

# Joseph R Ecker

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/382557/joseph-r-ecker-publications-by-citations.pdf>  
**Version:** 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

|                    |                          |                 |                 |
|--------------------|--------------------------|-----------------|-----------------|
| 299<br>papers      | 77,320<br>citations      | 135<br>h-index  | 277<br>g-index  |
| 335<br>ext. papers | 92,247<br>ext. citations | 19.6<br>avg, IF | 7.57<br>L-index |

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 299 | Genome-wide insertional mutagenesis of <i>Arabidopsis thaliana</i> . <i>Science</i> , <b>2003</b> , 301, 653-7  | 33.3 | 4165      |
| 298 | Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , <b>2015</b> , 518, 317-30   | 50.4 | 3849      |
| 297 | Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , <b>2009</b> , 462, 315-22   | 50.4 | 3401      |
| 296 | Highly integrated single-base resolution maps of the epigenome in <i>Arabidopsis</i> . <i>Cell</i> , <b>2008</b> , 133, 523-36  | 56.2 | 1896      |
| 295 | CTR1, a negative regulator of the ethylene response pathway in <i>Arabidopsis</i> , encodes a member of the raf family of protein kinases. <i>Cell</i> , <b>1993</b> , 72, 427-41 | 56.2 | 1640      |
| 294 | HIV-1 integration in the human genome favors active genes and local hotspots. <i>Cell</i> , <b>2002</b> , 110, 521-9  | 56.2 | 1376      |
| 293 | Genome-wide high-resolution mapping and functional analysis of DNA methylation in <i>Arabidopsis</i> . <i>Cell</i> , <b>2006</b> , 126, 1189-201                                  | 56.2 | 1366      |
| 292 | The NIH Roadmap Epigenomics Mapping Consortium. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1045-8  | 44.5 | 1284      |
| 291 | Global epigenomic reconfiguration during mammalian brain development. <i>Science</i> , <b>2013</b> , 341, 1237905   | 33.3 | 1283      |
| 290 | Genome-wide association study of 107 phenotypes in <i>Arabidopsis thaliana</i> inbred lines. <i>Nature</i> , <b>2010</b> , 465, 627-31  | 50.4 | 1257      |
| 289 | Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , <b>2011</b> , 471, 68-73   | 50.4 | 1241      |
| 288 | Ethylene biosynthesis and signaling networks. <i>Plant Cell</i> , <b>2002</b> , 14 Suppl, S131-51   | 11.6 | 1237      |
| 287 | Phased diploid genome assembly with single-molecule real-time sequencing. <i>Nature Methods</i> , <b>2016</b> , 13, 1050-1054   | 21.6 | 1015      |
| 286 | Assignment of 30 microsatellite loci to the linkage map of <i>Arabidopsis</i> . <i>Genomics</i> , <b>1994</b> , 19, 137-44  | 4.3  | 1011      |
| 285 | EIN2, a bifunctional transducer of ethylene and stress responses in <i>Arabidopsis</i> . <i>Science</i> , <b>1999</b> , 284, 2148-53  | 33.3 | 1010      |
| 284 | Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , <b>2015</b> , 518, 331-6  | 50.4 | 988       |
| 283 | Mitogen-activated protein kinase cascades in plants: a new nomenclature. <i>Trends in Plant Science</i> , <b>2002</b> , 7, 301-8  | 13.1 | 891       |

|     |  |      |     |
|-----|--|------|-----|
| 282 | Determination and inference of eukaryotic transcription factor sequence specificity. <i>Cell</i> , <b>2014</b> , 158, 1431-1443  | 56.2 | 866 |
| 281 | Empirical analysis of transcriptional activity in the Arabidopsis genome. <i>Science</i> , <b>2003</b> , 302, 842-6  | 33.3 | 782 |
| 280 | Activation of the ethylene gas response pathway in Arabidopsis by the nuclear protein ETHYLENE-INSENSITIVE3 and related proteins. <i>Cell</i> , <b>1997</b> , 89, 1133-44  | 56.2 | 776 |
| 279 | Genome-wide analysis of cAMP-response element binding protein occupancy, phosphorylation, and target gene activation in human tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 4459-64 | 11.5 | 756 |
| 278 | Arabidopsis RIN4 is a target of the type III virulence effector AvrRpt2 and modulates RPS2-mediated resistance. <i>Cell</i> , <b>2003</b> , 112, 379-89  | 56.2 | 731 |
| 277 | The ethylene signaling pathway: new insights. <i>Current Opinion in Plant Biology</i> , <b>2004</b> , 7, 40-9  | 9.9  | 729 |
| 276 | Retroviral DNA integration: ASLV, HIV, and MLV show distinct target site preferences. <i>PLoS Biology</i> , <b>2004</b> , 2, E234  | 9.7  | 706 |
| 275 | Functional genomic analysis of the AUXIN RESPONSE FACTOR gene family members in Arabidopsis thaliana: unique and overlapping functions of ARF7 and ARF19. <i>Plant Cell</i> , <b>2005</b> , 17, 444-63   | 11.6 | 699 |
| 274 | Evidence for network evolution in an Arabidopsis interactome map. <i>Science</i> , <b>2011</b> , 333, 601-7  | 33.3 | 689 |
| 273 | Plant responses to ethylene gas are mediated by SCF(EBF1/EBF2)-dependent proteolysis of EIN3 transcription factor. <i>Cell</i> , <b>2003</b> , 115, 667-77   | 56.2 | 689 |
| 272 | Genome-wide mapping of 5-hydroxymethylcytosine in embryonic stem cells. <i>Nature</i> , <b>2011</b> , 473, 394-7   | 50.4 | 653 |
| 271 | Widespread dynamic DNA methylation in response to biotic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E2183-91  | 11.5 | 640 |
| 270 | Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> , <b>2010</b> , 6, 479-91   | 18   | 630 |
| 269 | 1,135 Genomes Reveal the Global Pattern of Polymorphism in Arabidopsis thaliana. <i>Cell</i> , <b>2016</b> , 166, 481-491  | 50.1 | 620 |
| 268 | Independently evolved virulence effectors converge onto hubs in a plant immune system network. <i>Science</i> , <b>2011</b> , 333, 596-601   | 33.3 | 601 |
| 267 | Common sequence polymorphisms shaping genetic diversity in Arabidopsis thaliana. <i>Science</i> , <b>2007</b> , 317, 338-42  | 33.3 | 596 |
| 266 | Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1097-105   | 44.5 | 570 |
| 265 | Epigenomic analysis of multilineage differentiation of human embryonic stem cells. <i>Cell</i> , <b>2013</b> , 153, 1134-48  | 50.1 | 550 |

