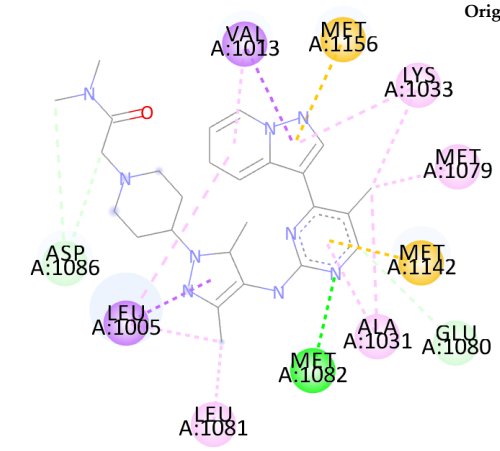
Table S1. The results of method validation between co-crystalized ligand at the original active site of IGFR (PDB ID: 5FXS)

Ligand	RMSD (Å)	Binding energy (kcal/mol)	Amino acid interaction		
			Hydrogen bond	Hydrophobic bond	Electrostatic bond
2-[4-[4-[[(6Z)-5-chloranyl-6-pyrazolo[1,5-a]pyridin-3-ylidene-1H-pyrimidin-2-yl]amino]-3,5-dimethyl-pyrazol-1-yl]piperidin-1-yl]-N,N-dimethyl-ethanamide (crystal structure)	Not determined	Not determined	GLU1080 MET1082	LEU1005 (2) VAL1013 ALA1031 LYS1033 MET1142 LEU1081	-
2-[4-[4-[[(6Z)-5-chloranyl-6-pyrazolo[1,5-a]pyridin-3-ylidene-1H-pyrimidin-2-yl]amino]-3,5-dimethyl-pyrazol-1-yl]piperidin-1-yl]-N,N-dimethyl-ethanamide (re-docking)	2.48	-9.88	GLU1080 MET1082 ASP1086 (2)	LEU1005 (3) VAL1013 (3) ALA1031 (2) LYS1033 (2) MET1079 LEU1081	-

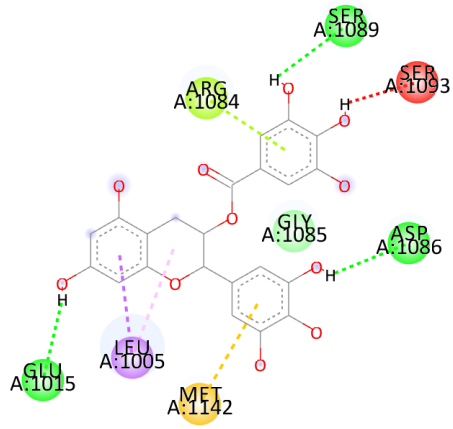
Original ligand



Interactions

- Conventional Hydrogen Bond
- Carbon Hydrogen Bond
- Pi-Sigma
- Pi-Sulfur
- Alkyl
- Pi-Alkyl

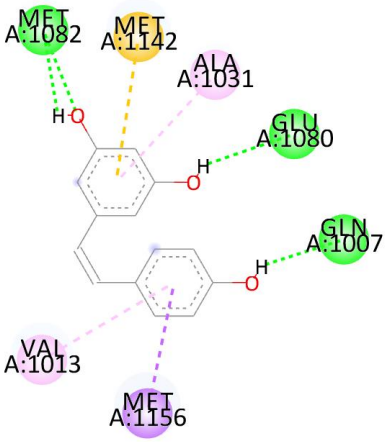
EGCG



Interactions

- van der Waals
- Conventional Hydrogen Bond
- Unfavorable Donor-Donor
- Pi-Sigma
- Pi-Sulfur
- Pi-Lone Pair
- Amide-Pi Stacked
- Alkyl
- Pi-Alkyl

