Names for RH (ISBT 004) Blood Group Alleles: RHCE Alleles

Intro

General description:	The Rh blood group system consists of 56 antigens. Many are encoded at the *RHCE* locus and a number are encoded by hybrid *RHCE* with *RHD*. The RhCE protein (CD240CE) consists of 12 membrane-spanning domains and 417 amino acids. The amino and carboxyl termini are predicted to be intracellular, and the initial methionine is cleaved post-translationally. The expression of Rh proteins requires functional RhAG proteins, predicted to form heterotrimers with Rh.
Gene name:	*RHCE*
Number of exons:	10
Initiation codon:	within exon 1
Stop codon:	within exon 10
Entrez Gene ID:	6006
LRG:	LRG_797
LRG sequence:	NG_009208.3 (genomic) corresponds to a *RHCE*01* allele NM_020485.8 (mRNA transcript) corresponds to a *RHCE*01* allele NP_065231.4 (protein) corresponds to a *RHCE*01* allele
Reference allele:	Preferred: *RHCE*01* (shaded) Acceptable: *RHCE*C, RHCE*c, RHCE*E or RHCE*e* when only testing for the specific polymorphism(s) associated with expression of that antigen.
Reference allele *RHCE*01* encodes:	RH4, RH5, RH6, RH17, RH18, RH19, RH26, RH29, RH31, RH34, RH44, RH46, RH47, RH51, RH57, RH58, RH59, RH61, RH62
Antithetical antigens:	[RH2 RH4] [RH3 RH5] [RH8/RH9 RH52] [RH26 RH55] [RH32 RH46] [RH43 RH58] [RH48 RH57]
Antigens commonly typed for include	RH2 (C), RH3 (E), RH4 (c), RH5 (e), RH8 (C^w), RH9 (C^x), RH10 (V) and RH20 (VS).
The less common include	RH11 (E^w), RH17 (Hr_0), RH18 (Hr), RH19 (hr^S), RH21 (C^G), RH26 (c-like), RH28 (hr^H), RH31 (hr^B), RH32, RH33, RH34 (Hr^B), RH35, RH36 (Be^a), RH39, RH41, RH42, RH43 (Crawford), RH44 (Nou), RH45 (Riv), RH46 (Sec), RH47 (Dav), RH48 (JAL), RH49 (STEM), RH51 (MAR), RH53 (JAHK), RH55 (LOCR), RH56 (CENR), RH57 (CEST), RH58 (CELO), RH59 (CEAG), RH60 (PARG), RH61 (CEVF) and RH63 (CETW).
Compound antigens include	RH6 (f), RH7 (Ce), RH22 (CE) and RH27 (cE).
Antigens encoded from either *RHCE* or *RHD* loci include	RH12 (G), RH50 (FPTT), RH52 (BARC), RH54 (DAK), RH29 and CEWA (RH62).

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:4 or c RH:5 or e RH:6 or f (ce)	*RHCE*01 or* *RHCE*ce*	c.307C c.676G	2 5	p.Pro103 p.Ala226	PMID: 8220426	NG_009208.3	rs676785 rs609320
RH:5 (e+ weak)	*RHCE*01.01* *RHCE*ce.01*	c.48G>C	1	p.Trp16Cys	PMID: 11380456	DQ266400	rs586178
RH:4 (c+ weak, partial) RH:5 (e+ weak, partial)	*RHCE*01.02.01* *RHCE*ce.02.01* *RHCE*ceTI*	c.48G>C c.1025C>T	1 7	p.Trp16Cys p.Thr342Ile	PMID: 22804620	KY369953	rs586178 rs1053374
	*RHCE*01.02.02* *RHCE*ce.02.02*	c.48G>C c.150C>T c.178C>A c.201A>G c.203A>G c.307C>T c.1025C>T	1 2 7	p.Trp16Cys p.Val50= p.Leu60Ile p.Ser67= p.Asn68Ser p.Pro103Ser p.Thr342Ilep	PMID: 25857637	LN680105	rs586178 rs200955066 rs181860403 rs1053343 rs1053344 rs676785 rs1053374
RH:5 (e+ partial)	*RHCE*01.03* *RHCE*ce.03*	c.1025C>T	7	p.Thr342Ile	PMID: 20088832	MH717897	rs1053374
RH:4 (c+ partial) RH:5 (e+ weak, partial) RH:10,–20 (V+ weak, VS–) RH:–18,–19 (Hr–, hr^S–)	*RHCE*01.04.01* *RHCE*ce.04.01* *RHCE*ceAR*	c.48G>C c.712A>G c.733C>G c.787A>G c.800T>A c.916A>G	1 5 6	p.Trp16Cys p.Met238Val p.Leu245Val p.Arg263Gly p.Met267Lys p.Ile306Val	PMID: 10590079	not found	rs586178 rs144163296 rs1053361 rs1132763 rs1132764 rs1132765
Inferred as *RHCE*01.04.01* *RHCE*ceAR*	*RHCE*01.04.02* *RHCE*ce.04.02*	c.48G>C c.697C>G c.712A>G c.733C>G c.787A>G c.800T>A c.916A>G	1 5 6	p.Trp16Cys p.Gln233Glu p.Met238Val p.Leu245Val p.Arg263Gly p.Met267Lys p.Ile306Val	(1), Abstract	KY369958	rs586178 rs142246017 rs144163296 rs1053361 rs1132763 rs1132764 rs1132765

