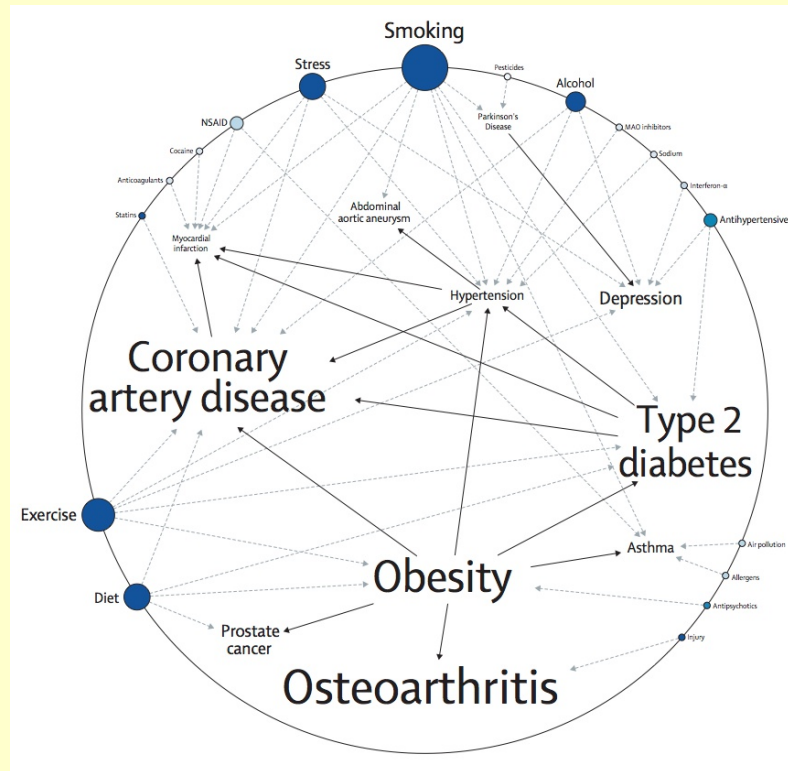


Your Genes and Your Health

<http://bio84.stanford.edu/>

What We Can Learn from Personal Genomics

<http://bio84.stanford.edu/06%20Personal%20Genomics.html>

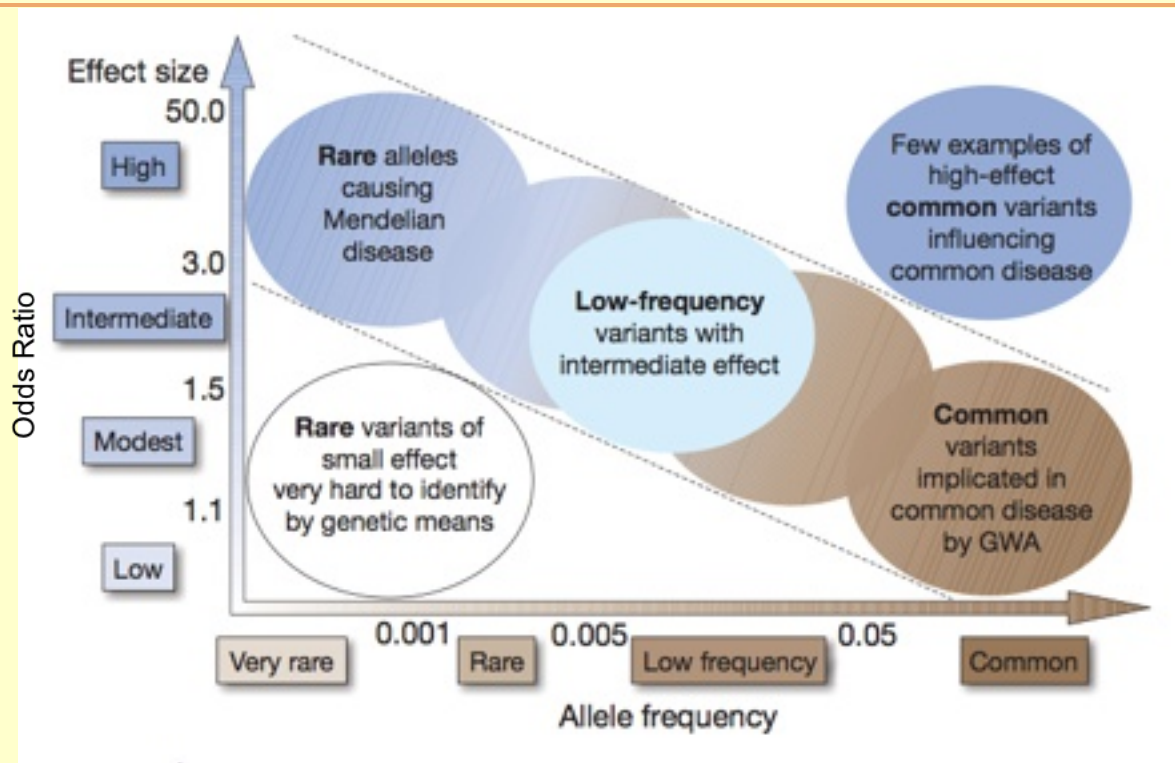


Doug Brutlag, Professor Emeritus of
Biochemistry & Medicine (by courtesy)
Stanford University School of Medicine

Genetic Penetrance of Inherited Diseases

- Many inherited diseases are Mendelian and highly penetrant
 - Sickle cell disease
 - Thalassemias
 - Huntington's disease
 - Color blindness
 - Cystic fibrosis
- Most common diseases are complex (multifactorial - caused by multiple genes or multiple pathways as well as multiple environmental factors) and of low penetrance
 - Familial
 - Predisposition to disease
 - Very large environmental and / or behavioral component
 - Type I diabetes and other autoimmune diseases (lupus, rheumatoid arthritis, hyperthyroidism, Crohn's disease, Celiac Sprue, irritable bowel disease etc.)
 - Type 2 diabetes
 - Coronary heart disease (atherosclerosis)
 - Asthma, COPD, pulmonary fibrosis
 - Many complex diseases can be avoided with diet, nutrition, exercise or behavioral modification
 - Many complex diseases can also be monitored by increased vigilance (another behavioral modification)

Common SNPs have Low Odds Ratio and Low Heritability



- Rare High Penetrance Variants Carry High Risk
- Common SNPs Carry Low Risk
- Multiple Variants May Increase Risk Synergistically
- Common SNPs Associated with Genes Containing High Risk Alleles
- Common SNPs Associations can Suggest Regions to Sequence in Cohorts or Trios or Subpopulations

So What Can We Learn from Personal Genomics?

- Disease risk for common diseases
 - Genetic predisposition towards a disease (relative risk or odds ratio)
 - Genetic versus environmental contributions to disease (penetrance)
 - How to alter your environment and behavior to avoid the disease
 - How to increase your vigilance for symptoms of specific diseases
- Disease carrier status
 - Premarital genetic counseling
 - Preimplantation genetic diagnosis
 - Neonatal diagnosis
 - Amniocentesis
 - Chorion villus sampling (CVS)
 - Non-Invasive Prenatal Testing tests for fetal DNA in pregnant mother's blood
- Drug susceptibility
 - Efficacy of common drugs
 - Adverse reactions to common drugs
- Ancestry
 - One can follow maternal line using mitochondrial DNA SNPs
 - Males can follow paternal line using Y chromosome SNPs
 - Shared haplotypes with close relatives (up to 5th cousins)
- Familial traits, diseases and relationships
 - Known family diseases (breast cancers, colorectal cancer, lysosome storage diseases, etc.)
 - Paternity (10% of people do not know their true biological father)
 - Maternity (about 1% of people do not know their true biological mother)
 - Inbreeding and incest lead to increased homozygosity and recessive diseases
 - Orphans can find family relations



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To **register** your kit,
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32.7%

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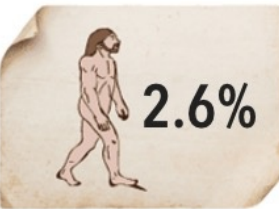
 ANCESTRY COMPOSITION



HEALTH OVERVIEW

CLOSE FAMILY	2nd & 3rd COUSINS	4th COUSINS	DISTANT COUSINS
2	22	302	534

DNA RELATIVES



2.6%

NEANDERTHAL ANCESTRY

23andMe Research

FEATURED SURVEY



ANCESTRY INFORMATION

TAKE SURVEY

FEATURED CONTENT




23andMe DNA Processing Lab Video

Then we make copies of it (amplification), so we have enough to analyze.

Surgical Complications

In the case of a surgical procedure, planned or unplanned, this set of your genetic results and health history information would be important to share with your doctor.



BASED ON YOUR 6 GENETIC REPORTS & 12 SURVEY ANSWERS

QUICK QUESTIONS

Q: Have you been diagnosed with rapid eye movement (REM) sleep behavior disorder or been told that you act out your dreams while lying asleep in bed (as opposed to sleepwalking)?

Yes


No

health overview

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Show results for Douglas Brutlag

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 23andMe Discoveries were made possible by 23andMe members who took surveys.

Disease Risks (120, 1 locked report) ?

