

Kyle Ellrott

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

12,473
citations

331670

21
h-index

254184

43
g-index

63
all docs

63
docs citations

63
times ranked

24456
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. <i>Cell Genomics</i> , 2022, 2, 100085. | 6.5 | 59 |
| 2 | A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5. | 6.2 | 15 |
| 3 | neopiscope improves neopeptide prediction with multivariate phasing. <i>Bioinformatics</i> , 2020, 36, 713-720. | 4.1 | 23 |
| 4 | A community effort to create standards for evaluating tumor subclonal reconstruction. <i>Nature Biotechnology</i> , 2020, 38, 97-107. | 17.5 | 58 |
| 5 | Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748. | 12.8 | 27 |
| 6 | A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020, 52, 448-457. | 21.4 | 104 |
| 7 | Exploring Integrative Analysis Using the BioMedical Evidence Graph. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 147-159. | 2.1 | 4 |
| 8 | Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. <i>Genome Biology</i> , 2019, 20, 195. | 8.8 | 19 |
| 9 | Population-level distribution and putative immunogenicity of cancer neopeptides. <i>BMC Cancer</i> , 2018, 18, 414. | 2.6 | 32 |
| 10 | Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7. | 6.2 | 605 |
| 11 | Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. <i>Genome Biology</i> , 2018, 19, 188. | 8.8 | 42 |
| 12 | Valection: design optimization for validation and verification studies. <i>BMC Bioinformatics</i> , 2018, 19, 339. | 2.6 | 2 |
| 13 | Germline contamination and leakage in whole genome somatic single nucleotide variant detection. <i>BMC Bioinformatics</i> , 2018, 19, 28. | 2.6 | 8 |
| 14 | A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017, 5, 485-497.e3. | 6.2 | 19 |
| 15 | TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. <i>Cancer Research</i> , 2017, 77, e111-e114. | 0.9 | 59 |
| 16 | Prophetic Granger Causality to infer gene regulatory networks. <i>PLoS ONE</i> , 2017, 12, e0170340. | 2.5 | 10 |
| 17 | Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. <i>Nature Methods</i> , 2015, 12, 623-630. | 19.0 | 282 |
| 18 | Abstract PR02: Multiple Pathway Learning accurately predicts gene essentiality in the Cancer Cell Line Encyclopedia. , 2015, , . | | 0 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Abstract A2-64: A signature catalog to classify tumor mixtures: Application to recognition of metastatic disease in prostate cancer. , 2015, , . | | 0 |
| 20 | Abstract PR10: Multiple Pathway Learning accurately predicts gene essentiality in the Cancer Cell Line Encyclopedia. , 2015, , . | | 0 |
| 21 | Abstract B1-37: A signature catalog to classify tumor mixtures: application to recognition of metastatic disease in prostate cancer. , 2015, , . | | 0 |
| 22 | Global optimization of somatic variant identification in cancer genomes with a global community challenge. <i>Nature Genetics</i> , 2014, 46, 318-319. | 21.4 | 42 |
| 23 | The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477. | 28.9 | 3,979 |
| 24 | The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120. | 21.4 | 6,265 |
| 25 | The UCSC Cancer Genomics Browser: update 2013. <i>Nucleic Acids Research</i> , 2013, 41, D949-D954. | 14.5 | 172 |
| 26 | Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas. <i>Nature Genetics</i> , 2013, 45, 1121-1126. | 21.4 | 102 |
| 27 | Abstract 2985: Predicting the impact of mutations in cancer using an integrated pathway approach. , 2012, , . | | 0 |
| 28 | Abstract 5087: UCSC Cancer Genomics Browser 2.0. , 2012, , . | | 0 |
| 29 | TOPSAN: a dynamic web database for structural genomics. <i>Nucleic Acids Research</i> , 2011, 39, D494-D496. | 14.5 | 17 |
| 30 | Abstract A39: The UCSC Cancer Genomics Browser. , 2011, , . | | 0 |
| 31 | The structure of KPN03535 (gi 152972051), a novel putative lipoprotein from <i>Klebsiella pneumoniae</i> , reveals an OB-fold. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1254-1260. | 0.7 | 3 |
| 32 | The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1174-1181. | 0.7 | 8 |
| 33 | The structure of BVU2987 from <i>Bacteroides vulgatus</i> reveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1265-1273. | 0.7 | 8 |
| 34 | Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of the <i>Bacillus</i> chorismate mutase fold and suggest a role in amino-acid metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1182-1189. | 0.7 | 3 |
| 35 | A conserved fold for fimbrial components revealed by the crystal structure of a putative fimbrial assembly protein (BT1062) from <i>Bacteroides thetaiotaomicron</i> at 2.2 Å resolution. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1281-1286. | 0.7 | 9 |
| 36 | Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved $\beta\alpha\beta$ core domain and an auxiliary C-terminal treble-clef zinc finger. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1335-1346. | 0.7 | 8 |