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
Inferred as *RHCE*01.04.01* *RHCE*ceAR*	*RHCE*01.04.03* *RHCE*ce.04.03*	c.48G>C c.455C>A c.712A>G c.733C>G c.787A>G c.800T>A c.916A>G	1 3 5 6	p.Trp16Cys p.Thr152Asn p.Met238Val p.Leu245Val p.Arg263Gly p.Met267Lys p.Ile306Val	(1), Abstract	KY369957	rs586178 rs35109888 rs144163296 rs1053361 rs1132763 rs1132764 rs1132765
Inferred as *RHCE*01.04.01* *RHCE*ceAR*	*RHCE*01.04.04* *RHCE*ce.04.04*	c.712A>G c.733C>G c.787A>G c.800T>A c.916A>G	5 6	p.Met238Val p.Leu245Val p.Arg263Gly p.Met267Lys p.Ile306Val	(22), Abstract	not found	rs144163296 rs1053361 rs1132763 rs1132764 rs1132765
RH:4 (c+ partial) RH:5 (e+ weak, partial) RH:–18,–19 (Hr–, hr^{S}–)	*RHCE*01.05.01* *RHCE*ce.05.01* *RHCE*ceEK*	c.48G>C c.712A>G c.787A>G c.800T>A	1 5	p.Trp16Cys p.Met238Val p.Arg263Gly p.Met267Lys	PMID: 12393640	AF510065 KU556685	rs586178 rs144163296 rs1132763 rs1132764
RH:4 (c+ partial) RH:5 (e+ partial) RH:–18,–19 (Hr–, hr^{S}–)	*RHCE*01.05.02* *RHCE*ce.05.02*	c.712A>G c.787A>G c.800T>A	5	p.Met238Val p.Arg263Gly p.Met267Lys	PMID: 32196693	not found	rs144163296 rs1132763 rs1132764
RH:5 (e+ weak, partial) RH:–59 (CEAG–) RH:–31 (hr^{B}–)	*RHCE*01.06.01* *RHCE*ce.06.01* *RHCE*ceAG*	c.254C>G	2	p.Ala85Gly	PMID: 26173592	GU810838	rs57992529
	*RHCE*01.06.02* *RHCE*ce.06.02*	c.254C>G c.733C>G	2 5	p.Ala85Gly p.Leu245Val	PMID: 25695437	not found	rs57992529 rs1053361
	*RHCE*01.06.03* *RHCE*ce.06.03*	c.254C>G c.733C>G c.941T>C	2 5 7	p.Ala85Gly p.Leu245Val p.Val314Ala	PMID: 26173592	KY243887	rs57992529 rs1053361 rs79321360
	*RHCE*01.06.04* *RHCE*ce.06.04*	c.254C>G c.697C>G	2 5	p.Ala85Gly p.Gln233Glu	PMID: 26173592	KY243888	rs57992529 rs142246017
RH:2 (C+ partial, robust C+ expression) RH:5 (e+)	*RHCE*01.06.05* *RHCE*ce.06.05*	c.254C>G c.307C>T	2	p.Ala85Gly p.Pro103Ser	PMID: 26173592	KY369954	rs57992529 rs676785

