

The Pharmacogene Variation (PharmVar) Consortium is a central repository for pharmacogene (PGx) variation that focuses on haplotype structure and allelic variation.

The information in this resource facilitates the interpretation of pharmacogenetic test results to guide precision medicine.



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Director, PharmVar





The Pharmacogene Variation (PharmVar) Consortium is a global consortium of scientists and clinicians who study pharmacogene (PGx) variation that focuses on haplotypes. The information in this resource facilitates basic and clinical interpretation of pharmacogenetic test results to guide

 PharmVar API Services are now available for third party use. For more information, visit the [API Service Documentation Page](#)

[What's New](#) **3**



## PharmVar Publications

Articles published by PharmVar are available on the [resources](#) page.



**NEW** September 03, 2024

#### Database Updated to Version 6.1.5

##### CYP2D6

- Added one new star allele, \*176
- Added one new \*1 suballele, \*1.065
- Confirmed definition of \*144

**NEW** August 28, 2024

#### Database Updated to Version 6.1.4

##### DPYD

- Added six intragenic deletion events: exon 4 deletion, exon 6 deletion, exon 9+10 deletion, exon 11 deletion, exon 12 deletion, and exon 14-16 deletion (listed at the bottom of the DPYD gene page)
- A new Structural Variation document is available on the DPYD gene page providing more information about copy number variation

**NEW** June 29, 2024

#### Database Updated to Version 6.1.3

##### CYP2D6

- Added three novel star alleles, \*173, \*174 and \*175
- Added two novel suballeles, \*2.034 (found as duplication) and \*4.034. In contrast to all other \*4 suballeles, \*4.034 is unique by having only the splice defect causing variant 1847G>A

# PharmVar

# gene pages

CYP2D6 CPIC guidelines

[CPIC guideline for atomoxetine based on CYP2D6 genotype](#)


[CPIC guideline for opioids based on CYP2D6, CYP2C19, and COMT genotype](#)

[CPIC guideline for ondansetron and tropisetron based on CYP2D6 genotype](#)

[CPIC guideline for tamoxifen based on CYP2D6 genotype](#)

[CPIC guideline for selective serotonin reuptake inhibitors based on CYP2D6 and CYP2C19 genotype](#)

[CPIC guideline for tricyclic antidepressants based on CYP2D6 and CYP2C19 genotype](#)



 PHARMGKB

 CYP2D6

RefSeq	5' limit Counting from the sequence start	5' limit Counting from the ATG translation start	3' limit Counting from the sequence start	3' limit Counting from the ATG translation start
NG_008376.4	3436	-1584	9501	4482

**All SNVs within the 5' and 3' limits must be submitted for haplotype (star allele) definitions.**  
This includes 5' flanking sequence, the 5' UTR, exons 1-9, introns 1-8, the 3' UTR, and the 3' flanking sequence.

**CYP2D6**

External Resources [CPIC](#) [PHARMGKB](#) [ClinGen](#) [ClinVar](#) [EntrezGene](#) [HGNC](#)

[Read Me for CYP2D6](#) [Change Log for CYP2D6](#) [Structural Variation for CYP2D6](#) [+ More Documents](#)

[Download Gene Data](#)

[Additional Data Download Information](#)

NG\_008376.4 (LRG\_303) [i](#)    NM\_000106.6 [i](#)    GRCh37 (NC\_000022.10) [i](#)    GRCh38 (NC\_000022.11) [i](#)    M33388 [i](#)

CAVE Compare View [↔](#)

Count From: Sequence Start   ATG Start

[Download Allele Data](#) [Core SNV](#)

# PharmVar

deposited by  
now has “year”  
the allele was  
posted

## citations

CYP2D6*27		PV00451		CPIC Clinical Function →
↓ <a href="#">CYP2D6*27.001</a>	CYP2D6*27	PV00130	Def	<a href="#">Marez et al. 1997</a> <a href="#">Sakuyama et al. 2008</a> deposited by Gelineau-Morel/PharmVar Team 2024 deposited by Nofziger et al 2024
↓ <a href="#">CYP2D6*27.002</a>		PV02496	Def	deposited by Nofziger et al 2024
↓ <a href="#">CYP2D6*27.003</a>		PV02497	Def	deposited by Nofziger et al 2024



Coming: more info about depositing author(s) in Change Log document

# PharmVar Variant Frequencies

CYP2D6\*10

100C>T (rs1065852, P34S)

4181G>C (rs11135)

## Variant Positions

Gene	NG_008376.4:g.5119C>T
Transcript	NM_000106.6:c.100C>T
GRCh37	NC_000022.10:g.42526694G>A
GRCh38	NC_000022.11:g.42130692G>A

Reference Sequence	Position	Reference	Variant
NG_008376.4			
Sequence Start	5119	C	> T
ATG Start	100	C	> T
NM_000106.6			
Sequence Start	119	C	> T
ATG Start	100	C	> T
GRCh37 (NC_000022.10)			

## Show Haplotypes With This Variant

External Resources:

[dbSNP:rs1065852](#)  
[PharmGKB:PA166156062](#)  
[GnomAD:rs1065852](#)

Variant Frequency:

0.212157 ([GnomAD](#))

# PharmVar Variant Frequencies

link to PharmGKB  
variant/SNP page

rs1065852

gnomAD Genome

gnomAD Exome

1000 Genomes

ALFA



Based on v3 genome data from the [Genomes Aggregation Database](#) (gnomAD) retrieved from the [Ensembl](#) API.

