

Look Up Full Text

Full Text Options



Save to EndNote online

Add to Marked List

◀ 1 of 1 ▶

## Interaction of monomeric Ebola VP40 protein with a plasma membrane: A coarse-grained molecular dynamics (CGMD) simulation study

by: YUSOFF, MIAMI (YUSOFF, Muhammad Ariff Mohamad)<sup>[1]</sup>; Hamid, AAA (Hamid, Azzmer Azzar Abdul)<sup>[1]</sup>; Bunori, NM (Bunori, Noraslinda Mohammad)<sup>[1]</sup>; Abd Halim, KB (Abd Halim, Khairul Bariyyah)<sup>[1]</sup>

[View ResearcherID and ORCID](#)

JOURNAL OF MOLECULAR GRAPHICS & MODELLING

Volume: 82 Pages: 137-144

DOI: 10.1016/j.jmglm.2018.04.010

Published: JUN 2018

Document Type: Article

[View Journal Impact](#)

### Abstract

Ebola virus is a lipid-enveloped filamentous virus that affects human and non-human primates and consists of several types of protein: nucleoprotein, VP30, VP35, L protein, VP40, VP24, and transmembrane glycoprotein. Among the Ebola virus proteins, its matrix protein VP40 is abundantly expressed during infection and plays a number of critical roles in oligomerization, budding and egress from the host cell. VP40 exists predominantly as a monomer at the inner leaflet of the plasma membrane, and has been suggested to interact with negatively charged lipids such as phosphatidylinositol 4,5-bisphosphate (PIP2) and phosphatidylserine (PS) via its cationic patch. The hydrophobic loop at the C-terminal domain has also been shown to be important in the interaction between the VP40 and the membrane. However, details of the molecular mechanisms underpinning their interactions are not fully understood. This study aimed at investigating the effects of mutation in the cationic patch and hydrophobic loop on the interaction between the VP40 monomer and the plasma membrane using coarse-grained molecular dynamics simulation (CGMD). Our simulations revealed that the interaction between VP40 and the plasma membrane is mediated by the cationic patch residues. This led to the clustering of PIP2 around the protein in the inner leaflet as a result of interactions between some cationic residues including R52, K127, K221, K224, K225, K256, K270, K274, K275 and K279 and PIP2 lipids via electrostatic interactions. Mutation of the cationic patch or hydrophobic loop amino acids caused the protein to bind at the inner leaflet of the plasma membrane in a different orientation, where no significant clustering of PIP2 was observed around the mutated protein. This study provides basic understanding of the interaction of the VP40 monomer and its mutants with the plasma membrane. (C) 2018 Elsevier Inc. All rights reserved.

### Keywords

**Author Keywords:** VP40; Ebola; PIP2; Coarse-grained; Plasma membrane; Molecular dynamics

**KeyWords Plus:** VIRUS MATRIX PROTEIN; MARTINI FORCE-FIELD; BINDING PROPERTIES; LIPID-BILAYER; VIRAL-EGRESS; ASSOCIATION; OLIGOMERIZATION; ORGANIZATION; MODEL

### Author Information

**Reprint Address:** Abd Halim, KB (reprint author)

Int Islamic Univ Malaysia, Kulliyyah Sci, Dept Biotechnol, Kuantan 25200, Pahang, Malaysia.

**Addresses:**

[ 1 ] Int Islamic Univ Malaysia, Kulliyyah Sci, Dept Biotechnol, Kuantan 25200, Pahang, Malaysia

**E-mail Addresses:** [kbariyyah@iium.edu.my](mailto:kbariyyah@iium.edu.my)

### Funding

Funding Agency	Grant Number
Ministry of Higher Education, Malaysia	FRGS15-207-0448 FRGS15-208-0449

[View funding text](#)

### Publisher

### Citation Network

In Web of Science Core Collection

0

Times Cited

[Create Citation Alert](#)

37

Cited References

[View Related Records](#)

### Use in Web of Science

Web of Science Usage Count

8

13

Last 180 Days

Since 2013

[Learn more](#)

