

Supplementary Table 1 – MD simulation of membrane potential.

| Orientation | Choline presence | Electric field [mV] | Occupancy* | Release time (ns) |
|----------------|---------------------|---------------------|------------|-------------------|
| Outward-facing | In solution [380mM] | 0 | 12.46 | n.a.** |
| Outward-facing | In solution [380mM] | 0 | 1.3 | n.a. |
| Outward-facing | In solution [380mM] | 0 | 80.62 | n.a. |
| Outward-facing | In cavity | 0 | 19.4 | 348 |
| Outward-facing | In cavity | 0 | 99 | n.r.*** |
| Outward-facing | In cavity | 0 | 98.4 | n.r. |
| Inward-facing | In cavity | 0 | 70.7 | 895 |
| Inward-facing | In cavity | 0 | 92.8 | n.r. |
| Inward-facing | In cavity | 0 | 100 | n.r. |
| Outward-facing | In solution [380mM] | -200 | 50.55 | n.a. |
| Outward-facing | In solution [380mM] | -200 | 73.43 | n.a. |
| Outward-facing | In solution [380mM] | -200 | 0 | n.a. |
| Outward-facing | In cavity | -200 | 98.38 | n.r. |
| Outward-facing | In cavity | -200 | 99.59 | n.r. |
| Outward-facing | In cavity | -200 | 99.29 | n.r. |
| Inward-facing | In cavity | -200 | 100 | n.r. |
| Inward-facing | In cavity | -200 | 64.4 | 662 |
| Inward-facing | In cavity | -200 | 17.4 | 675 |

* Percentage of the trajectory in which at least one choline molecule is closer than 5 Å to the center of mass of TRP 102.

** n.a.: not applicable

***n.r.: no release observed

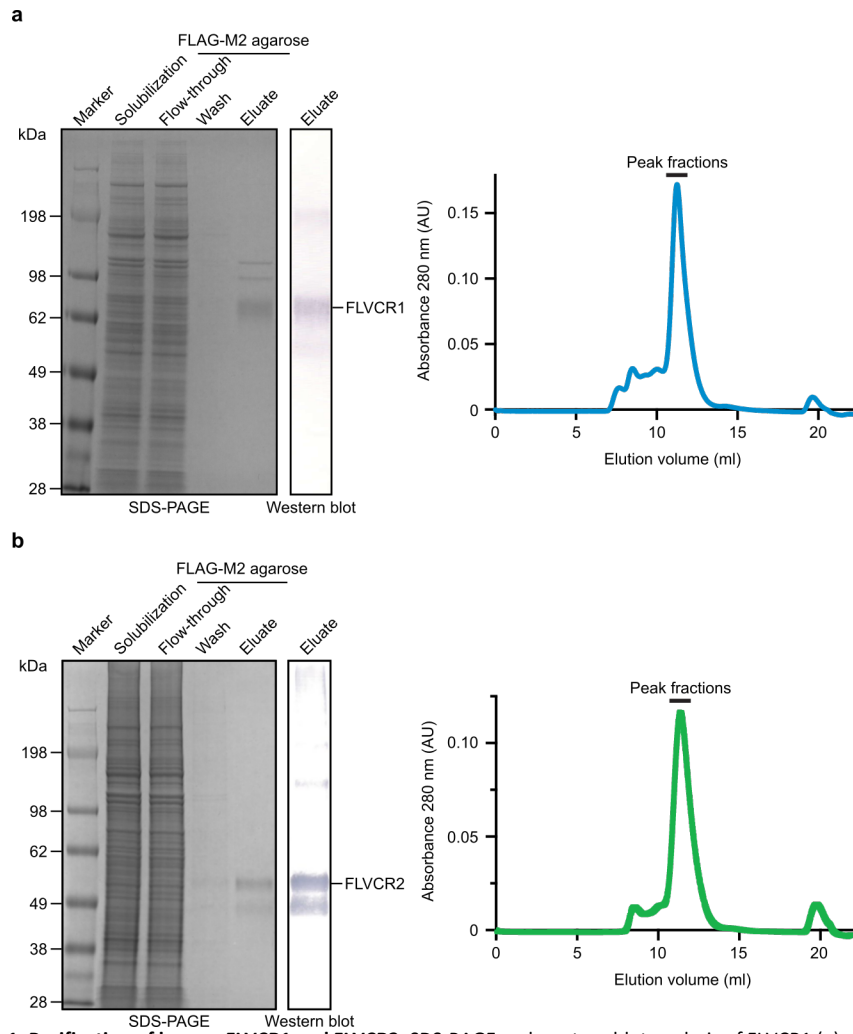
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Supplementary Table 3 – Amino acid sequences of human FLVCR variants used in this study.

