

SUPPLEMENTARY INFORMATION

Identification of novel GSK-3 β hits using competitive biophysical assays

Beatrice Balboni^{1,2}, Shailesh Kumar Tripathi¹, Marina Veronesi³, Debora Russo³, Ilaria Penna³, Barbara Giabbai⁴, Tiziano Bandiera³, Paola Storici⁴, Stefania Giroto^{1} and Andrea Cavalli^{1,2*}*

¹Computational and Chemical Biology, Istituto Italiano di Tecnologia, Via Morego 30, 16163 Genova, Italy

²Department of Pharmacy and Biotechnology, University of Bologna, Via Belmeloro 6, 40126 Bologna, Italy.

³D3 Pharmachemistry, Istituto Italiano di Tecnologia, Via Morego 30, 16163 Genova, Italy.

⁴Structural Biology Lab, Elettra Sincrotrone Trieste S.C.p.A., 34149, Basovizza, Trieste, Italy

**Andrea Cavalli, Computational and Chemical Biology, Istituto Italiano di Tecnologia, Via Morego 30, 16163 Genoa, Italy, phone: +39 0102897403; Stefania Giroto, Computational and Chemical Biology, Istituto Italiano di Tecnologia, Via Morego 30, 16163 Genoa, Italy, phone: +39 0102896983*

Email: andrea.cavalli@iit.it, stefania.giroto@iit.it

Supplementary figures

Supplementary Figure S1

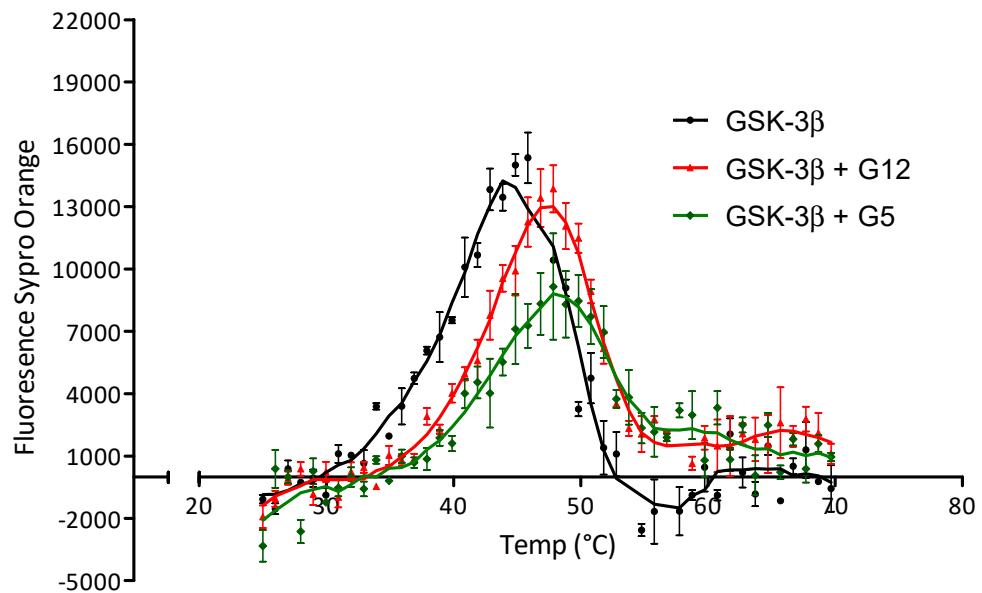


Figure S1. Thermal Shift Assay of GSK-3 β alone (black trace), in the presence of G5 (green trace) and G12 (red trace) compounds. G5 and G12 stabilize GSK-3 β protein and lead to an increase in melting temperature (T_m) of 3.2 °C and 2.5 °C, respectively. Error bars denote Standard Deviation (SD).

