

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. [↗](#)

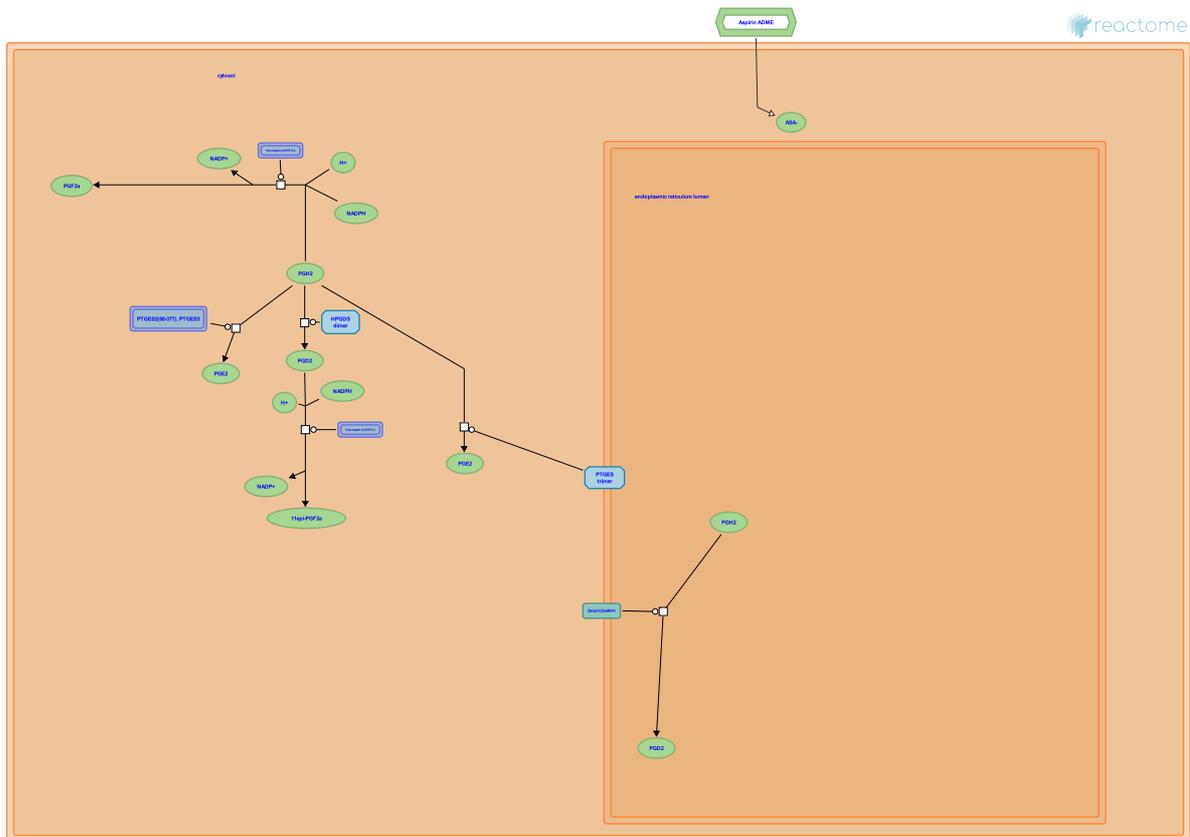
Reactome database release: 83

This document contains 1 pathway and 6 reactions ([see Table of Contents](#))

Synthesis of Prostaglandins (PG) and Thromboxanes (TX) ↗

Stable identifier: R-DME-2162123

Inferred from: [Synthesis of Prostaglandins \(PG\) and Thromboxanes \(TX\) \(Homo sapiens\)](#)



