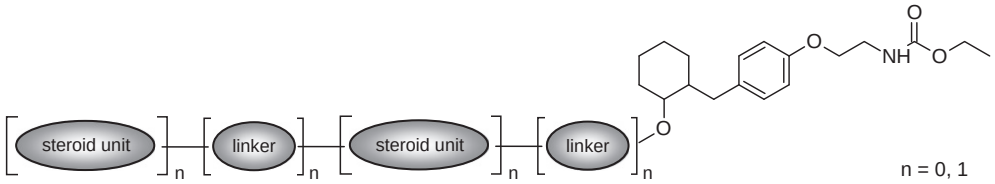


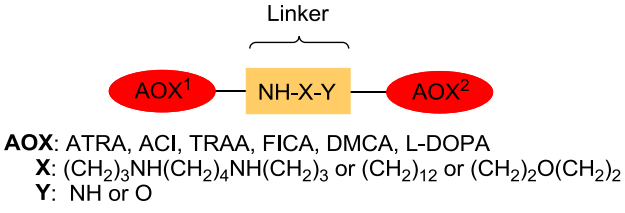


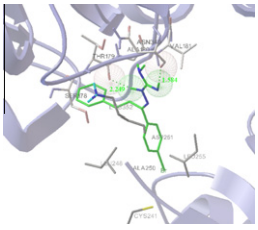


The replacement of the oxo group with the thioxo group in 3-(4-alkylphenyl)-2*H*-1,3-benzoxazine-2,4(3*H*)-diones (**1**) increases the antimycobacterial activity. The most active derivatives are more active than isonicotinhydrazide (INH).



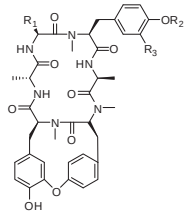




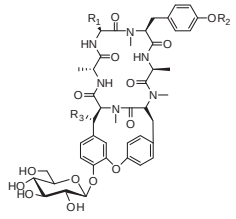


Compound **4q** showed the most potent biological activity (IC_{50} = 0.09 ± 0.01 μM for MCF-7 and IC_{50} = 8.4 ± 0.6 μM for tubulin), which is comparable to the positive controls. Docking simulation was performed to position compound **4q** into the colchicine binding site to determine the probable binding model, which suggested probable inhibition mechanism. Antitubulin polymerization, antiproliferative assay and docking simulation results showed the compound **4q** was a potential anticancer agent.

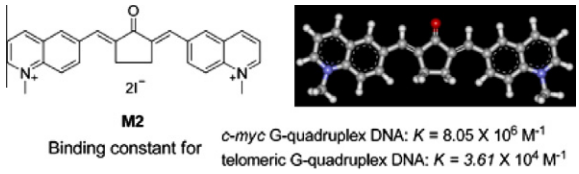
Six new (**1**–**6**) and five known (**7**–**11**) cyclic hexapeptides were isolated from the roots of *Rubia yunnanensis*. This is the first time it is being reported that compounds **2** and **7**–**10** significantly inhibited TNF-α-induced NF-κB pathway activation.



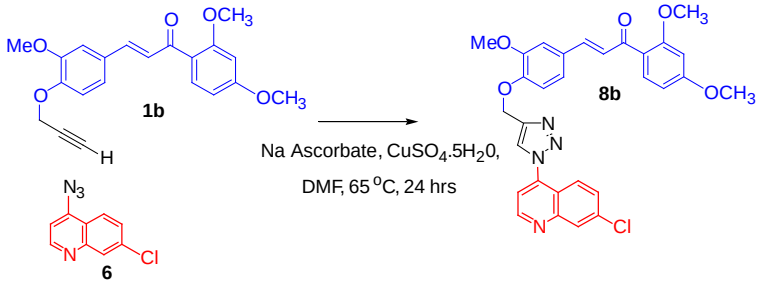
	R_1	R_2	R_3
1	$CH_2CH_2COOCH_3$	CH_3	H
2	CH_2CH_2COOH	H	H
3	CH_2CH_2COOH	CH_3	OH

