



5th International Electronic Conference on Medicinal Chemistry

1-30 November 2019

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Enhancing anticancer activity of spiropyrazoline oxindoles by disrupting p53-MDMs PPIs

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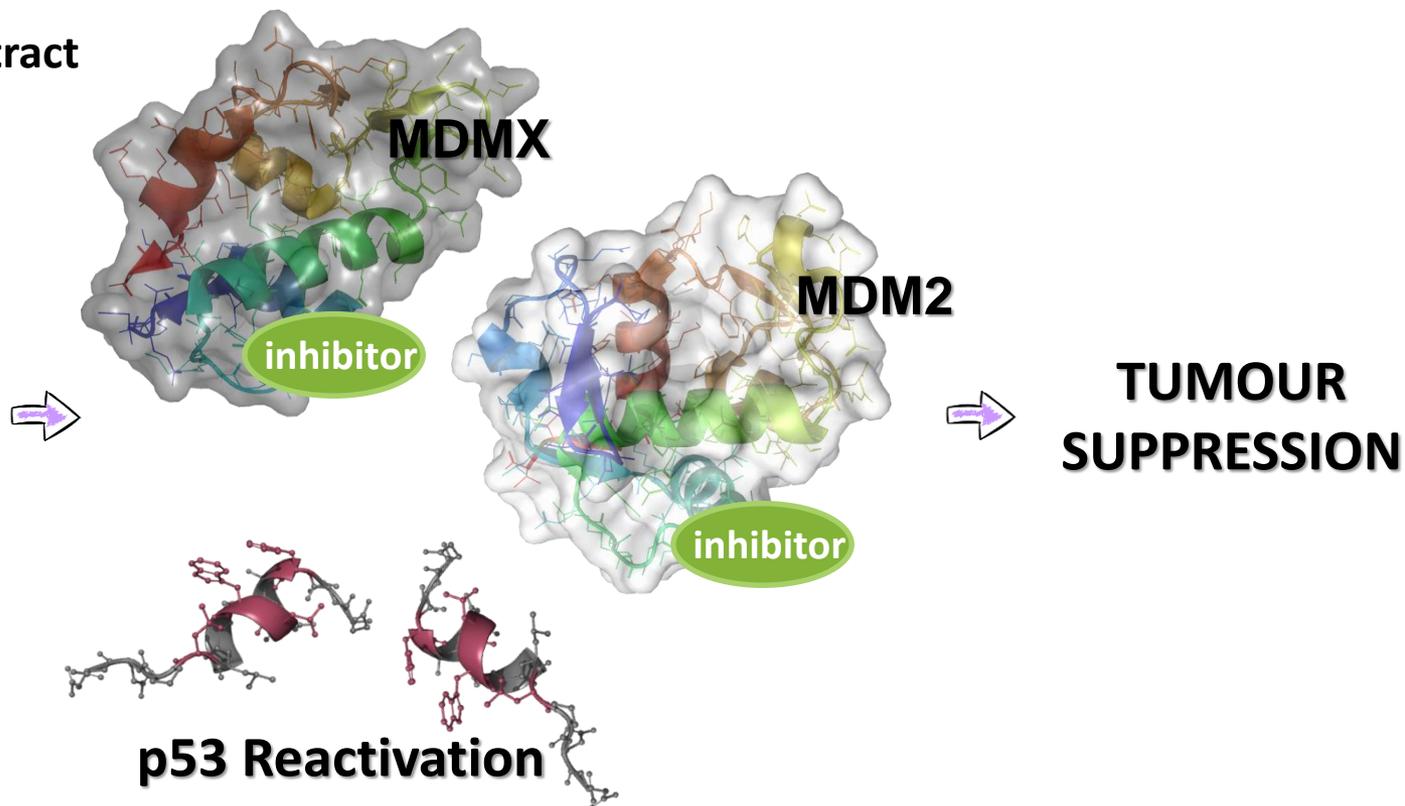
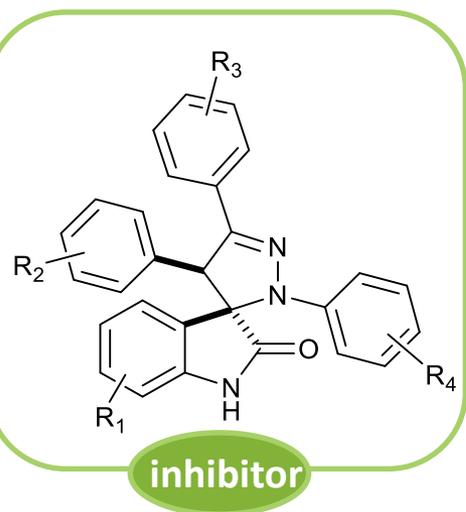
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Enhancing anticancer activity of spiropyrazoline oxindoles by disrupting p53-MDMs PPIs

