

Supporting information

New prodrugs and analogs of the phenazine 5,10-dioxide natural products iodinin and myxin promote selective cytotoxicity towards human acute myeloid leukemia cells

Elvar Örn Viktorsson^{a,b}, Reidun Aesoy^c, Sindre Støa^a, Viola Lekve^c, Stein Ove Døskeland^d, Lars Herfindal^c and Pål Rongved^a

^a School of Pharmacy, Department of Pharmaceutical Chemistry, University of Oslo, PO Box 1068 Blindern, N0316 Oslo, Norway.

^b School of Health Sciences, Faculty of Pharmaceutical Sciences, University of Iceland, Hofsvallagata 53, IS-107 Reykjavik, Iceland

^c Centre for Pharmacy, Department of Clinical Science, University of Bergen, Jonas Lies vei 87, N-5021 Bergen, Norway

^d Department of Biomedicine, University of Bergen, Jonas Lies vei 91, N-5021 Bergen, Norway

*Corresponding author: pal.rongved@farmasi.uio.no

KPLS-model of activity of iodinin-analogs towards MOLM-13 and NRK cells, and for identification of hypoxia-relevant moieties.

1: Generation of a KPLS model

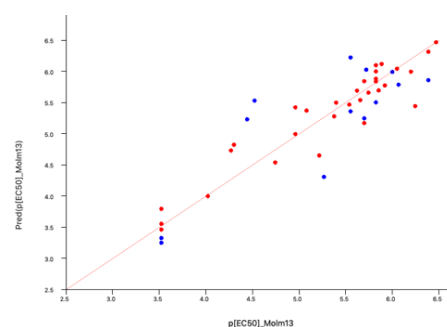
All analogs listed in Table 1 in the main article as well as some from a previous publication on iodinin analogs [1] were imported into Canvas (ver. 4.1.013, MMshare Version 4.7.013, Schrödinger Software Modules, LLC, NY, 2019) [2] from .mol files.

The activity towards cell lines (EC50 from Table 1 or from [1]) were presented as $-\log(EC50)$ or $p(\text{activity})$ to linearize data and to ensure that the data were presented with higher value corresponding to high activity. The physico-chemical properties of all compounds were generated in Canvas using Task>properties>calculate. The properties were: Molecular weight (MW), hydrogen bond acceptor number (HBA), hydrogen bond donors (HBD), number of rotatable bonds (RB), heavy atom count, chiral center count, ring count, electronegativity state (Estate), molar refractivity (MR), partition coefficient (AlogP), polar surface area (PSA). See Table S1 at the end of this document for a list of all compounds and experimental and calculated properties. Next, dendritic fingerprint of each compound was created and kerne-based partial least square (KPLS) model was built using activity towards a given cell lines or hypoxia/normoxia as Y variable, and the calculated binary fingerprint as the X variable. Further settings were: Maximum number of KPLS factors = 3, 70% training set and 30% test set, where the same seed was used for all activities to ensure that the same compounds were used as training and test compounds at the different conditions. Images were exported from the visualize model function in the KPLS window. Atoms contributing to high activity is labelled green, whereas atoms contributing to low activity is labelled red.

2: Regression analyses and correlation fits for the KPLS models

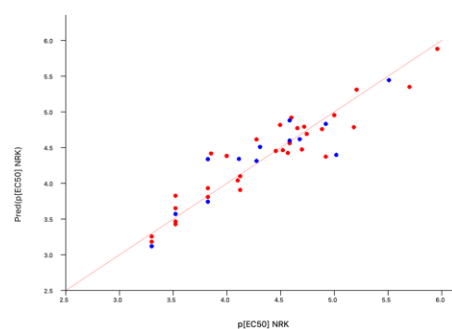
2.1 Results from Molm-13 normoxiadata:

R^2 after 2 KPLS factors was 0.8435 for the training set, and the Q^2 (correlation fit) for the test set was 0.7092, which was considered satisfactory. The scatter plot shows nice correlation. This suggests that the model can predict the activity of a compound based on its structure with acceptable accuracy.