 Elevated Risks	Your Risk	Average Risk
Prostate Cancer 	22.4%	17.8%
Colorectal Cancer	7.1%	5.6%
Melanoma	6.0%	2.9%
Chronic Kidney Disease	4.2%	3.4%
Restless Legs Syndrome	2.5%	2.0%

[See all 120 risk reports...](#)

Carrier Status (49) ?

Alpha-1 Antitrypsin Deficiency	Variant Absent
Bloom's Syndrome	Variant Absent
BRCA Cancer Mutations (Selected)	Variant Absent
Canavan Disease	Variant Absent
Cystic Fibrosis	Variant Absent
DPD Deficiency	Variant Absent
Familial Dysautonomia	Variant Absent
Factor XI Deficiency	Variant Absent

[See all 49 carrier status...](#)

Traits (57) ?

Alcohol Flush Reaction	Does Not Flush
Bitter Taste Perception	Can Taste
Earwax Type	Wet
Eye Color	Likely Brown
Hair Curl 	Straighter Hair on Average

[See all 57 traits...](#)

Drug Response (21) ?

Clopidogrel (Plavix®) Efficacy	Greatly Reduced
Abacavir Hypersensitivity	Typical
Alcohol Consumption, Smoking and Risk of Esophageal Cancer	Typical
Fluorouracil Toxicity	Typical
Response to Hepatitis C Treatment	Typical

[See all 21 drug response...](#)

disease risk

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Show results for Douglas Brutlag

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23andMe Discoveries were made possible by 23andMe members who took surveys.

Locked Reports ?

Name	Confidence	Your Risk	Avg. Risk	Compared to Average
Alzheimer's Disease	★★★★	🔒	🔒	🔒

Elevated Risk ?

Name	Confidence	Your Risk	Avg. Risk	Compared to Average
Prostate Cancer ♂	★★★★	22.4%	17.8%	1.26x 📈
Colorectal Cancer	★★★★	7.1%	5.6%	1.27x 📈
Melanoma	★★★★	6.0%	2.9%	2.10x 📈
Chronic Kidney Disease	★★★★	4.2%	3.4%	1.22x 📈
Restless Legs Syndrome	★★★★	2.5%	2.0%	1.25x 📈
Exfoliation Glaucoma	★★★★	2.2%	0.7%	2.90x 📈
Abdominal Aortic Aneurysm	★★★			📈
Ankylosing Spondylitis	★★★			📈
Asthma	★★★			📈

23andMe Prostate Cancer Risks

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Prostate Cancer

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Prostate Cancer

 [Printable Version](#)

Prostate cancer is by far the most common cancer affecting men. (Women don't have prostate glands and therefore cannot get prostate cancer, but can pass markers to their children.) About one in six men will develop prostate cancer over their lifetimes, according to the American Cancer Society. Fortunately, most prostate tumors grow slowly, and if detected early, treatment may help control their size. Until recently, the only well-known risk factors for prostate cancer were age, ethnicity, and family history. Although advanced age increases a person's risk for any type of cancer, the involvement of ethnicity and family history suggests that there is a strong genetic component as well.

The following results are based on ★★★★★ **Established Research** for 12 reported markers, updated [November 4th, 2010](#).

[Learn more about the biology of Prostate Cancer...](#)
[Major discoveries in Prostate Cancer...](#)



1 of 3. Prostate cancer affects about 1 in 6 men. (Women don't have prostate glands and therefore cannot get prostate cancer.)

23andMe Prostate Cancer Risks

Your Genetic Data

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Show information for assuming ethnicity and an age range of

[Where's mine?](#)



Douglas Brutlag

22.4 out of 100

men of European ethnicity who share Douglas Brutlag's genotype will develop Prostate Cancer between the ages of 35 and 79.



Average

17.8 out of 100

men of European ethnicity will develop Prostate Cancer between the ages of 35 and 79.

What does the Odds Calculator show me?

Use the ethnicity and age range selectors above to see the estimated incidence of Prostate Cancer due to genetics for men with **Douglas Brutlag's** genotype. The 23andMe Odds Calculator assumes that a person is free of the condition at the lower age in the range. You can use the name selector above to see the estimated incidence of Prostate Cancer for the genotypes of other people in your account.

The 23andMe Odds Calculator only takes into account effects of markers with known associations that are also on our genotyping chip. Keep in mind that aside from genetics, environment and lifestyle may also contribute to one's risk for Prostate Cancer.

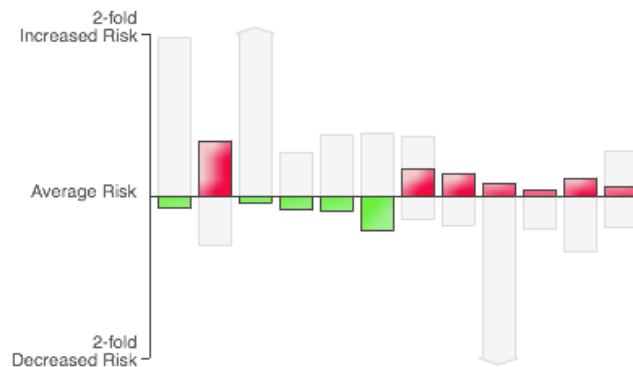
Genes vs. Environment

42-57 %
Attributable to
Genetics

The **heritability** of **prostate cancer** is estimated to be 42-57%. This means that genetic and **environmental factors** contribute nearly equally to differences in risk for this condition. (If you are a woman, you have no chance of getting this type of cancer, but if you have sons, their risk may be affected by what they inherit from you.) Genetic factors that play a role in prostate cancer include both unknown factors and known factors such as the SNPs we describe. Other factors that can increase your risk include being older, having African ancestry, or living in North America, Northwestern Europe, Australia, or the Caribbean islands. The effect of nationality may be tied to diet, as a diet high in red meat and high-fat dairy products, and low in fruits and vegetables, may also put you at increased risk.

[\(sources\)](#)

Marker Effects



What does this chart show?

The chart shows the approximate effects of the selected person's genotype at the 12 reported markers. Higher, **red bars** indicate **increased risk** from the average, while lower, **green bars** indicate **decreased risk** from the average. The light gray bars show the maximum possible effects for the possible genotypes at the marker.

Mouse over individual bars to view additional information about each marker. Click on a bar to view detailed information about that marker below. You can read more about all markers in the [technical report](#).

8q24 (region 1)

Marker: **rs1447295**

Three SNPs in the same area of the [genome](#) have recently been found to be independently associated with [prostate cancer](#) risk. This region is called 8q24, because it lies within band 24 on the long arm (named the "q" arm) of chromosome 8. The three SNPs are not close to known genes (although there are others located farther away). But other studies have looked at [DNA](#) from prostate tumors and found that in the cancerous cells, this area of the genome often has unusual duplications, or extra copies of DNA.

The duplications might contribute to the progression of prostate cancer (for example, by increasing the number of genes related to [cell](#) growth), or they might simply be a side effect of the high mutation rate seen in all types of cancer cells. Similarly, the risk-associated versions of the SNPs in the 8q24 region might directly affect activity levels of genes involved in prostate cancer, or they might somehow make it easier for DNA duplications to occur. (And, they might only be linked to yet-unknown SNPs that are directly involved.)

One study has investigated this association in Japanese Americans. Although the [SNP](#) also appears to be associated with prostate cancer risk in this population, evidence suggests that the effect of this SNP on risk may differ between populations. Therefore, the exact association in populations with Asian ancestry still needs to be confirmed.

The genotyping services of 23andMe are performed in LabCorp's CLIA-certified laboratory. The tests have not been cleared or approved by the FDA but have been analytically validated according to CLIA standards. The information on this page is intended for research and educational purposes only, and is not for diagnostic use.

Citations

- [Amundadottir et al. \(2006\)](#) . "A common variant associated with prostate cancer in European and African populations." *Nat Genet* 38(6):652-8.
- [Freedman et al. \(2006\)](#) . "Admixture mapping identifies 8q24 as a prostate cancer risk locus in African-American men." *Proc Natl Acad Sci U S A* 103(38):14068-73.
- [Severi et al. \(2007\)](#) . "The common variant rs1447295 on chromosome 8q24 and prostate cancer risk: results from an Australian population-based case-control study." *Cancer Epidemiol Biomarkers Prev* 16(3):610-2.
- [Yeager et al. \(2007\)](#) . "Genome-wide association study of prostate cancer identifies a second risk locus at 8q24." *Nat Genet* 39(5):645-9.
- [Gudmundsson et al. \(2007\)](#) . "Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24." *Nat Genet* 39(5):631-7.
- [Wang et al. \(2007\)](#) . "Two common chromosome 8q24 variants are associated with increased risk for prostate cancer." *Cancer Res* 67(7):2944-50.
- [Schumacher et al. \(2007\)](#) . "A common 8q24 variant in prostate and breast cancer from a large nested case-control study." *Cancer Res* 67(7):2951-2956.
- [Suuriniemi et al. \(2007\)](#) . "Confirmation of a positive association between prostate cancer risk and a locus at chromosome 8q24." *Cancer Epidemiol Biomarkers Prev* 16(4):809-14.
- [Cheng et al. \(2008\)](#) . "8q24 and prostate cancer: association with advanced disease and meta-analysis." *Eur J Hum Genet* 16(4):496-505.
- [Zheng et al. \(2008\)](#) . "Cumulative association of five genetic variants with prostate cancer." *N Engl J Med* 358(9):910-9.



