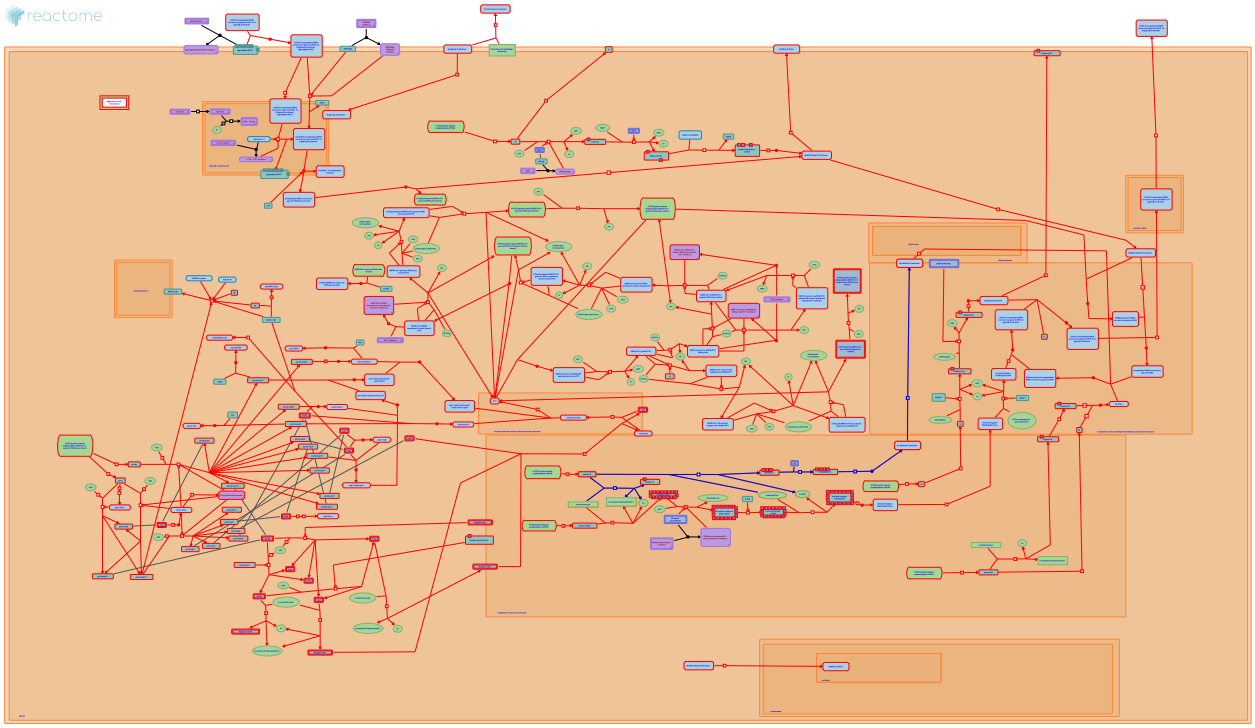
Maturation of protein E



Acencio, ML., D'Eustachio, P., Mazein, A., Stephan, R.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

03/05/2024

Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.
The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

