

Identification of potential therapeutic targets of fatty acids for inflammatory bowel diseases: An *in silico* approach

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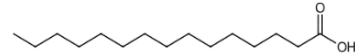
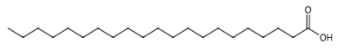
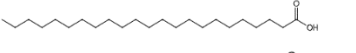
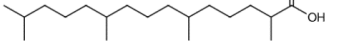
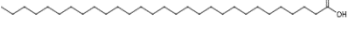
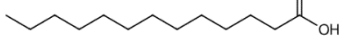
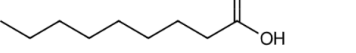
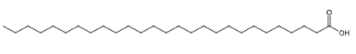
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Supplementary data

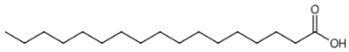
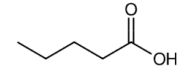
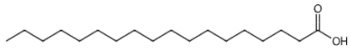
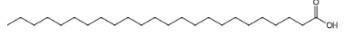
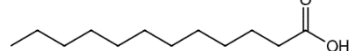
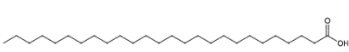
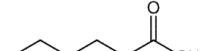
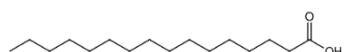
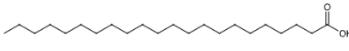
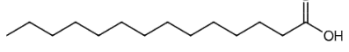

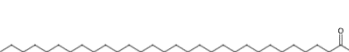
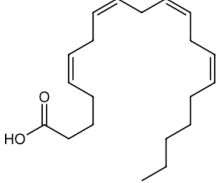
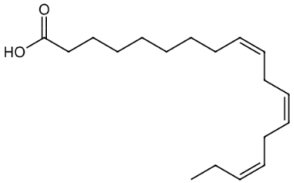
Suppl. Table 1 — Site-specific docking XYZ coordinates and radius of the sphere (Å)

| Protein (PDB ID) | XYZ Co-ordinates | Radius of the sphere (Å) |
|--|---|--------------------------|
| Interleukin-6 (8D82) | X = 198.918961, Y = 236.898380, and Z = 228.863648. | 18 |
| Interleukin-17 (7AMA) | X = -15.516853, Y = -12.893235, and Z = -16.562309. | 12 |
| Tumor necrosis factor- α (2AZ5) | X = -19.409600, Y = 74.650750, and Z = 33.849550. | 15 |
| Phosphoinositide 3-kinase(8EXU) | X = -17.458794, Y = 13.166471, and Z = 29.347353. | 15 |
| Protein Kinase B (AKT) (3CQW) | X = 5.990263, Y = 3.014000, and Z = 17.344895. | 12 |
| Hypoxia-inducible factor 1(8II0) | X = 23.184115, Y = -25.673308, and Z = 3.448577. | 12 |

Suppl. Table 2 — ADME analysis of odd-chain and even-chain FAs

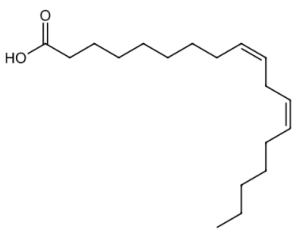
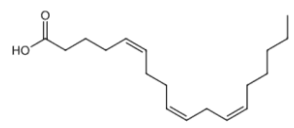
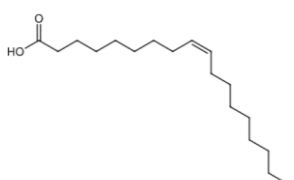
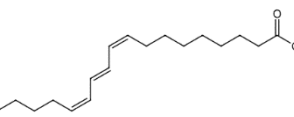
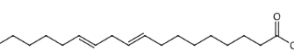
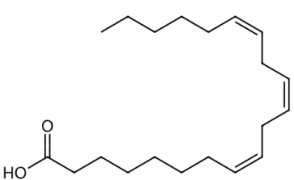
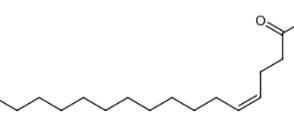
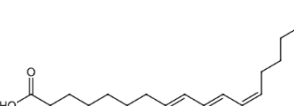
| Fatty acid | MW(≤ 500 D) | Odd-chain FAs | | | Structure |
|--------------------|-------------------|---|---------------|--------------|---|
| | | Bioavailability Score (OB $\geq 30\%$) | GI absorption | BBB permeant | |
| Pentadecanoic acid | 242.4 | 0.85 | High | Yes |  |
| Heneicosylic acid | 326.56 | 0.85 | Low | No |  |
| Tricosylic acid | 354.61 | 0.85 | Low | No |  |
| Pristanic acid | 298.5 | 0.85 | High | No |  |
| Nonacosanoic acid | 438.77 | 0.85 | Low | No |  |
| Tridecylic acid | 214.34 | 0.85 | High | Yes |  |
| Pelargonic acid | 158.24 | 0.85 | High | Yes |  |
| Carboceric acid | 410.72 | 0.85 | Low | No |  |

