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## Modeling of new VHR inhibitors based on 4H-1,3,5-oxadiazine derivatives.

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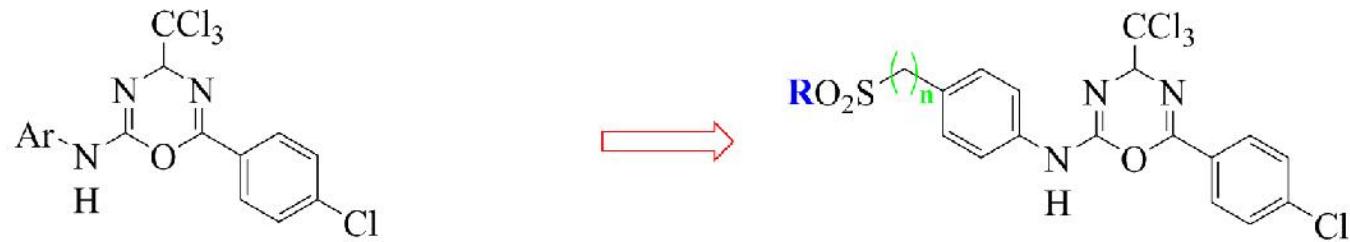
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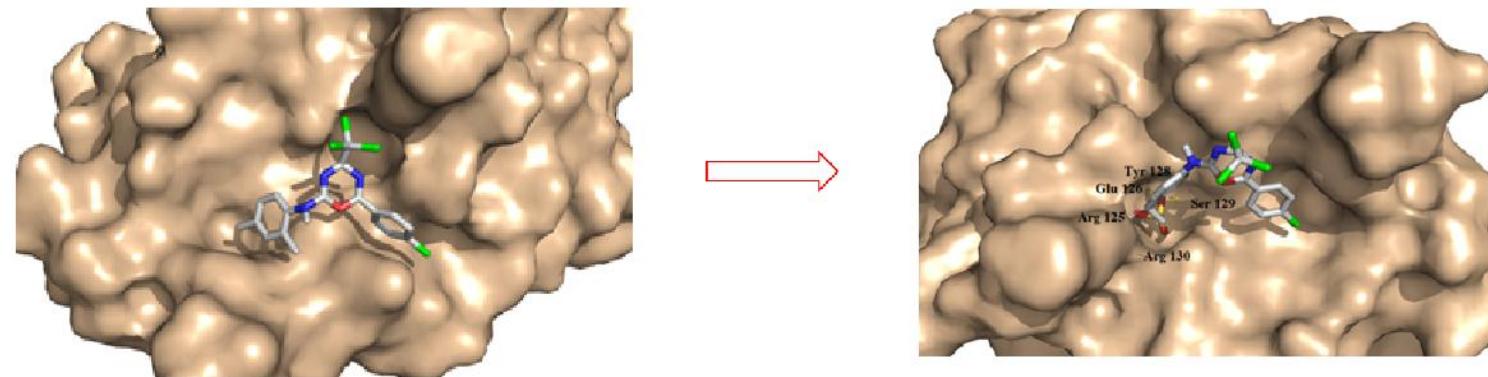
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# Modeling of new VHR inhibitors based on 4H-1,3,5-oxadiazine derivatives.

## Graphical Abstract



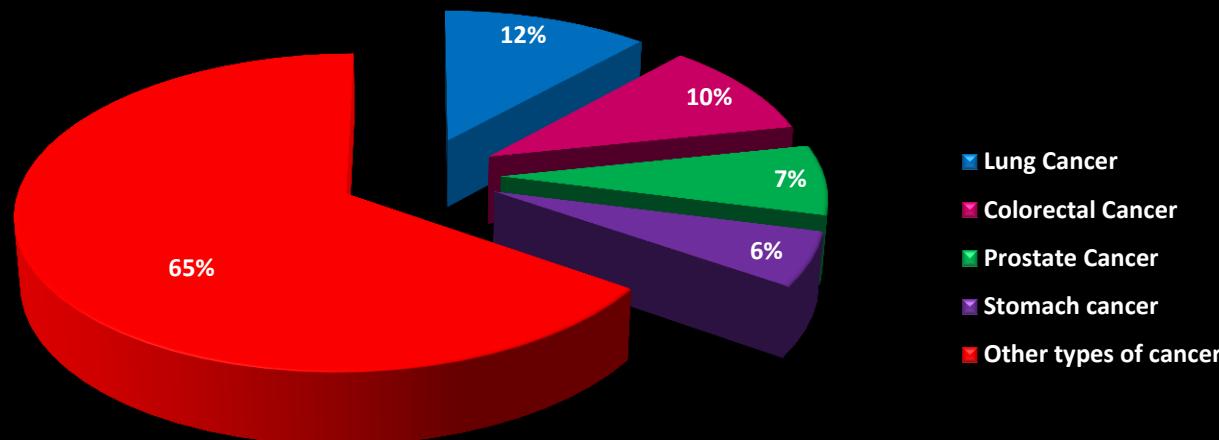
$\text{R} = \text{OH}, \text{OCH}_3, \text{NH}_2;$   
 $n = 0, 1, 2, 3.$