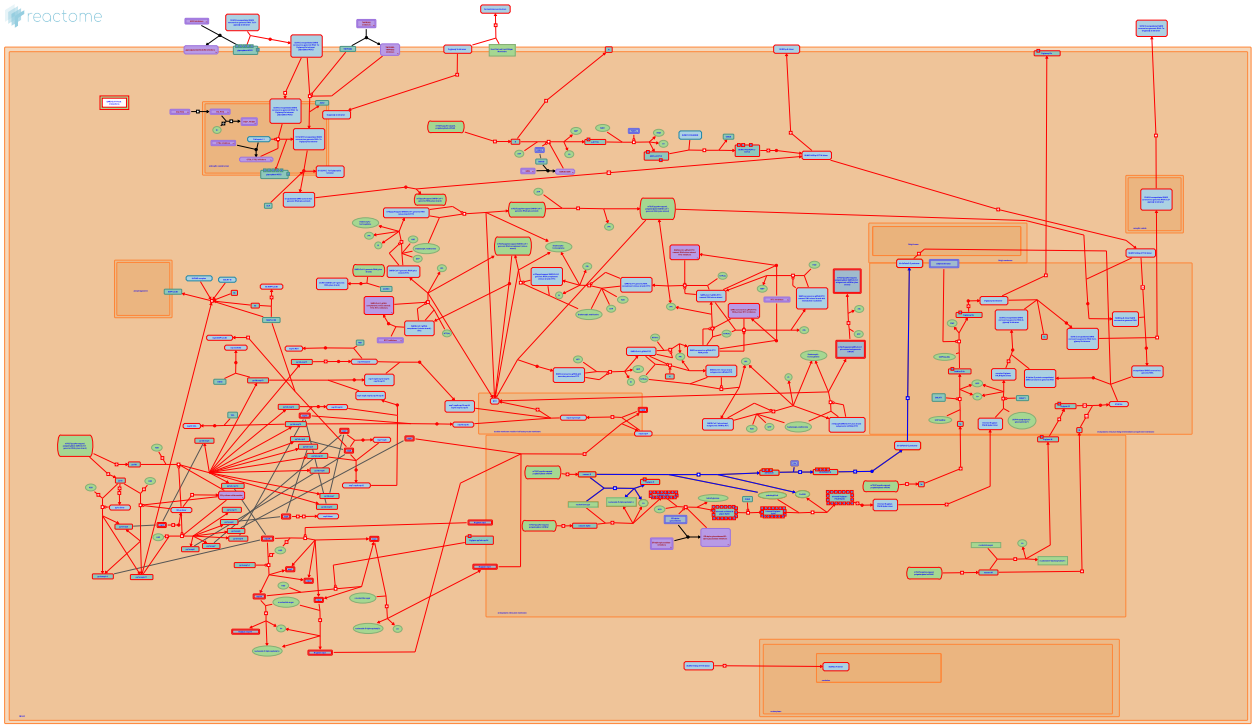
Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Maturation of protein E ↗

Stable identifier: R-HSA-9683683

Diseases: severe acute respiratory syndrome



The envelope protein (E) gets palmitoylated and ubiquitinated after translation. It forms trimers that show porin activity but does not localize to the cell membrane (Tan et al, 2004; Liao et al, 2006; Alvarez et al, 2011).

Literature references

Liu, DX., Liao, Y., Tam, JP., Lescar, J. (2004). Expression of SARS-coronavirus envelope protein in Escherichia coli cells alters membrane permeability. *Biochem. Biophys. Res. Commun., 325*, 374-80. ↗

Liu, DX., Liao, Y., Tam, JP., Yuan, Q., Torres, J. (2006). Biochemical and functional characterization of the membrane association and membrane permeabilizing activity of the severe acute respiratory syndrome coronavirus envelope protein. *Virology, 349*, 264-75. ↗

Marcos-Villar, L., Jiménez-Guardeño, JM., DeDiego, ML., Enjuanes, L., Nieto-Torres, JL., Alvarez, E. (2010). The envelope protein of severe acute respiratory syndrome coronavirus interacts with the non-structural protein 3 and is ubiquitinated. *Virology, 402*, 281-91. ↗

Editions

2020-04-08	Authored	Stephan, R.
2020-05-21	Edited	D'Eustachio, P.
2020-05-27	Reviewed	Mazein, A., Acencio, ML.

