Reproduction
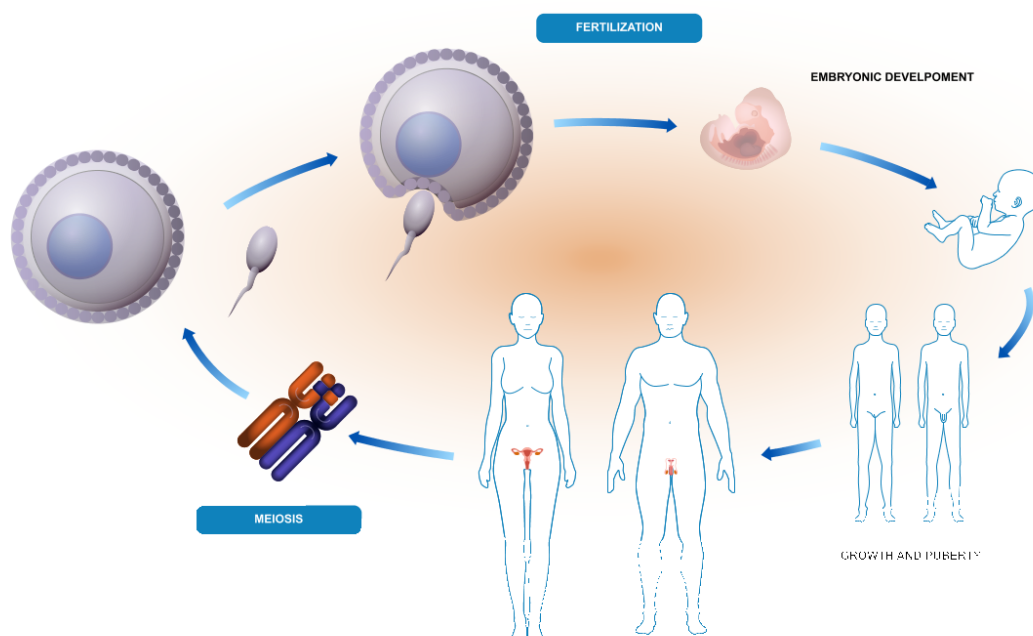

Bolcun-Filas, E., Cohen, PE., Gillespie, ME., Holloway, JK., Lishko, PV., Lyndaker, A., May, B., Schimenti, JC., Strong, E.

14/09/2021

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

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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: 77

This document contains 3 pathways (see Table of Contents)

Reproduction ↗

Stable identifier: R-HSA-1474165
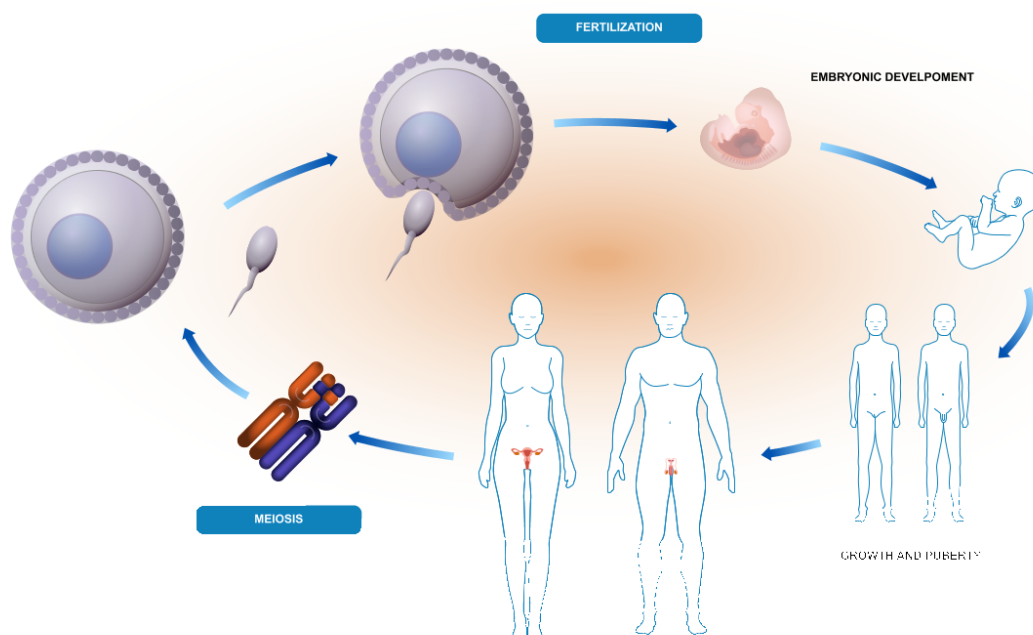
Human reproduction mixes the genomes of two individuals creating a new organism. The offspring individuals produced by sexual reproduction differ from their parents and from their siblings. Reproduction includes the reproductive system, sperm and egg production (haploid cells), fertilization, and the early stages embryo development.