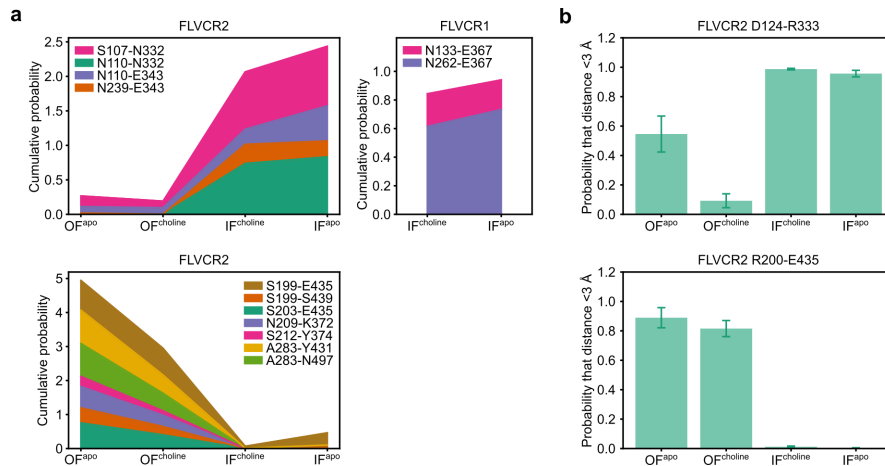
| Variant | Amino acid sequence |
|---------------------|--|
| FLVCR1a (wild-type) | MARPDEEGAAVAPGHPLAKGYLPLPRGAPVVGKESVELQNGPKAGTFPVNGAPRDSLAAASGVLGGPQTPLAPEEETQARLLP AGAGAETPGAESSPLTLTALSRRFVLLIFSLYSLVNAFQWIQYSISNVFEGFYGVTLHIDWLSMVYMLAYVPLIFPATWLLDTR GLRLTALLGSGLNCLGAWIKCGSVQQHLFWVTMLGQCLCSVAQVFILGLPSRIASVWFGPKEVSTACATAVLGNQLGTAVGFLL PPVLPNTQNDTNLLACNISTMFYGTSAVATLLFILTAIAFKEKPRYPSSQAQAALQDSPPEEYSYKKSIRNLFKNIPFVLLITYGIM TGAFYSVSTLLNQMILTYEGEEVNAGRIGLTLVVAGMVGSLCGLWLDYTKYKQTTLIVYILSFIGMVIFFTLRLYIIIVFVTGG VLGFFMTGYLPLGFEFAVEITYPESEGTSSGLLNASAQIFGILFLAQGKLTSDYGPKAGNIFLCVWWMFIGIILTALIKSDLRRHNINI GITNVDVKAIPADSPTDQEPKTVMLSKQSESAIDYKDDDDK |
| FLVCFR2 (wild-type) | MVNEGPNQEESDDTPVPESALQADPSVSVHPSVSVHPSVSNPSVSVHPSSSAHPSALAQPGLAHPSSSGPELDSVIKVSRRR WAVVLVFCSCYMCNSFQWIQYGSINIFMHFYGVSAFAIDWLSMCMYMLTYIPLLLPVAWVLEKFGRLTIALTGSALNCLGAWVK LGSLKPHLFPVTVVGGQLICVAQVFLGMPRIASVWFGANEVSTACSVAVFGNQLGIAIGFLVPPVLPNIEDRDELAYHISIMFYI IGGVATLLILVIVFKEKPKYPPSRAQSLSYALTSPDASYLGSARLFKNLNFVLLVITYGLNAGAFYALSTLLNRMVIVHYPGEEVN AGRIGLTIAGMLGAVISGIWLDRSKTYKETTLLVYIMTLVGMVVYFTLNLGHLWVVVITAGTMGFFMTGYLPLGFEFAVELTY PESEGSSGLLNISAQVFGIIFTISQGGIIDNYGTPGNIFLCVFLTLGAALTAFAIKADLRRQKANKETLENKLQEEEEESNTSKVPTAV SEDHLDYKDDDDK |