Supplementary Figure S2

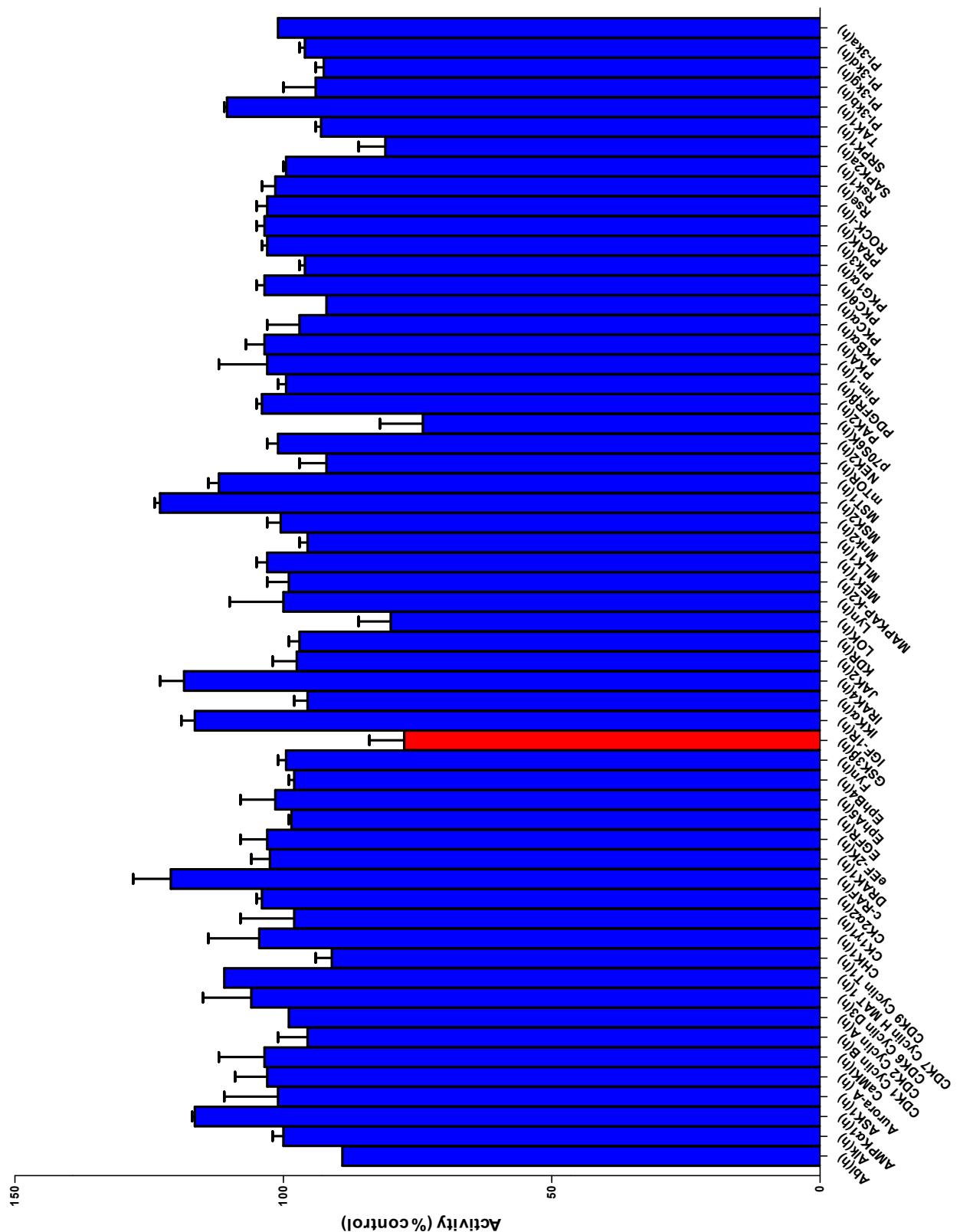


Figure S2. Bar Graphs showing G5 inhibitory effect on different kinases of the commercial panel (Eurofins service); all the experiments were performed using 20 μ M of compound and ATP concentrations \pm 15 μ M of each K_m . Error bars denote SD.