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>

PGH2 is reduced to PGF2a by AKR1C3 ↗

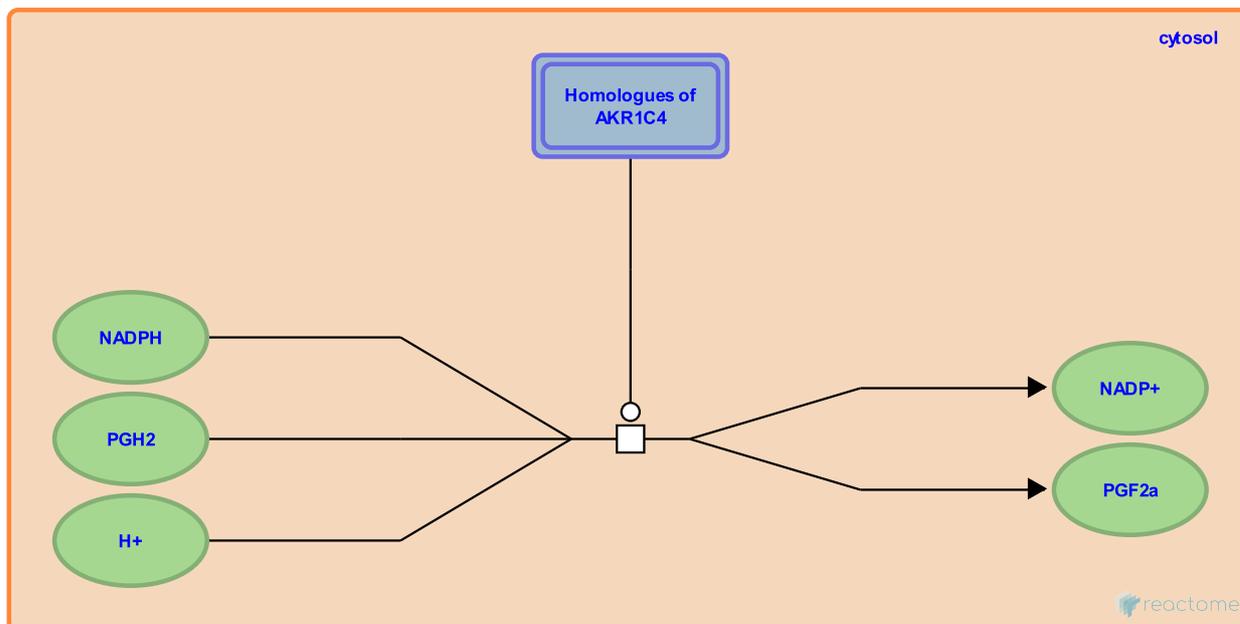
Location: Synthesis of Prostaglandins (PG) and Thromboxanes (TX)

Stable identifier: R-DME-2161549

Type: transition

Compartments: cytosol

Inferred from: PGH2 is reduced to PGF2a by AKR1C3 (Homo sapiens)



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

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PGH2 is isomerised to PGE2 by PTGES ↗

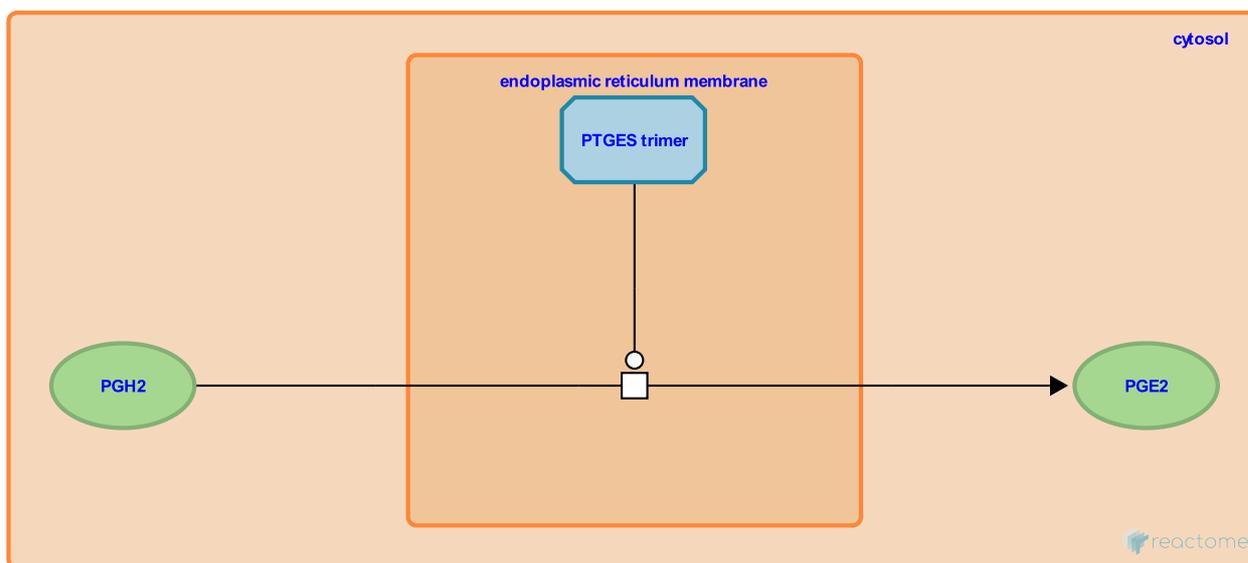
Location: [Synthesis of Prostaglandins \(PG\) and Thromboxanes \(TX\)](#)