Graphical Abstract



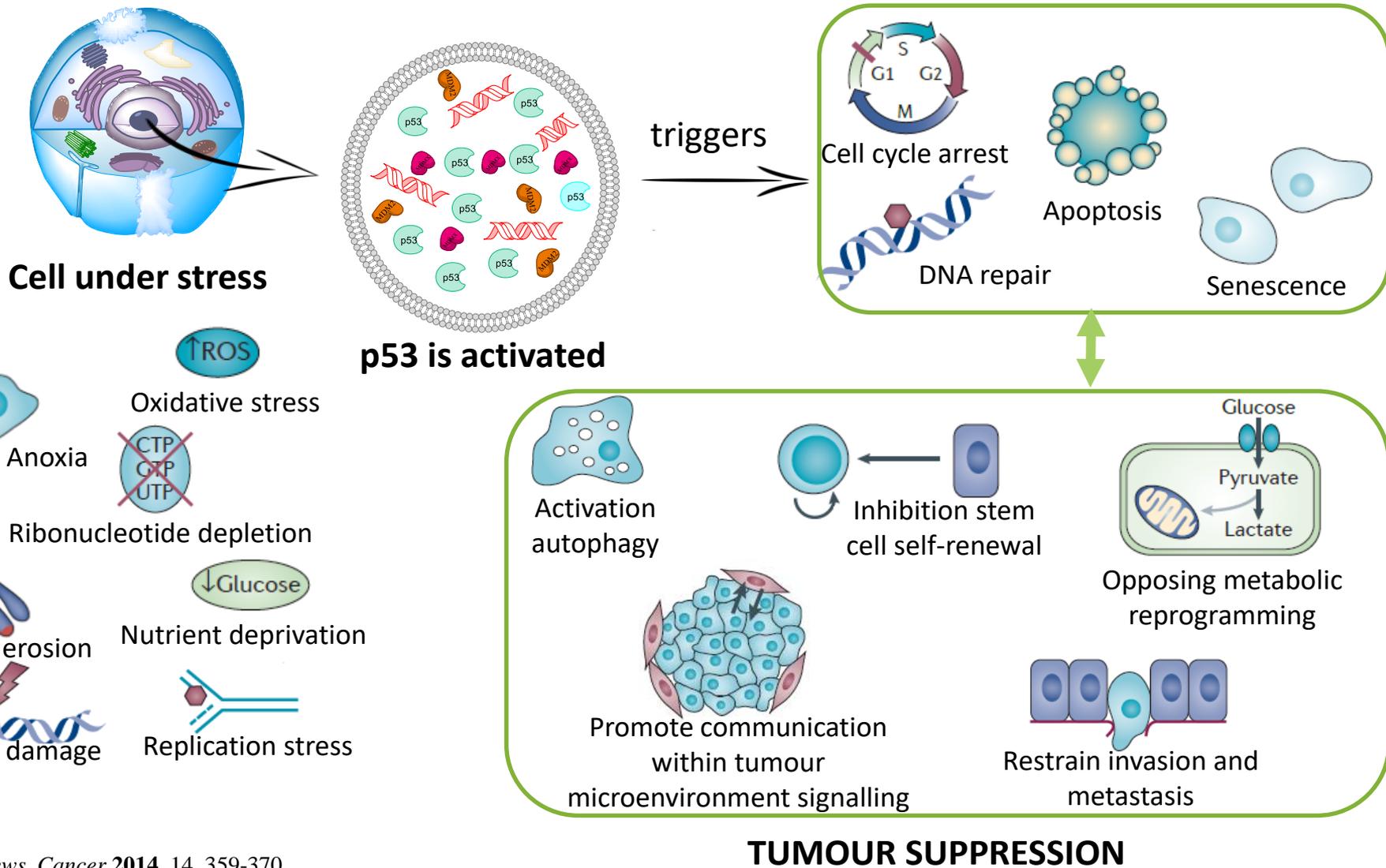
Abstract:

The protein p53 is an attractive target in oncology because it can modulate several additional cellular processes that are relevant for the suppression of tumour development. In all types of human cancers, the p53 tumour suppressor function is inactivated by mutation or gene deletion or by negative regulators. For the full reactivation of wild-type p53, both interactions of p53 with the negative regulators have to be inhibited. Due to the lack of dual p53-MDM2/X PPIs inhibitors in clinical trials, it is urgent to develop small molecules that inhibit these interactions. Our research team has been working on the development of spiropyrazoline oxindoles to obtain dual p53-MDM2/X PPIs inhibitors. Hence, we have already developed derivatives with good antiproliferative activities in HCT-116 p53^(+/+) human colorectal carcinoma cell line, which induce apoptosis and cell cycle arrest at G0/G1 phase, and lead to a decrease of MDM2 levels. In this communication, we report the *hit-to-lead* optimization of this chemical family for the development of novel p53-MDM2/X interactions inhibitors. Furthermore, we report our most recent optimization of the synthesis of these new spiropyrazoline oxindoles derivatives and the first preliminary biological results.

Keywords: p53 activation, spiropyrazoline oxindoles, MDM2, MDMX



Introduction – p53 tumour suppressor



Nature Reviews. Cancer 2014, 14, 359-370.