Supplementary Figure S3

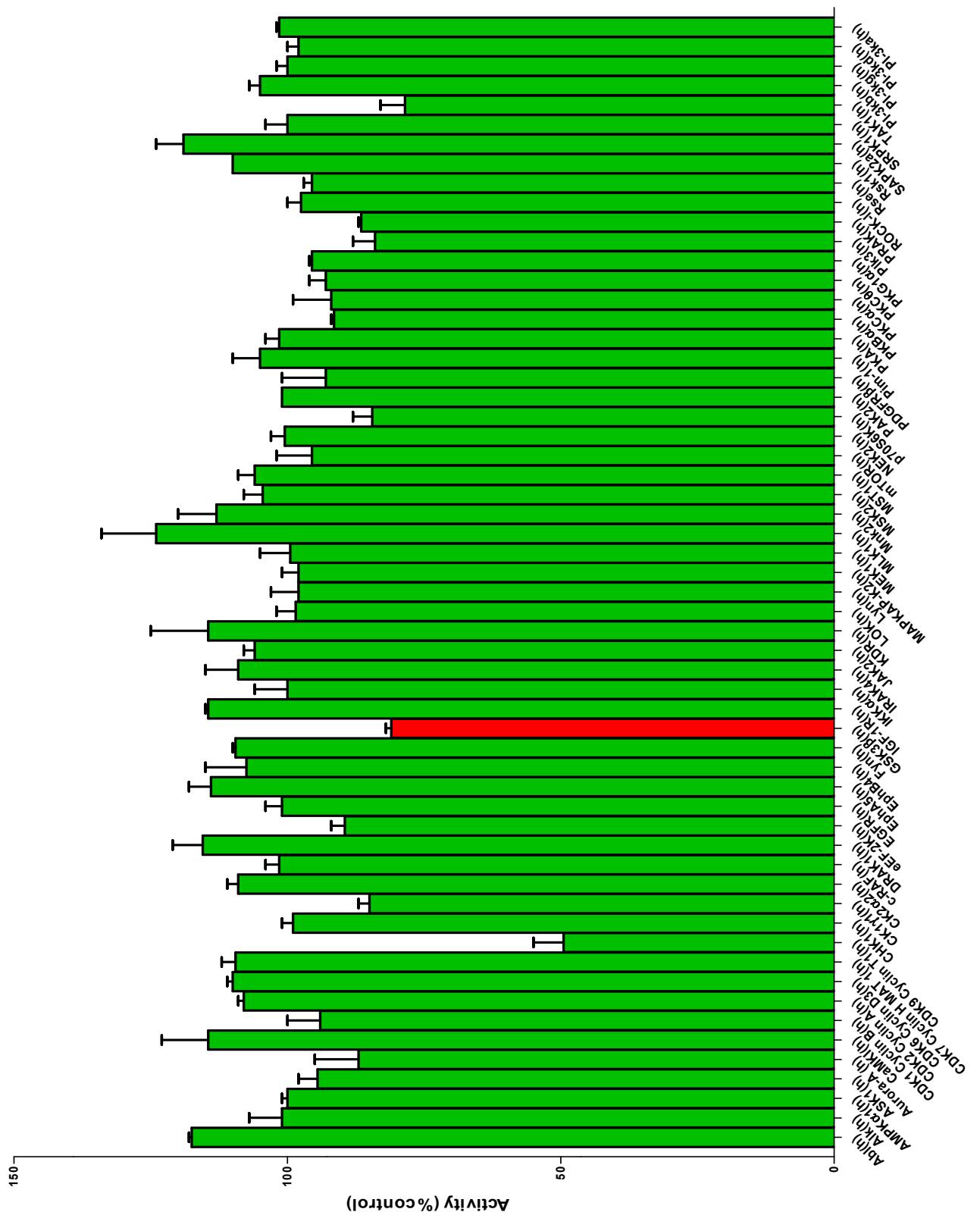


Figure S3. Bar Graphs showing G12 inhibitory effect on different kinases of the commercial panel (Eurofins service); all the experiments were performed using 20 μ M of compound and ATP concentrations \pm 15 μ M of each K_m . Error bars denote SD.

Supplementary Table

	G5	G12
Data reduction		
Resolution (Å)	2.5-48.8 (2.5-2.59)	2.2-89 (2.2-2.26)
Rmerge	0.388 (3.619)	0.319 (3.86)
Mean(I/sd(I))	7.9(0.8)	6.9 (0.6)
Completeness	100(100)	95.6 (87.8)
Unique Reflections	44494 (4582)	61582(4107)
Multiplicity	13.4 (12.9)	12.2(11.4)
CC_{1/2}	0.992 (0.39)	0.993(0.37)
Refinement		
Resolution (Å)	2.5-48.8	2.2-89
Rwork/Rfree	0.225/0.268	0.24/0.27
RMS bonds (Å)	0.0086	0.0075
RMS angles (°)	1.808	1.573

Table S1. Table reporting refinement statistics and values used for solving structure of GSK-3 β in complex with G5 and G12 compounds