

# Alan H Schulman

## List of Publications by Year in descending order

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130  
papers

16,391  
citations

31976

53  
h-index

17105

122  
g-index

139  
all docs

139  
docs citations

139  
times ranked

14502  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic regions associated with chocolate spot ( <i>Botrytis fabae</i> Sard.) resistance in faba bean ( <i>Vicia</i> ) Tj ETQq1 1 0.784314 rgBT /Ove	2.1	8
2	Transposon-Based Tagging In Silico Using FastPCR Software. <i>Methods in Molecular Biology</i> , 2021, 2250, 245-256.	0.9	4
3	Recent advances in faba bean genetic and genomic tools for crop improvement. , 2021, 3, e75.		38
4	Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. <i>Nature Genetics</i> , 2021, 53, 564-573.	21.4	138
5	Palindromic Sequence-Targeted (PST) PCR, Version 2: An Advanced Method for High-Throughput Targeted Gene Characterization and Transposon Display. <i>Frontiers in Plant Science</i> , 2021, 12, 691940.	3.6	11
6	VC1 catalyses a key step in the biosynthesis of vicine in faba bean. <i>Nature Plants</i> , 2021, 7, 923-931.	9.3	34
7	European Court of Justice delivers no justice to Europe on genome-edited crops. <i>Plant Biotechnology Journal</i> , 2020, 18, 8-10.	8.3	31
8	Why do crop models diverge substantially in climate impact projections? A comprehensive analysis based on eight barley crop models. <i>Agricultural and Forest Meteorology</i> , 2020, 281, 107851.	4.8	35
9	Immunochemical analysis of oat avenins in an oat cultivar and landrace collection. <i>Journal of Cereal Science</i> , 2020, 95, 103053.	3.7	11
10	High-throughput retrotransposon-based genetic diversity of maize germplasm assessment and analysis. <i>Molecular Biology Reports</i> , 2020, 47, 1589-1603.	2.3	16
11	The impact of GM crops on agriculture. , 2020, , 195-213.		5
12	Long Tandem Arrays of Cassandra Retroelements and Their Role in Genome Dynamics in Plants. <i>International Journal of Molecular Sciences</i> , 2020, 21, 2931.	4.1	27
13	Eliminating vicine and convicine, the main anti-nutritional factors restricting faba bean usage. <i>Trends in Food Science and Technology</i> , 2019, 91, 549-556.	15.1	84
14	Genome Sequence of <i>Striga asiatica</i> Provides Insight into the Evolution of Plant Parasitism. <i>Current Biology</i> , 2019, 29, 3041-3052.e4.	3.9	109
15	The genome of cowpea ( <i>Vigna unguiculata</i> [L.] Walp.). <i>Plant Journal</i> , 2019, 98, 767-782.	5.7	264
16	Microsatellite Diversity, Complexity, and Host Range of Mycobacteriophage Genomes of the Siphoviridae Family. <i>Frontiers in Genetics</i> , 2019, 10, 207.	2.3	17
17	Palindromic sequence-targeted (PST) PCR: a rapid and efficient method for high-throughput gene characterization and genome walking. <i>Scientific Reports</i> , 2019, 9, 17707.	3.3	21
18	TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. <i>Genome Biology</i> , 2019, 20, 284.	8.8	179

