

Computational Screening and Design of G-quadruplex Ligands Targeting *c-MYC* in Breast Cancer



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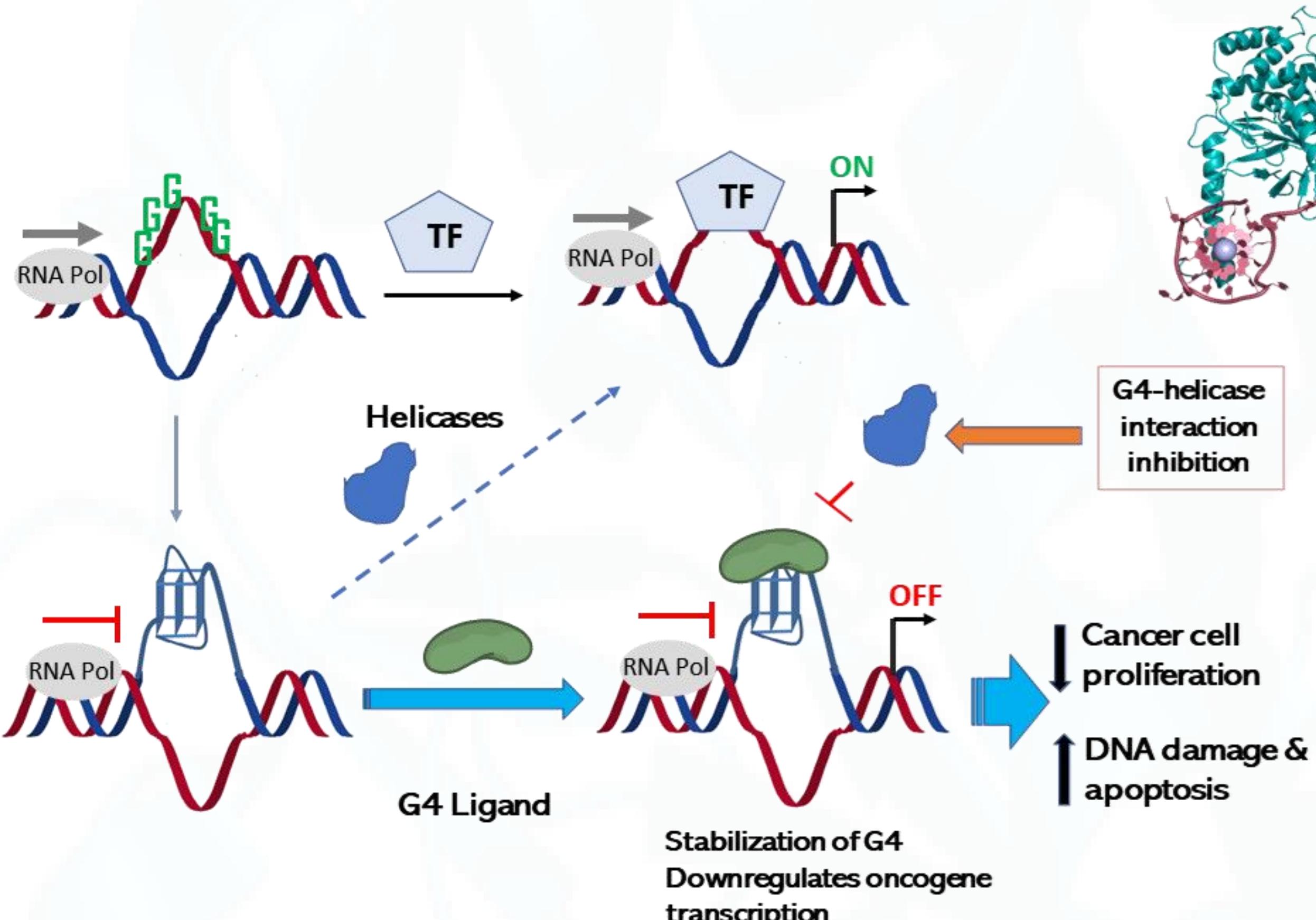
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Introduction

- G-quadruplexes (G4) are four-stranded nucleic acid secondary structures formed by guanine-rich sequences of DNA or RNA.
- G4 in *c-MYC* oncogene has biological functions in cancer cells [1].
- G4 in the *c-MYC* promoter is reported to be unwound by the helicase DHX36, that recognizes specifically G4s and promotes the regulation of DNA transcription[1,2].



