

Agostino Bruno,¹ Francesca Giordano,³ Alessandra Nigro,² Paolo Vincetti,¹ Gabriele Costantino,¹
 Francesca Aiello^{3,*} and Marco Radi^{1,*}

¹*P4T Group, Dipartimento di Farmacia, Università degli Studi di Parma, Viale delle Scienze, 27/A, 43124 Parma, Italy.* ²*Dipartimento di Biologia, Ecologia e Scienze della Terra, Università della Calabria, Via P. Bucci 87036 Arcavacata di Rende (CS), Italy* ³*Dipartimento di Farmacia e Scienze della Salute e della Nutrizione, Università della Calabria, Edificio Polifunzionale, 87036 Arcavacata di Rende (CS), Italy*

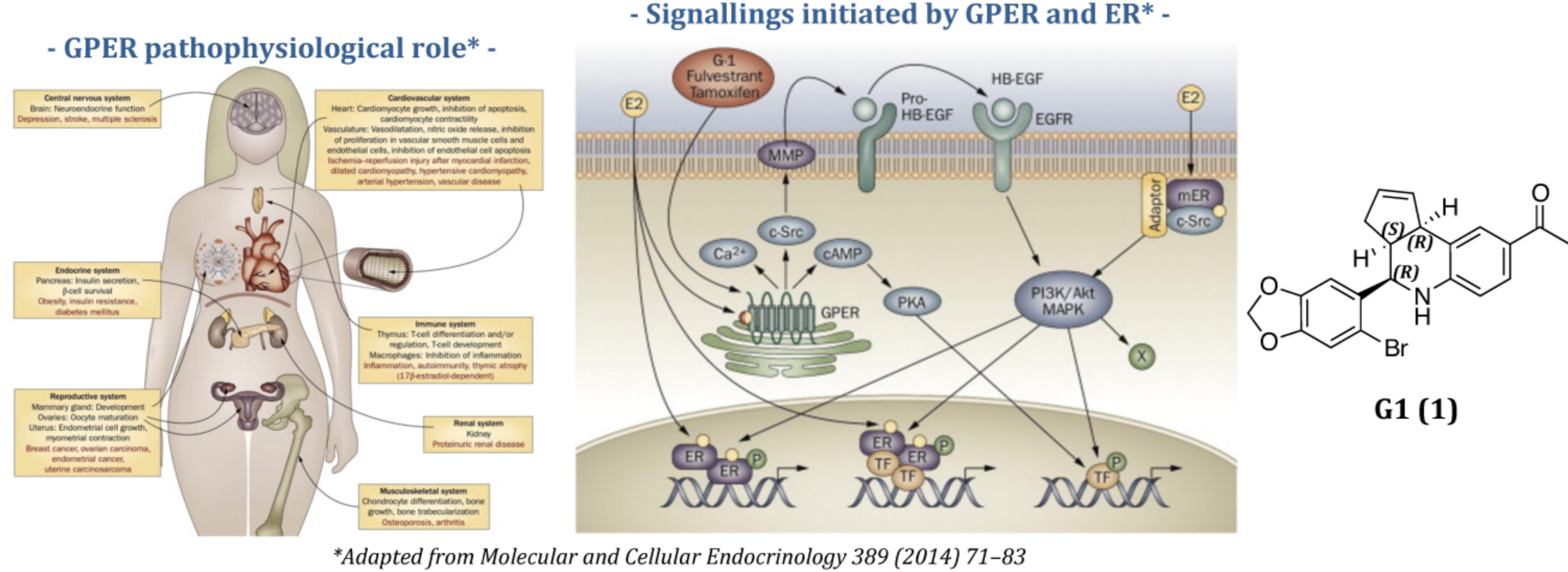


marco.radi@unipr.it
<http://p4t.farmacia.unipr.it>



Background

Together with ER α/β , GPER (G protein-coupled estrogen receptor 1, or GPR30) mediates important pathophysiological signaling pathways induced by estrogens and is currently regarded as a promising target for ER-negative and triple-negative breast cancer [1]. To better distinguish the role of GPER from nuclear ER α/β , selective ligands are essential. In this context **G1** (1) was proposed as a promising tool, being able to selectively bind GPER over ER α/β [2]. However, subsequent studies showed contradictory results on the effect of **G1** in the proliferation of cancer cells, leaving unsettled the need for better chemical tools [3-4].