Stable identifier: R-DME-2161660

Type: transition

Compartments: endoplasmic reticulum membrane, cytosol

Inferred from: [PGH2 is isomerised to PGE2 by PTGES \(Homo sapiens\)](#)



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.

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Prostaglandin E synthase isomerizes PGH2 to PGE2 ↗

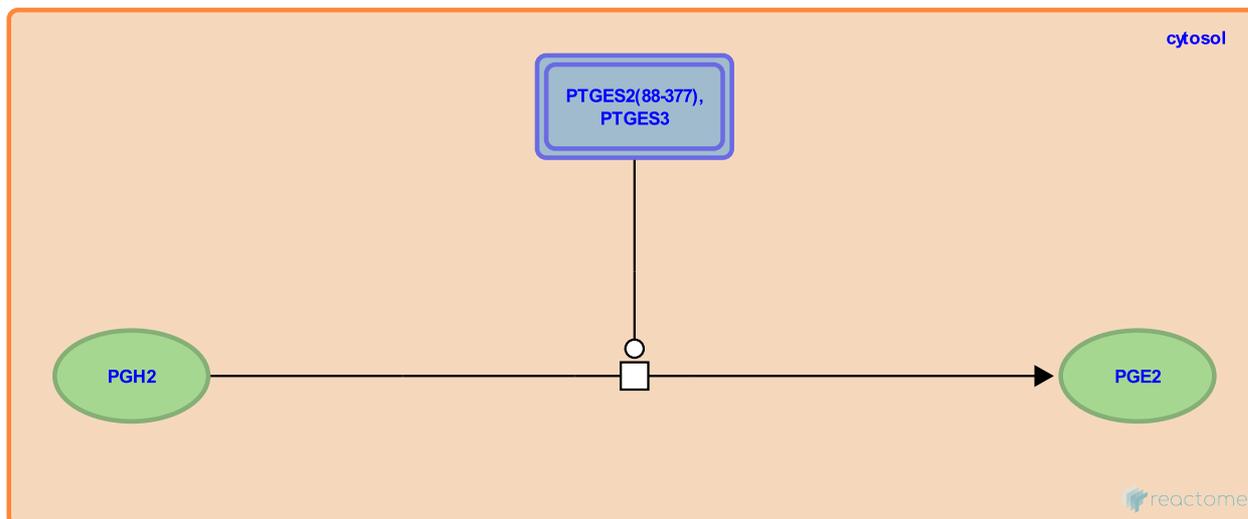
Location: [Synthesis of Prostaglandins \(PG\) and Thromboxanes \(TX\)](#)

Stable identifier: R-DME-265295

Type: transition

Compartments: cytosol

Inferred from: [Prostaglandin E synthase isomerizes PGH2 to PGE2 \(Homo sapiens\)](#)



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.

