

Client: Example Client ABC123  
123 Test Drive  
Salt Lake City, UT 84108  
UNITED STATES

Physician: Doctor, Example

**Patient: Patient, Example**

**DOB:** 11/17/1992  
**Gender:** Female  
**Patient Identifiers:** 01234567890ABCD, 012345  
**Visit Number (FIN):** 01234567890ABCD  
**Collection Date:** 00/00/0000 00:00

**Cytochrome P450 Genotyping Panel, with GeneDose Access**

ARUP test code 3004255

CYP PANEL Specimen whole blood

CYP2C19 Genotype \*1/\*1

CYP2C19 Phenotype Normal

CYP2C8 Genotype \*1/\*1

CYP2C8 Phenotype Normal

CYP2C9 Genotype \*1/\*1

CYP2C9 Phenotype Normal

CYP2C Cluster Geno Negative

CYP2C Cluster Pheno Normal

CYP2D6 Genotype \*1/\*1

CYP2D6 Phenotype Normal

CYP3A4 Genotype \*1/\*1

**H=High, L=Low, \*=Abnormal, C=Critical**

Unless otherwise indicated, testing performed at:

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CYP3A4 Phenotype	Normal
CYP3A5 Genotype	*1/*1
CYP3A5 Phenotype	Normal
CYP2B6 Genotype	*1/*1
CYP2B6 Phenotype	Normal
CYP PANEL Interpretation	See Note

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H=High, L=Low, \*=Abnormal, C=Critical

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The following CYP2C19 allele(s) were detected: \*1/\*1. This result predicts the normal metabolizer phenotype.

Recommendation: Guidelines for genotype-based dosing are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and other organizations. See : <https://www.pharmgkb.org/>

The following CYP2C8 allele(s) were detected: \*1/\*1. This result predicts the normal metabolizer phenotype.

The following CYP2C9 allele(s) were detected: \*1/\*1. This result predicts the normal metabolizer phenotype, with an activity score of 2.

Recommendation: Guidelines for genotype-based dosing are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and other organizations. See: <https://www.pharmgkb.org/>

The 2C cluster variant (rs12777823) was not detected. This result predicts a normal phenotype and is not expected to contribute to warfarin dosing estimates.

The following CYP2D6 allele(s) were detected: \*1/\*1. This result predicts the normal metabolizer phenotype with an activity score estimated at 2 of 2.

Recommendation: Guidelines for genotype-based dosing are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and other organizations. See: <https://www.pharmgkb.org/>

The following CYP3A4 allele(s) were detected: \*1/\*1. This result predicts the normal metabolizer phenotype.

The following CYP3A5 allele(s) were detected: \*1/\*1. This result predicts the normal metabolizer phenotype.

Recommendation: Guidelines for genotype-based dosing are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and can be found at: <https://www.pharmgkb.org/>.

The following CYP2B6 alleles were detected: \*1/\*1. This result predicts the normal metabolizer phenotype.

Recommendation: Guidelines for gene-based dosing are published by the Clinical Pharmacogenetics Implementation Consortium (CPIC) and other organizations. See [https://www.pharmgkb.org](https://www.pharmgkb.org/)

This result has been reviewed and approved by [REDACTED]

#### BACKGROUND INFORMATION: Cytochrome P450 Genotyping Panel

Characteristics: The cytochrome P450 (CYP) isozymes 2B6, 2C19, 2C8, 2C9, 2D6 and the CYP3A subfamily are involved in the metabolism of many drugs. Variants in the genes that code for CYP2B6, CYP2C19, CYP2C8, CYP2C9, CYP2D6, CYP3A4, and CYP3A5, and CYP2C cluster (rs12777823) loci, influence pharmacokinetics of respective substrates, and may predict or explain nonstandard dose requirements, therapeutic failure, or adverse reactions. Inheritance: Autosomal codominant.

Cause: Gene variants affect enzyme function.

Variants Tested:

(Variants are numbered according to the following transcripts: CYP2C19 NM\_000769, CYP2C8 NM\_000770, CYP2C9 NM\_000771, 2C cluster rs12777823, CYP2D6 M33388 sequence, CYP3A4 NM\_017460 and CYP3A5 NM\_000777, CYP2B6 NM\_000767).