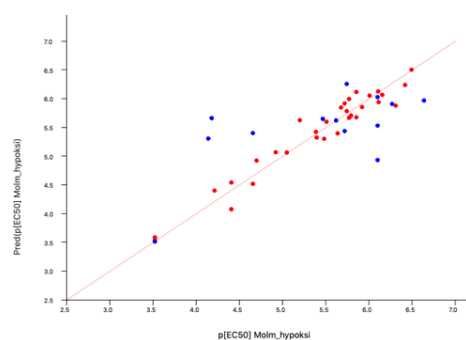
2.2 Results from NRK normoxia data

R^2 after 2 KPLS factors was 0.8139, and after 3 factors, it was 0.8755. The Q^2 was 0.8542 after 2 factors, and 0.8135 after 3 factors. The scatter plot after 3 factors confirms the good correlation, and this model can be used to predict structures based on activity.



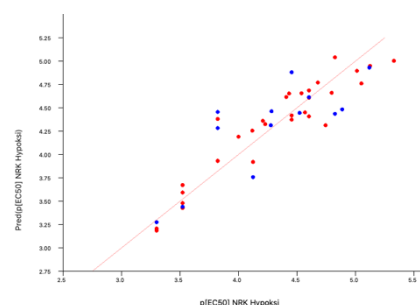
2.3 Results from Molm-13 hypoxia data

R^2 after 3 KPLS factors was 0.9431, and the Q^2 for the test set was 0.3966. There are obviously a few compounds or chemical moieties which are difficult to predict with respect to activity under hypoxic conditions. The scatter plot shows that the activity of structure **12** and **13** are heavily overestimated, whereas the activity of structure 3 (iodinin) is underestimated by a value of around one ($p[EC50]$ value, means a factor of ten in concentration). For structure **12** and **13**, the problem can be that both have very low permeability (see Table 1 in the main article), perhaps due to chelation with cations in the medium. Such events are not predicted by the model. Furthermore, hypoxia experiments are very dependent on stable conditions, and small variations in oxygen saturation in the incubators would have larger impact on these data compared to those obtained under normoxic conditions.



2.4 Results from NRK hypoxia data

R^2 after 3 KPLS factors was 0.8738, and the Q^2 for the test set was 0.6267. This is a bit lower than for NRK normoxia data, but still decent correlation, and we conclude that this model can be used to predict activity under hypoxic conditions. There were two outliers, where the predicted activity was overestimated. As with Molm-13 data, these were structure **12** and **13**.

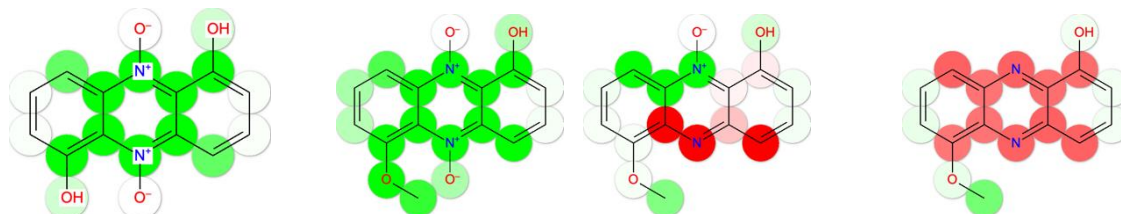


3: Comparison between predictions for activity, MOLM-13 vs. NRK.

Here, we compare the predicted contribution of each parts of the molecules with respect to activity towards MOLM-13 and NRK. We focus on differences between activity towards Molm-13 and NRK cells, and between MOLM-13 cells cultured under normoxic and hypoxic conditions.

