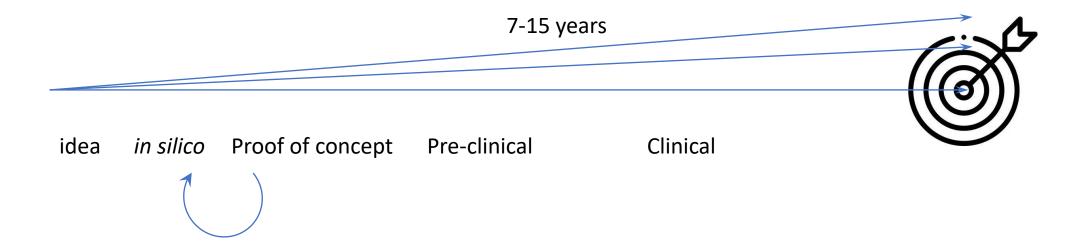
# In silico small molecule drug discovery from the pharma company point of view

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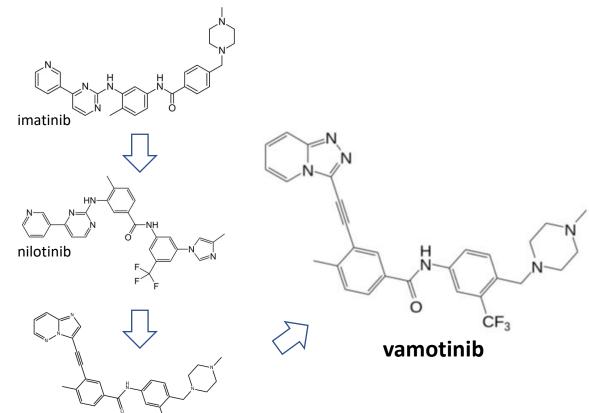
## Why in silico stage matters a lot



- The drug discovery and development process takes many years from the idea to drug approval, and it does not get easier because of regulatory landscape changes and competition from different drug products and drug modalities
- Slight deviations from the desired product profile at the beginning may result into big differences in the properties of the final product which may not fit market expectations
- Therefore, alignment of the desired product profile with in silico modeling stage and further translation into proof of concept stage is crucial

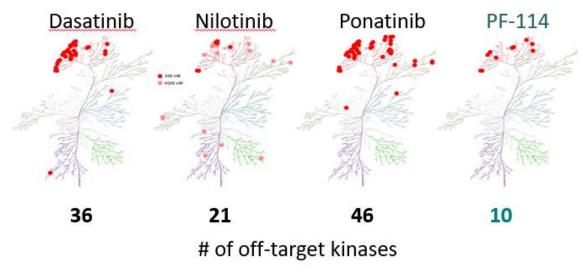
# Case study: vamotinib - a 3<sup>rd</sup> generation Bcr-Abl inhibitor

- Vamotinib (PF-114): 3<sup>rd</sup> generation inhibitor of Bcr-Abl (following 1<sup>st</sup> generation inhibitor imatinib and 2<sup>nd</sup> generation nilotinib)
- Rationally designed to avoid multiple off-target effects and improve safety compared to another 3<sup>rd</sup> generation inhibitor ponatinib
- Current status: filed for marketing authorization in Russia



ponatinib

#### Kinase inhibition profile of ATP-competitive drugs



## in silico stage setup

## Key indicators

- Clearly defined therapeutic target (target discovery stage completed)
- Clearly defined mode of action
- translated into a hypothesis for the new molecular entity (which unique properties should a new molecule have)
- a feasible proof of concept

## Implementation



Bcr-Abl fusion protein, kinase activity



 ATP-competitive binding site (alternatively – allosteric site)



 A molecule with affinity towards an Abl kinase mutant of interest and no affinity to off-target kinases



 Activity vs certain Abl mutants and a better kinase selectivity profile; no severe toxicity in animal models

### Capture the "physics" of a target

- "Simple" ligand binding in the existing site (e.g. competitive enzyme inhibitors)
- Allosteric binding where the binding site emerges during the protein structure movement
- Functional influence on the protein (aiding CFTR channel function, blocking/activating other ion channels, etc)
- PDB structure may not be sufficient!

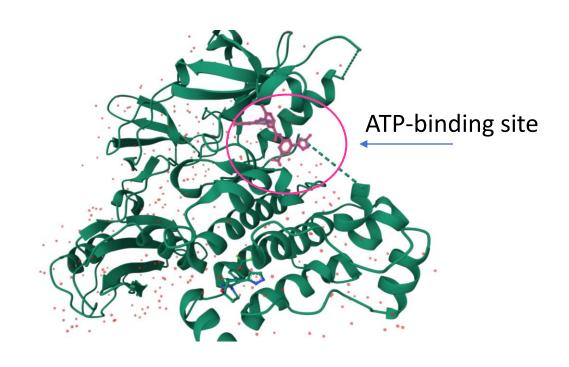
## • Full atomic modeling of a protein target interaction

