



Article

# Dynamical behavior of the human ferroportin homologue from *Bdellovibrio bacteriovorus*. Insight into the ligand recognition mechanism.

Valentina Tortosa<sup>1</sup>, Maria Carmela Bonaccorsi di Patti<sup>2</sup>, Federico Iacovelli<sup>3</sup>, Andrea Pasquadibisceglie<sup>1</sup>, Mattia Falconi<sup>3</sup>, Giovanni Musci<sup>4</sup>, Fabio Polticelli<sup>1,5\*</sup>

<sup>1</sup>Department of Sciences, Roma Tre University, 00146 Rome, Italy; valentina.tortosa@uniroma3.it (V.T.); andrea.pasquadibisceglie@uniroma3.it (A.P.)

<sup>2</sup>Department of Biochemical Sciences, Sapienza University of Roma, 00185 Rome, Italy; mariacarmela.bonaccorsi@uniroma1.it (M.C.B.P.)

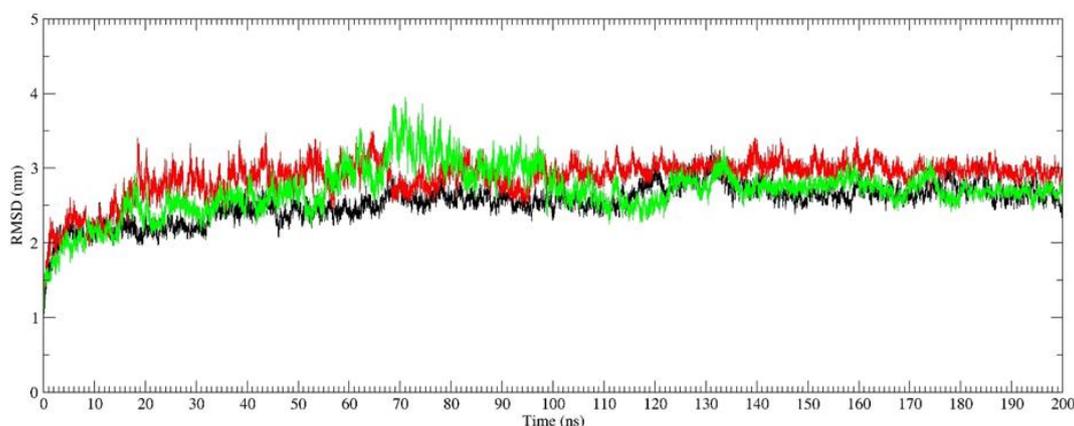
<sup>3</sup>Department of Biology, University of Rome Tor Vergata, 00133 Rome, Italy; federico.iacovelli@uniroma2.it (F.I.); falconi@uniroma2.it (M.F.)

<sup>4</sup>Department Biosciences and Territory, University of Molise, 86090 Pesche, Italy; giovanni.musci@unimol.it (G.M.)

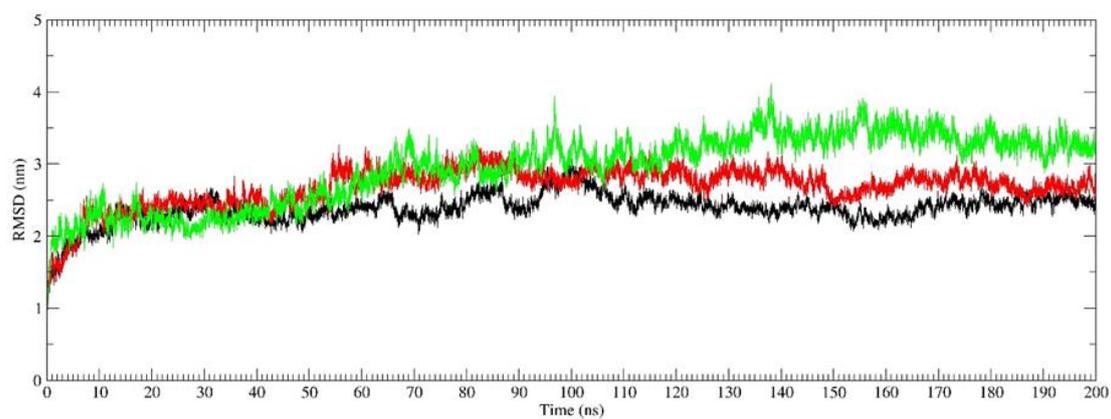
<sup>5</sup>National Institute of Nuclear Physics, Roma Tre Section, 00146 Rome, Italy