**This record is from:**

Web of Science Core Collection  
- Science Citation Index Expanded

**Suggest a correction**

*If you would like to improve the quality of the data in this record, please [suggest a correction](#).*

ELSEVIER SCIENCE INC, 360 PARK AVE SOUTH, NEW YORK, NY 10010-1710 USA

**Journal Information**Impact Factor: [Journal Citation Reports](#)**Categories / Classification**

Research Areas: Biochemistry &amp; Molecular Biology; Computer Science; Crystallography; Mathematical &amp; Computational Biology

Web of Science Categories: Biochemical Research Methods; Biochemistry &amp; Molecular Biology; Computer Science, Interdisciplinary Applications; Crystallography; Mathematical &amp; Computational Biology

**See more data fields**

◀ 1 of 1 ▶

**Cited References: 37**Showing 30 of 37 [View All in Cited References page](#)*(from Web of Science Core Collection)*

1. [Interactions of the EGFR juxtamembrane domain with PIP2-containing lipid bilayers: Insights from multiscale molecular dynamics simulations](#) Times Cited: 25  
 By: Abd Halim, Khairul Bariyyah; Koldso, Heidi; Sansom, Mark S. P.  
 BIOCHIMICA ET BIOPHYSICA ACTA-GENERAL SUBJECTS Volume: 1850 Issue: 5 Special Issue: SI Pages: 1017-1025 Published: MAY 2015
2. [Investigation of Ebola VP40 Assembly and Oligomerization in Live Cells Using Number and Brightness Analysis](#) Times Cited: 27  
 By: Adu-Gyamfi, Emmanuel; Digman, Michelle A.; Gratton, Enrico; et al.  
 BIOPHYSICAL JOURNAL Volume: 102 Issue: 11 Pages: 2517-2525 Published: JUN 6 2012
3. [The Ebola Virus Matrix Protein Penetrates into the Plasma Membrane A KEY STEP IN VIRAL PROTEIN 40 \(VP40\) OLIGOMERIZATION AND VIRAL EGRESS](#) Times Cited: 38  
 By: Adu-Gyamfi, Emmanuel; Soni, Smita P.; Xue, Yi; et al.  
 JOURNAL OF BIOLOGICAL CHEMISTRY Volume: 288 Issue: 8 Pages: 5779-5789 Published: FEB 22 2013
4. [Host Cell Plasma Membrane Phosphatidylserine Regulates the Assembly and Budding of Ebola Virus](#) Times Cited: 20  
 By: Adu-Gyamfi, Emmanuel; Johnson, Kristen A.; Fraser, Mark E.; et al.  
 JOURNAL OF VIROLOGY Volume: 89 Issue: 18 Pages: 9440-9453 Published: SEP 2015
5. [Interaction of Monotopic Membrane Enzymes with a Lipid Bilayer: A Coarse-Grained MD Simulation Study](#) Times Cited: 35  
 By: Balali-Mood, Kia; Bond, Peter J.; Sansom, Mark S. P.  
 BIOCHEMISTRY Volume: 48 Issue: 10 Pages: 2135-2145 Published: MAR 17 2009
6. [A hydrophobic gating mechanism for nanopores](#) Times Cited: 210  
 By: Beckstein, O; Biggin, PC; Sansom, MSP  
 JOURNAL OF PHYSICAL CHEMISTRY B Volume: 105 Issue: 51 Pages: 12902-12905 Published: DEC 27 2001
7. [Coarse-grained molecular dynamics simulations of membrane proteins and peptides](#) Times Cited: 236  
 By: Bond, Peter J.; Holyoake, John; Ivetac, Anthony; et al.  
 JOURNAL OF STRUCTURAL BIOLOGY Volume: 157 Issue: 3 Pages: 593-605 Published: MAR 2007
8. [Structural Rearrangement of Ebola Virus VP40 Begets Multiple Functions in the Virus Life Cycle](#) Times Cited: 80  
 By: Bornholdt, Zachary A.; Noda, Takeshi; Abelson, Dafna M.; et al.  
 CELL Volume: 154 Issue: 4 Pages: 763-774 Published: AUG 15 2013
9. [Self-assembly of a simple membrane protein: Coarse-grained molecular dynamics simulations of the influenza M2 channel](#) Times Cited: 62  
 By: Carpenter, Timothy; Bond, Peter J.; Khalid, Syma; et al.  
 BIOPHYSICAL JOURNAL Volume: 95 Issue: 8 Pages: 3790-3801 Published: OCT 15 2008
10. Title: [not available] Times Cited: 1  
 By: De Jong, D. H.; Singh, G.; Bennett, W. F. D.; et al.