**Abstract:** Vaccinia H1-related phosphatase (VHR) is a dual-specific phosphatase that is a promising potential target for the treatment of many human diseases. In this work, we have proposed a series of 6-(4-chlorophenyl)-N-aryl-4-(trichloromethyl)-4H-1,3,5-oxadiazin-2-amines as potential VHR inhibitors. The SuperPred online server predicts VHR inhibition for the studied compounds with a probability of 88.88-98.51%. To establish the efficiency of binding of 4H-1,3,5-oxadiazine derivatives to the active site of VHR (PDB ID: 3F81) in the AutoDock Vina program, we have carried out molecular docking studies. According to its results, the studied compounds effectively interact with the hydrophobic region of the VHR active site due to aromatic rings and the trichloromethyl group, but the polar catalytic cavity is not involved, and therefore inhibition cannot be effective. In this regard, we have built a number of model compounds containing a sulfate group and its derivatives (methyl ester and amide) in the *para*-position of the arylamine fragment. According to the results of molecular docking, these compounds effectively bind to the polar catalytic cavity of the enzyme due to hydrogen bonds, but due to the relative rigidity of their molecules, hydrophobic interactions are not fully realized. Therefore, in these model compounds between the arylamine fragment and the sulfo group, we introduced a spacer with a length of one to three methylene groups. Hit compounds have been selected - 2-(4-((6-(4-chlorophenyl)-4-(trichloromethyl)-4H-1,3,5-oxadiazin-2-yl)amino)phenyl)ethane-1-sulfonic acid and its amide.

