Jane Doe
Sex Assigned at Birth: Female
Date of Birth: 11/15/1962
Sample ID: SM-0000232
Sample Type: BLOOD
Collection Date: 02/01/2024
Received Date: 02/03/2024

Clinic: Cardiovascular Health Center
Physician: Test Provider, M.D., Ph.D.
Phone: 510-555-0000
NPI: 1234567890

Requisition ID:
RQ-0000059
Report Number:
RP12345
Report Date:
08/22/2025

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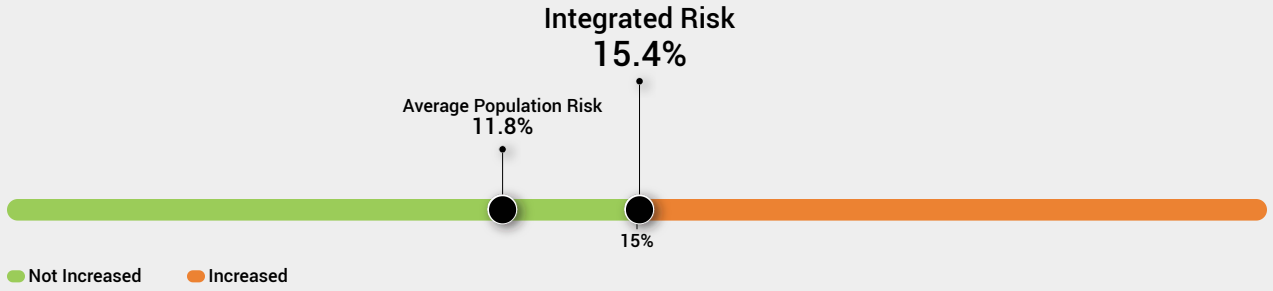
Increased Risk

Based on the integrated risk score, this patient has a 15.4% chance of developing type 2 diabetes in the next 10 years.

10-YEAR ABSOLUTE RISK OF TYPE 2 DIABETES



Integrated Risk: The chance of developing type 2 diabetes in the next 10 years based on the combination of a polygenic risk score (PRS) and clinical risk factors.

Average Population Risk: The chance of developing type 2 diabetes in the next 10 years for someone of the same age and sex in the general population.

Based on the integrated risk score, this patient has a 15.4% chance of developing type 2 diabetes in the next 10 years.

This test determined that the patient is at increased risk for type 2 diabetes, defined as an absolute 10-year integrated risk greater than 15%. Being at increased risk for type 2 diabetes does not mean that the patient will definitely develop the disease. There may be other genetic and non-genetic factors not considered here that influence the patient's risk.

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Report Information:
Jane Doe
DOB: 11/15/1962
Requisition ID: RQ-0000059

Lab Director:
Brynn Levy M.Sc.(Med)., Ph.D., FACMG
CLIA #05D2203070 CAP #8939502

NEXT STEPS

The ADA recommends all patients follow a heart-healthy lifestyle, including smoking cessation, regular physical activity, and a balanced diet.

For patients with an increased risk for 10-year type 2 diabetes, the ADA recommends a combination of lifestyle changes and screening. Lifestyle modifications include regular exercise, maintaining a healthy body weight, and eating a heart-healthy diet. Screening includes assessing for symptoms of diabetes, such as excessive urination and weight changes, and checking hemoglobin A1c and fasting glucose [3].

CLINICAL MEASUREMENTS

The clinical measurements used to estimate the patient's risk of developing type 2 diabetes were provided by the ordering physician and detailed below. Changes in these measurements may result in a change in the patient's risk estimation.

Age	63	**Systolic Blood Pressure**	182 mm Hg
Sex Assigned at Birth	Female	**Waist Circumference**	118 cm
Smoking Status	Former smoker	**HDL Cholesterol**	75 mg/dL
Body Mass Index	19 kg/m²	**Fasting Glucose Level**	212 mg/dL
First Degree Relatives with T2D	Yes	**Triglyceride Level**	155 mg/dL