|     |  |      |     |
|-----|--|------|-----|
| 264 | Class III homeodomain-leucine zipper gene family members have overlapping, antagonistic, and distinct roles in Arabidopsis development. <i>Plant Cell</i> , <b>2005</b> , 17, 61-76  | 11.6 | 530 |
| 263 | Cistrome and Epicistrome Features Shape the Regulatory DNA Landscape. <i>Cell</i> , <b>2016</b> , 165, 1280-1292   | 56.2 | 528 |
| 262 | Type-A Arabidopsis response regulators are partially redundant negative regulators of cytokinin signaling. <i>Plant Cell</i> , <b>2004</b> , 16, 658-71  | 11.6 | 503 |
| 261 | Localization of iron in Arabidopsis seed requires the vacuolar membrane transporter VIT1. <i>Science</i> , <b>2006</b> , 314, 1295-8   | 33.3 | 496 |
| 260 | A role for LEDGF/p75 in targeting HIV DNA integration. <i>Nature Medicine</i> , <b>2005</b> , 11, 1287-9   | 50.5 | 489 |
| 259 | Transgenerational epigenetic instability is a source of novel methylation variants. <i>Science</i> , <b>2011</b> , 334, 369-73   | 33.3 | 485 |
| 258 | Chloroplast to nucleus communication triggered by accumulation of Mg-protoporphyrinIX. <i>Nature</i> , <b>2003</b> , 421, 79-83  | 50.4 | 484 |
| 257 | EIN4 and ERS2 are members of the putative ethylene receptor gene family in Arabidopsis. <i>Plant Cell</i> , <b>1998</b> , 10, 1321-32  | 11.6 | 476 |
| 256 | Trp-dependent auxin biosynthesis in Arabidopsis: involvement of cytochrome P450s CYP79B2 and CYP79B3. <i>Genes and Development</i> , <b>2002</b> , 16, 3100-12   | 12.6 | 467 |
| 255 | Auxin response factors ARF6 and ARF8 promote jasmonic acid production and flower maturation. <i>Development (Cambridge)</i> , <b>2005</b> , 132, 4107-18   | 6.6  | 464 |
| 254 | CDPKs CPK6 and CPK3 function in ABA regulation of guard cell S-type anion- and Ca(2+)-permeable channels and stomatal closure. <i>PLoS Biology</i> , <b>2006</b> , 4, e327   | 9.7  | 446 |
| 253 | Human body epigenome maps reveal noncanonical DNA methylation variation. <i>Nature</i> , <b>2015</b> , 523, 212-6  | 50.4 | 442 |
| 252 | ABA-activated SnRK2 protein kinase is required for dehydration stress signaling in Arabidopsis. <i>Plant and Cell Physiology</i> , <b>2002</b> , 43, 1473-83   | 4.9  | 441 |
| 251 | Della proteins and gibberellin-regulated seed germination and floral development in Arabidopsis. <i>Plant Physiology</i> , <b>2004</b> , 135, 1008-19  | 6.6  | 431 |
| 250 | Epigenomic Signatures of Neuronal Diversity in the Mammalian Brain. <i>Neuron</i> , <b>2015</b> , 86, 1369-84  | 13.9 | 430 |
| 249 | The ethylene gas signal transduction pathway: a molecular perspective. <i>Annual Review of Genetics</i> , <b>1998</b> , 32, 227-54   | 14.5 | 423 |
| 248 | CBF2/DREB1C is a negative regulator of CBF1/DREB1B and CBF3/DREB1A expression and plays a central role in stress tolerance in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 3985-90 | 11.5 | 413 |
| 247 | GUN4, a regulator of chlorophyll synthesis and intracellular signaling. <i>Science</i> , <b>2003</b> , 299, 902-6  | 33.3 | 411 |

|     |   |      |     |
|-----|---|------|-----|
| 246 | Patterns of population epigenomic diversity. <i>Nature</i> , <b>2013</b> , 495, 193-8   | 50.4 | 406 |
| 245 | Phototropin-related NPL1 controls chloroplast relocation induced by blue light. <i>Nature</i> , <b>2001</b> , 410, 952-4  | 50.4 | 405 |
| 244 | Involvement of NRAMP1 from <i>Arabidopsis thaliana</i> in iron transport. <i>Biochemical Journal</i> , <b>2000</b> , 347, 749-755   | 3.8  | 405 |
| 243 | Recombination and linkage disequilibrium in <i>Arabidopsis thaliana</i> . <i>Nature Genetics</i> , <b>2007</b> , 39, 1151-5   | 36.3 | 400 |
| 242 | HOOKLESS1, an ethylene response gene, is required for differential cell elongation in the <i>Arabidopsis</i> hypocotyl. <i>Cell</i> , <b>1996</b> , 85, 183-94  | 56.2 | 391 |
| 241 | Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , <b>2012</b> , 22, 246-58  | 9.7  | 385 |
| 240 | Expanded encyclopaedias of DNA elements in the human and mouse genomes. <i>Nature</i> , <b>2020</b> , 583, 699-710  | 10.4 | 360 |
| 239 | Epigenomic Diversity in a Global Collection of <i>Arabidopsis thaliana</i> Accessions. <i>Cell</i> , <b>2016</b> , 166, 492-505   | 56.2 | 353 |
| 238 | RESPONSIVE-TO-ANTAGONIST1, a Menkes/Wilson disease-related copper transporter, is required for ethylene signaling in <i>Arabidopsis</i> . <i>Cell</i> , <b>1999</b> , 97, 383-93  | 56.2 | 351 |
| 237 | Enhanced fitness conferred by naturally occurring variation in the circadian clock. <i>Science</i> , <b>2003</b> , 302, 1049-53   | 33.3 | 347 |
| 236 | Regulation of ethylene gas biosynthesis by the <i>Arabidopsis</i> ETO1 protein. <i>Nature</i> , <b>2004</b> , 428, 945-50   | 50.4 | 341 |
| 235 | Linking photoreceptor excitation to changes in plant architecture. <i>Genes and Development</i> , <b>2012</b> , 26, 785-90  | 12.6 | 334 |
| 234 | Processing and subcellular trafficking of ER-tethered EIN2 control response to ethylene gas. <i>Science</i> , <b>2012</b> , 338, 390-3  | 33.3 | 333 |
| 233 | Ethylene-induced stabilization of ETHYLENE INSENSITIVE3 and EIN3-LIKE1 is mediated by proteasomal degradation of EIN3 binding F-box 1 and 2 that requires EIN2 in <i>Arabidopsis</i> . <i>Plant Cell</i> , <b>2010</b> , 22, 2384-401 | 11.6 | 328 |
| 232 | A link between RNA metabolism and silencing affecting <i>Arabidopsis</i> development. <i>Developmental Cell</i> , <b>2008</b> , 14, 854-66  | 10.2 | 328 |
| 231 | Applications of DNA tiling arrays for whole-genome analysis. <i>Genomics</i> , <b>2005</b> , 85, 1-15   | 4.3  | 325 |
| 230 | LUX ARRHYTHMO encodes a Myb domain protein essential for circadian rhythms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 10387-92                                      | 11.5 | 316 |
| 229 | Multiple type-B response regulators mediate cytokinin signal transduction in <i>Arabidopsis</i> . <i>Plant Cell</i> , <b>2005</b> , 17, 3007-18   | 11.6 | 315 |