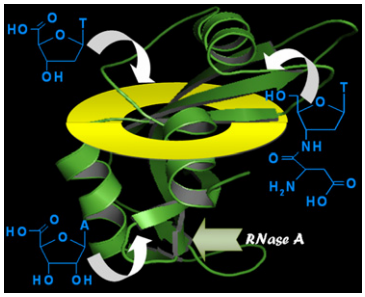


	R_1	R_2	R_3
4	$CH_2CH_2CONH_2$	CH_3	H
5	CH_3	H	H
6	CH_3	CH_3	OH

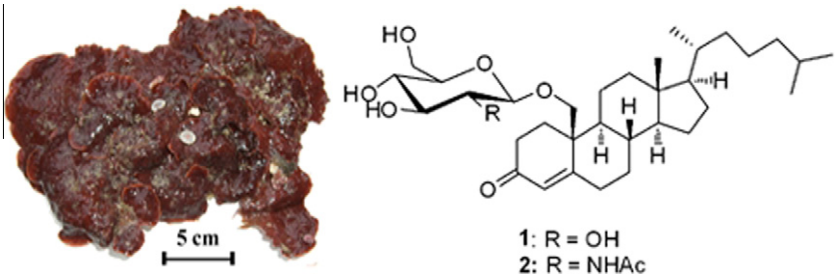


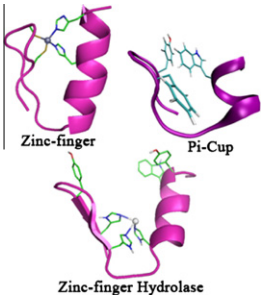
A series of bisaryldiketene derivatives were designed and synthesized as a new class of specific G-quadruplex ligands. The primary binding affinity of ligand **M2** for *c-myc* G-quadruplex DNA was over 200 times larger than that for telomere G-quadruplex DNA.

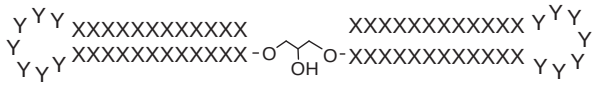


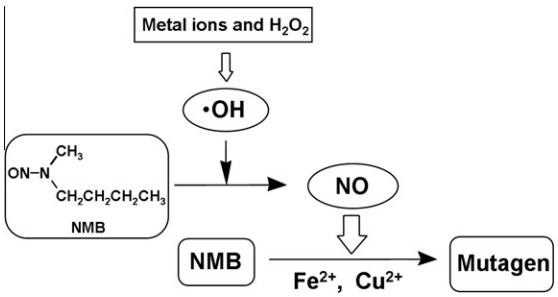


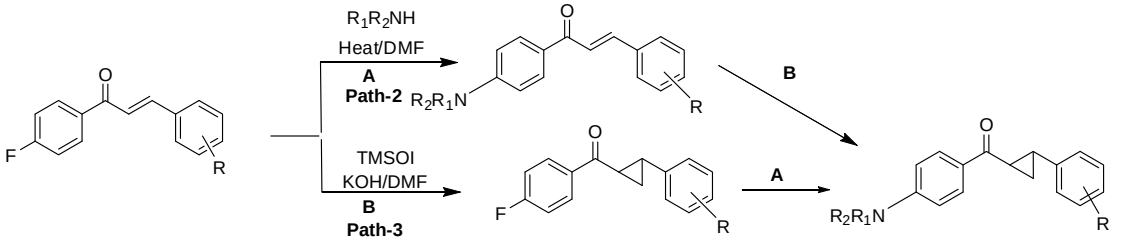
Modification of nucleoside molecules at 5′- and 3′-position with polar ionisable group improve their inhibitory potential on ribonuclease A.



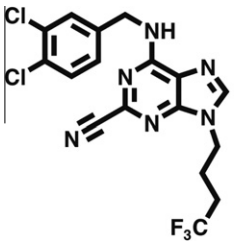




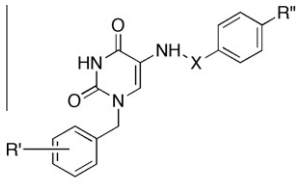




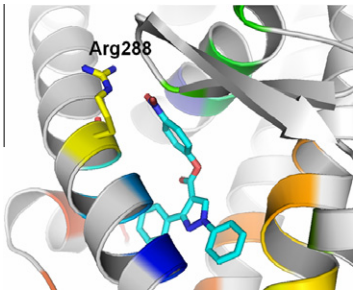
Antitubercular and antimalrial agents
FAS-II inhbitors, in silico screening