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|----|---|------|-----------|
| 37 | Structure of the Î³-D-glutamyl-L-diamino acid endopeptidase YkfC from <i>Bacillus cereus</i> in complex with L-Ala-Î³-D-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1354-1364. | 0.7 | 64 |
| 38 | Structure of a membrane-attack complex/perforin (MACPF) family protein from the human gut symbiont <i>Bacteroides thetaiotaomicron</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1297-1305. | 0.7 | 30 |
| 39 | Structure of <i>Bacteroides thetaiotaomicron</i> BT2081 at 2.05 Å resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1287-1296. | 0.7 | 2 |
| 40 | Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1274-1280. | 0.7 | 11 |
| 41 | The crystal structure of a bacterial Sufu-like protein defines a novel group of bacterial proteins that are similar to the N-terminal domain of human Sufu. <i>Protein Science</i> , 2010, 19, 2131-2140. | 7.6 | 12 |
| 42 | Expansion of the Protein Repertoire in Newly Explored Environments: Human Gut Microbiome Specific Protein Families. <i>PLoS Computational Biology</i> , 2010, 6, e1000798. | 3.2 | 52 |
| 43 | Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. <i>Journal of Molecular Biology</i> , 2010, 396, 31-46. | 4.2 | 32 |
| 44 | Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. <i>Journal of Biological Chemistry</i> , 2009, 284, 25268-25279. | 3.4 | 23 |
| 45 | A Historical Perspective of Template-Based Protein Structure Prediction. , 2008, 413, 3-42. | | 20 |
| 46 | IMPROVING THE PERFORMANCE OF PROTEIN THREADING USING INSERTION/DELETION FREQUENCY ARRAYS. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 585-602. | 0.8 | 1 |
| 47 | IMPROVEMENT IN PROTEIN SEQUENCE-STRUCTURE ALIGNMENT USING INSERTION/DELETION FREQUENCY ARRAYS. , 2007, , . | | 6 |
| 48 | Improvement in protein sequence-structure alignment using insertion/deletion frequency arrays. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007, 6, 335-42. | 0.4 | 5 |
| 49 | A generalized threading model using integer programming that allows for secondary structure element deletion. <i>Genome Informatics</i> , 2006, 17, 248-58. | 0.4 | 0 |
| 50 | PROSPECT-PSPP: an automatic computational pipeline for protein structure prediction. <i>Nucleic Acids Research</i> , 2004, 32, W522-W525. | 14.5 | 20 |
| 51 | A computational pipeline for protein structure prediction and analysis at genome scale. <i>Bioinformatics</i> , 2003, 19, 1985-1996. | 4.1 | 23 |
| 52 | PROSPECT II: protein structure prediction program for genome-scale applications. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 641-650. | 2.1 | 89 |
| 53 | Identifying transcription factor binding sites through Markov chain optimization. <i>Bioinformatics</i> , 2002, 18, S100-S109. | 4.1 | 71 |