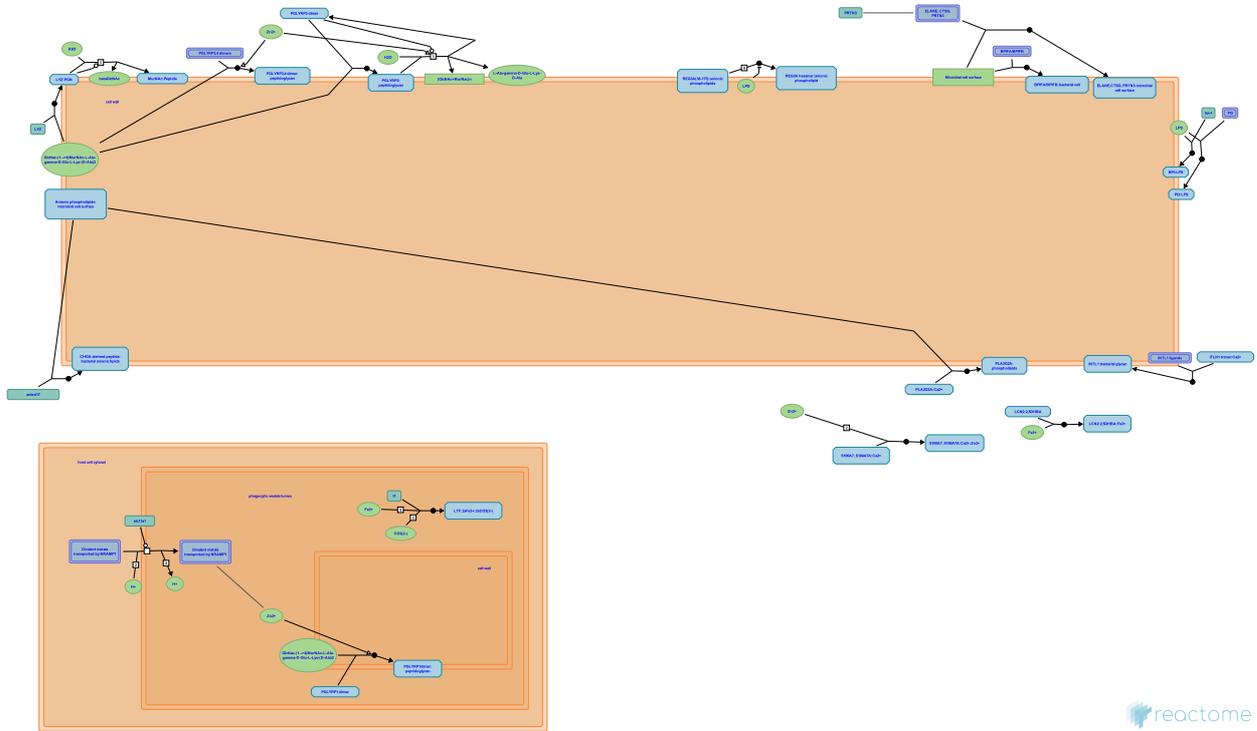


Antimicrobial peptides



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

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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).

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- 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. [↗](#)