23andMe Disease Risks

Decreased Risk

Name	Confidence	Your Risk	Avg. Risk	Compared to Average
Type 2 Diabetes	★★★★★	19.2%	25.7%	0.75x
Age-related Macular Degeneration	★★★★★	2.9%	6.5%	0.44x
Rheumatoid Arthritis	★★★★★	1.2%	2.4%	0.52x
Esophageal Squamous Cell Carcinoma (ESCC)	★★★★★	0.29%	0.36%	0.80x
Crohn's Disease	★★★★★	0.26%	0.53%	0.50x
Multiple Sclerosis	★★★★★	0.20%	0.34%	0.59x
Stomach Cancer (Gastric Cardia Adenocarcinoma)	★★★★★	0.18%	0.23%	0.77x
Type 1 Diabetes	★★★★★	0.07%	1.02%	0.07x
Primary Biliary Cirrhosis	★★★★★	0.05%	0.08%	0.66x
Celiac Disease	★★★★★	0.03%	0.12%	0.28x
Atrial Fibrillation: Preliminary Research	★★★			



Type 2 Diabetes

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Type 2 Diabetes

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The most common type of diabetes, [type 2 diabetes mellitus](#) occurs when chronically high blood sugar levels cause a breakdown of the body's natural response to eating sweets and starches. Left untreated, type 2 diabetes can result in kidney failure, blindness, and circulatory problems that increase the risk of heart attack or stroke. In the United States, almost 21 million children and adults have diabetes, but the rate of new diagnoses is increasing.

The following results are based on ★★★★★ [Established Research](#) for 11 reported markers, updated [March 24th, 2011](#).

[Learn more about the biology of Type 2 Diabetes...](#)

[Major discoveries in Type 2 Diabetes...](#)



1 of 3. Smart choices about diet can help delay or prevent type 2 diabetes.

23andMe Type 2 Diabetes Risks

Your Genetic Data

» [Share your health results](#)

Show information for assuming ethnicity
 and an age range of

[Why are there limited choices of ethnicity in risk reports?](#)



Douglas Brutlag

19.2 out of 100

men of European ethnicity who share Douglas Brutlag's genotype will develop Type 2 Diabetes between the ages of 20 and 79.



Average

25.7 out of 100

men of European ethnicity will develop Type 2 Diabetes between the ages of 20 and 79.

What does the Odds Calculator show me?

Use the ethnicity and age range selectors above to see the estimated incidence of Type 2 Diabetes due to genetics for men with **Douglas Brutlag's** genotype. The 23andMe Odds Calculator assumes that a person is free of the condition at the lower age in the range. You can use the name selector above to see the estimated incidence of Type 2 Diabetes for the genotypes of other people in your account.

The 23andMe Odds Calculator only takes into account effects of markers with known associations that are also on our genotyping chip. Keep in mind that aside from genetics, environment and lifestyle may also contribute to one's risk for Type 2 Diabetes.

Genes vs. Environment

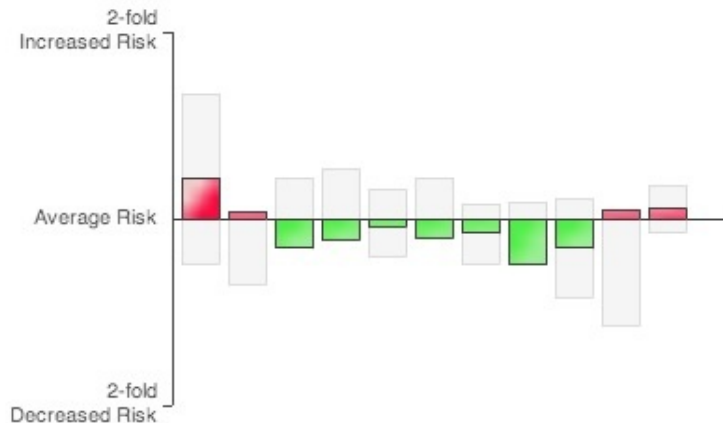
26 %
 Attributable to
 Genetics



The **heritability** of type 2 diabetes is estimated to be 26%. This means that **environmental factors** contribute more to differences in risk for this condition than genetic factors. Genetic factors that play a role in type 2 diabetes include both unknown factors and known factors such as the SNPs we describe here. Environmental factors include **obesity**, gestational diabetes, giving birth to at least one baby weighing nine pounds or more, high blood pressure, abnormal cholesterol levels, physical inactivity, polycystic ovarian syndrome, other clinical conditions associated with **insulin** resistance, a history of impaired **glucose** tolerance or impaired fasting glucose, and a history of cardiovascular disease. ([sources](#))

23andMe Type 2 Diabetes Risks

Marker Effects



What does this chart show?

The chart shows the approximate effects of the selected person's genotype at the 11 reported markers. Higher, **red bars** indicate **increased risk** from the average, while lower, **green bars** indicate **decreased risk** from the average. The light gray bars show the maximum possible effects for the possible genotypes at the marker.

Mouse over individual bars to view additional information about each marker. Click on a bar to view detailed information about that marker below. You can read more about all markers in the [technical report](#).

TCF7L2

Marker: [rs7903146](#)

This **SNP** is located in the **TCF7L2 gene**, which encodes a **protein** involved in **cell** signalling. How TCF7L2 affects the development of type 2 diabetes is not completely understood. TCF7L2 has been shown to be involved in the development of pancreatic islets, which contain **insulin**-producing beta cells. Studies suggest that the T version of this SNP is associated with impaired baseline insulin secretion.

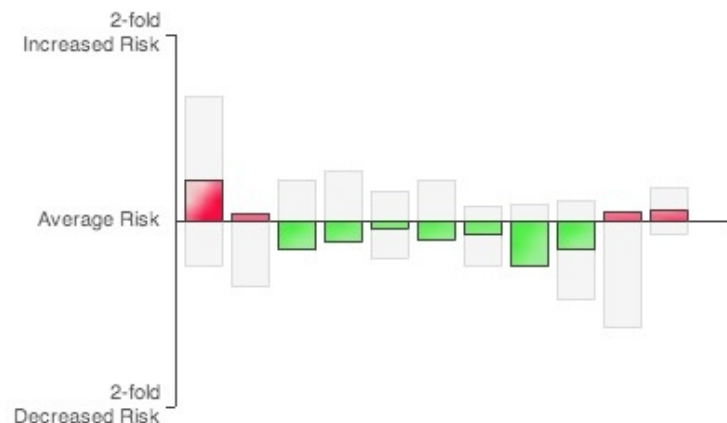
The T version of this SNP is also associated with increased odds of gestational diabetes, a form of diabetes that occurs only during pregnancy. Gestational diabetes can lead to complications for both mother— such as difficult delivery due to unusually large infant size— and baby, such as low blood sugar and breathing problems.

Citations

- [Grant et al. \(2006\)](#) . "Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes." *Nat Genet* 38(3):320-3.
- [Saxena et al. \(2006\)](#) . "Common single nucleotide polymorphisms in TCF7L2 are reproducibly associated with type 2 diabetes and reduce the insulin response to glucose in nondiabetic individuals." *Diabetes* 55(10):2890-5.
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- [Sladek et al. \(2007\)](#) . "A genome-wide association study identifies novel risk loci for type 2 diabetes." *Nature* 445(7130):881-5.
- [Saxena et al. \(2007\)](#) . "Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels." *Science* 316(5829):1331-6.
- [Zeggini et al. \(2007\)](#) . "Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes." *Science* 316(5829):1336-41.

23andMe Type 2 Diabetes Risks

Marker Effects



What does this chart show?

The chart shows the approximate effects of the selected person's genotype at the 11 reported markers. Higher, **red bars** indicate **increased risk** from the average, while lower, **green bars** indicate **decreased risk** from the average. The light gray bars show the maximum possible effects for the possible genotypes at the marker.

Mouse over individual bars to view additional information about each marker. Click on a bar to view detailed information about that marker below. You can read more about all markers in the [technical report](#).

MTNR1B

Marker: [rs1387153](#)

This SNP is located near the MTNR1B gene, which encodes a pancreatic beta cell protein that interacts with a hormone called melatonin. In healthy individuals, insulin secretion follows a circadian rhythm with peaks during the day and troughs at night. Melatonin levels have the opposite pattern being highest during the night and thus may inhibit insulin secretion, possibly through the MTNR1B protein. Studies have shown that melatonin receptors like MTNR1B are overexpressed in pancreatic islets of individuals with type 2 diabetes compared to non-diabetic individuals.

Multiple studies have confirmed this association in populations with European ancestry. This association has not been studied in Asian or African populations.

Citations

- Voight BF et al. (2010) . "Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis." *Nat. Genet.* 42(7):579-89.
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- Prokopenko I et al. (2009) . "Variants in MTNR1B influence fasting glucose levels." *Nat. Genet.* 41(1):77-81.
- Peschke E (2008) . "Melatonin, endocrine pancreas and diabetes." *J. Pineal Res.* 44(1):26-40.



23andMe Carrier Status

carrier status

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23andMe Discoveries were made possible by 23andMe members who took surveys.