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:4 (c+ partial) RH:5 (e+ weak, partial) RH:–19 (hr^{S}–) RH:–31 (hr^{B}–) RH:–61 (CEVF–)	*RHCE*01.07.01* *RHCE*ce.07.01* *RHCE*ceMO.01*	c.48G>C c.667G>T	1 5	p.Trp16Cys p.Val223Phe	PMID: 11380457 PMID: 23772606	not found	rs586178 rs147357308
RH:4 (c+ partial) RH:5 (e+ weak, partial) RH:–19 (hr^{S}–) RH:–31 (hr^{B}–) RH:–61 (CEVF–)	*RHCE*01.07.02* *RHCE*ce.07.02* *RHCE*ceMO.02*	c.667G>T	5	p.Val223Phe	PMID: 23772606	not found	rs147357308
RH:5 (e+ partial, weak to neg) RH:–18,–19 (Hr–, hr^{S}–) RH:49 (STEM+)	*RHCE*01.08* *RHCE*ce.08* *RHCE*ceBI*	c.48G>C c.712A>G c.818C>T c.1132C>G	1 5 6 8	p.Trp16Cys p.Met238Val p.Ala273Val p.Leu378Val	PMID: 12393640	AF510066	rs586178 rs144163296 rs147094099 rs138917454
RH:5 (e+ positive to negative) RH:–18 (Hr–), inferred RH:–19 (hr^{S}–) Rh:49 (STEM+ weak)	*RHCE*01.09* *RHCE*ce.09* *RHCE*ceSM*	c.48G>C c.712A>G c.818C>T	1 5 6	p.Trp16Cys p.Met238Val p.Ala273Val	PMID: 22738288	GU474431	rs586178 rs144163296 rs147094099
RH:5 (e+ weak) Some monoclonal anti-D cross-react	*RHCE*01.10.01 .01* *RHCE*ce.10.01 .01* *RHCE*ceSL .01.01*	c.48G>C c.365C>T	1 3	p.Trp16Cys p.Ser122Leu	PMID: 16686844	not found	rs586178 rs201407774
RH:5 (e+ weak) Some monoclonal anti-D cross-react	*RHCE*01.10.01.02* *RHCE*ce.10.01.02* *RHCE*ceSL.01.02*	c.48G>C c.105C>T c.365C>T	1 2 3	p.Trp16Cys p.Asp35= p.Ser122Leu	PMID: 16686844	not found	rs586178 rs142971926 rs201407774
RH:5 (e+ weak) Some monoclonal anti-D cross-react	*RHCE*01.10.02* *RHCE*ce.10.02* *RHCE*ceSL.02*	c.365C>T	3	p.Ser122Leu	PMID: 16686844	AM072960	rs201407774
RH:5 (e+ weak) Some monoclonal anti-D cross-react	*RHCE*01.11* *RHCE*ce.11* *RHCE*ceRT*	c.461G>C	3	p.Arg154Thr	PMID: 12919427	AM072961	rs747471048
RH:5 (e+ weak)	*RHCE*01.12* *RHCE*ce.12* *RHCE*ceRA*	c.48G>C c.538G>C	1 4	p.Trp16Cys p.Gly180Arg	PMID: 16836572	not found	rs586178 not found

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:5 (e+ very weak) RH:58 (CELO+ weak)	*RHCE*01.13* *RHCE*ce.13* *RHCE*ceBP*	c.687_689delAAG	5	p.Arg229del	PMID: 14996197	not found	rs1437180947
RH:4 (c+ weak) RH:5 (e+ weak) RH:36 (Be[a]+)	*RHCE*01.14* *RHCE*ce.14* *RHCE*ceBE*	c.662C>G	5	p.Pro221Arg	PMID: 19453979 PMID: 19951310	AM295500	rs141398055
RH:4 (c+ weak) RH:5 (e+ weak) RH:55 (LOCR+) RH:–26	*RHCE*01.15* *RHCE*ce.15* *RHCE*ceLOCR*	c.286G>A	2	p.Gly96Ser	PMID: 9426634 PMID: 17002624	not found	rs144348222
RH:5 (e+ weak)	*RHCE*01.16* *RHCE*ce.16*	c.48G>C c.1170C>T c.1193T>A	1 9	p.Trp16Cys p.Leu390= p.Val398Glu	PMID: 27113036	KU234778	rs586178 rs630931 rs630612
Some monoclonal anti-D crossreact	*RHCE*01.17* *RHCE*ce.17*	c.505C>A c.509G>T c.514T>A	4	p.Leu169Met p.Arg170Met p.Phe172Ile	(27), Abstract	MW924818	rs1020280601 rs987753117 rs1053349
RH:5 (e+ weak)	*RHCE*01.18* *RHCE*ce.18*	c.939G>A	6	p.Pro313=	PMID: 30919985	not found	rs754703211
RH:4 (c+ partial) RH:5 (e+ partial) RH:10,20 (V+VS+) RH:31 (hr[B]+ very weak to neg)	*RHCE*01.20.01* *RHCE*ce.20.01* *RHCE*ceVS.01*	c.733C>G	5	p.Leu245Val	PMID: 8759908 PMID: 9256293 PMID: 9024488	not found	rs1053361
RH:4 (c+ partial) RH:5 (e+ partial) RH:10,20 (V+VS+) RH:–31 (hr[B]–)	*RHCE*01.20.02.01* *RHCE*ce.20.02.01* *RHCE*ceVS.02.01*	c.48G>C c.733C>G	1 5	p.Trp16Cys p.Leu245Val	PMID: 9024488	not found	rs586178 rs1053361
Inferred as *RHCE*01.20.02.01*	*RHCE*01.20.02.02* *RHCE*ce.20.02.02* *RHCE*ceVS.02.02*	c.48G>C c.105C>T c.733C>G	1 2 5	p.Trp16Cys p.Asp35= p.Leu245Val	PMID: 31002175	not found	rs586178 rs186534432 rs1053361
RH:4 (c+ partial) RH:5 (e+ partial) RH:–10,20 (V–VS+) RH:–31 (hr[B]–)	*RHCE*01.20.03* *RHCE*ce.20.03* *RHCE*ceVS.03* *RHCE*ceS*	c.48G>C c.733C>G c.1006G>T	1 5 7	p.Trp16Cys p.Leu245Val p.Gly336Cys	PMID: 9767746	not found	rs586178 rs1053361 rs116261244