**Keywords:** 4H-1,3,5-oxadiazine; molecular docking; VHR; cancer; inhibitor

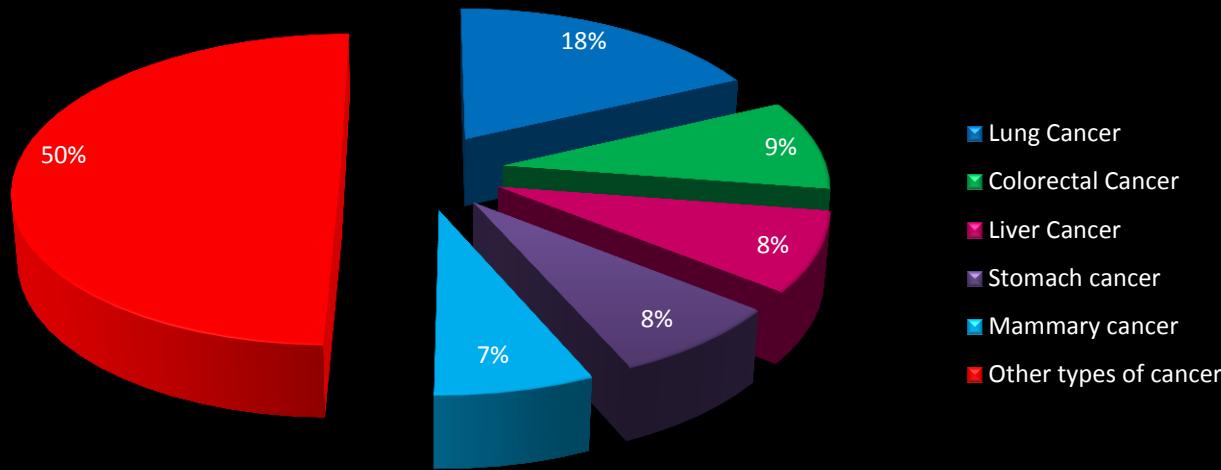
## Introduction



**Figure 1.** Ratio of some newly diagnosed cancers in 2020.

Sung, H.; Ferlay, J.; Siegel, R.L.; Laversanne, M.; Soerjomataram, I.; Jemal, A.; Bray, F. Global Cancer Statistics 2020: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries. *CA Cancer J. Clin.* **2021**, *71*, 209-249.  
<https://doi.org/10.3322/caac.21660>

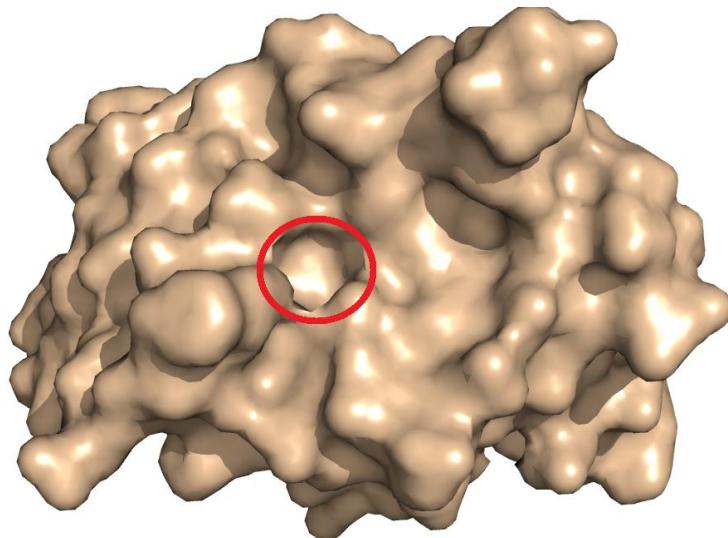
## Introduction



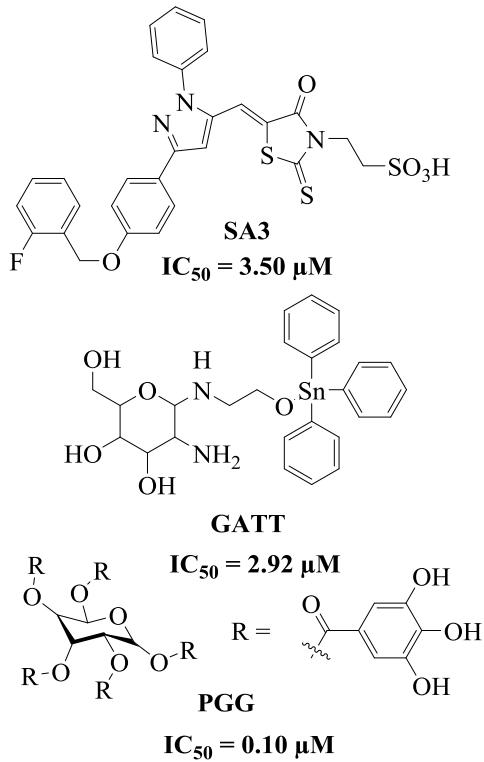
**Figure 2.** The ratio of deaths from certain types of cancer as of 2020.

Sung, H.; Ferlay, J.; Siegel, R.L.; Laversanne, M.; Soerjomataram, I.; Jemal, A.; Bray, F. Global Cancer Statistics 2020: GLOBOCAN Estimates of Incidence and Mortality Worldwide for 36 Cancers in 185 Countries. *CA Cancer J. Clin.* **2021**, *71*, 209-249.  
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# Introduction



(a)



(b)

