

Supplementary Material to

Genetic bases of C7 deficiency: systematic review and report of a novel deletion determining functional hemizygoty

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Search strategy

Databases	PubMed/Medline, Scopus, Embase	
Total	363	
Database	n	Search
PubMed	90	((((((((((C7 deficient[Title/Abstract]) OR (C7 deficiency[Title/Abstract])) OR (C7 deficiencies[Title/Abstract])) OR (seventh complement deficient[Title/Abstract])) OR (seventh complement deficiency[Title/Abstract])) OR (seventh complement deficiencies[Title/Abstract])) OR (7th complement deficient[Title/Abstract]) OR (7th complement deficiency[Title/Abstract])) OR (7th complement deficiencies[Title/Abstract])) OR (complement 7 deficient[Title/Abstract])) OR (complement 7 deficiency[Title/Abstract])) OR (complement 7 deficiencies [Title/Abstract]))
Scopus	166	(TITLE-ABS-KEY(c7 AND deficient) OR TITLE-ABS-KEY(c7 AND deficiency) OR TITLE-ABS-KEY(c7 AND deficiencies) OR TITLE-ABS-KEY(seventh AND complement AND deficient) OR TITLE-ABS-KEY(seventh AND complement AND deficiency) OR TITLE-ABS-KEY(seventh AND complement AND deficiencies) OR TITLE-ABS-KEY(7th AND complement AND deficient) OR TITLE-ABS-KEY(7th AND complement AND deficiency) OR TITLE-ABS-KEY(7th AND complement AND deficiencies) OR TITLE-ABS-KEY(complement 7 deficient) OR TITLE-ABS-KEY(complement 7 deficiency) OR TITLE-ABS-KEY(complement 7 deficiencies)) AND (LIMIT-TO (LANGUAGE,"English")) AND (EXCLUDE (DOCTYPE,"re")) AND (LIMIT-TO (EXACTKEYWORD,"Complement Component C7"))
Embase	107	('c7 deficient':ti,ab,kw OR 'c7 deficiency':ti,ab,kw OR 'c7 deficiencies':ti,ab,kw OR 'seventh complement deficient':ti,ab,kw OR 'seventh complement deficiency':ti,ab,kw OR 'seventh complement deficiencies':ti,ab,kw OR '7th complement deficient':ti,ab,kw OR '7th complement deficiency':ti,ab,kw OR '7th complement deficiencies':ti,ab,kw OR 'complement 7 deficient':ti,ab,kw OR 'complement 7 deficiency':ti,ab,kw OR 'complement 7 deficiencies':ti,ab,kw) AND [english]/lim

Supplementary Table 1. Variants identified in the C7 gene (NM_000587.4) of the patient by Sanger sequencing.

Variant	Effect	Zigosity	rs	MAF	Interpretation
c.983-230T>G	n.a.	hom	n.a.	n.a.	n.a.
c.983-9C>T	n.a.	hom	rs1450656	C=0.35640	benign
c.1135G>C	p.G379R	het	rs121964921	C=0.00013	pathogenetic
c.1166G>C	p.S389T	hom	rs1063499	G=0.4300	benign
c.1661+444A>T	n.a.	het	n.a.	n.a.	n.a.
c.1759A>C	p.T587P	het	rs13157656	C=0.240352	benign
c.1883-134A>G	n.a.	het	n.a.	n.a.	n.a.
c.2166-37A>T	n.a.	het	rs2876849	T=0.3106	benign
c.*99_*101delTCT	n.a.	het	n.a.	n.a.	n.a.

Abbreviations: hom: homozygosis; het: heterozygosis; n.a.: not available; MAF: minor allele frequency.