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19	Contribution of crop model structure, parameters and climate projections to uncertainty in climate change impact assessments. <i>Global Change Biology</i> , 2018, 24, 1291-1307.	9.5	149
20	Cloning of the wheat Yr15 resistance gene sheds light on the plant tandem kinase-pseudokinase family. <i>Nature Communications</i> , 2018, 9, 3735.	12.8	204
21	Retrotransposon-Based Genetic Diversity Assessment in Wild Emmer Wheat ( <i>Triticum turgidum</i> ssp.) Tj ETQq1 1 0.784314 rgBT /Ove	3.0	23
22	The Repetitive Landscape of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 123-138.	0.5	6
23	The pseudogenes of barley. <i>Plant Journal</i> , 2018, 93, 502-514.	5.7	14
24	Copy-number variation of housekeeping gene rpl13a in rat strains selected for nervous system excitability. <i>Molecular and Cellular Probes</i> , 2017, 33, 11-15.	2.1	5
25	Gene Deletion in Barley Mediated by LTR-retrotransposon BARE. <i>Scientific Reports</i> , 2017, 7, 43766.	3.3	13
26	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. <i>Nature Genetics</i> , 2017, 49, 904-912.	21.4	221
27	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	27.8	1,365
28	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	5.3	130
29	Designing future barley ideotypes using a crop model ensemble. <i>European Journal of Agronomy</i> , 2017, 82, 144-162.	4.1	84
30	The repetitive landscape of the 5100 Mbp barley genome. <i>Mobile DNA</i> , 2017, 8, 22.	3.6	49
31	Assessment of genetic diversity in Nordic timothy ( <i>Phleum pratense</i> L.). <i>Hereditas</i> , 2016, 153, 5.	1.4	6
32	Genetics and Genomics of <i>Brachypodium</i> . <i>Plant Genetics and Genomics: Crops and Models</i> , 2016, , .	0.3	22
33	Evaluation of marker-assisted selection for the stripe rust resistance gene Yr15, introgressed from wild emmer wheat. <i>Molecular Breeding</i> , 2015, 35, 1.	2.1	74
34	Genome Size and the Role of Transposable Elements. <i>Plant Genetics and Genomics: Crops and Models</i> , 2015, , 81-106.	0.3	3
35	Retrotransposon molecular markers resolve cocoyam ( <i>Xanthosoma sagittifolium</i> ) and taro ( <i>Colocasia esculenta</i> ) by type and variety. <i>Euphytica</i> , 2015, 206, 541-554.	1.2	25
36	Development of IRAP- and REMAP-derived SCAR markers for marker-assisted selection of the stripe rust resistance gene Yr15 derived from wild emmer wheat. <i>Theoretical and Applied Genetics</i> , 2015, 128, 211-219.	3.6	35

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37	Analysis of CACTA transposases reveals intron loss as major factor influencing their exon/intron structure in monocotyledonous and eudicotyledonous hosts. <i>Mobile DNA</i> , 2014, 5, 24.	3.6	10
38	The <i>Glanville</i> fritillary genome retains an ancient karyotype and reveals selective chromosomal fusions in Lepidoptera. <i>Nature Communications</i> , 2014, 5, 4737.	12.8	196
39	FastPCR Software for PCR, In Silico PCR, and Oligonucleotide Assembly and Analysis. <i>Methods in Molecular Biology</i> , 2014, 1116, 271-302.	0.9	73
40	The <i>Tyv1</i> retrotransposon family is conserved between plant genomes separated by over 100 million years. <i>Theoretical and Applied Genetics</i> , 2014, 127, 1223-1235.	3.6	21
41	Transposon-Based Tagging: IRAP, REMAP, and iPBS. <i>Methods in Molecular Biology</i> , 2014, 1115, 233-255.	0.9	52
42	Retrotransposon replication in plants. <i>Current Opinion in Virology</i> , 2013, 3, 604-614.	5.4	53
43	Anchoring and ordering <i>NGS</i> contig assemblies by population sequencing ( <i>POPSEQ</i> ). <i>Plant Journal</i> , 2013, 76, 718-727.	5.7	264
44	Retrotransposon <i>BARE</i> displays strong tissue-specific differences in expression. <i>New Phytologist</i> , 2013, 200, 1000-1008.	7.3	16
45	Detection of genetic relationships among spring and winter triticale ( <i>Triticosecale</i> Witt.) and rye cultivars ( <i>Secale cereale</i> L.) by using retrotransposon-based markers. <i>Czech Journal of Genetics and Plant Breeding</i> , 2013, 49, 171-174.	0.8	8
46	Structural and Temporal Variation in Genetic Diversity of European Spring Two-Row Barley Cultivars and Association Mapping of Quantitative Traits. <i>Plant Genome</i> , 2013, 6, plantgenome2013.03.0007.	2.8	95
47	<i>BARE</i> Retrotransposons Are Translated and Replicated via Distinct RNA Pools. <i>PLoS ONE</i> , 2013, 8, e72270.	2.5	25
48	Integrating cereal genomics to support innovation in the Triticeae. <i>Functional and Integrative Genomics</i> , 2012, 12, 573-583.	3.5	39
49	A physical, genetic and functional sequence assembly of the barley genome. <i>Nature</i> , 2012, 491, 711-716.	27.8	1,416
50	Hitching a Ride: Nonautonomous Retrotransposons and Parasitism as a Lifestyle. <i>Topics in Current Genetics</i> , 2012, , 71-88.	0.7	10
51	Differential effects of mild chronic stress on cortisol and S-IgA responses to an acute stressor. <i>Biological Psychology</i> , 2012, 91, 307-311.	2.2	27
52	The Application of LTR Retrotransposons as Molecular Markers in Plants. <i>Methods in Molecular Biology</i> , 2012, 859, 115-153.	0.9	58
53	Ancient diversity of splicing motifs and protein surfaces in the wild emmer wheat ( <i>Triticum</i> ) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Pathology, 2012, 13, 276-287.	4.2	45
54	Java web tools for PCR, in silico PCR, and oligonucleotide assembly and analysis. <i>Genomics</i> , 2011, 98, 137-144.	2.9	146