Aim of study

In silico identification and chemical synthesis of Indoloisoquinolones derivatives

G4 Stabilizers

Inhibitors of Helicase interaction

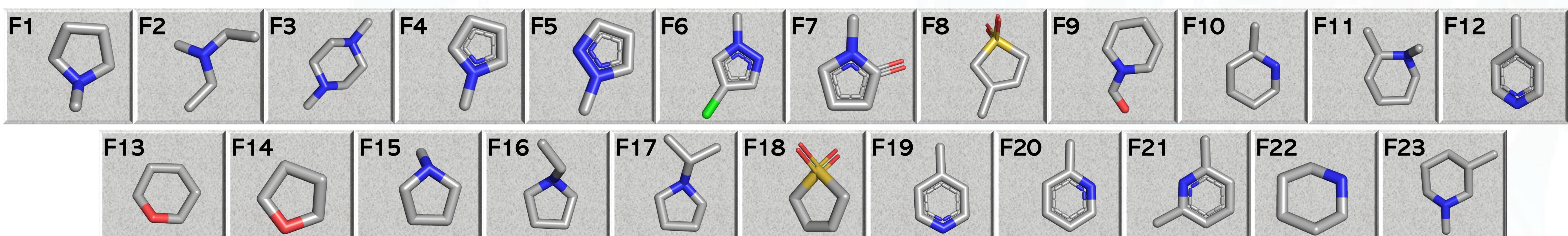
Workflow

SOFTWARES : Vinardo
Autodock Vina 1.1.2
Autodock Vina 1.2.2
DockER ranking

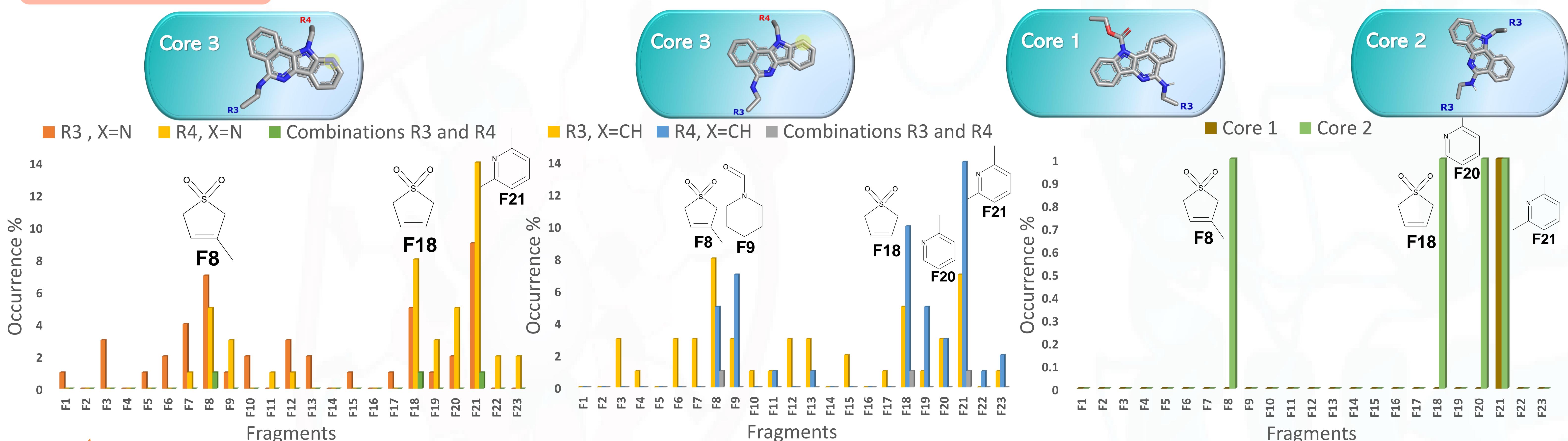
Docking with different scoring functions

Library of (23 fragments with ligands3 cores) 1104

Build compounds (smiles and 3D)



Results



 Fragments showing higher occurrence in docking consensus calculations : F8, F18, F21, F9, and F20

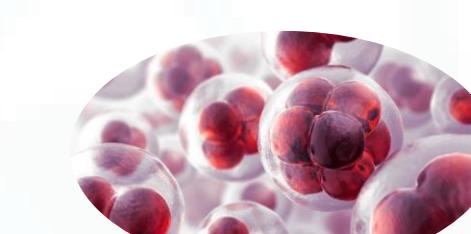
Conclusion

- Core 3 derivative compounds were the ones showing higher binding affinity to *c-MYC* G4.
- We have identified the most promising indoloisoquinolones stabilizers of *c-MYC* G4.

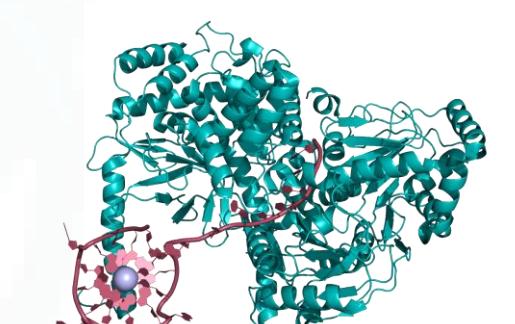
Next Step ...



Chemical synthesis of fragments



In vitro test.



Optimization of the compounds with molecular dynamics

CORE 1_F21