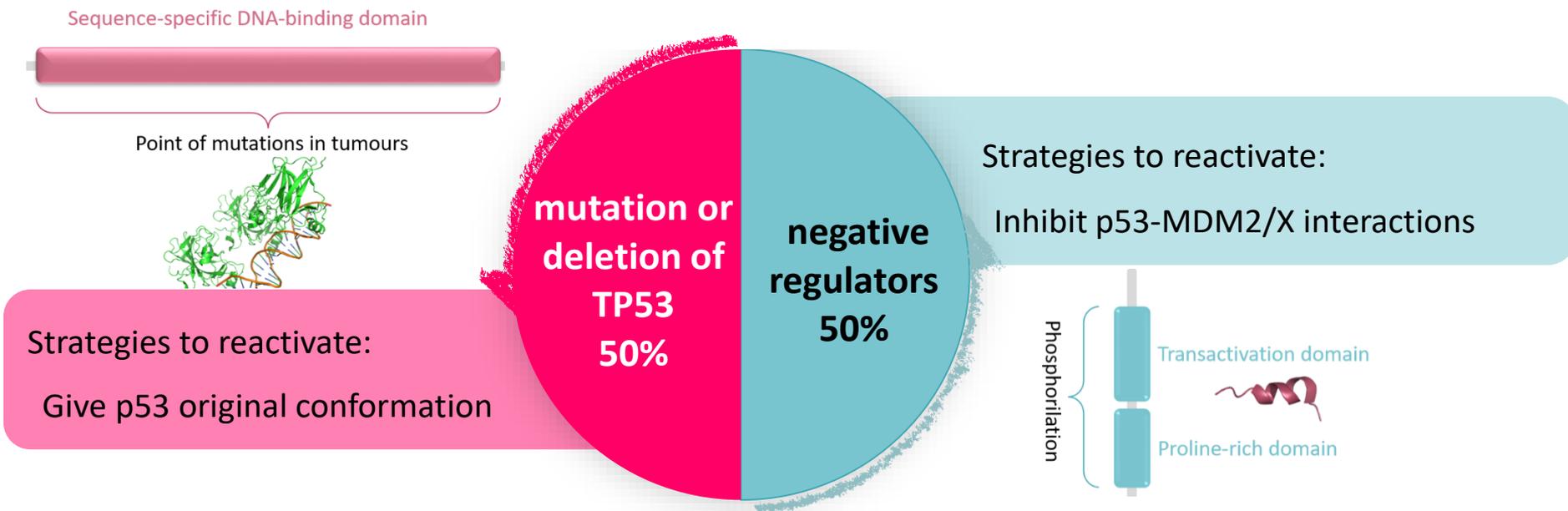


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Introduction – p53 inactivation in tumours

The p53 tumour suppressor function is **inactivated in all** tumours

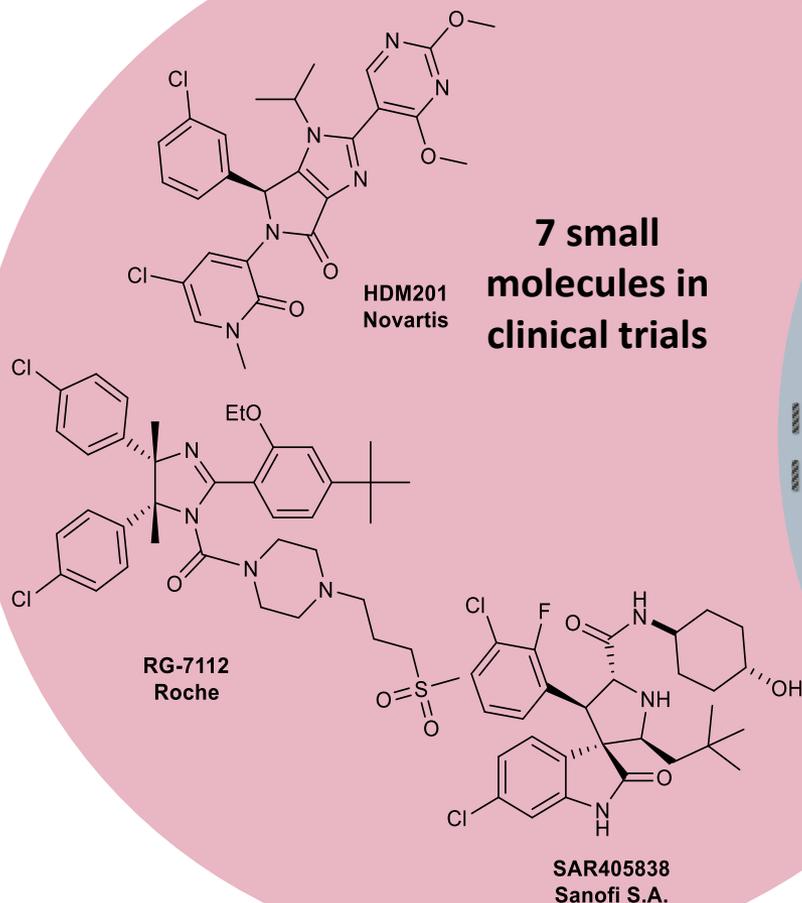


Full reactivation of p53 can only be achieved by inhibition of dual p53-MDM2 and p53-MDMX PPIs