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55	Analysis of plant diversity with retrotransposon-based molecular markers. <i>Heredity</i> , 2011, 106, 520-530.	2.6	213
56	Rapid linkage disequilibrium decay in the Lr10 gene in wild emmer wheat ( <i>Triticum dicoccoides</i> ) populations. <i>Theoretical and Applied Genetics</i> , 2011, 122, 175-187.	3.6	17
57	Genetic diversity of cultivated flax ( <i>Linum usitatissimum</i> L.) germplasm assessed by retrotransposon-based markers. <i>Theoretical and Applied Genetics</i> , 2011, 122, 1385-1397.	3.6	127
58	A doubled haploid rye linkage map with a QTL affecting $\alpha$ -amylase activity. <i>Journal of Applied Genetics</i> , 2011, 52, 299-304.	1.9	12
59	iPBS: a universal method for DNA fingerprinting and retrotransposon isolation. <i>Theoretical and Applied Genetics</i> , 2010, 121, 1419-1430.	3.6	223
60	Transposable elements in a marginal plant population: temporal fluctuations provide new insights into genome evolution of wild diploid wheat. <i>Mobile DNA</i> , 2010, 1, 6.	3.6	85
61	Genome sequencing and analysis of the model grass <i>Brachypodium distachyon</i> . <i>Nature</i> , 2010, 463, 763-768.	27.8	1,685
62	The International Barley Sequencing Consortium "At the Threshold of Efficient Access to the Barley Genome". <i>Plant Physiology</i> , 2009, 149, 142-147.	4.8	195
63	Copia and Gypsy retrotransposons activity in sunflower ( <i>Helianthus annuus</i> L.). <i>BMC Plant Biology</i> , 2009, 9, 150.	3.6	38
64	Genetic variability in sunflower ( <i>Helianthus annuus</i> L.) and in the <i>Helianthus</i> genus as assessed by retrotransposon-based molecular markers. <i>Theoretical and Applied Genetics</i> , 2009, 119, 1027-1038.	3.6	66
65	Reply: A unified classification system for eukaryotic transposable elements should reflect their phylogeny. <i>Nature Reviews Genetics</i> , 2009, 10, 276-276.	16.3	41
66	Genomics of Transposable Elements in the Triticeae. , 2009, , 387-405.		4
67	Reme1, a Copia retrotransposon in melon, is transcriptionally induced by UV light. <i>Plant Molecular Biology</i> , 2008, 66, 137-150.	3.9	56
68	A universal classification of eukaryotic transposable elements implemented in Repbase. <i>Nature Reviews Genetics</i> , 2008, 9, 414-414.	16.3	5
69	<i>BARE</i> retrotransposons produce multiple groups of rarely polyadenylated transcripts from two differentially regulated promoters. <i>Plant Journal</i> , 2008, 56, 40-50.	5.7	22
70	<i>Cassandra</i> retrotransposons carry independently transcribed 5S RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5833-5838.	7.1	127
71	The first doubled haploid linkage map for cultivated oat. <i>Genome</i> , 2008, 51, 560-569.	2.0	33
72	Life without GAG: The BARE-2 retrotransposon as a parasite's parasite. <i>Gene</i> , 2007, 390, 166-174.	2.2	48