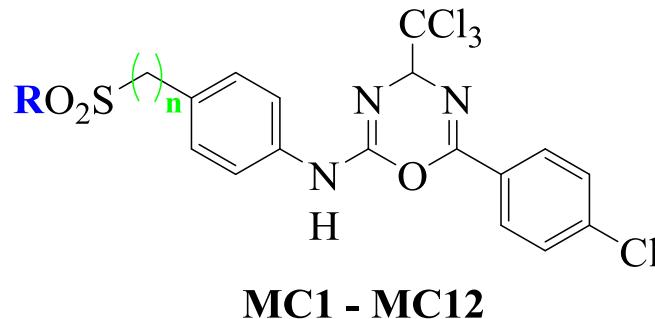
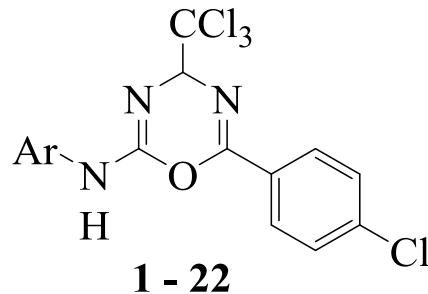
Figure 3. Structure of VHR (a) and some of its inhibitors (b).

Wu, S.; Vossius, S.; Rahmouni, S.; Miletic, A.V.; Vang, T.; Vazquez-Rodriguez, J.; Cerignoli, F.; Arimura, Y.; Williams, S.; Hayes, T.; Moutschen, M.; Vasile, S.; Pellecchia, M.; Mustelin, T.; Tautz, L. Multidentate small-molecule inhibitors of vaccinia H1-related (VHR) phosphatase decrease proliferation of cervix cancer cells. *J. Med. Chem.* **2009**, *52*, 6716-6723. <https://doi.org/10.1021/jm901016k>

Shi, Z.; Tabassum, S.; Jiang, W.; Zhang, J.; Mathur, S.; Wu, J.; Shi, Y. Identification of a potent inhibitor of human dual-specific phosphatase, VHR, from computer-aided and NMR-based screening to cellular effects. *ChemBioChem* **2007**, *8*, 2092-2099. <https://doi.org/10.1002/cbic.200700397>

Yoon, S.Y.; Kim, D.H.; Min Roh, K.; Ahn, D.; Jin Kang, H.; Chung, S.J. Identification of Vaccinia-H1 Related Phosphatase as an Anticancer Target for 1,2,3,4,6-O-Pentagalloylglucose. *Chem. Biodivers.* **2020**, *17*, e1900414. <https://doi.org/10.1002/cbdv.201900414>

# Introduction



**R** = OH,  $\text{OCH}_3$ ,  $\text{NH}_2$ ;  
**n** = 0, 1, 2, 3.

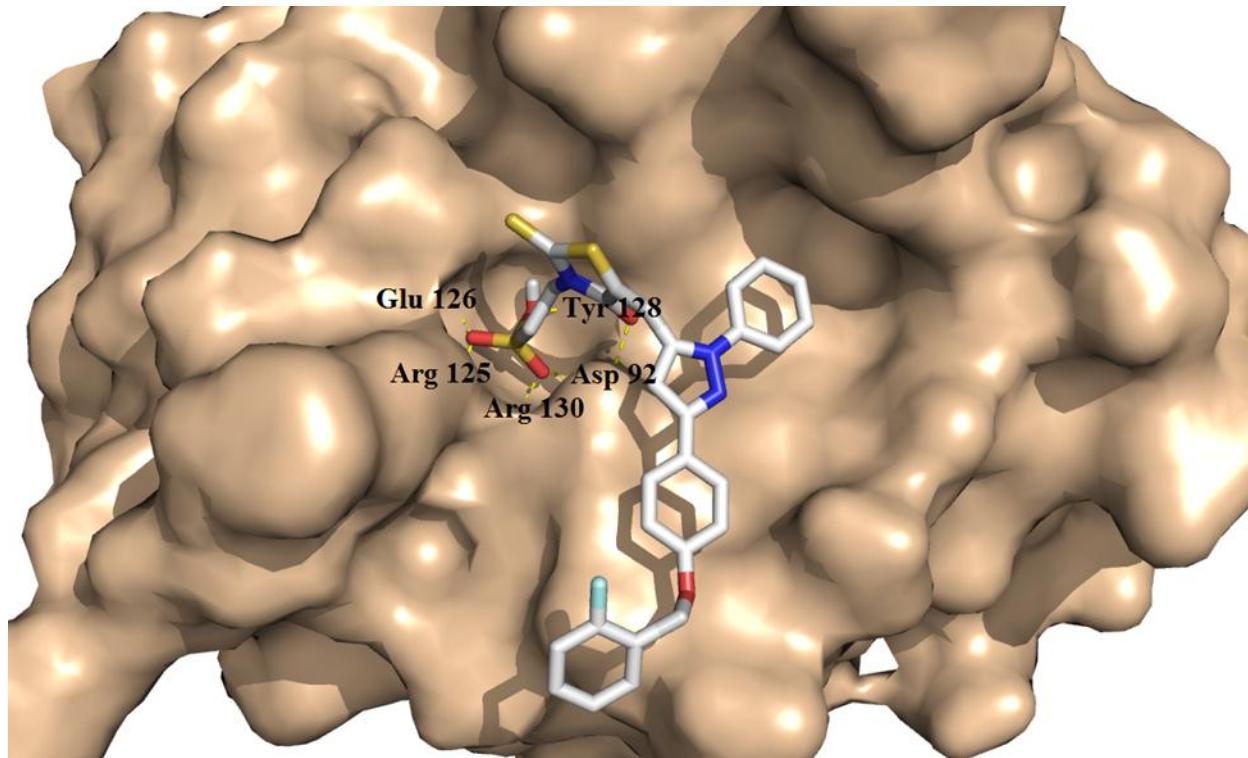
**Figure 4.** Structures of the studied compounds as potential VHR inhibitors.