(Contd.)

| Suppl. Table 2 — ADME analysis of odd-chain, even-chain FAs(Contd.) | | | | | |
|---|------------|---------------------------------|--------------|--------------|---|
| Margaric acid | 270.45 | 0.85 | High | Yes |  |
| Valeric acid | 102.13 | 0.85 | High | Yes |  |
| Even-chain saturated FAs | | | | | |
| Fatty acid | MW(≤500 D) | Bioavailability Score (OB≥ 30%) | GIabsorption | BBB permeant | Structure |
| Stearic acid | 284.48 | 0.85 | High | No |  |
| Lignoceric acid | 368.64 | 0.85 | Low | No |  |
| Lauric acid | 200.32 | 0.85 | High | Yes |  |
| Cerotic acid | 396.69 | 0.85 | Low | No |  |
| Caproic acid | 116.16 | 0.85 | High | Yes |  |
| Palmitic acid | 256.42 | 0.85 | High | Yes |  |
| Behenic acid | 340.58 | 0.85 | Low | No |  |
| Myristic acid | 228.37 | 0.85 | High | Yes |  |
| Caprylic acid | 144.21 | 0.85 | High | Yes |  |
| Melissic acid | 452.8 | 0.85 | Low | No |  |
| Even-chain unsaturated FAs | | | | | |
| Fatty acid | MW(≤500 D) | Bioavailability Score(OB≥ 30%) | GIabsorption | BBB permeant | Structure |
| Arachidonic acid | 304.47 | 0.85 | Low | No |  |
| α -Linolenic acid | 278.43 | 0.85 | High | Yes |  |

(Contd.)

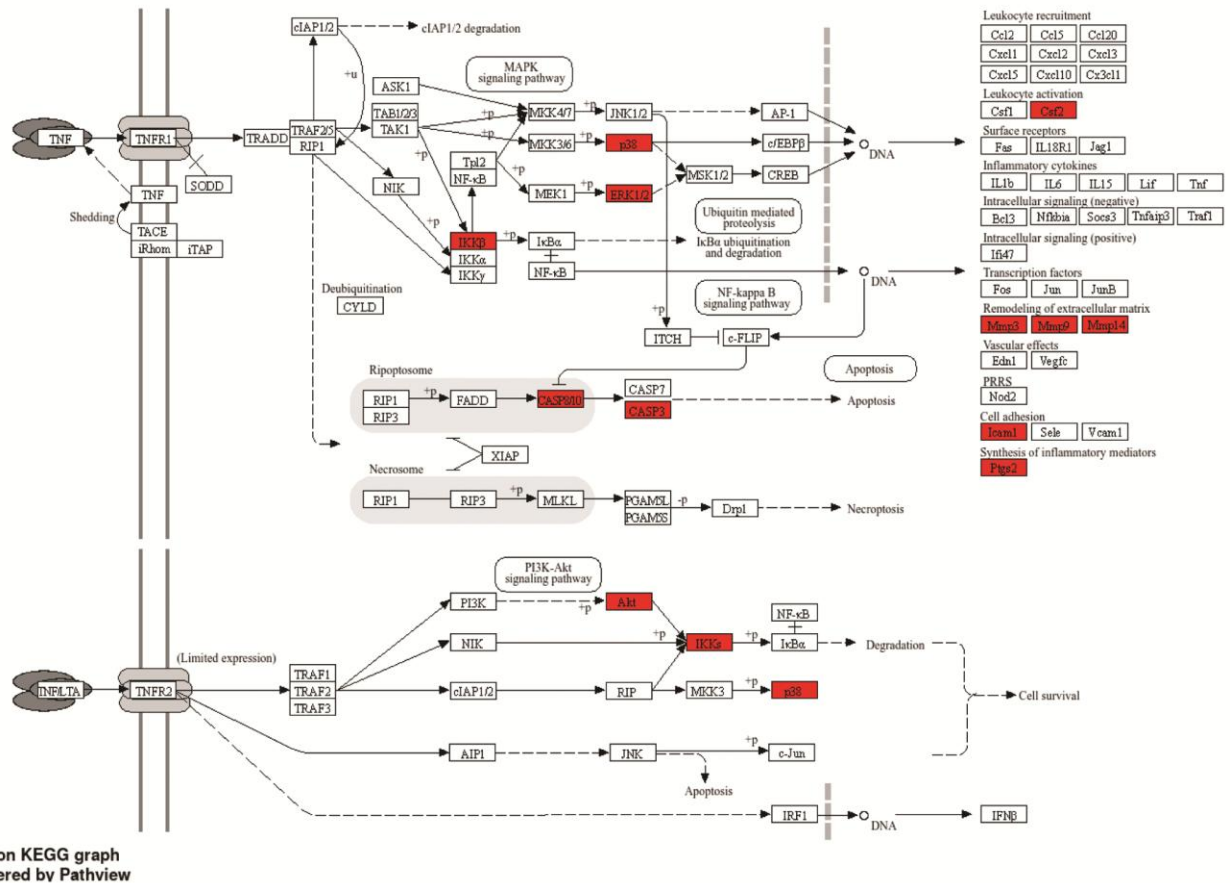
Suppl. Table 2 — ADME analysis of odd-chain, even-chain FAs (*Contd.*)

