

FIRST NAME: Oscar
LAST NAME: Meyer
DOB: 01/01/1964
PATIENT ID: HDHD-1-1

SAMPLE ID: ASDFG123
SAMPLE TYPE: Buccal swab
COLLECTION DATE: 01/06/2026
ORDERING PROVIDER: Sherlock Holmes

ORDERING PROVIDER INSTITUTION:
Baker Street Medical Center
ORDER REQUISITION: XXXXX
DATA RECEIVED: 01/08/2026
REPORT DATE: 01/18/2026

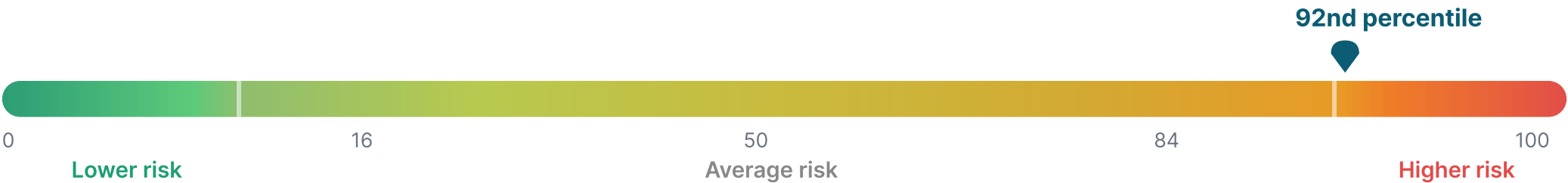
Arboretum CAD PRS Test (Coronary Artery Disease Polygenic Risk Score)

TEST RESULTS

RISK CLASSIFICATION

This individual's polygenic risk score (PRS) for coronary artery disease (CAD) falls at the 92nd percentile compared to individuals of similar genetic ancestry. This score reflects a higher than average inherited genetic predisposition to CAD.

Higher risk

 | 92 nd percentile

TEST DETAIL

RISK CATEGORY

Higher Risk (Above the 84th percentile)

Genetic factors suggest a higher than average predisposition to coronary artery disease compared to individuals of similar genetic ancestry.

INTERPRETATION

The polygenic risk score is calculated from approximately 1.3 million genetic variants and normalized to account for ancestral background. The percentile reflects the patient's relative genetic risk position compared to a reference population of similar ancestry.

Percentile and risk classification reflect relative genetic predisposition and do not represent an absolute probability of developing coronary artery disease.

- This score is not a diagnosis. It does not take into account non-genetic factors, such as lifestyle habits and history of other diseases, which could affect overall risk.
- Other limitations of this polygenic score include:
 - It does not look for rare genetic variants that cause disease such as familial hypercholesterolemia - present in 1 in every 250 people - that can greatly increase risk for coronary artery disease
 - For people belonging to ancestry groups that are less represented, genetics research, these scores may be less accurate.

FOLLOW UP RECOMMENDATIONS

It is recommended that you discuss the results with a certified genetic counselor or other healthcare professional with genetics expertise.

Detailed findings continued on next page.

FIRST NAME: Oscar LAST NAME: Meyer DOB: 12/01/1964 ORDER REQUISITION: XXXXX

TECHNICAL AND REGULATORY INFORMATION

TEST METHODOLOGY

The Arboretum CAD PRS Test is performed on genomic DNA extracted from buccal swabs, saliva, or whole blood. Next-generation sequencing is performed using a blended approach combining low-coverage whole genome sequencing with high-coverage exome sequencing. Variant calling and genotype imputation are performed with alignment to reference build GRCh38. Imputation utilizes Illumina's IRPv2.1 reference panel to achieve high-accuracy genotype calls across the genome.

The polygenic risk score is calculated using a multi-ancestry algorithm incorporating approximately 1.3 million genetic variants associated with coronary artery disease risk. Raw polygenic scores undergo ancestry-specific normalization using a principal component analysis-based calibration model trained on diverse population data to ensure equivalent risk interpretation across all major continental ancestry groups. The final score is converted to a standardized z-score and classified into risk categories (Lower, Average, Higher) based on population percentiles. Corresponding percentile is reported alongside the risk category. Quality control metrics include: minimum mean coverage $\geq 2x$, overall genotype concordance $\geq 98\%$, and technical reproducibility with coefficient of variation $\leq 5\%$.