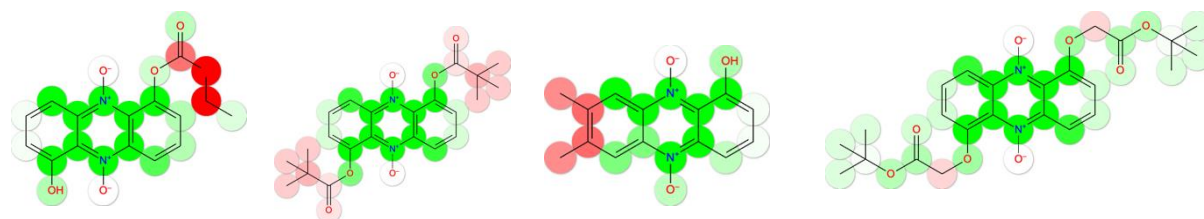
3.1 Visualization of KPLS model on MOLM-13 cells

We noticed first that the oxygens, but not the nitrogens, of the N-oxides were considered neutral. The charged nitrogens are predicted with high activity. One explanation to why the N-oxides fail to be predicted with high activity contrary to our findings with myxin-analogs lacking N-oxides [1], can be that such moieties are considered weak spots for in silico modelling [3]. Interestingly, the oxygen of the N-oxides was considered important for Molm-13 activity when there was an -OMe substituent in position 6 instead of -OH (as in iodinin). Further, structures **1-12** and **1-14** (myxin, but lacking one or both oxygens on the nitrogens) was correctly predicted as having very low activity, and here the non-oxygenated nitrogen was associated with reduced activity. The -OH groups in position 1 and 6 are associated with high activity but not to the same extent as the nitrogens (positions 5 and 10 of the scaffold).



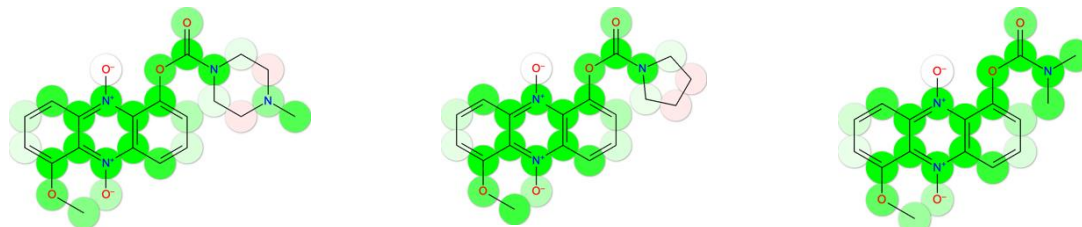
Structure **3** (iodinin) and **4** (myxin) and the de-oxygenated forms of myxin (**1-12** and **1-14**).

Substituents which stood out as having negative impact on activity towards MOLM-13 cells were the pivalate esters on compound **11**, the valerate esters of compound **12** and the ethyl carbonate side chain on compound **13**. The methyl groups in positions 7 and 8 (compounds **44**, **48** and **52**) resulted in negative impact on MOLM-13 activity as well. All two-ring compounds were correctly predicted as having poor activity. According to the model, the linker was also important for activity, and when *O-tert*butyl acetate side chains (2-(*tert*-butoxy)-2-oxoethoxy) was attached to the phenols (structure **1-18**) instead of the pivalic esters (structure **11**) they were associated with high activity. This means that not only the end-substituent, but also the linker is important for activity. This can be explained with the concept of prodrug, where the stability of the linker in medium and in the cytoplasm can be a determinant for activity.



Structure **13**, **11**, **44**, and **1-18**. Notice the difference between the *tert*-butyl based substituents in structure **11** and **1-18**, suggesting that the linker is a determining factor for activity for these structures.

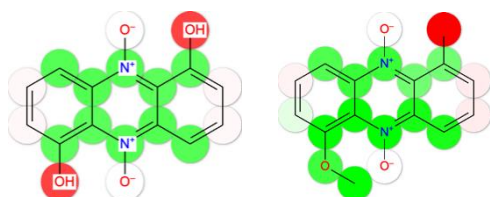
In general, a short linker consisting of carbamate bond was associated with high activity even when added different substituents like the pyrrolidine ring in structure **19**, the *N,N*-dimethyl of structure **20** or the piperazine of structure **18**. Note that in all these cases, the linker ends with a nitrogen (a carbamate), whereas in structure **13** (a carbonate), the linker ends with an oxygen, which is associated with low activity.