|     |  |      |     |
|-----|--|------|-----|
| 228 | Arabidopsis basic helix-loop-helix transcription factors MYC2, MYC3, and MYC4 regulate glucosinolate biosynthesis, insect performance, and feeding behavior. <i>Plant Cell</i> , <b>2013</b> , 25, 3117-32                                       | 11.6 | 313 |
| 227 | The Arabidopsis histidine phosphotransfer proteins are redundant positive regulators of cytokinin signaling. <i>Plant Cell</i> , <b>2006</b> , 18, 3073-87   | 11.6 | 313 |
| 226 | Five components of the ethylene-response pathway identified in a screen for weak ethylene-insensitive mutants in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 2992-7 | 11.5 | 312 |
| 225 | NPH4/ARF7 and ARF19 promote leaf expansion and auxin-induced lateral root formation. <i>Plant Journal</i> , <b>2005</b> , 43, 118-30   | 6.9  | 312 |
| 224 | Cryptochromes Interact Directly with PIFs to Control Plant Growth in Limiting Blue Light. <i>Cell</i> , <b>2016</b> , 164, 233-245   | 56.2 | 295 |
| 223 | Molecular Criteria for Defining the Naive Human Pluripotent State. <i>Cell Stem Cell</i> , <b>2016</b> , 19, 502-515   | 18   | 291 |
| 222 | Single-cell methylomes identify neuronal subtypes and regulatory elements in mammalian cortex. <i>Science</i> , <b>2017</b> , 357, 600-604   | 33.3 | 279 |
| 221 | Retroviral DNA integration: viral and cellular determinants of target-site selection. <i>PLoS Pathogens</i> , <b>2006</b> , 2, e60   | 7.6  | 273 |
| 220 | Finding the fifth base: genome-wide sequencing of cytosine methylation. <i>Genome Research</i> , <b>2009</b> , 19, 959-66  | 9.7  | 271 |
| 219 | The beta-subunit of the Arabidopsis G protein negatively regulates auxin-induced cell division and affects multiple developmental processes. <i>Plant Cell</i> , <b>2003</b> , 15, 393-409   | 11.6 | 269 |
| 218 | Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. <i>ELife</i> , <b>2013</b> , 2, e00675  | 8.9  | 265 |
| 217 | Functional genomic analysis of the AUXIN/INDOLE-3-ACETIC ACID gene family members in Arabidopsis thaliana. <i>Plant Cell</i> , <b>2005</b> , 17, 3282-300  | 11.6 | 265 |
| 216 | The Arabidopsis phytochrome-interacting factor PIF7, together with PIF3 and PIF4, regulates responses to prolonged red light by modulating phyB levels. <i>Plant Cell</i> , <b>2008</b> , 20, 337-52   | 11.6 | 261 |
| 215 | Genome-wide high-resolution mapping of exosome substrates reveals hidden features in the Arabidopsis transcriptome. <i>Cell</i> , <b>2007</b> , 131, 1340-53   | 56.2 | 258 |
| 214 | Abnormalities in human pluripotent cells due to reprogramming mechanisms. <i>Nature</i> , <b>2014</b> , 511, 177-83  | 50.4 | 255 |
| 213 | RF1 knockout allows ribosomal incorporation of unnatural amino acids at multiple sites. <i>Nature Chemical Biology</i> , <b>2011</b> , 7, 779-86   | 11.7 | 255 |
| 212 | Convergence of signaling pathways in the control of differential cell growth in Arabidopsis. <i>Developmental Cell</i> , <b>2004</b> , 7, 193-204  | 10.2 | 253 |
| 211 | Dynamic DNA methylation: In the right place at the right time. <i>Science</i> , <b>2018</b> , 361, 1336-1340   | 33.3 | 246 |

|     |   |      |     |
|-----|---|------|-----|
| 210 | The phytochrome-interacting transcription factor, PIF3, acts early, selectively, and positively in light-induced chloroplast development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 16091-8 | 11.5 | 244 |
| 209 | Convergent targeting of a common host protein-network by pathogen effectors from three kingdoms of life. <i>Cell Host and Microbe</i> , <b>2014</b> , 16, 364-75  | 23.4 | 242 |
| 208 | A transcription factor hierarchy defines an environmental stress response network. <i>Science</i> , <b>2016</b> , 354,  | 33.3 | 241 |
| 207 | Comparison of the transcriptional landscapes between human and mouse tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 17224-9   | 11.5 | 239 |
| 206 | Interplay between ethylene, ETP1/ETP2 F-box proteins, and degradation of EIN2 triggers ethylene responses in Arabidopsis. <i>Genes and Development</i> , <b>2009</b> , 23, 512-21   | 12.6 | 238 |
| 205 | Next is now: new technologies for sequencing of genomes, transcriptomes, and beyond. <i>Current Opinion in Plant Biology</i> , <b>2009</b> , 12, 107-18   | 9.9  | 238 |
| 204 | Literature-curated protein interaction datasets. <i>Nature Methods</i> , <b>2009</b> , 6, 39-46   | 21.6 | 237 |
| 203 | The Arabidopsis heavy metal P-type ATPase HMA5 interacts with metallochaperones and functions in copper detoxification of roots. <i>Plant Journal</i> , <b>2006</b> , 45, 225-36  | 6.9  | 237 |
| 202 | Integration of omic networks in a developmental atlas of maize. <i>Science</i> , <b>2016</b> , 353, 814-8   | 33.3 | 232 |
| 201 | Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements. <i>ELife</i> , <b>2015</b> , 4,  | 8.9  | 208 |
| 200 | A combinatorial interplay among the 1-aminocyclopropane-1-carboxylate isoforms regulates ethylene biosynthesis in Arabidopsis thaliana. <i>Genetics</i> , <b>2009</b> , 183, 979-1003   | 4    | 208 |
| 199 | Cerebral Organoids Recapitulate Epigenomic Signatures of the Human Fetal Brain. <i>Cell Reports</i> , <b>2016</b> , 17, 3369-3384   | 10.6 | 207 |
| 198 | Three redundant brassinosteroid early response genes encode putative bHLH transcription factors required for normal growth. <i>Genetics</i> , <b>2002</b> , 162, 1445-56  | 4    | 202 |
| 197 | Circadian oscillations of protein-coding and regulatory RNAs in a highly dynamic mammalian liver epigenome. <i>Cell Metabolism</i> , <b>2012</b> , 16, 833-45   | 24.6 | 199 |
| 196 | Prepublication data sharing. <i>Nature</i> , <b>2009</b> , 461, 168-70  | 50.4 | 197 |
| 195 | Moving forward in reverse: genetic technologies to enable genome-wide phenomic screens in Arabidopsis. <i>Nature Reviews Genetics</i> , <b>2006</b> , 7, 524-36   | 30.1 | 197 |
| 194 | Genomics: ENCODE explained. <i>Nature</i> , <b>2012</b> , 489, 52-5   | 50.4 | 191 |
| 193 | MethylC-seq library preparation for base-resolution whole-genome bisulfite sequencing. <i>Nature Protocols</i> , <b>2015</b> , 10, 475-83   | 18.8 | 190 |