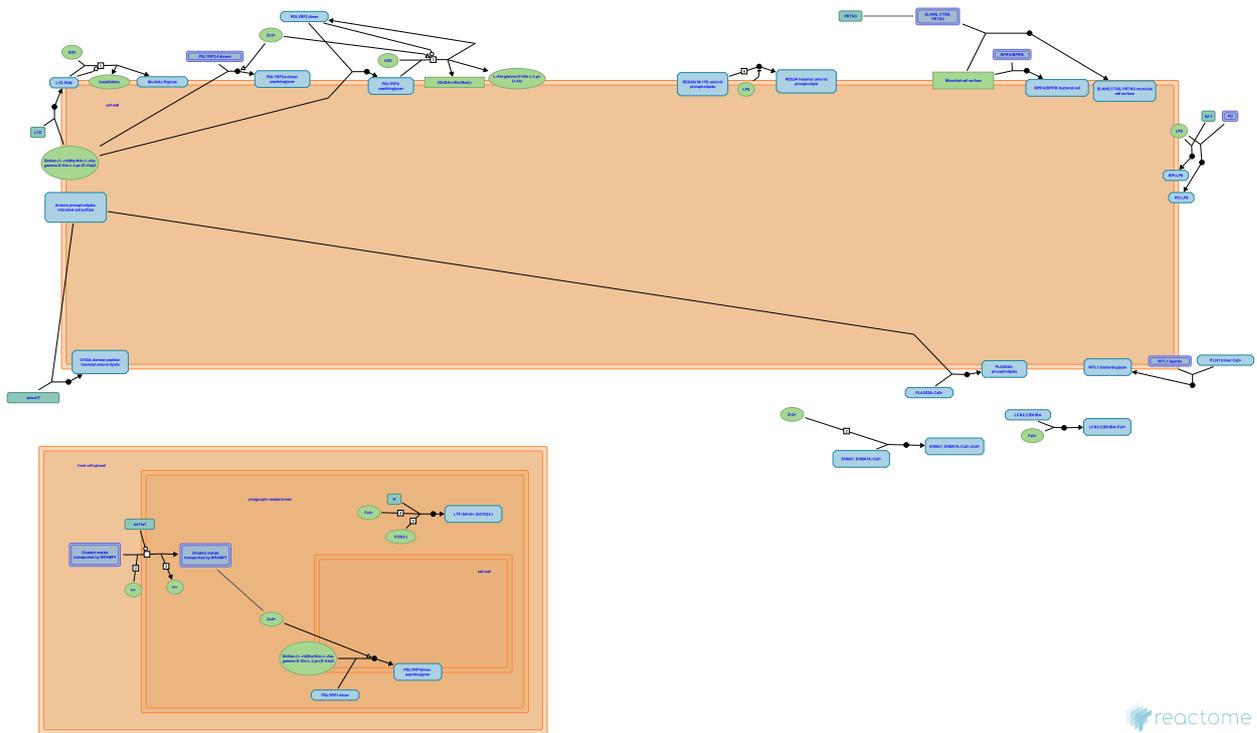
Reactome database release: 74

This document contains 3 pathways and 14 reactions ([see Table of Contents](#))

Antimicrobial peptides ↗

Stable identifier: R-XTR-6803157

Inferred from: Antimicrobial peptides (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

PGLYRP1 binds bacterial peptidoglycan ↗

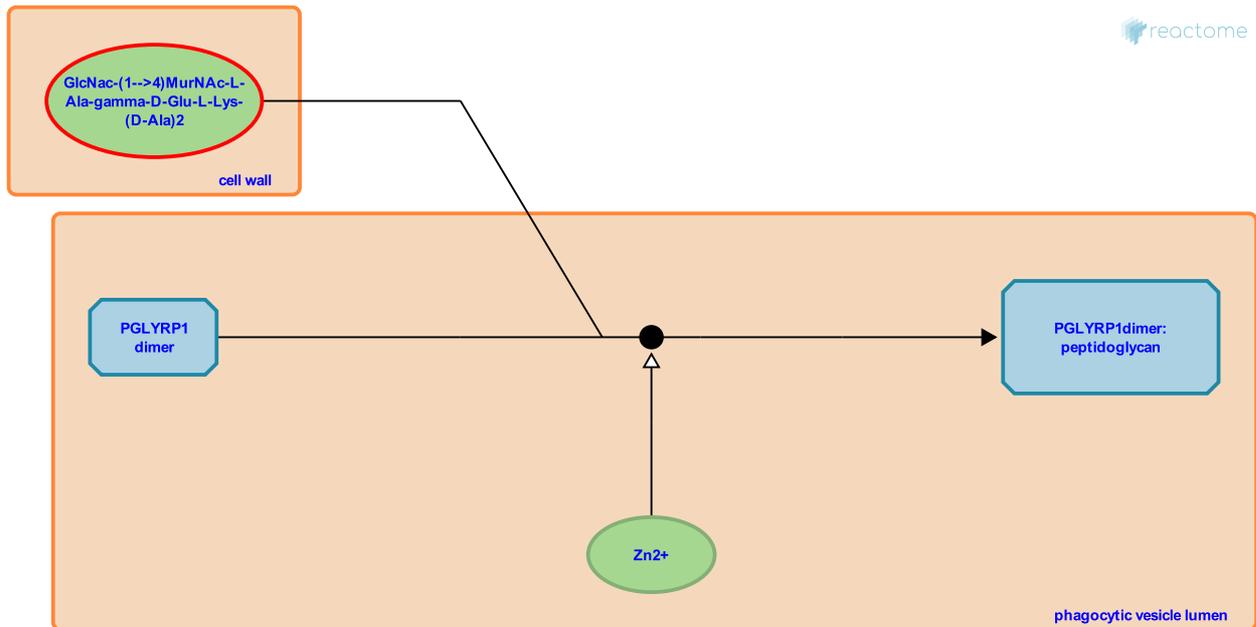
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6789072