\*Correspondence: fabio.polticelli@uniroma3.it; Tel.: +39-06-5733-6362

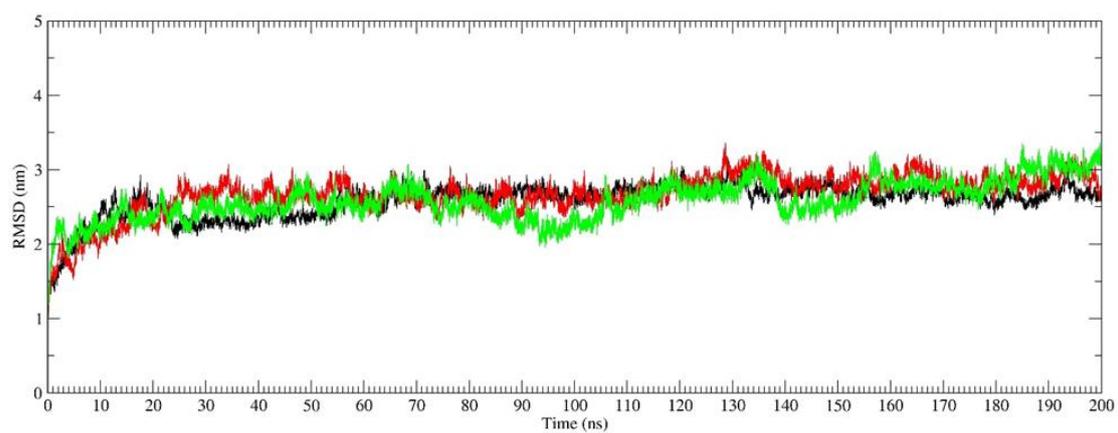
## Supplementary Materials



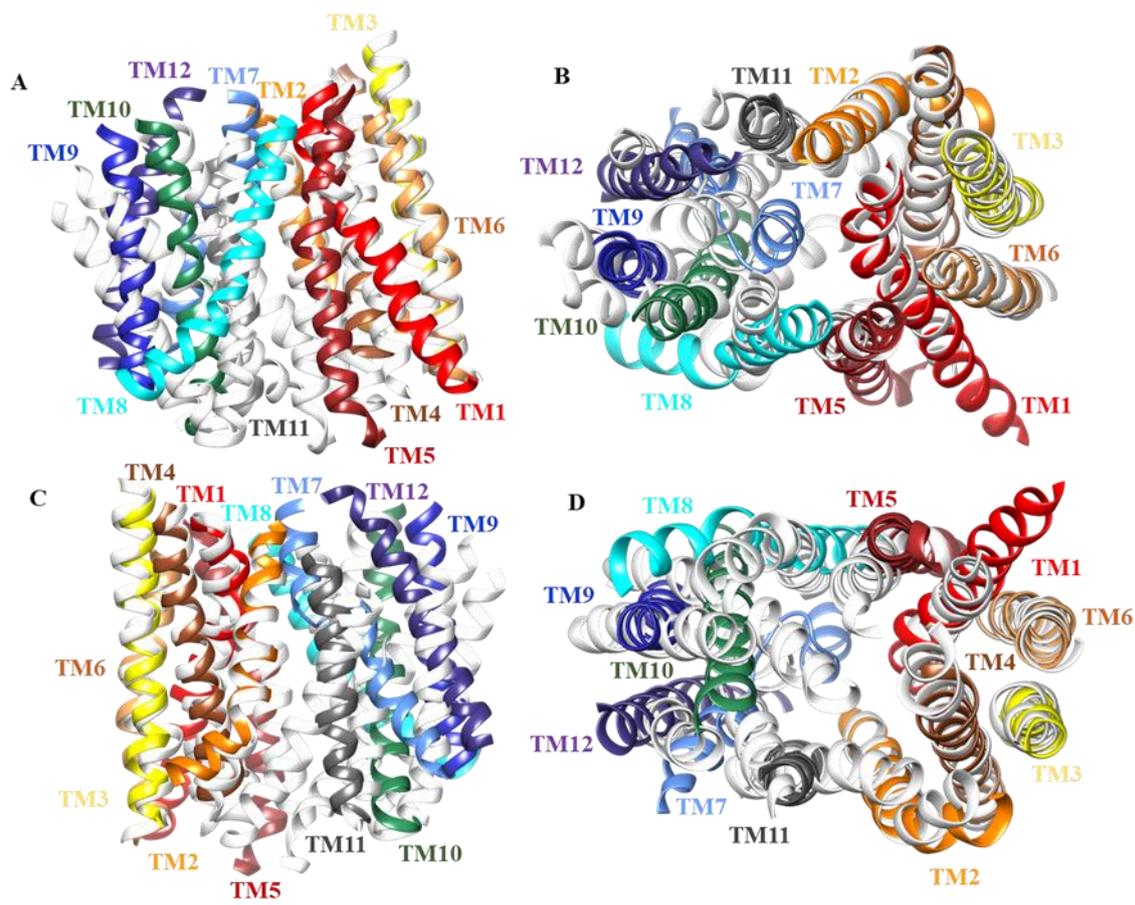
**Figure S1.** Root mean-square deviation (RMSD) values calculated on protein heavy atoms for the three simulation replicas of the inward-facing conformation as a function of simulation time.