- Validation of a model using true positive and true negative examples
- Select proper method for model validation (docking, flexible docking, molecular dynamics, FEP)
- Gain understanding of ligand binding at structural biology level



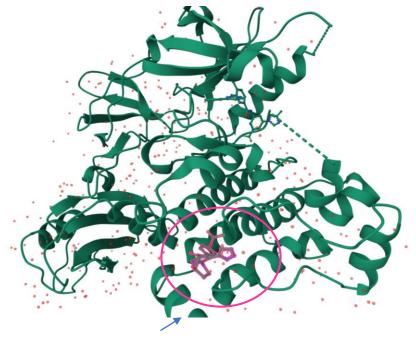
 Increase the success rate of designing a proper binder and shorten the time of drug candidate optimization vs large scale screening and empiric optimization of ligand structure

**Bcr-Abl inhibitors:** Bcr-Abl – is a sole cause of disease, 2 inhibitor binding sites available



Resistant mutations: T315I, G250E, Y253H/F, E255K/V, H396P/R, F359V/C/I, L248V, M351T

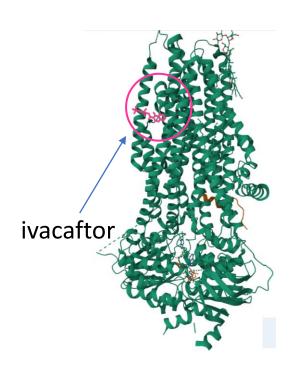
~4% of patients develop mutations upon treatment with nilotinib front line

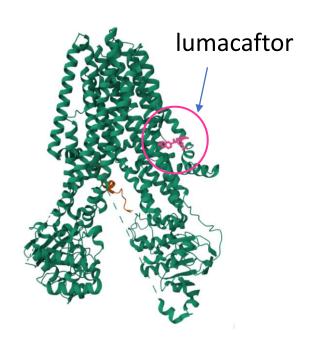


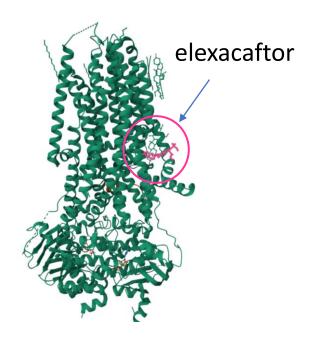
#### Allosteric binding site

Resistant mutations: A337V/T, P465S, C464W, V468F, G463S, I502L, M244V, L248V, F317L, F359C/I/V 4% of patients develop mutations upon treatment with asciminib front line

**CFTR ion channel:** different opportunities to assist functioning of inactivated mutant protein





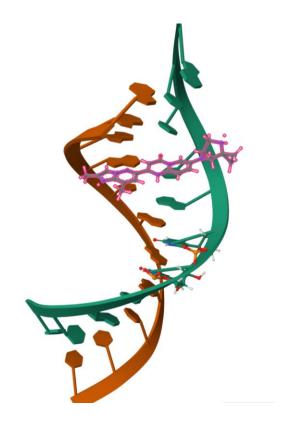


Ivacaftor stabilizes open conformation of a channel

Lumacaftor stabilizes the correctly folded conformation of a channel

Elexacaftor stabilizes protein interface and dimerization

#### Even more complicated modality: Risdiplam mechanism of action

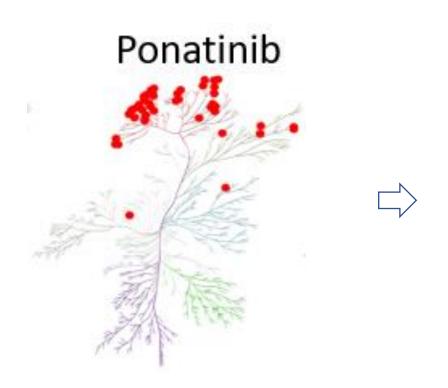


A-1 splicing modifier	IC <sub>50</sub> [nM]	KD [μM]
NH SMN-C5	30 nMª	28 ± 9 μM <sup>f</sup>
NH SMN-CX	36 nM⁵	74 ± 17 μM <sup>f</sup>
N N N N N N N N N N N N N N N N N N N	23 nM°	12 ± 1 μM <sup>g</sup>
H <sub>2</sub> N SMN-CY	29 nM <sup>d</sup>	60 ± 13 μM <sup>f</sup>
h <sub>2</sub> N branaplam	20 nM <sup>e</sup>	18 ± 1 μM <sup>g</sup>