REFERENCES

1. Ratman, D. et al. (2024, June). Utility of Polygenic Risk Scores for Prediction of Incident Type 2 Diabetes. Poster presented at: The European Human Genetics Conference; Berlin, Germany.
2. Tshiaba, Placede et al. Genetics in Medicine Open, Volume 1, Issue 1, 100361.
3. American Diabetes Association Professional Practice Committee. Prevention or Delay of Diabetes and Associated Comorbidities: Standards of Care in Diabetes- 2025. Diabetes Care. 2025;48(1 Supp 1):S50-S58. PMID: 39651971
4. American Diabetes Association Professional Practice Committee. Diagnosis and Classification of Diabetes: Standards of Care in Diabetes-2025. Diabetes Care. 2025; 48(48):S27-S49. PMID: 39651986
5. US Preventative Services Task Force. Screening for Prediabetes and Type 2 Diabetes. JAMA. 2021;326;(8):736-743. PMID: 34427594

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TEST METHODS

- Patient data is provided by the ordering physician. Specimen receipt, accessioning, data analysis and interpretation is performed by MyOme, Inc., 1455 Adams Dr., Ste 1150, Menlo Park, CA 94025, CLIA#05D2203070. Blended Genome-Exome sequencing, excluding data analysis and interpretation, is performed by Broad Clinical Labs LLC, 27 Blue Sky Dr, Burlington, MA 01803, CLIA#22D2055652.
- Genomic DNA obtained from the submitted sample was used to construct a PCR-free whole genome library and an exome library and sequenced using Illumina technology generating low-coverage whole-genome and higher coverage exome data. Reads were aligned to the NCBI GRCh38.p14 reference assembly.
- Genotype likelihoods are estimated for bases covered by at least one sequencing read. Genotypes at additional sites are imputed based on a genotype reference panel.
- A polygenic risk score (PRS) is calculated for each of 5 continental ancestries of which the patient is a part as the sum of the patient's risk alleles weighted by the allele-specific effect sizes. The raw scores are centered using four principal components and standardized with a population-specific standard deviation. Standardized PRSs weighted by fractional ancestry and ancestry-specific effect sizes are summed (caPRS) [2].
- The standardized PRS is integrated with non-genetic risk factors, including age, sex, BMI, waist circumference, smoking status, systolic blood pressure, family history of T2D and clinical measurements (fasting glucose, HDL-C, triglycerides) to estimate the patient's 10-year risk of developing T2D.
- The 15% increased-risk cutoff was set to match the risk associated with BMI ≥ 25 kg/m² (overweight), as defined in the literature [5].

TEST LIMITATIONS

- This tool cannot be used to detect rare variants including those in genes associated with monogenic diabetes.
- The clinical risk was calculated based on the patient data provided by the ordering physician. Incorrect information will impact this calculation and the integrated risk score.
- A risk calculation will not be performed for individuals younger than 35 or older than 70 years old, individuals with prior T2D diagnosis (based on any ADA criteria) or those using insulin or oral antidiabetic medications.
- The type 2 diabetes integrated risk is a risk assessment tool and is not diagnostic. These results should be interpreted in the context of the individual's personal medical history and family history.
- Performance of this tool may be reduced in certain populations.
- A history of stem cell or bone marrow transplantation, or recent blood transfusion may impact the accuracy of the results.
- Like most tests, this test caries a risk of false negative or false positive results, which may be caused by, without limitation, sample contamination from biological or non-biological sources, specimen marking issues, rare genetic variants interfering with analysis, and other technical issues and limitations.

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DISCLAIMERS

- This test was developed, and its performance characteristics were determined, by MyOme, Inc., a clinical laboratory certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) and College of American Pathologist (CAP) accredited to perform high complexity clinical laboratory testing. This test has not been cleared or approved by the U.S. Food and Drug Administration (FDA).
- Like most tests, this test carries a risk of false negative or false positive results. Testing is unavailable for samples damaged by human error, lost/destroyed due to weather, transit issues or other problems beyond the control of MyOme. Test results should always be interpreted by a clinician in the context of clinical and familial data with the availability of genetic counseling when appropriate. MyOme is not responsible for the content of third-party websites referenced in this report.
- The interpretation of variants is based on our current understanding of the genome. These interpretations may change over time as more information about these alterations becomes available. Possible diagnostic errors include variant call errors, sample misidentification, and other sources.

REVIEWED BY

MyOme

MyOme Example Lab Director

08/22/2025

Date

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