**Figure S2.** RMSD values calculated on protein heavy atoms for the three simulation replicas of the outward-facing conformation as a function of the simulation time.

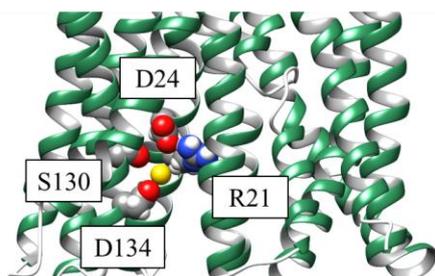


**Figure S3.** RMSD values calculated on protein heavy atoms for the three simulation replicas of the Fe\_WT as a function of the simulation time.

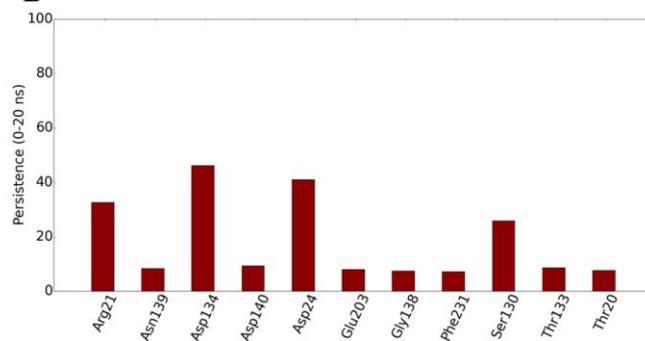


**Figure S4** Structural comparison of the inward-facing (rainbow helices) and outward-facing states (white helices), (A front view; B front view rotated of 180°; C extracellular view; D intracellular view).