Type: binding

Compartments: phagocytic vesicle lumen, cell wall

Inferred from: [PGLYRP1 binds bacterial peptidoglycan \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

PGLYRP2 binds bacterial peptidoglycan ↗

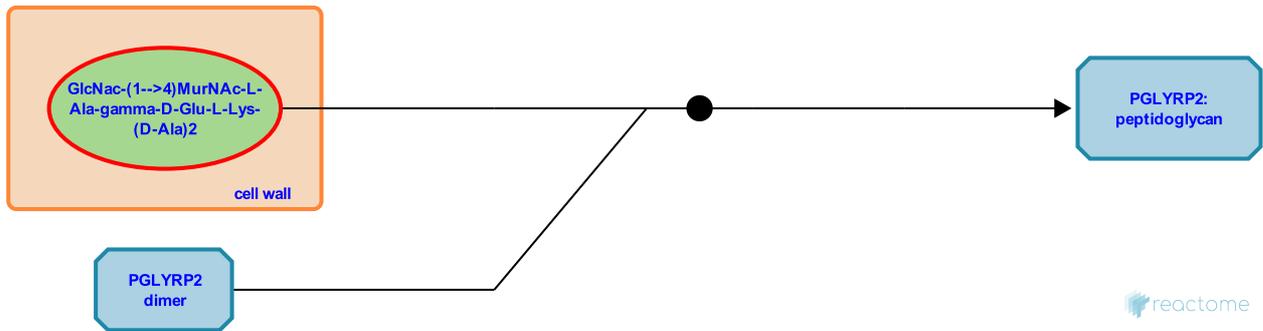
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6799981

Type: binding

Compartments: extracellular region, cell wall

Inferred from: [PGLYRP2 binds bacterial peptidoglycan \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [PGLYRP2 hydrolyzes bacterial peptidoglycan](#)

PGLYRP2 hydrolyzes bacterial peptidoglycan ↗

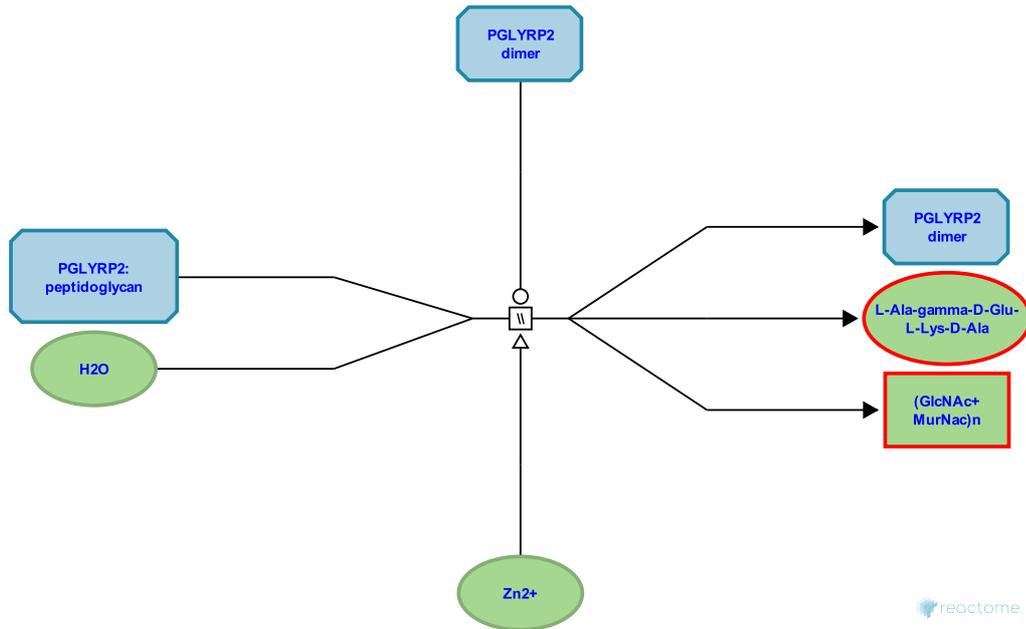
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6799977

