

CDKN2A

Gene Report

REPORT CATEGORIES —



COGNITION



HEART & BLOOD
VESSELS



INFLAMMATION &
AUTOIMMUNITY



CANCER

Sample Client

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DISCLAIMER

This report does not diagnose this or any other health conditions. Please talk to a healthcare professional if this condition runs in your family, you think you might have this condition, or you have any concerns about your results.

Personal information

NAME

Sample Client

SEX AT BIRTH

Male

HEIGHT

5ft 5" 165cm

WEIGHT

137lb 62kg



How this works

Our Wellness Reports analyze how your DNA influences your health.
We then use this analysis to give you personalized risk estimates and recommendations.



Similarly, our Trait Reports look at how your DNA influences your traits.



Your DNA is like an instruction manual — it contains a lot of information.
You can think of it as a blueprint for your body.

Genetic variants are parts of DNA that differ from person to person. Some can make you more vulnerable to certain health issues, while others may influence traits such as eye color.



We use artificial intelligence and machine learning to analyze all this information.
We then summarize your results as a risk score or display it on a gauge.

In total, we analyze up to 83 million genetic variants.

When we give a risk score, the risk icon tells you if you are at a higher or lower risk compared to other people:



Genotype color info:

AA

You don't have any risk alleles

AA

You have 1 risk allele

AA

You have 2 risk alleles

Your risk is also displayed as a percentile. This will tell you how your risks compare to our sample population. The lower your percentile number, the lower your risk. The "50th percentile" would be an average risk.

Similarly, the gauge tells you your relative risk score compared to our sample population, or it indicates a specific trait or haplotype you are more likely to have based on your genetic variants.

When applicable, we also list top evidence-based recommendations that may help lower your risk. The focus is on recommendations that may be of benefit to you, based on your genetics.

Our recommendations come in four categories: lifestyle, diet, supplements and drugs.
The following icons tell you which category a recommendation falls into:



Our team of scientists also ranks each recommendation.
We rank based on impact and the strength of evidence in the medical literature.

Impact shows how strongly a recommendation will affect your health in a certain area.
Evidence is how much scientific support there is for the recommendation. Rankings are from 1 to 5 (low to high):



Impact

Impact scores range from 1-5. These scores reflect how much of an effect each recommendation can have. An impact score of 5 predicts the biggest effect.

When a recommendation affects something we can measure, we use those measurements to assign the impact score. For example, a recommendation that decreases cholesterol by 20% will have a higher impact score than one that decreases it by 5%.

Some recommendations affect things that we cannot directly measure, like stress or mood. For these, the impact score is based on how well they work relative to other recommendations and standard treatments. The best ones get the highest scores.

If there is a lot of research that shows a recommendation works especially well for your genotype, the impact score gets increased.

Recommendation Evidence

- 5 / 5
- Recommendations that are considered effective and generally recommended by experts and medical bodies.
-
- 4 / 5
- Recommendations that are considered likely effective and that have multiple independent meta-analyses and a great many studies supporting them.
-
- 3 / 5
- Recommendations that are considered possibly effective and have many studies supporting them
-
- 2 / 5
- Recommendations that have insufficient evidence, with two or several clinical trials supporting them, or many studies but with ambiguous results.
-
- 1 / 5
- Recommendations that have insufficient evidence, with a single clinical trial, or with many studies most of which didn't find support for the recommendation.
-
- 0 / 5
- No evidence in humans.

Genotype-specific Evidence

- High-quality
- Direct evidence that a recommendation helps more in people with your gene variant (many clinical trials, a few large clinical trials, or a meta-analysis).
- Medium-quality
- Direct evidence that a recommendation helps more in people with your gene variant (a few clinical trials or one large clinical trial).
- Low-quality
- Direct evidence that a recommendation helps more in people with your gene variant (a single clinical trial or more trials with inconsistent results).
- Indirect
- A recommendation may help more in people with your gene variant because it targets a specific gene or protein affected by your variant (e.g., MTHFR, dopamine).
- In theory
- A recommendation may help more in people with your gene variant because it targets a specific mechanism affected by your variant (e.g., inflammation, oxidative stress).

Some things to keep in mind:

- Genetics doesn’t play a considerable role in a condition or a trait.
- There is not enough research available to estimate a genetic predisposition.
- There are technical limitations to estimating or presenting a genetic predisposition.
- The topic is sensitive, and a genetic predisposition should only be estimated and presented by a healthcare professional.