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:5 (e+ partial) RH:10,20 (V+VS+) Probable RH:–31 (hr^{B}–)	*RHCE*01.20.04.01* *RHCE*ce.20.04.01* *RHCE*ceVS.04.01* *RHCE*ceTI type 2*	c.48G>C c.733C>G c.1025C>T	1 5 7	p.Trp16Cys p.Leu245Val p.Thr342Ile	PMID: 20088832	KY652757	rs586178 rs1053361 rs1053374
Inferred as *RHCE*01.20.04.01* *RHCE*ceTI type 2*	*RHCE*01.20.04.02* *RHCE*ce.20.04.02* *RHCE*ceVS.04.02*	c.48G>C c.105C>T c.733C>G c.744T>C c.1025C>T	1 5 7	p.Trp16Cys p.Asp35= p.Leu245Val p.Ser248= p.Thr342Ile		not found	rs586178 rs142971926 rs1053361 rs149352457 rs1053374
RH:5 (e+ partial) RH:–10,20 (V–VS+) RH:–31 (hr^{B}–)	*RHCE*01.20.05* *RHCE*ce.20.05* *RHCE*ceVS.05*	c.733C>G c.1006G>T	5 7	p.Leu245Val p.Gly336Cys	PMID: 9767746	not found	rs1053361 rs116261244
RH:4 (c+ partial) RH:5 (e+ partial, positive to negative) RH:20 (VS+) RH:–19,–31 (hr^{S}–, hr^{B}–) RH:43 (Crawford+) RH:–58 (CELO–) Some monoclonal anti-D cross-react	*RHCE*01.20.06* *RHCE*ce.20.06* *RHCE*ceVS.06* *RHCE*ceCF*	c.48G>C c.697C>G c.733C>G	1 5	p.Trp16Cys p.Gln233Glu p.Leu245Val	PMID: 16934069 PMID: 20609196	DQ178642	rs586178 rs142246017 rs1053361
Some monoclonal anti-D cross-react	*RHCE*01.20.06.02* *RHCE*ce.20.06.02* *RHCE*ceVS.06.02*	c.697C>G c.733C>G	5	p.Gln233Glu p.Leu245Val	(27), Abstract	MW924817	rs142246017 rs1053361
RH:4 (c+ partial, weak to neg) RH:5 (e+ partial, weak to neg) RH:10 (V+ weak to neg) RH:19 (hr^{S}+ weak to neg) RH:20 (VS+ weak to neg) RH:31 (hr^{B}+ weak to neg) RH:48 (JAL+) RH:–57 (CEST–)	*RHCE*01.20.07* *RHCE*ce.20.07* *RHCE*ceVS.07* *RHCE*ceJAL*	c.340C>T c.733C>G	3 5	p.Arg114Trp p.Leu245Val	PMID: 12393640 PMID: 19207167 PMID: 19170983	AF510067	rs148487630 rs1053361

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:5 (e+ weak) RH:10,20 (V+VS+) Probable RH:–31 (hr^{B}–)	*RHCE*01.20.08* *RHCE*ce.20.08* *RHCE*ceVS.08*	c.48G>C c.733C>G c.748G>A	1 5	p.Trp16Cys p.Leu245Val p.Val250Met	PMID: 12393640	AF510068	rs586178 rs1053361 not found
RH:5 (e+ weak) RH:10,20 (V+VS+) RH:31 (hr^{B}+ weak)	*RHCE*01.20.09* *RHCE*ce.20.09* *RHCE*ceVS.09*	c.48G>C c.733C>G c.941T>C	1 5 7	p.Trp16Cys p.Leu245Val p.Val314Ala	PMID: 20576012 allele reported with c.1006G>T (possible error)	KX279465	rs586178 rs1053361 rs79321360
Probable RH:4 (c+ partial) Probable RH:5 (e+ partial)	*RHCE*01.20.10* *RHCE*ce.20.10* *RHCE*ceVS.10*	c.48G>C c.712A>G c.733C>G	1 5	p.Trp16Cys p.Met238Val p.Leu245Val	(1), Abstract	KY369955	rs586178 rs144163296 rs1053361
	*RHCE*01.20.11* *RHCE*ce.20.11* *RHCE*ceVS.11*	c.48G>C exons 2-3 D c.186G>T c.410C>T c.455A>C c.733C>G c.1006G>T	1 2 3 5 7	p.Trp16Cys p.Leu62Phe p.ALa137Val p.Asn152Thr p.Leu245Val p.Gly336Cys	(2), Abstract	KY926711	rs586178 rs199509194 rs113982491 rs17418085 rs1053361 rs116261244
Some monoclonal anti-D cross-react	*RHCE*01.20.12* *RHCE*ce.20.12* *RHCE*ceVS.12*	c.48G>C c.462G>T c.733C>G c.1006G>T	1 3 5 7	p.Trp16Cys p.Arg154Ser p.Leu245Val p.Gly336Cys	(3), Abstract	MW349827	rs586178 not found rs1053361 rs116261244
RH:5 (e+) RH:9 (C^{X}+) RH:20 (VS+)	*RHCE*01.20.13* *RHCE*ce.20.13* *RHCE*ceVS.13*	c.48G>C c.106G>A c.733C>G	1 5	p.Trp16Cys p.Ala36Thr p.Leu245Val	PMID: 22288371	not found	rs586178 rs145034271 rs1053361
RH:5 (e+ weak) RH:48 (JAL+)	*RHCE*01.21.01* *RHCE*ce.21.01*	c.341G>A	3	p.Arg114Gln	PMID: 19207167	AJ548432	rs1238030431
RH:5 (e+ weak) RH:48 (JAL+)	*RHCE*01.21.02* *RHCE*ce.21.02*	c.48G>C c.187G>C c.341G>A	1 2 3	p.Trp16Cys p.Gly63Arg p.Arg114Gln	PMID: 19453979	AM295498	rs586178 not found rs1238030431