Type: omitted

Compartments: extracellular region

Inferred from: [PGLYRP2 hydrolyzes bacterial peptidoglycan \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [PGLYRP2 binds bacterial peptidoglycan](#)

PGLYRP3,4 binds bacterial peptidoglycan ↗

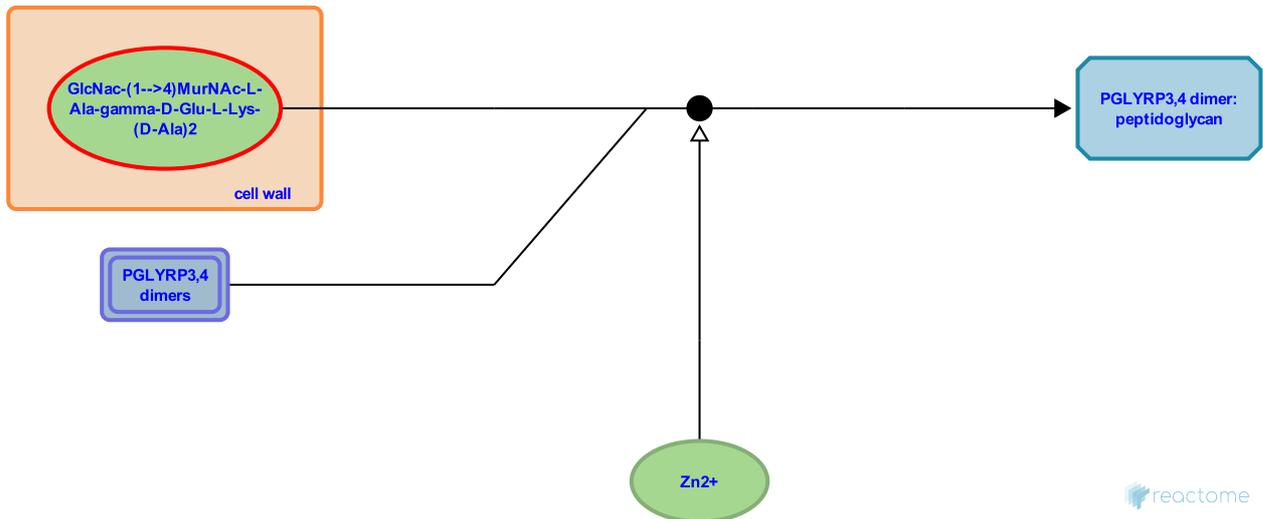
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6799959

Type: binding

Compartments: extracellular region

Inferred from: [PGLYRP3,4 binds bacterial peptidoglycan \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

REG3A oligomerize to form a pore complex ↗

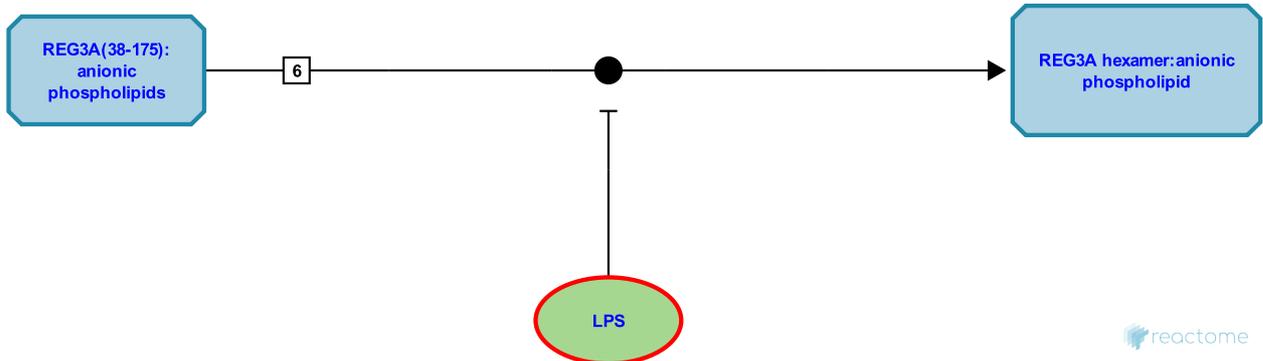
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6801762

Type: binding

Compartments: extracellular region

Inferred from: [REG3A oligomerize to form a pore complex \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