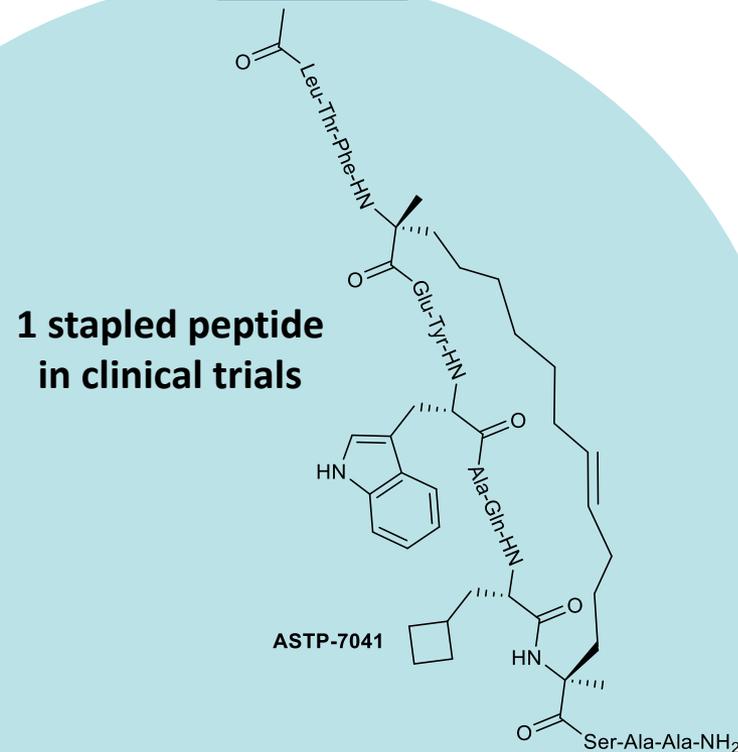


Introduction – p53-MDM2 and p53-MDMX PPIs inhibitors in clinic

MDM2



MDMX



**NO DUAL
INHIBITORS
IN CLINICAL
TRIALS**

Curr. Topics Med. Chem. **2018**, 18, 647-660.



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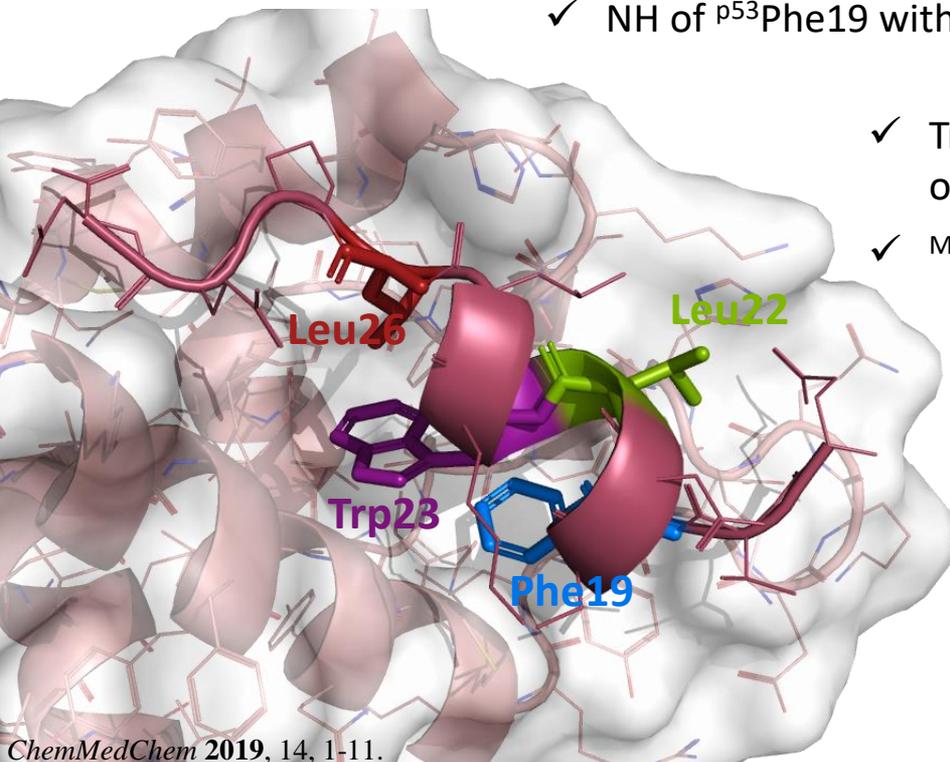
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Introduction – Understanding MDM2 and MDMX pockets

MDM2

- ✓ Interacts with p53 by 4 amino acid residues: p^{53} Phe19, p^{53} Leu22, p^{53} Trp23, p^{53} Leu26
- ✓ Intermolecular van der Waals contacts
- ✓ Two hydrogen bonds
 - ✓ NH of p^{53} Trp23 with $MDM2$ Leu54 (2.8Å)
 - ✓ NH of p^{53} Phe19 with $MDM2$ Gln72 (3.0Å)

Important
pharmacophore
feature



- ✓ Trp23 sub-pocket can adapt its side chain depending on the groups in the Trp23 and Leu26 sub-pockets
- ✓ $MDM2$ His96 (Leu26 sub-pocket) can adapt its side chain

Other important features:

- ✓ π - π stacking interaction with $MDM2$ His96 (enthalpic based binding)
- ✓ $MDM2$ Tyr67 “out conformation” of Phe19 sub-pocket enlarges the space and leads to higher affinity

ChemMedChem 2019, 14, 1-11.