Name	Confidence	Confidence ▾
Alpha-1 Antitrypsin Deficiency	★★★★★	Variant Absent
Bloom's Syndrome	★★★★★	Variant Absent
BRCA Cancer Mutations (Selected)	★★★★★	Variant Absent
Canavan Disease	★★★★★	Variant Absent
Cystic Fibrosis	★★★★★	Variant Absent
DPD Deficiency	★★★★★	Variant Absent
Familial Dysautonomia	★★★★★	Variant Absent
Factor XI Deficiency	★★★★★	Variant Absent
Fanconi Anemia (FANCC-related)	★★★★★	Variant Absent
Familial Hypercholesterolemia Type B	★★★★★	Variant Absent
Familial Mediterranean Fever	★★★★★	Variant Absent
G6PD Deficiency	★★★★★	Variant Absent
Gaucher Disease	★★★★★	Variant Absent
Glycogen Storage Disease Type 1a	★★★★★	Variant Absent
Hemochromatosis (HFE-related)	★★★★★	Variant Absent
Limb-girdle Muscular Dystrophy	★★★★★	Variant Absent
Maple Syrup Urine Disease Type 1B	★★★★★	Variant Absent

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Alpha-1 Antitrypsin Deficiency

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Community (5)

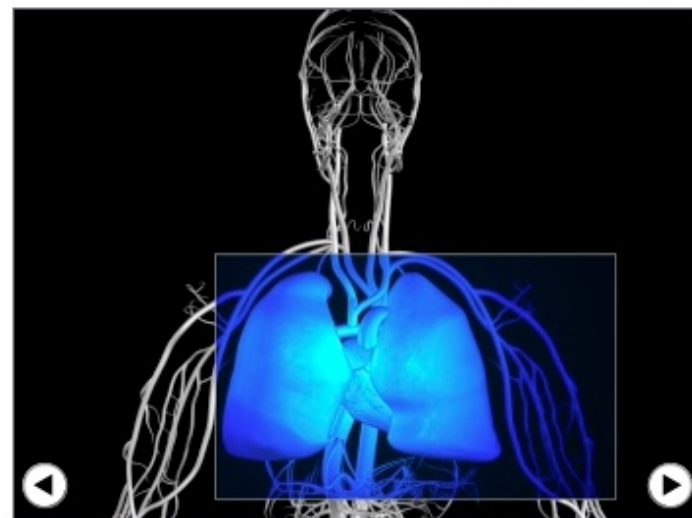
Alpha-1 Antitrypsin Deficiency

 [Printable Version](#)

The alpha-1 antitrypsin (AAT) [protein](#) protects the body, especially fragile lung tissues, from the damaging effects of a powerful enzyme called neutrophil elastase that is released from white blood cells. In AAT deficiency, a genetic mutation reduces levels of the protective protein in the bloodstream. AAT deficiency can lead to chronic obstructive pulmonary disease (COPD), specifically [emphysema](#), and liver disease. Smoking, which can inhibit what little AAT protein an affected person does have, increases the risk of lung disease.

The following results are based on [★★★★ Established Research](#) for 2 reported markers.

[Learn more about the biology of Alpha-1 Antitrypsin Deficiency...](#)



1 of 3. Low levels of alpha-1 antitrypsin can lead to COPD.


23andMe Drug Responses

drug response

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 23andMe Discoveries were made possible by 23andMe members who took surveys.

Name	Confidence ▾	Status
Clopidogrel (Plavix®) Efficacy	★★★★★	Greatly Reduced
Abacavir Hypersensitivity	★★★★★	Typical
Alcohol Consumption, Smoking and Risk of Esophageal Cancer	★★★★★	Typical
Fluorouracil Toxicity	★★★★★	Typical
Response to Hepatitis C Treatment	★★★★★	Typical
Pseudocholinesterase Deficiency	★★★★★	Typical
Thiopurine Methyltransferase Deficiency	★★★★★	Typical
Warfarin (Coumadin®) Sensitivity	★★★★★	Typical
Oral Contraceptives, Hormone Replacement Therapy and Risk of Venous Thromboembolism ♀	★★★★★	Not Applicable
Caffeine Metabolism	★★★	Fast Metabolizer
Hepatitis C Treatment Side Effects	★★★	See Report
Metformin Response	★★★	Typical Odds of Positive Response
Antidepressant Response	★★	See Report

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- Carrier Status
- [Drug Response](#)
- Traits
- Health Labs

- [My Ancestry](#)
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- Paternal Line
- Relative Finder
- Ancestry Painting
- Global Similarity
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- Compare Genes
- Family Inheritance
- 23andMe Community
- Genome Sharing

- [23andWe](#)
- Research Surveys (24)
- Research Snippets

drug response

Clopidogrel (Plavix®) Efficacy ★★★★★ ?

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Established Research report on 5 reported markers.

- Your Data**
- How It Works
- Resources
- Technical Report

[Next ▶](#)
Floxacin Toxicity

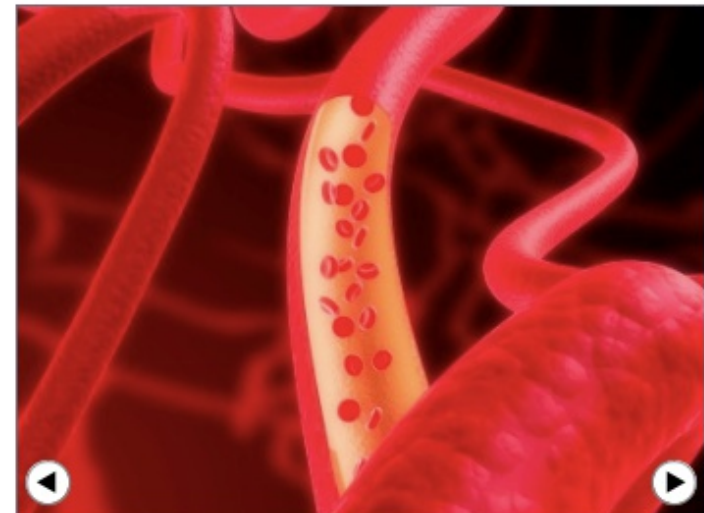
Only a medical professional can determine whether clopidogrel is the right medication for a particular patient. The information contained in this report should not be used to independently establish a clopidogrel regimen, or abolish or adjust an existing course of treatment.

About Clopidogrel Efficacy

 [Printable Version](#)

[Clopidogrel](#) (sold under the trade names Plavix®, Iscover®, Clopilet® and Ceruvin®) is a drug commonly prescribed in combination with aspirin to help prevent blood clots that can block blood flow and cause a heart attack or stroke. However, clopidogrel doesn't inhibit clotting to the same extent in everyone. For some people, genetic variations that prevent the drug from being converted into its active form in the body are the cause. Studies have shown that people who are taking clopidogrel who have these genetic variations may have reduced protection from heart attacks, strokes and death from cardiovascular causes.

[Learn more about the biology of Clopidogrel Efficacy...](#)



1 of 3. Clopidogrel keeps platelets from sticking together and prevents blood clots.

Plavix Ad with Genetic Requirement



[My Home](#)

Inbox (3)

[My Health](#)

Disease Risk

Carrier Status

Drug Response

► [Traits](#)

Health Labs

My Ancestry

Maternal Line

Paternal Line

Relative Finder

Ancestry Painting

Global Similarity

Ancestry Labs

Sharing & Community

Compare Genes

Family Inheritance

23andMe Community

Genome Sharing

23andWe

Research Surveys (21)

Research Snippets

Research Initiatives

Research Discoveries

traits

Share my health results with family and friends

Show results for

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23andWe Discoveries were made possible by 23andMe members who took surveys.

Name	Confidence ▲	Outcome
Alcohol Flush Reaction	★★★★★	Does Not Flush
Bitter Taste Perception	★★★★★	Can Taste
Earwax Type	★★★★★	Wet
Eye Color	★★★★★	Likely Brown
Hair Curl	★★★★★	Straighter Hair on Average
Lactose Intolerance	★★★★★	Likely Tolerant
Malaria Resistance (Duffy Antigen)	★★★★★	Not Resistant
Male Pattern Baldness ♂	★★★★★	Decreased Odds
Muscle Performance	★★★★★	Likely Sprinter
Non-ABO Blood Groups	★★★★★	See Report
Norovirus Resistance	★★★★★	Not Resistant
Resistance to HIV/AIDS	★★★★★	Not Resistant
Smoking Behavior	★★★★★	Typical
Adiponectin Levels new	★★★	See Report
Asparagus Metabolite Detection	★★★	Typical Odds of Detecting
Birth Weight	★★★	See Report
Blood Glucose	★★★	5.18 mmol/L on Average
Breastfeeding and IQ	★★★	See Report
C-reactive Protein Level	★★★	2.09 mg/L on Average

Choice of GWAS Studies

- Common traits of broad interest
 - Prevalence of $> 1\%$
 - Report Mendelian traits when possible
 - Focus on drug responses
- Avoid false discoveries
 - Large case-control studies > 750 cases
 - Highly significant expectation values (< 0.01 errors)
 - Published in reputable journals
 - Studies that have been replicated
- May impute highly linked missing SNPs
- Calculate likelihood and odds ratio using customers ethnicity as detected
- Distinguish preliminary studies (non-replicated or smaller sample sizes) from established research.



ancestry overview

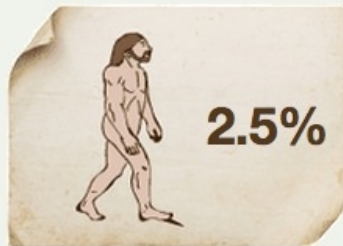
Your Father's Line

Your father's line was likely in eastern Africa 50,000 years ago. Today that line is still found primarily in Africa.