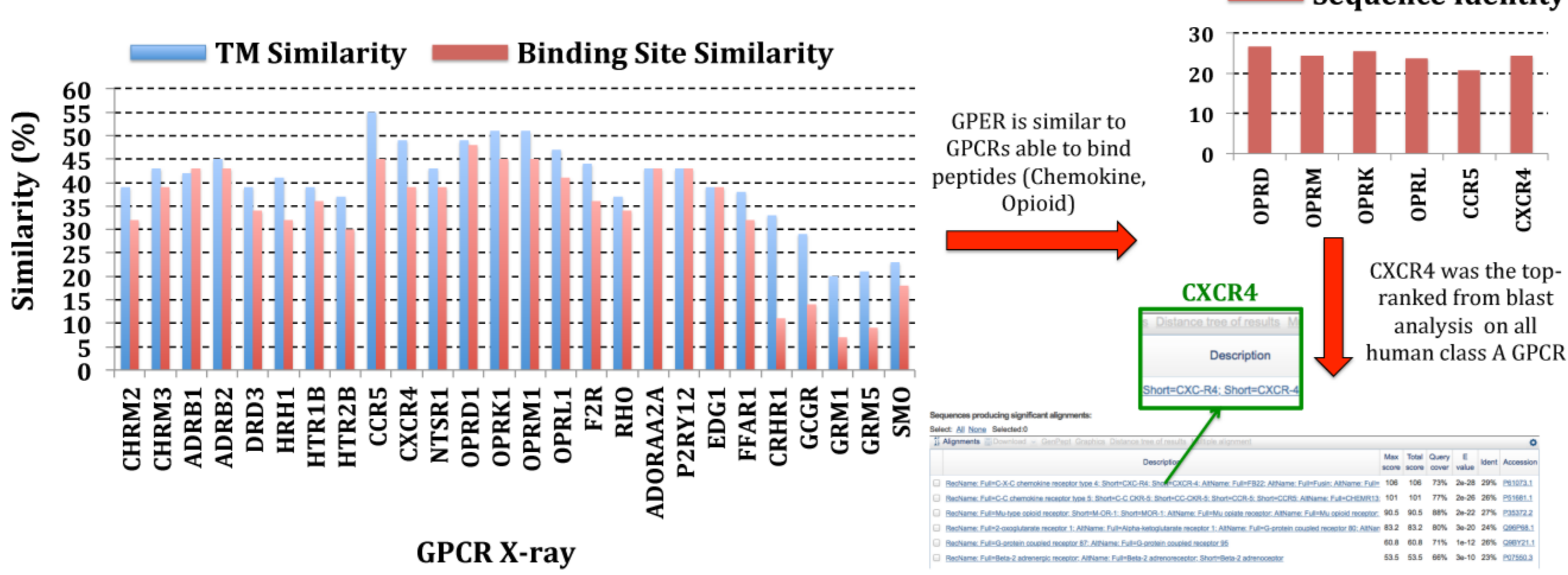
Aim

With the aim to **identify new GPER-selective anticancer probes**, we generated the GPER-G1 complex that was refined by extensive MD simulations, and used to perform Virtual Screening studies. The top-ranked compounds were biologically evaluated in selected cell lines showing different level of GPER expression, such as MCF-7, SKBR-3 and HEK293.