Structures **18**, **19**, and **20**. Note that the nitrogen in the carbamate functional group is associated with high activity, whereas in structure **13**, the nitrogen is replaced by an oxygen forming a carbonate functionality and results in low activity.

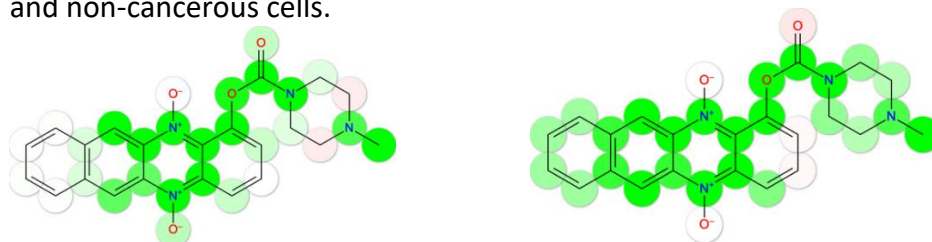
3.2 Visualization of KPLS model on NRK cells

In general, the effect of the different analogs on MOLM-13 cells was reflected in their activity towards NRK, except that most analogs were much less potent towards NRK cells. A large difference in predictions was therefore not expected. However, it was predicted that the two -OH groups in position 1 and 6 on iodinin (**3**) was linked to low activity. This was also the case for all structures with one or more phenols (-OH). As such, it appears that mono-substituted analogues should have higher selectivity towards Molm-13 cells than di-substituted analogues.



Structure **3** (iodinin) and **4** (myxin). Note that the phenol -OH in position 1 and 6 are associated with low activity, in contrast to the model on MOLM-13.

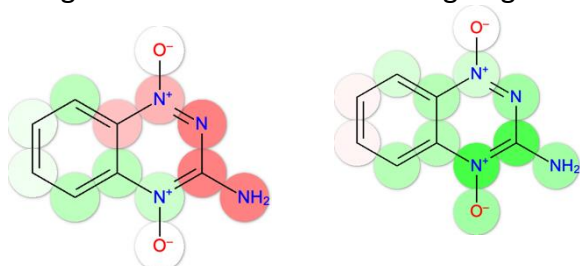
Besides this, there were several molecular elements which were common for high activity in MOLM-13 and NRK cells, such as the pivalate esters in structure **11** being a predictor for low activity whereas the carbamate nitrogen atom in structures **16**, **17**, **15**, **20**, and **18** was associated with high activity. The fourth ring in the tetracyclic structure **53** was associated with high activity in NRK-cells but was neutral in the model for MOLM-13 cells. This suggests that the introduction of a fourth ring shifts the activity of the compounds from being AML selective to a more general cytotoxic activity which does not discriminate between cancerous and non-cancerous cells.



The predicted atomic contribution of structure **53** towards AML activity (left) or NRK activity (right). Notice that while the terminal aromatic ring is predicted to be neutral towards AML cells, it is predicted to contribute to high activity in NRK-cells.

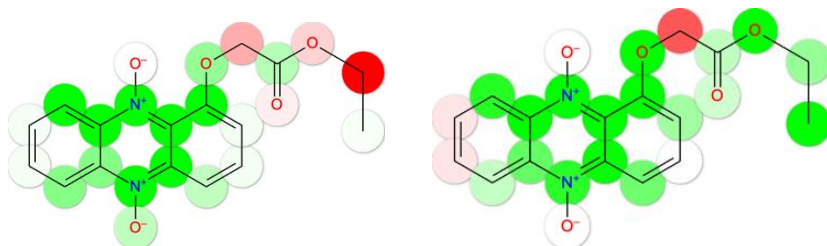
3.3 Comparison of the KPLS models on MOLM-13 activity cells obtained under normoxic and hypoxic conditions

Here, we can see a clear difference in the two models for tirapazamine (structure **10**). Whereas the nitrogens are clearly associated with poor activity in normoxic conditions, they are associated with high activity in hypoxic conditions. Although this could give indications on how to create hypoxia-dependent analogues, this is only one example, and more analogs of tirapazamine should be part of a KPLS-model before we can conclude on the importance of the nitrogens in the *N*-oxide-containing ring.