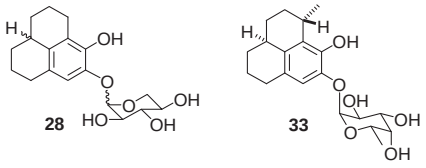
IC_{50} vs. TbcatB	0.6 μM
EC_{50} vs. *T. brucei*	0.53 μM
plasma $t_{1/2}$	177 hrs
microsome $t_{1/2}$	stable
mouse NAETL	>1000 mg/kg
peak plasma conc.	>10 μM



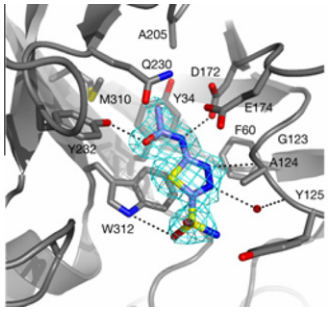
Target pyrimidines



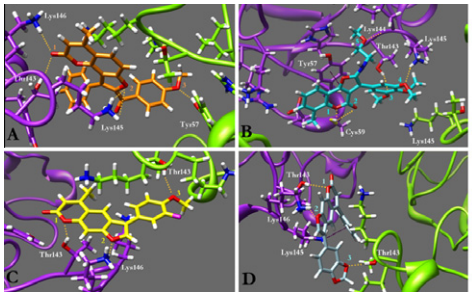
This study presents new findings of pyrazole derivatives as PPAR partial agonists and significantly improves the understanding of their SARs.

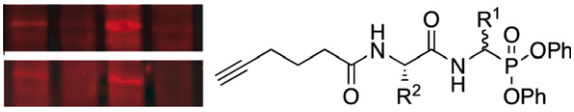


New synthetic pseudopterosin analogues have been shown to possess strong in vivo anti-inflammatory activity, which is conserved over a wide range of structural modifications.

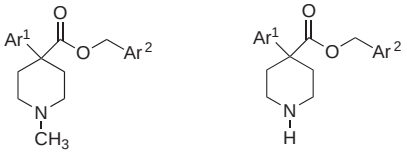


Four commercial available furocoumarin derivatives were selected from VS studies of a focus library against NF-κB for further biological evaluation. Three of the identified molecules (**6f**, **7f** and **9f**) significantly inhibited NF-κB dependent biological functions and might be of interest for experimental therapy of cystic fibrosis.



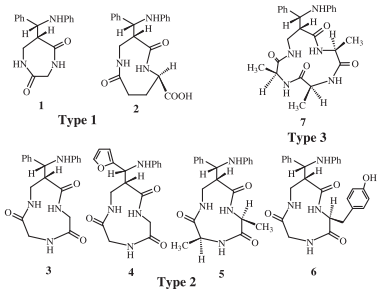


Eight dipeptidyl phosphonate probes were synthesized and used for substrate-based protease identification in soluble brain and pituitary gland proteomes.