INTL1 binds bacterial glycans ↗

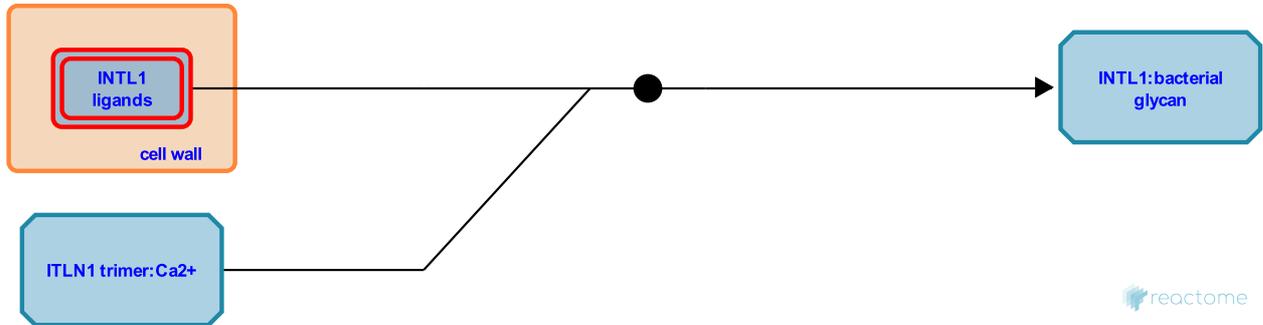
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6804527

Type: binding

Compartments: extracellular region, cell wall

Inferred from: [INTL1 binds bacterial glycans \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

BPI binds LPS on the bacterial surface ↗

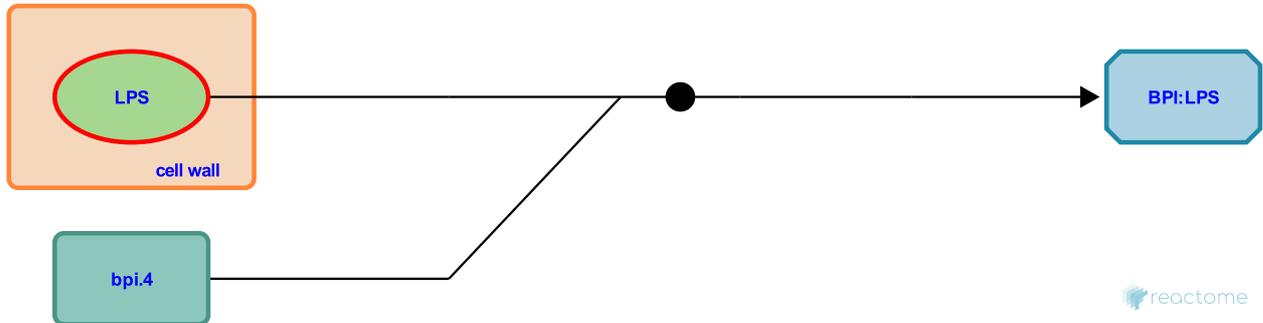
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6807585

Type: binding

Compartments: extracellular region, cell wall

Inferred from: [BPI binds LPS on the bacterial surface \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

CHGA-derived peptide binds the bacterial cell surface ↗

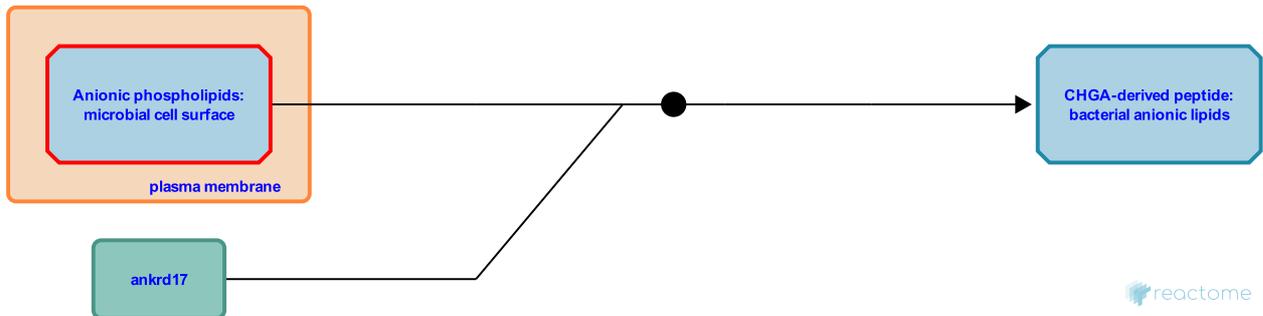
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6808566