Neanderthal Ancestry

You have an estimated **2.5%** Neanderthal DNA, which puts you in the **39th** percentile among Northern European 23andMe members.



Your Extended DNA Family

Guess what? If you have a large piece of identical DNA in common with someone, then you're related. You have **505** DNA relatives in 23andMe. Explore their info to learn more about your own ancestry.

Close Family 1st-2nd Cousins 3rd-4th Cousins Distant Cousins

2 0 60 443

Your Mother's Line

Along your mother's line, you have ancestry in **Europe/the Near East** in the past few hundred years, that traces back to eastern Africa around 50,000 years ago.



From Your Ancestry Expert

It's remarkable what you can discover from a little saliva. On this page are the highlights of what we've learned about your ancestry, based just on your DNA. Enjoy!

Dr. Joanna Mountain, PhD

Joanna Mountain is 23andMe's Senior Director of Research. A former Stanford professor, she has traveled the world studying genetics and human history.

AS SEEN ON



A N D E R S O N

Ancestry Help

Send Feedback

Top Relative Surnames

Surname	Count	Enrichment
Anderson	5	10
Smith	5	1

Maternal Haplogroup: U5b2a

Share

Map

History

Haplogroup Tree

Community

Maternal Haplogroup: U5b2a

U5b2a is a subgroup of U5, which is described below.

Locations of haplogroup U5 circa 500 years ago, before the era of intercontinental travel.



Haplogroup U5 arose among early colonizers of Europe around 40,000 years ago; maternal descendants of those early colonizers persist in the region to this day. After the last Ice Age two subgroups of U5 expanded across Europe and into northern Africa and the Near East. Today, one subgroup, U5b1b, is shared by groups as diverse as the northern African desert-dwelling Berbers and the Scandinavian Arctic-dwelling Saami, also known as the Lapps.

Human Prehistory Videos



[Human Prehistory: Prologue](#)



[Out of \(Eastern\) Africa](#)

Haplogroup: U5, a subgroup of [R](#)

Age: 40,000 years

Region: Europe, Near East, North Africa

Populations: Basques, Saami (Lapps) of northern Scandinavia

Highlight: Though primarily a European haplogroup, U5 was recently found in mitochondrial DNA extracted from the remains of a 6th-century AD Chinese chieftain.

Your Family and Friends

A2	Samantha Hill
D4e2	Japanese Person
D5a2a'c	Chinese Person
H3	Lilly Mendel (Mom), Erin Mendel (Daughter), Alan Mendel (Son), Ian Mendel (Son), Margo Fisher (Grandma)
H4a1	Ron Fisher (Grandpa)
K1a1b1a	Benjamin Brutlag, Pauline Brutlag, Simone Brutlag
L3e2b2	Nigerian Person
M35b	renu heller

Paternal Haplogroup: E1b1b1a2*

Share

Map

History

Haplogroup Tree

Community

Paternal Haplogroup: E1b1b1a2*

E1b1b1a2* is a subgroup of E1b1b1a, which is described below.

Locations of haplogroup E1b1b1a circa 500 years ago, before the era of intercontinental travel.



E1b1b1a is most common in northern Africa and southern Europe. It arose about 23,000 years ago in eastern Africa and spread into the Mediterranean region after the Ice Age.

E1b1b1a, a subgroup of E1b1b, expanded out of the Near East 8,000 years ago into northern Africa and southern Europe. Today it is one of the most common haplogroups in those regions.

Haplogroup: E1b1b1a, a subgroup of [E1b1b](#)

Age: 23,000 years

Region: Northern Africa, Southern Europe

Populations: Berbers, Iberians, Balkans

Highlight: Two different migrations brought E1b1b1a into Europe.

Your Family and Friends

[D2a1b](#) Japanese Person

[E1b1a8a1...](#) Nigerian Person

[E1b1b1a2...](#) Douglas Brutlag, Benjamin Brutlag

[G2a](#) Brian Becker

[I1*](#) Greg Mendel (Dad), Alan Mendel (Son), Ian Mendel (Son), Fred Mendel (Grandpa)



ancestry overview

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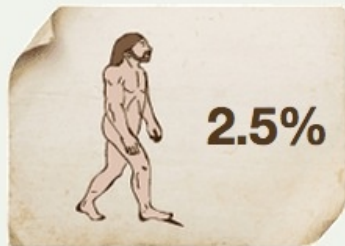
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AS SEEN ON



A N D E R S O N

[Ancestry Help](#)

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Top Relative Surnames

Surname	Count	Enrichment
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Smith	5	1

Ancestry Composition

ancestry composition

Douglas Brutlag

Standard Estimate

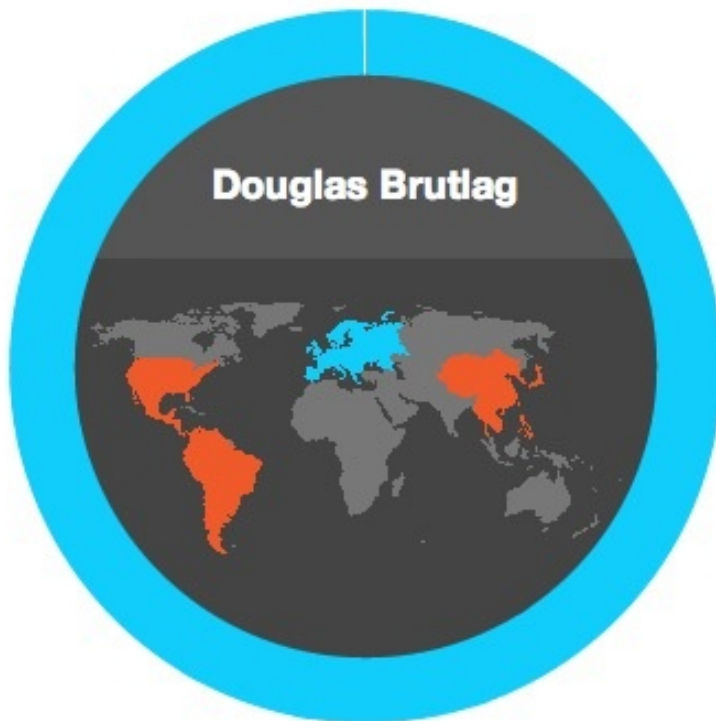


Map View

Global Resolution



Ancestry Composition tells you what percent of your DNA comes from each of 22 populations worldwide. The analysis includes DNA you received from all of your ancestors, on both sides of your family. The results reflect where your ancestors lived 500 years ago, before ocean-crossing ships and airplanes came on the scene.



99.9% European

< 0.1% East Asian & Native American

0.1% Unassigned

100.0% **Douglas Brutlag**

[show all populations](#)

Ancestry Composition

ancestry composition

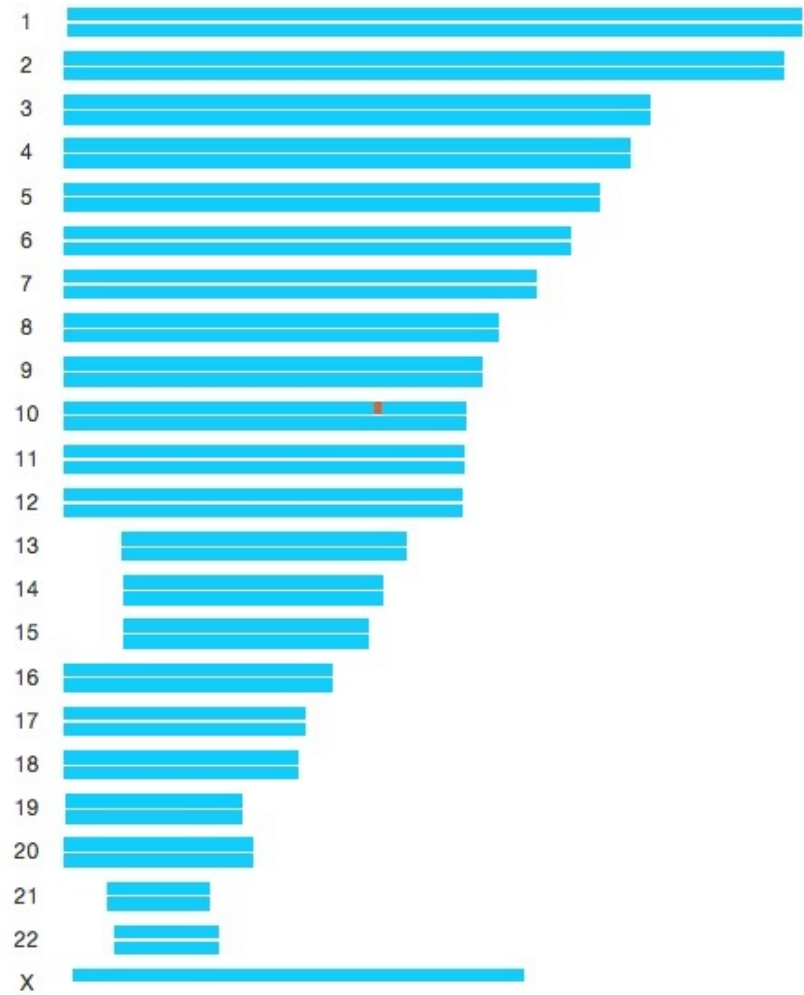
Douglas Brutlag

Speculative Estimate



Chromosome View

Global Resolution



Ancestry Composition tells you what percent of your DNA comes from each of 22 populations worldwide. The analysis includes DNA you received from all of your ancestors, on both sides of your family. The results reflect where your ancestors lived 500 years ago, before ocean-crossing ships and airplanes came on the scene.

