

# ANTXR1-bound pagA(197-794) forms oligomers

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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.

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## 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. [↗](#)

Reactome database release: 88

This document contains 1 reaction ([see Table of Contents](#))

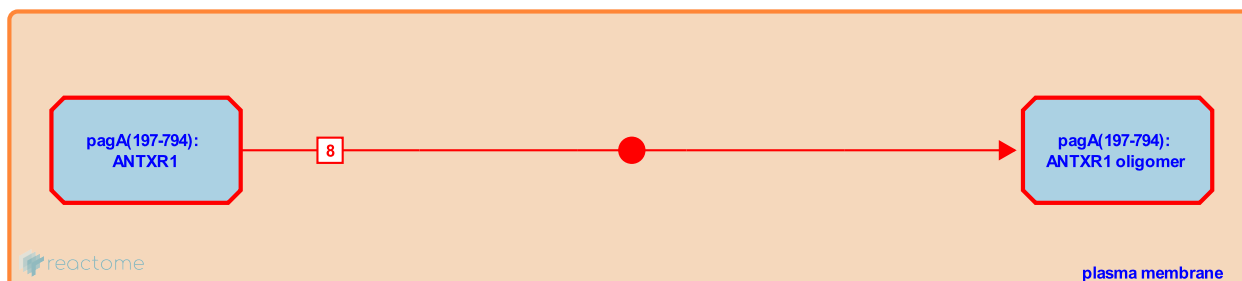
## ANTXR1-bound pagA(197-794) forms oligomers [↗](#)

**Stable identifier:** R-HSA-5210909

**Type:** binding

**Compartments:** plasma membrane

**Diseases:** anthrax disease



ANTXR1 (Anthrax Receptor 1)-bound pagA(197-794) (protective antigen, large fragment) forms oligomers in the target cell plasma membrane. Initial studies indicated that these were heptamers (Lacy et al. 2004; Santelli et al. 2004; Wigelsworth et al. 2004; Young and Collier 2007). More recent work has established that octamers also form and suggests that the octameric structure is more stable under physiological conditions (Kintzer et al. 2009, 2010). Formation of the latter structure is thus annotated here.

### Literature references

- Young, JA., Collier, RJ. (2007). Anthrax toxin: receptor binding, internalization, pore formation, and translocation. *Annu. Rev. Biochem.*, 76, 243-65. [↗](#)
- Wigelsworth, DJ., Melnyk, RA., Lacy, DB., Collier, RJ., Harrison, SC. (2004). Structure of heptameric protective antigen bound to an anthrax toxin receptor: a role for receptor in pH-dependent pore formation. *Proc. Natl. Acad. Sci. U.S.A.*, 101, 13147-51. [↗](#)
- Abdul-Gader, A., Krantz, BA., Williams, ER., Miles, AJ., Sterling, HJ., Tang, II. et al. (2010). Role of the protective antigen octamer in the molecular mechanism of anthrax lethal toxin stabilization in plasma. *J. Mol. Biol.*, 399, 741-58. [↗](#)
- Wigelsworth, DJ., Krantz, BA., Lacy, DB., Collier, RJ., Juris, SJ., Christensen, KA. (2004). Binding stoichiometry and kinetics of the interaction of a human anthrax toxin receptor, CMG2, with protective antigen. *J. Biol. Chem.*, 279, 23349-56. [↗](#)
- Santelli, E., Leppla, SH., Liddington, RC., Bankston, LA. (2004). Crystal structure of a complex between anthrax toxin and its host cell receptor. *Nature*, 430, 905-8. [↗](#)

### Editions

2013-12-13	Authored	D'Eustachio, P.
2014-05-19	Reviewed	Leppla, SH.
2014-05-23	Reviewed	Turk, BE.
2014-05-28	Reviewed	Moayeri, M., Liu, S.