Literature references

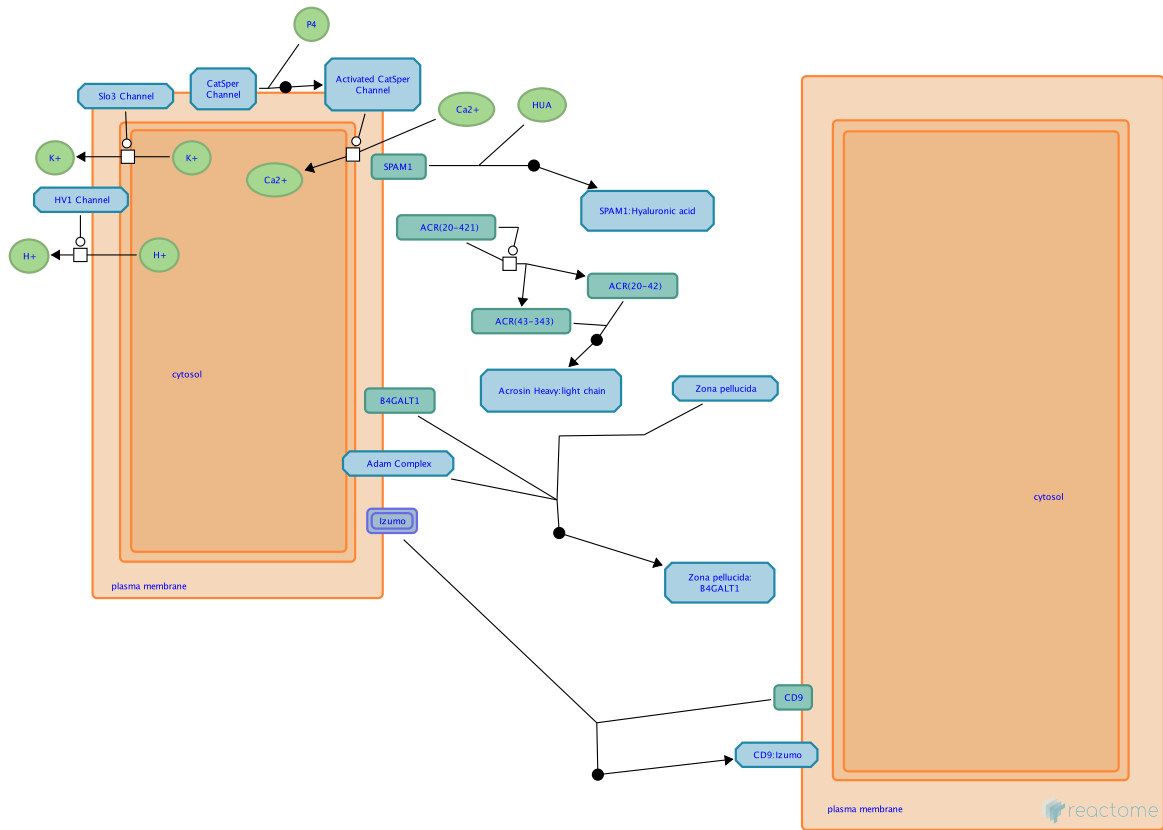Evan Jones, R., López, KH. (2006). Human reproductive biology. *Academic Press*.

Editions

2013-02-13	Authored	Gillespie, ME.
2013-05-21	Reviewed	Lishko, PV.
2013-05-23	Edited	Gillespie, ME.

Fertilization ↗

Location: Reproduction

Stable identifier: R-HSA-1187000

Mammalian fertilization comprises sperm migration through the female reproductive tract, biochemical and morphological changes to sperm, and sperm-egg interaction in the oviduct. Although the broad concepts of fertilization are well defined, our understanding of the biochemical mechanisms underlying sperm-egg binding is limited.

