

# Gerard R Lazo

## List of Publications by Year in descending order

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68  
papers

8,141  
citations

61984

43  
h-index

102487

66  
g-index

68  
all docs

68  
docs citations

68  
times ranked

8361  
citing authors

#	ARTICLE	IF	CITATIONS
1	GrainGenes: a data-rich repository for small grains genetics and genomics. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	22
2	OUP accepted manuscript. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	50
3	Gene Space and Transcriptome Assemblies of Leafy Spurge ( <i>Euphorbia esula</i> ) Identify Promoter Sequences, Repetitive Elements, High-Quality Markers, and a Full-Length Chloroplast Genome. Weed Science, 2018, 66, 355-367.	1.5	11
4	AgBioData consortium recommendations for sustainable genomics and genetics databases for agriculture. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	52
5	The art of curation at a biological database: Principles and application. Current Plant Biology, 2017, 11-12, 2-11.	4.7	30
6	A whole-genome, radiation hybrid mapping resource of hexaploid wheat. Plant Journal, 2016, 86, 195-207.	5.7	23
7	Radiation hybrid maps of the D-genome of <i>Aegilops tauschii</i> and their application in sequence assembly of large and complex plant genomes. BMC Genomics, 2015, 16, 800.	2.8	31
8	Development of a D genome specific marker resource for diploid and hexaploid wheat. BMC Genomics, 2015, 16, 646.	2.8	6
9	Comparative Systems Biology Reveals Allelic Variation Modulating Tocochromanol Profiles in Barley ( <i>Hordeum vulgare</i> L.). PLoS ONE, 2014, 9, e96276.	2.5	10
10	De Novo Transcriptome Assembly and Analyses of Gene Expression during Photomorphogenesis in Diploid Wheat <i>Triticum monococcum</i> . PLoS ONE, 2014, 9, e96855.	2.5	55
11	A SNP Genotyping Array for Hexaploid Oat. Plant Genome, 2014, 7, plantgenome2014.03.0010.	2.8	63
12	Quantitative trait loci of barley malting quality trait components in the Stellar/01Ab8219 mapping population. Molecular Breeding, 2014, 34, 59-73.	2.1	12
13	A new genetic linkage map of barley ( <i>Hordeum vulgare</i> L.) facilitates genetic dissection of height and spike length and angle. Field Crops Research, 2013, 154, 91-99.	5.1	18
14	Farinin: Characterization of a Novel Wheat Endosperm Protein Belonging to the Prolamin Superfamily. Journal of Agricultural and Food Chemistry, 2013, 61, 2407-2417.	5.2	37
15	Wheat Zapper: a flexible online tool for colinearity studies in grass genomes. Functional and Integrative Genomics, 2013, 13, 11-17.	3.5	9
16	SNP Discovery and Chromosome Anchoring Provide the First Physically-Anchored Hexaploid Oat Map and Reveal Synteny with Model Species. PLoS ONE, 2013, 8, e58068.	2.5	73
17	A 4-gigabase physical map unlocks the structure and evolution of the complex genome of <i>Aegilops tauschii</i> , the wheat D-genome progenitor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 7940-7945.	7.1	214
18	PIECE: a database for plant gene structure comparison and evolution. Nucleic Acids Research, 2013, 41, D1159-D1166.	14.5	50