| | | | | | |
|----------------------------------|--------|------|------|-----|---|
| Linoleic acid | 280.45 | 0.85 | High | No |  |
| Pinolenic acid | 278.43 | 0.85 | High | Yes |  |
| Oleic acid | 282.46 | 0.85 | High | No |  |
| Punicic acid | 278.43 | 0.85 | High | Yes |  |
| Linoelaidic acid | 280.45 | 0.85 | High | Yes |  |
| Dihomo- γ -linolenic acid | 306.48 | 0.85 | Low | No |  |
| 4-Hexadecenoic acid | 254.41 | 0.85 | High | Yes |  |
| Calendic acid | 278.43 | 0.85 | High | Yes |  |

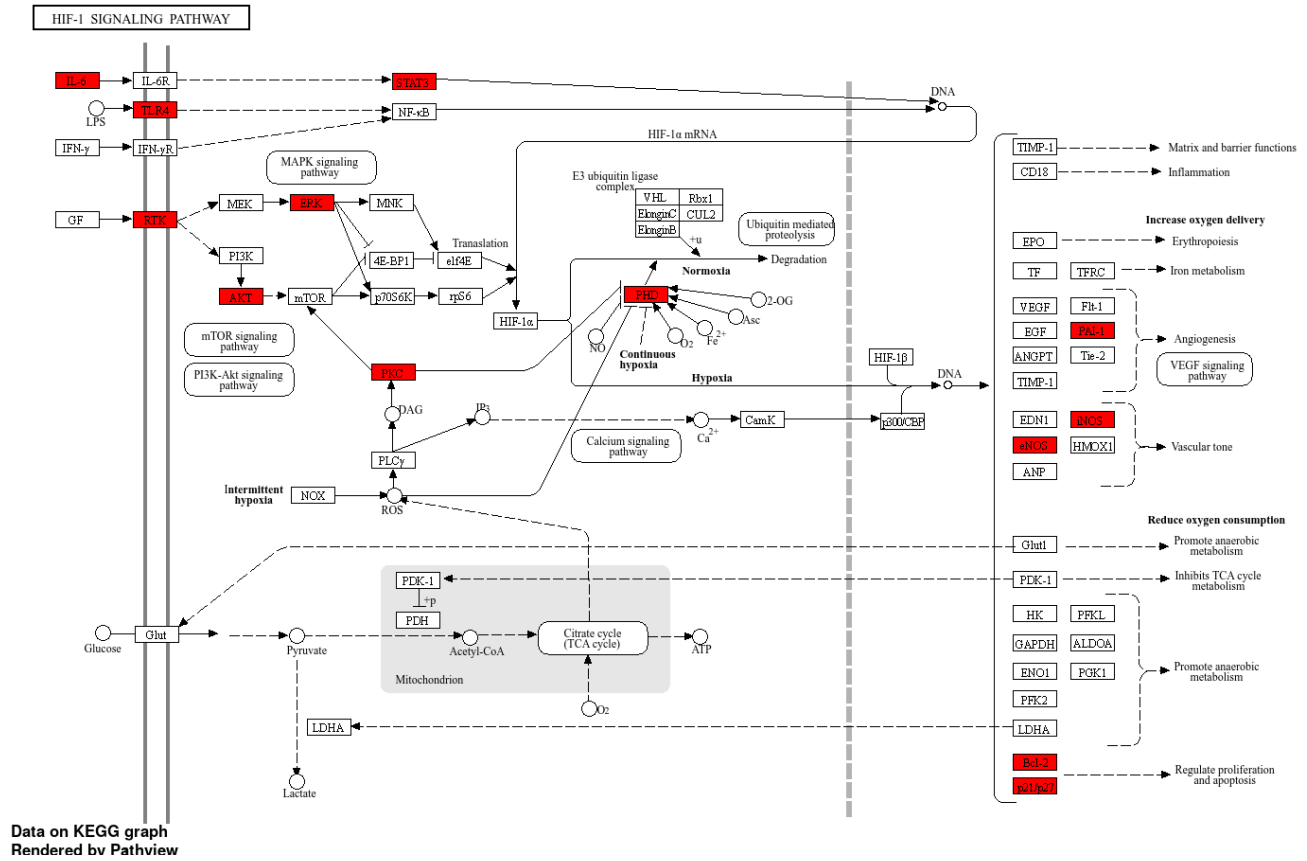
*MW-Molecular Weight; OB-Oral Bio-availability; GI – Gastro-intestinal; BBB – Blood brain barrier