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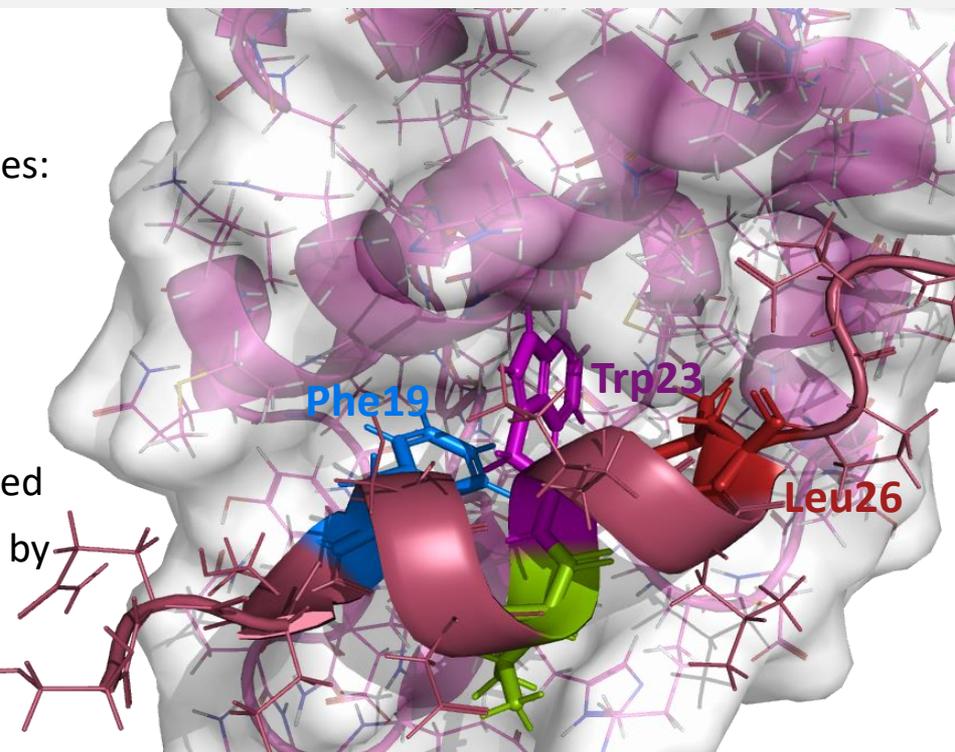


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Introduction – Understanding MDM2 and MDMX pockets

MDMX

- ✓ Interacts with p53 by 4 amino acid residues: p53Phe19, p53Leu22, p53Trp23, p53Leu26
- ✓ Phe19 sub-pocket similar to MDM2
- ✓ Trp23 sub-pocket is 2.0 Å shorter
- ✓ MDM2His96 is replaced by MDMXPro96 residue
 - ✓ No longer π - π stacking interaction is needed
- ✓ MDM2Leu54 and MDM2Ile99 are replaced by MDMXMet54 and MDMXLeu99
 - ✓ Leu26 pocket is more shallow and deeper



Other important features:

- ✓ Carboxylate group can induce a flip of His55 enabling a strong hydrogen bond
 - ✓ Water-mediated hydrogen bond with Lys51
- ✓ Interactions with His55 can compensate weaker interactions in the Leu26 and Trp23 sub-pockets
- ✓ Induction of dimerization of MDMX complexes

ChemMedChem 2019, 14, 1-11.



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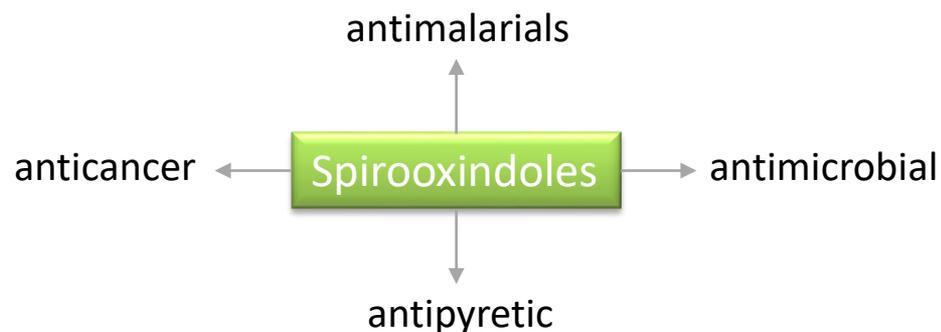
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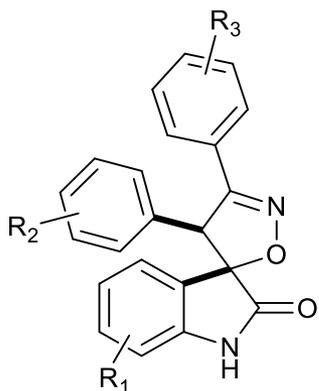
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Introduction – Spirooxindoles

Biological activities of spirooxindoles



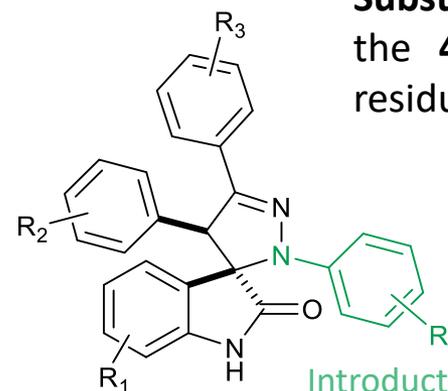
First spirooxindole derivative synthesized by our group



Spiroisoxazoline oxindoles

- ✓ Library of 18 new compounds;
- ✓ Tested in human colorectal carcinoma cell lines
- ✓ p53-MDM2 interaction inhibitor.