>	AGGREGATED POPULATIONS ⓘ	DISTRIBUTION	A ↕	G ↕
✓	All populations n=150,496		19.06%	80.94%
:	AER n=40,586		12.46%	87.54%
:	AMJ n=898		30.07%	69.93%
:	AMR n=15,142		15.30%	84.70%
:	ASJ n=3,462		24.58%	75.42%
:	EAS n=5,104		54.13%	45.87%
:	FIN n=10,590		11.26%	88.74%
:	NFE n=67,574		22.25%	77.75%
:	QTH n=2,060		17.72%	82.28%
:	SAS n=4,764		16.81%	83.19%

This SNP is presents the frequency of ALL star alleles  
including \*4 and \*10

# PharmVar Allele Window

**CYP2D6**

External Resources [CPI](#) [PHARMCKB](#) [ClinGen](#) [ClinVar](#) [EntrezGene](#) [HGNC](#)

[Read Me for CYP2D6](#) [Change Log for CYP2D6](#) [Structural Variation for CYP2D6](#) [+ More Documents](#)

NG\_008376.4 (LRG\_303) ⌵      NM\_000106.6 ⌵      GRCh37 (NC\_000022.10) ⌵      GRCh38 (NC\_000022.11) ⌵      M33388


[CAVE Compare View](#) ↔

[Download Allele Data](#) [Core SNV](#)

Allele Name	Legacy Label	PharmVar ID	Variants (rsIDs, Impact) <b>variant</b> = variants with dbSNP rsID
<a href="#">CYP2D6*10</a>		PV00435	<a href="#">100C&gt;T (rs1065852, P34S)</a> <a href="#">4181G&gt;C (rs1135840, S486T)</a>
<a href="#">CYP2D6*10.001</a>	CYP2D6*10A	PV00179	<a href="#">100C&gt;T (rs1065852, P34S)</a> <a href="#">1662G&gt;C (rs1058164)</a> <a href="#">4181G&gt;C (rs1135840, S486T)</a>
<a href="#">CYP2D6*10.002</a>	CYP2D6*10B	PV00178	<a href="#">-1426C&gt;T (rs28588594)</a> <a href="#">-1235A&gt;G (rs28735595)</a> <a href="#">-1000G&gt;A (rs1080989)</a> <a href="#">100C&gt;T (rs1065852, P34S)</a> <a href="#">310G&gt;T (rs28371699)</a> <a href="#">842T&gt;G (rs28371702)</a> <a href="#">1038C&gt;T (rs1081003)</a> <a href="#">1662G&gt;C (rs1058164)</a> <a href="#">2098A&gt;G (rs2267447)</a> <a href="#">3385A&gt;C (rs1985842)</a> <a href="#">3583A&gt;G (rs2004511)</a> <a href="#">4181G&gt;C (rs1135840, S486T)</a> <a href="#">4402C&gt;T (rs28371738)</a>
<a href="#">CYP2D6*10.003</a>	CYP2D6*10D	PV02177	<a href="#">-1426C&gt;T (rs28588594)</a> <a href="#">-1235A&gt;G (rs28735595)</a> <a href="#">-1000G&gt;A (rs1080989)</a> <a href="#">100C&gt;T (rs1065852, P34S)</a> <a href="#">310G&gt;T (rs28371699)</a> <a href="#">842T&gt;G (rs28371702)</a> <a href="#">1038C&gt;T (rs1081003)</a> <a href="#">1662G&gt;C (rs1058164)</a> <a href="#">2098A&gt;G (rs2267447)</a> <a href="#">3385A&gt;C (rs1985842)</a> <a href="#">3583A&gt;G (rs2004511)</a> <a href="#">4181G&gt;C (rs1135840, S486T)</a> <a href="#">4445A&gt;G (rs148648640)</a>

# PharmVar Allele Window

## Allele Details

CYP2D6*10		Function
PV00435		
		decreased function
Reference	Variants	
⌵ NG_008376.4		
Sequence Start	<a href="#">5119C&gt;T</a> (P34S), <a href="#">9200G&gt;C</a> (S486T)	
ATG Start	<a href="#">100C&gt;T</a> (P34S), <a href="#">4181G&gt;C</a> (S486T)	
NM_000106.6		
Sequence Start	<a href="#">119C&gt;T</a> (P34S), <a href="#">1476G&gt;C</a> (S486T)	
ATG Start	<a href="#">100C&gt;T</a> (P34S), <a href="#">1457G&gt;C</a> (S486T)	
⌵ GRCh37		
Sequence Start	<a href="#">42523943A&gt;G</a> , <a href="#">42526694G&gt;A</a> (P34S)	
⌵ GRCh38		
Sequence Start	<a href="#">42126611C&gt;G</a> (S486T), <a href="#">42130692G&gt;A</a> (P34S)	
⌵ M33388		
Sequence Start	<a href="#">1719C&gt;T</a> (P34S), <a href="#">5799G&gt;C</a> (S486T)	
ATG Start	<a href="#">100C&gt;T</a> (P34S), <a href="#">4180G&gt;C</a> (S486T)	

## External Resources and Star Allele Frequency Information

 PHARMGKB





# PharmVar Allele Window

 CYP2D6\*10

## Frequencies

CPIC

All of Us

UK Biobank

Based on [CPIC Frequency Tables](#).