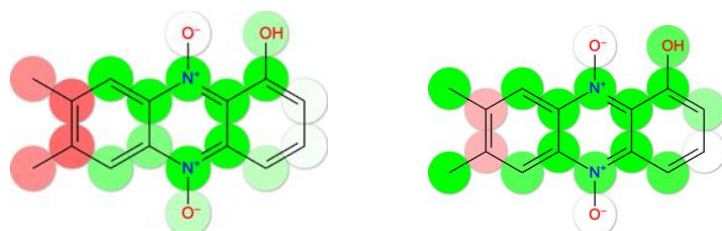
The atomic contribution for low and high activity of structure 10 (tirapazamine) in normoxic (left) and hypoxic (right) conditions.

No large differences were found in structure 3 (iodinin), or structure 4 (myxin). Some of the linkers, such as the ethyl- and *tert*butyl acetate side chains in structures **24** and **25** were connected to poor activity to a higher degree in hypoxia, which could be related to the activation of the prodrug being slower in hypoxic conditions.



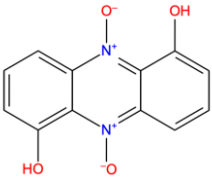
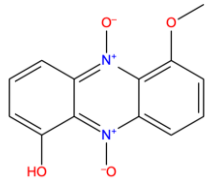
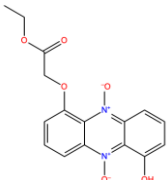
Predicted atomic contribution for activity for structures **24** under normoxic (left) and hypoxic (right) conditions. Note that the -CH₂- in the linker is predicted to be associated with low activity.

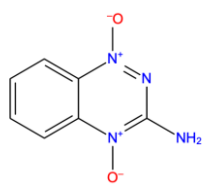
Another difference was the influence of methyl groups in positions 7 and 8 on the phenazine scaffold, where the methyl groups were linked to high activity in hypoxic conditions, but not in normoxic conditions. This was evident in structures **44** (illustrated), **48**, and **52**.



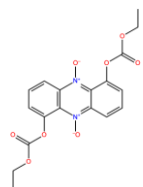
Structure **44**, with predicted atomic contribution to activity in normoxic (left) and hypoxic (right) conditions. Note the Me-substituents in position 7 and 8.

Table 1: Structures and their cytotoxicity and molecular properties used to create dendritic fingerprinting. Structures 1-11 to 1-20 corresponds to a previously published study (reference no.: 2, Viktorsson et al. 2017)

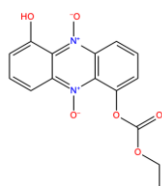
Structure	Name	Permeability (Log)	p[EC50] MOLM-13	p[EC50] NRK	p[EC50] Molm hypoksi	p[EC50] NRK Hypoksi	MW	HB A	HBD	RB	Heavy Atom Count	Chiral Center Count	Chiral Center Count All Possible	Ring Count	Estate	MR	AlogP	PSA
	Structure_3	-5,64	5,699	4,125	6,102	4,125	244,2029	2	2	5,699	5,699	0	0	3	56,002	56,169	-2,8556	94,34
	Structure_4	-4,94	5,854	4,114	6,114	4,119	258,2295	2	1	5,854	5,854	0	0	3	55,502	60,9381	-2,6046	83,34
	Structure_7	-4,84	6,244	4,921	6,31	4,744	330,2922	4	1	6,244	6,244	0	0	3	70,669	76,5398	-2,5487	109,64



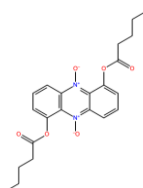
Structure_10 -5,79 4,022 3,824 4,658 4,456 178,1481 1 -5,79 -5,79 4,022 0 0 2 42,001 42,7503 -2,3606 92,79



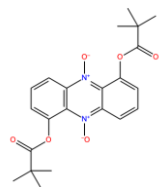
Structure_14 -4,75 5,215 4,456 5,398 4,456 388,3282 6 0 5,215 5,215 0 0 3 82,336 87,7888 -0,8014 124,94