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\*1: Indicative of no detected targeted variants and an assumption of functional allele.

CYP2C19\*2: rs4244285, c.681G>A; rs12769205, c.332-23A>G  
CYP2C19\*3: rs4986893, c.636G>A  
CYP2C19\*4A: rs28399504, c.1A>G  
CYP2C19\*4B: rs28399504, c.1A>G; rs12248560, c.-806C>T  
CYP2C19\*5: rs56337013, c.1297C>T  
CYP2C19\*6: rs72552267, c.395G>A  
CYP2C19\*7: rs72558186, c.819+2T>A  
CYP2C19\*8: rs41291556, c.358T>C  
CYP2C19\*9: rs17884712, c.431G>A  
CYP2C19\*17: rs12248560, c.-806C>T  
CYP2C19\*35: rs12769205, c.332-23A>G

CYP2C8\*2: rs11572103, c.805A>T  
CYP2C8\*3: rs10509681, c.1196A>G  
CYP2C8\*4: rs1058930, c.792C>G

CYP2C rs12777823, g.96405502 G>A

CYP2C9\*2: rs1799853, c.430C>T  
CYP2C9\*3: rs1057910, c.1075A>C  
CYP2C9\*4: rs56165452, c.1076T>C  
CYP2C9\*5: rs28371686, c.1080C>G  
CYP2C9\*6: rs9332131, c.818del  
CYP2C9\*8: rs7900194, c.449G>A  
CYP2C9\*11: rs28371685, c.1003C>T  
CYP2C9\*12: rs9332239, c.1465C>T

CYP2D6\*2: rs16947, g.2850C>T; rs1135840, g.4180G>C  
CYP2D6\*2A: rs1080985, g.-1584C>G; rs16947, g.2850C>T; rs1135840, g.4180G>C  
CYP2D6\*3: rs35742686, g.2549del  
CYP2D6\*4: rs1065852, g.100C>T; rs3892097, g.1846G>A; rs1135840, g.4180G>C  
CYP2D6\*5: gene deletion  
CYP2D6\*6: rs5030655, g.1707del  
CYP2D6\*7: rs5030867, g.2935A>C  
CYP2D6\*8: rs5030865, g.1758G>T; rs16947, g.2850C>T; rs1135840, g.4180G>C  
CYP2D6\*9: rs5030656, g.2615\_2617del  
CYP2D6\*10: rs1065852, g.100C>T; rs1135840, g.4180G>C  
CYP2D6\*11: rs1080985, g.-1584C>G; rs201377835, g.883G>C; rs16947, g.2850C>T; rs1135840, g.4180G>C  
CYP2D6\*13: a CYP2D7-derived exon 1 conversion  
CYP2D6\*14: rs5030865, g.1758G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C  
CYP2D6\*15: rs774671100, g.137\_138insT  
CYP2D6\*17: rs28371706, g.1023C>T; rs16947, g.2850C>T; rs1135840, g.4180G>C  
CYP2D6\*29: rs16947, g.2850C>T; rs59421388, g.3183G>A; rs1135840, g.4180G>C  
CYP2D6\*35: rs769258, g.31G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C; rs1080985, g.-1584C>G  
CYP2D6\*36: a CYP2D6\*10 carrying a CYP2D7-derived exon 9 conversion  
CYP2D6\*36-\*10: a CYP2D6\*36 and a CYP2D6\*10 in tandem  
CYP2D6\*40: rs28371706, g.1023C>T, rs16947, g.2850C>T; rs1135840, g.4180G>C; rs72549356, g.1863\_1864ins TTTCGCCCTTCGCCCC  
CYP2D6\*41: rs16947, g.2850C>T; rs28371725, g.2988G>A; rs1135840, g.4180G>C  
CYP2D6\*42: rs16947, g.2850C>T; rs1135840, g.4180G>C; rs72549346, g.3260\_3261insGT  
CYP2D6\*49: rs1065852, g.100C>T; rs1135822, g.1611T>A; rs1135840, g.4180G>C  
CYP2D6\*69: rs1065852, g.100C>T; rs16947, g.2850C>T; rs28371725, g.2988G>A; rs1135840, g.4180G>C  
CYP2D6\*114: rs1065852, g.100C>T; rs5030865, g.1758G>A; rs16947, g.2850C>T; rs1135840, g.4180G>C