Improved Parameter for the Martini Coarse-grained Protein Force Field Published: 2012

URL: <https://doi-org.ezaccess.library.uitm.edu.my/>

[Show additional data]

11. **Crystal structure of the matrix protein VP40 from Ebola virus** Times Cited: 115  
By: Dessen, A; Volchkov, V; Dolnik, O; et al.  
EMBO JOURNAL Volume: 19 Issue: 16 Pages: 4228-4236 Published: AUG 15 2000
  
12. **Ebola haemorrhagic fever** Times Cited: 591  
By: Feldmann, Heinz; Geisbert, Thomas W.  
LANCET Volume: 377 Issue: 9768 Pages: 849-862 Published: MAR 5 2011
  
13. **The Ebola virus protein VP40 hexamer enhances the clustering of PI(4,5)P-2 lipids in the plasma membrane** Times Cited: 10  
By: Gc, Jeevan B.; Gerstman, Bernard S.; Stahelin, Robert V.; et al.  
PHYSICAL CHEMISTRY CHEMICAL PHYSICS Volume: 18 Issue: 41 Pages: 28409-28417 Published: NOV 7 2016
  
14. **The matrix protein VP40 from Ebola virus octamerizes into pore-like structures with specific RNA binding properties** Times Cited: 86  
By: Gomis-Roth, FX; Dessen, A; Timmins, J; et al.  
STRUCTURE Volume: 11 Issue: 4 Pages: 423-433 Published: APR 2003
  
15. **Structural insights how PIP2 imposes preferred binding orientations of FAK at lipid membranes** Times Cited: 1  
By: Herzog, F. A.; Braun, L; Schoen, I.; et al.  
J. Phys. Chem. B Pages: 1-34 Published: 2017  
URL: <https://doi-org.ezaccess.library.uitm.edu.my/>  
[Show additional data]
  
16. **VMD: Visual molecular dynamics** Times Cited: 20,856  
By: Humphrey, W; Dalke, A; Schulten, K  
JOURNAL OF MOLECULAR GRAPHICS & MODELLING Volume: 14 Issue: 1 Pages: 33-38 Published: FEB 1996
  
17. **Lipid Organization of the Plasma Membrane** Times Cited: 201  
By: Ingolfsson, Helgi I.; Melo, Manuel N.; van Eerden, Floris J.; et al.  
JOURNAL OF THE AMERICAN CHEMICAL SOCIETY Volume: 136 Issue: 41 Pages: 14554-14559 Published: OCT 15 2014
  
18. **Ebola virus VP40-induced particle formation and association with the lipid bilayer** Times Cited: 172  
By: Jasenosky, LD; Neumann, G; Lukashovich, I; et al.  
JOURNAL OF VIROLOGY Volume: 75 Issue: 11 Pages: 5205-5214 Published: JUN 2001
  
19. **Membrane association and localization dynamics of the Ebola virus matrix protein VP40** Times Cited: 3  
By: Jeevan, B. G. C.; Gerstman, Bernard S.; Chapagain, Prem P.  
BIOCHIMICA ET BIOPHYSICA ACTA-BIOMEMBRANES Volume: 1859 Issue: 10 Pages: 2012-2020 Published: OCT 2017
  
20. **The Ebola Virus matrix protein, VP40, requires phosphatidylinositol 4,5-bisphosphate (PI(4,5)P-2) for extensive oligomerization at the plasma membrane and viral egress** Times Cited: 19  
By: Johnson, Kristen A.; Taghon, Geoffrey J. F.; Scott, Jordan L.; et al.  
SCIENTIFIC REPORTS Volume: 6 Article Number: 19125 Published: JAN 12 2016
  