|     |   |      |     |
|-----|---|------|-----|
| 192 | Epigenome-wide inheritance of cytosine methylation variants in a recombinant inbred population. <i>Genome Research</i> , <b>2013</b> , 23, 1663-74  | 9.7  | 189 |
| 191 | De-etiolated 1 and damaged DNA binding protein 1 interact to regulate Arabidopsis photomorphogenesis. <i>Current Biology</i> , <b>2002</b> , 12, 1462-72  | 6.3  | 188 |
| 190 | An Arabidopsis circadian clock component interacts with both CRY1 and phyB. <i>Nature</i> , <b>2001</b> , 410, 487-90   | 50.4 | 183 |
| 189 | Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana. <i>Nature</i> , <b>2000</b> , 408, 816-20  | 50.4 | 183 |
| 188 | Leveling the playing field for analyses of single-base resolution DNA methylomes. <i>Trends in Genetics</i> , <b>2012</b> , 28, 583-5   | 8.5  | 182 |
| 187 | Forward and reverse genetics through derivation of haploid mouse embryonic stem cells. <i>Cell Stem Cell</i> , <b>2011</b> , 9, 563-74  | 18   | 180 |
| 186 | Direct transcriptional control of the Arabidopsis immune receptor FLS2 by the ethylene-dependent transcription factors EIN3 and EIL1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 14502-7 | 11.5 | 177 |
| 185 | Potential sites of bioactive gibberellin production during reproductive growth in Arabidopsis. <i>Plant Cell</i> , <b>2008</b> , 20, 320-36   | 11.6 | 175 |
| 184 | An alternative pluripotent state confers interspecies chimaeric competency. <i>Nature</i> , <b>2015</b> , 521, 316-21   | 50.4 | 167 |
| 183 | Quantitative trait locus mapping and DNA array hybridization identify an FLM deletion as a cause for natural flowering-time variation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 2460-5 | 11.5 | 167 |
| 182 | High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell. <i>Nature Communications</i> , <b>2018</b> , 9, 541  | 17.4 | 164 |
| 181 | The BRAIN Initiative Cell Census Consortium: Lessons Learned toward Generating a Comprehensive Brain Cell Atlas. <i>Neuron</i> , <b>2017</b> , 96, 542-557  | 13.9 | 159 |
| 180 | Isolation and characterization of phyC mutants in Arabidopsis reveals complex crosstalk between phytochrome signaling pathways. <i>Plant Cell</i> , <b>2003</b> , 15, 1962-80   | 11.6 | 159 |
| 179 | Active DNA demethylation at enhancers during the vertebrate phylotypic period. <i>Nature Genetics</i> , <b>2016</b> , 48, 417-26  | 36.3 | 157 |
| 178 | Genome-wide identification of CCA1 targets uncovers an expanded clock network in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E4802-10  | 11.5 | 156 |
| 177 | Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , <b>2015</b> , 518, 350-354  | 50.4 | 155 |
| 176 | Non-CG Methylation in the Human Genome. <i>Annual Review of Genomics and Human Genetics</i> , <b>2015</b> , 16, 55-77   | 9.7  | 154 |
| 175 | Mobile small RNAs regulate genome-wide DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E801-10   | 11.5 | 153 |



|     |   |      |     |
|-----|---|------|-----|
| 174 | Ethylene signaling: from mutants to molecules. <i>Current Opinion in Plant Biology</i> , <b>2000</b> , 3, 353-60  | 9.9  | 149 |
| 173 | ETHYLENE-INSENSITIVE5 encodes a 5'→3' exoribonuclease required for regulation of the EIN3-targeting F-box proteins EBF1/2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 13286-93 | 11.5 | 148 |
| 172 | GCR1 can act independently of heterotrimeric G-protein in response to brassinosteroids and gibberellins in Arabidopsis seed germination. <i>Plant Physiology</i> , <b>2004</b> , 135, 907-15  | 6.6  | 148 |
| 171 | Mutations in the Ca <sup>2+</sup> /H <sup>+</sup> transporter CAX1 increase CBF/DREB1 expression and the cold-acclimation response in Arabidopsis. <i>Plant Cell</i> , <b>2003</b> , 15, 2940-51  | 11.6 | 148 |
| 170 | Genome-wide patterns of single-feature polymorphism in Arabidopsis thaliana. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 12057-62   | 11.5 | 147 |
| 169 | Arabidopsis homologs of a c-Jun coactivator are present both in monomeric form and in the COP9 complex, and their abundance is differentially affected by the pleiotropic cop/det/fus mutations. <i>Plant Cell</i> , <b>1998</b> , 10, 1779-90  | 11.6 | 144 |
| 168 | Mapping genome-wide transcription-factor binding sites using DAP-seq. <i>Nature Protocols</i> , <b>2017</b> , 12, 1659-1672   | 11.6 | 142 |
| 167 | Linking genotype to phenotype using the Arabidopsis unimutant collection. <i>Plant Journal</i> , <b>2010</b> , 61, 928-40   | 11.4 | 141 |
| 166 | A complete BAC-based physical map of the Arabidopsis thaliana genome. <i>Nature Genetics</i> , <b>1999</b> , 22, 271-5  | 11.3 | 140 |
| 165 | PHYTOCHROME KINASE SUBSTRATE 1 is a phototropin 1 binding protein required for phototropism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2006</b> , 103, 10134-9                                | 11.5 | 138 |
| 164 | Phytochrome-specific type 5 phosphatase controls light signal flux by enhancing phytochrome stability and affinity for a signal transducer. <i>Cell</i> , <b>2005</b> , 120, 395-406  | 56.2 | 133 |
| 163 | Dynamic DNA methylation reconfiguration during seed development and germination. <i>Genome Biology</i> , <b>2017</b> , 18, 171  | 18.3 | 132 |
| 162 | Regulation of flowering time in Arabidopsis by K homology domain proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 12759-64   | 11.5 | 128 |
| 161 | FRIGIDA-independent variation in flowering time of natural Arabidopsis thaliana accessions. <i>Genetics</i> , <b>2005</b> , 170, 1197-207   | 4    | 128 |
| 160 | The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Cell Biology</i> , <b>2007</b> , 178, 477-88   | 7.3  | 127 |
| 159 | Unique cell-type-specific patterns of DNA methylation in the root meristem. <i>Nature Plants</i> , <b>2016</b> , 2, 16058   | 11.5 | 125 |
| 158 | Arabidopsis ETO1 specifically interacts with and negatively regulates type 2 1-aminocyclopropane-1-carboxylate synthases. <i>BMC Plant Biology</i> , <b>2005</b> , 5, 14  | 5.3  | 125 |
| 157 | Short-term growth responses to ethylene in Arabidopsis seedlings are EIN3/EIL1 independent. <i>Plant Physiology</i> , <b>2004</b> , 136, 2921-7   | 6.6  | 123 |