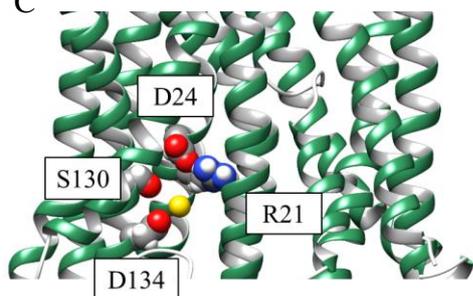
A



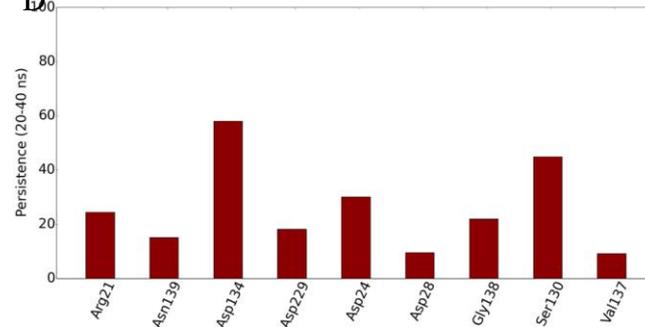
B



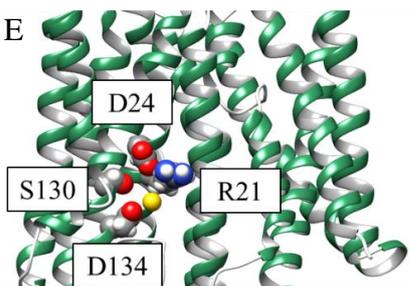
C



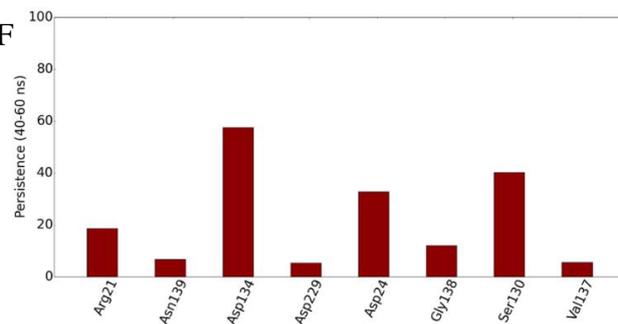
D



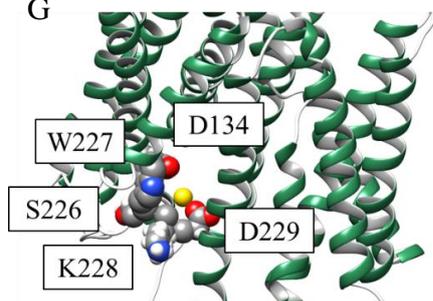
E



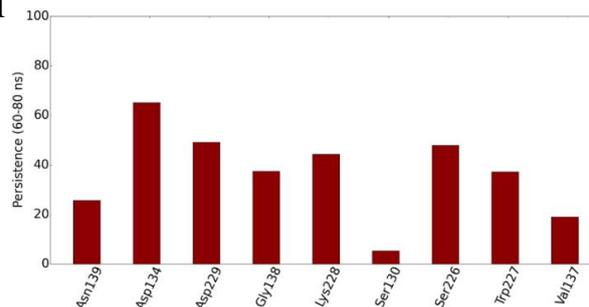
F

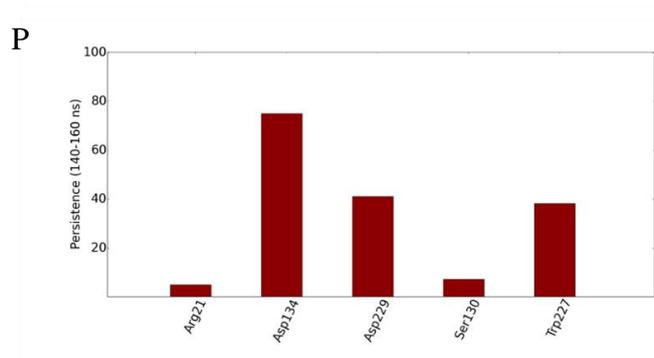