POPULATION ⓘ	CYP2D6*10 OBSERVED ⬆	ALLELES TOTAL ⬆	FREQUENCY ⬆
African American/Afro-Caribbean	777	20368	3.82%
American	127	8768	1.45%
Central/South Asian	339	4488	7.56%
East Asian	16973	39616	42.84%
European	1750	111390	1.57%
Latino	423	16098	2.63%
Near Eastern	313	4626	6.77%
Oceanian	114	1998	5.71%
Sub-Saharan African	220	4518	4.87%

# DPYD

## Get-RM study

Reference Materials

# AMP

Clinical testing recommendations

## **Characterization of Reference Materials for DPYD – A GeT-RM Collaborative Project**

Gaedigk, Turner, Moyer, Zubiaur, Boone, Wang, Broeckel and Kalman

*J Mol Diag (Epub July 18, 2024)*

## **DPYD Genotyping Recommendations: A Joint Consensus Recommendation of the AMP, ACMG, CPIC, American Pathologists, DPWG, ESPG, PharmGKV and PharmVar**

Pratt, Cavallari, Fulmer, Gaedigk, Hachad, Ji, Kalman, Ly, Moyer, Scott,  
Turner, van Scaik, Whirl-Carrillo and Weck

*J Mol Diag (Epub July 18, 2024)*

# DPYD

## PharmVar now lists six intragenic exon deletion events

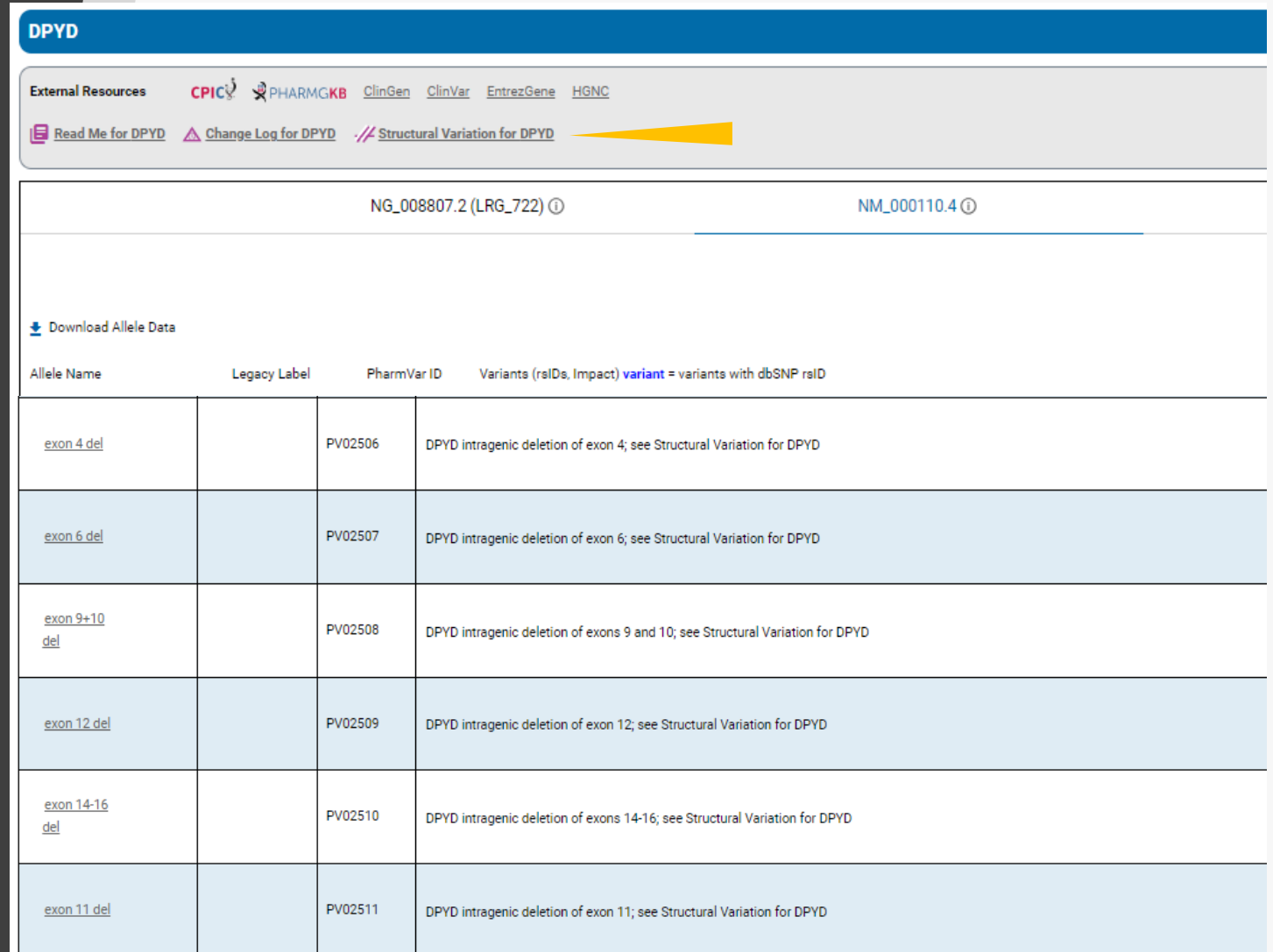
GeT-RM study revealed samples with an exon 4 and an exon 11 deletion, respectively