|     |  |      |     |
|-----|--|------|-----|
| 156 | The Arabidopsis 14-3-3 protein RARE COLD INDUCIBLE 1A links low-temperature response and ethylene biosynthesis to regulate freezing tolerance and cold acclimation. <i>Plant Cell</i> , <b>2014</b> , 26, 3326-42                                      | 11.6 | 122 |
| 155 | Involvement of NRAMP1 from Arabidopsis thaliana in iron transport. <i>Biochemical Journal</i> , <b>2000</b> , 347, 749   | 3.8  | 121 |
| 154 | Sigma factor-mediated plastid retrograde signals control nuclear gene expression. <i>Plant Journal</i> , <b>2013</b> , 73, 1-13  | 6.9  | 117 |
| 153 | A genome-scale resource for the functional characterization of Arabidopsis transcription factors. <i>Cell Reports</i> , <b>2014</b> , 8, 622-32  | 10.6 | 116 |
| 152 | Spatial and functional relationships among Pol V-associated loci, Pol IV-dependent siRNAs, and cytosine methylation in the Arabidopsis epigenome. <i>Genes and Development</i> , <b>2012</b> , 26, 1825-36   | 12.6 | 115 |
| 151 | Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells. <i>ELife</i> , <b>2018</b> , 7,   | 8.9  | 114 |
| 150 | The developmental potential of iPSCs is greatly influenced by reprogramming factor selection. <i>Cell Stem Cell</i> , <b>2014</b> , 15, 295-309  | 18   | 112 |
| 149 | An Arabidopsis NPR1-like gene, NPR4, is required for disease resistance. <i>Plant Journal</i> , <b>2005</b> , 41, 304-18   | 6.9  | 112 |
| 148 | A reevaluation of the role of the heterotrimeric G protein in coupling light responses in Arabidopsis. <i>Plant Physiology</i> , <b>2003</b> , 131, 1623-7   | 6.6  | 112 |
| 147 | The POLARIS peptide of Arabidopsis regulates auxin transport and root growth via effects on ethylene signaling. <i>Plant Cell</i> , <b>2006</b> , 18, 3058-72  | 11.6 | 109 |
| 146 | The central role of PhEIN2 in ethylene responses throughout plant development in petunia. <i>Plant Physiology</i> , <b>2004</b> , 136, 2900-12   | 6.6  | 109 |
| 145 | Two plant viral suppressors of silencing require the ethylene-inducible host transcription factor RAV2 to block RNA silencing. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1000729   | 7.6  | 107 |
| 144 | RACK1 mediates multiple hormone responsiveness and developmental processes in Arabidopsis. <i>Journal of Experimental Botany</i> , <b>2006</b> , 57, 2697-708  | 7    | 107 |
| 143 | An ABA-increased interaction of the PYL6 ABA receptor with MYC2 Transcription Factor: A putative link of ABA and JA signaling. <i>Scientific Reports</i> , <b>2016</b> , 6, 28941  | 4.9  | 103 |
| 142 | Small RNA-mediated chromatin silencing directed to the 3' region of the Arabidopsis gene encoding the developmental regulator, FLC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 3633-8 | 11.5 | 102 |
| 141 | Downregulation of ClpR2 leads to reduced accumulation of the ClpPRS protease complex and defects in chloroplast biogenesis in Arabidopsis. <i>Plant Cell</i> , <b>2006</b> , 18, 1704-21   | 11.6 | 100 |
| 140 | An adapter ligation-mediated PCR method for high-throughput mapping of T-DNA inserts in the Arabidopsis genome. <i>Nature Protocols</i> , <b>2007</b> , 2, 2910-7  | 18.8 | 96  |
| 139 | Exploring the transcriptional landscape of plant circadian rhythms using genome tiling arrays. <i>Genome Biology</i> , <b>2009</b> , 10, R17   | 18.3 | 93  |

|     |   |      |    |
|-----|---|------|----|
| 138 | Flagellin is not a major defense elicitor in <i>Ralstonia solanacearum</i> cells or extracts applied to <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , <b>2004</b> , 17, 696-706                 | 3.6  | 90 |
| 137 | Regulation of membrane trafficking and organ separation by the NEVERSHED ARF-GAP protein. <i>Development (Cambridge)</i> , <b>2009</b> , 136, 1909-18   | 6.6  | 89 |
| 136 | Development of large DNA methods for plants: molecular cloning of large segments of <i>Arabidopsis</i> and carrot DNA into yeast. <i>Nucleic Acids Research</i> , <b>1988</b> , 16, 11091-105                                 | 20.1 | 89 |
| 135 | ERRs Mediate a Metabolic Switch Required for Somatic Cell Reprogramming to Pluripotency. <i>Cell Stem Cell</i> , <b>2015</b> , 16, 547-55   | 18   | 87 |
| 134 | CrY2H-seq: a massively multiplexed assay for deep-coverage interactome mapping. <i>Nature Methods</i> , <b>2017</b> , 14, 819-825   | 21.6 | 86 |
| 133 | Release factor one is nonessential in <i>Escherichia coli</i> . <i>ACS Chemical Biology</i> , <b>2012</b> , 7, 1337-44  | 4.9  | 85 |
| 132 | Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , <b>2019</b> , 16, 999-1006   | 21.6 | 84 |
| 131 | Epigenomic landscapes of retinal rods and cones. <i>ELife</i> , <b>2016</b> , 5, e11613   | 8.9  | 83 |
| 130 | Plant Stress Tolerance Requires Auxin-Sensitive Aux/IAA Transcriptional Repressors. <i>Current Biology</i> , <b>2017</b> , 27, 437-444  | 6.3  | 80 |
| 129 | JAZ2 controls stomata dynamics during bacterial invasion. <i>New Phytologist</i> , <b>2017</b> , 213, 1378-1392   | 9.8  | 80 |
| 128 | Rapid array mapping of circadian clock and developmental mutations in <i>Arabidopsis</i> . <i>Plant Physiology</i> , <b>2005</b> , 138, 990-7   | 6.6  | 80 |
| 127 | A homolog of prokaryotic thiol disulfide transporter CcdA is required for the assembly of the cytochrome b6f complex in <i>Arabidopsis</i> chloroplasts. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 32474-82 | 5.4  | 79 |
| 126 | Auxin-sensitive Aux/IAA proteins mediate drought tolerance in <i>Arabidopsis</i> by regulating glucosinolate levels. <i>Nature Communications</i> , <b>2019</b> , 10, 4021  | 17.4 | 78 |
| 125 | Epigenetic and epigenomic variation in <i>Arabidopsis thaliana</i> . <i>Trends in Plant Science</i> , <b>2012</b> , 17, 149-54  | 13.1 | 76 |
| 124 | An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , <b>2020</b> , 583, 744-751   | 50.4 | 76 |
| 123 | A B-ARR-mediated cytokinin transcriptional network directs hormone cross-regulation and shoot development. <i>Nature Communications</i> , <b>2018</b> , 9, 1604   | 17.4 | 75 |
| 122 | Light-response quantitative trait loci identified with composite interval and eXtreme array mapping in <i>Arabidopsis thaliana</i> . <i>Genetics</i> , <b>2004</b> , 167, 907-17  | 4    | 74 |
| 121 | A family of bacterial cysteine protease type III effectors utilizes acylation-dependent and -independent strategies to localize to plasma membranes. <i>Journal of Biological Chemistry</i> , <b>2009</b> , 284, 15867-79     | 5.4  | 73 |