Introduction

The [CDKN2A](#) gene encodes several proteins, including p16(INK4a) and p14(ARF). Both function as tumor suppressors, which means they keep cells from growing and dividing too rapidly or in an uncontrolled way. These proteins help regulate the cell cycle [\[R\]](#).

The p16(INK4A) protein binds to two other proteins called CDK4 and CDK6 that help regulate the cell cycle. CDK4 and CDK6 normally stimulate the cell to continue through the cycle and divide. However, binding of p16(INK4A) blocks CDK4's or CDK6's ability to stimulate cell cycle progression. Cells begin to produce p16(INK4A) when they are no longer able to undergo cell division [\[R\]](#).

The p14(ARF) protein protects p53 from being broken down. This protein is an important tumor suppressor that is essential for regulating cell division, senescence, and death. By protecting p53, p14(ARF) also helps prevent tumor formation. The p14(ARF) and p53 proteins are often made in cells that are unable to undergo cell division [\[R\]](#).

Mutations in this gene are associated with several cancer types, including bladder cancer, head and neck cancer, lung cancer, and melanoma [\[R\]](#).

CDKN2A Genetics

The minor ‘G’ allele of [rs2811712](#) may decrease *CDKN2A* expression and was associated with reduced physical impairment in a study of 938 older participants [\[R\]](#), [\[R\]](#).

However, this allele has also been associated with:

- Cerebral small vessel disease [\[R\]](#)
- Acute lymphoblastic leukemia [\[R\]](#)

Another variant reducing gene expression, ‘T’ at [rs3731249](#) (Ala148Thr), has been associated with acute lymphoblastic leukemia in several studies [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#).

This variant has also been associated with

- Ovarian cancer [\[R\]](#)
- Coronary artery disease [\[R\]](#)
- Cognitive decline in Alzheimer’s disease [\[R\]](#)

Another minor allele, ‘G’ at [rs11515](#), has been associated with an increased risk and worse prognosis of:

- Breast cancer [\[R\]](#)
- Glioblastoma [\[R\]](#)
- Alzheimer’s disease [\[R\]](#)

However, this variant has also been associated with a decreased risk of thyroid cancer [\[R\]](#)

In contrast, the minor ‘C’ allele of [rs3731217](#) seems to increase gene expression and has been associated with a decreased risk of:

- Thyroid cancer [\[R\]](#)
- Endometrial cancer [\[R\]](#)
- Acute lymphoblastic leukemia (with mixed results) [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#), [\[R\]](#)
- Death from oropharyngeal cancer [\[R\]](#)

Similarly, the minor ‘A’ allele of [rs3088440](#) impairs the binding of a protein that prevents *CDKN2A* expression and has been associated with an increased risk and severity of [\[R\]](#):

- Coronary artery disease [\[R\]](#)



TYPICAL ACTIVITY

Likely typical CDKN2A activity based on 6 genetic variants we looked at

Your top variants that most likely impact your genetic predisposition:

GENE	SNP	GENOTYPE
CDKN2A	rs3731217	AA
CDKN2A	rs3088440	GG
CDKN2B	rs3217992	TT
CDKN2B	rs11515	GC
CDKN2A	rs3731249	CC
CDKN2B	rs2811712	AA

The number of "risk" variants in this table doesn't necessarily reflect your overall result.

- Acute lymphoblastic leukemia [\[R\]](#), [\[R\]](#)
- Endometrial cancer [\[R\]](#)
- Melanoma [\[R\]](#)

However, this variant may decrease the risk of:

- Head and neck cancer [\[R\]](#), [\[R\]](#)
- Esophageal cancer [\[R\]](#)
- Cervical cancer [\[R\]](#), [\[R\]](#)
- DNA damage in workers exposed to vinyl chloride [\[R\]](#)

Finally, the ‘T’ allele of [rs3217992](#) may impair the binding of a regulatory protein to the gene and has been associated with a decreased risk of [\[R\]](#), [\[R\]](#):

- Acute lymphoblastic leukemia [\[R\]](#)
- Breast cancer [\[R\]](#)
- Lung cancer [\[R\]](#)
- Rheumatoid arthritis [\[R\]](#)
- Psoriasis [\[R\]](#)

However, this allele has been associated with an increased risk and severity of:

- Myocardial infarction and cardiovascular disease [\[R\]](#), [\[R\]](#)
- Periodontitis [\[R\]](#)
- Pancreatic cancer [\[R\]](#)
- Osteosarcoma [\[R\]](#)