E protein gets N-glycosylated ↗

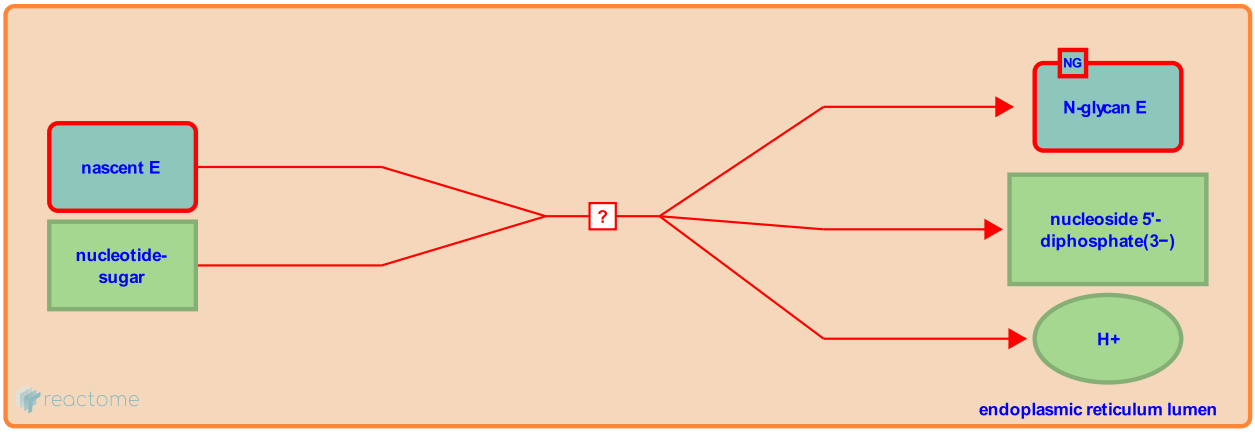
Location: Maturation of protein E

Stable identifier: R-HSA-9683669

Type: uncertain

Compartments: endoplasmic reticulum lumen

Diseases: severe acute respiratory syndrome



A minor proportion of the SARS-CoV E protein is modified by N-linked glycosylation at the N66 residue. This variant appears to be more likely to form multimers, and it shows a different membrane topology than the main variant (Yuan et al, 2006).

Literature references

Feldmann, H., Feldmann, F., Rudd, PM., Stroeher, U., Royle, L., Harvey, DJ. et al. (2010). Identification of N-linked carbohydrates from severe acute respiratory syndrome (SARS) spike glycoprotein. *Virology, 399*, 257-69. ↗

Editions

2020-04-08	Authored	Stephan, R.
2020-05-21	Edited	D'Eustachio, P.

E protein gets palmitoylated ↗

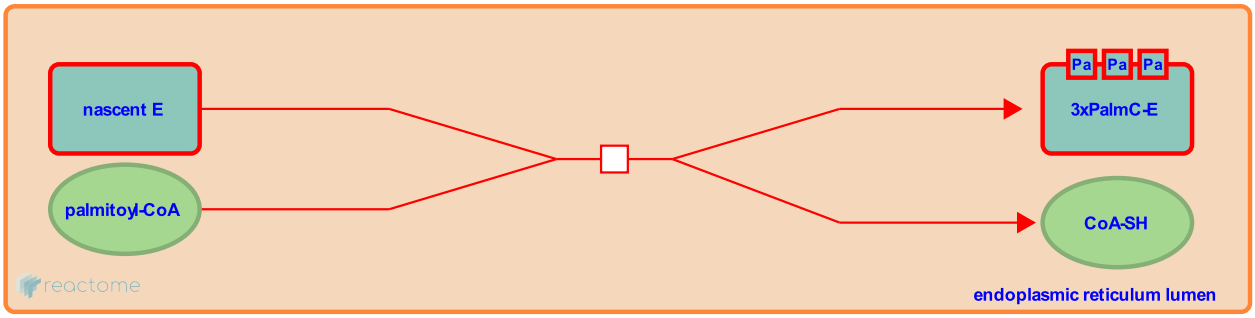
Location: Maturation of protein E

Stable identifier: R-HSA-9683720

Type: transition

Compartments: endoplasmic reticulum lumen

Diseases: severe acute respiratory syndrome



SARS-CoV E protein is modified by palmitoylation at all three cysteine residues. In general, palmitoylation is usually non-enzymatic (Liao et al, 2006, Veit, 2012).