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19	Physical mapping resources for large plant genomes: radiation hybrids for wheat D-genome progenitor <i>Aegilops tauschii</i> . <i>BMC Genomics</i> , 2012, 13, 597.	2.8	33
20	Generation and Characterization of the Western Regional Research Center Brachypodium T-DNA Insertional Mutant Collection. <i>PLoS ONE</i> , 2012, 7, e41916.	2.5	109
21	Transcriptome and gene expression analysis in cold-acclimated guayule ( <i>Parthenium argentatum</i> ) rubber-producing tissue. <i>Phytochemistry</i> , 2012, 79, 57-66.	2.9	40
22	Leymus EST linkage maps identify 4NsL-5NsL reciprocal translocation, wheat-Leymus chromosome introgressions, and functionally important gene loci. <i>Theoretical and Applied Genetics</i> , 2012, 124, 189-206.	3.6	42
23	Comparison of a high-density genetic linkage map to genome features in the model grass <i>Brachypodium distachyon</i> . <i>Theoretical and Applied Genetics</i> , 2011, 123, 455-464.	3.6	70
24	Model SNP development for complex genomes based on hexaploid oat using high-throughput 454 sequencing technology. <i>BMC Genomics</i> , 2011, 12, 77.	2.8	84
25	Nucleotide diversity maps reveal variation in diversity among wheat genomes and chromosomes. <i>BMC Genomics</i> , 2010, 11, 702.	2.8	189
26	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
27	RJPrimers: unique transposable element insertion junction discovery and PCR primer design for marker development. <i>Nucleic Acids Research</i> , 2010, 38, W313-W320.	14.5	34
28	ConservedPrimers 2.0: A high-throughput pipeline for comparative genome referenced intron-flanking PCR primer design and its application in wheat SNP discovery. <i>BMC Bioinformatics</i> , 2009, 10, 331.	2.6	28
29	A BAC-based physical map of <i>Brachypodium distachyon</i> and its comparative analysis with rice and wheat. <i>BMC Genomics</i> , 2009, 10, 496.	2.8	42
30	The wheat $\gamma$ -gliadin genes: structure and EST analysis. <i>Functional and Integrative Genomics</i> , 2009, 9, 397-410.	3.5	50
31	Structural characterization of <i>Brachypodium</i> genome and its syntenic relationship with rice and wheat. <i>Plant Molecular Biology</i> , 2009, 70, 47-61.	3.9	71
32	Genome comparisons reveal a dominant mechanism of chromosome number reduction in grasses and accelerated genome evolution in Triticeae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15780-15785.	7.1	190
33	Plant and Crop Databases. <i>Methods in Molecular Biology</i> , 2009, 513, 243-262.	0.9	7
34	The nuclear genome of <i>Brachypodium distachyon</i> : analysis of BAC end sequences. <i>Functional and Integrative Genomics</i> , 2008, 8, 135-147.	3.5	83
35	BatchPrimer3: A high throughput web application for PCR and sequencing primer design. <i>BMC Bioinformatics</i> , 2008, 9, 253.	2.6	707
36	The complete chloroplast genome sequence of <i>Brachypodium distachyon</i> : sequence comparison and phylogenetic analysis of eight grass plastomes. <i>BMC Research Notes</i> , 2008, 1, 61.	1.4	65

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37	Comparative Genomics in Switchgrass Using 61,585 High-Quality Expressed Sequence Tags. <i>Plant Genome</i> , 2008, 1, .	2.8	57
38	GenoProfiler: batch processing of high-throughput capillary fingerprinting data. <i>Bioinformatics</i> , 2007, 23, 240-242.	4.1	58
39	Transcriptional profiling of wheat caryopsis development using cDNA microarrays. <i>Plant Molecular Biology</i> , 2007, 63, 651-668.	3.9	82
40	Types and Rates of Sequence Evolution at the High-Molecular-Weight Glutenin Locus in Hexaploid Wheat and Its Ancestral Genomes. <i>Genetics</i> , 2006, 174, 1493-1504.	2.9	83
41	Use of a large-scale Triticeae expressed sequence tag resource to reveal gene expression profiles in hexaploid wheat ( <i>Triticum aestivum</i> L.). <i>Genome</i> , 2006, 49, 531-544.	2.0	26
42	Construction and characterization of two BAC libraries from <i>Brachypodium distachyon</i> , a new model for grass genomics. <i>Genome</i> , 2006, 49, 1099-1108.	2.0	64
43	Analysis of the wheat endosperm transcriptome. <i>Journal of Applied Genetics</i> , 2006, 47, 287-302.	1.9	30
44	EST sequencing and phylogenetic analysis of the model grass <i>Brachypodium distachyon</i> . <i>Theoretical and Applied Genetics</i> , 2006, 113, 186-195.	3.6	117
45	Analysis of expressed sequence tags and the identification of associated short tandem repeats in switchgrass. <i>Theoretical and Applied Genetics</i> , 2005, 111, 956-964.	3.6	50
46	Hybsweeper: a resource for detecting high-density plate gridding coordinates. <i>BioTechniques</i> , 2005, 39, 320-324.	1.8	10
47	GrainGenes 2.0. An Improved Resource for the Small-Grains Community. <i>Plant Physiology</i> , 2005, 139, 643-651.	4.8	74
48	Charting Contig-Component Relationships within the Triticeae. , 2005, , 109-120.		0
49	Analysis of Expressed Sequence Tag Loci on Wheat Chromosome Group 4. <i>Genetics</i> , 2004, 168, 651-663.	2.9	90
50	Chromosome Bin Map of Expressed Sequence Tags in Homoeologous Group 1 of Hexaploid Wheat and Homoeology With Rice and Arabidopsis. <i>Genetics</i> , 2004, 168, 609-623.	2.9	78
51	A Chromosome Bin Map of 2148 Expressed Sequence Tag Loci of Wheat Homoeologous Group 7. <i>Genetics</i> , 2004, 168, 687-699.	2.9	68
52	Construction and Evaluation of cDNA Libraries for Large-Scale Expressed Sequence Tag Sequencing in Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 595-608.	2.9	57
53	Deletion Mapping of Homoeologous Group 6-Specific Wheat Expressed Sequence Tags. <i>Genetics</i> , 2004, 168, 677-686.	2.9	43
54	A 2500-Locus Bin Map of Wheat Homoeologous Group 5 Provides Insights on Gene Distribution and Colinearity With Rice. <i>Genetics</i> , 2004, 168, 665-676.	2.9	67

