

Pro-angiogenic and wound healing potential of baicalein: *In vitro*, *in ovo* and *in silico* evaluation

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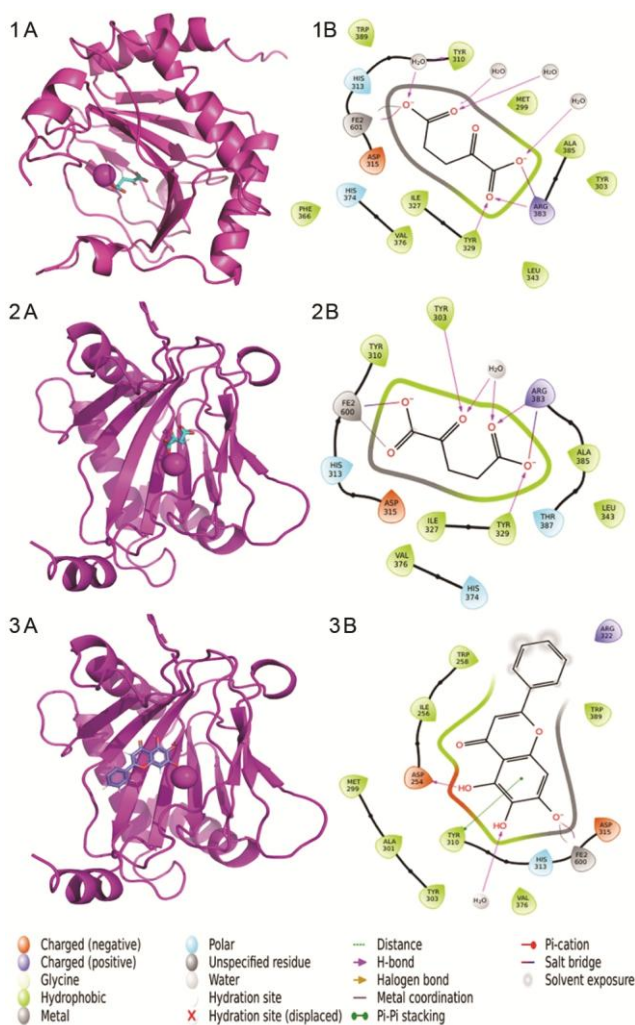
Supplementary Data

Supplementary Table 1 - Sequence of primers utilised for qPCR studies in HaCaT cells

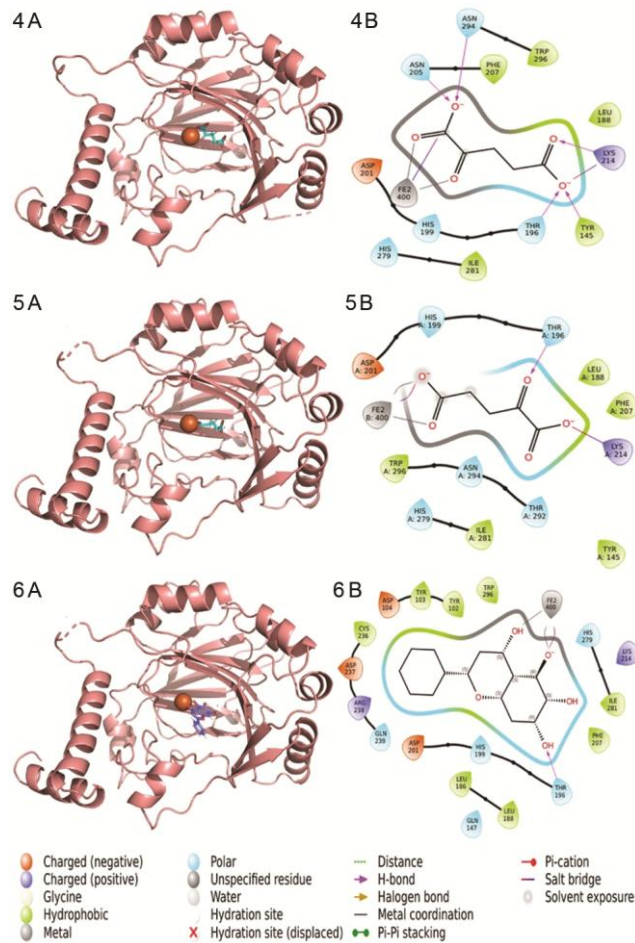
Gene name	Primer Sequence
KERATIN 10(F)	CAACCTAACTGATAATGCC
KERATIN 10(R)	GTCTTTCATTTCTCCTCGT
B ACTIN (F)	AAGAGAGGCATCCTCACCCCT
B ACTIN (R)	TACATCGCTGGGGTGTGAA

Suppl. Table S2 — List of grid information of each of the PDB IDs used for molecular docking

PDB IDs	Grid Dimensions (X, Y, Z Grid Points)
3OJU	20.1321, -18.6997, -9.7257
2G1M	41.5151, 20.5021, 10.8543
1MZF	22.6111, 25.6396, 31.0952
1MZE	22.7316, 25.4835, 30.8092
7E2E	48.6009, 56.5831, -10.9864



Suppl. Fig. 1 — 3D ribbon model (A) and stick model (B) diagrams of protein-ligand complexes generated via *in silico* docking experiments on PHD2. (A) The binding pocket of each protein and corresponding ligand (stick model) are given. The interacting amino acid moieties and the type of interactions involved are illustrated. The legend in the lower margin of the figure enlists the structural scheme of the molecules and interaction involved. The protein (PDB ID) - ligand complexes are (1) 3OJU-2OG, (2) 2G1M-2OG, and (3) 2G1M-Baicalein. Fe (II) ion is depicted as the ball-like structure in the centre of the protein structure.



Suppl. Fig. 2 — Readouts of the docking experiment done on FIH1 protein are represented as 3D ribbon model (A) and stick model (B) structural diagrams. (A) The binding pocket of each protein-ligand complex generated *in silico* is given. The amino acids taking part in the protein-ligand interaction are shown. A scheme representing the molecules and interactions involved is provided as a legend. Fe (II) ion, ordinarily present inside the protein molecule, is also identified in the structural representation of the interaction interphase. The protein (PDB ID) - ligand complexes are (4) 1MZF-2OG, (5) 1MZE-2OG, and (6) 1MZE-Baicalein, respectively.