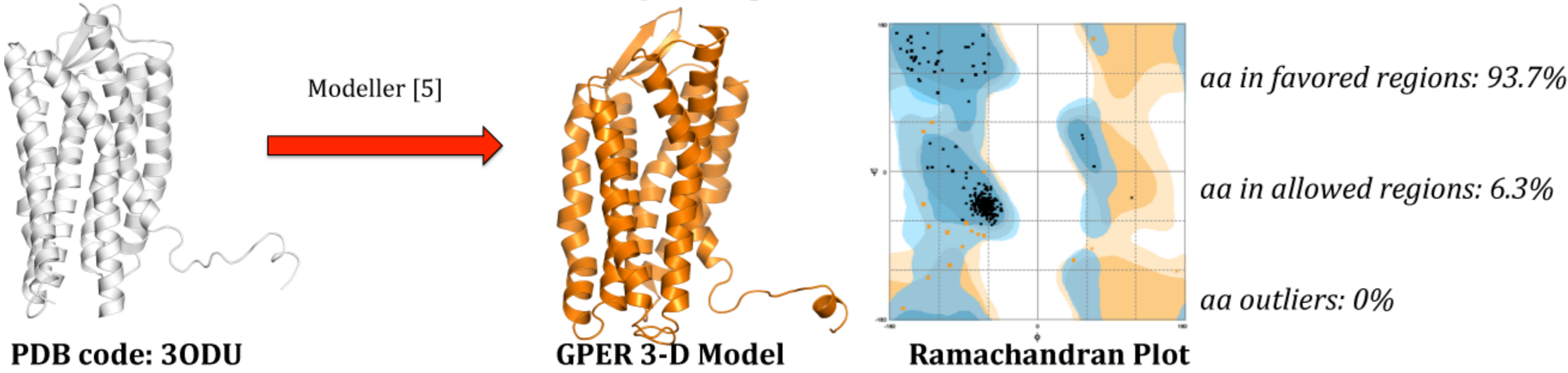
GPER 3-D Model

Several GPCRs X-ray crystal structures were solved so far, for class A, B, C and F. Unfortunately, for GPER no 3D structural information are currently available. Therefore, we decided to build a reliable model of GPER by means of homology modeling techniques.

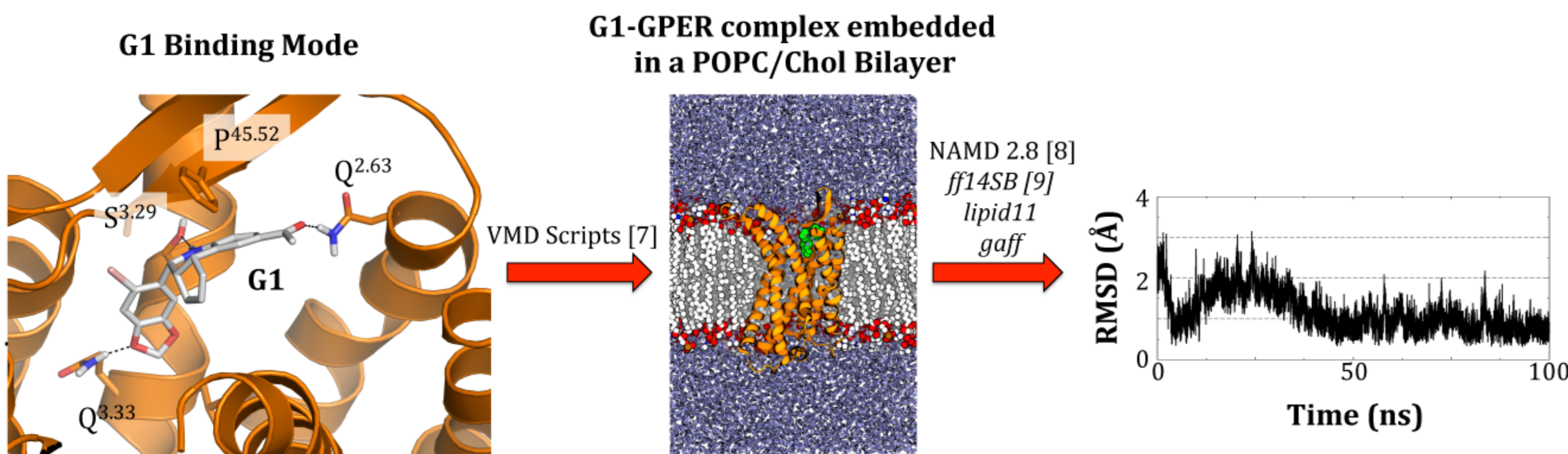
Template selection: among the GPCRs X-ray crystal structures available we need to identify the closest GPER homologs, as templates.



Model construction: CXCR4 was used as template to generate the 3-D Model of GPER



Model Validation: **G1** was docked into GPER structure, by means of Glide [6], and the selected binding mode was evaluated by molecular dynamics simulations by means of NAMD 2.8.