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55	Group 3 Chromosome Bin Maps of Wheat and Their Relationship to Rice Chromosome 1. <i>Genetics</i> , 2004, 168, 639-650.	2.9	81
56	A Chromosome Bin Map of 16,000 Expressed Sequence Tag Loci and Distribution of Genes Among the Three Genomes of Polyploid Wheat. <i>Genetics</i> , 2004, 168, 701-712.	2.9	369
57	Development of an Expressed Sequence Tag (EST) Resource for Wheat ( <i>Triticum aestivum</i> L.). <i>Genetics</i> , 2004, 168, 585-593.	2.9	87
58	A 2600-Locus Chromosome Bin Map of Wheat Homoeologous Group 2 Reveals Interstitial Gene-Rich Islands and Colinearity With Rice. <i>Genetics</i> , 2004, 168, 625-637.	2.9	78
59	Bioinformatics and Triticeae Genomics: Resources and Future Developments. , 2004, , 425-446.		1
60	GrainGenes, the genome database for small-grain crops. <i>Nucleic Acids Research</i> , 2003, 31, 183-186.	14.5	87
61	The Organization and Rate of Evolution of Wheat Genomes Are Correlated With Recombination Rates Along Chromosome Arms. <i>Genome Research</i> , 2003, 13, 753-763.	5.5	298
62	Structural organization of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes. <i>Genome</i> , 2003, 46, 1084-1097.	2.0	61
63	Synteny perturbations between wheat homoeologous chromosomes caused by locus duplications and deletions correlate with recombination rates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10836-10841.	7.1	159
64	Comparative DNA Sequence Analysis of Wheat and Rice Genomes. <i>Genome Research</i> , 2003, 13, 1818-1827.	5.5	369
65	Frequencies of Ty1-copia and Ty3-gypsy retroelements within the Triticeae EST databases. <i>Theoretical and Applied Genetics</i> , 2002, 104, 840-844.	3.6	45
66	Molecular mapping and characterization of traits controlling fiber quality in cotton. <i>Euphytica</i> , 2001, 121, 163-172.	1.2	168
67	A DNA Transformationâ€“Competent <i>Arabidopsis</i> Genomic Library in <i>Agrobacterium</i> . <i>Bio/technology</i> , 1991, 9, 963-967.	1.5	918
68	Conservation of Plasmid DNA Sequences and Pathovar Identification of Strains of <i>Xanthomonas campestris</i> . <i>Phytopathology</i> , 1987, 77, 448.	2.2	71