99.9% European

0.1% East Asian & Native American

100.0% Douglas Brutlag

[show all populations](#)

23andMe Relative Finder

relative finder

? List view Map view Surname view

search matches: Show: both sides Sort: relationship 25 per page 1 - 25 of 504

Male You U5b... E1b1b1... [Update Your Profile](#)

 **Benjamin Brutlag**
Male, b. 1980
Son
47.7% shared, 22 segments
United Sta... Southern Euro...
K1a1b... E1b1b1...

[Sharing Genomes](#)
[Send a Message](#)

 **Pauline Brutlag**
Female
Daughter
53.1% shared, 25 segments
United Sta... Northern Euro...
K1a1b...

[Sharing Genomes](#)
[Send a Message](#)

Male
3rd to 4th Cousin
0.77% shared, 3 segments
... I2...

[Send an Introduction](#)

Male
3rd to 5th Cousin
0.47% shared, 3 segments
... R1a...

[Send an Introduction](#)

 **Larry Vongroven**
Male
3rd to 5th Cousin
0.54% shared, 2 segments
United Sta... Alen, Nor...
Haltalen, Nor... Voss, Nor...
8 m... Northern Euro...
Vongroven (Vongrav... Bakk...
Good... 11 m... U4b1...
R1a...

[Introduction Received](#)
[Respond](#)
[View Family Tree](#)

 **Carolyn Otterness**
Female, b. 1941
3rd to 5th Cousin
0.47% shared, 2 segments
United Sta...
Otsego, Wisconsin, Dodge County, C...
Northern Euro... Ottern...
Brandsn... Gjerne... 5 m...
K1a...

[Public Match](#)
[Send a Message](#)

 **Gale Enger**
Male, b. 1925
3rd to 5th Cousin
0.41% shared, 2 segments
United Sta...
Norway, Denmark, Minnesota, Wisco...
Northern Euro... En... Lars...
Mest... 6 m... K1... ...

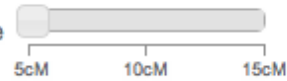
[Introduction Received](#)
[Respond](#)



Hide Advanced Controls

Number of grandparents from the same country

Minimum Segment Size



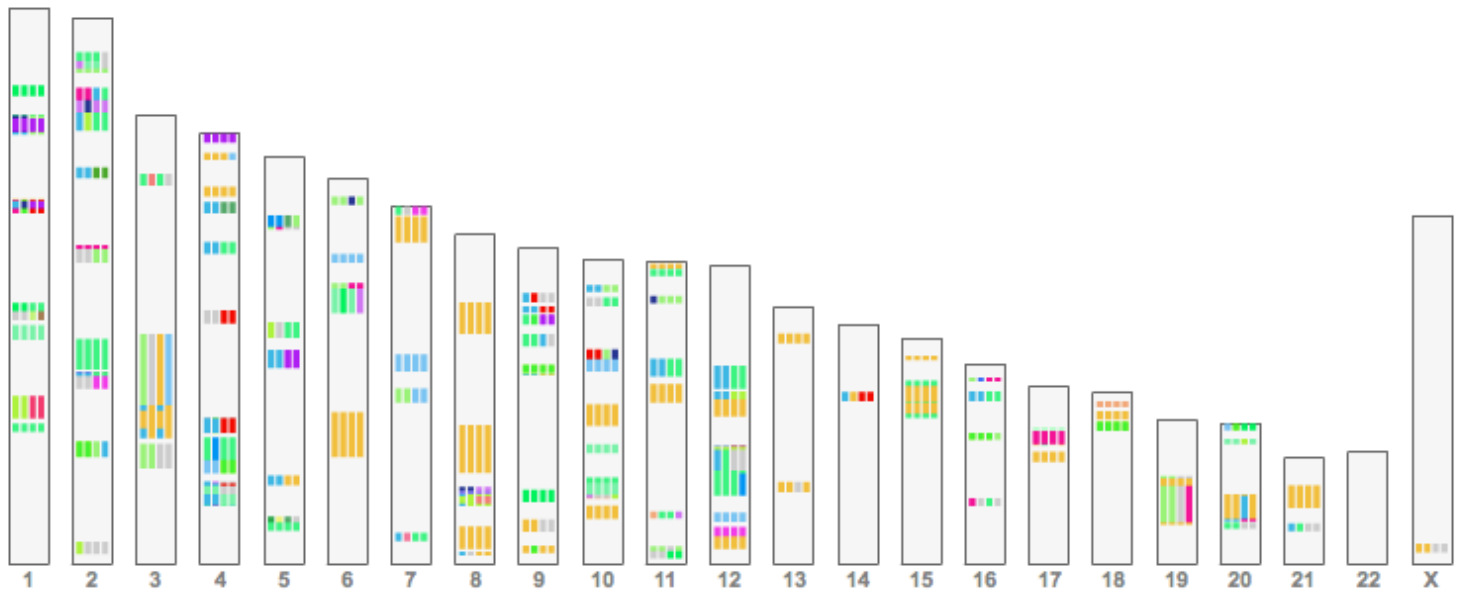
Include matches primarily from US, Canada, Australia, New Zealand & South Africa

Indicate segments declared to be of Ashkenazi Jewish ancestry.

Only show segments belonging to public individuals.

[Learn more about Advanced Controls](#)

Country	Color	Percent of Douglas Brutlag's Genome Covered
Norway		3.4% – 5.2%
Germany		1.6% – 6.1%
Ireland		0.7% – 1.5%
Denmark		0.4% – 1.7%
Russia		0.4% – 0.9%
Sweden		0.3% – 1.0%
Netherlands		0.3% – 0.7%
Finland		0.3% – 0.7%



What is a Fifth Cousin?

So You're

23andWe Discoveries

23andWe discoveries



You answer questions.



Other 23andMe members answer questions.



23andMe scientists work their magic.



And make discoveries!

Your contributions

These articles are based on surveys you've taken.



New Genetic Factors for Hypothyroidism



Thanks! You took a survey that fueled this discovery.

[view discovery](#)



Ancestry and Disease Risk



Thanks! You took a survey that fueled this discovery.

[view discovery](#)



Genes and Geography



Thanks! You took a survey that fueled this discovery.

[view discovery](#)

A new paradigm for genetic research.



[Read our open letter to the science community](#)

23andMe is a new, more efficient way of doing genetic research. Even though new technologies have made it possible to link genes to diseases, traits and conditions more effectively than ever before, collecting the data for this research can be a costly, time-consuming and logistically difficult process. Progress is hindered by the fact that these studies require both genetic and personal information from thousands – sometimes tens of thousands – of people.

23andMe involves our customers in research as collaborators, advisers and contributors by conducting studies that correlate their responses to online surveys with their genetic data. The idea is to enable large studies that would be infeasible using current methods, which typically involve recruiting patients through physicians' practices and other means. We plan to share the results of our research and show you how your contributions are making an impact by posting regular updates on this web site.

▶▶ [Next: How does research work at 23andMe?](#)



Join a research community



Parkinson's Disease

Recent discoveries suggest that genetics plays a greater role in Parkinson's disease than was previously thought. You can advance research into the genetic roots of Parkinson's disease.



Alzheimer's Disease

More than 5 million Americans have Alzheimer's Disease. 23andMe and Genentech have teamed up to find out how genetics might protect against Alzheimer's Disease. This research could lead to new scientific knowledge or possibly a drug that could prevent or slow Alzheimer's Disease.

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Genetic Expertise

- ✓ Cancer Genetics
- ✓ Reproductive Genetics
- ✓ Cardiac Genetics
- ✓ Ocular Genetics
- ✓ Neurogenetics
- ✓ Adult Genetics

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- ✓ Ample Appointment Availability
- ✓ Insurance Authorization
- ✓ Genetic Test Coordination
- ✓ Expert Test Interpretation
- ✓ Personalized Healthcare Reports

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- Our services
- FAQs
- Tools
- Set up your practice
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What other physicians say:

“We believe that Navigenics’ preventive genomics service has the potential to be an innovation that could significantly enhance patient care.”

-Edward Goldman, M.D.,
Former CEO, MDVIP, Inc.

We care about the science, your patients, and you

Make personalized genomic medicine and pharmacogenomics part of your practice. And provide your patients with a powerful tool for change.



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Your patients trust you; you can trust us.

- Founders, practicing physician [David Agus, M.D.](#), and geneticist [Dietrich Stephan, Ph.D.](#), came together so that they could create a powerful new tool for personalized medicine.
- Focused on prevention, pharmacogenomics, and longitudinal health outcome studies.