An exon 4 deletion has been reported in cases with 5-FU toxicity

The exon 4 deletion has been found at a frequency of 2.4% in a Finnish cohort

Other intragenic deletions have also been described in the literature

**\*\*New\*\*** Structural Variation document



DPYD

External Resources [CPIC](#) [PHARMGKB](#) [ClinGen](#) [ClinVar](#) [EntrezGene](#) [HGNC](#)

[Read Me for DPYD](#) [Change Log for DPYD](#) [Structural Variation for DPYD](#)

NG\_008807.2 (LRG\_722) [i](#) NM\_000110.4 [i](#)

[Download Allele Data](#)

Allele Name	Legacy Label	PharmVar ID	Variants (rsIDs, Impact) <a href="#">variant</a> = variants with dbSNP rsID
<a href="#">exon 4 del</a>		PV02506	DPYD intragenic deletion of exon 4; see Structural Variation for DPYD
<a href="#">exon 6 del</a>		PV02507	DPYD intragenic deletion of exon 6; see Structural Variation for DPYD
<a href="#">exon 9+10 del</a>		PV02508	DPYD intragenic deletion of exons 9 and 10; see Structural Variation for DPYD
<a href="#">exon 12 del</a>		PV02509	DPYD intragenic deletion of exon 12; see Structural Variation for DPYD
<a href="#">exon 14-16 del</a>		PV02510	DPYD intragenic deletion of exons 14-16; see Structural Variation for DPYD
<a href="#">exon 11 del</a>		PV02511	DPYD intragenic deletion of exon 11; see Structural Variation for DPYD

# PharmVar publications



## Pharmacogene Variation Consortium: A Global Resource and Repository for Pharmacogene Variation

Andrea Gaedigk<sup>1,2,\*</sup>, Scott T. Casey<sup>3</sup>, Michelle Whirl-Carrillo<sup>4</sup>, Neil A. Miller<sup>3</sup> and Teri E. Klein<sup>4,5</sup>

Please cite!

## PharmVar Tutorial on *CYP2D6* Structural Variation Testing and Recommendations on Reporting

CLINICAL PHARMACOLOGY & THERAPEUTICS | VOLUME 114 NUMBER 6 | December 2023

Amy J. Turner<sup>1,2</sup>, Charity Nofziger<sup>3</sup>, Bronwyn E. Ramey<sup>4</sup>, Reynold C. Ly<sup>5</sup>, Chad A. Bousman<sup>6</sup>, José A. G. Agúndez<sup>7,8</sup>, Katrin Sangkuhl<sup>9</sup>, Michelle Whirl-Carrillo<sup>9</sup>, Simone Vanoni<sup>3</sup>, Henry M. Dunnenberger<sup>10</sup>, Gualberto Rúaño<sup>11,12</sup>, Martin A. Kennedy<sup>13</sup>, Michael S. Phillips<sup>14</sup>, Houda Hachad<sup>15</sup>, Teri E. Klein<sup>16</sup>, Ann M. Moyer<sup>17</sup> and Andrea Gaedigk<sup>18,19,\*</sup>

## PharmVar GeneFocus: *CYP2A6*

Epub Jul 2024

Alec W.R. Langlois<sup>1,2</sup>, Meghan J. Chenoweth<sup>1,2,3</sup>, David Twesigomwe<sup>4</sup>, Giada Scantamburlo<sup>5</sup>, Michelle Whirl-Carrillo<sup>6</sup>, Katrin Sangkuhl<sup>6</sup>, Teri E. Klein<sup>6,7</sup>, Charity Nofziger<sup>5</sup>, Rachel F. Tyndale<sup>1,2,3</sup> and Andrea Gaedigk<sup>8,9,\*</sup>

## PharmVar GeneFocus: *CYP4F2*

Epub Aug 2024

Pablo Zubiaur<sup>1</sup>, Cristina Rodríguez-Antona<sup>2,3</sup>, Erin C. Boone<sup>4</sup>, Ann K. Daly<sup>5</sup>, Evangelia Eirini Tsermpini<sup>6</sup>, Lubna Q. Khasawneh<sup>7</sup>, Katrin Sangkuhl<sup>8</sup>, Jorge Duconge<sup>9</sup>, Mariana R. Botton<sup>10,11</sup>, Jessica Savio<sup>12</sup>, Charity Nofziger<sup>13</sup>, Michelle Whirl-Carrillo<sup>8</sup>, Teri E. Klein<sup>8,14</sup> and Andrea Gaedigk<sup>4,15,\*</sup>



PharmVar GeneFocus: *NAT2* (in preparation)

# CYP2D6

this panel keeps busy...

