Kyle Ellrott

List of Publications by Year in descending order

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	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
2	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
3	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
4	Combining tumor genome simulation with crowdsourcing to benchmark somatic single-nucleotide-variant detection. Nature Methods, 2015, 12, 623-630.	19.0	282
5	The UCSC Cancer Genomics Browser: update 2013. Nucleic Acids Research, 2013, 41, D949-D954.	14.5	172
6	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
7	Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas. Nature Genetics, 2013, 45, 1121-1126.	21.4	102
8	PROSPECT II: protein structure prediction program for genome-scale applications. Protein Engineering, Design and Selection, 2003, 16, 641-650.	2.1	89
9	Identifying transcription factor binding sites through Markov chain optimization. Bioinformatics, 2002, 18, S100-S109.	4.1	71
10	Structure of the γ-<scp>D</scp>-glutamyl-<scp>L</scp>-diamino acid endopeptidase YkfC from<i>Bacillus cereus</i>in complex with<scp>L</scp>-Ala-γ-<scp>D</scp>-Glu: insights into substrate recognition by NlpC/P60 cysteine peptidases. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1354-1364.	0.7	64
11	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. Cancer Research, 2017, 77, e111-e114.	0.9	59
12	Inverting the model of genomics data sharing with the NHGRI Genomic Data Science Analysis, Visualization, and Informatics Lab-space. Cell Genomics, 2022, 2, 100085.	6.5	59
13	A community effort to create standards for evaluating tumor subclonal reconstruction. Nature Biotechnology, 2020, 38, 97-107.	17.5	58
14	Expansion of the Protein Repertoire in Newly Explored Environments: Human Gut Microbiome Specific Protein Families. PLoS Computational Biology, 2010, 6, e1000798.	3.2	52
15	Global optimization of somatic variant identification in cancer genomes with a global community challenge. Nature Genetics, 2014, 46, 318-319.	21.4	42
16	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. Genome Biology, 2018, 19, 188.	8.8	42
17	Bacterial Pleckstrin Homology Domains: A Prokaryotic Origin for the PH Domain. Journal of Molecular Biology, 2010, 396, 31-46.	4.2	32
18	Population-level distribution and putative immunogenicity of cancer neoepitopes. BMC Cancer, 2018, 18, 414.	2.6	32

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19	Structure of a membrane-attack complex/perforin (MACPF) family protein from the human gut symbiontBacteroides thetaiotaomicron. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1297-1305.	0.7	30
20	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
21	A computational pipeline for protein structure prediction and analysis at genome scale. Bioinformatics, 2003, 19, 1985-1996.	4.1	23
22	Structural and Functional Characterizations of SsgB, a Conserved Activator of Developmental Cell Division in Morphologically Complex Actinomycetes. Journal of Biological Chemistry, 2009, 284, 25268-25279.	3.4	23
23	<tt>neoepiscope</tt>improves neoepitope prediction with multivariant phasing. Bioinformatics, 2020, 36, 713-720.	4.1	23
24	PROSPECT-PSPP: an automatic computational pipeline for protein structure prediction. Nucleic Acids Research, 2004, 32, W522-W525.	14.5	20
25	A Historical Perspective of Template-Based Protein Structure Prediction. , 2008, 413, 3-42.		20
26	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
27	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. Genome Biology, 2019, 20, 195.	8.8	19
28	TOPSAN: a dynamic web database for structural genomics. Nucleic Acids Research, 2011, 39, D494-D496.	14.5	17
29	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. Cell Systems, 2021, 12, 827-838.e5.	6.2	15
30	The crystal structure of a bacterial Sufuâ€‌like protein defines a novel group of bacterial proteins that are similar to the Nâ€‌terminal domain of human Sufu. Protein Science, 2010, 19, 2131-2140.	7.6	12
31	Structure of BT_3984, a member of the SusD/RagB family of nutrient-binding molecules. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1274-1280.	0.7	11
32	Prophetic Granger Causality to infer gene regulatory networks. PLoS ONE, 2017, 12, e0170340.	2.5	10
33	A conserved fold for fimbrial components revealed by the crystal structure of a putative fimbrial assembly protein (BT1062) from<i>Bacteroides thetaiotaomicron</i>at 2.2â€‌Ã… resolution. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1281-1286.	0.7	9
34	The structure of the first representative of Pfam family PF09836 reveals a two-domain organization and suggests involvement in transcriptional regulation. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1174-1181.	0.7	8
35	The structure of BVU2987 fromBacteroides vulgatusreveals a superfamily of bacterial periplasmic proteins with possible inhibitory function. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1265-1273.	0.7	8
36	Structures of three members of Pfam PF02663 (FmdE) implicated in microbial methanogenesis reveal a conserved Î±+Î² core domain and an auxiliary C-terminal treble-clef zinc finger. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1335-1346.	0.7	8

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37	Germline contamination and leakage in whole genome somatic single nucleotide variant detection. BMC Bioinformatics, 2018, 19, 28.	2.6	8
38	IMPROVEMENT IN PROTEIN SEQUENCE-STRUCTURE ALIGNMENT USING INSERTION/DELETION FREQUENCY ARRAYS. , 2007, , .		6
39	Improvement in protein sequence-structure alignment using insertion/deletion frequency arrays. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 335-42.	0.4	5
40	Exploring Integrative Analysis Using the BioMedical Evidence Graph. JCO Clinical Cancer Informatics, 2020, 4, 147-159.	2.1	4
41	The structure of KPN03535 (gi|152972051), a novel putative lipoprotein fromKlebsiella pneumoniae, reveals an OB-fold. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1254-1260.	0.7	3
42	Structures of the first representatives of Pfam family PF06684 (DUF1185) reveal a novel variant of theBacilluschorismate mutase fold and suggest a role in amino-acid metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1182-1189.	0.7	3
43	Structure of<i>Bacteroides thetaiotaomicron</i>BT2081 at 2.05â€¦Ã… resolution: the first structural representative of a new protein family that may play a role in carbohydrate metabolism. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 1287-1296.	0.7	2
44	Valection: design optimization for validation and verification studies. BMC Bioinformatics, 2018, 19, 339.	2.6	2
45	IMPROVING THE PERFORMANCE OF PROTEIN THREADING USING INSERTION/DELETION FREQUENCY ARRAYS. Journal of Bioinformatics and Computational Biology, 2008, 06, 585-602.	0.8	1
46	Abstract A39: The UCSC Cancer Genomics Browser. , 2011, , .		0
47	Abstract 2985: Predicting the impact of mutations in cancer using an integrated pathway approach. , 2012, , .		0
48	Abstract 5087: UCSC Cancer Genomics Browser 2.0. , 2012, , .		0
49	Abstract PR02: Multiple Pathway Learning accurately predicts gene essentiality in the Cancer Cell Line Encyclopedia. , 2015, , .		0
50	Abstract A2-64: A signature catalog to classify tumor mixtures: Application to recognition of metastatic disease in prostate cancer. , 2015, , .		0
51	Abstract PR10: Multiple Pathway Learning accurately predicts gene essentiality in the Cancer Cell Line Encyclopedia. , 2015, , .		0
52	Abstract B1-37: A signature catalog to classify tumor mixtures: application to recognition of metastatic disease in prostate cancer. , 2015, , .		0
53	A generalized threading model using integer programming that allows for secondary structure element deletion. Genome Informatics, 2006, 17, 248-58.	0.4	0