|     |  |      |    |
|-----|--|------|----|
| 120 | HIV integration site selection: targeting in macrophages and the effects of different routes of viral entry. <i>Molecular Therapy</i> , <b>2006</b> , 14, 218-25   | 11.7 | 73 |
| 119 | NPSN11 is a cell plate-associated SNARE protein that interacts with the syntaxin KNOLLE. <i>Plant Physiology</i> , <b>2002</b> , 129, 530-9  | 6.6  | 73 |
| 118 | Ethylene gas: perception, signaling and response. <i>Current Opinion in Plant Biology</i> , <b>1998</b> , 1, 393-8   | 9.9  | 72 |
| 117 | Ethylene gas: it's not just for ripening any more!. <i>Trends in Genetics</i> , <b>1993</b> , 9, 356-62  | 8.5  | 71 |
| 116 | Genome-wide DNA methylation patterns in LSH mutant reveals de-repression of repeat elements and redundant epigenetic silencing pathways. <i>Genome Research</i> , <b>2014</b> , 24, 1613-23                          | 9.7  | 67 |
| 115 | Higher plants possess two different types of ATX1-like copper chaperones. <i>Biochemical and Biophysical Research Communications</i> , <b>2007</b> , 354, 385-90   | 3.4  | 66 |
| 114 | Robust single-cell DNA methylome profiling with snmC-seq2. <i>Nature Communications</i> , <b>2018</b> , 9, 3824  | 17.4 | 66 |
| 113 | The ACC synthase TOE sequence is required for interaction with ETO1 family proteins and destabilization of target proteins. <i>Plant Molecular Biology</i> , <b>2006</b> , 62, 427-37                                | 4.6  | 64 |
| 112 | Functional characterization of type-B response regulators in the Arabidopsis cytokinin response. <i>Plant Physiology</i> , <b>2013</b> , 162, 212-24   | 6.6  | 63 |
| 111 | The DNA methylome. <i>FEBS Letters</i> , <b>2011</b> , 585, 1994-2000  | 3.8  | 63 |
| 110 | The complex architecture and epigenomic impact of plant T-DNA insertions. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1007819  | 6    | 61 |
| 109 | Perspectives on ENCODE. <i>Nature</i> , <b>2020</b> , 583, 693-698   | 50.4 | 61 |
| 108 | Comprehensive analysis of single cell ATAC-seq data with SnapATAC. <i>Nature Communications</i> , <b>2021</b> , 12, 1337   | 17.4 | 61 |
| 107 | Improved regulatory element prediction based on tissue-specific local epigenomic signatures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E1633-E1640 | 11.5 | 60 |
| 106 | A growth regulatory loop that provides homeostasis to phytochrome a signaling. <i>Plant Cell</i> , <b>2003</b> , 15, 2966-78   | 11.6 | 60 |
| 105 | Integrated multi-omics framework of the plant response to jasmonic acid. <i>Nature Plants</i> , <b>2020</b> , 6, 290-302   | 1.5  | 59 |
| 104 | Plant genomics: the third wave. <i>Annual Review of Genomics and Human Genetics</i> , <b>2004</b> , 5, 443-77  | 9.7  | 59 |
| 103 | EIN2-dependent regulation of acetylation of histone H3K14 and non-canonical histone H3K23 in ethylene signalling. <i>Nature Communications</i> , <b>2016</b> , 7, 13018  | 17.4 | 58 |

|     |  |      |    |
|-----|--|------|----|
| 102 | Unexpected Diversity of Chloroplast Noncoding RNAs as Revealed by Deep Sequencing of the Arabidopsis Transcriptome. <i>G3: Genes, Genomes, Genetics</i> , <b>2011</b> , 1, 559-70  | 3.2  | 58 |
| 101 | Functional Human Oocytes Generated by Transfer of Polar Body Genomes. <i>Cell Stem Cell</i> , <b>2017</b> , 20, 112-119  | 11.9 | 57 |
| 100 | The Arabidopsis Auxin Receptor F-Box Proteins AFB4 and AFB5 Are Required for Response to the Synthetic Auxin Picloram. <i>G3: Genes, Genomes, Genetics</i> , <b>2016</b> , 6, 1383-90  | 3.2  | 54 |
| 99  | Mapping the genome landscape using tiling array technology. <i>Current Opinion in Plant Biology</i> , <b>2007</b> , 10, 534-42   | 9.9  | 54 |
| 98  | Reentry of the Ethylene MPK6 Module. <i>Plant Cell</i> , <b>2004</b> , 16, 3169-3173   | 11.6 | 54 |
| 97  | A WD40 domain cyclophilin interacts with histone H3 and functions in gene repression and organogenesis in Arabidopsis. <i>Plant Cell</i> , <b>2007</b> , 19, 2403-16   | 11.6 | 53 |
| 96  | Integration site selection by HIV-based vectors in dividing and growth-arrested IMR-90 lung fibroblasts. <i>Molecular Therapy</i> , <b>2006</b> , 13, 366-73   | 11.7 | 53 |
| 95  | Chimeric Activators and Repressors Define HY5 Activity and Reveal a Light-Regulated Feedback Mechanism. <i>Plant Cell</i> , <b>2020</b> , 32, 967-983  | 11.6 | 52 |
| 94  | Mapping transcription factor interactome networks using HaloTag protein arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, E4238-47                         | 11.5 | 52 |
| 93  | A user's guide to the Arabidopsis T-DNA insertion mutant collections. <i>Methods in Molecular Biology</i> , <b>2015</b> , 1284, 323-42   | 1.4  | 52 |
| 92  | PFGE and YAC analysis of the Arabidopsis genome. <i>Methods</i> , <b>1990</b> , 1, 186-194   | 4.6  | 51 |
| 91  | Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , <b>2017</b> , 214, 808-819  | 9.8  | 49 |
| 90  | methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 313   | 3.6  | 48 |
| 89  | SnapATAC: A Comprehensive Analysis Package for Single Cell ATAC-seq  |      | 48 |
| 88  | A multimodal cell census and atlas of the mammalian primary motor cortex. <i>Nature</i> , <b>2021</b> , 598, 86-102  | 50.4 | 44 |
| 87  | Dynamic and rapid changes in the transcriptome and epigenome during germination and in developing rice ( <i>Oryza sativa</i> ) coleoptiles under anoxia and re-oxygenation. <i>Plant Journal</i> , <b>2017</b> , 89, 805-824 | 6.9  | 43 |
| 86  | Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons. <i>ELife</i> , <b>2019</b> , 8,   | 8.9  | 41 |
| 85  | Extraction of Distinct Neuronal Cell Types from within a Genetically Continuous Population. <i>Neuron</i> , <b>2020</b> , 107, 274-282.e6  | 13.9 | 41 |