We can help answer your questions.

- Medical education programs, resources and board-certified genetic counseling.
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Partner with the leader in genomic health, just as we partner with the leaders in medicine.

- We collaborate with Mayo Clinic, Scripps Genomic Medicine, Duke, and others.

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- Downloads**
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 - [The Science Behind the Navigenics Health Compass Service](#)
 - [Conditions We Cover](#)
- Quick links**
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 - [Our testing services](#)
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Free Information Kit



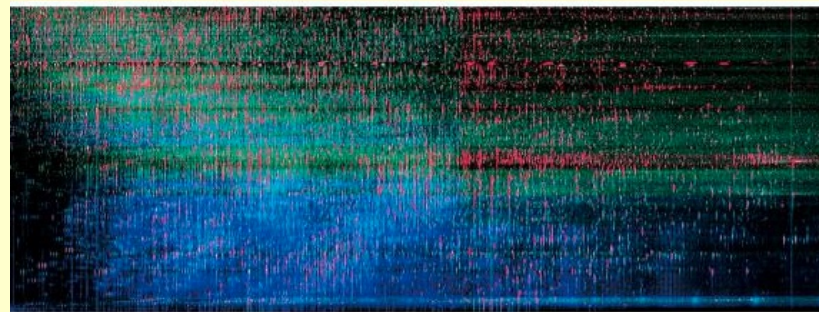
Navigenics physician kit

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THE END *of* ILLNESS



David B. Agus, MD

\$12 Paperback
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DNAdirect: Clinical Genetic Testing









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- » Hospitals
- » Physicians
- » Consumers

Our Products

- » Policy & Benefit Support Program
- » Coverage Management
- » Clinical Testing Programs
- » Decision Support Program
- » Home Biometrics
- » Genomic Medicine Network
- » About Personalized Medicine
- » Newsroom
- » About Us

DNA Direct brings the power of personalized medicine to payors, providers and patients.

 THE RIGHT PERSON	 THE RIGHT TEST	 THE RIGHT INTERPRETATION
<p>Finding the right people to benefit from genomic medicine can improve disease management and lower healthcare costs.</p>	<p>Getting the wrong test can misinform medical decisions and increase healthcare costs.</p>	<p>Delivers the full value of genetic information and enables physicians to make appropriate management decisions.</p>
		

Hospital Plan Webinar

Strategies to Optimize Personalize Medicine: How to Integrate Genomic Services into Your Hospital Community

Dr. Derek Kelly, Vice President, Medical Management at Swedish Covenant Hospital in Chicago discusses integrating genomic services into their clinical care.

Health Plan Webinar

How a Health Plan Successfully Integrated Genomic Services into Its System

Dr. Charles Stemple, Medical Director, Personalized Medicine/Genomics at Humana discusses their genetic guidance program.

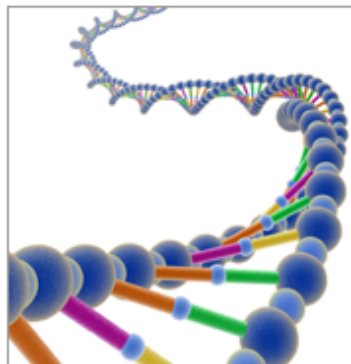
About Personalized Medicine

Our Customers

- » Health Plans
- » Employers
- » Hospitals
- » Physicians
- » Consumers

Our Products

- » Policy & Benefit Support Program
- » Coverage Management
- » Clinical Testing Programs
- » Decision Support Program
- » Home Biometrics
- » Genomic Medicine Network



Personalized medicine, also referred to as genomic medicine, is changing the landscape of healthcare. By harnessing the power of genetic testing, physicians can make more informed healthcare decisions and better target treatments and drug therapies. The result is better healthcare outcomes.

Genetic tests are used in all areas of medicine – from prevention and screening to diagnosis and treatment. G2 Intelligence estimated that the market was \$14.3B in 2010 and growing rapidly at 16% per year¹ and the Food and Drug Administration (FDA) states that more than 100 medications have pharmacogenomic information included in their drug labels². Research by the Tufts Center for the Study of Drug Development indicates that oncology leads

other therapeutic areas in the number of targeted therapies on the market as well as in the pipeline, with the expectation that within the decade all oncology drugs will have a related diagnostic. Other key therapeutic areas in which personalized medicine is impacting clinical decision-making include cardiovascular, neurologic, and immunologic therapies, whereas personalized medicine development is just getting started for metabolic and respiratory therapies, as well as virology³. With the advent of all of this new technology and information available to healthcare professionals and consumers, it will be critical to stay abreast of the new developments.

Low-cost whole genome sequencing (WGS) is on the horizon as well, adding a profound new dimension to the personalized medicine arsenal. Healthcare providers and consumers will be challenged with how best to interpret the information available to them.

As advances in personalized medicine continue, patients benefit from the deeper knowledge that genomics brings to healthcare decision making and outcomes.

1. G2 Intelligence: Lab Industry Strategic Outlook 2011: Market Trends & Analysis



2. www.fda.gov/drugs/scienceresearch/researchareas/pharmacogenetics/ucm083378.htm

3. *Personalized Medicine Is Playing A Growing Role In Development Pipelines* November/December 2010 Tufts CSDD Impact Report ; Vol12:6

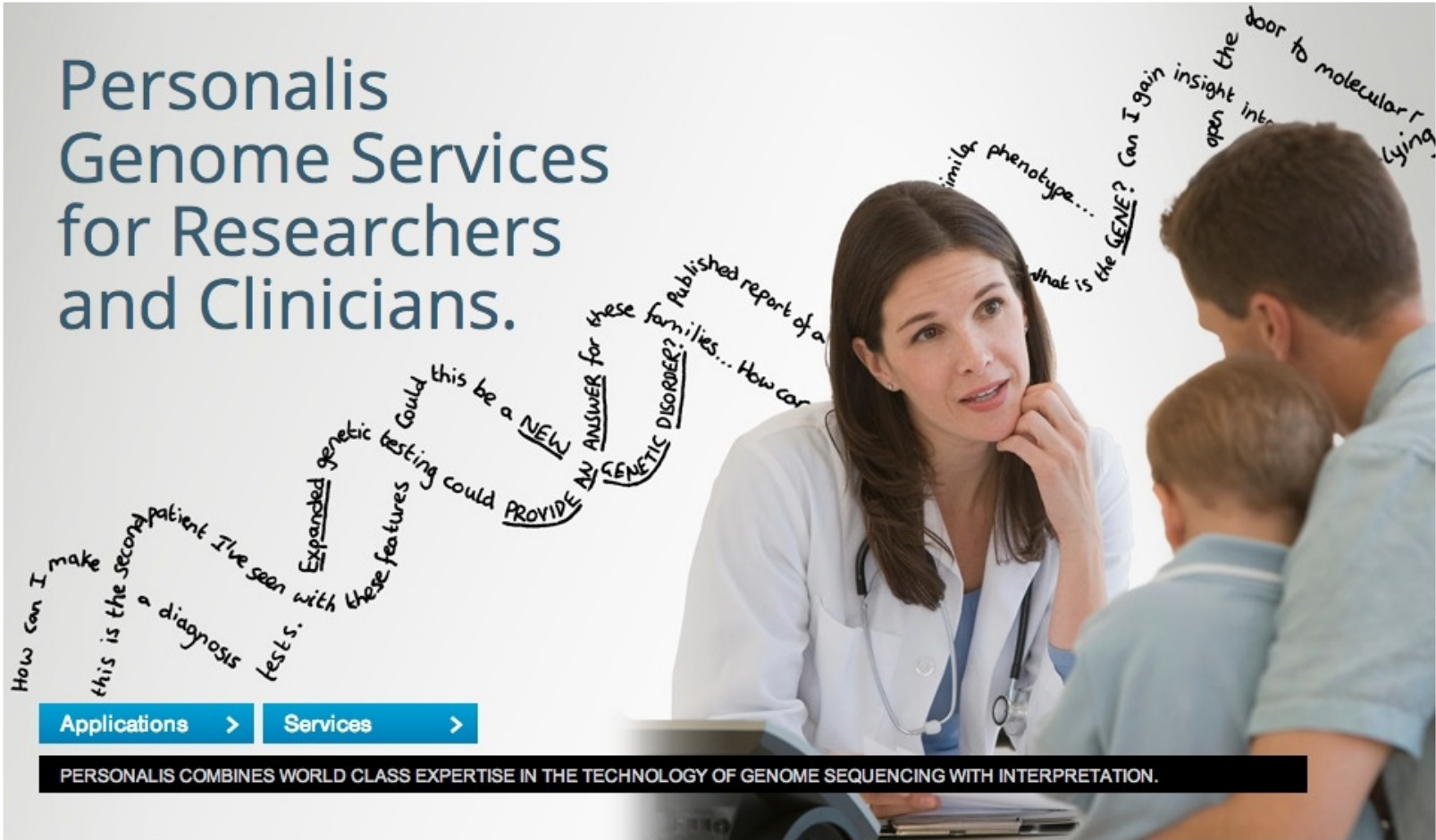


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Genomes

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**The variant interpretation and reporting platform
of choice for the UK 100,000 Genomes Project,
LabCorp and clinical labs worldwide.**

Accurately report on causative variants from gene panels, exomes, and whole genomes.

