

Practical session:

Variants & diseases

- Exploring ClinGen and ClinVar resources to find out relationships between genetic diseases and genes/variants implicated.



ACTGATGGTATGGGGCCAAGAGATATATCT
CAGGTACGGCTGTCATCACTTAGACCTCAC
CAGGGCTGGGCATAAAAGTCAGGGCAGAGC
CCATGGTGCATCTGACTCCTGAGGAGAAGT
GCAGGTTGGTATCAAGGTTACAAGACAGGT
GGCACTGACTCTCTCTGCCTATTGGTCTAT

ClinVar

ClinVar aggregates information about genomic variation and its relationship to human health.

Using ClinVar

[About ClinVar](#)[Data Dictionary](#)[Downloads/FTP site](#)[FAQ](#)[Contact Us](#)[RSS feed/What's new?](#)[Factsheet](#)

Tools

[ACMG Recommendations for Reporting of Incidental Findings](#)[ClinVar Submission Portal](#)[Submissions](#)[Variation Viewer](#)[Clinical Remapping - Between assemblies and RefSeqGenes](#)[RefSeqGene/LRG](#)

Related Sites

[ClinGen](#)[GeneReviews®](#)[GTR®](#)[MedGen](#)[OMIM®](#)[Variation](#)

Example: Workflow for a monogenic disease: sickle cell anemia

<https://www.ncbi.nlm.nih.gov/clinvar/?term=sickle%20cell%20anemia>

Variation Location		Gene(s)	Condition(s)	Clinical significance (Last reviewed)	Review status
<input type="checkbox"/>	UGT1A1*28	UGT1A , UGT1A10 , UGT1A8 , UGT1A7 , UGT1A6 , UGT1A5 , UGT1A9 , UGT1A4 , UGT1A1 , UGT1A3	Bilirubin, serum level of, quantitative trait locus 1, Lucey-Driscoll syndrome, Crigler-Najjar syndrome, type II,	Conflicting interpretations of pathogenicity, Affects, association, drug response, other (Apr 4, 2018)	criteria provided, conflicting interpretations

Interpretation ?

Go

Clinical significance:

[Conflicting interpretations of pathogenicity, Affects, association, drug response, other](#)
Benign(1);Pathogenic(2)

Last evaluated:

Apr 4, 2018

Number of submission(s):

7

Condition(s):

- Bilirubin, serum level of, quantitative trait locus 1 [\[MedGen - OMIM\]](#)
- Lucey-Driscoll syndrome [\[MedGen - Orphanet - OMIM\]](#)
- Crigler-Najjar syndrome, type II [\[MedGen - Orphanet - OMIM\]](#)
- Gilbert's syndrome [\[MedGen - OMIM\]](#)
- Irinotecan response [\[MedGen\]](#)

[See supporting ClinVar records](#) 

Assertion and evidence details

Clinical assertions

Summary evidence

Supporting observations

Allele(s) ?

Go

UGT1A1*28

Allele ID:

27314

Variant type:

Duplication

Cytogenetic location:

2q37.1

Genomic location:

- Chr2: 233760235 - 233760236 (on Assembly GRCh38)
- Chr2: 234668881 - 234668882 (on Assembly GRCh37)

Other names:

- A(TA)7TAA
- (TA)7TAA

HGVS:

- NG_002601.2:g.175492_175493[8]
- NG_033238.1:g.4963_4964[8]
- NM_000463.2:c.-53_-52[8]

[...more](#)

Note:

Until October 16, 2017, this allele had conflicting molecular definitions. UGT1A1*28 is the allele with 8 copies of the TA repeat (1 copy more than reference). We deleted the representations that reported 7 copies and refreshed the database.

Links:

- OMIM: [191740.0011](#)
- dbSNP: [rs34983651](#)
- dbSNP: [rs606231201](#)
- dbSNP: [rs8175347](#)

NCBI 1000 Genomes Browser: [rs34983651](#)

Molecular consequence:

NM_000463.2:c.-41_-40dupTA: 2KB upstream variant [\[Sequence Ontology SO:0001636\]](#)

Explore ClinVar and ClinGen resources

Task: Create a **relational lists**

Disease

Sickle cell anemia

...

Thalassaemia
Sickle cell anemia
Haemophilia
Cystic Fibrosis
Tay sachs disease
Fragile X syndrome
Huntington's disease

Gene

UGT11

...

Variant

HGVS (id)

...

<http://www.hgvs.org/mutnomen/recs-DNA.html>

[About ClinGen](#)[Working Groups & Expert Panels](#)[Resources & Tools](#)[GenomeConnect](#)[Share Your Data](#)[Curation Activities](#)

Defining the clinical relevance of genes & variants for precision medicine and research...

1496

ClinGen Curated Genes

31

Expert Groups

10446

Expert Reviewed Variants in ClinVar



Knowledge Base Search

Sharing Data. Building Knowledge. Improving Care.

ClinGen is dedicated to building an authoritative central resource that defines the clinical relevance of genes and variants for use in precision medicine and research. Learn more about our organization and our ongoing efforts below.