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:5 (e+ weak) RH:33 (DHAR+) RH:50 (FPPT+) Some monoclonal anti-D cross-react	*RHCE*01.22.01* *RHCE*ce.22.01* *RHCE*ceHAR.01*	c.667G>T c.697C>G c.712A>G c.733C>G c.744T>C c.787A>G c.800T>A	5	p.Val223Phe p.Gln233Glu p.Met238Val p.Leu245Val p.Ser248= p.Arg263Gly p.Met267Lys	PMID: 8616049	not found	rs147357308 rs142246017 rs144163296 rs1053361 rs149352457 rs1132763 rs1132764
Inferred as *RHCE*01.22.01* *RHCE*ceHAR.01*	*RHCE*01.22.02* *RHCE*ce.22.02* *RHCE*ceHAR.02*	c.48G>C c.667G>T c.697C>G c.712A>G c.733C>G c.744T>C c.787A>G c.800T>A	1 5	p.Trp16Cys p.Val223Phe p.Gln233Glu p.Met238Val p.Leu245Val p.Ser248= p.Arg263Gly p.Met267Lys	(22), Abstract	not found	rs586178 rs147357308 rs142246017 rs144163296 rs1053361 rs149352457 rs1132763 rs1132764
RH:5 (e+ weak)	*RHCE*01.23* *RHCE*ce.23*	c.649T>C	5	p.Trp217Arg	PMID: 19453980	FJ486162	not found
RH:5 (e+ weak)	*RHCE*01.24* *RHCE*ce.24*	c.512A>G	4	p.His171Arg	PMID: 19453979	AM182448	rs781037009
RH:5 (e+ weak)	*RHCE*01.25* *RHCE*ce.25*	c.730G>A	5	p.Ala244Thr	PMID: 19453979	AM260938	rs1307519228
RH:5 (e+ weak)	*RHCE*01.26* *RHCE*ce.26*	c.872C>T	6	p.Pro291Leu	PMID: 19453979	AM183927	rs374399829
RH:5 (e+ weak)	*RHCE*01.27* *RHCE*ce.27*	c.1154G>C	9	p.Gly385Ala	PMID: 19453979	AM295499	rs1412021250
RH:4 (c+ weak)	*RHCE*01.28* *RHCE*ce.28*	c.1254A>C	10	p.Ter418Tyr	PMID: 19453979	AM295503	not found
RH:4,–5 (c+e–)	*RHCE*01.29* *RHCE*ce.29* *RHCE*ceBOL*	RHD exons 4-9	4-9		PMID: 7994050	not found	NA
RH:5 (e+ weak)	*RHCE*01.30* *RHCE*ce.30*	c.526G>A	4	p.Ala176Thr	PMID: 21166680	not found	rs753965768

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:5 (e+ weak)	*RHCE*01.31* *RHCE*ce.31*	c.695T>C	5	p.Ile232Thr	PMID: 21166680	not found	not found
	*RHCE*01.32* *RHCE*ce.32*	c.827C>A	6	p.Ala276Glu	PMID: 21166680	not found	not found
RH:5 (e+ partial, weak to neg) RH:–31 (hr^{B}–)	*RHCE*01.33* *RHCE*ce.33*	c.506T>C	4	p.Leu169Pro	(1), Abstract	KX714949	not found
RH:4 (c+ partial) RH:–5 (e–)	*RHCE*01.34* *RHCE*ce.34*	RHD exons 4-7	4-7		(4), Abstract	KY652756	NA
	*RHCE*01.35* *RHCE*ce.35*	c.202A>G	2	p.Asn68Asp	PMID: 26435076	KP136911	rs772058645
RH:2 (robust C+ expression) RH:–4 (c–)	*RHCE*01.36* *RHCE*ce.36*	c.307C>T	2	p.Pro103Ser	PMID: 26435076	KP136912	rs676785
	*RHCE*01.37* *RHCE*ce.37*	c.697C>G c.712A>G c.733C>G c.744T>C	5	p.Gln233Glu p.Met238Val p.Leu245Val p.Ser248=	PMID: 26435076	KP136915	rs142246017 rs144163296 rs1053361 rs149352457
RH:5 (e+ weak)	*RHCE*01.38* *RHCE*ce.38*	c.1-10C>T	5'UTR	promoter region	PMID: 19453979	FM866412	rs369957834
RH:2 (C+ weak) RH:–4 (c–)	*RHCE*01.39* *RHCE*ce.39*	c.308C>T	2	p.Pro103Leu	PMID: 27338008	KU319432	rs747882675
RH:4 (c+ weak)	*RHCE*01.40* *RHCE*ce.40*	c.340C>T	3	p.Arg114Trp	(5), Abstract	KR060081	rs148487630
RH:–8 (C^{W}–) RH:9 (C^{X}+ weak) Rh:–51 (MAR–) RH:–62 (PARG–)	*RHCE*01.41* *RHCE*ce.41* *RHCE*ceWA*	c.114A>C	2	p.Leu38Phe	(6), Abstract	not found	not found
Some monoclonal anti-D crossreact	*RHCE*01.42* *RHCE*ce.42* *RHCE*ceRG*	c.508A>G	4	p.Arg170Gly	(7), Abstract	KX236061	not found