Type: binding

Compartments: extracellular region, plasma membrane

Inferred from: [CHGA-derived peptide binds the bacterial cell surface \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

PI3 binds the bacterial surface ↗

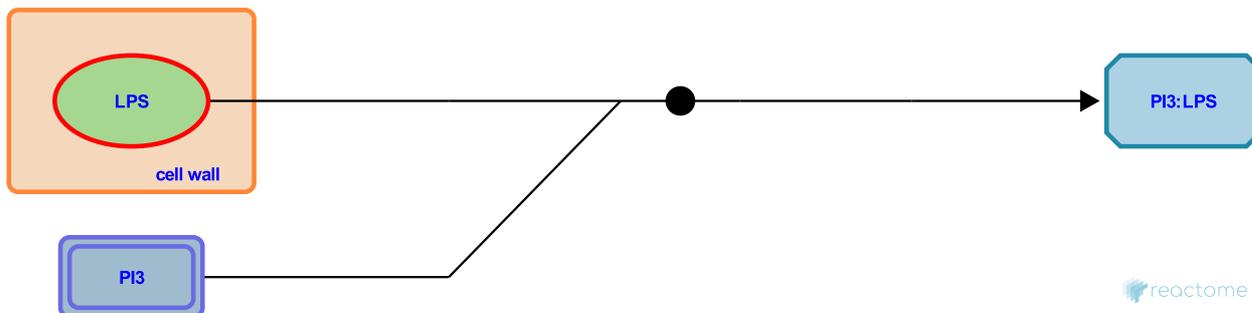
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6810724

Type: binding

Compartments: extracellular region, cell wall

Inferred from: [PI3 binds the bacterial surface \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

BPIF binds bacteria ↗

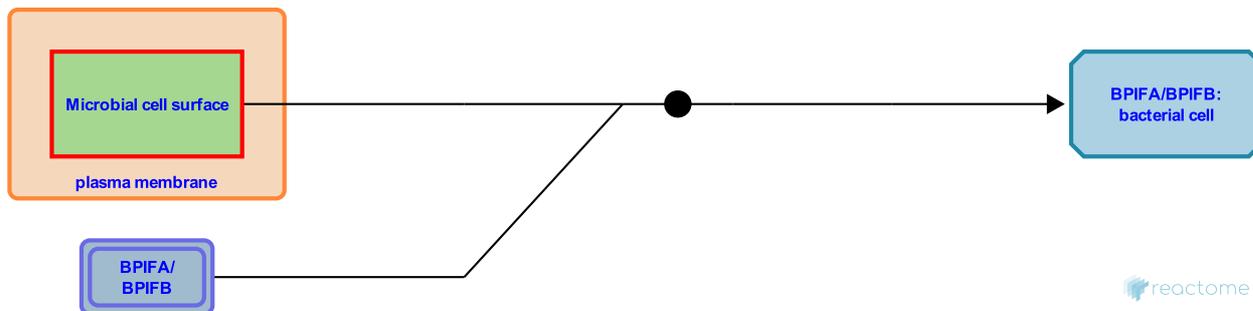
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6809521

Type: binding

Compartments: extracellular region, plasma membrane

Inferred from: [BPIF binds bacteria \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

LYZ binds bacterial peptidoglycan ↗

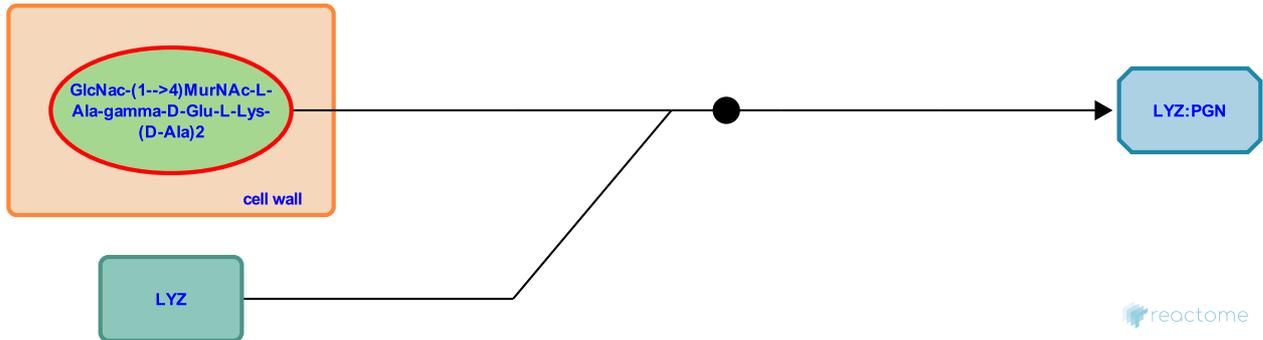
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-8862300