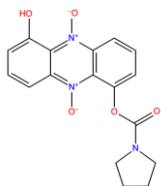
Structure_13 -7,32 4,301 3,824 4,181 3,824 316,2656 4 1 4,301 4,301 0 0 3 69,169 71,9789 -1,8285 109,64



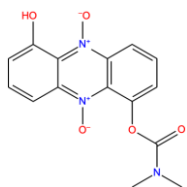
Structure_12 -7,74 4,444 3,824 4,658 3,824 412,4358 4 0 4,444 4,444 0 0 3 81,336 102,703
4 0,3732 106,48



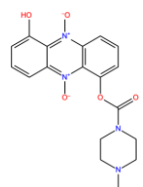
Structure_11 -6,06 4,959 3,824 5,051 3,824 412,4358 4 0 4,959 4,959 0 0 3 82,836 102,450 0,3072 106,48
4



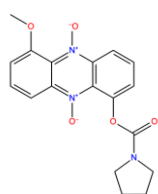
Structure_16 -4,74 6,066 5,018 6,102 4,824 341,3181 3 1 6,066 6,066 0 0 4 70,169 82,0156 -1,6332 103,65



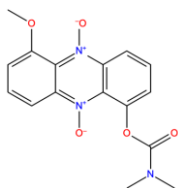
Structure_17 -5,06 6,051 4,31 6,155 4,208 315,2808 3 1 6,051 6,051 0 0 3 68,169 74,4754 -2,0942 103,65



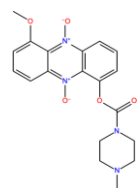
Structure_15 -5,96 5,824 4,276 5,854 4,229 370,3593 3 1 5,824 5,824 0 0 4 74,169 90,5255 -2,1369 106,89



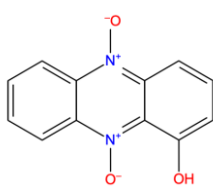
Structure_19 -5,1 5,699 4,495 5,745 4,456 355,3447 3 0 5,699 5,699 0 0 4 69,669 86,7847 -1,3822 92,65



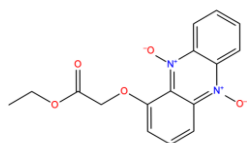
Structure_20 -5,1 5,721 4,658 5,77 4,538 329,3074 3 0 5,721 5,721 0 0 3 67,669 79,2445 -1,8432 92,65



Structure_18 -5,74 6 4,585 6,009 4,409 384,3859 3 0 6 6 0 0 4 73,669 95,2946 -1,8859 95,89

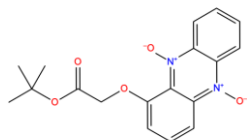


Structure_21 -4,74 4,959 4,102 4,921 3,824 228,2035 1 1 4,959 4,959 0 0 3 50,335 54,4749 -2,5882 74,11



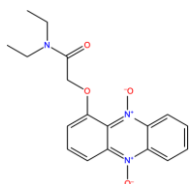
Structure_24

-4,93 5,824 4,585 5,77 4,602 314,2928 3 0 5,824 5,824 0 0 3 65,002 74,8457 -2,2813 89,41



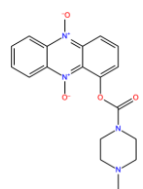
Structure_25

-4,76 5,657 4,585 5,721 4,602 342,3459 3 0 5,657 5,657 0 0 3 68,752 83,9015 -1,6988 89,41



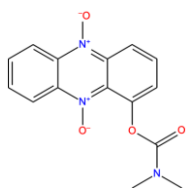
Structure_26

-5,2 5,921 4,886 5,854 4,796 341,3612 2 0 5,921 5,921 0 0 3 67,002 86,4402 -2,3739 83,42

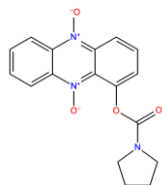


Structure_27

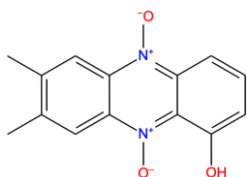
-4,85 5,824 4,602 5,721 4,432 354,3599 2 0 5,824 5,824 0 0 4 68,502 88,8314 -1,8695 86,66



