

Exploring Structural Flexibility and Classification Methods for Identifying Intermediate States of Hepatic ABCB Transporters

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Cryo-EM advances in Single Particle Analysis focuses nowadays in the study of the diverse conformations of the macromolecules beyond traditional 3D classification. Continuous flexibility methods, such as cryodrgn or Zernike3D [1, 2], allow to study intermediate states as well as transitions between them, characterizing the full structural spectrum. In this work we have combined flexibility methods, together with static classification consensus strategies, to study the conformational landscape of ABCB4. This receptor is an ATP-binding cassette transporter expressed in hepatocytes that plays a crucial role in the formation of bile by translocating phosphatidylcholine (PC) into canaliculi [3]. While previous studies [4] have provided valuable insights into the structural basis of PC translocation, the precise transition mechanism between discrete conformations remains elusive. Although further characterization is needed to fully understand the mechanism of PC translocation, preliminary studies using these developing flexibility analysis tools [1,5] revealed what might be possible new intermediate states.

References:

[1] Herreros D, Lederman RR, Krieger JM, Jiménez-Moreno A, Martínez M, Myška D, Strelak D, Filipovic J, Sorzano COS, Carazo JM. Estimating conformational landscapes from Cryo-EM particles by 3D Zernike polynomials. *Nat Commun.* 2023; 14:154.

[2] Zhong, E.D., Bepler, T., Berger, B. et al. CryoDRGN: reconstruction of heterogeneous cryo-EM structures using neural networks. *Nat Methods* 18, 176–185 (2021).

[3] Olsen JA, Alam A, Kowal J, Stieger B, Locher KP. Structure of the human lipid exporter ABCB4 in a lipid environment. *Nat Struct Mol Biol.* 2020; 27:62-70.

[4] Nosol K, Bang-Sørensen R, Irobalieva RN, Erramilli SK, Stieger B, Kossiakoff AA, Locher KP. Structures of ABCB4 provide insight into phosphatidylcholine translocation. *Proc Natl Acad Sci U S A.* 2021; 118:e2106702118.

[5] Jiménez de la Morena J, Conesa P, Fonseca YC, de Isidro-Gómez FP, Herreros D, Fernández-Giménez E, Strelak D, Moebel E, Buchholz TO, Jug F, Martínez-Sánchez A, Harastani M, Jonic S, Conesa JJ, Cuervo A, Losana P, Sánchez I, Iceta M, Del Cano L, Gragera M, Melero R, Sharov G, Castaño-Díez D, Koster A, Piccirillo JG, Vilas JL, Otón J, Marabini R, Sorzano COS, Carazo JM. *J Struct Biol.* 2022; 214:107872.

The authors also acknowledge “Comunidad Autónoma de Madrid” (Grant: S2022/BMD-7232) and European Union (EU) and Horizon 2020 through grant HighResCells (ERC - 2018 - SyG, Proposal: 810057).