Zadorozhnii, P.V.; Kiselev, V.V.; Pokotylo, I.O.; Kharchenko, A.V. A new method for the synthesis of 4H-1,3,5-oxadiazine derivatives. *Heterocycl. Commun.* **2017**, 23, 369-374. <https://doi.org/10.1515/hc-2017-0083>

Zadorozhnii, P.V.; Kiselev, V.V.; Pokotylo, I.O.; Okhtina, O.V.; Kharchenko, A.V. Synthesis and mass spectrometric fragmentation pattern of 6-(4-chlorophenyl)-N-aryl-4-(trichloromethyl)-4H-1,3,5-oxadiazin-2-amines. *Heterocycl. Commun.* **2018**, 24, 273-278. <https://doi.org/10.1515/hc-2018-0082>

Zadorozhnii, P.V.; Pokotylo, I.O.; Kiselev, V.V.; Kharchenko, A.V.; Okhtina, O.V. Synthesis and Spectral Characteristics of Some New 4H-1,3,5-Oxadiazine Derivatives. *Res. J. Pharm., Biol. Chem. Sci.* **2019**, 10, 1508-1515.

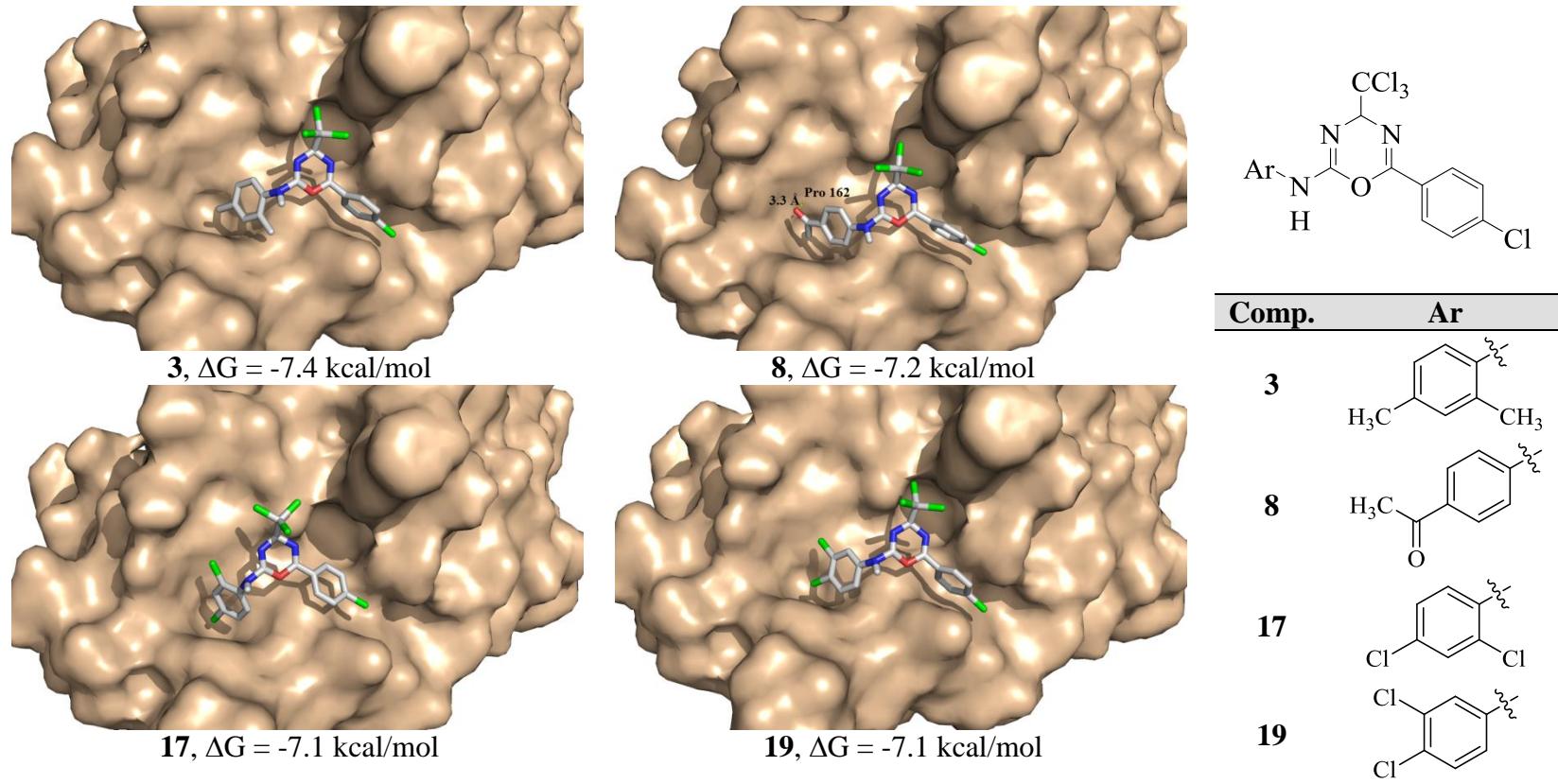
## Results and discussion



Hydrogen bonds	
Amino acid	Length, Å
Asp 92	3.0
Arg 125	3.4
Glu 126	3.0
Tyr 128	3.1
Ser 129	2.9
Arg 130	3.0, 3.2, 3.3

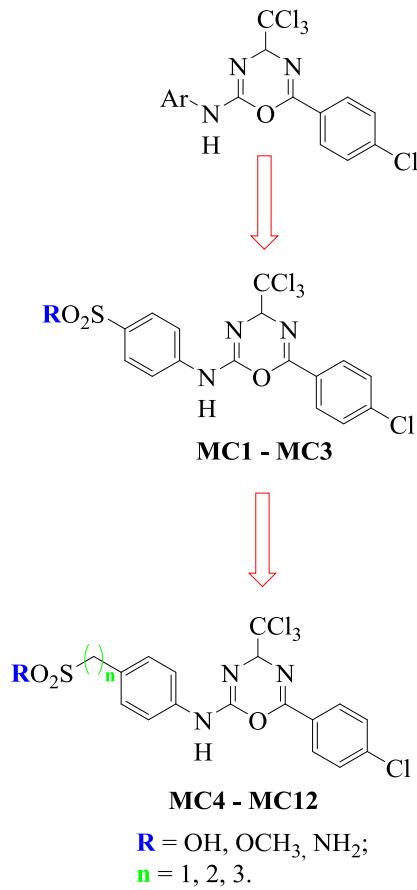
**Figure 5.** The position of the SA3 molecule in the active site of the VHR according to the results of molecular docking studies.