**H=High, L=Low, \*=Abnormal, C=Critical**

DUP: complete gene duplications

CYP2B6\*4: rs2279343, c.785A>G  
 CYP2B6\*6: rs3745274, c.516G>T; rs2279343, c.785A>G  
 CYP2B6\*7: rs3745274, c.516G>T; rs2279343, c.785A>G; rs3211371, c.1459C>T  
 CYP2B6\*9: rs3745274, c.516G>T  
 CYP2B6\*18: rs28399499, c.983T>C  
 CYP2B6\*22: rs34223104, c.-82T>C  
 CYP2B6\*36: rs34223104, c.-82T>C; rs3745274, c.516G>T; rs2279343, c.785A>G

CYP3A4\*1A: rs2740574, c.-392G>A  
 CYP3A4\*22: rs35599367, c.522-191C>T

CYP3A5\*3: rs776746, c.219-237A>G  
 CYP3A5\*6: rs10264272, c.624G>A  
 CYP3A5\*7: rs41303343, c.1035dup

Methodology: Polymerase chain reaction (PCR) and fluorescence monitoring. Sequencing is only performed if needed to characterize a duplicated CYP2D6 gene.

Analytic Sensitivity and Specificity: Greater than 99 percent.

Limitations: Only the targeted variants will be detected by this panel, and assumptions about phase and content are made to assign alleles. Publicly available sources such as the [www.pharmvar.org](http://www.pharmvar.org) or [www.pharmgkb.org](http://www.pharmgkb.org) provide guidance on phenotype predictions and allele frequencies. A combination of the CYP2D6\*5 (gene deletion) and a CYP2D6 gene duplication cannot be specifically identified; however, this combination is not expected to adversely affect the phenotype prediction. The assay used to detect \*40 allele, cannot distinguish between insertions of 1 or 2 copies; it also cannot distinguish between heterozygous and homozygous mutant samples due to unavoidable cross reactivity with the wild type sequence. Additional assays will be used to help differentiate the \*40 allele from other CYP2D6 star alleles. Diagnostic errors can occur due to rare sequence variations. Risk of therapeutic failure or adverse reactions with gene substrates may be affected by genetic and nongenetic factors that are not detected by this test. This result does not replace the need for therapeutic drug or clinical monitoring.

Please note the information contained in this report does not contain medication recommendations, and should not be interpreted as recommending any specific medications. Any dosage adjustments or other changes to medications should be evaluated in consultation with a medical provider.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration. This test was performed in a CLIA-certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

CYP PANEL, GeneDose Link

See Note

To access GeneDose LIVE, visit the URL below and enter the ARUP Accession number to continue:

**H=High, L=Low, \*=Abnormal, C=Critical**

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INTERPRETIVE INFORMATION: CYP PANEL, GeneDose Link

GeneDose LIVE content is provided by Coriell Life Sciences and not by ARUP Laboratories.

Any dosage adjustments or other changes to medications should be evaluated in consultation with a medical provider.

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EER Cytochrome P450 Panel, GeneDose

See Note

Authorized individuals can access the ARUP Enhanced Report using the following link:

[REDACTED]

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**H=High, L=Low, \*=Abnormal, C=Critical**

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VERIFIED/REPORTED DATES				
Procedure	Accession	Collected	Received	Verified/Reported
CYP PANEL Specimen	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C19 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C19 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C8 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C8 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C9 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C9 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C Cluster Geno	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2C Cluster Pheno	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2D6 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2D6 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A4 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A4 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A5 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP3A5 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2B6 Genotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP2B6 Phenotype	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP PANEL Interpretation	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
CYP PANEL, GeneDose Link	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Cytochrome P450 Panel, GeneDose	24-323-113996	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

H=High, L=Low, \*=Abnormal, C=Critical