- New star alleles, suballeles and structural variants keep coming – just posted *CYP2D6\*176!*
- “Clean-up” efforts
  - Looking into alleles with limited evidence that were first defined using methods we would not accept today
    - Confirmed \*27, there are now three suballeles, one found as \*27.002x2
    - *Need to confirm* \*20, \*23, \*24, \*25, \*26, \*30, \*34, \*37 and some \*2, \*3, \*4, \*6, \*12, \*19 suballeles
  - Concerns that some of these alleles do not exist as defined
    - Retire some alleles if no evidence can be found in the literature or databases supporting the allele in question?
  - Can we identify samples with SNV(s) of interest for reanalysis?

Role	Name	Institution	Country
Chair	Andrea Gaedigk	Children's Mercy/PharmVar	USA
Vice Chair	Houda Hachad	AccessDx	USA
PharmVar Representative	Michael Phillips	Precision Medicine Advisers	Canada
PharmGKB/CPIC Representative	Teri Klein	Stanford, PharmGKB	USA
PharmGKB/CPIC Representative	Katrin Sangkuhl	Stanford, PharmGKB	USA
PharmGKB/CPIC Representative	Michelle Whirl-Carrillo	Stanford, PharmGKB	USA
Member	Jose Agundez	Universidad de Extremadura	Spain
Member	Chad Bousman	University of Calgary	Canada
Member	Mark Dunnenberger	NorthShore University HealthSystem	USA
Member	Martin Kennedy	University of Otago	New Zealand
Member	Reynold Ly	Nationwide Children's Hospital	USA
Member	Ann Meyer	Mayo Clinic	USA
Member	Charity Nofziger	PharmGenetics GmbH	Austria
Member	Bronwyn Ramey	Let's Get Checked	USA
Member	Guillermo Ruano	Institute of Living at Hartford Hospital	USA
Member	Amy Turner	Medical College of Wisconsin, RPRD Diagnostics, LLC	USA

CYP2D6 expert panel

▶ If you have data for alleles with a “Limited” or “Moderate” evidence level, please consider submitting to PharmVar

# CYP1A2 curation underway

CYP1A2 Gene Expert Panel			
Role	Name	Institution	Country
Chair	Andrea Gaedigk	Children's Mercy Research Institute	USA
Vice Chair	Pablo Zubiaur	Universidad Autonoma de Madrid	Spain
PharmGKB/CPIC Representative	Michelle Whirl-Carrillo	Stanford, PharmGKB	USA
PharmGKB/CPIC Representative	Teri Klein	Stanford, PharmGKB	USA
Member	Solomon Adams	Base5	USA
Member	Matthias König	Humboldt University	Germany
Member	Dora Koller	University of Barcelona	Spain
Member	Volker Lauschke	Karolinska Institutet and Institute of Clinical Pharmacology	Sweden, Germany
Member	Martin Lewis	South Australia Health & Medical Research Institute, Adelaide	Australia
Member	Katalin Monostory	HUN-REN Research Centre for Natural Sciences	Hungary
Member	Mohamed Nagy	Children's Cancer Hospital	Egypt
Member	Amy Turner	Medical College of Wisconsin, RPRD Diagnostics, LLC	USA
Member	David Twesigomwe	Brenner Institute, University of the Witwatersrand	South Africa
Trainee	Gonzalo Villapalos-García	Hospital Universitario de La Princesa and Children's Mercy Research Institute	Spain, USA
Data Specialist	Erin Boone	Children's Mercy Research Institute	USA
Ad Hoc Member	Chad Bousman	University of Calgary	Canada

CYP1a2 expert panel

- No CPIC or DPWG guidelines
  - PharmGKB level 3/4
  - PharmVar Priority Level low
- Tested by many PGx panels
- Many [current] star alleles are poorly characterized
- Many common haplotypes are not defined
- **There will be major updates!**

▶ **Transition of CYP1A2 into the PharmVar database coming soon**

## ***NAT2* was transferred from the NAT database to PharmVar!**

- PharmVar *NAT2* gene page launched in March 2024
- *NAT2* “legacy” content still available at the DUTH site
- *NAT1* and non-human *NATs* will continue to be hosted by DUTH

DEMOCRITUS UNIVERSITY of THRACE

DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

HOME

BACKGROUND

PROKARYOTIC *NAT* GENES

EUKARYOTIC *NAT* GENES

**Human *NAT* alleles/haplotypes**

[NAT1 alleles](#)