Spiropyrazoline oxindoles



Substituents mimic the 4 amino acid residues of p53:

- ✓ Phe19
- ✓ Leu22
- ✓ Trp23
- ✓ Leu26

Introduction of a fourth substituent

Bioorg. Med. Chem. **2014**, *22*, 577-584



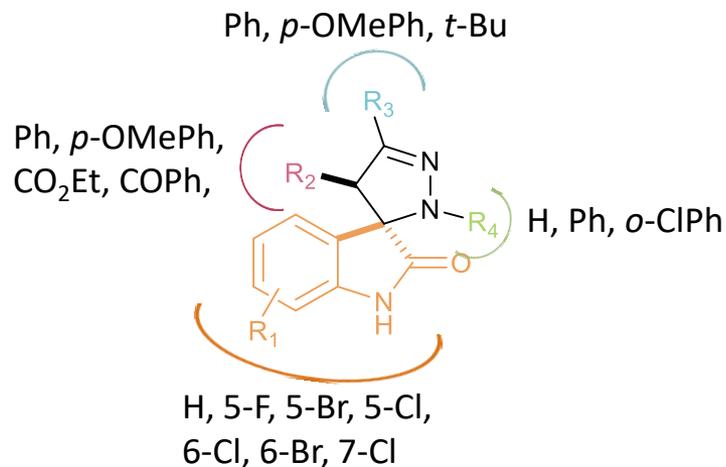
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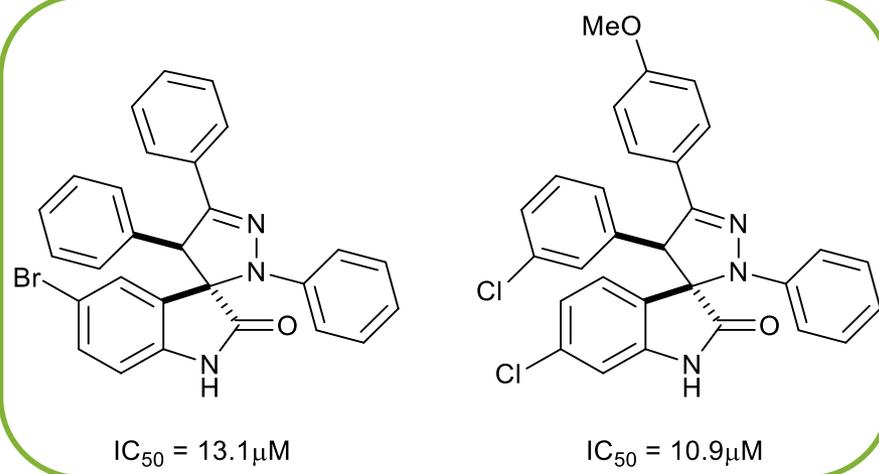
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Introduction – *Spiropyrazoline oxindoles*



- ✓ Library of 32 new compounds
- ✓ Evaluated in human colorectal carcinoma cell line HCT-116 *p53*^(+/+) (*wild-type p53*)
- ✓ Non-cytotoxic against HEK293T cell line up to 100 μM

Identified as *hit* compounds



Selected for further studies, including molecular docking

- ✓ Disrupt p53-MDM2 PPI (BiFC assay)
- ✓ Decrease MDM2 level
 - ✓ Other mechanisms besides p53-dependent effects
- ✓ Induce apoptosis
- ✓ Induce cell cycle arrest in G₀/G₁ phase in a time-dependent manner

Eur. J. Med. Chem. **2014**, 79, 266-272. *Eur. J. Med. Chem.* **2017**, 139, 168-179.



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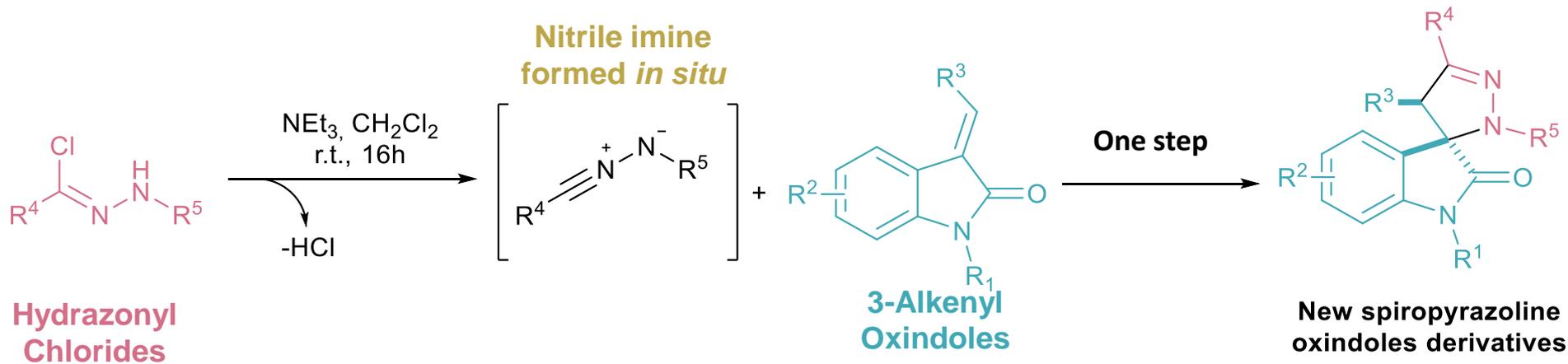
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Results and discussion – *Synthesis*

1,3-dipolar cycloaddition



- ✓ High yields
- ✓ Commercially available starting materials

Eur. J. Med. Chem. **2014**, 79, 266-272. *Eur. J. Med. Chem.* **2017**, 139, 168-179. *Frontiers in Chemistry* **2019**, 7, article 15.