|    |   |      |    |
|----|---|------|----|
| 84 | A MYC2/MYC3/MYC4-dependent transcription factor network regulates water spray-responsive gene expression and jasmonate levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 23345-23356                | 11.5 | 38 |
| 83 | Utilizing tiling microarrays for whole-genome analysis in plants. <i>Plant Journal</i> , <b>2008</b> , 53, 636-44   | 6.9  | 38 |
| 82 | CG hypomethylation in Lsh <sup>-/-</sup> mouse embryonic fibroblasts is associated with de novo H3K4me1 formation and altered cellular plasticity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 5890-5 | 11.5 | 37 |
| 81 | Allele-specific non-CG DNA methylation marks domains of active chromatin in female mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E2882-E2890   | 11.5 | 35 |
| 80 | Spatiotemporal DNA methylome dynamics of the developing mouse fetus. <i>Nature</i> , <b>2020</b> , 583, 752-759   | 50.4 | 35 |
| 79 | Surveillance of 30Noncoding Transcripts Requires FIERY1 and XRN3 in Arabidopsis. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 487-98  | 3.2  | 33 |
| 78 | Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse  |      | 33 |
| 77 | Robust single-cell Hi-C clustering by convolution- and random-walk-based imputation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 14011-14018  | 11.5 | 32 |
| 76 | Genomic Decoding of Neuronal Depolarization by Stimulus-Specific NPAS4 Heterodimers. <i>Cell</i> , <b>2019</b> , 179, 373-391.e27   | 56.2 | 31 |
| 75 | The ethylene pathway: a paradigm for plant hormone signaling and interaction. <i>Science Signaling</i> , <b>2001</b> , 2001, re1  | 8.8  | 31 |
| 74 | Comparative cellular analysis of motor cortex in human, marmoset and mouse. <i>Nature</i> , <b>2021</b> , 598, 111-119  | 50.4 | 31 |
| 73 | Ethylene signaling in Arabidopsis: Events from the membrane to the nucleus. <i>Plant Physiology and Biochemistry</i> , <b>1998</b> , 36, 103-113  | 5.4  | 30 |
| 72 | Sequencing and functional validation of the JGI Brachypodium distachyon T-DNA collection. <i>Plant Journal</i> , <b>2017</b> , 91, 361-370  | 6.9  | 29 |
| 71 | OGT binds a conserved C-terminal domain of TET1 to regulate TET1 activity and function in development. <i>ELife</i> , <b>2018</b> , 7,  | 8.9  | 27 |
| 70 | A Proposal Regarding Best Practices for Validating the Identity of Genetic Stocks and the Effects of Genetic Variants. <i>Plant Cell</i> , <b>2016</b> , 28, 606-9  | 11.6 | 25 |
| 69 | The JA-pathway MYC transcription factors regulate photomorphogenic responses by targeting HY5 gene expression. <i>Plant Journal</i> , <b>2020</b> , 102, 138-152  | 6.9  | 24 |
| 68 | A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex. <i>Nature</i> , <b>2021</b> , 598, 103-110  | 50.4 | 23 |
| 67 | Single nucleus multi-omics links human cortical cell regulatory genome diversity to disease risk variants   |      | 23 |



|    |   |      |    |
|----|---|------|----|
| 66 | An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types  |      | 23 |
| 65 | A blueprint for an international cancer epigenome consortium. A report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , <b>2012</b> , 72, 6319-24  | 10.1 | 21 |
| 64 | Epigenomic programming contributes to the genomic drift evolution of the F-Box protein superfamily in Arabidopsis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 16927-32 | 11.5 | 20 |
| 63 | Detection of allele-specific methylation through a generalized heterogeneous epigenome model. <i>Bioinformatics</i> , <b>2012</b> , 28, i163-71   | 7.2  | 19 |
| 62 | Genetic and physical linkage of the Arabidopsis genome: Methods for anchoring Yeast Artificial Chromosomes <b>1992</b> , 144-169  |      | 19 |
| 61 | Losing Dnmt3a dependent methylation in inhibitory neurons impairs neural function by a mechanism impacting Rett syndrome. <i>ELife</i> , <b>2020</b> , 9,   | 8.9  | 19 |
| 60 | Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in Arabidopsis thaliana. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008492   | 6    | 19 |
| 59 | The emergence of the brain non-CpG methylation system in vertebrates. <i>Nature Ecology and Evolution</i> , <b>2021</b> , 5, 369-378  | 12.3 | 19 |
| 58 | Diversity and dynamics of DNA methylation: epigenomic resources and tools for crop breeding. <i>Breeding Science</i> , <b>2019</b> , 69, 191-204  | 2    | 18 |
| 57 | BRI-ghtening the pathway to steroid hormone signaling events in plants. <i>Cell</i> , <b>1997</b> , 90, 825-7   | 56.2 | 18 |
| 56 | Genome and time-of-day transcriptome of link morphological minimization with gene loss and less growth control. <i>Genome Research</i> , <b>2020</b> ,  | 9.7  | 17 |
| 55 | Profiling of transcription factor binding events by chromatin immunoprecipitation sequencing (ChIP-seq). <i>Current Protocols in Plant Biology</i> , <b>2016</b> , 1, 293-306   | 2.8  | 16 |
| 54 | Challenges and recommendations for epigenomics in precision health. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 1128-1132   | 44.5 | 16 |
| 53 | DNA topoisomerase 1 promotes transcriptional silencing of transposable elements through DNA methylation and histone lysine 9 dimethylation in Arabidopsis. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004446                            | 6    | 16 |
| 52 | Epigenetic silencing of a multifunctional plant stress regulator. <i>ELife</i> , <b>2019</b> , 8,   | 8.9  | 16 |
| 51 | Systematic mapping of chromatin state landscapes during mouse development   |      | 15 |
| 50 | DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , <b>2021</b> , 598, 120-128  | 50.4 | 14 |
| 49 | Variation in the structure of varicella-zoster virus DNA. <i>Intervirology</i> , <b>1984</b> , 21, 25-37  | 2.5  | 13 |