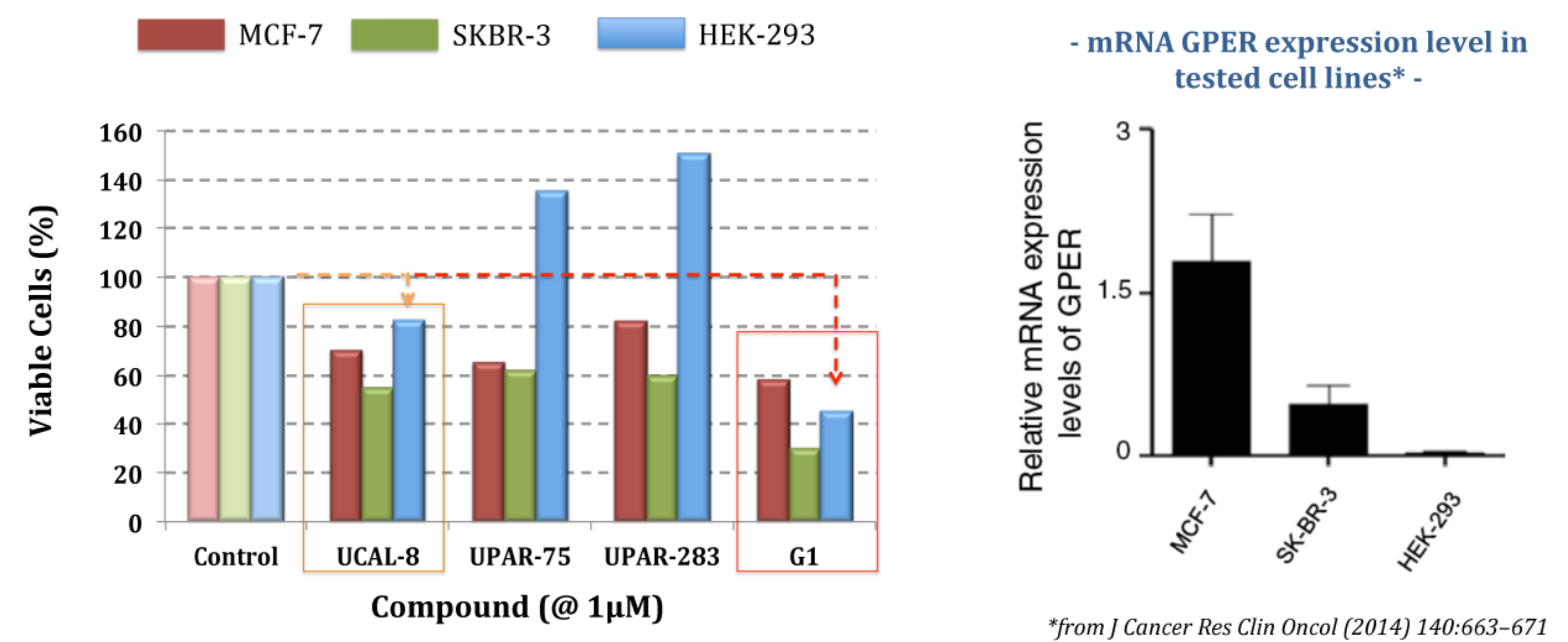


VS Protocol

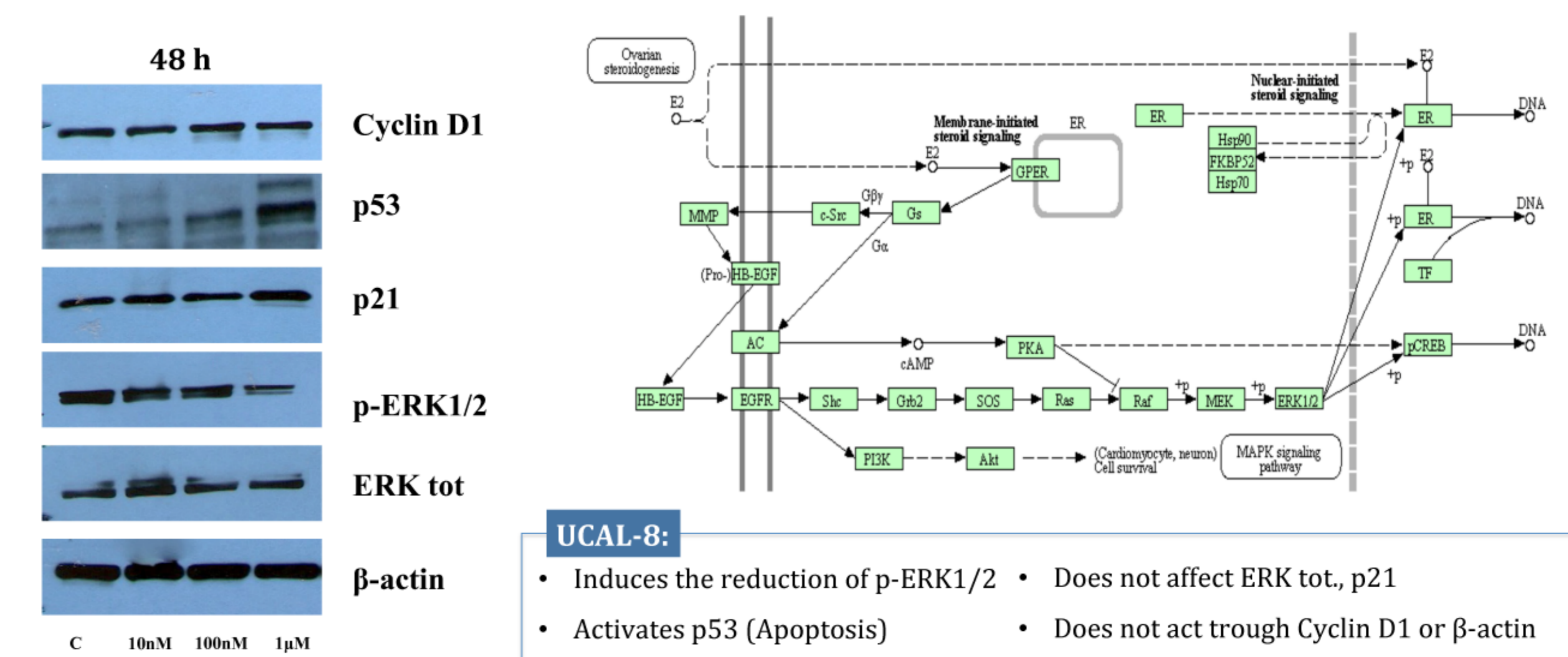
The refined **G1-GPER** complex was used to perform a Virtual Screening campaigns using in-house libraries (~1000 compounds). The VS was performed by using the virtual screening workflow implemented in Glide [6]. The 10% top ranked compounds were initially selected, and among such compounds, only those showing a similar pattern of interaction with respect to **G1** were finally selected for biological evaluation (3 compounds).

