

Charles H Langley

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

3,381
citations

236925

25
h-index

377865

34
g-index

38
all docs

38
docs citations

38
times ranked

3712
citing authors

#	ARTICLE	IF	CITATIONS
1	Complete genomic and epigenetic maps of human centromeres. <i>Science</i> , 2022, 376, eabl4178.	12.6	204
2	SNPs in a Large Genomic Scaffold Are Strongly Associated with <i>Cr1R</i> , Major Gene for Resistance to White Pine Blister Rust in Range-Wide Samples of Sugar Pine (<i>Pinus</i>). <i>Tj ETQq0 0 0 rgBT /Overlap 10 Tf 50 697 Td</i> (
3	Dissecting the Polygenic Basis of Cold Adaptation Using Genome-Wide Association of Traits and Environmental Data in Douglas-fir. <i>Genes</i> , 2021, 12, 110.	2.4	14
4	Comparative genomics of six <i>Juglans</i> species reveals disease-associated gene family contractions. <i>Plant Journal</i> , 2020, 102, 410-423.	5.7	25
5	Genomic basis of white pine blister rust quantitative disease resistance and its relationship with qualitative resistance. <i>Plant Journal</i> , 2020, 104, 365-376.	5.7	32
6	Development of a highly efficient Axiom [®] 70 K SNP array for <i>Pyrus</i> and evaluation for high-density mapping and germplasm characterization. <i>BMC Genomics</i> , 2019, 20, 331.	2.8	40
7	Genomic architecture of complex traits in loblolly pine. <i>New Phytologist</i> , 2019, 221, 1789-1801.	7.3	60
8	A new genomic tool for walnut (<i>Juglans regia</i> L.): development and validation of the high-density Axiom [®] J. <i>Regia</i> 700K SNP genotyping array. <i>Plant Biotechnology Journal</i> , 2019, 17, 1027-1036.	8.3	79
9	Haplotypes spanning centromeric regions reveal persistence of large blocks of archaic DNA. <i>ELife</i> , 2019, 8, .	6.0	54
10	Genomic Variation Among and Within Six <i>Juglans</i> Species. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2153-2165.	1.8	73
11	From Pine Cones to Read Clouds: Rescaffolding the Megagenome of Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1563-1568.	1.8	19
12	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3157-3167.	1.8	103
13	An improved assembly of the loblolly pine mega-genome using long-read single-molecule sequencing. <i>GigaScience</i> , 2017, 6, 1-4.	6.4	71
14	Assessing the Gene Content of the Megagenome: Sugar Pine (<i>Pinus lambertiana</i>). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3787-3802.	1.8	51
15	First Draft Assembly and Annotation of the Genome of a California Endemic Oak <i>Quercus lobata</i> (Fagaceae). <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 3485-3495.	1.8	95
16	Hubby and Lewontin on Protein Variation in Natural Populations: When Molecular Genetics Came to the Rescue of Population Genetics. <i>Genetics</i> , 2016, 203, 1497-1503.	2.9	12
17	Sequence of the Sugar Pine Megagenome. <i>Genetics</i> , 2016, 204, 1613-1626.	2.9	169
18	The walnut (<i>Juglans regia</i>) genome sequence reveals diversity in genes coding for the biosynthesis of non-structural polyphenols. <i>Plant Journal</i> , 2016, 87, 507-532.	5.7	233

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19	The <i>Drosophila</i> Genome Nexus: A Population Genomic Resource of 623 <i>Drosophila melanogaster</i> Genomes, Including 197 from a Single Ancestral Range Population. <i>Genetics</i> , 2015, 199, 1229-1241.	2.9	273
20	Nucleosomes Shape DNA Polymorphism and Divergence. <i>PLoS Genetics</i> , 2014, 10, e1004457.	3.5	38
21	Decoding the massive genome of loblolly pine using haploid DNA and novel assembly strategies. <i>Genome Biology</i> , 2014, 15, R59.	9.6	424
22	Combination of multipoint maximum likelihood (MML) and regression mapping algorithms to construct a high-density genetic linkage map for loblolly pine (<i>Pinus taeda</i> L.). <i>Tree Genetics and Genomes</i> , 2013, 9, 1529-1535.	1.6	23
23	Genomic Variation in Natural Populations of <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2012, 192, 533-598.	2.9	325
24	Circumventing Heterozygosity: Sequencing the Amplified Genome of a Single Haploid <i>Drosophila melanogaster</i> Embryo. <i>Genetics</i> , 2011, 188, 239-246.	2.9	51
25	Algorithms to Distinguish the Role of Gene-Conversion from Single-Crossover Recombination in the Derivation of SNP Sequences in Populations. <i>Journal of Computational Biology</i> , 2007, 14, 1273-1286.	1.6	14
26	Both Naturally Occurring Insertions of Transposable Elements and Intermediate Frequency Polymorphisms at the achaete-scute Complex Are Associated With Variation in Bristle Number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 2000, 154, 1255-1269.	2.9	99
27	Linkage Disequilibria and the Site Frequency Spectra in the <i>su(s)</i> and <i>su(wa)</i> Regions of the <i>Drosophila melanogaster</i> X Chromosome. <i>Genetics</i> , 2000, 156, 1837-1852.	2.9	137
28	Genetic Variation in Rates of Nondisjunction: Association of Two Naturally Occurring Polymorphisms in the Chromokinesin nod With Increased Rates of Nondisjunction in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1999, 152, 1605-1614.	2.9	93
29	Classic Weinstein: Tetrad Analysis, Genetic Variation and Achiasmate Segregation in <i>Drosophila</i> and Humans. <i>Genetics</i> , 1999, 152, 1615-1629.	2.9	21
30	quemao, a <i>Drosophila</i> Bristle Locus, Encodes Geranylgeranyl Pyrophosphate Synthase. <i>Genetics</i> , 1998, 149, 1051-1061.	2.9	37
31	Two Sites in the Delta Gene Region Contribute to Naturally Occurring Variation in Bristle Number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1998, 149, 999-1017.	2.9	189
32	DNA Polymorphism in <i>Lycopersicon</i> and Crossing-Over per Physical Length. <i>Genetics</i> , 1998, 150, 1585-1593.	2.9	151
33	Endogenous proviruses as "elementos". <i>Nature</i> , 1997, 388, 840-840.	27.8	5
34	Genetic Interactions Between Naturally Occurring Alleles at Quantitative Trait Loci and Mutant Alleles at Candidate Loci Affecting Bristle Number in <i>Drosophila melanogaster</i> . <i>Genetics</i> , 1996, 144, 1497-1510.	2.9	145
35	Restriction map polymorphism in the forked and vermilion regions of <i>Drosophila melanogaster</i> . <i>Japanese Journal of Genetics</i> , 1994, 69, 297-305.	1.0	6