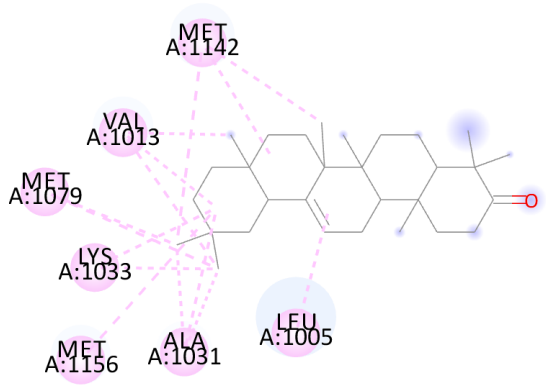
Resveratrol



Interactions

- Conventional Hydrogen Bond
- Pi-Sigma
- Pi-Sulfur
- Pi-Alkyl

Olean-12-en-3-one



Interactions

- Alkyl

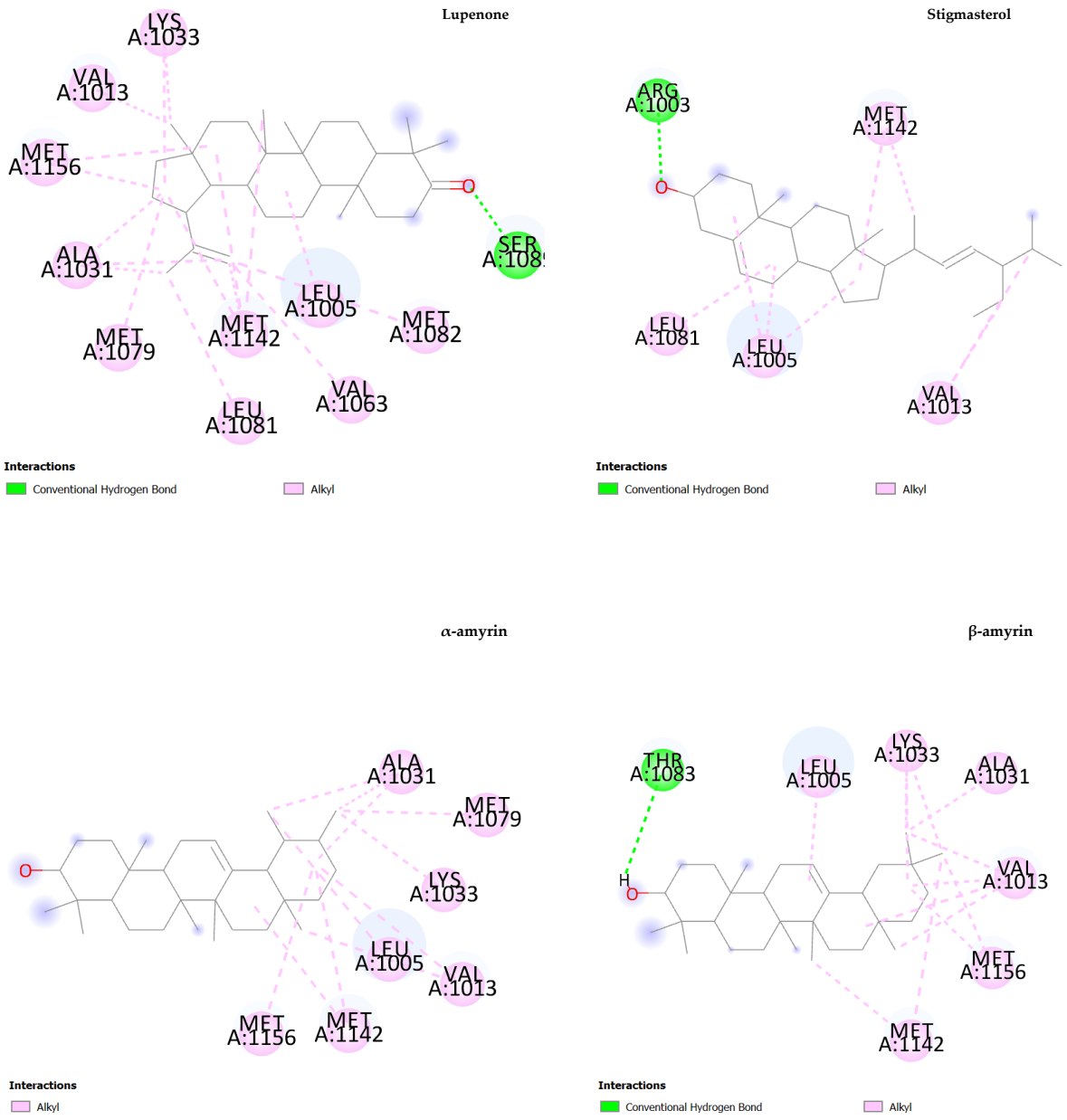


Figure S1. The results of the molecular docking study of IGFR were represented by 2D diagram of phytochemical-receptor interactions.