Type: binding

Compartments: extracellular region, cell wall

Inferred from: [LYZ binds bacterial peptidoglycan \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Followed by: [LYZ hydrolyzes peptidoglycans in the bacterial cell wall](#)

LYZ hydrolyzes peptidoglycans in the bacterial cell wall ↗

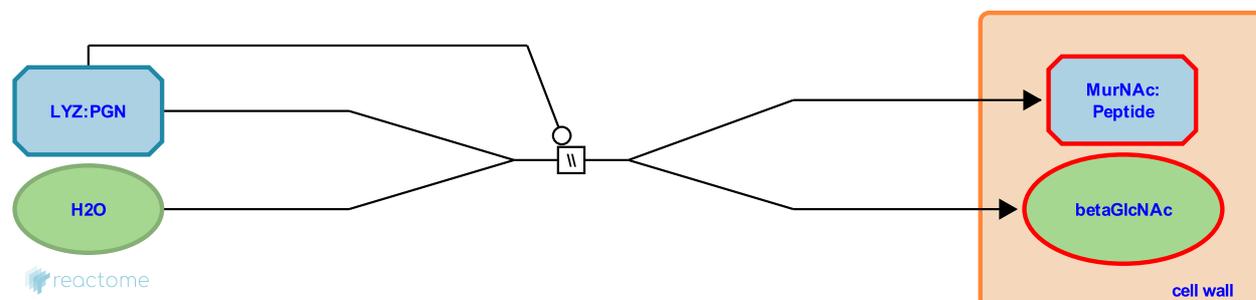
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-8862320

Type: omitted

Compartments: extracellular region, cell wall

Inferred from: [LYZ hydrolyzes peptidoglycans in the bacterial cell wall \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Preceded by: [LYZ binds bacterial peptidoglycan](#)

ELANE, CTSG or PRTN3 binds bacteria ↗

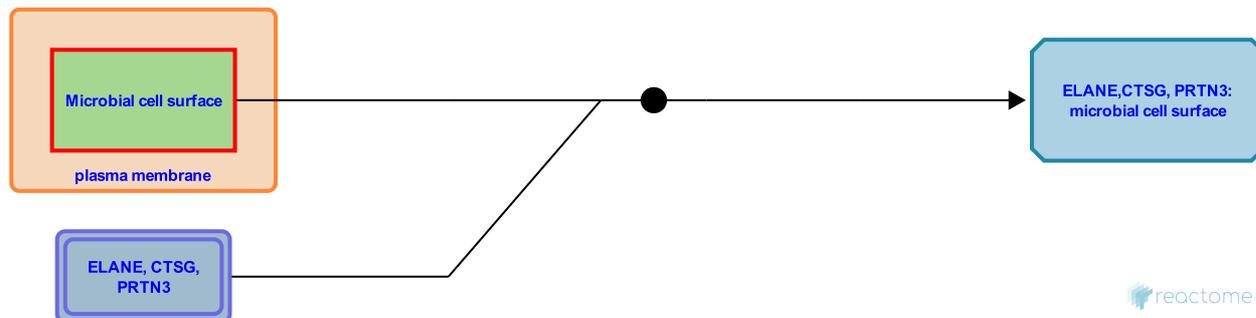
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-6813659

Type: binding

Compartments: extracellular region, plasma membrane

Inferred from: [ELANE, CTSG or PRTN3 binds bacteria \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