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PGH2 is isomerised to PGD2 by PTGDS ↗

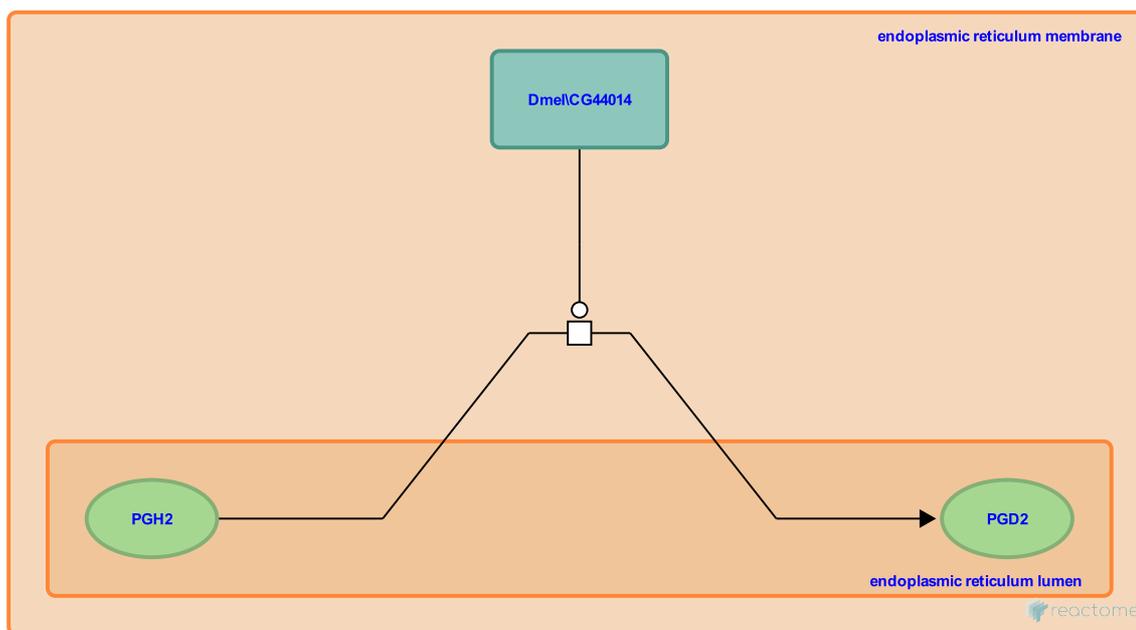
Location: [Synthesis of Prostaglandins \(PG\) and Thromboxanes \(TX\)](#)

Stable identifier: R-DME-2161620

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Inferred from: [PGH2 is isomerised to PGD2 by PTGDS \(Homo sapiens\)](#)



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>

PGH2 is isomerised to PGD2 by HPGDS ↗

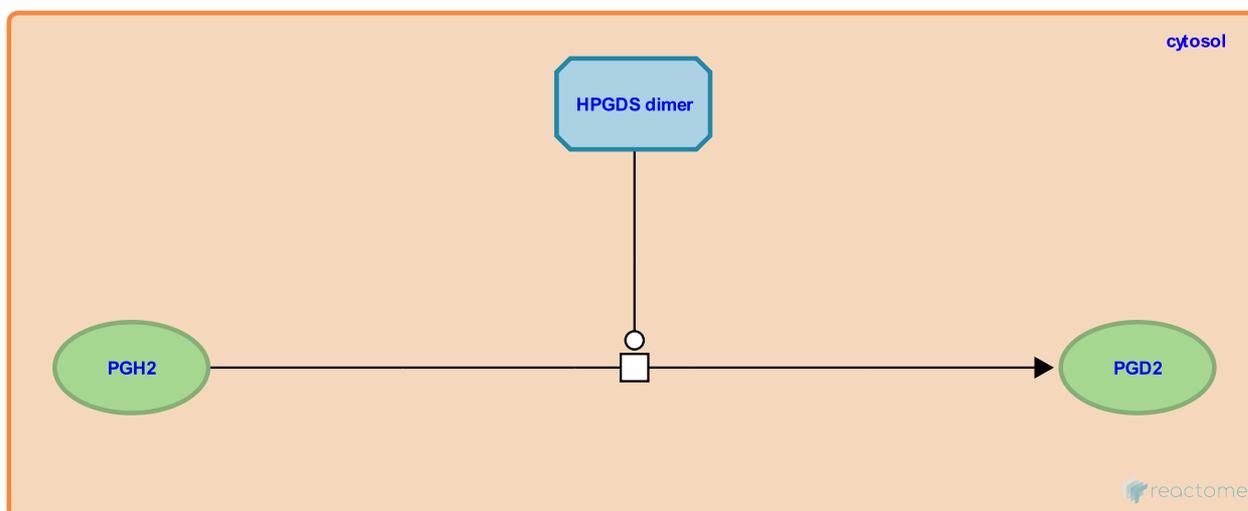
Location: [Synthesis of Prostaglandins \(PG\) and Thromboxanes \(TX\)](#)