Supplementary Table 4 – Cryo-EM and model data statistics.

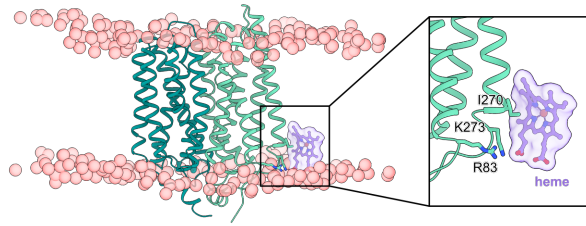
| | FLVCR1-IF ^{apo} (EMD-18334; PDB 8QCS) | FLVCR1-IF ^{choline} (EMD-18335; PDB 8QCT) | FLVCR2-IF ^{apo} (EMD-18336; PDB 8QCX) | FLVCR2-OF ^{apo} (EMD-18337; PDB 8QCY) | FLVCR2-OF ^{heme} (EMD-18338; PDB 8QCZ) | FLVCR2-IF ^{choline} (EMD-18337; PDB 8QD0) |
|---|--|--|--|--|---|--|
| Data collection and processing | | | | | | |
| Magnification | 215,000 | 215,000 | 215,000 | 215,000 | 105,000 | 215,000 |
| Voltage (kV) | 300 | 300 | 300 | 300 | 300 | 300 |
| Electron dose (e ⁻ /Å ²) | 55 | 55 | 80 | 80 | 80 | 57 |
| Defocus range (µm) | -1.1 to -2.1 | -1.1 to -2.1 | -1.1 to -2.1 | -1.1 to -2.1 | -1.1 to -2.1 | -1.1 to -2.1 |
| Pixel size (Å) | 0.573 | 0.573 | 0.573 | 0.573 | 0.837 | 0.573 |
| Symmetry imposed | C1 | C1 | C1 | C1 | C1 | C1 |
| Initial particle images (no.) | 3,247,307 | 3,251,081 | 3,497,517 | 3,497,517 | 5,419,952 | 4,790,154 |
| Final particle images (no.) | 56,664 | 25,873 | 50,167 | 49,532 | 51,266 | 51,511 |
| Map resolution (Å) | 2.9 | 2.6 | 3.1 | 2.9 | 3.1 | 2.8 |
| FSC threshold | 0.143 | 0.143 | 0.143 | 0.143 | 0.143 | 0.143 |
| Map resolution range (Å) | 2.4–6.5 | 2.6–4.9 | 2.8–5.5 | 2.7–3.8 | 2.7–5.8 | 2.6–3.8 |
| Refinement | | | | | | |
| Initial model used | AlphaFold model (AF-Q9Y5Y0-F1) | | AlphaFold model (AF-Q9UPI3-F1) | | | |
| Model resolution (Å) | 3.4 | 3.1 | 3.6 | 3.4 | 3.6 | 3.3 |
| FSC threshold | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 | 0.5 |
| Model resolution range (Å) | | | | | | |
| Map sharpening B factor (Å ²) | -80 | -30 | -120 | -100 | -60 | -30 |
| Model composition | | | | | | |
| Non-hydrogen atoms | 3,255 | 3,273 | 3283 | 3,273 | 3,316 | 3,290 |
| Protein residues | 417 | 418 | 422 | 421 | 421 | 422 |
| Ligands | NAG: 1 | NAG: 1 CHT: 1 | – | – | HEM: 1 | CHT: 1 |
| Average B factors (Å ²) | | | | | | |
| Protein | 87.45 | 40.28 | 76.93 | 82.55 | 109.15 | 63.63 |
| Ligand | 144.11 | 68.46 | – | – | 183.4 | 31.72 |
| R.m.s. deviations | | | | | | |
| Bond lengths (Å) | 0.003 | 0.003 | 0.003 | 0.004 | 0.004 | 0.003 |
| Bond angles (°) | 0.570 | 0.512 | 0.512 | 0.592 | 0.631 | 0.641 |
| Validation | | | | | | |
| MolProbity score | 1.50 | 1.40 | 1.20 | 1.31 | 1.43 | 1.31 |
| Clashscore | 6.82 | 7.22 | 4.20 | 5.71 | 7.24 | 5.68 |
| Poor rotamers (%) | 2.5 | 3.1 | 0.6 | 0.0 | 1.4 | 2.8 |
| Ramachandran plot | | | | | | |
| Favored (%) | 97.3 | 98.1 | 99.0 | 98.6 | 98.1 | 99.0 |
| Allowed (%) | 2.7 | 1.9 | 1.0 | 1.4 | 1.9 | 1.0 |
| Disallowed (%) | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 |