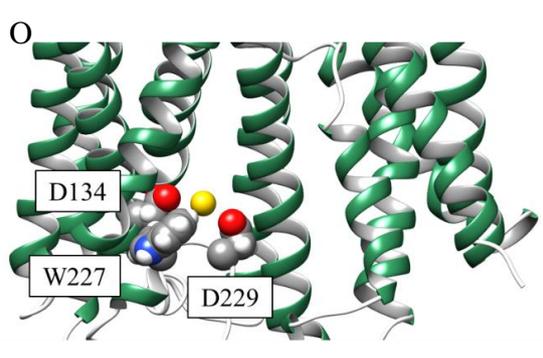
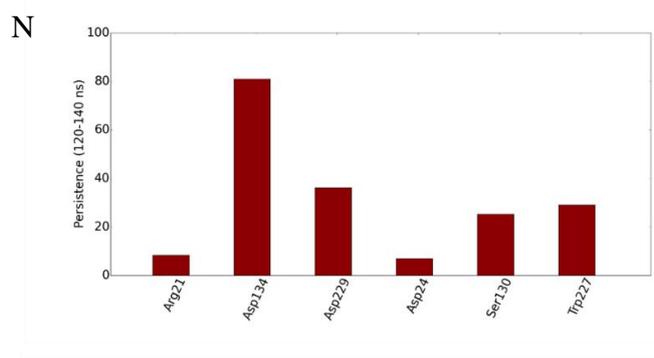
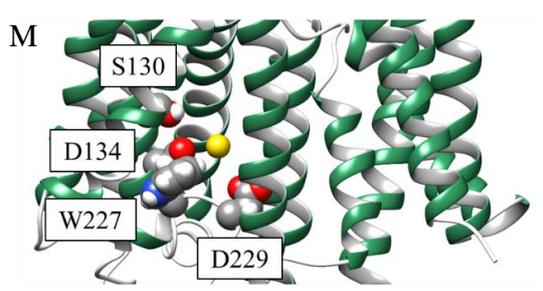
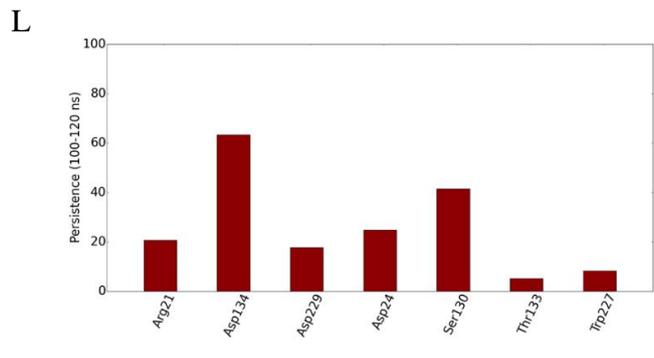
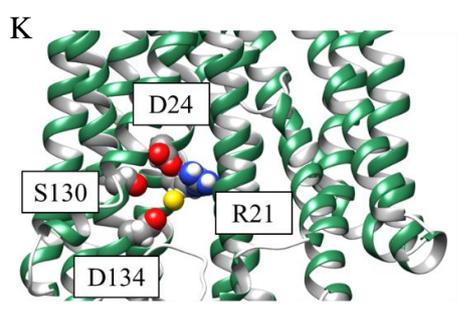
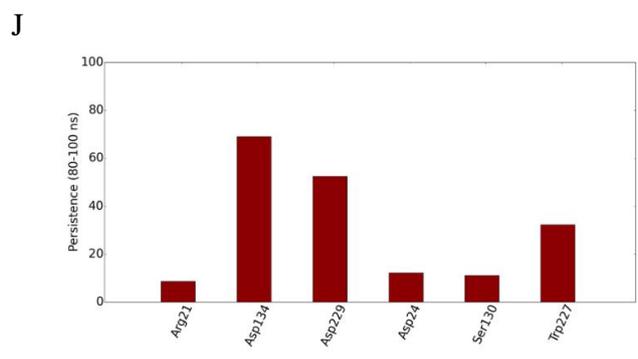
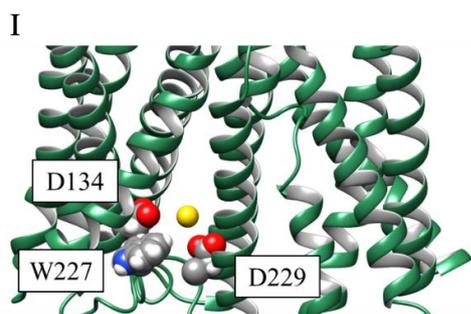