Biological Assays

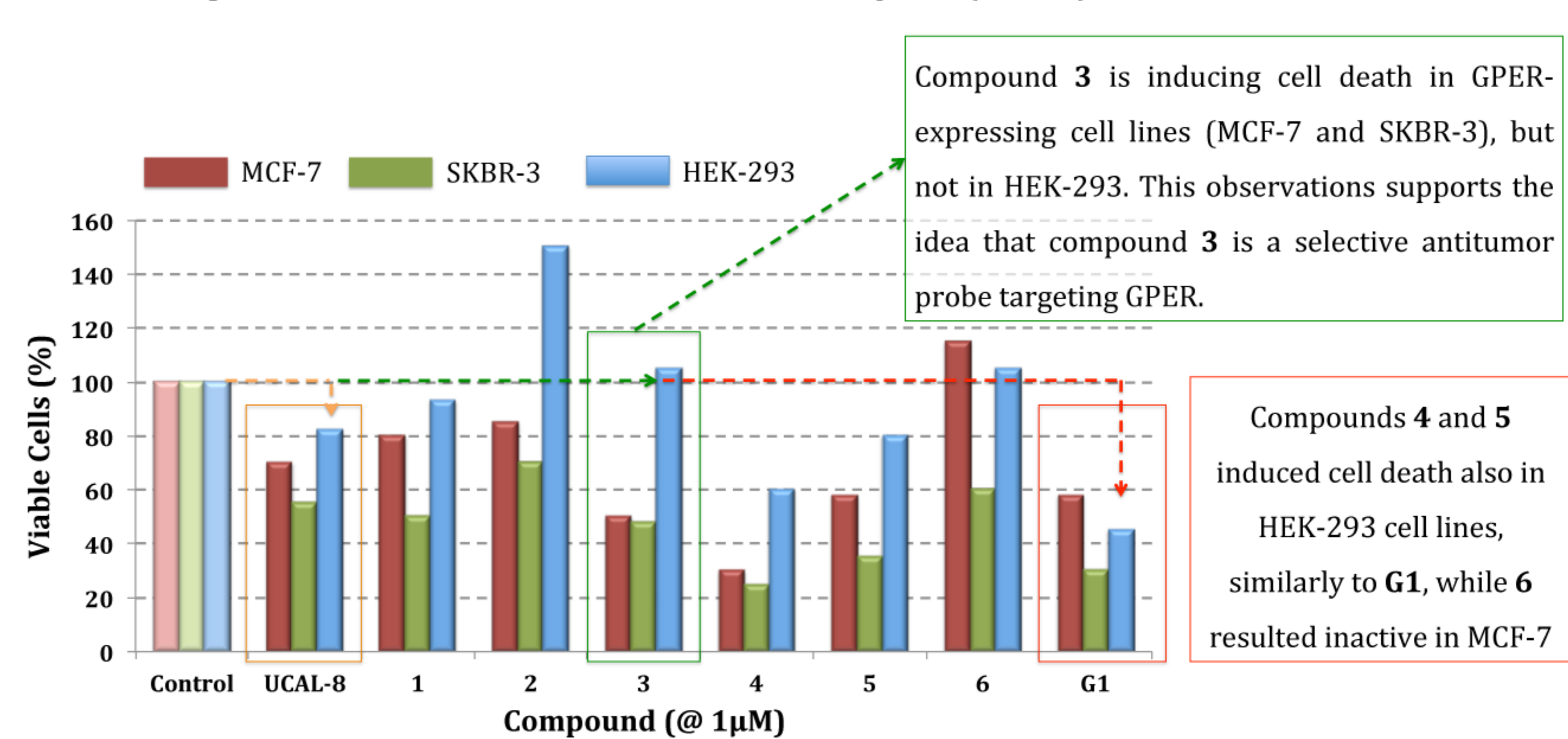
The selected compounds (UCAL-8, UPAR-75, UPAR-283) were evaluated for their **antitumor activity** in three different cell lines showing different level of GPER expression, such as MCF-7, SKBR-3 and HEK293.



MoA elucidation: UCAL-8 was analyzed for its ability to activate specific intracellular effectors



Hit-to-lead optimization: structural modification of the hit compound (UCAL-8)



Conclusions

- The 3-D structural **model of GPER** was used to identify new chemical entities as modulator of the GPER receptor
- The 3-D model of GPER was validated by biological assays, leading to the **discovery of at least three new GPER modulators**
- Among the new GPER modulators identified, one (**UCAL-8**) is structurally related to **G1**, while **UPAR-75** and **UPAR-283** are structurally unrelated to **G1**, leading to the discovery of **two new chemotypes** as potential modulators of GPER
- In our assays **G1 induced cell death in a GPER-independent manner** (HEK-293), while **UCAL-8** effects on cell survival is tightly linked to the GPER expression even if its selectivity profile is not fully characterized yet.
- UCAL-8 reduce the phosphorylation of ERK1/2** with no interference on cyclin D1 or β -actin, further supporting a GPER-dependent mechanism,
- Structural optimization of **UCAL-8** led to the **discovery of the lead compound 3**, which showed an improved activity profile and should be submitted to further biological investigation.

Future Perspectives

- The protocol herein described led to the discovery of two new chemotypes (**UPAR-75** and **UPAR-283**) as potential modulators of GPER, which will be further expanded to get clear SARs and to elucidate their MoA.
- The **lead 3** will be submitted to further biological investigation to clarify its MoA and define its biological potential.

References

- Lappano, R. et al. Front. Endocrinol. 2014, 5, 1-6. [2]. Bologna, C.G. et al. Nat. Chem. Biol., 2006, 2, 207-212.
- Weissenborn, C. et al. J. Cancer Res. Clin. Oncol. 2014, 140, 663-671. [4]. Wang, C. et al. Am. J. Transl. Res. 2012, 4, 390-402.
- https://saliilab.org/modeller/ [6]. http://www.schrodinger.com [7]. http://www.ks.uiuc.edu/Research/vmd/ [8]. http://www.ks.uiuc.edu/Research/namd/ [9]. http://ambermd.org