Supplementary Figures:

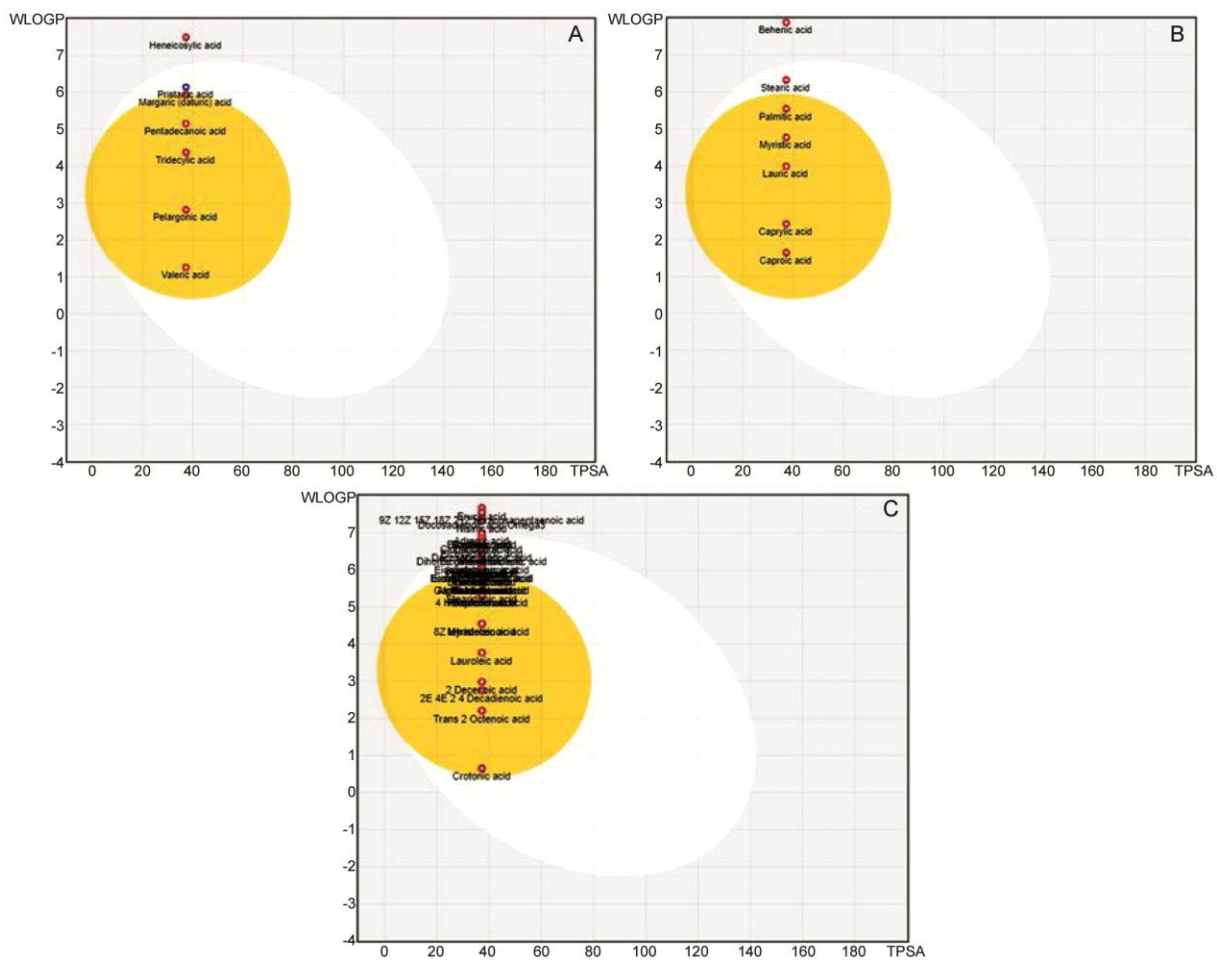
A TNF SIGNALING PATHWAY



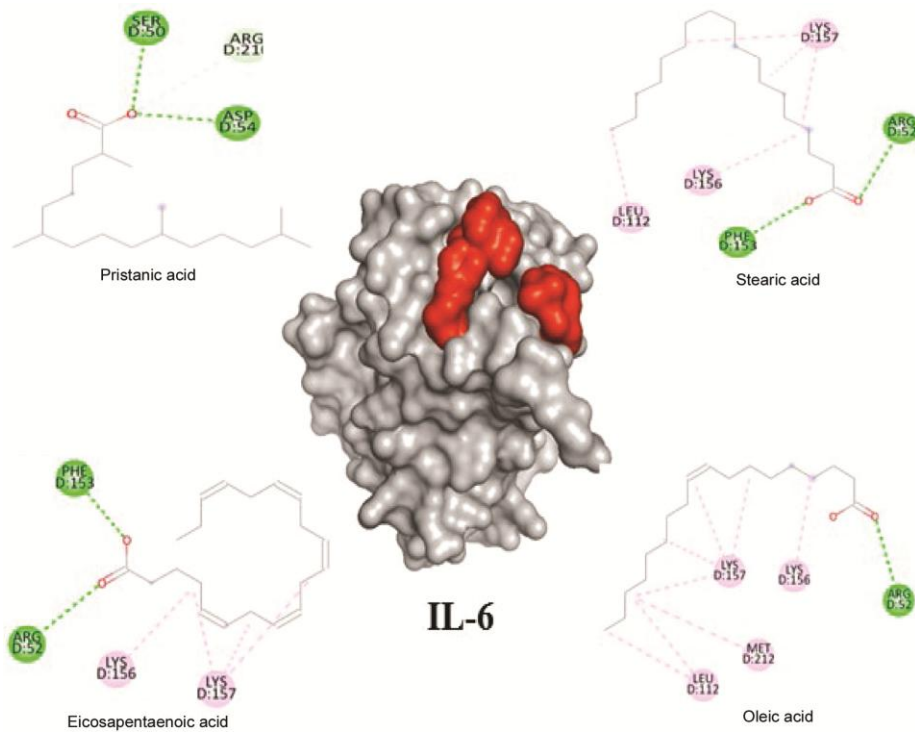
Suppl. Fig. 1A — KEGG pathway analysis: Odd-chain FA targets that target the component of the TNF signaling pathway. The figure illustrates the potential gene targets within the TNF signaling pathway that is associated with inflammatory bowel diseases (IBD). In this visual representation, the enriched gene targets are highlighted in red, indicating their relevance and potential impact in the context of IBD. This highlighting emphasizes the critical nodes within the pathway that may serve as focal points for therapeutic intervention.