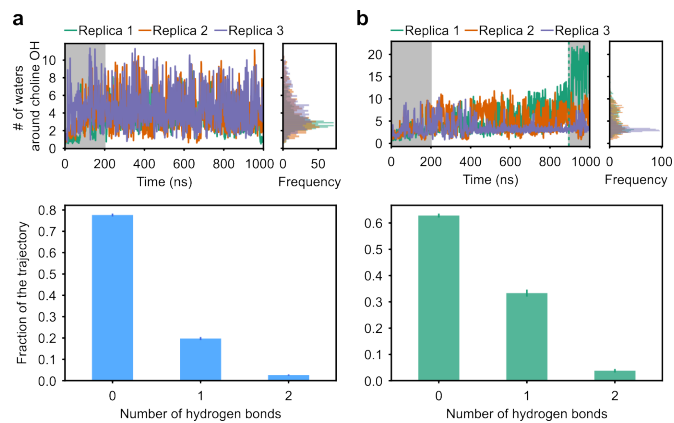
Supplementary Fig. 1: Purification of human FLVCR1 and FLVCR2. SDS-PAGE and western blot analysis of FLVCR1 (a) and FLVCR2 (b) affinity purification (left) and subsequent size-exclusion chromatography (SEC; right).



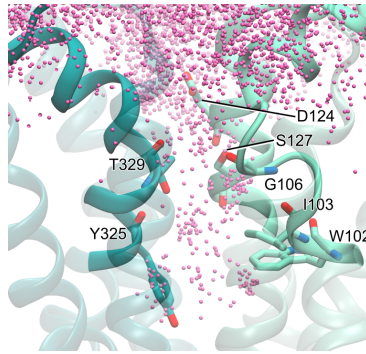
Supplementary Fig. 2: Persistence of critical interactions for stabilization of FLVCR1 and FLVCR2 in MD simulations. **a**, Cumulative probability of inter-domain hydrogen bond formation at the external gate (top) and the internal gate (bottom) with or without choline in the binding cavity. For each pair of residues, the probability was calculated as the fraction of the trajectory in which the distance between the residues remained below 3 Å. **b**, Stability of salt bridges within the external gate (top) and internal gate (bottom) of FLVCR2 in MD simulations. The displayed data represents the mean values obtained from three independent replicas, with error bars representing standard errors of the mean (s.e.m.).