[NAT2 alleles](#)

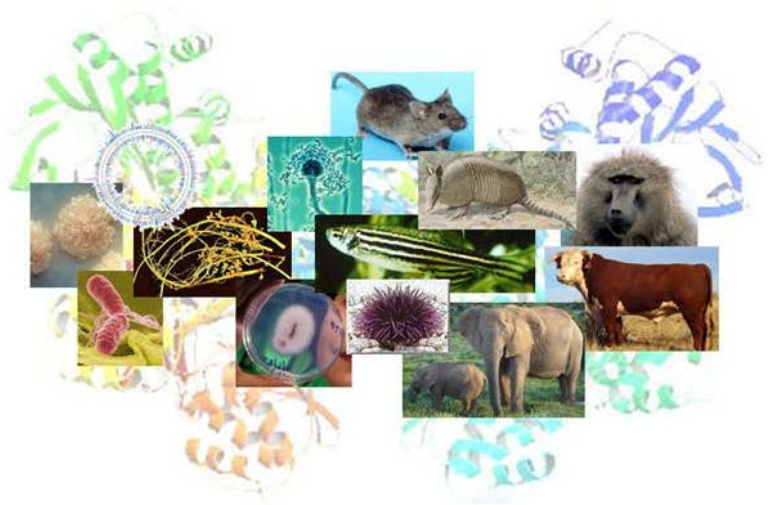
**Non-human *NAT* alleles/haplotypes**

[NAT1 alleles](#)

[NAT2 alleles](#)

[NAT3 alleles](#)

Welcome to the database of arylamine *N*-acetyltransferases (*NATs*)



Images are from the public domain  
Salmonella *NAT* is pdb 1E2T

**The Arylamine *N*-acetyltransferase Gene Nomenclature Committee:**

Dr. Sotiria Boukouvala  
Department of Molecular Biology & Genetics,  
Democritus University of Thrace, Greece.

Prof. David W. Hein  
Department of Pharmacology & Toxicology,  
University of Louisville, USA.

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Eirini Vagena  
Vasiliki Garefalaki  
for collection, annotation and presentation of the data

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68100, Greece.  
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**Big “Thank You” to all who provided *NAT2* nomenclature in the past and/or served on the PharmVar expert panel to make the transition happen**

# NAT2

## New nomenclature

used for the CPIC guideline on *NAT2* and hydralazine

NAT2 Gene Expert Panel			
Role	Name	Institution	Country
Chair	Andrea Gaedigk	Children's Mercy Research Institute	USA
Chair	Sotiria (Rea) Boukourvala	Democritus University of Thrace	Greece
PharmGKB/CPIC Representative	Michelle Whinn-Carrillo	Stanford, PharmGKB	USA
PharmGKB/CPIC Representative	Katrin Sangkuhl	Stanford, PharmGKB	USA
PharmGKB/CPIC Representative	Teri Klein	Stanford, PharmGKB	USA
Member	Jose Agundez	Universidad de Extremadura	Spain
Member	Giannoulis Fakis	Democritus University of Thrace	Greece
Member	Mariam Habil	University of Louisville	USA
Member	David Hein	University of Louisville	USA
Member	Rod Minchin	University of Queensland	Australia
Trainee	Georgia Papanikolaou	Democritus University of Thrace	Greece
Member	Estella Poloni	University of Geneva	Switzerland
Member	Adalberto Rezende Santos	Oswaldo Cruz Foundation	Brazil
Member	Raquel Teixeira	Laboratório de Biologia Molecular Aplicada a Micobactérias	Brazil
Data Specialist	Erin Boone	Children's Mercy Research Institute	USA

NAT2 expert panel

- Allele definitions include the 5' and 3' untranslated regions
- Star allele definitions use NG\_012246.1
- The “new” *NAT2*\*1 allele matches NG\_012246.1 and GRCh38 (and the “old” \*12A)
- Used 1000 Genomes 30X WGS data to confirm existing allele definitions (and discover some new ones)
- Not all previously defined star alleles were transferred to PharmVar
- Many alleles received a new star allele number to conform with PharmVar rules



# *NAT2*

Alleles not transferred

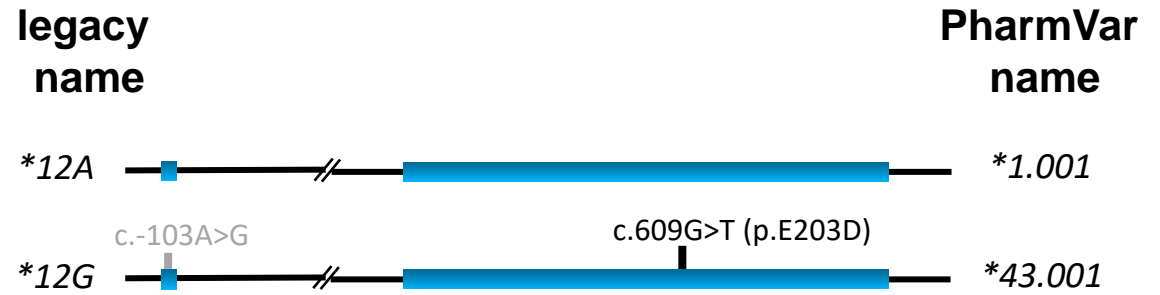


to PharmVar

- Numerous alleles defined based on computational inference
- Papers provide limited/no information about
  - about method
  - SNPs present in subjects(s) with “new” haplotype
  - Possible/alternate diplotype
  - Inferred to be present in one/few subjects
- Concerns about whether these exist
- Efforts underway by panel experts to reanalyze samples, if available
- Experts concurred that experimental validation is needed before transfer to PharmVar to ensure high-quality content of *NAT2* star alleles in PharmVar