21. **Interactions of Phosphatase and Tensin Homologue (PTEN) Proteins with Phosphatidylinositol Phosphates: Insights from Molecular Dynamics Simulations of PTEN and Voltage Sensitive Phosphatase** Times Cited: 23  
By: Kalli, Antreas C.; Devaney, Isabel; Sansom, Mark S. P.  
BIOCHEMISTRY Volume: 53 Issue: 11 Pages: 1724-1732 Published: MAR 25 2014
  
22. **Lipid Clustering Correlates with Membrane Curvature as Revealed by Molecular Simulations of Complex Lipid Bilayers** Times Cited: 74  
By: Koldso, Heidi; Shorthouse, David; Helie, Jean; et al.  
PLOS COMPUTATIONAL BIOLOGY Volume: 10 Issue: 10 Article Number: e1003911 Published: OCT 2014
  
23. **Membrane proteins: molecular dynamics simulations** Times Cited: 205  
By: Lindahl, Erik; Sansom, Mark S. P.  
CURRENT OPINION IN STRUCTURAL BIOLOGY Volume: 18 Issue: 4 Pages: 425-431 Published: AUG 2008

24. **The MARTINI force field: Coarse grained model for biomolecular simulations** Times Cited: **2,254**  
By: Marrink, Siewert J.; Risselada, H. Jelger; Yefimov, Serge; et al.  
JOURNAL OF PHYSICAL CHEMISTRY B Volume: 111 Issue: 27 Pages: 7812-7824 Published: JUL 12 2007
25. **Coarse grained model for semiquantitative lipid simulations** Times Cited: **1,305**  
By: Marrink, SJ; de Vries, AH; Mark, AE  
JOURNAL OF PHYSICAL CHEMISTRY B Volume: 108 Issue: 2 Pages: 750-760 Published: JAN 15 2004
26. **PIP2 AND proteins: Interactions, organization, and information flow** Times Cited: **555**  
By: McLaughlin, S; Wang, JY; Gambhir, A; et al.  
ANNUAL REVIEW OF BIOPHYSICS AND BIOMOLECULAR STRUCTURE Volume: 31 Pages: 151-175 Published: 2002
27. **The MARTINI coarse-grained force field: Extension to proteins** Times Cited: **1,148**  
By: Monticelli, Luca; Kandasamy, Senthil K.; Periole, Xavier; et al.  
JOURNAL OF CHEMICAL THEORY AND COMPUTATION Volume: 4 Issue: 5 Pages: 819-834 Published: MAY 2008
28. **BIN1/M-Amphiphysin2 induces clustering of phosphoinositides to recruit its downstream partner dynamin** Times Cited: **28**  
By: Picas, Laura; Viaud, Julien; Schauer, Kristine; et al.  
NATURE COMMUNICATIONS Volume: 5 Article Number: 5647 Published: DEC 2014
29. **Helix-helix interactions in membrane proteins: Coarse-grained simulations of glycoporphin a helix dimerization** Times Cited: **68**  
By: Psachoulia, Emi; Fowler, Philip W.; Bond, Peter J.; et al.  
BIOCHEMISTRY Volume: 47 Issue: 40 Pages: 10503-10512 Published: OCT 7 2008
30. **CHARMM-GUI Martini Maker for Coarse-Grained Simulations with the Martini Force Field** Times Cited: **45**  
By: Qi, Yifei; Ingolfsson, Helgi I.; Cheng, Xi; et al.  
JOURNAL OF CHEMICAL THEORY AND COMPUTATION Volume: 11 Issue: 9 Pages: 4486-4494 Published: SEP 2015

Showing 30 of 37 [View All in Cited References page](#)

Clarivate

Accelerating innovation

© 2019 Clarivate [Copyright notice](#) [Terms of use](#) [Privacy statement](#) [Cookie policy](#)

[Sign up for the Web of Science newsletter](#) [Follow us](#)