Solution structure of Risdiplam bound to the RNA, PDB 8R62

## In silico driven hypothesis for the drug candidate

**Hypothesis:** a more selective kinase inhibitor is required for improved safety



Kinase inhibition profile

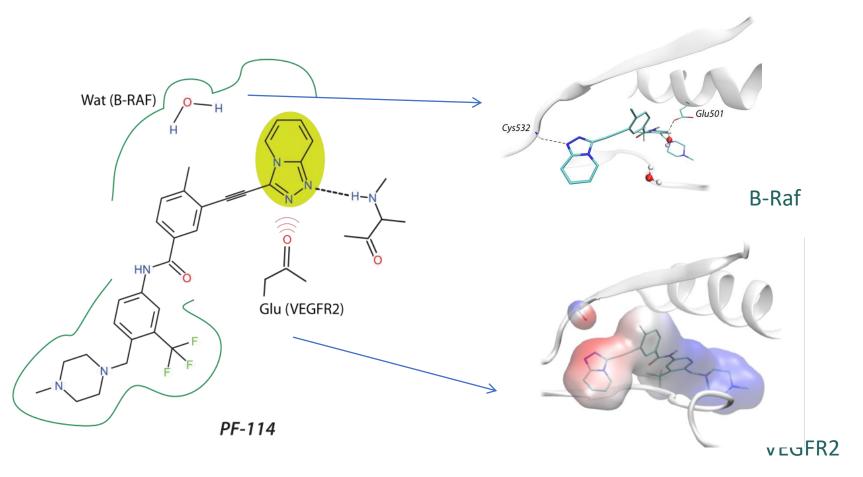
# WARNING: ARTERIAL OCCLUSION, VENOUS THROMBOEMBOLISM, HEART FAILURE, and HEPATOTOXICITY

See full prescribing information for complete boxed warning.

- Arterial occlusion has occurred in at least 35% of Iclusig-treated patients including fatal myocardial infarction, stroke, stenosis of large arterial vessels of the brain, severe peripheral vascular disease, and the need for urgent revascularization procedures. Patients with and without cardiovascular risk factors, including patients less than 50 years old, experienced these events. Interrupt or stop Iclusig immediately for arterial occlusion. A benefit-risk consideration should guide a decision to restart Iclusig (5.1).
- Venous thromboembolism has occurred in 6% of Iclusig-treated patients. Monitor for evidence of thromboembolism. Consider dose modification or discontinuation of Iclusig in patients who develop serious venous thromboembolism (5.2).
- Heart failure, including fatalities, occurred in 9% of Iclusig-treated patients. Monitor cardiac function. Interrupt or stop Iclusig for new or worsening heart failure (5.3).
- Hepatotoxicity, liver failure and death have occurred in Iclusigtreated patients. Monitor hepatic function. Interrupt Iclusig if hepatotoxicity is suspected (2.3, 5.4).

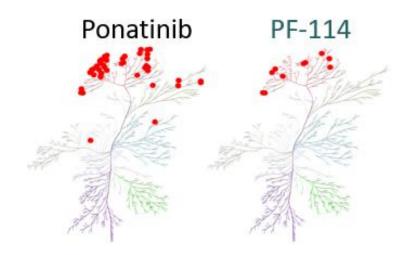
## In silico driven hypothesis for the drug candidate

Selectivity of vamotinib by design: disrupting typical off-target interactions e.g. with VEGFR2 and B-Raf

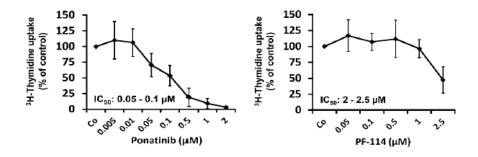


## In silico driven hypothesis for the drug candidate

Kinase selectivity profile of vamotinib (PF-114) may explain its reduced cardio toxicity



 PF-114 <u>as opposed to ponatinib</u> is not toxic to human umbilical vein endothelial cells (Medical University of Vienna, Prof. Peter Valent lab)



 PF-114 <u>as opposed to ponatinib</u> is not toxic to cardiomyocytes, does not cause ventricular fractional shortening in zebrafish, does not induce cardiac dysfunction in ApoE null mice as compared to ponatinib (University if Vanderbilt, Prof. Hind Lal lab)

Basing on the comparison of strongly inhibited kinases by ponatinib vs vamotinib and other inhibitors the following kinases may stand for cardiovascular toxicity: EPHA6, EPHA7, TAK1, TIE2, VEGFR2, ZAK

# Other molecular properties of interest: cost of manufacturing

- For a company working in the other-the-counter (OTC) segment the cost of drug is crucial.
- In Russia, the cost of API per monthly course of an OTC drug should not exceed ~5 USD, which translates to 2-4k USD/kg of API
- Considering obesity as an indication for OTC drug therapy:
- Monthly cost of semaglutide in Russia is ~70 USD
   How can small molecule chemicals like orforgliprone reach that price level?
- In silico tools to be evaluated: Rondaxe CoGS, ChemPrice, CoPriNet, MolPrice, RetroPriceNet

## Other molecular properties of interest: intellectual property

- Novelty
  - Your molecule does not appear somewhere else explicitly
- Inventive step
  - Your molecule differs from existing ones in a non-trivial for an expert way
- Freedom to operate
  - Your molecule and all related to it (manufacturing, use, etc) does not violate the IP rights of others
- Patenting salt forms of a drug molecule, crystal forms
  - Worth for prolongation of patent protection