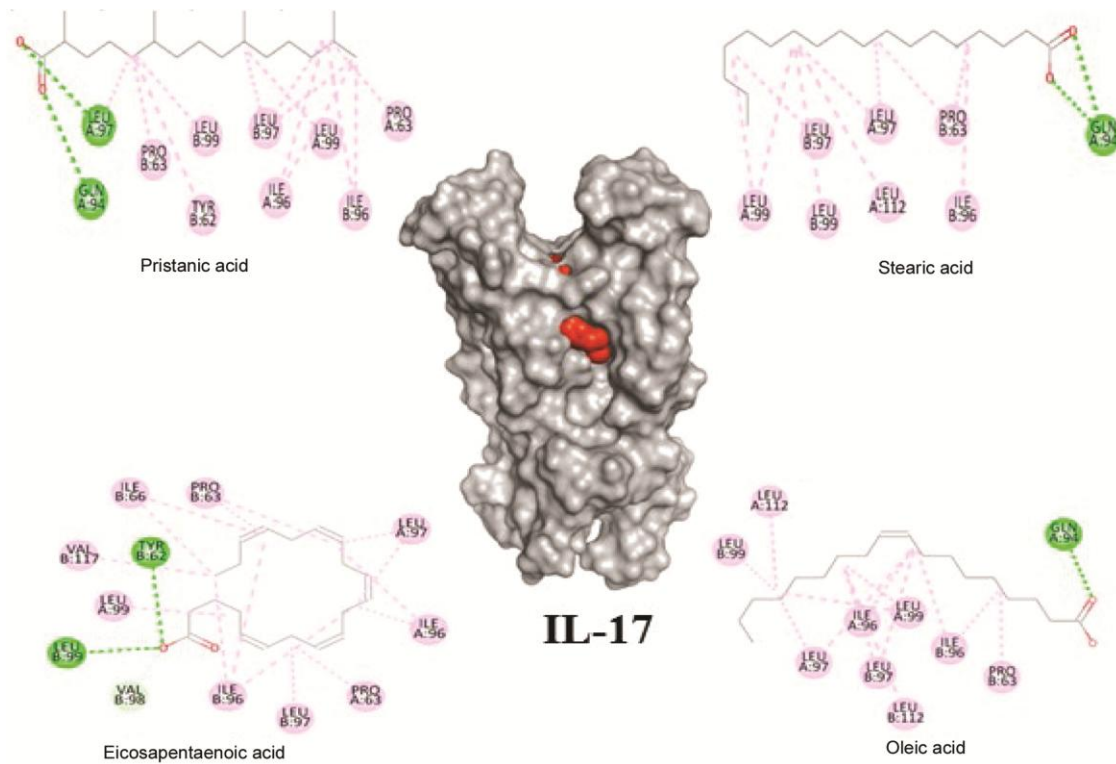
Suppl. Fig. 1B — KEGG pathway analysis: Even-chain FA targets that target the HIF-1 signaling pathway. The figure illustrates the potential gene targets within the HIF-1 signaling pathway that are associated with inflammatory bowel diseases (IBD). In this visual representation, the enriched gene targets are highlighted in red, indicating their relevance and potential impact in the context of IBD. This highlighting emphasizes the critical nodes within the pathway that may serve as focal points for therapeutic options.



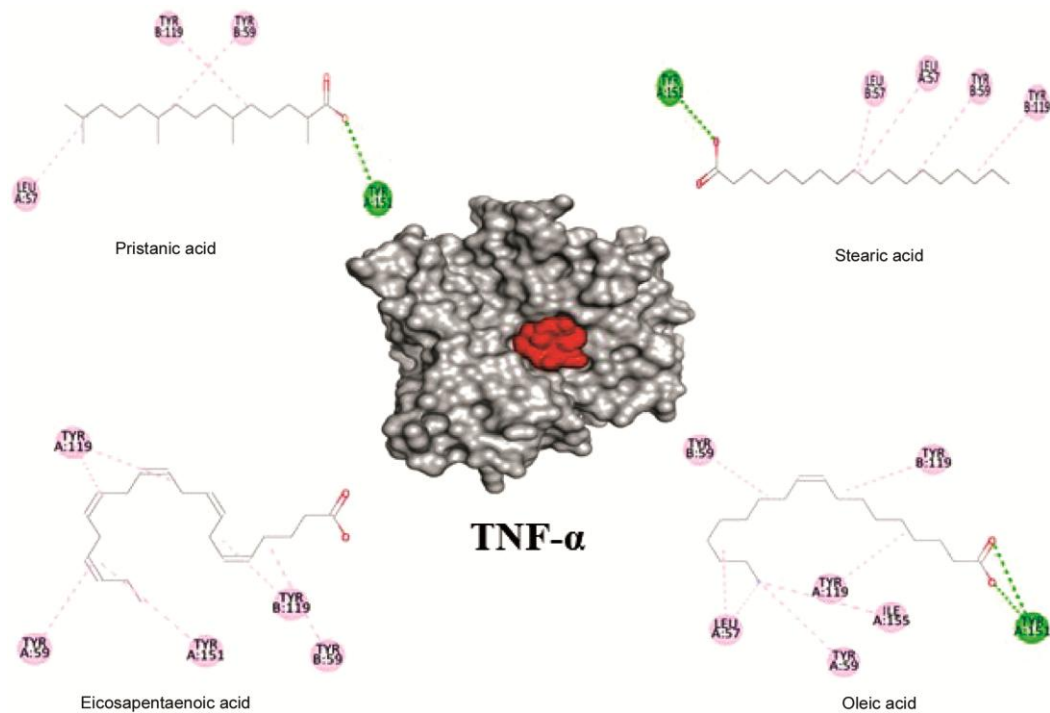
Suppl. Fig. 2 — BOILED-egg plots obtained for the FAs studied. (A) For odd-chain FAs; (B) For even-chain FAs (Saturated); and (C) For even-chain FAs (unsaturated)



