

Cumhur Gökhan Ekmekci MD, PhD

Independent Researcher — Computational Oncology & Drug Discovery · Istanbul, Türkiye
Principal Investigator / Founder · academic affiliation with Atlas University, Istanbul (in progress)

ABOUT

Independent computational oncology researcher combining 25+ years in molecular and clinical genetics with 7+ years of in-silico drug discovery (26 SCI publications). I build self-contained computational pipelines — from causal target identification and neoantigen/biomarker design to structure-based lead discovery — that plug into experimental and clinical consortia as a discrete, fully-defined work package. As a Widening-country partner I am eligible for the Horizon Europe Hop-on Facility and actively seek Cluster 1 Health, Cancer Mission, EIC, ERDERA and TRANSCAN consortia.

KEY WORDS

Computational drug discovery Neoantigen & TMB Molecular docking (AutoDock Vina) Molecular dynamics (GROMACS/AMBER) MM-GBSA AlphaFold / AlphaFold-Multimer
Virtual screening QSAR Mendelian randomization Biomarker discovery Precision oncology Rare-disease pharmacological chaperones Nonsense-readthrough (PERT)
Blood-brain barrier (CLDN5) Bioinformatics (Python, RDKit)

PROJECT COOPERATION

Offering: a computational drug-discovery & biomarker work package for Health / Cancer-Mission / rare-disease consortia

I offer a ready-to-integrate in-silico work package: target identification (incl. Mendelian randomization), neoantigen and TMB-based biomarker design, structure-based drug discovery (docking, molecular dynamics, MM-GBSA, AlphaFold), virtual screening and patient stratification. Seeking: prospective coordinators plus wet-lab and clinical partners to validate and translate these outputs. Role sought: beneficiary / work-package partner (also eligible as a Widening-country partner for the Hop-on Facility). Open to Pillar 2 Health, Cancer Mission, EIC Pathfinder, ERDERA and TRANSCAN topics.

EXPERTISE

- Neoantigen identification/prioritisation & HLA-aware epitope ranking
- TMB panel design & optimisation
- Structure-based drug discovery & ternary-complex/degrader modelling
- Rare-disease pharmacological chaperones & drug repurposing
- Genome-scale nonsense-readthrough (PERT) feasibility atlases
- CLDN5 / blood-brain-barrier modulation (eight-platform framework)
- NGS / exome analysis; variant structural modelling

SELECTED OUTPUTS

- Ni C, ..., Ekmekci C, et al. *Nature Cell Biology* (2025).
- USP7 inhibitor discovery — ECC10, Antwerp (2026).
- Pan-cancer neoantigens & TMB panels — ESMO TAT 2026, Paris.
- Computational DIPG dual ALK5/ALK2 (galunisertib-class) study.
- PERT readthrough atlases (cancer / metabolic / neuromuscular).

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