

Title: Primary Autosomal Recessive Microcephalies and Seckel Syndrome Spectrum Disorders *GeneReview* Tables 16 – 18

Authors: Verloes A, Drunat S, Gressens P, Passemard S

Updated: October 2013

Note: The following information is provided by the authors listed above and has not been reviewed by *GeneReviews* staff.

**Table 16. Published Pathogenic *ATR* Allelic Variants (Based on NM\_001184 Reference Sequences)**

DNA Nucleotide Change	Protein Amino Acid Change
Large deletion (chr3: g.(143,446,412_143,475,187)_(144,013,999_144,022,947)del.) [Mokrani-Benhelli et al 2013]	p.0
c.2022A>G (2101A>G or IVS9-57A>G) [O'Driscoll et al 2003]	Aberrant splicing of exon 9
c.3477G>T [Ogi et al 2012]	p.Met1159Ile
c.5635G>T [Mokrani-Benhelli et al 2013]	p.Asp1879Tyr
c.6897+464C>G [Ogi et al 2012]	p.Val2300Glyfs75Ter

See [Quick Reference](#) for an explanation of nomenclature. *GeneReviews* follows the standard naming conventions of the Human Genome Variation Society ([www.hgvs.org](http://www.hgvs.org)).

**Table 17. Published Pathogenic *RBBP8* Allelic Variants (Based on NM\_002894.2 and NP\_002885.1 Reference Sequences)**

DNA Nucleotide Change (Alias <sup>1</sup> )	Protein Amino Acid Change
c.1808_1809delTA (1868delTA) [Qvist et al 2011]	p.Ile603LysfTer7
(2347+53T>G) [Qvist et al 2011]	Missplicing and premature termination of protein

See [Quick Reference](#) for an explanation of nomenclature. *GeneReviews* follows the standard naming conventions of the Human Genome Variation Society ([www.hgvs.org](http://www.hgvs.org)).

1. Variant designation that does not conform to current naming conventions

**Table 18. Published Pathogenic *CEP63* Allelic Variants**

DNA Nucleotide Change	Protein Amino Acid Change
c.129G>A [Sir et al 2011]	p.Trp43Ter

See [Quick Reference](#) for an explanation of nomenclature. *GeneReviews* follows the standard naming conventions of the Human Genome Variation Society ([www.hgvs.org](http://www.hgvs.org)).

## References

Mokrani-Benhelli H, Gaillard L, Biasutto P, Le Guen T, Touzot F, Vasquez N, Komatsu J, Conseiller E, P'icard C, Gluckman E, Francannet C, Fischer A, Durandy A, Soulier J, de Villartay JP, Cavazzana-Calvo M, Revy P. Primary microcephaly, impaired DNA replication, and genomic instability caused by compound heterozygous ATR mutations. *Hum Mutat.* 2013;34:374-84.

O'Driscoll M, Ruiz-Perez VL, Woods CG, Jeggo PA, Goodship JA. A splicing mutation affecting expression of ataxia-telangiectasia and Rad3-related protein (ATR) results in Seckel syndrome. *Nat Genet.* 2003;33:497-501.

Ogi T, Walker S, Stiff T, Hobson E, Limsirichaikul S, Carpenter G, Prescott K, Suri M, Byrd PJ, Matsuse M, Mitsutake N, Nakazawa Y, Vasudevan P, Barrow M, Stewart GS, Taylor AM, O'Driscoll M, Jeggo PA. Identification of the first ATRIP-deficient patient and novel mutations in ATR define a clinical spectrum for ATR-ATRIP Seckel Syndrome. *PLoS Genet.* 2012;8:e1002945.

Qvist P, Huertas P, Jimeno S, Nyegaard M, Hassan MJ, Jackson SP, Børglum AD. CtIP Mutations Cause Seckel and Jawad Syndromes. *PLoS Genet.* 2011;7:e1002310.

Sir JH, Barr AR, Nicholas AK, Carvalho OP, Khurshid M, Sossick A, Reichelt S, D'Santos C, Woods CG, Gergely F. A primary microcephaly protein complex forms a ring around parental centrioles. *Nat Genet.* 2011;43:1147-53.