

ABCA4 locus as a model for complex genetics in monogenic diseases = ABCA4 lookus kui monogeensete haiguste kompleksse geneetika mudel

Zernant, Jana 2019 <https://digi.lib.ttu.ee/?i/212387> https://www.ester.ee/record=b5235122*est

Analyses of non-coding somatic drivers in 2,658 cancer whole genomes

Rheinbay, Esther; Nielsen, Morten Muhlig; Abascal, Federico; Wala, Jeremiah A.; Shapira, Ofer; Tiao, Grace; Hornshøj, Henrik; Hess, Julian M.; Juul, Randi Istrup; **Uusküla-Reimand, Liis** Nature 2020 / 10 p. : ill <https://doi.org/10.1038/s41586-020-1965-x> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

ASK1, a SKP1 homolog, is required for nuclear reorganization, presynaptic homolog juxtaposition and the proper distribution of cohesin during meiosis in Arabidopsis

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Author Correction: A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns (Nature Communications, (2020), 11, 1, (728), 10.1038/s41467-019-13825-8)

Jiao, Wei; Atwal, Gurmit; Polak, Paz; Karlic, Rosa; Cuppen, Edwin; Al-Shahrour, Fatima; Bailey, Peter J.; Biankin, Andrew V.; Boutros, Paul C.; **Uusküla-Reimand, Liis** Nature Communications 2022 / Art. 7573 <https://doi.org/10.1038/s41467-022-32329-6> [Journal metrics](#) [at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

Author Correction: Analyses of non-coding somatic drivers in 2,658 cancer whole genomes (Nature, (2020), 578, 7793, (102-111), 10.1038/s41586-020-1965-x)

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Author Correction: Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing (Nature Genetics, (2020), 52, 3, (331-341), 10.1038/s41588-019-0576-7)

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Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing

Cortés-Ciriano, Isidro; Lee, Jake June-Koo; Xi, Ruibin; Jain, Dhawal; Jung, Youngsook Lucy; Yang, Lixing; Gordenin, Dmitry; Klimczak, Leszek J.; **Uusküla-Reimand, Liis** Nature Genetics 2020 / p. 331-341 <https://doi.org/10.1038/s41588-019-0576-7> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

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A deep learning system accurately classifies primary and metastatic cancers using passenger mutation patterns

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Divergent mutational processes distinguish hypoxic and normoxic tumours

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High-coverage whole-genome analysis of 1220 cancers reveals hundreds of genes deregulated by rearrangement-mediated cis-regulatory alterations

Zhang, Yiqun; Chen, Fengju; Fonseca, Nuno A.; He, Yao; Fujita, Masashi; Nakagawa, Hidewaki; Zhang, Zemin; Brazma, Alvis; Amin, Samirkumar B.; **Uusküla-Reimand, Liis** Nature Communications 2020 / Art. nr. 736 <https://doi.org/10.1038/s41467-019-13885-w>
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Introducing Pitt-Hopkins syndrome-associated mutations of TCF4 to Drosophila daughterless

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Pathway and network analysis of more than 2500 whole cancer genomes

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Reconstructing evolutionary trajectories of mutation signature activities in cancer using TrackSig

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Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples

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