Followed by: Ubiquination of protein E

Literature references

Veit, M. (2012). Palmitoylation of virus proteins. *Biol. Cell, 104*, 493-515. ↗

Liu, DX., Liao, Y., Tam, JP., Yuan, Q., Torres, J. (2006). Biochemical and functional characterization of the membrane association and membrane permeabilizing activity of the severe acute respiratory syndrome coronavirus envelope protein. *Virology, 349*, 264-75. ↗

Editions

2020-04-08	Authored	Stephan, R.
2020-05-21	Edited	D'Eustachio, P.

Ubiquination of protein E ↗

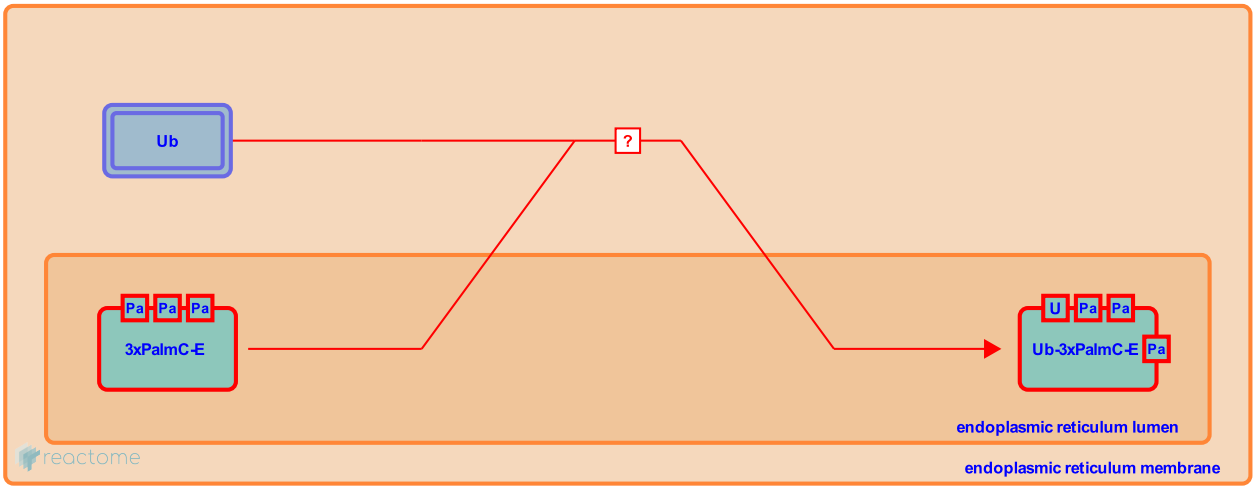
Location: Maturation of protein E

Stable identifier: R-HSA-9683679

Type: uncertain

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Diseases: severe acute respiratory syndrome



SARS-CoV E protein is ubiquitinated both in vitro and in cells (Alvarez et al, 2011).

Preceded by: E protein gets palmitoylated

Followed by: Protein E forms a homopentamer

Literature references

Marcos-Villar, L., Jiménez-Guardeño, JM., DeDiego, ML., Enjuanes, L., Nieto-Torres, JL., Alvarez, E. (2010). The envelope protein of severe acute respiratory syndrome coronavirus interacts with the non-structural protein 3 and is ubiquitinated. *Virology, 402*, 281-91. ↗

Editions

2020-04-08	Authored	Stephan, R.
2020-05-21	Edited	D'Eustachio, P.

