

☆ Alopecia areata (Petukhova, 2010)

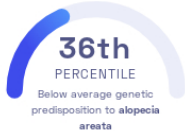
Lynn Petukhova, et al.
Nature

Autoimmunity Appearance

STUDY SUMMARY

Identification of 16 genomic regions associated with alopecia areata, an *autoimmune* disease that causes hair loss.

YOUR RESULT



STUDY DESCRIPTION

Alopecia areata occurs when the immune system attacks *hair follicles*, resulting in hair loss. Alopecia areata affects over 6.8 million people in the United States. The genetic basis of alopecia areata remains largely unknown. By examining the genomes of 4,332 individuals, this study identified 16 independent genetic variants that are associated with alopecia areata. Most of these genetic variants are within or near genes that play a role in the immune system. Interestingly, this study implicated ULBP genes, which encode *natural killer cell receptor ligands*, that have not been previously linked to this or other *autoimmune* diseases. These *natural killer cell receptor ligands* act as “danger signals” to the immune system.



Circular bald patches are typical for alopecia areata.

DID YOU KNOW?

Common treatment options for alopecia areata include steroid injections or topical irritants. However, recently, there has been success in treating alopecia areata patients with Xeljanz, which is used to treat rheumatoid arthritis. Many patients see hair growth after 2 or 3 months.

YOUR DETAILED RESULTS

To calculate your genetic predisposition to alopecia areata we summed up the effects of genetic variants that were linked to alopecia areata 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 alopecia areata. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to alopecia areata. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to alopecia areata. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for alopecia areata to be 4.20**. 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 alopecia areata is in the **36th percentile**. This means that it is higher than the polygenic scores 36% of people. We consider this to be a **below average genetic predisposition to alopecia areata**. 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 [Ⓞ]	YOUR GENOTYPE [Ⓞ]	EFFECT SIZE [Ⓞ]	VARIANT FREQUENCY [Ⓞ]	SIGNIFICANCE [Ⓞ]
rs9275572_G	A / G	0.79 (↑)	59%	1.38×10^{-35}
rs16898264_A	G / G	0.67 (-)	37%	1.66×10^{-32}
rs9479482_T	T / T	0.50 (↑)	57%	4.49×10^{-19}
rs3130320_C	T / C	0.63 (↑)	64%	5.64×10^{-19}
rs2009345_C	C / C	0.42 (↑)	39%	4.43×10^{-17}
rs3763312_A	G / G	0.53 (-)	20%	2.53×10^{-16}
rs6910071_G	A / A	0.45 (-)	18%	2.95×10^{-13}
rs1024161_T	T / C	0.36 (↑)	40%	3.55×10^{-13}
rs3118470_C	T / T	0.34 (-)	30%	1.74×10^{-12}
rs4147359_A	G / G	0.26 (-)	33%	2.22×10^{-8}
rs1701704_G	T / T	0.29 (-)	33%	3.21×10^{-8}
rs3096851_C	A / C	0.28 (↑)	31%	3.58×10^{-8}
rs7682241_T	G / T	0.29 (↑)	33%	4.27×10^{-8}