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73	A major gene for grain cadmium accumulation in oat ( <i>Avena sativa</i> L.). <i>Genome</i> , 2007, 50, 588-594.	2.0	60
74	A unified classification system for eukaryotic transposable elements. <i>Nature Reviews Genetics</i> , 2007, 8, 973-982.	16.3	2,396
75	Template switching can create complex LTR retrotransposon insertions in Triticeae genomes. <i>BMC Genomics</i> , 2007, 8, 247.	2.8	25
76	Molecular markers to assess genetic diversity. <i>Euphytica</i> , 2007, 158, 313-321.	1.2	114
77	Mapping of major spot-type and net-type net-blotch resistance genes in the Ethiopian barley line CI 9819. <i>Genome</i> , 2006, 49, 1564-1571.	2.0	73
78	IRAP and REMAP for retrotransposon-based genotyping and fingerprinting. <i>Nature Protocols</i> , 2006, 1, 2478-2484.	12.0	224
79	Integrase diversity and transcription of the maize retrotransposon Grande. <i>Genome</i> , 2006, 49, 558-562.	2.0	12
80	Generation of SNP markers for short straw in oat ( <i>Avena sativa</i> L.). <i>Genome</i> , 2006, 49, 282-287.	2.0	24
81	Parasitism and the retrotransposon life cycle in plants: a hitchhiker's guide to the genome. <i>Heredity</i> , 2006, 97, 381-388.	2.6	136
82	An atlas of gene expression from seed to seed through barley development. <i>Functional and Integrative Genomics</i> , 2006, 6, 202-211.	3.5	138
83	TRIM retrotransposons occur in apple and are polymorphic between varieties but not sports. <i>Theoretical and Applied Genetics</i> , 2006, 112, 999-1008.	3.6	79
84	Retrotransposons: Metaparasites and Agents of Genome Evolution. <i>Israel Journal of Ecology and Evolution</i> , 2006, 52, 319-330.	0.6	3
85	Variability, Recombination, and Mosaic Evolution of the Barley BARE-1 Retrotransposon. <i>Journal of Molecular Evolution</i> , 2005, 61, 275-291.	1.8	62
86	Genome constitution and classification using retrotransposon-based markers in the orphan crop banana. <i>Journal of Plant Biology</i> , 2005, 48, 96-105.	2.1	77
87	A movable feast: diverse retrotransposons and their contribution to barley genome dynamics. <i>Cytogenetic and Genome Research</i> , 2005, 110, 598-605.	1.1	49
88	The Application of LTR Retrotransposons as Molecular Markers in Plants. , 2004, 260, 145-174.		85
89	Large Retrotransposon Derivatives: Abundant, Conserved but Nonautonomous Retroelements of Barley and Related Genomes. <i>Genetics</i> , 2004, 166, 1437-1450.	2.9	157
90	Organization of Retrotransposons and Microsatellites in Cereal Genomes. , 2004, , 83-118.		6

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91	Comparison of the utility of barley retrotransposon families for genetic analysis by molecular marker techniques. <i>Molecular Genetics and Genomics</i> , 2003, 269, 464-474.	2.1	87
92	Development of new marker methodsâ€”an example from oil palm. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , 2003, 1, 103-113.	0.8	8
93	Retrotransposons and Genomic Stability in Populations of the Young Allopolyploid Species <i>Spartina anglica</i> C.E. Hubbard (Poaceae). <i>Molecular Biology and Evolution</i> , 2002, 19, 1218-1227.	8.9	168
94	A high-density cytogenetic map of the <i>Aegilops tauschii</i> genome incorporating retrotransposons and defense-related genes: insights into cereal chromosome structure and function. <i>Plant Molecular Biology</i> , 2002, 48, 767-789.	3.9	95
95	Mapping of genes affecting linolenic acid content in <i>Brassica rapa</i> ssp. <i>oleifera</i> . <i>Molecular Breeding</i> , 2002, 10, 51-62.	2.1	23
96	Copia-Like Retrotransposons in the Rice Genome: Few and Assorted. <i>Journal of Genome Science and Technology</i> , 2002, 1, 35-47.	0.5	23
97	<i>Envelope</i> -Class Retrovirus-Like Elements Are Widespread, Transcribed and Spliced, and Insertionally Polymorphic in Plants. <i>Genome Research</i> , 2001, 11, 2041-2049.	5.5	86
98	Active Retrotransposons Are a Common Feature of Grass Genomes. <i>Plant Physiology</i> , 2001, 125, 1283-1292.	4.8	188
99	Barley Mutagenesis. <i>Progress in Botany Fortschritte Der Botanik</i> , 2001, , 34-50.	0.3	3
100	Characterisation of Dextrins Solubilised by Î±-Amylase from Barley Starch Granules. <i>Starch/Staerke</i> , 2000, 52, 160-163.	2.1	6
101	Application of BARE-1 retrotransposon markers to the mapping of a major resistance gene for net blotch in barley. <i>Molecular Genetics and Genomics</i> , 2000, 264, 325-334.	2.1	135
102	Genome evolution of wild barley ( <i>Hordeum spontaneum</i> ) by <i>BARE</i> -1 retrotransposon dynamics in response to sharp microclimatic divergence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000, 97, 6603-6607.	7.1	553
103	A Contiguous 66-kb Barley DNA Sequence Provides Evidence for Reversible Genome Expansion. <i>Genome Research</i> , 2000, 10, 908-915.	5.5	285
104	Grain filling and starch synthesis in barley. <i>Developments in Crop Science</i> , 2000, 26, 147-167.	0.1	3
105	Structure, functionality, and evolution of the BARE-1 retrotransposon of barley. , 2000, , 53-63.		0
106	Retrotransposon BARE-1 and Its Role in Genome Evolution in the Genus <i>Hordeum</i> . <i>Plant Cell</i> , 1999, 11, 1769.	6.6	4
107	Retrotransposon <i>BARE-1</i> and Its Role in Genome Evolution in the Genus <i>Hordeum</i> . <i>Plant Cell</i> , 1999, 11, 1769-1784.	6.6	333
108	Retrotransposon BARE-1: expression of encoded proteins and formation of virus-like particles in barley cells. <i>Plant Journal</i> , 1999, 20, 413-422.	5.7	55