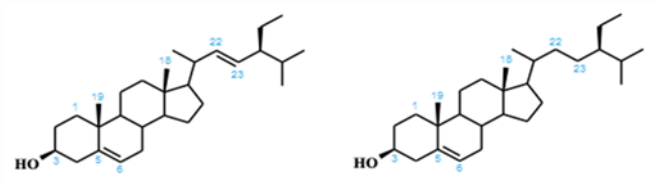


Figure S2. Structure of compound 1 (stigmasterol) and compound 2 (β-sitosterol) from fraction ACH3.

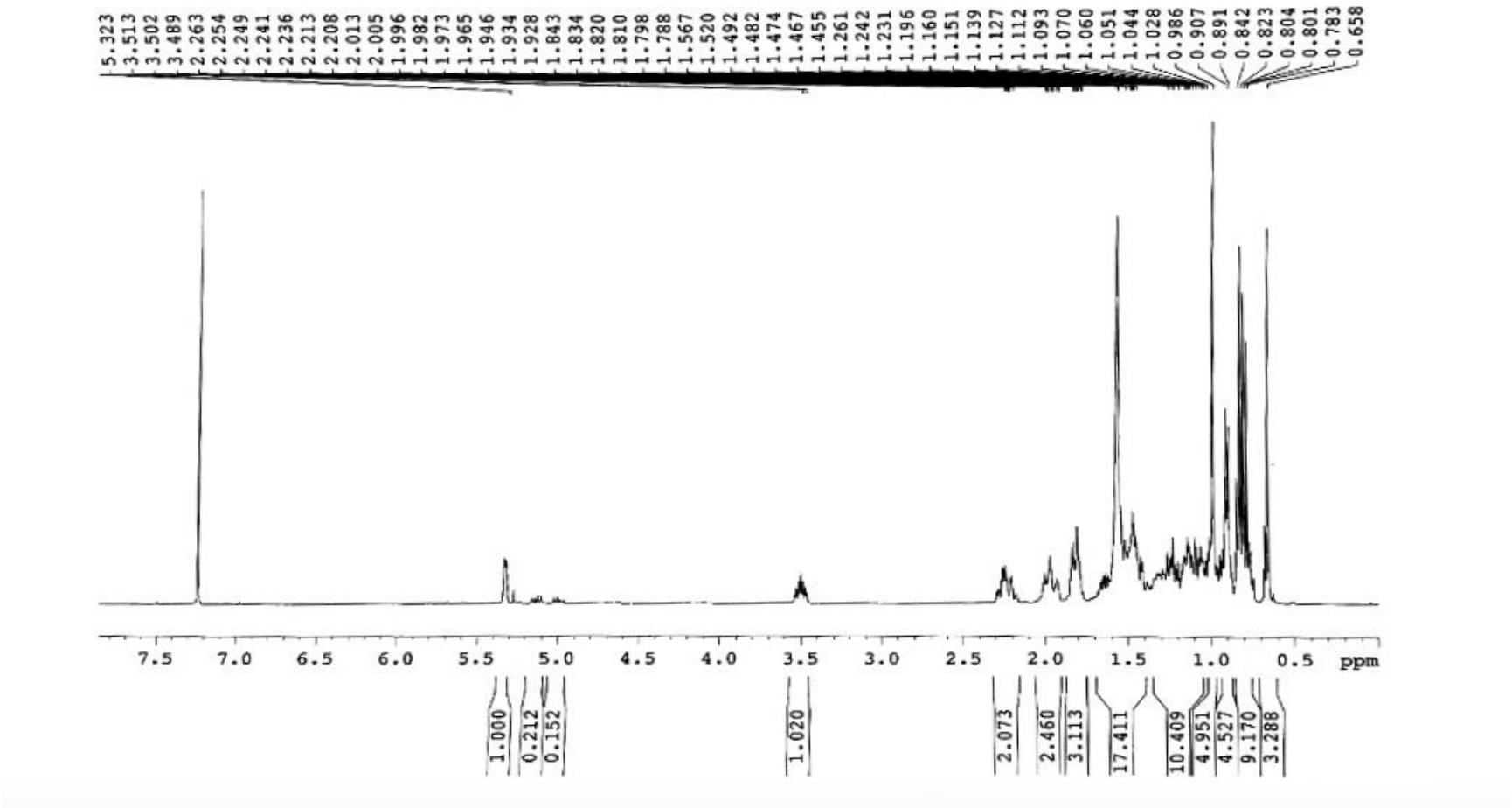


Figure S3. ^{1}H-NMR spectrum of a mixture of β-sitosterol and stigmastrol (compound 1 and 2) in $CDCl_3$