Stable identifier: R-DME-2161701

Type: transition

Compartments: cytosol

Inferred from: [PGH2 is isomerised to PGD2 by HPGDS \(Homo sapiens\)](#)



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: [PGD2 is reduced to 11-epi-PGF2a by AKRIC3](#)

PGD2 is reduced to 11-epi-PGF2a by AKRIC3 ↗

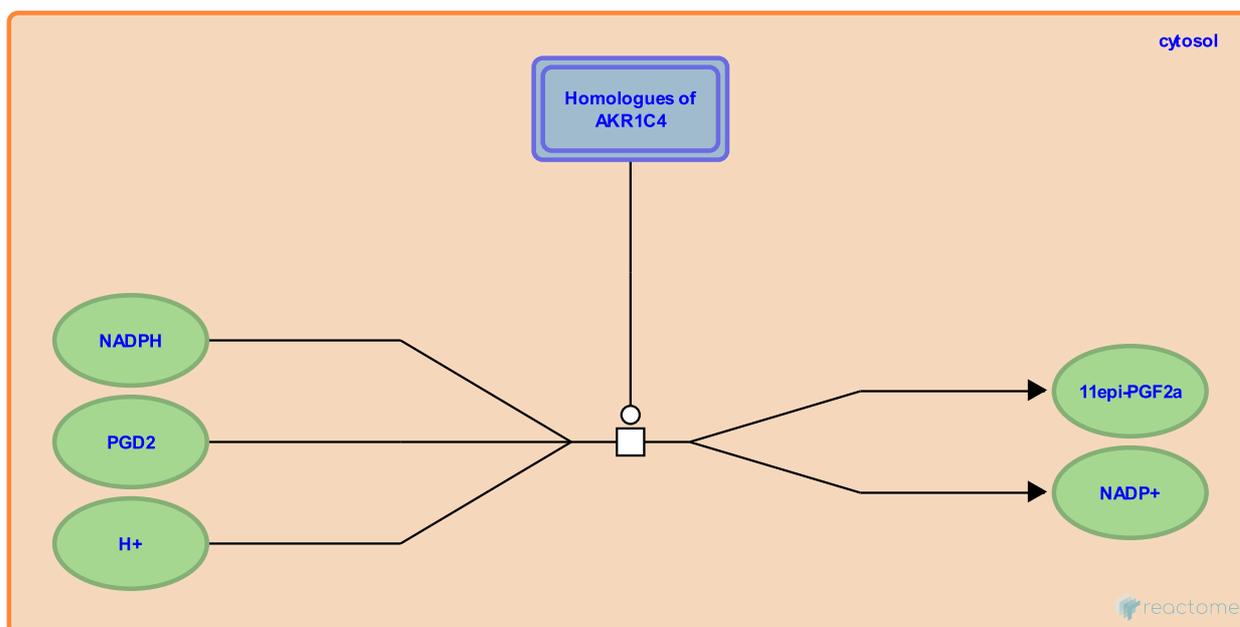
Location: [Synthesis of Prostaglandins \(PG\) and Thromboxanes \(TX\)](#)

Stable identifier: R-DME-2161614

Type: transition

Compartments: cytosol

Inferred from: [PGD2 is reduced to 11-epi-PGF2a by AKRIC3 \(Homo sapiens\)](#)



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: [PGH2 is isomerised to PGD2 by HPGDS](#)

Table of Contents

Introduction	1
☒ Synthesis of Prostaglandins (PG) and Thromboxanes (TX)	2
↳ PGH2 is reduced to PGF2a by AKR1C3	3
↳ PGH2 is isomerised to PGE2 by PTGES	4
↳ Prostaglandin E synthase isomerizes PGH2 to PGE2	5
↳ PGH2 is isomerised to PGD2 by PTGDS	6
↳ PGH2 is isomerised to PGD2 by HPGDS	7
↳ PGD2 is reduced to 11-epi-PGF2a by AKR1C3	8
Table of Contents	9