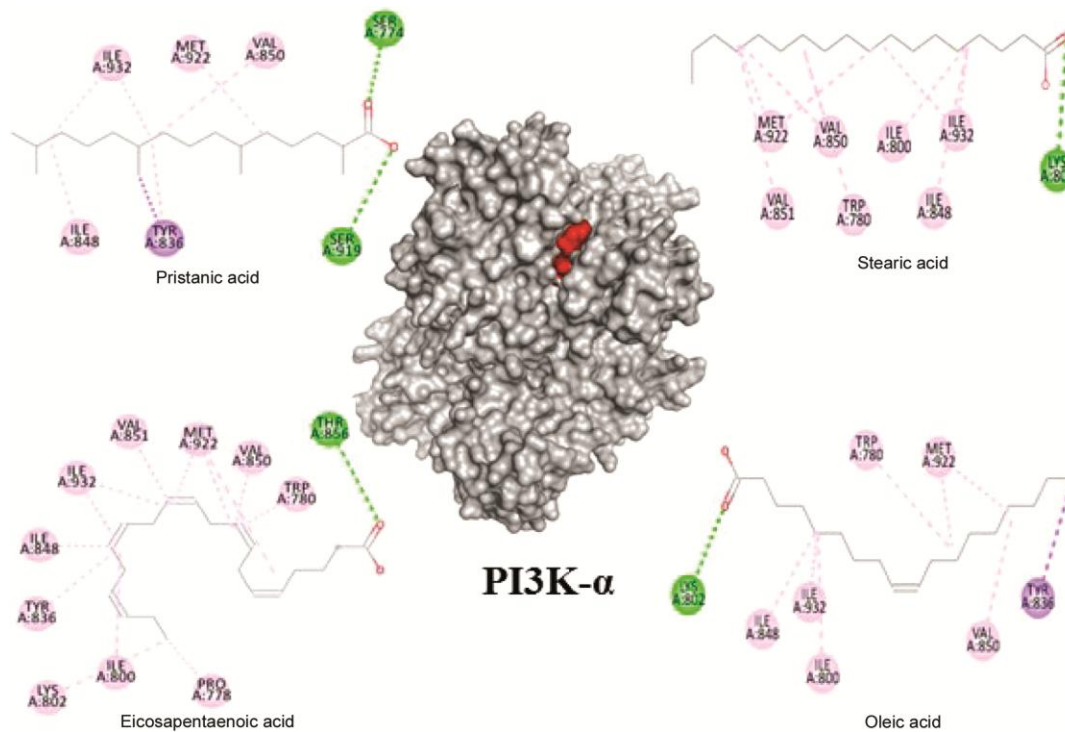
Suppl. Fig. 3 — Interactions of IL-6 with fatty acids. The protein (gray) and ligands (red) are shown in surface representation; hydrogen bonds (green) and hydrophobic interactions (pink) are depicted as dotted lines



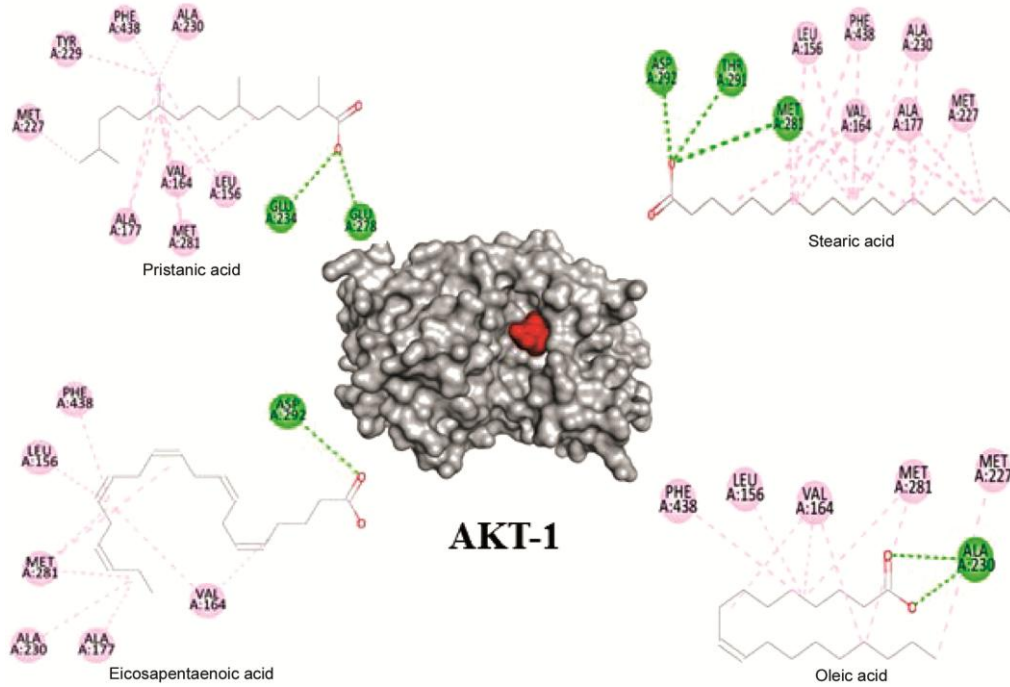
Suppl. Fig. 4 — Interactions of IL-17 with fatty acids. The protein (gray) and ligands (red) are shown in surface representation; hydrogen bonds (green) and hydrophobic interactions (pink) are depicted as dotted lines