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109	Structure, functionality, and evolution of the BARE-1 retrotransposon of barley. <i>Genetica</i> , 1999, 107, 53-63.	1.1	43
110	Phylogeny and transpositional activity of Ty1-copia group retrotransposons in cereal genomes. <i>Molecular Genetics and Genomics</i> , 1999, 261, 883-891.	2.4	86
111	IRAP and REMAP: two new retrotransposon-based DNA fingerprinting techniques. <i>Theoretical and Applied Genetics</i> , 1999, 98, 704-711.	3.6	468
112	Plant cells sell plants. <i>Trends in Biotechnology</i> , 1998, 16, 1-2.	9.3	0
113	Gypsy-like retrotransposons are widespread in the plant kingdom. <i>Plant Journal</i> , 1998, 13, 699-705.	5.7	166
114	The effect of growth temperature on gelatinization properties of barley starch. <i>Acta Agriculturae Scandinavica - Section B Soil and Plant Science</i> , 1998, 48, 85-90.	0.6	12
115	The core domain of retrotransposon integrase in <i>Hordeum</i> : predicted structure and evolution. <i>Molecular Biology and Evolution</i> , 1998, 15, 1135-1144.	8.9	25
116	HEAT-INDUCED STRUCTURAL CHANGES OF SMALL AND LARGE BARLEY STARCH GRANULES. <i>Journal of the Institute of Brewing</i> , 1998, 104, 343-349.	2.3	36
117	Bare-1 insertion site preferences and evolutionary conservation of RNA and cDNA processing sites. <i>Genetica</i> , 1997, 100, 219-230.	1.1	44
118	BARE-1 insertion site preferences and evolutionary conservation of RNA and cDNA processing sites. <i>Contemporary Issues in Genetics and Evolution</i> , 1997, , 219-230.	0.9	25
119	The genome sizes of <i>Hordeum</i> species show considerable variation. <i>Genome</i> , 1996, 39, 730-735.	2.0	26
120	Retrotransposon BARE-1 is a major, dispersed component of the barley ( <i>Hordeum vulgare</i> L.) genome. <i>Plant Molecular Biology</i> , 1996, 30, 1321-1329.	3.9	128
121	The BARE-1 retrotransposon is transcribed in barley from an LTR promoter active in transient assays. <i>Plant Molecular Biology</i> , 1996, 31, 295-306.	3.9	121
122	Structural analysis of starch from normal and shx (shrunken endosperm) barley ( <i>Hordeum vulgare</i> ) Tj ETQq0 0 0 rgBTj/Overlock 10 Tf 50	2.3	36
123	Metabolism of starch synthesis in developing grains of the shx shrunken mutant of barley ( <i>Hordeum</i> ) Tj ETQq1 1 0.784314 rgBTj/Overlo	5.2	15
124	The Effect of the Shrunken Endosperm Mutation shx on Starch Granule Development in Barley Seeds. <i>Journal of Cereal Science</i> , 1994, 19, 49-55.	3.7	13
125	BARE-1, a copia-like retroelement in barley ( <i>Hordeum vulgare</i> L.). <i>Plant Molecular Biology</i> , 1993, 22, 829-846.	3.9	197
126	An analysis of soluble starch synthase isozymes from the developing grains of normal and shx cv. Bomi barley ( <i>Hordeum vulgare</i> ). <i>Physiologia Plantarum</i> , 1993, 89, 835-841.	5.2	14



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127	Swelling and Gelatinization of Cereal Starches. V. RisÃ, Mutants of Bomi and Carlsberg II Barley Cultivars. <i>Journal of Cereal Science</i> , 1993, 17, 1-9.	3.7	60
128	An analysis of soluble starch synthase isozymes from the developing grains of normal and shx cv. Bomi barley ( <i>Hordeum vulgare</i> ). <i>Physiologia Plantarum</i> , 1993, 89, 835-841.	5.2	9
129	Purification of Barley Starch by Protein Extraction. <i>Starch/Staerke</i> , 1991, 43, 387-389.	2.1	11
130	A novel shrunken endosperm mutant of barley. <i>Physiologia Plantarum</i> , 1990, 78, 583-589.	5.2	18