## David E Larson

## List of Publications by Year in descending order

Source: https:/|exaly.com/author-pdf/1405829/publications.pdf
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Bam-readcount - rapid generation of basepair-resolution sequence metrics. Journal of Open Source
Software, 2022, 7, 3722.

Association of structural variation with cardiometabolic traits in Finns. American Journal of Human Genetics, 2021, 108, 583-596.

Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly
associated with metabolic traits via cell-type composition differences. Human Genomics, 2021, 15, 34.

4 The clonal evolution of metastatic colorectal cancer. Science Advances, 2020, 6, eaay9691.
10.3

Mapping and characterization of structural variation in 17,795 human genomes. Nature, 2020, 583,
83-89.

Exome sequencing of Finnish isolates enhances rare-variant association power. Nature, 2019, 572, 323-328.
27.8

161

7 svtools: population-scale analysis of structural variation. Bioinformatics, 2019, 35, 4782-4787.
4.1

51
$8 \quad$ Functional equivalence of genome sequencing analysis pipelines enables harmonized variant calling across human genetics projects. Nature Communications, 2018, 9, 4038.

9 The prognostic effects of somatic mutations in ER-positive breast cancer. Nature Communications,
2018, 9, 3476.

CIViC is a community knowledgebase for expert crowdsourcing the clinical interpretation of variants
21.4

11 Comprehensive discovery of noncoding RNAs in acute myeloid leukemia cell transcriptomes.
Experimental Hematology, 2017, 55, 19-33.

Brief Report: The Role of Rare Proteinâ€€oding Variants in Antiâ€"Tumor Necrosis Factor Treatment
12 Response in Rheumatoid Arthritis. Arthritis and Rheumatology, 2017, 69, 735-741.
5.6

8

13 Truncating Prolactin Receptor Mutations Promote Tumor Growth in Murine Estrogen Receptor-Alpha Mammary Carcinomas. Cell Reports, 2016, 17, 249-260.

Rare Variation in <i>TET2</i> Is Associated with Clinically Relevant Prostate Carcinoma in African Americans. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1456-1463.

Aromatase inhibition remodels the clonal architecture of estrogen-receptor-positive breast cancers.
Nature Communications, 2016, 7, 12498.
12.8

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Comprehensive genomic analysis reveals FLT3 activation and a therapeutic strategy for a patient with relapsed adult B-lymphoblastic leukemia. Experimental Hematology, 2016, 44, 603-613.
Patterns and functional implications of rare germline variants across 12 cancer types. Nature
Communications, 2015, 6, 10086.

Identification of Functional Variants for Cleft Lip with or without Cleft Palate in or near PAX7, FGFR2, and NOG by Targeted Sequencing of GWAS Loci. American Journal of Human Genetics, 2015, 96, 397-411.
6.2

150

Association Between Mutation Clearance After Induction Therapy and Outcomes in Acute Myeloid
7.4
$21 \quad \begin{aligned} & \text { Association Between Mutation Clearance After Induction Therapy and Outcomes } \\ & \text { Leukemia. JAMA - Journal of the American Medical Association, 2015, 314, 811. }\end{aligned}$
302

TYK2 Protein-Coding Variants Protect against Rheumatoid Arthritis and Autoimmunity, with No
Evidence of Major Pleiotropic Effects on Non-Autoimmune Complex Traits. PLoS ONE, 2015, 10, e0122271.
2.5

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Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at CWAS Loci. PLoS
Genetics, 2014, 10, e1004147.
3.5

Exome-Based Mapping and Variant Prioritization for Inherited Mendelian Disorders. American Journal of Human Genetics, 2014, 94, 373-384.
6.2

37Using SomaticSniper to Detect Somatic Single Nucleotide Variants. Current Protocols in

Using SomaticSniper to Detect Somatic Single Nucleotide Variants. Current Protocols in
Bioinformatics, 2014, 45, 15.5.1-8.
25.8

4

BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current
Protocols in Bioinformatics, 2014, 45, 15.6.1-11.
25.8

135
2

Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014,
5, 3156.
12.8

253

28 DGIdb: mining the druggable genome. Nature Methods, 2013, 10, 1209-1210.
19.0

443

> Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal
> of Medicine, 2013, 368, 2059-2074.
$27.0 \quad 4,139$

SomaticSniper: identification of somatic point mutations in whole genome sequencing data.
30 Bioinformatics, 2012, 28, 311-317.
4.1

566

Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature,
27.8

1,795
2012, 481, 506-510.

VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing.
5.5

4,086