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:3 (E+ weak to neg)	*RHCE*01.43* *RHCE*ce.43*	c.499A>G	4	p.Met167Val	PMID: 33399221 PMID: 30418133	not found	rs779408591
RH:4 (c+ partial, weak) RH:5 (e+ partial, weak)	*RHCE*01.44* *RHCE*ce.44*	RHD exons 5-6	5 and 6		(8), Abstract	MW349828	NA
Null phenotypes							
RH:–4,–5,–17 (c–e–)	*RHCE*01N.01* *RHCE*ceN.01*	c.80_84delTCTTC	1	p.Tyr29Phefs*5	PMID: 10827273	not found	not found
RH:–4,–5,–17 (c–e–)	*RHCE*01N.02* *RHCE*ceN.02*	c.963delG	7	p.Iso322Phefs*37	PMID: 16271106	not found	not found
RH:–4,–5,–17 (c–e–)	*RHCE*01N.03* *RHCE*ceN.03*	c.634+1G>T	i4	Splice site	PMID: 9657766	not found	not found
RH:–4,–5,–17 (c–e–), inferred (ce in trans)	*RHCE*01N.04* *RHCE*ceN.04*	c.676delG	5	p.Ala226Leufs*3	PMID: 30284287	KY652755	not found
RH:–5 (e–) (cE in trans)	*RHCE*01N.05* *RHCE*ceN.05*	c.335+3A>T	i2	Splice site	PMID: 30284287	KX714951	not found
RH:–4,–5,–17 (c–e–)	*RHCE*01N.06* *RHCE*ceN.06*	c.679_683delCTGCT	5	p.Leu227Glufs*89	PMID: 23252593	not found	not found
RH:–4 (c–) (ce or Ce in trans)	*RHCE*01N.07* *RHCE*ceN.07*	c.1074-2A>G	i7	Splice site	PMID: 23252593	not found	not found
RH:–4,–5,–17 (c–e–)	*RHCE*01N.08* *RHCE*ceN.08*	c.801+1G>A	5	Splice site	PMID: 28470789	KY229720	not found
RH:–4,–5,–17 (c–e–)	*RHCE*01N.09* *RHCE*ceN.09*	c.1044_1050dupGCTTCAT	7	p.Thr351Alafs*52	PMID: 25413218	not found	not found
RH:–4,–5 (c–e–)	*RHCE*01N.10* *RHCE*ceN.10*	c.807T>A	6	p.Tyr269Ter	(9), Abstract	not found	rs780267740
RH:–4 (c–) (Ce in trans)	*RHCE*01N.11* *RHCE*ceN.11*	c.1154-1G>A	i8	Splice site	(10), Abstract	MT374825	not found
RH:-4 (c–) (Ce in trans)	*RHCE*01N.12*	c.48G>C c.366delG	1 3	p.Trp16Cys p.Val123Cysfs*1	PMID: 34046910	MW773845	not found

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:–4 (c–) (Ce in trans)	*RHCE*01N.13* *RHCE*ceN.13*	c.486+1G>A	i3	Splice site	*provisional (partially sequenced Exons 1-7)* (24), Abstract	not found	not found
RH:2 or C RH:5 or e RH:7 or Ce	*RHCE*02 or* *RHCE*Ce*	Reference nucleotides c.48G>C c.150C>T c.178C>A c.201A>G c.203A>G c.307C>T c.676G	 1 2 5	 p.Trp16Cys p.Val50= p.Leu60Ile p.Ser67= p.Asn68Ser p.Pro103Ser p.Ala226	PMID: 8220426	BC075081	 rs586178 rs200955066 rs181860403 rs1053343 rs1053344 rs676785 rs609320
RH:2 (C+ weak to neg) RH:5 (e+ weak) RH:48 (JAL+)	*RHCE*02.01* *RHCE*Ce.01* *RHCE*CeMA* *RHCE*CeJAL*	c.340C>T	3	p.Arg114Trp	PMID: 12084172	AJ548431 AM183925	rs148487630
RH:2 (C+) RH:5 (e+)	*RHCE*02.02* *RHCE*Ce.02* *RHCE*CeFV*	c.667G>T c.697C>G c.712A>G	5	p.Val223Phe p.Gln233Glu p.Met238Val	PMID: 19453980	AJ867777	rs147357308 rs142246017 rs144163296
RH:2 (C+ weak to neg) RH:5 (e+ weak) RH:53 (JAHK+)	*RHCE*02.03* *RHCE*Ce.03* *RHCE*CeJAHK*	c.365C>T	3	p.Ser122Leu	PMID: 16078918	AM999773 (called CeSI in GenBank)	rs201407774
RH:2 (C+ partial, weak to neg)	*RHCE*02.04* *RHCE*Ce.04* *RHCE*CeVA*	c.667G>T c.697C>G c.712A>G c.733C>G c.744T>C c.787A>G c.800T>A	5	p.Val223Phe p.Gln233Glu p.Mer238Val p.Leu245Val p.Ser248= p.Arg263Gly p.Met267Lys	PMID: 12084172	not found	rs147357308 rs142246017 rs144163296 rs1053361 rs149352457 rs1132763 rs1132764

