SOAPsnp

**RRID:** SCR_010602  
**Type:** Tool

**Proper Citation**

SOAPsnp (RRID:SCR_010602)

**Resource Information**

**URL:** [http://soap.genomics.org.cn/soapsnp.html](http://soap.genomics.org.cn/soapsnp.html)

**Description:** Software providing a method based on Bayes' theorem (the reverse probability model) to call consensus genotype by carefully considering the data quality, alignment, and recurring experimental errors.

**Resource Name:** SOAPsnp

**Proper Citation:** SOAPsnp (RRID:SCR_010602)

**Resource Type:** Resource, software resource

**Resource ID:** SCR_010602

**Website Status:** Last checked up

**Alternate IDs:** OMICS_00078

**Abbreviations:** SOAPsnp

**Mentions Count:** 102

**Ratings and Alerts**

No rating or validation information has been found for SOAPsnp.

No alerts have been found for SOAPsnp.

**Data and Source Information**
Usage and Citation Metrics

We found 102 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [scicrunch](https://scicrunch.org).


Zhang T, et al. (2019) Human macular Müller cells rely more on serine biosynthesis to combat oxidative stress than those from the periphery. eLife, 8.


Hong S, et al. (2019) Clinical utility in infants with suspected monogenic conditions through next-generation sequencing. Molecular genetics & genomic medicine, 7(6), e684.