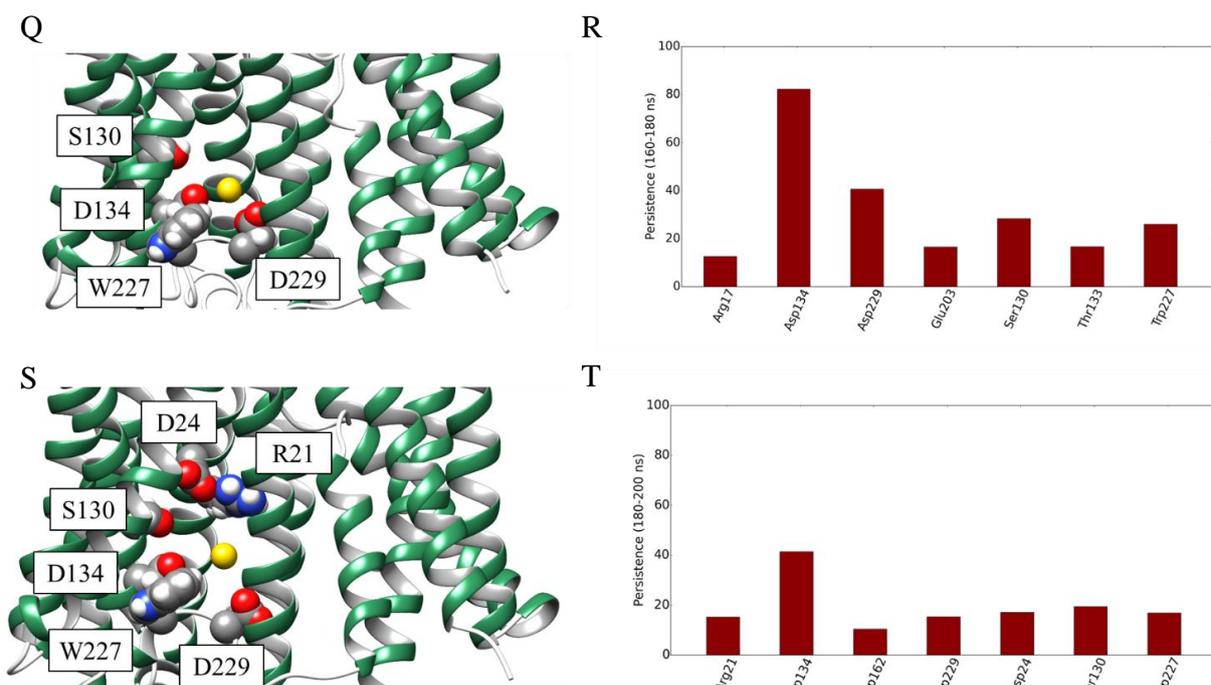
G



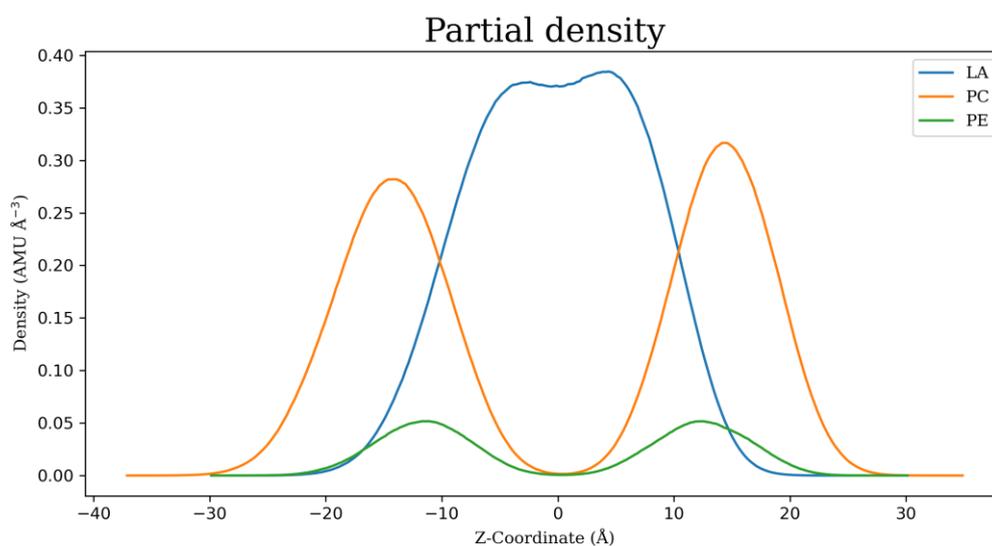
H



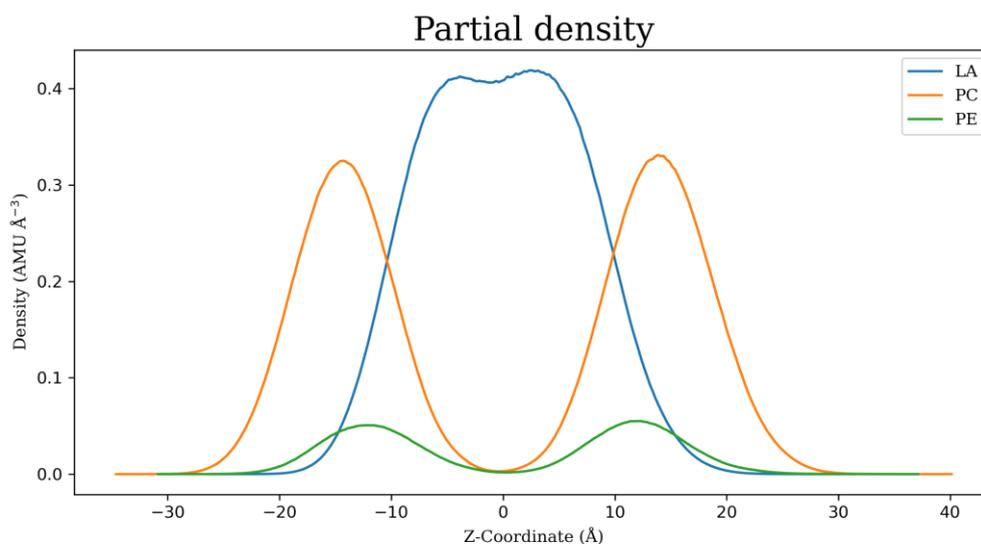




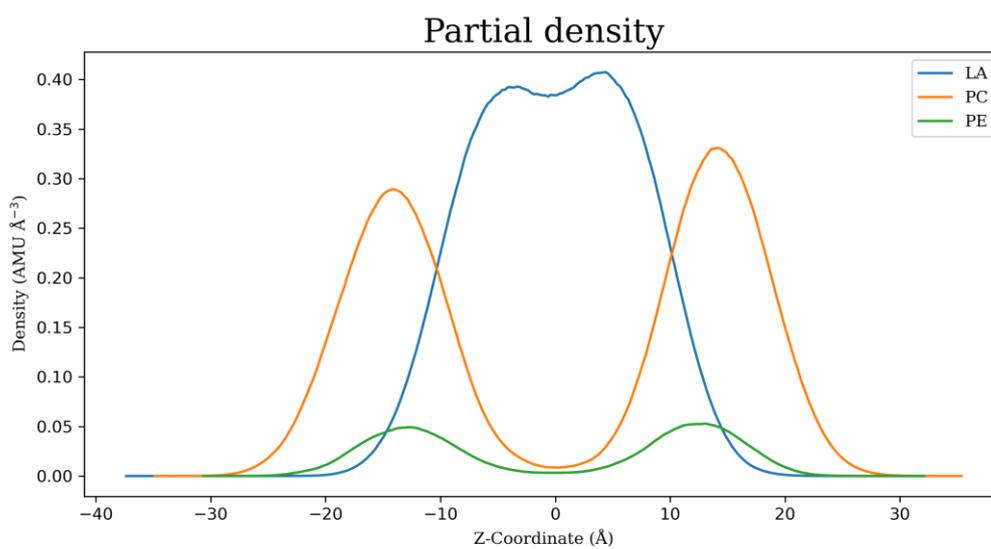
**Figure S5.** Structural representation of the main iron interacting residues (panels A,C,E,G,I,K,M,O,Q,S), and iron persistence histogram (in percent of the simulation time) (panels B,D,F,H,J,L,N,P,R,T), for every 20 ns interval. The persistence