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.04.01* *RHCE*Ce.04.01*	c.667G>T c.697C>G c.712A>G c.733C>G c.744T>C c.787A>G	5	p.Val223Phe p.Gln233Glu p.Mer238Val p.Leu245Val p.Ser248= p.Arg263Gly	PMID: 19453979	AM999774	rs147357308 rs142246017 rs144163296 rs1053361 rs149352457 rs1132763
RH:60 (PARG+)	*RHCE*02.05* *RHCE*Ce.05* *RHCE*CePARG*	c.501G>A	4	p.Met167Ile	PMID: 28144953	not found	not found
RH:2 (C+ partial) RH:5 (e+ partial) RH:8 (C^{W}+) RH:–51 (MAR–)	*RHCE*02.08.01* *RHCE*Ce.08.01* *RHCE*CeCW*	c.122A>G	1	p.Gln41Arg	PMID: 7620172 (25), Abstract	not found	rs138268848
RH:8 (C^{W}+) RH:–56 (CENR–)	*RHCE*02.08.02* *RHCE*Ce.08.02* *RHCE*CeNR*	c.122A>G RHD exon 6-10	1 6-10	p.Gln41Arg	PMID: 15225246	not found	rs138268848
RH:2 (C+ partial) RH:9 (C^{X}+) RH:–51 (MAR–)	*RHCE*02.09* *RHCE*Ce.09* *RHCE*CeCX*	c.106G>A	1	p.Ala36Thr	PMID: 7620172	not found	rs145034271
RH:1 (D+) in the absence of conventional D RH:2 (C+ partial, weak to neg) RH:5 (e+ partial, weak) RH:32 RH:54 (DAK+) RH:–46 (Sec–)	*RHCE*02.10.01* *RHCE*Ce.10.01* *RHCE*CeRN*	c.505C>A c.509G>T c.514T>A c.544A>T c.577A>G c.594T>A c.602G>C	4	p.Leu169Met p.Arg170Met p.Phe172Ile p.Thr182Ser p.Lys193Glu p.Asn198Lys p.Arg201Thr	PMID: 8639859 (21), Abstract	not found	rs1132761 rs1132762 rs1053349 rs1053350 rs1384157219 rs1053354 rs141398055
RH:2 (C+ partial, weak to neg) RH:5 (e+ partial, weak) RH:32 RH:54 (DAK+) RH:–46 (Sec–)	*RHCE*02.10.02* *RHCE*Ce.10.02* (allele existence?)	c.455C>A c.505C>A c.509G>T c.514T>A c.544A>T c.577A>G c.594T>A c.602G>C	3 4	p.Thr152Asn p.Leu169Met p.Arg170Met p.Phe172Ile p.Thr182Ser p.Lys193Glu p.Asn198Lys p.Arg201Thr	PMID: 8639859	not found	rs35109888 rs1132761 rs1132762 rs1053349 rs1053350 rs1384157219 rs1053354 rs141398055