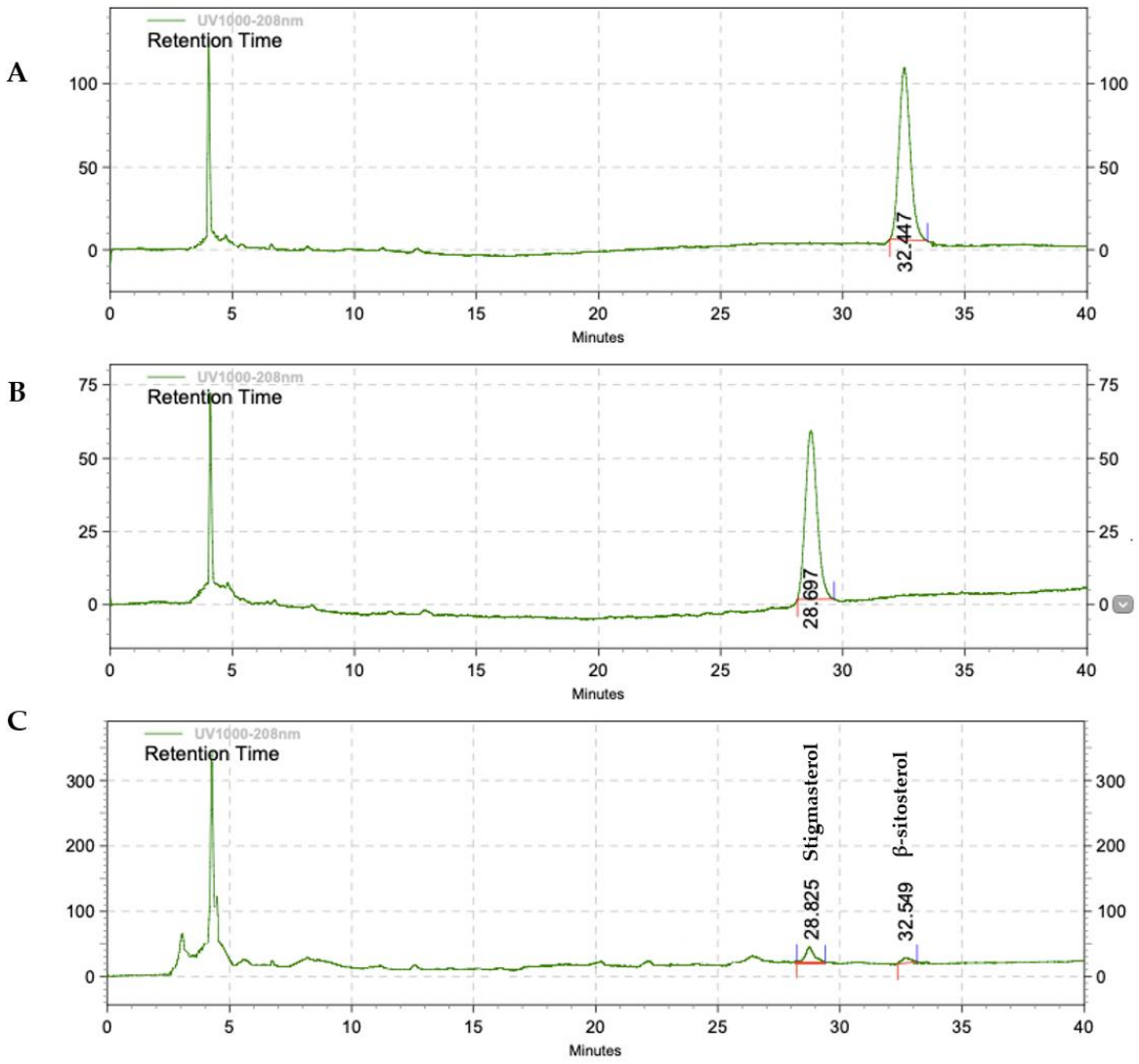


Figure S4. Reverse-phase HPLC analysis of standard β-sitosterol (A) and stigmasterol (B). The extract of ACH showing the presence of both β-sitosterol and stigmasterol (C).