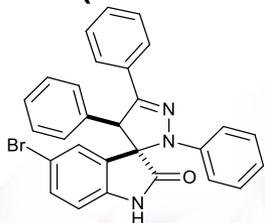
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Results and discussion – *In silico* design

Docking pose of the binding of *hit compound* already identified and MDM2 (PDB ID 4WT2)



cation- π interaction
Ph ring and aromatic
ring of ^{MDM2}His96

π - π interaction
Ph ring and
^{MDM2}Tyr67

Hydrogen bond
NH of indole moiety and
C=O of ^{MDM2}Leu54

Ligand energy minimization: SZYBK1
(force field MMFF94S)
Software: Fred 3.2.0.2 (rigid receptor)
Validation with redocking of SAR405838



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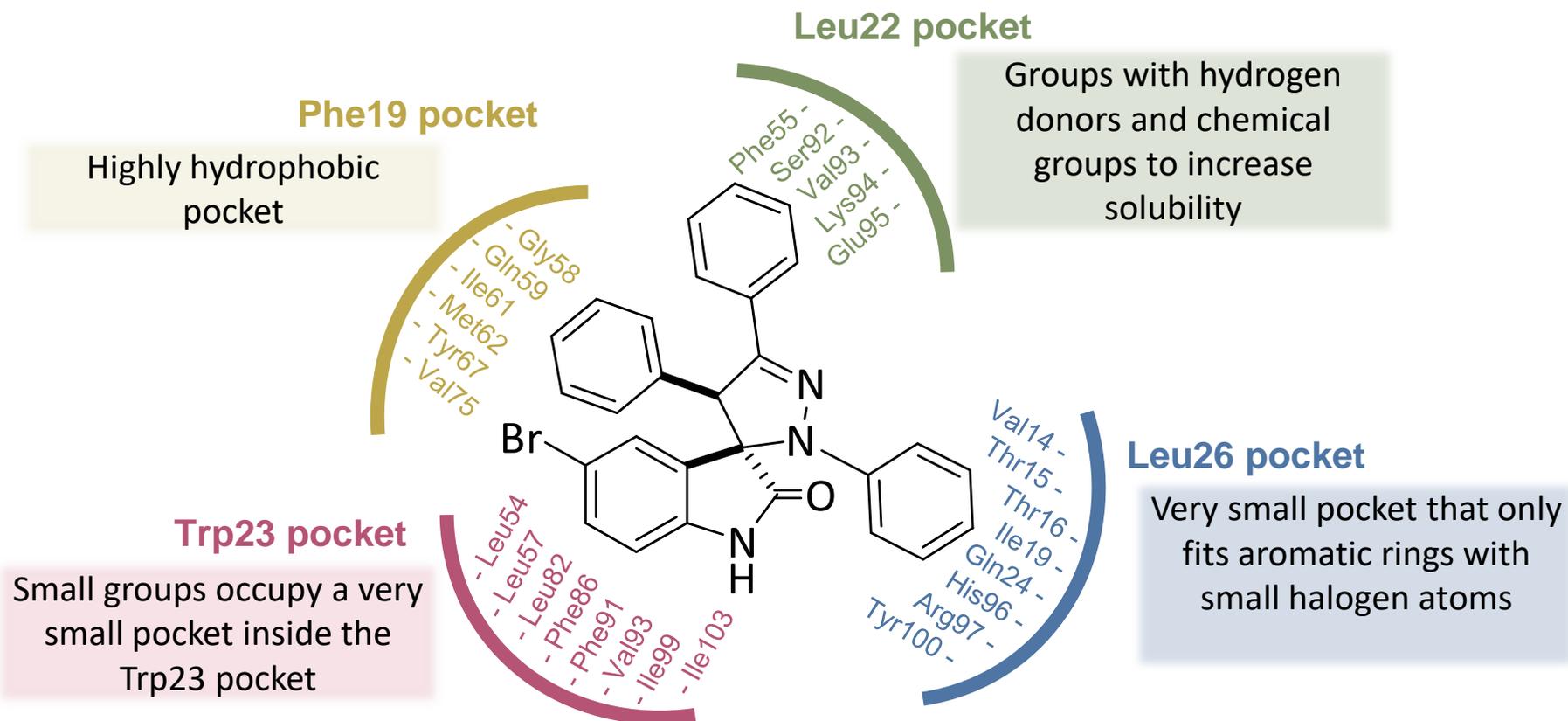
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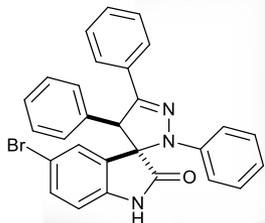
Results and discussion – *In silico* design

MDM2 optimizations



Results and discussion – *In silico* design

Docking pose of the binding of *hit* compound already identified and MDMX (PDB ID 3LBJ)



MDMX

Mainly hydrophobic interactions
No hydrogen bonds

Ligand energy minimization: SZYBKI (force field MMFF94S)