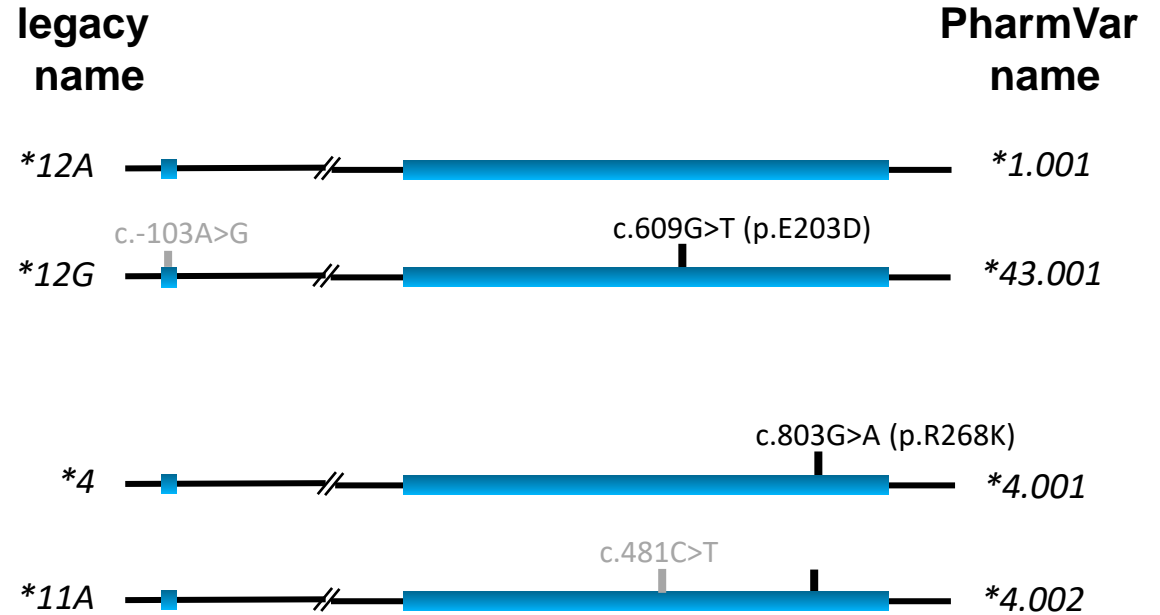
# ***NAT2***

Renamed alleles  
to conform to PharmVar rules



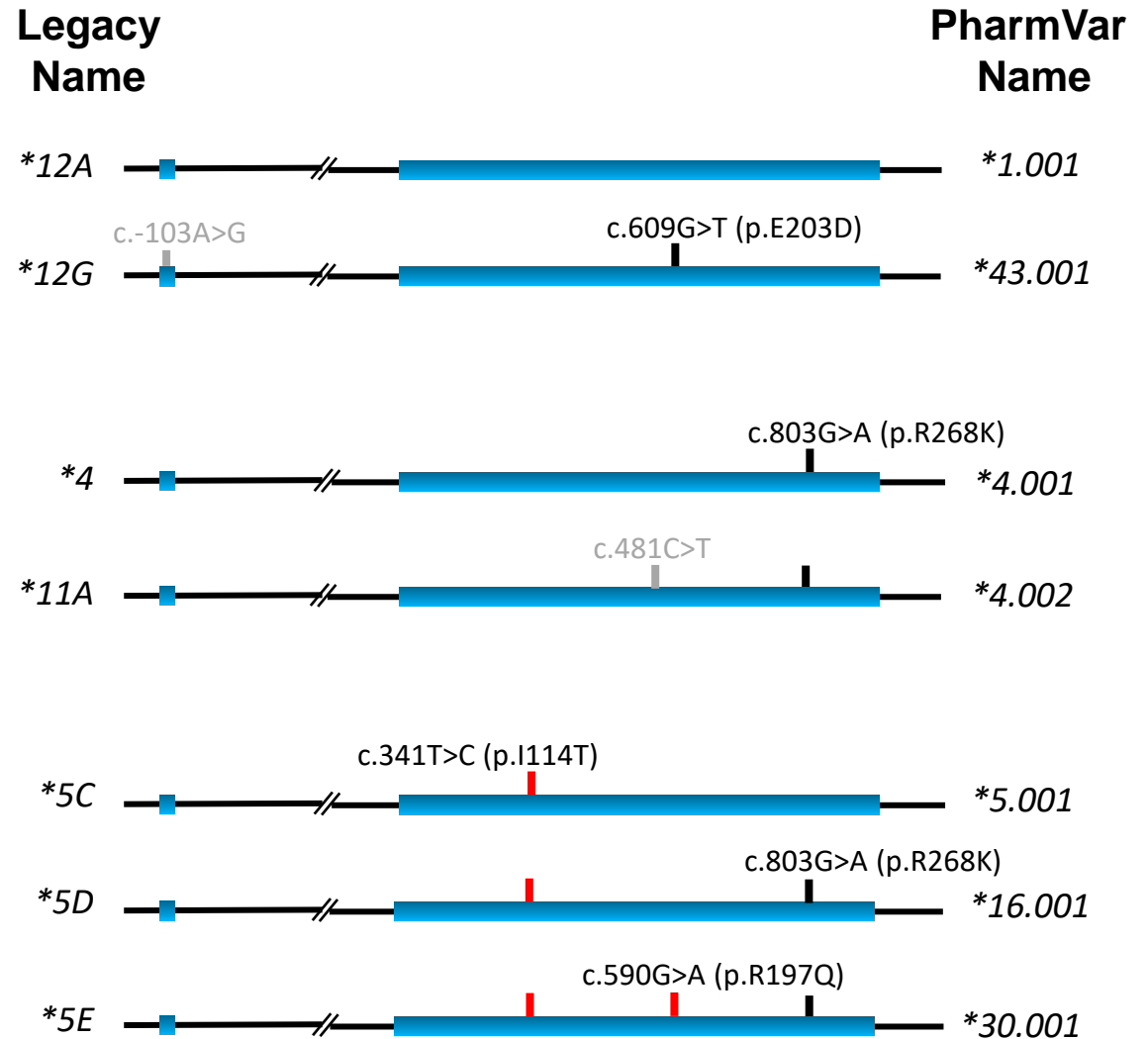
# NAT2

Renamed alleles  
to conform to PharmVar rules



# NAT2

Renamed alleles  
to conform to PharmVar rules



# NAT2

New nomenclature

Look it up!

NAT2

External Resources



[ClinGen](#)

[ClinVar](#)

[EntrezGene](#)

[HGNC](#)

[Read Me for NAT2](#)

[Change Log for NAT2](#)

[More Documents](#)



# NAT2

## New nomenclature

## Look-up table

Legacy name	PharmVar Name <sup>1</sup>	Transferred Yes/No	PharmVar data base version if transferred OR why allele was not transferred
*10	*10.001	yes	6.1 (March 11, 2024)
*11A	*4.002	yes	6.1 (March 11, 2024)
*12A	*1.001	yes	6.1 (March 11, 2024)
*12B	*1.002	yes	6.1 (March 11, 2024)
*12C	*1.003	yes	6.1 (March 11, 2024)
*12D	*48.001	yes	6.1 (March 11, 2024)
*12E	*41.001	yes	6.1 (March 11, 2024)
*11B	n/a	no	allele retired from NAT nomenclature site
*12K	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar
*12L	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar
*12M	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar
*13B	*13 reserved	no	evidence review in progress; if transferred, allele will keep its original star number
*13C	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar

### NAT2

#### External Resources

[ClinGen](#)[ClinVar](#)[EntrezGene](#)[HGNC](#)[Read Me for NAT2](#)[Change Log for NAT2](#)[+ More Documents](#)