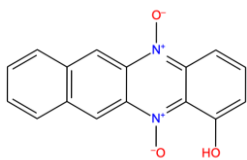
Structure_28 -4,95 5,886 4,721 5,678 4,602 299,2814 2 0 5,886 5,886 0 0 3 62,502 72,7813 -1,8268 83,42



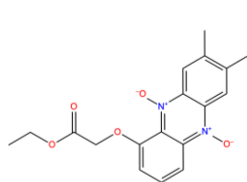
Structure29 -4,91 5,824 4,744 5,921 4,678 325,3187 2 0 5,824 5,824 0 0 4 64,502 80,3215 -1,3658 83,42



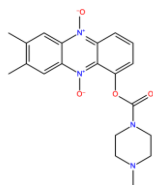
Structure_44 -5,45 5,553 4,125 5,638 4,125 256,2567 1 1 5,553 5,553 0 0 3 53,669 64,5573 -1,6158 74,11



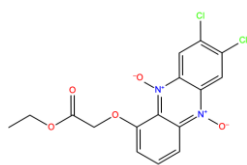
Structure_45 -7,23 4,523 4 4,699 4 278,2622 1 1 4,523 4,523 0 0 4 57,669 70,9251 -1,6798 74,11



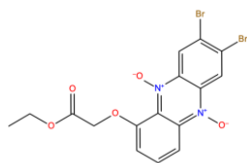
Structure_48 -4,93 5,081 3,854 5,201 3,824 342,3459 3 0 5,081 5,081 0 0 3 68,336 84,9281 -1,3089 89,41



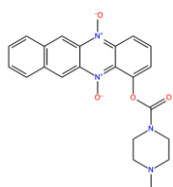
Structure_52 -4,97 6,201 4,921 6,268 4,886 382,4131 2 0 6,201 6,201 0 0 4 71,836 98,9138 -0,8971 86,66



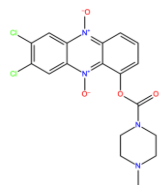
Structure_50 -5,16 6,387 5,509 6,42 5,328 383,1829 3 0 6,387 6,387 0 0 3 72,558 84,4553 -0,9525 89,41



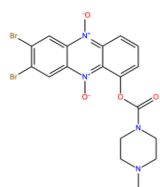
Structure_51 -5,24 5,62 5 5,796 5,013 472,0849 3 0 5,62 5,62 0 0 3 69,836 90,0913 -0,7845 89,41



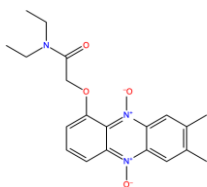
Structure_53 -5,26 5,553 5,699 5,745 5,125 404,4186 2 0 5,553 5,553 0 0 5 75,836 105,281
6 -0,9611 86,66



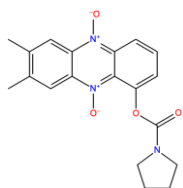
Structure_54 -4,97 6,469 5,959 6,495 4,824 423,25 2 0 6,469 6,469 0 0 4 76,058 98,441
-0,5407 86,66



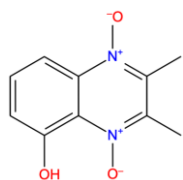
Structure_55 -4,88 6,387 5,208 6,638 5,119 512,152 2 0 6,387 6,387 0 0 4 73,336 104,077
-0,3727 86,66



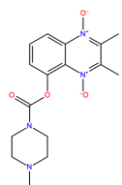
Structure_56 -5,18 5,745 4,678 5,469 4,284 369,4143 2 0 5,745 5,745 0 0 3 70,336 96,5226
-1,4015 83,42



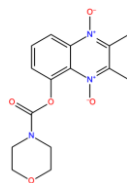
Structure_57 -4,85 5,823 5,181 6,108 5,051 353,3719 2 0 5,823 5,823 0 0 4 67,836 90,4039 -0,3934 83,42



