

### **Adenylate kinase and metabolic signaling in cancer cells**

Klepinin, Aleksandr; Zhang, Song; **Klepinina, Ljudmila; Rebane-Klemm, Egle**; Terzic, Andre; Käämbre, Tuuli; Dzeja, Petras  
Frontiers in oncology 2020 / art. 660, 9 p <https://doi.org/10.3389/fonc.2020.00660>

### **Alternative splicing of TAF4 : a dynamic switch between distinct cell functions = TAF4 alternatiivne splaining kui raku funktsioonide dünaamilise reguleerimise lüliti**

Kazantseva, Jekaterina 2014 [https://www.ester.ee/record=b4437535\\*est](https://www.ester.ee/record=b4437535*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](#)

### **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)**

Rheinbay, Esther; Nielsen, Morten Muhlig; Abascal, Federico; Wala, Jeremiah A.; Shapira, Ofer; Tiao, Grace; Hornshøj, Henrik; Hess, Julian M.; Juul, Randi Istrup; Lin, Ziao; Feuerbach, Lars; Sabarinathan, Radhakrishnan; **Uusküla-Reimand, Liis** Nature 2023 / p. E40 <https://doi.org/10.1038/s41586-022-05599-9> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

### **Author Correction: Butler enables rapid cloud-based analysis of thousands of human genomes (Nature Biotechnology, (2020), 38, 3, (288-292), 10.1038/s41587-019-0360-3)**

Yakneen, Sergei; Waszak, Sebastian M.; Aminou, Brice; Bartolome, Javier; Boroevich, Keith A.; Boyce, Rich; Brooks, Angela N.; Buchanan, Alex; Buchhalter, Ivo; Butler, Adam P.; Byrne, Niall J.; Cafferkey, Andy; **Uusküla-Reimand, Liis** Author Correction: Butler enables rapid cloud-based analysis of thousands of human genomes (Nature Biotechnology, (2020), 38, 3, (288-292), 10.1038/s41587-019-0360-3) 2023 / p. 577 <https://doi.org/10.1038/s41587-022-01554-1> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

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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)**

Cortés-Ciriano, Isidro; Lee, Jake June-Koo; Xi, Ruibin; Jain, Dhawal; Jung, Youngsook Lucy; Yang, Lixing; Gordenin, Dmitry A.; Klimczak, Leszek J.; Zhang, Cheng-Zhong; Pellman, David S.; Akdemir, Kadir Caner; Alvarez, Eva Garcia; **Uusküla-Reimand, Liis** Nature Genetics 2023 / p. 1076 <https://doi.org/10.1038/s41588-023-01315-z> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

### **Author Correction: Comprehensive molecular characterization of mitochondrial genomes in human cancers (Nature Genetics, (2020), 52, 3, (342-352), 10.1038/s41588-019-0557-x)**

Yuan, Yuan; Ju, Young Seok; Kim, Youngwook; Li, Jun; Wang, Yumeng; Yoon, Christopher J.; Yang, Yang; Martincorena, Inigo; Creighton, Chad J.; Weinstein, John N.; Xu, Yanxun; Han, Leng; **Uusküla-Reimand, Liis** Nature Genetics 2023 / p. 892 <https://doi.org/10.1038/s41588-020-0629-y> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

### **Author Correction: Comprehensive molecular characterization of mitochondrial genomes in human cancers (Nature Genetics, (2020), 52, 3, (342-352), 10.1038/s41588-019-0557-x)**

Yuan, Yuan; Ju, Young Seok; Kim, Youngwook; Li, Jun; Wang, Yumeng; Yoon, Christopher J.; Yang, Yang; Martincorena, Inigo; Creighton, Chad J.; Weinstein, John N.; Xu, Yanxun; Han, Leng; **Uusküla-Reimand, Liis** Nature Genetics 2023 / p. 1078 <https://doi.org/10.1038/s41588-023-01317-x> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

### **Author Correction: Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer (Nature Genetics, (2020), 52, 3, (294-305), 10.1038/s41588-019-0564-y)**

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**Author Correction: Genomic basis for RNA alterations in cancer (Nature, (2020), 578, 7793, (129-136), 10.1038/s41586-020-1970-0)**

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**Author Correction: Genomic footprints of activated telomere maintenance mechanisms in cancer (Nature Communications, (2020), 11, 1, (733), 10.1038/s41467-019-13824-9)**

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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 2022 / Art. nr. 7572 <https://doi.org/10.1038/s41467-022-32333-w>

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**Combined burden and functional impact tests for cancer driver discovery using DriverPower**

Shuai, Shimin; Abascal, Federico; Amin, Samirkumar B.; Bader, Gary D.; Bandopadhyay, Pratiti; Barenboim, Jonathan; Beroukhim, Rameen; Bertl, Johanna; Boroevich, Keith A.; **Uusküla-Reimand, Liis** Nature Communications 2020 / art. 734 <https://doi.org/10.1038/s41467-019-13929-1> [Journal metrics at Scopus](#) [Article at Scopus](#) [Journal metrics at WOS](#) [Article at WOS](#)

**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](#)

**Comprehensive molecular characterization of mitochondrial genomes in human cancers**

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**Divergent mutational processes distinguish hypoxic and normoxic tumours**

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