# NAT2

## New nomenclature

## Look-up table

Legacy name	PharmVar Name <sup>1</sup>	Transferred Yes/No	PharmVar data base version if transferred OR why allele was not transferred
*10	*10.001	yes	6.1 (March 11, 2024)
*11A	*4.002	yes	6.1 (March 11, 2024)
*12A	*1.001	yes	6.1 (March 11, 2024)
*12B	*1.002	yes	6.1 (March 11, 2024)
*12C	*1.003	yes	6.1 (March 11, 2024)
*12D	*48.001	yes	6.1 (March 11, 2024)
*12E	*41.001	yes	6.1 (March 11, 2024)
*11B	n/a	no	allele retired from NAT nomenclature site
*12K	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar
*12L	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar
*12M	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar
*13B	*13 reserved	no	evidence review in progress; if transferred, allele will keep its original star number
*13C	n/a	no	computationally inferred; experimental evidence needed to confirm haplotype and transfer to PharmVar

### NAT2

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### NAT2

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***TPMT?***

***ABCG2?***

***VCORC1?***

***UGT1A1?***

***Other?***

**Can't do this without**

**Gene Champions and Experts**



감사합니다 Natick  
Grazie Danke Ευχαριστίες Dalu Obrigado  
Thank You Köszönöm  
Tack  
Спасибо Dank Gracias  
Seé  
谢谢 Merci ありがとう

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## PharmVar

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Erin Boone (data)

Wendy Wang (lab, submissions)

**Expert Panelists**

**Submitters**

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