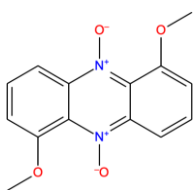
Structure_60 -4,35 3,523 3,301 3,523 3,301 206,198 1 1 3,523 3,523 0 0 2 46,335 48,5679 -3,7884 74,11



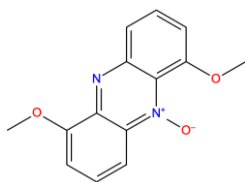
Structure_61 -4,48 3,523 3,301 3,523 3,301 332,3544 2 0 3,523 3,523 0 0 3 64,502 82,9244 -3,0697 86,66



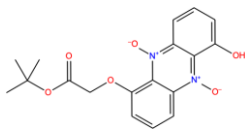
Structure_62 -4,65 3,523 3,301 3,523 3,301 319,3126 3 0 3,523 3,523 0 0 3 64,002 75,9488 -3,3393 92,65



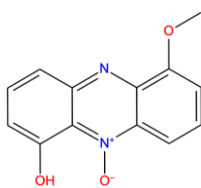
Structure_1_11 -5,1 5,398 4,699 5,509 4,602 272,2561 2 -5,1 -5,1 5,398 0 0 3 55,002 65,7072 -2,3536 72,34



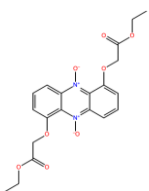
Structure_1_13 -5,1 5,267 3,522 5,387 3,523 256,2567 3 -5,1 -5,1 5,268 0 0 3 47,002 65,8951 0,3366 58,29



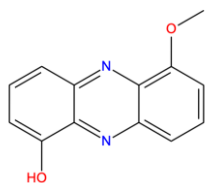
Structure_1_17 -5,04 5,538 4,276 5,62 4,276 358,3453 4 -5,04 -5,04 5,538 0 0 3 74,419 85,5956 -1,9662 109,64



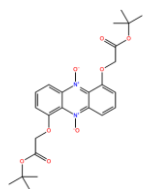
Structure_1_12 -5,09 3,523 3,523 4,143 3,523 242,2301 3 -5,09 -5,09 3,523 0 0 3 47,502 61,126 0,0856 69,29



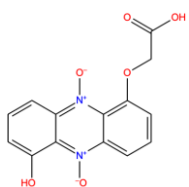
Structure_1_16 -5,17 5,699 4,523 6,102 4,523 416,3814 6 -5,17 -5,17 5,699 0 0 3 85,336 96,9106 -2,2418 124,94



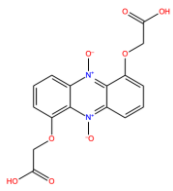
Structure_1_14 -5,08 3,523 3,523 4,409 3,523 226,2307 4 -5,08 -5,08 3,523 0 0 3 39,502 61,3139 2,7758 55,24



Structure_1_18 -5,2 5,377 4,569 5,482 4,569 472,4877 6 -5,5 -5,5 5,377 0 0 3 92,836 115,022
2 -1,0768 124,94



Structure_1_19 -7,16 4,268 3,523 4,215 3,523 302,239 2 -7,16 -7,16 4,268 0 0 3 70,669 67,0227 -3,1485 120,64



Structure_1_20

-7,2

4,745

3,523

4,409

3,523

360,2751

2

-7,2

-7,2

4,745

0

0

3

85,336

77,8764

-3,4414

146,94

References

1. Viktorsson, E.O., et al., *Total synthesis and antileukemic evaluations of the phenazine 5,10-dioxide natural products iodinin, myxin and their derivatives*. *Bioorg Med Chem*, 2017. **25**(7): p. 2285-2293.
2. Duan, J., et al., *Analysis and comparison of 2D fingerprints: insights into database screening performance using eight fingerprint methods*. *J Mol Graph Model*, 2010. **29**(2): p. 157-70.
3. Eros, D., et al., *Reliability of logP predictions based on calculated molecular descriptors: a critical review*. *Curr Med Chem*, 2002. **9**(20): p. 1819-29.