Software: Fred 3.2.0.2 (rigid receptor)

Validation with redocking of WK298 (MDMX)



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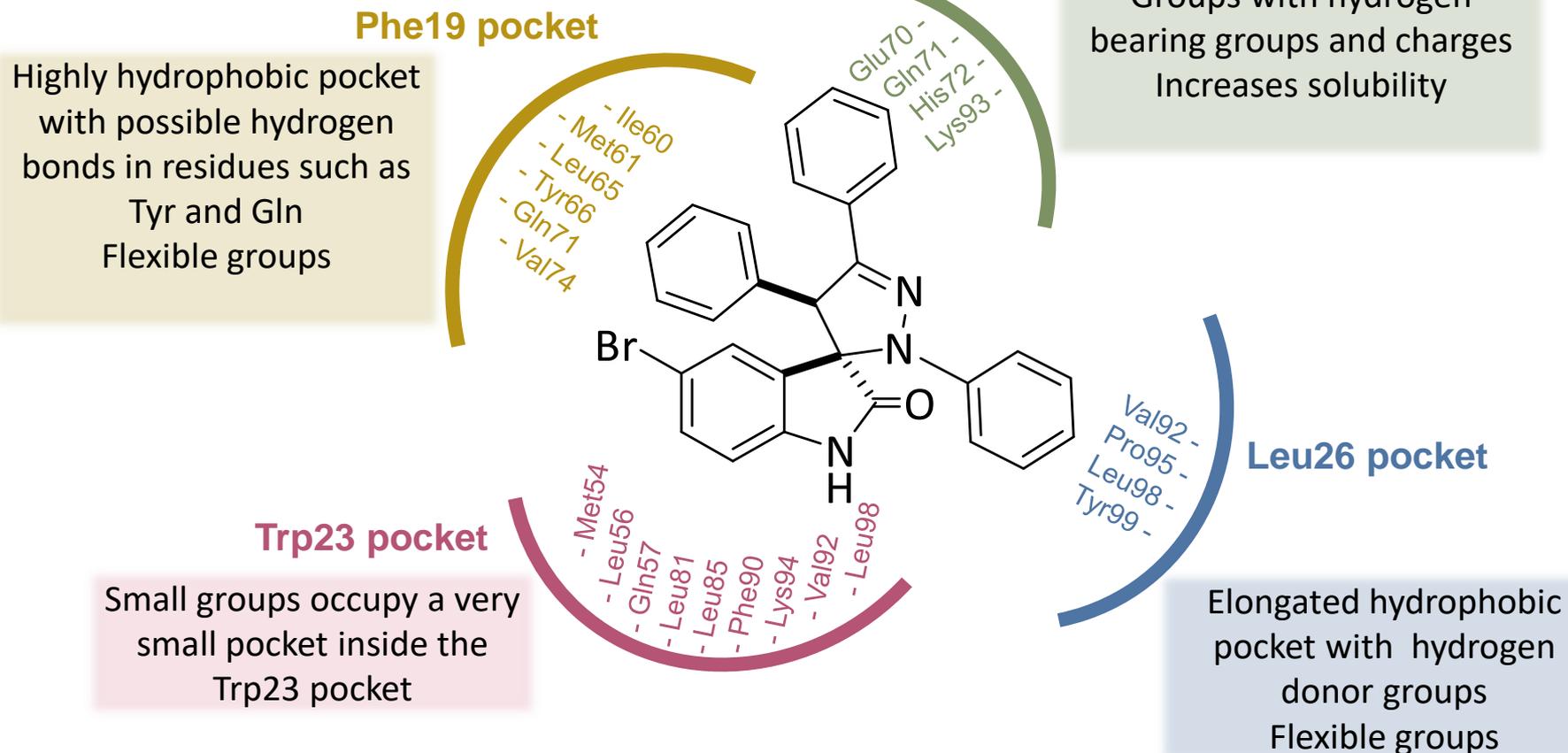
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Results and discussion – *In silico* design

MDMX optimizations



Results and discussion – *Biological evaluation*

A NEW CHEMICAL LIBRARY OF 30 COMPOUNDS



- ✓ MDM2 fluorescence polarization (FP) competitive binding assay

Hit compound ($IC_{50}=10\mu M$)



- ✓ Screening of the new library in human colorectal carcinoma cell lines
 - ✓ HCT116 p53^(+/+)
 - ✓ HCT116 p53^(-/-)

Current work



2 new compounds more active than the positive control



Conclusions

Synthesis

- ✓ Spiropyrazoline oxindoles are synthesized by 1,3-dipolar cycloaddition between 2-indolinones and nitrile imines formed *in situ* from hydrazonoyl chlorides.

In silico design

- ✓ Spiropyrazoline oxindoles establish the two important pharmacophore interactions: the hydrogen bond between ^{MDM2}Leu54 and NH of the indole moiety and π - π stacking interaction with ^{MDM2}His96
- ✓ Possible interactions around MDMX binding pocket can lead to extra interaction between MDMX and spiropyrazoline oxindoles and help to keep the ligand in the binding pocket.

Biological evaluation

- ✓ It was identified a *hit* compound by MDM2 fluorescence polarization (FP) competitive binding assay.
- ✓ Currently, it is being performed a screening in several cancer cell lines with *wild-type* p53.
- ✓ MDMX competitive binding assay – FUTURE WORK



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