TEST LIMITATIONS

All tests have limitations. This polygenic risk score reflects inherited genetic predisposition to coronary artery disease but does not account for environmental factors, lifestyle habits, medication use, or other non-genetic risk factors that significantly influence disease development. The score does not constitute a diagnosis and cannot predict with certainty whether an individual will or will not develop coronary artery disease. This test is designed specifically for coronary artery disease risk assessment and does not evaluate risk for other cardiovascular conditions or diseases. The assay does not screen for rare monogenic variants such as those causing familial hypercholesterolemia or other single-gene disorders that can substantially increase cardiovascular risk.

Performance may be reduced for individuals from populations underrepresented in genomic research, including but not limited to Native American, Pacific Islander, and some Central Asian ancestries. Individuals with complex admixed ancestry or from consanguineous populations may experience reduced accuracy. The test is validated for germline constitutional specimens only and is not appropriate for somatic tissue analysis.

Technical limitations include: samples with mean coverage $< 2x$ are considered sample failures; individuals with significant germline mosaicism ($> 20\%$ variant allele frequency deviation) may yield inaccurate scores; bone marrow transplant recipients tested using blood-derived samples will reflect donor rather than recipient genotype.

Risk score interpretation may be affected by age, sex, and population-specific factors not explicitly modeled in the current algorithm. The score should be interpreted in conjunction with traditional cardiovascular risk factors and clinical assessment.

LABORATORY INFORMATION

This test was performed by Arboretum Clinical, LLC, 6901 Quaker Ave. Ste 300, Lubbock TX 79413 CLIA: 45D2331659, CAP: 7734236. Laboratory Director: Owatha Tatum, Ph.D., HCLD/CC(ABB). Sequencing services were provided by GenebyGene, Ltd., 1445 North Loop West, Suite 820 Houston, TX 77008, CLIA: ID 45D1102202, CAP: 7212851, Laboratory Director: Dr. Feng Zhou, PhD, HCLD(ABB), MB(ASCP). Both laboratories are authorized under the Clinical Laboratory Improvement. Amendments (CLIA) to develop and perform high complexity clinical laboratory testing. This test was developed and its performance characteristics determined by Arboretum Clinical. It has not been cleared or approved by the U.S. Food and Drug Administration. It is a laboratory-developed test (LDT) not reviewed by the U.S. Food and Drug Administration.

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RELEVANT RESOURCES

- Blumenthal RS et al. 2026 ACC/AHA/AACVPR/ABC/ACPM/ADA/AGS/APhA/ASPC/NLA/PCNA Guideline on the Management of Dyslipidemia: A Report of the American College of Cardiology/American Heart Association Joint Committee on Clinical Practice Guidelines. J Am Coll Cardiol. 2026 Mar 13:S0735-1097(25)10254-4. doi: 10.1016/j.jacc.2025.11.016. Epub ahead of print. PMID: 41824590.
- Khera AV et al. Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. Nat Genet. 2018 Sep;50(9):1219-1224. doi: 10.1038/s41588-018-0183-z. Epub 2018 Aug 13. PMID: 30104762; PMCID: PMC6128408.
- Adams DR et al. Next-Generation Sequencing to Diagnose Suspected Genetic Disorders. N Engl J Med. 2018 Oct 4;379(14):1353-1362. doi: 10.1056/NEJMr1711801. PMID: 30281996.
- Mars N et al. Polygenic and clinical risk scores and their impact on age at onset and prediction of cardiometabolic diseases and common cancers. Nat Med. 2020 Apr;26(4):549-557. doi: 10.1038/s41591-020-0800-0. Epub 2020 Apr 7. PMID: 32273609.
- Patel AP et al. A multi-ancestry polygenic risk score improves risk prediction for coronary artery disease. Nat Med. 2023 Jul;29(7):1793-1803. doi: 10.1038/s41591-023-02429-x. Epub 2023 Jul 6. PMID: 37414900; PMCID: PMC10353935.