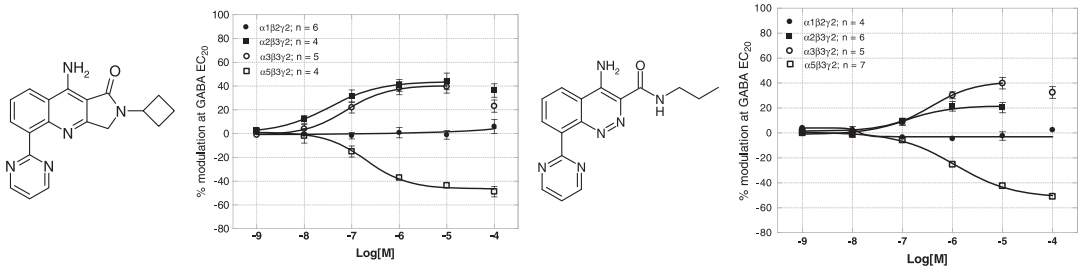


Ar^1 = 4-Cl-Ph, 3,4-Cl_2-Ph, 4-I-Ph, 2-naphthyl

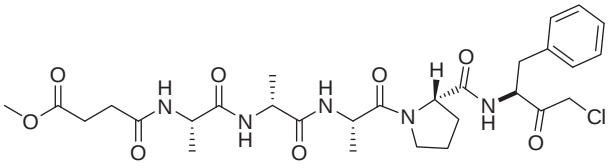
Ar^2 = Ph, 4-BrPh, 4-I-Ph, 4-CH_3OPh, 4-NO_2Ph, 4-CF_3Ph, 4-Ph-Ph, 3,4-Cl_2Ph, 2-naphthyl



Compound	K_i(μM)
1	140.2 ±10
2	36.3 ±8.5
3	85.5 ±7.3
4	215.4 ±12
5	220.2 ±11
6	8.0 ±.20
7	199.1 ±10

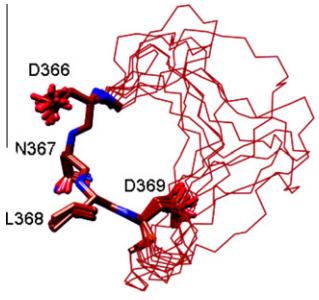


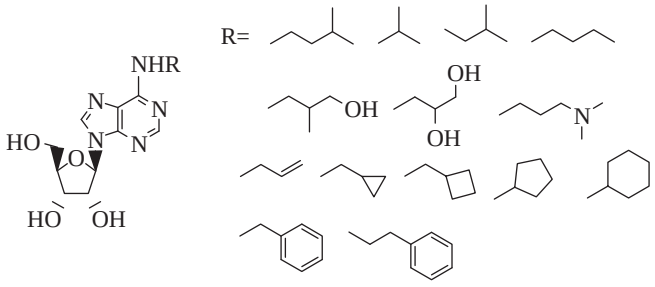
New structural classes of dual functional benzodiazepine-site allosteric modulators of $GABA_A$ receptors are reported.

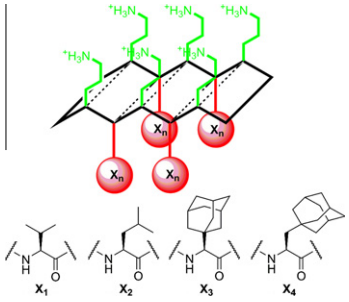


Design, synthesis and proteolytic inhibitor function of new modified pentapeptide MeOSuc-AAAPF-CH_2Cl **6** is described.

In this study we present the use of a cyclic peptide library with conformational diversity for selecting an active and stable peptide that mimics the structure and activity of the HIV-1 integrase (IN) binding loop from its cellular cofactor LEDGF/p75 (residues 361–370). Shown is the NMR solution structure ensemble of *c*(MZ 4-1), the most active LEDGF 361–370-derived cyclic peptide, in the presence of IN. The backbone RMSD for the final ensemble of structures of the unbound *c*(MZ 4-1) was 1.74 Å, and the local RMSD for residues 366–369 (sticks) was 0.46 Å. In the presence of IN the local RMSD of the same region decreased to 0.04 Å (sticks) while the rest of the cyclic peptide is flexible. Our results indicate that this cyclic peptide, when coupled with FDA-approved drugs, may show combined improved anti-HIV activity. c(MZ 4-1) mimics the bioactive conformation of LEDGF/p75 361–370.







OTHER CONTENT

*Corresponding author
Supplementary data available via ScienceDirect

COVER

An insight into biologically relevant chemical space showing the scaffolds of potential natural-product based inhibitors orbiting their target, the protein structure of protein 11-beta steroid dehydrogenase (PDB code 1xu7). Graphic produced using Pymol (http://www.pymol.org). [M. A. Koch, A. Schuffenhauer, M. Scheck, S. Wetzel, M. Casaulta, A. Odermatt, P. Ertl, H. Waldmann, Charting biologically relevant chemical space: A structural classification of natural products (SCONP), *PNAS* **2005**, *102*, 17272–17277 and S. Wetzel, H. Waldmann, Cheminformatic analysis of natural products and their chemical space, *Chimia* **2007**, *61*(6), 355–360].

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