Omicia's Opal Clinical system is a robust, scalable platform developed in collaboration with leading testing labs to accelerate the clinical interpretation of NGS data.

Learn how your lab can optimize report turnaround time and increase diagnostic yield with NGS testing. Schedule a free Opal demo today.

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Omicia Movie

<http://www.omicia.com/>





Our Story

Watch our video to learn more about Sure Genomics' full DNA sequencing process and platform.



Your **Full DNA Sequence**

We are enabling consumers to obtain, access and review their full Genomic DNA sequence through a system we call **Get Look Plan™**

Genome Voyager™ ALPHA



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Complete Genomics is a leader in accurate whole human genomic sequencing. Using our proprietary sequencing instruments, chemistry, and software, we have sequenced more than 15,000 whole human genomes for our research customers over the past three years. Our mission is to provide the technology for sequencing one million human genomes, enabling researchers and clinicians to improve human health through the prevention, diagnosis, and treatment of genetic diseases and conditions.

BGI-Shenzhen
Completes
Acquisition of
Complete Genomics

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nature
Read the
ground
breaking
Nature paper
on LFR
Technology

[Read More](#)

Genome Voyager DX from Genos Research

<https://voyager-staging.genosresearch.com/index.html#case/13356/sample/33/workspace>

Cases > 41
Case ID: 13356

Case Overview

View: Variants

Filter: Exome

Search Gene, Location, or rsID

11255 RESULTS

Sort by: Community Assessment

PATHOGENIC

NM_013339.3(ALG6): c.391T>C (p.Y131H)
chr1:63,872,031-63,872,032
1:2

NM_000036.2(AMPD1): c.242C>T (p.P81L)
chr1:115,231,253-115,231,254
1:1

NM_000036.2(AMPD1): c.133C>T (p.Q45*)
chr1:115,236,056-115,236,057
1:2

NM_001002294.2(FMO3): c.472G>A (p.E158K)
chr1:171,076,965-171,076,966
1:1

NM_001002294.2(FMO3): c.769G>A (p.V257M)

Karyogram Cytogenomic Circos

Chromosome	CNVs	Small Var	Genes
1	44	348K	2520
2	22	364K	1597
3	14	305K	1354
4	12	328K	957
5	20	277K	1096
6	11	284K	1286
7	17	255K	1222
8	10	234K	904
9	24	182K	1042
10	22	224K	966
11	7	228K	1524
12	9	211K	1236
13	4	172K	519
14	6	146K	828
15	4	133K	881
16	17	135K	1021
17	9	128K	1424
18	1	123K	370
19	7	107K	1673
20	5	92K	701
21	2	64K	316
22	5	58K	593
X	21	157K	1052
M	47	37	Genes

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chr1:171,076,965-171,076,966
1:1
- NM_001002294.2(FMO3): c.769G>A (p.V257M)**
chr1:171,080,079-171,080,080
1:1
- NM_001002294.2(FMO3): c.923A>G (p.E308G)**
chr1:171,083,241-171,083,242
1:1

NM_013339.3(ALG6): c.391T>C (p.Y131H)

Pinned

Create Interpretation

No KB Assessments | No Case Assessments | Pathogenic 1:2

Interpre... | Genome... | Technic... | Knowled... | Case Ass... | Commu... | Variant... | External...

Copy Number

Allele Specific Copy Number

Small Variations

5' C A T A C C T G C A G T G G T T T T G T A C T G T T G T T G C T T A A A

Genes

ALG6 >

I P A V V L Y C C C L K

A T A C C T G C A G T G G T T T T G T A C T G T T G T T G C T T A A A

H

C A C



Genome Voyager DX

Cases > 41
Case ID: 13356

Case Overview

View: Variants



Filter: Exome

Search Gene, Location, or rsID

11255 RESULTS

Sort by: Community Assessment

PATHOGENIC



NM_013339.3(ALG6): c.391T>C (p.Y131H)

chr1:63,872,031-63,872,032

1:2



NM_000036.2(AMPD1): c.242C>T (p.P81L)

chr1:115,231,253-115,231,254

1:1



NM_000036.2(AMPD1): c.133C>T (p.Q45*)

chr1:115,236,056-115,236,057

2:2



NM_001002294.2(FMO3): c.472G>A (p.E158K)

chr1:171,076,965-171,076,966

1:1



NM_001002294.2(FMO3): c.769G>A (p.V257M)

chr1:171,080,079-171,080,080

1:1



Pinned

NM_013339.3(ALG6): c.391T>C (p.Y131H)

Create Interpretation

No KB Assessments

No Case Assessments

Pathogenic 1:2

Interpre...

Genome ...

Technic...

Knowned...

Case Ass...

Commu...

Variant ...

Genomic Coordinates

Chromosome: chr1

Position: 63,872,031 - 63,872,032

Cytoband: 1p31.3

Reference Genome: GRCh37

DNA Change

Reference Sequence: T

Called Sequence: C

Small Variation Type: snv

Zygosity: Heterozygous-Ref

Haplink ID:

Allele Frequencies

1000 Genomes Allele Freq: 2.000% (2184)

ESP6500 Allele Freq: 2.922% (13006)

Complete Genomics Allele Freq: 1.852% (108)

Welllderley Allele Freq: Not Found

Genome Voyager DX

Cases > 41
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chr1:171,076,965-171,076,966
 **1:1**

 **NM_001002294.2(FMO3): c.769G>A (p.V257M)**
chr1:171,080,079-171,080,080
 **1:1**

NM_013339.3(ALG6): c.391T>C (p.Y131H)



Create Interpretation

No KB Assessments

No Case Assessments

 **Pathogenic 1:2**

Interpre...

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ESP6500 Allele Freq: **2.922% (13006)**

Complete Genomics Allele Freq: **1.852% (108)**

Welllderley Allele Freq: **Not Found**

Gene Annotations

Gene Symbol: [ALG6](#)

Associated KB Conditions: [Congenital disorder of glycosylation, type 1c](#)

mRNA Acc (Transcript)	Nucleotide Change	Protein Change	Gene Region	Functional Impact
NM_013339.3	c.391T>C	p.Y131H	CDS, Exon(6)	Missense

Cross References

dbSNP ID: [rs35383149](#)

DGV ID: **Not Found**

pFam ID: **Not Found**

mirBase ID: **Not Found**

Cosmic ID: **Not Found**

Genome Voyager DX

Cases > 41

Case ID: 13356

Case Overview

View: Variants


Filter: Exome



Search Gene, Location, or rsID



11255 RESULTS



Sort by: Community Assessment



PATHOGENIC

 **NM_013339.3(ALG6): c.391T>C (p.Y131H)**
chr1:63,872,031-63,872,032
 **1:2**

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 **1:1**

 **NM_000036.2(AMPD1): c.133C>T (p.Q45*)**
chr1:115,236,056-115,236,057
 **2:2**

 **NM_001002294.2(FMO3): c.472G>A (p.E158K)**
chr1:171,076,965-171,076,966
 **1:1**

 **NM_001002294.2(FMO3): c.769G>A (p.V257M)**
chr1:171,080,079-171,080,080
 **1:1**

NM_013339.3(ALG6): c.391T>C (p.Y131H)



Pinned

Create Interpretation

No KB Assessments

No Case Assessments

Pathogenic 1:2

Interpre...

Genome ...

Technic...

Knowned...

Case Ass...

Commu...

Variant ...

1000 Genomes Allele Freq: 2.000% (2184)

ESP6500 Allele Freq: 2.922% (13006)

Complete Genomics Allele Freq: 1.852% (108)

Welllderley Allele Freq: Not Found

Gene Annotations

Gene Symbol: [ALG6](#)

Associated KB Conditions: [Congenital disorder of glycosylation, type Ic](#)

mRNA Acc (Transcript)	Nucleotide Change	Protein Change	Gene Region	Functional Impact
NM_013339.3	c.391T>C	p.Y131H	CDS, Exon(6)	Missense

Cross References

dbSNP ID: [rs35383149](#)

DGV ID: Not Found

pFam ID: Not Found

mirBase ID: Not Found

Cosmic ID: Not Found

Genome Voyager DX Genos Research

Cases > 41
Case ID: 13356

Case Overview

View: Variants

Filter: Exome

Search Gene, Location, or rsID

11255 RESULTS

Sort by: Community Assessment

PATHOGENIC

NM_013339.3(ALG6): c.391T>C (p.Y131H)
chr1:63,872,031-63,872,032
1:2

NM_000036.2(AMPD1): c.242C>T (p.P81L)
chr1:115,231,253-115,231,254
1:1

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chr1:115,236,056-115,236,057
2:2

NM_001002294.2(FMO3): c.472G>A (p.E158K)
1:171,074,015-171,074,016

NM_013339.3(ALG6): c.391T>C (p.Y131H)

Create Interpretation

No KB Assessments | No Case Assessments | Pathogenic 1:2

Interpr... | Genome... | Technic... | Knowle... | Case As... | Commu... | Variant ... | Externa...

Genome Browsers

UCSC |> DGV |>
DBVar |> Ensembl |>

Public Resources

Pubmed |> Gene Reviews |>
Locus Specific DBs |> GET-Evidence |>
NHGRI CGD |> Google |>
Uniprot |>

Personal Genomics References

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