

6th International Electronic Conference on Medicinal Chemistry

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Optimizing the oxazoloisoindolinone family: identification and biological evaluation of a potent and selective indolebased p53 activator in human colorectal cancer

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FACULDADE DE FARMÁCIA Optimizing the oxazoloisoindolinone family: identification and biological evaluation of a potent and selective indole-based p53 activator in human colorectal cancer



Graphical Abstract



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Abstract:

With 1.8 million new cases in 2018, Colorectal Cancer (CRC) is considered one of the most malignant cancers due to its frequency and high rate of mortality. The molecular pathogenesis of CRC involves in 40-50% of cases mutation of protein p53, a longestablished tumor suppressor which inactivation occurs in all human cancers either by protein-protein interaction with its main inhibitors MDM2/X or by hotspot mutation. Unfortunately, patients with mutated p53 gene are likely to develop multidrug resistance, thus likely leading to therapy failure. Our group of research is actively involved in the identification of new p53 modulators and in this work, we want to share our latest results in the identification of **compound 1**, an optimized (R)tryptophanol-derived oxazoloisoindolinone that was found to be six-fold more active than our hit compound SLMP53-1 in colon carcinoma HCT116 cell line (see Graphical abstract). Interestingly, in vitro results show that compound 1 was found to have increased selectivity for HCT116 cells with p53, and with low toxicity in normal cells. Molecular docking simulations and binding assays, reported in this study, give important insights about why this novel enantiopure oxazoloisoindolinone analogue cannot be consider a MDM2 inhibitor.

Keywords: Colorectal cancer; p53; anticancer drug; oxazoloisoindolinones.



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Introduction: Colorectal cancer at a glance



Colorectal cancer (CRC) is the third most common malignancy worldwide







By 2030, the incidence of CRC could soar by 90% and 124 % for patients with age 20 to 34 years old



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p53 and colorectal cancer



It's the most frequently inactivated tumor suppressor

When active p53 regulates

- Apoptosis
- **Cell cycle arrest**
- DNA repair
- Senescence
- Autophagy



50% of cases p53 is inactivated by hotspot mutations on its DNA-binding domain

292

325

356

393

DNA binding domain DBD

62

94

p53 mutation develops in about 40-50% of CRC. Patients with mutated p53 gene gain multidrug resistance



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Hunting p53 activators

To date, most strategies of reactivation of p53 are focused on the inhibition of its main negative regulator MDM2 (a), or on the pharmacological restoration of wild-type-like activity to mutant p53 forms (b).

Our research group have identified several small molecules that are able to activate the p53 pathway



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a)

b)

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Results and discussion: Hit-to-lead optimization strategy



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Screening the oxazoloisoindolinone family in HCT-116 cell line





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25 Oxazoloisoindolinones present a GI₅₀ lower than the hit SLMP53-1

ChemMedChem 2020, doi: 10.1002/cmdc.202000522



20·

15

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GI₅₀ (д)

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Selectivity in HCT-116 cell line for the p53 pathway

Table 1. Phenotypic activity of tryptophanol-derived isoindolinones against HCT116 $p53^{+/+}$ and $p53^{-/-}$ cell growth.			
Compound	HCT116 p53 ^{+/+} Gl ₅₀ [μM]	HCT116 p53 ^{-/-} Gl ₅₀ [μM]	SIª
1	15.5±1.6 ^[30]	$34.0 \pm 3.5^{[30]}$	2.2
10	9.7±0.4	9.7 ± 0.3	1.0
11	8.4±1.1 ^[32]	$17.7 \pm 2.3^{[32]}$	2.1
13	6.35 ± 0.2	7.0 ± 1.1	1.1
14	8.5±0.1	9.5 ± 1.5	1.1
17	4.55 ± 0.1	3.8±0.3	0.8
19	6.2±0.3	7.4 ± 0.1	1.2
20	4.2±0.1	4.8 ± 0.3	1.1
21	8.35 ± 1.65	8.95 ± 0.75	1.1
22	5.2±0.4	5.6±0.7	1.1
23	4.75 ± 0.05	6.3±0.4	1.3
24	5.7±0.2	7.0 ± 0.5	1.2
25	9.6±1.3	16.7 ± 1.9	1.7
26	9.2±0.4	7.3 ± 0.9	0.8
27	6.5 ± 0.6	10.0 ± 1.3	1.5
28	8.0±0.3	5.4 ± 0.4	0.7
29	5.1±0.2	3.6±0.2	0.7
30	7.2±0.2	9.9 ± 1.3	1.4
31	6.7 ± 0.5	9.0±0.4	1.3
32	2.6±0.5	8.6±0.4	3.3
34	7.5±0.9	10.2±0.8	1.4
[a] Selectivity in GI ₅₀ HCT116 p53	dex toward HCT116 p53 3 ^{-/-} /Gl ₅₀ HCT116 p53 ^{+/-}	+/+, which is express	ed by the ratio





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Evaluation of compound 32 as MDM2 inhibitor

p53-MDM2 protein-protein interaction consists of a steric complementary interface between the MDM2 cleft and the hydrophobic residues Phe19, Leu22, Trp23 and Leu26 of the α-helix of p53



- polarization (FP) competitive binding assay was used to evaluate if the molecular target for the activation of p53 observed for compound 32 is MDM2
- Compound 32 was not able to compete with the fluorescent probe molecule that binds potently to MDM2

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Evaluation of compound 32 as MDM2 inhibitor: molecular docking



- indole moiety projected to the Leu26 pocket
- the oxazolidine moiety projected to the Phe19 pocket
- both compounds are unable to fill the four pockets of the MDM2 hydrophobic binding site

SLMP53-1

- does not fill the Trp23 and the Leu22 pockets
- only one hydrogen interaction with the carbonyl group of the backbone of His96

Compound 32

- 9b-phenyl group is projected to the Leu22 solvent-exposed pocket,
- the Trp23 pocket remains unfilled
- the nitro group establishes a hydrogen bond with the nitrogen of the Met6 residue



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Conclusions

In this presentation we briefly described:

synthetic strategy

structure-activity study

of a chemical library of 34 enantiopure tryptophanolderived oxazoloisoindolinones as p53 activators Screening in human colon adenocarcinoma cell line leads to identification of compound 32 (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) + (+) +



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regulator (MDM2)



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