|    |   |      |    |
|----|---|------|----|
| 48 | A multimodal cell census and atlas of the mammalian primary motor cortex  |      | 12 |
| 47 | Iterative single-cell multi-omic integration using online learning. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 1000-1007   | 14.5 | 12 |
| 46 | Spatiotemporal DNA Methylome Dynamics of the Developing Mammalian Fetus   |      | 11 |
| 45 | PHYTOCHROME-INTERACTING FACTORs trigger environmentally responsive chromatin dynamics in plants. <i>Nature Genetics</i> , <b>2021</b> , 53, 955-961                                   | 36.3 | 11 |
| 44 | Activity-dependent modulation of synapse-regulating genes in astrocytes. <i>ELife</i> , <b>2021</b> , 10,   | 8.9  | 11 |
| 43 | Mutant analysis as an experimental approach towards understanding plant hormone action. <i>Seminars in Developmental Biology</i> , <b>1993</b> , 4, 3-13                              |      | 10 |
| 42 | Exploiting the Triple Response of Arabidopsis to Identify Ethylene-Related Mutants. <i>Plant Cell</i> , <b>1990</b> , 2, 513  | 11.6 | 10 |
| 41 | Epigenetics. Exceptional epigenetics in the brain. <i>Science</i> , <b>2015</b> , 348, 1094-5   | 33.3 | 9  |
| 40 | STAR: an integrated solution to management and visualization of sequencing data. <i>Bioinformatics</i> , <b>2013</b> , 29, 3204-10  | 7.2  | 9  |
| 39 | Divergent perspectives on GM food. <i>Nature Biotechnology</i> , <b>2002</b> , 20, 1195-6; author reply 1197  | 44.5 | 9  |
| 38 | Analysis of interruptions in the phosphodiester backbone of herpes simplex virus DNA. <i>Virology</i> , <b>1981</b> , 110, 213-6  | 3.6  | 9  |
| 37 | Epigenomic diversity of cortical projection neurons in the mouse brain. <i>Nature</i> , <b>2021</b> , 598, 167-173  | 50.4 | 9  |
| 36 | Piecing together cis-regulatory networks: insights from epigenomics studies in plants. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2018</b> , 10, e1411 | 6.6  | 9  |
| 35 | An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , <b>2021</b> , 598, 129-136  | 50.4 | 8  |
| 34 | Single nucleus multi-omics regulatory landscape of the murine pituitary. <i>Nature Communications</i> , <b>2021</b> , 12, 2677  | 17.4 | 8  |
| 33 | Chromosomal mapping of the ubiquitin gene family in <i>Saccharomyces cerevisiae</i> by pulsed field gel electrophoresis. <i>Nucleic Acids Research</i> , <b>1989</b> , 17, 3611-2     | 20.1 | 7  |
| 32 | Author response: Transcriptional and epigenomic landscapes of CNS and non-CNS vascular endothelial cells <b>2018</b> ,  |      | 7  |
| 31 | Molecular and Genetic Analysis of the Constitutive Ethylene Response Mutation Ctr1 <b>1994</b> , 193-201  |      | 7  |

|    |   |      |   |
|----|---|------|---|
| 30 | High contiguity Arabidopsis thaliana genome assembly with a single nanopore flow cell   |      | 7 |
| 29 | A massively parallel barcoded sequencing pipeline enables generation of the first ORFeome and interactome map for rice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 11836-11842 | 11.5 | 6 |
| 28 | Genotypic variation of gene expression during the soybean innate immunity response. <i>Plant Genetic Resources: Characterisation and Utilisation</i> , <b>2014</b> , 12, S27-S30  | 1    | 6 |
| 27 | DNA Methylation Atlas of the Mouse Brain at Single-Cell Resolution  |      | 6 |
| 26 | Profiling Interactome Networks with the HaloTag-NAPPA In Situ Protein Array. <i>Current Protocols in Plant Biology</i> , <b>2018</b> , 3, e20071  | 2.8  | 6 |
| 25 | Systematic mapping of occluded genes by cell fusion reveals prevalence and stability of cis-mediated silencing in somatic cells. <i>Genome Research</i> , <b>2014</b> , 24, 267-80  | 9.7  | 5 |
| 24 | Author response: Stress induced gene expression drives transient DNA methylation changes at adjacent repetitive elements <b>2015</b> ,  |      | 5 |
| 23 | Response to perspective: "separation anxiety: an analysis of ethylene-induced cleavage of EIN2". <i>Plant Signaling and Behavior</i> , <b>2013</b> , 8,   | 2.5  | 4 |
| 22 | EIN4 and ERS2 Are Members of the Putative Ethylene Receptor Gene Family in Arabidopsis. <i>Plant Cell</i> , <b>1998</b> , 10, 1321  | 11.6 | 4 |
| 21 | Epigenomic Diversity of Cortical Projection Neurons in the Mouse Brain  |      | 4 |
| 20 | Iterative Refinement of Cellular Identity from Single-Cell Data Using Online Learning   |      | 4 |
| 19 | Single nucleus multi-omics identifies human cortical cell regulatory genome diversity.. <i>Cell Genomics</i> , <b>2022</b> , 2,   |      | 4 |
| 18 | Multi-omic profiling of transcriptome and DNA methylome in single nuclei with molecular partitioning  |      | 3 |
| 17 | Ethylene Responses in Seedling Growth and Development <b>2010</b> , 358-376   |      | 2 |
| 16 | Dnmt3a knockout in excitatory neurons impairs postnatal synapse maturation and is partly compensated by repressive histone modification H3K27me3  |      | 2 |
| 15 | A plant-specific syntaxin-6 protein contributes to the intracytoplasmic route for the begomovirus CabLCV. <i>Plant Physiology</i> , <b>2021</b> , 187, 158-173  | 6.6  | 2 |
| 14 | The biology of time: dynamic responses of cell types to developmental, circadian and environmental cues. <i>Plant Journal</i> , <b>2021</b> ,   | 6.9  | 1 |
| 13 | The complex architecture of plant transgene insertions  |      | 1 |

|    |   |      |
|----|---|------|
| 12 | Loss of Dnmt3a dependent methylation in inhibitory neurons impairs neural function through a mechanism that impacts Rett syndrome   | 1    |
| 11 | Genome and time-of-day transcriptome of <i>Wolffia australiana</i> link morphological extreme minimization with un-gated plant growth   | 1    |
| 10 | Single nucleus multi-omics regulatory atlas of the murine pituitary   | 1    |
| 9  | Global DNA methylation remodeling during direct reprogramming of fibroblasts to neurons   | 1    |
| 8  | Single-cell multi-omic profiling of chromatin conformation and DNA methylome  | 1    |
| 7  | PHYTOCHROME INTERACTING FACTORs Trigger Environmentally Responsive Chromatin Dynamics   | 1    |
| 6  | The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>Journal of Experimental Medicine</i> , <b>2007</b> , 204, i22-i22 | 16.6 |
| 5  | The phosphatase laforin crosses evolutionary boundaries and links carbohydrate metabolism to neuronal disease. <i>FASEB Journal</i> , <b>2008</b> , 22, 102.2                       | 0.9  |
| 4  | Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> <b>2019</b> , 15, e1008492                                      |      |
| 3  | Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> <b>2019</b> , 15, e1008492                                      |      |
| 2  | Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> <b>2019</b> , 15, e1008492                                      |      |
| 1  | Common alleles of CMT2 and NRPE1 are major determinants of CHH methylation variation in <i>Arabidopsis thaliana</i> <b>2019</b> , 15, e1008492                                      |      |