has been calculated by an in-house written script. Residues are colored by atom type; iron is colored in yellow.



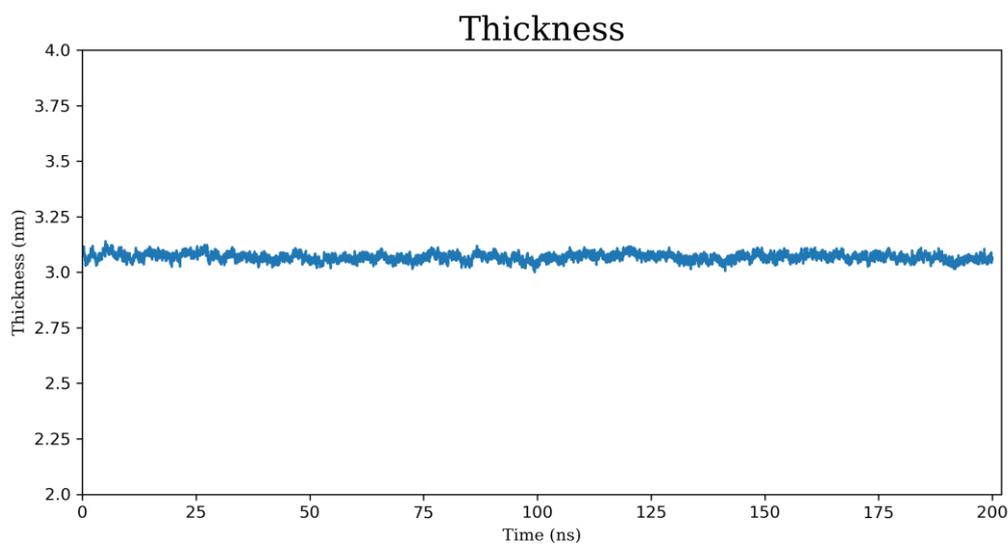
**Figure S6.** Density calculated for the lipids headgroups (phosphatidylcholine, PC; phosphatidylethanolamine, PE) and for the acyl chains (lauroyl, LA) of the membrane, averaged along the trajectory and the surface area of the inward-facing BdFpn structure.