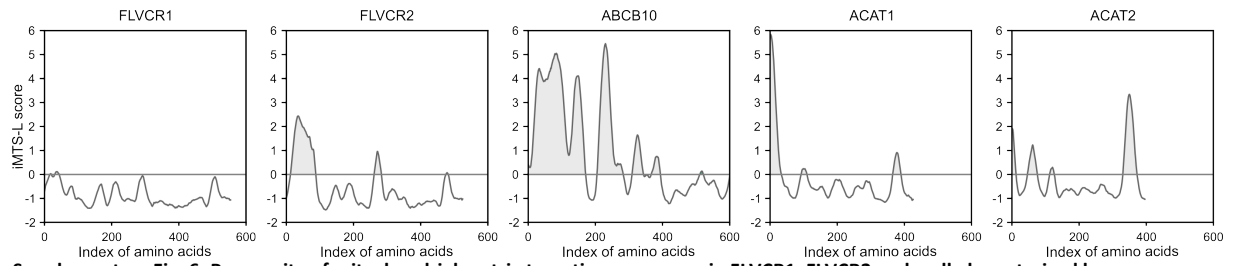
Supplementary Fig. 3: Snapshot of new, stable interactions formed between heme and FLVCR2 within the lipid bilayer in MD simulations. The heme molecule is shown in ball-and-stick representation and the phosphates of POPE/POPG are shown as red spheres. The right panel shows the close-up view of the heme molecule and the interacting residues of FLVCR2.



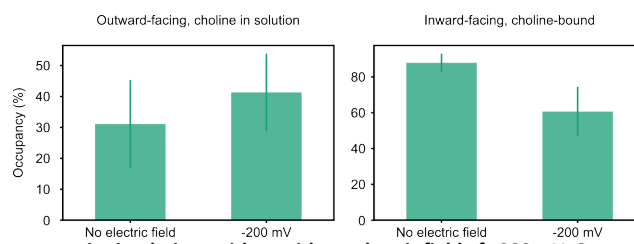
Supplementary Fig. 4: Hydration of choline in MD simulations. Interactions between choline and water in the binding site of inward-facing FLVCR1 (a) and FLVCR2 (b). The upper panels indicate the number of water molecules in the proximity of the hydroxyl group of choline with a cutoff of 5 Å in the $O^{\text{choline}}-O^{\text{water}}$ distance. The first 200 ns of simulations were considered as equilibration and thus not included in the histograms. The last 105 ns of replica 1 in the FLVCR2 simulation were discarded as well due to choline release. The lower panels represent the hydrogen bond formation between waters and the hydroxyl group of choline in the simulations with a distance and angle cut-off of 3 Å and 20°, respectively. Error bars represent s.e.m.



Supplementary Fig. 5: Choline entry from solution into the outward-facing cavity of FLVCR2 in MD simulations. Residues that interact with choline frequently are shown as sticks. Pink dots represent choline positions in all frames of one 1- μ s trajectory.



Supplementary Fig. 6: Propensity of mitochondrial matrix targeting sequences in FLVCR1, FLVCR2 and well-characterized human mitochondrial proteins. The propensity scores of internal matrix targeting signal-like sequences (iMTS-Ls) for FLVCR1, FLVCR2, and other known mitochondrial proteins, including ATP Binding Cassette Subfamily B Member 10 (ABCB10), Acetyl-CoA acetyltransferase 1 (ACAT1) and Acetyl-CoA acetyltransferase 2 (ACAT2), were computed with iMLP (<https://csb-iimp.bio.rptu.de>). Curve areas with propensity score >0 are coloured grey.



Supplementary Fig. 7: Choline occupancy in simulations with or without electric field of -200 mV. Occupancy was defined as the percentage of the trajectory in which at least one choline molecule is closer than 5 Å to the centre of mass of W102. The average values of three replicas are shown. Error bars represent standard errors of the mean (s.e.m.).