Protein E forms a homopentamer ↗

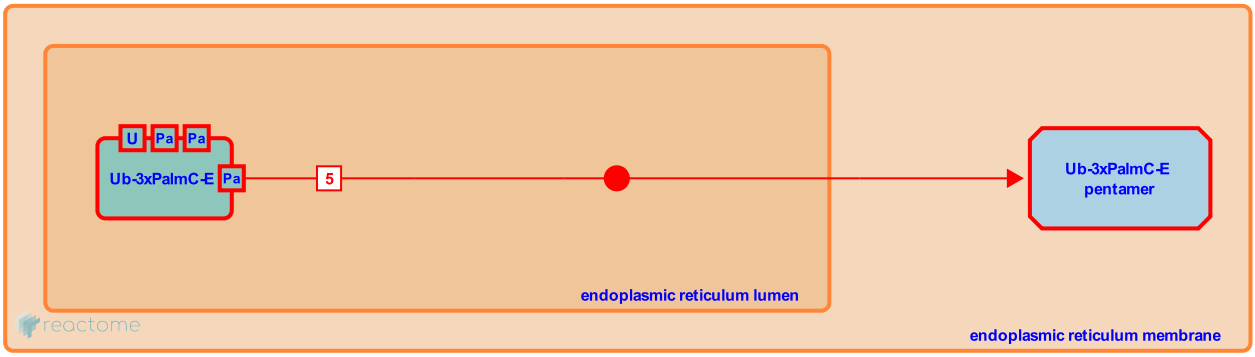
Location: Maturation of protein E

Stable identifier: R-HSA-9683670

Type: binding

Compartments: endoplasmic reticulum lumen

Diseases: severe acute respiratory syndrome



Protein E forms a pentamer of monomers without disulfide bonds (Parthasarathy et al, 2012).

Preceded by: Ubiquination of protein E

Followed by: E pentamer is transported to the Golgi

Literature references

Liu, DX., Liao, Y., Tam, JP., Lescar, J. (2004). Expression of SARS-coronavirus envelope protein in Escherichia coli cells alters membrane permeability. *Biochem. Biophys. Res. Commun., 325*, 374-80. ↗

Editions

2020-04-08	Authored	Stephan, R.
2020-05-21	Edited	D'Eustachio, P.

E pentamer is transported to the Golgi

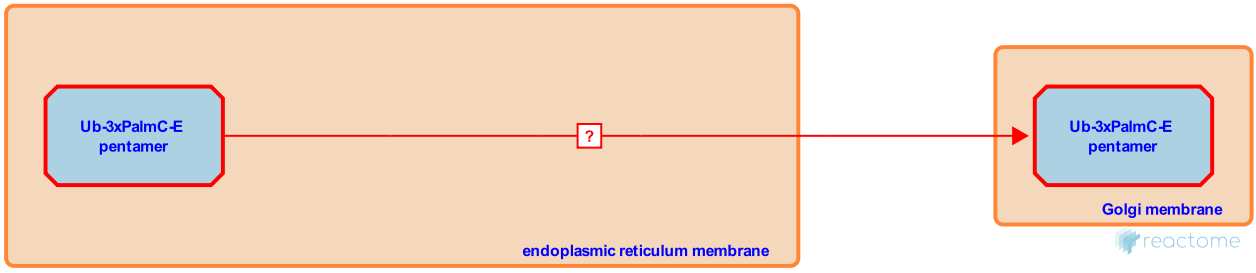
Location: Maturation of protein E

Stable identifier: R-HSA-9683635

Type: uncertain

Compartments: endoplasmic reticulum membrane, Golgi membrane

Diseases: severe acute respiratory syndrome



Both a predicted beta-hairpin motif and the N-terminal part of SARS-Cov protein E are sufficient for its localization to the Golgi membrane. Although porin activity has been shown for protein E it cannot be detected in the plasma membrane of infected cells (Liao et al, 2006; Cohen et al, 2011; Nieto-Torres, 2011).

Preceded by: Protein E forms a homopentamer

Literature references

Lin, LD., Cohen, JR., Machamer, CE. (2011). Identification of a Golgi complex-targeting signal in the cytoplasmic tail of the severe acute respiratory syndrome coronavirus envelope protein. *J. Virol., 85*, 5794-803.

Regla-Nava, JA., Jiménez-Guardeño, JM., DeDiego, ML., Enjuanes, L., Llorente, M., Shuo, S. et al. (2011). Subcellular location and topology of severe acute respiratory syndrome coronavirus envelope protein. *Virology, 415*, 69-82.

Editions

2020-04-08	Authored	Stephan, R.
2020-05-21	Edited	D'Eustachio, P.

Table of Contents