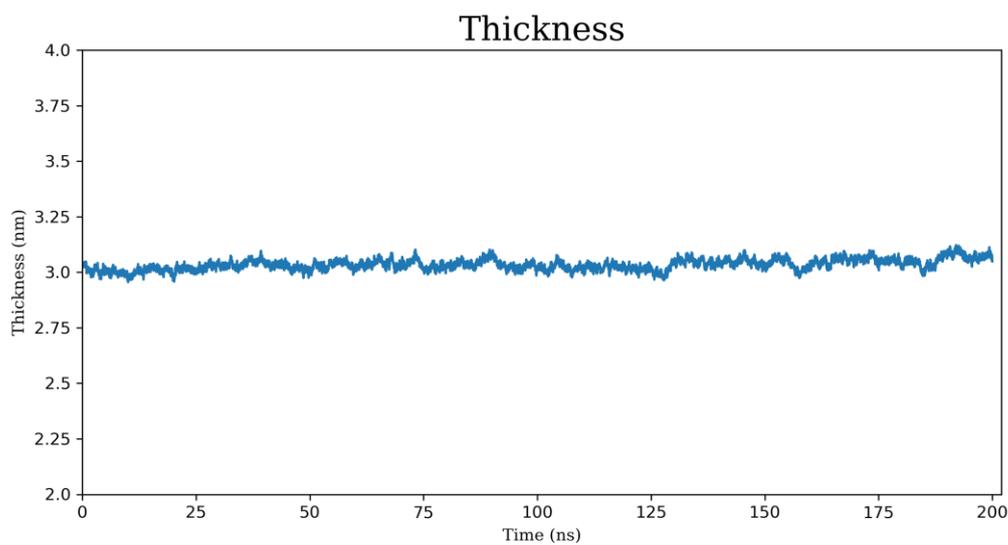
**Figure S7.** Density calculated for the lipids headgroups (phosphatidylcoline, PC; phosphatidylethanolamine, PE) and for the acyl chains (lauroyl, LA) of the membrane, averaged along the trajectory and the surface area of the outward-facing BdFpn structure.



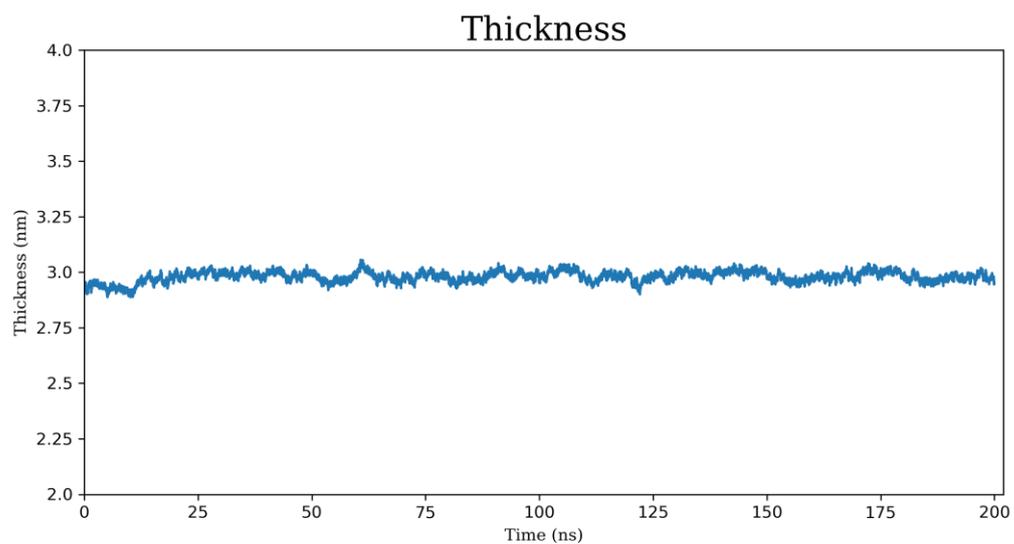
**Figure S8.** Density calculated for the lipids headgroups (phosphatidylcoline, PC; phosphatidylethanolamine, PE) and for the acyl chains (lauroyl, LA) of the membrane, averaged along the trajectory and the surface area of the inward-facing BdFpn structure with an excess of Fe<sup>2+</sup> ions.



**Figure S9.** Thickness of the membrane bilayer of the inward-facing BdFpn structure measured along the trajectory.



**Figure S10.** Thickness of the membrane bilayer of the outward-facing BdFpn structure measured along the trajectory.



**Figure S11.** Thickness of the membrane bilayer of the inward-facing BdFpn structure with an excess of  $\text{Fe}^{2+}$  ions measured along the trajectory.