Curation Status: Complete

id: ISCA-30165

Date last evaluated: 2016-08-22

Issue Type: ClinGen Gene Curation

Gene type: protein-coding

Entrez Gene: <https://www.ncbi.nlm.nih.gov/gene/1080>

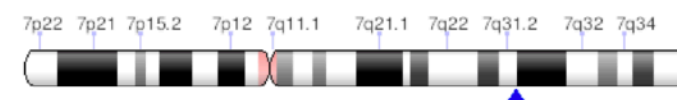
OMIM: <https://omim.org/entry/602421>

Gene Reviews: <https://www.ncbi.nlm.nih.gov/books/NBK1116/>

term=CFTR%5Bgenesymbol%5D

ClinGen Haploinsufficiency Score: [Gene associated with autosomal recessive phenotype](#)

ClinGen Triplosensitivity Score: Not yet evaluated



Location Information

7q31.2

GRCh37/hg19 chr7: 117,120,017-117,308,719

View: [NCBI](#) | [Ensembl](#) | [UCSC](#)

GRCh38/hg38 chr7: 117,478,367-117,668,665

View: [NCBI](#) | [Ensembl](#) | [UCSC](#)

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Pathogenic regions (nstd45)

Curation of the ACMG 59 Genes

FTP

[Report information on a gene](#)

[Print Full Report](#)

Genome View Evidence for Haploinsufficiency Phenotypes Evidence for Triplosensitive Phenotypes

Select assembly: **GRCh37/hg19 chr7: 117,120,017-117,308,719** (NC_000007.13)

The image shows a genome browser interface. At the top, there are three tabs: "Genome View", "Evidence for Haploinsufficiency Phenotypes", and "Evidence for Triplosensitive Phenotypes". Below the tabs, a dropdown menu shows the selected assembly: "GRCh37/hg19 chr7: 117,120,017-117,308,719" with a link to "(NC_000007.13)". The main panel displays a genomic track for the CFTR gene. The track is labeled "NC_000007.13" and "Find:". The track shows the gene structure with exons represented by blue boxes and introns by lines with arrows. The gene is labeled "CFTR" and "NM_000492.3". The track also shows the gene structure for "NP_000493.3". The track is zoomed in on the region from 117,120 K to 117,320 K. The track shows the gene structure with exons represented by blue boxes and introns by lines with arrows. The gene is labeled "CFTR" and "NM_000492.3". The track also shows the gene structure for "NP_000493.3". The track is zoomed in on the region from 117,120 K to 117,320 K. The track shows the gene structure with exons represented by blue boxes and introns by lines with arrows. The gene is labeled "CFTR" and "NM_000492.3". The track also shows the gene structure for "NP_000493.3". The track is zoomed in on the region from 117,120 K to 117,320 K.

Phenotypes

[Find tests for this gene in the NIH Genetic Testing Registry \(GTR\)](#)

Review eQTL and phenotype association data in this region using PheGenI

Associated conditions

Description	Tests
Bronchiectasis with or without elevated sweat chloride 1 MedGen: C2749757 , OMIM: 211400 , GeneReviews: Not available	Compare labs
Congenital bilateral absence of the vas deferens MedGen: C0403814 , OMIM: 277180 , GeneReviews: Cystic Fibrosis and Congenital Absence of the Vas Deferens	Compare labs
Cystic fibrosis MedGen: C0010674 , OMIM: 219700 , GeneReviews: Cystic Fibrosis and Congenital Absence of the Vas Deferens	Compare labs
Hereditary pancreatitis MedGen: C0238339 , OMIM: 167800 , GeneReviews: PRSS1-Related Hereditary Pancreatitis , Pancreatitis Overview	Compare labs
Ivacaftor response MedGen: CN185459 , GeneReviews: Not available	Compare labs

From genes to diseases...

Gene/locus	Gene name	Chromosomal location [#]	Gene product: protein function	Disease
<i>CFTR</i>	CF transmembrane conductance regulator	7q31.2	Ion channel: chloride transport	CF
<i>SERPINE1</i>	α 1-antitrypsin	14q32.13	Serine protease inhibitor	α 1-antitrypsin deficiency (COPD, emphysema, liver disease)
<i>DNAI1</i>	Dynein, axonemal, intermediate chain 1	9p13.3	Dynein arm: ciliary function	CILD1, with or without situs inversus (Kartagener syndrome)
<i>CYBB</i>	p91-phox (phagocyte oxidase): beta subunit of cytochrome b, component of the phagocyte NADPH oxidase complex	Xp11.4	Killing of microbes in phagocytes by generation of reactive oxygen species	CGD, X-linked
<i>CYBA</i>	p22-phox (phagocyte oxidase): alpha subunit of cytochrome b, component of the phagocyte NADPH oxidase complex	16q24.3	Killing of microbes in phagocytes by generation of reactive oxygen species	CGD, autosomal recessive
<i>SFTPC</i>	Surfactant, pulmonary-associated protein C	8p21.3	Surfactant proteins are essential for lung function, preventing lung collapse by lowering surface tension	Respiratory distress syndrome of prematurity
<i>SFTPB</i>	Surfactant, pulmonary-associated protein B	2p11.2	Surfactant proteins are essential for lung function, preventing lung collapse by lowering surface tension	Respiratory distress syndrome of prematurity