

# ☆ Asthma, hay fever and eczema (Johansson, 2019)

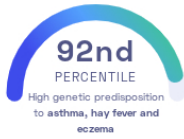
Åsa Johansson, et al.  
Human Molecular Genetics

Allergy

## STUDY SUMMARY

This study discovered 41 new genetic variants that are associated with asthma, hay fever, *eczema* or a combination of the three.

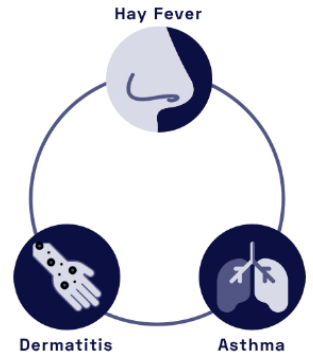
### YOUR RESULT



### STUDY DESCRIPTION

Asthma, hay fever, and *eczema* are common immunological diseases. All three conditions are linked to the body's immune system response to an irritant or allergen, though their symptoms are different. Previous genome studies have discovered few variants that explain the genetics of these diseases. To expand this understanding, in this genome-wide association study, 346,545 individuals of European ancestry were analyzed to identify loci associated with asthma, hay fever, *eczema*, or some combination of the three.

The study discovered 41 new loci, 16 of which are associated with all three diseases. However, some of these variants have significantly larger effects on one of the three diseases.



### DID YOU KNOW?

Avoiding the allergen altogether is the best way to prevent allergic reactions. Creams that contain corticosteroids can help against eczema. Nasal rinses and antihistamines are commonly prescribed against hay fever.

### YOUR DETAILED RESULTS

To calculate your genetic predisposition to asthma, hay fever and eczema we summed up the effects of genetic variants that were linked to asthma, hay fever and eczema in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to asthma, hay fever and eczema. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to asthma, hay fever and eczema. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to asthma, hay fever and eczema. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for asthma, hay fever and eczema to be 0.15**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for asthma, hay fever and eczema is in the **92nd percentile**. This means that it is higher than the polygenic scores 92% of people. We consider this to be a **high genetic predisposition to asthma, hay fever and eczema**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our [Nebula Library tutorial](#).

VARIANT <sup>Ⓞ</sup>	YOUR GENOTYPE <sup>Ⓞ</sup>	EFFECT SIZE <sup>Ⓞ</sup>	VARIANT FREQUENCY <sup>Ⓞ</sup>	SIGNIFICANCE <sup>Ⓞ</sup>
rs62379371_A	G / G	-0.09 (-)	5%	$1.13 \times 10^{-13}$
rs6066184_G	C / C	-0.05 (-)	26%	$1.19 \times 10^{-13}$
rs9816107_A	C / A	-0.04 (↓)	34%	$6.80 \times 10^{-11}$
rs2230624_A	NA	-0.14 (-)	2%	$2.64 \times 10^{-9}$
rs9379628_G	C / C	0.03 (-)	37%	$2.71 \times 10^{-9}$
rs3768212_T	C / C	0.03 (-)	37%	$2.99 \times 10^{-9}$
rs7114923_T	C / T	0.03 (↑)	37%	$3.74 \times 10^{-9}$
rs2606504_A	A / G	0.04 (↑)	29%	$5.45 \times 10^{-9}$
rs7410883_C	T / T	-0.05 (-)	11%	$7.00 \times 10^{-9}$
rs4381663_A	T / T	-0.03 (-)	33%	$7.81 \times 10^{-9}$
rs3116590_G	A / G	0.04 (↑)	21%	$1.52 \times 10^{-8}$
rs12966924_A	G / A	0.03 (↑)	31%	$1.52 \times 10^{-8}$
rs10419921_T	T / T	0.03 (↑)	30%	$1.67 \times 10^{-8}$
rs61976764_A	G / A	0.03 (↑)	47%	$2.65 \times 10^{-8}$
rs1330303_T	T / C	-0.03 (↓)	35%	$2.84 \times 10^{-8}$

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.