

## Lab of Plant Genomic Recombination since 2017 at POSTECH

### Journals

Cell: <https://www.cell.com/>  
Nature: <https://www.nature.com/>  
Science: <https://science.sciencemag.org/>  
Nature Genetics: <https://www.nature.com/ng/>  
PNAS: <https://www.pnas.org/>  
eLife: <https://elifesciences.org/>  
Genes & Development: <http://genesdev.cshlp.org/>  
PLoS Genetics: <https://journals.plos.org/plosgenetics/>

Nature Plants: <https://www.nature.com/nplants/>  
Molecular Plant: <https://www.cell.com/molecular-plant/home>  
Plant Cell: <http://www.plantcell.org/>  
Plant Journal: <https://onlinelibrary.wiley.com/journal/1365313x>  
Plant Physiology: <http://www.plantphysiol.org/>  
New Phytologist: <https://nph.onlinelibrary.wiley.com/journal/14698137>  
Plant Methods: <https://plantmethods.biomedcentral.com/>  
Plant Biotechnology Journal: <https://onlinelibrary.wiley.com/journal/14677652>

### Useful websites

- TAIR: <http://www.arabidopsis.org/index.jsp>  
[ASO design]: [http://mtweb.cs.ucl.ac.uk/mus/www/19genomes/variants.SDI/ler\\_0.v7c.sdi](http://mtweb.cs.ucl.ac.uk/mus/www/19genomes/variants.SDI/ler_0.v7c.sdi)  
<http://signal.salk.edu/atg1001/3.0/gebrowser.php>  
Both websites are helpful for designing ASO for pollen-typing
  - Conversion:weight-moles for nucleic acids: [http://www.molbiol.edu.ru/eng/scripts/01\\_07.html](http://www.molbiol.edu.ru/eng/scripts/01_07.html)
  - LALIGN(sequence alignment): [https://embnet.vital-it.ch/software/LALIGN\\_form.html](https://embnet.vital-it.ch/software/LALIGN_form.html)
  - Primer3(primer design): [http://biotools.umassmed.edu/bioapps/primer3\\_www.cgi](http://biotools.umassmed.edu/bioapps/primer3_www.cgi)
  - AtRTPrimer(qRT PCR primer design): <http://pombe.kaist.ac.kr/blan/genoPP.pl>
  - INDEL/CAPS markers: [http://signal.salk.edu/genome/SSLP\\_info/SSLPsordered.html](http://signal.salk.edu/genome/SSLP_info/SSLPsordered.html)  
<http://amp.genomics.org.cn/>
  - Dcaps Finder2.0(dCAPS marker design tool): <http://helix.wustl.edu/dcaps/dcaps.html>
  - Oligo Calc: <http://biotools.nubic.northwestern.edu/OligoCalc.html>
  - OligoAnalyzer 3.1: <https://sg.idtdna.com/calc/analyzer>
  - NEBcutter V2.0(RE cut number, site): <http://nc2.neb.com/NEBcutter2/>
  - NEBcloner(double digestion condition): <https://nebcloner.neb.com/#!/redigest>
  - Isoschizomers: <https://www.neb.com/tools-and-resources/selection-charts/isoschizomers>
  - e-FP Browser: <http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi>
  - SUBA(Subcellular Location of Proteins): <http://suba.live/>
  - BioGRID, IntAct(Protein interaction): <https://thebiogrid.org/> <https://www.ebi.ac.uk/intact/>
  - Araport: <https://www.araport.org/>
  - NCBI: <https://www.ncbi.nlm.nih.gov/>
  - T-DNA Express(T-DNA insertion line DB): <http://signal.salk.edu/cgi-bin/tdnaexpress>
  - Plant Cistrome Database: [http://neomorph.salk.edu/dap\\_web/pages/aj\\_browsers.php](http://neomorph.salk.edu/dap_web/pages/aj_browsers.php)
  - phylome DB(phylogenetic tree): [http://phylomedb.org/?q=search\\_tree&seqid=Q94AW8](http://phylomedb.org/?q=search_tree&seqid=Q94AW8)
  - <http://www.startbioinfo.com/>
  - <https://www.expasy.org/>
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