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Variant: NM_001369.3(DNAH5):c.10815del (p.Pro3606fs)

Version: 1.0

CA339772

65636 (ClinVar)

Gene: DNAH5 (HGNC:1767)
Condition: primary ciliary dyskinesia 3 (MONDO:0012085)
Inheritance Mode: Autosomal recessive inheritance
UUID: 8f286f60-da57-4194-9500-39f3188038b2
Approved on: Wed, 18 Nov 2026 00:00:00 +0000
Published on: Wed, 18 Nov 2026 00:00:00 +0000

HGVS expressions

NM_001369.3(DNAH5):c.10815del (p.Pro3606fs)
NM_001369.3:c.10815del
NM_001369.3:c.10815delT
NC_000005.10:g.13753290del
CM000667.2:g.13753290del
NC_000005.9:g.13753399del
CM000667.1:g.13753399del
NC_000005.8:g.13806399del
NG_013081.1:g.196191del
NG_013081.2:g.196191del
ENST00000265104.5:c.10815del
ENST00000681290.1:c.10770del
ENST00000265104.4:c.10815del
NM_001369.2:c.10815del

Pathogenic

Met criteria codes 4

PP1 PP4 PM3_Supporting PVS1

Not Met criteria codes 2

PM2 BS1

Evidence Links 0

Expert Panel

Motile Ciliopathy VCEP

Criteria Specification Information

Criteria Specification: *ClinGen Motile Ciliopathy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for DNAH5 Version 1.0*
Criteria Specification Approval History
Criteria Specifications for this VCEP

Evidence submitted by expert panel

Motile Ciliopathy VCEP

NM_001369.3(DNAH5):c.10815del (p.Pro3606HisfsTer23) is a frameshift variant that introduces a premature stop codon into exon 63 of 79, and is predicted to lead to nonsense-mediated decay in a gene in which loss-of-function is an established mechanism of disease (PVS1, PMIDs: 16627867, 34556108). This variant is present in gnomAD v.4.1.1 at a Grpmax allele frequency of 0.00051, with 638 alleles / 1,179,900 total alleles in the European (non-Finnish) population, which is lower than the BS1 threshold of >0.0006. The variant has a total

allele frequency of 0.000411 combined across all populations, which is higher than the ClinGen Motile Ciliopathy VCEP PM2_Supporting threshold of <0.00006, so no population code is met. This variant is a known founder with relatively high rates of heterozygous occurrence in the control population, and is considered eligible for inclusion in the PM3 code despite not meeting PM2_Supporting. This variant has been reported in at least 1 proband with primary ciliary dyskinesia who was homozygous for the variant (0.5 points, PMID: 16627867, PMID: 20301301, PM3_Supporting). This variant has also been reported in at least 4 probands with primary ciliary dyskinesia who were compound heterozygous with either the NM_001369.3(DNAH5):c.232C>T (p.Arg78Ter) variant confirmed in trans (PMID: 16627867, PMID: 31879361), the NM_001369.3(DNAH5):c.13458dup (p.Asn4487Ter) confirmed in trans (PMID: 16627867, 39115449), or the NM_001369.3:c.13486C>T (p.Arg4496Ter) (PMID: 16627867) confirmed in trans, all of which were previously classified pathogenic by the ClinGen Motile Ciliopathy VCEP, which were not counted for PM3 in order to avoid circularity. At least one proband harboring this variant exhibits a phenotype including: absent outer dynein arms (4 pt), productive cough (1 pt), decreased nasal nitric oxide (1 pt), neonatal respiratory distress (1 pt), sinusitis, rhinitis, chronic otitis media (1 pt) and situs inversus totalis (1 pt), which together are specific for primary ciliary dyskinesia 3 (total 9 points, PMID:23477994, PP4). The variant has been reported to co-segregate with primary ciliary dyskinesia through at least one segregation within the family of the proband, with the variant present in the compound heterozygous state (PMID: 23477994, PP1). In summary, this variant meets the criteria to be classified as Pathogenic for primary ciliary dyskinesia 3 based on the ACMG/AMP criteria applied, as specified by the ClinGen Motile Ciliopathy VCEP: PVS1, PM3_Supporting, PP4, and PP1. (VCEP specifications version 1.0.0).

Met criteria codes

PP1	✔	The variant has been reported to co-segregate with primary ciliary dyskinesia through at least one segregation within the family of the proband, with the variant present in the compound heterozygous state (PMID: 23477994, PP1).
PP4	✔	At least one proband harboring this variant exhibits a phenotype including: absent outer dynein arms (4 pt), productive cough (1 pt), decreased nasal nitric oxide (1 pt), neonatal respiratory distress (1 pt), sinusitis, rhinitis, chronic otitis media (1 pt) and situs inversus totalis (1 pt), which together are specific for primary ciliary dyskinesia 3 (total 9 points, PMID:23477994, PP4).
PM3_Supporting	✔	This variant has been reported in at least 1 proband with primary ciliary dyskinesia who was homozygous for the variant (0.5 points, PMID: 16627867, PMID: 20301301, PM3_Supporting). This variant has also been reported in at least 4 probands with primary ciliary dyskinesia who were compound heterozygous with either the NM_001369.3(DNAH5):c.232C>T (p.Arg78Ter) variant confirmed in trans (PMID: 16627867, PMID: 31879361), the NM_001369.3(DNAH5):c.13458dup (p.Asn4487Ter) confirmed in trans (PMID: 16627867, 39115449), or the NM_001369.3:c.13486C>T (p.Arg4496Ter) (PMID: 16627867) confirmed in trans, all of which were previously classified pathogenic by the ClinGen Motile Ciliopathy VCEP, which were not counted for PM3 in order to avoid circularity.
PVS1	✔	This is a frameshift variant that introduces a premature stop codon into exon 63 of 79, and is predicted to lead to nonsense-mediated decay in a gene in which loss-of-function is an established mechanism of disease (PVS1; PMIDs: 16627867, 34556108).

Not Met criteria codes

PM2	✖	This variant is present in gnomAD v.4.1.1 at a Grpmax allele frequency of 0.00051, with 638 alleles / 1,179,900 total alleles in the European (non-Finnish) population, which is lower than the BS1 threshold of >0.0006. The variant has a total allele frequency of 0.000411 combined across all populations, which is higher than the ClinGen Motile Ciliopathy VCEP PM2_Supporting threshold of <0.00006, so no population code is met.

BS1	ℹ	✖	This variant is present in gnomAD v.4.1.1 at a Grpmax allele frequency of 0.00051, with 638 alleles / 1,179,900 total alleles in the European (non-Finnish) population, which is lower than the BS1 threshold of >0.0006. The variant has a total allele frequency of 0.000411 combined across all populations, which is higher than the ClinGen Motile Ciliopathy VCEP PM2_Supporting threshold of <0.00006, so no population code is met.

Curation History

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See Report	Preferred Variant Title	Classification	Condition	Published Date	Version	Criteria Specification	Gene
View	NM_001369.3(DNAH5):c.10815del (p.Pr...	Pathogenic	Primary Ciliary Dyskinesia 3	2026-11-18	1.0	ClinGen Motile Ciliopathy Expert Panel Specifications to the ACMG/AMP Variant Interpretation Guidelines for DNAH5 Version 1.0	DNAH5

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