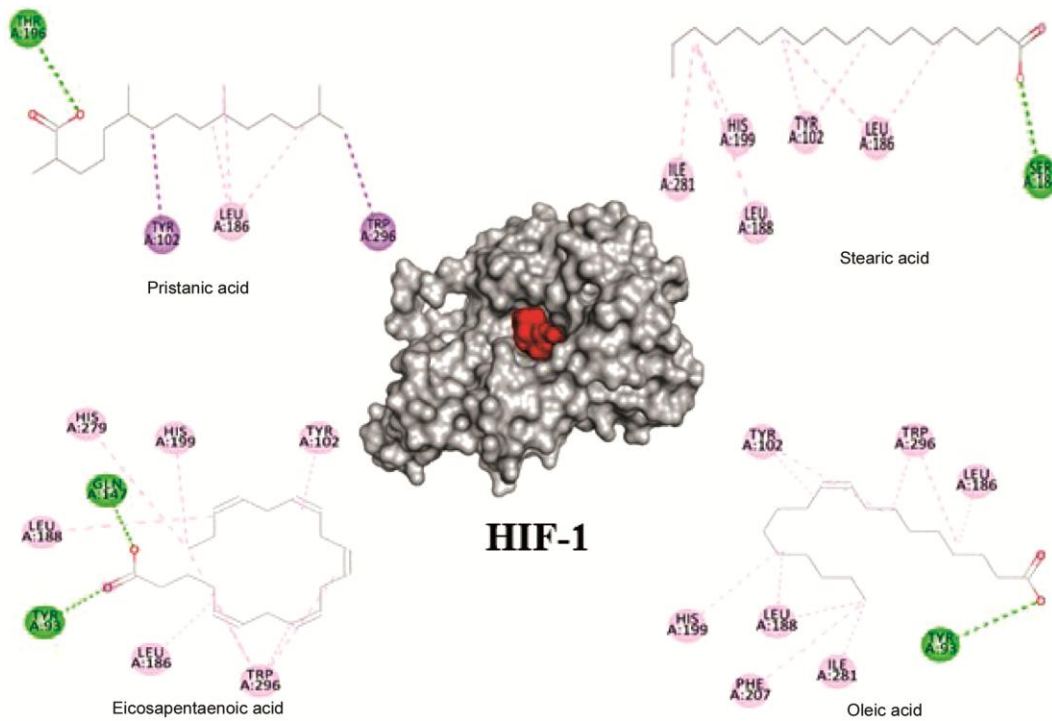
Suppl. Fig. 5 — Interactions of TNF- α with fatty acids. The protein (gray) and ligands (red) are shown in surface representation; hydrogen bonds (green) and hydrophobic interactions (pink) are depicted as dotted lines



Suppl. Fig. 6 — Interactions of PI3K- α with fatty acids. The protein (gray) and ligands (red) are shown in surface representation; hydrogen bonds (green) and hydrophobic interactions (pink) are depicted as dotted lines



Suppl. Fig. 7 — Interactions of AKT-1 with fatty acids. The protein (gray) and ligands (red) are shown in surface representation; hydrogen bonds (green) and hydrophobic interactions (pink) are depicted as dotted lines



Suppl. Fig. 8 — Interactions of HIF-1 with fatty acids. The protein (gray) and ligands (red) are shown in surface representation; hydrogen bonds (green) and hydrophobic interactions (pink) are depicted as dotted lines