Literature references

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Evans, JP., Florman, HM. (2002). The state of the union: the cell biology of fertilization. *Nat Cell Biol, 4*, s57-63. ↗
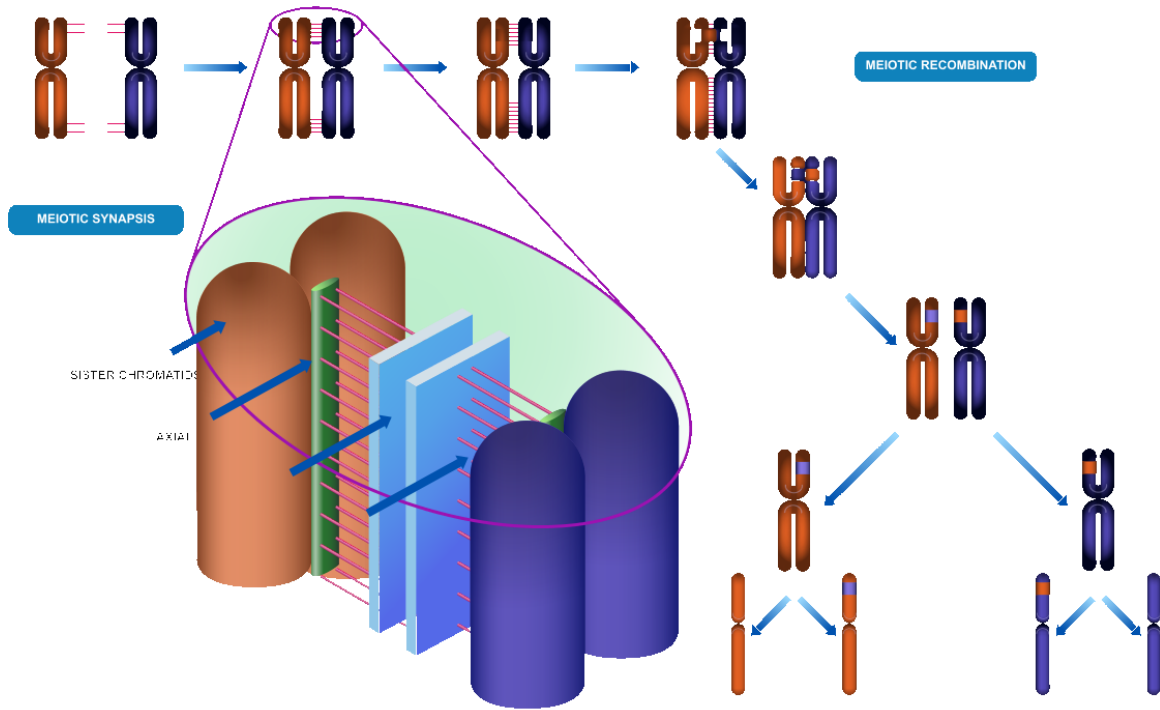
Editions

2013-02-13	Authored	Gillespie, ME.
2013-05-21	Reviewed	Lishko, PV.
2013-05-23	Edited	Gillespie, ME.

Meiosis ↗

Location: Reproduction

Stable identifier: R-HSA-1500620

Compartments: nuclear envelope, nucleoplasm

During meiosis the replicated chromosomes of a single diploid cell are segregated into 4 haploid daughter cells by two successive divisions, meiosis I and meiosis II. In meiosis I, the distinguishing event of meiosis, pairs (bivalents) of homologous chromosomes in the form of sister chromatids are paired by **synapsis** along their regions of homologous DNA (Yang and Wang 2009), and then segregated, resulting in haploid daughters containing sister chromatids paired at their centromeres (Cohen et al. 2006, Handel and Schimenti 2010). The sister chromatids are then separated and segregated during meiosis II.

Recombination between chromosomal homologues but not between sister chromatids occurs during prophase of meiosis I (Inagaki et al. 2010). Though hundreds of recombination events are initiated, most are resolved without crossovers and only tens proceed to become crossovers. In mammals recombination events are required between homologues for normal pairing, synapsis, and segregation.

Literature references

Inagaki, A., Schoenmakers, S., Baarends, WM. (2010). DNA double strand break repair, chromosome synapsis and transcriptional silencing in meiosis. *Epigenetics, 5*. ↗

Cohen, PE., Pollack, SE., Pollard, JW. (2006). Genetic analysis of chromosome pairing, recombination, and cell cycle control during first meiotic prophase in mammals. *Endocr Rev, 27*, 398-426. ↗

Handel, MA., Schimenti, JC. (2010). Genetics of mammalian meiosis: regulation, dynamics and impact on fertility. *Nat Rev Genet, 11*, 124-36. ↗

Yang, F., Wang, PJ. (2009). The Mammalian synaptonemal complex: a scaffold and beyond. *Genome Dyn, 5*, 69-80. ↗

Editions

2011-02-05	Reviewed	Schimenti, JC., Cohen, PE., Holloway, JK.
2011-02-25	Reviewed	Bolcun-Filas, E., Lyndaker, A., Strong, E.
2011-08-19	Authored, Edited	May, B.

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