PLA2G2A binds bacterial phospholipids ↗

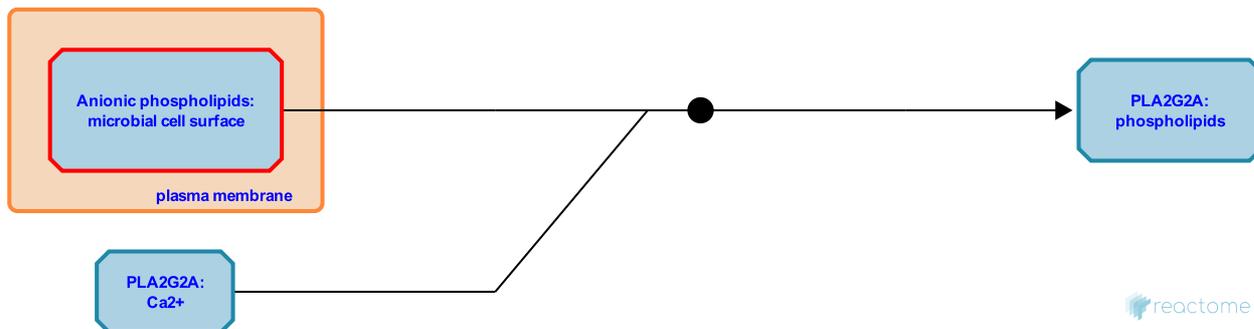
Location: [Antimicrobial peptides](#)

Stable identifier: R-XTR-8862771

Type: binding

Compartments: extracellular region, plasma membrane

Inferred from: [PLA2G2A binds bacterial phospholipids \(Homo sapiens\)](#)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

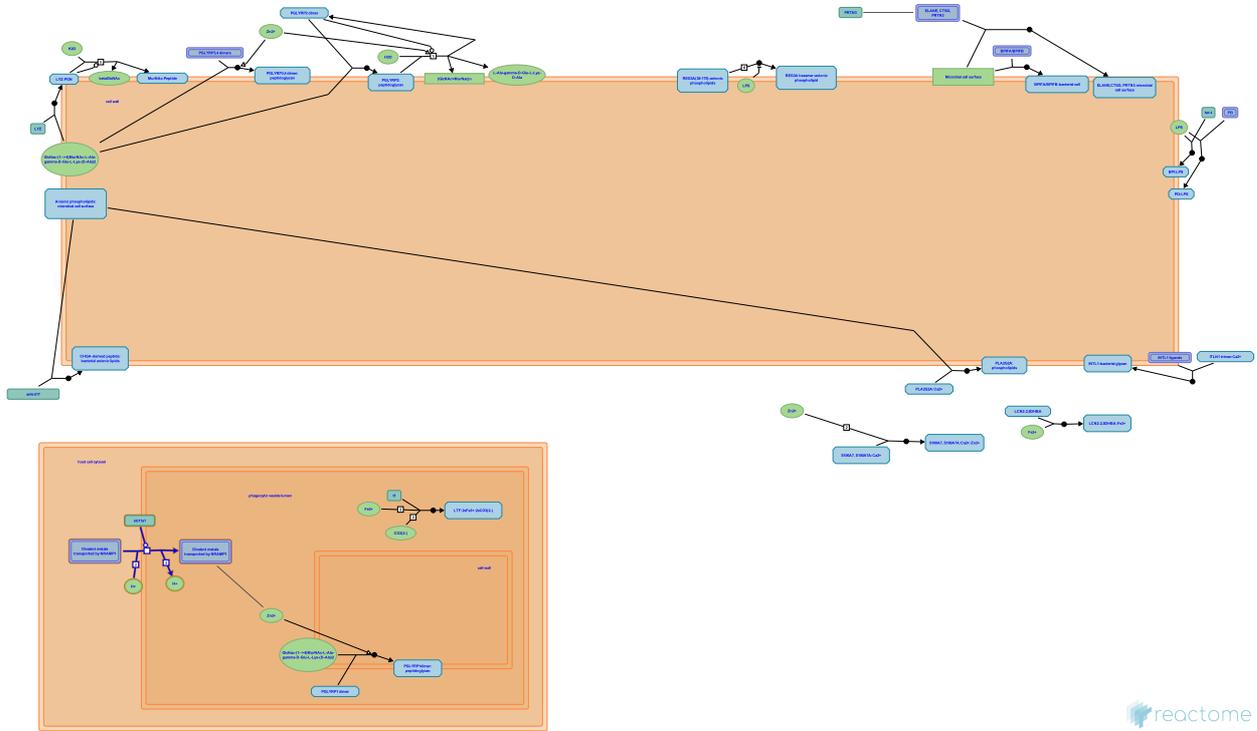
[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

Ion influx/efflux at host-pathogen interface ↗

Location: Antimicrobial peptides

Stable identifier: R-XTR-6803544

Inferred from: Ion influx/efflux at host-pathogen interface (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](/electronic_inference_compara.html) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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