## Results and discussion

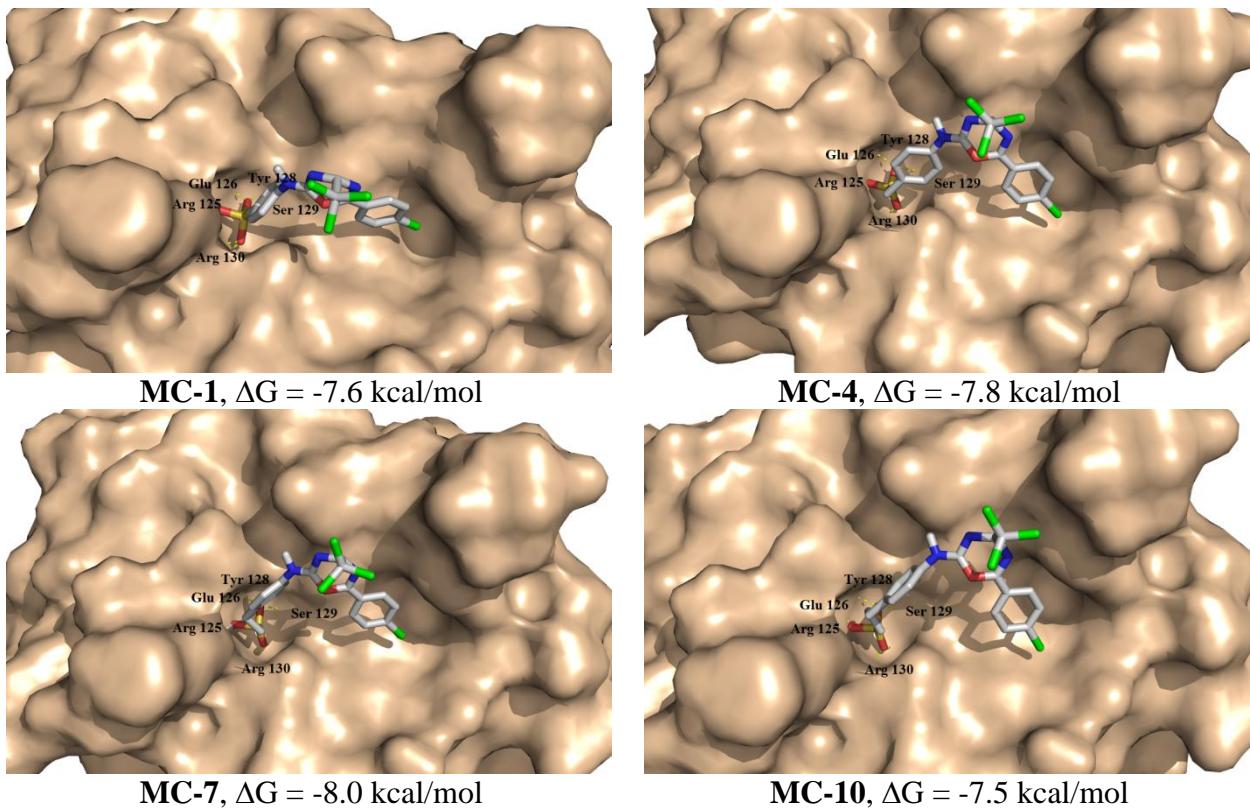


**Figure 6.** Position of molecules **3**, **8**, **17**, and **19** in the VHR active site from molecular docking studies.

# Results and discussion



**Figure 7.** Algorithm for creating model connections **MC1-MC12**.



**Figure 8.** Differences in the position of the molecules of the model compounds in the VHR active site depending on the length of the spacer between the sulfo group and the aromatic ring.

## Conclusions

In this work, using the methods of SAR prediction and molecular docking, we have tested 22 derivatives of 1,3,5-oxadiazine for the potential ability to inhibit VHR. It has been shown that the studied compounds effectively interact with the hydrophobic region of the VHR active site due to aromatic rings and the trichloromethyl group, but interaction with the polar catalytic cavity requires the additional introduction of a highly polar group into the aromatic substituent. In this regard, based on the principles of rational design, we have constructed a series of model compounds containing, directly or through a spacer, a sulfate group and its derivatives (methyl ester and amide) in the *para*- position of the arylamine fragment. According to the results of molecular docking, the most stable complexes with VHR are formed by model compounds containing sulfate or sulfamide groups and a spacer of two methylene groups. Hit compounds have been selected - 2-(4-((6-(4-chlorophenyl)-4-(trichloromethyl)-4*H*-1,3,5-oxadiazin-2-yl)amino)phenyl)ethane-1-sulfonic acid and its amide, which are superior to the known SA3 inhibitor in terms of binding strength to VHR.

# Thank you for your attention!

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