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:2 (C+ weak) RH:5 (e+) RH:55 (LOCR+)	*RHCE*02.11* *RHCE*Ce.11*	c.286G>A	2	p.Gly96Ser	PMID: 19453979 (23), Abstract	AM295502	rs144348222
RH:2 (C+ weak)	*RHCE*02.12* *RHCE*Ce.12*	c.344T>G	3	p.Leu115Arg	PMID: 19453979	AJ867774	not found
RH:5 (e+ weak)	*RHCE*02.13* *RHCE*Ce.13*	c.364T>C	3	p.Ser122Pro	PMID: 19453980	FJ486157	not found
RH:2 (C+ weak)	*RHCE*02.14* *RHCE*Ce.14*	c.497A>T	4	p.His166Leu	PMID: 19453980	FJ486159	not found
RH:5 (e+ weak)	*RHCE*02.15* *RHCE*Ce.15*	c.689G>C	5	p.Ser230Thr	PMID: 19453979	AM182449	not found
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.16* *RHCE*Ce.16*	c.728A>G	5	p.Tyr243Cys	PMID: 19453979	FM165579	rs555090649
RH:5 (e+ weak)	*RHCE*02.17* *RHCE*Ce.17*	c.800T>A	5	p.Met267Lys	PMID: 19453980	FJ486164	rs1132764
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.18* *RHCE*Ce.18*	c.890T>C	6	p.Leu297Pro	PMID: 19453979	AM295501	rs763017817
RH:5 (e+ weak)	*RHCE*02.19* *RHCE*Ce.19*	c.464T>G c.1118C>T	3 8	p.Met155Arg p.Ala373Val	PMID: 19453979	AM295506	not found not found
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.20* *RHCE*Ce.20*	c.79_81delCTC	1	p.Leu27del	PMID: 19453979	AM410878	not found
RH:2 (C+ weak)	*RHCE*02.21* *RHCE*Ce.21*	c.527C>T	4	p.Ala176Val	PMID: 21166680	KM975479	not found
RH:2 (C+ weak) RH:5 (e+ partial, weak)	*RHCE*02.22* *RHCE*Ce.22*	c.667G>T	5	p.Val223Phe	PMID: 21166680	not found	rs147357308
RH:2 (C+ weak)	*RHCE*02.23* *RHCE*Ce.23*	c.941T>C	7	p.Val314Ala	PMID: 21166680	not found	rs79321360
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.24* *RHCE*Ce.24*	c.1007G>A	7	p.Gly336Asp	PMID: 21166680	not found	rs760319839
RH:2 (C+ weak)	*RHCE*02.25* *RHCE*Ce.25*	c.1007G>T	7	p.Gly336Val	PMID: 21166680	not found	rs760319839

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.26* *RHCE*Ce.26*	c.460A>G	3	p.Arg154Gly	PMID: 27282785	KU744002	rs755299894
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.27* *RHCE*Ce.27*	c.375C>G	3	p.Ile125Met	(1), Abstract (5), Abstract	KM078027	rs143715642
RH:2,5 (C+e+) RH:9 (C^X+)	*RHCE*02.28* *RHCE*Ce.28*	c.919G>A	6	p.Gly307Arg	(1), Abstract	KY190222	rs200950594
RH:2 (C+) RH:3 (E+ pos to neg) RH:5 (e+)	*RHCE*02.29* *RHCE*Ce.29*	c.674C>G	5	p.Ser225Cys	(11), Abstract	KY190223	rs200087488
RH:2,5 (C+ e+) RH:10,20 (V+VS+)	*RHCE*02.30* *RHCE*Ce.30*	c.733C>G	5	p.Leu245Val	PMID: 26435076	KP136918	rs1053361
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.31* *RHCE*Ce.31*	c.487-5T>G	i3	Splice site	PMID: 19453979	FM866415	rs776819527
RH:2 (C+ weak)	*RHCE*02.32* *RHCE*Ce.32*	c.1228-2A>G	i9	Splice site	PMID: 19453979	FM866417	not found
RH:2 (C+ weak)	*RHCE*02.33* *RHCE*Ce.33*	c.98A>C	1	p.His33Pro	(5), Abstract	not found	not found
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.34* *RHCE*Ce.34*	c.473G>A	3	p.Ser158Asn	(5), Abstract	not found	rs758173067
RH:2 (C+ weak)	*RHCE*02.35* *RHCE*Ce.35*	c.491A>G	4	p.Asp164Gly	(5), Abstract	not found	rs548044758
RH:2 (C+ weak)	*RHCE*02.36* *RHCE*Ce.36*	c.494A>C	4	p.Tyr165Ser	(5), Abstract	not found	rs746303049
RH:2 (C+)	*RHCE*02.37* *RHCE*Ce.37*	Lacking the 109bp insert	i2		(12), Abstract	not found	
RH:2 (C+ weak) RH:5 (e+ weak)	*RHCE*02.38* *RHCE*Ce.38*	c.939G>A	6	p.Pro313=	PMID: 30919985	not found	rs754703211
RH:2 (C+ very weak)	*RHCE*02.39* *RHCE*Ce.39*	c.1154G>T	9	p.Gly385Val	(28), Abstract	MW427217	rs1412021250

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:2 (C+ weak, mixed field) RH:–10 (V–)	*RHCE*02.40* *RHCE*Ce.40* *RHCE*CeAR*	c.712A>G c.733C>G c.787A>G c.800T>A c.916A>G	5 6	p.Met238Val p.Leu245Val p.Arg263Gly p.Met267Lys p.Ile306Val	(22), Abstract	not found	rs586178 rs144163296 rs1053361 rs1132763 rs1132764
Null phenotypes							
RH:–2,–5,–17 (C–e–)	*RHCE*02N.01* *RHCE*CeN.01*	c.966_968delinsC	7	p.His323Profs*77	PMID: 9657766 PMID: 9657769	not found	not found
RH:–2 (C–) RH:–5 (e–), inferred RH:–17, inferred	*RHCE*02N.02* *RHCE*CeN.02*	c.659G>A	5	p.Trp220Ter	PMID: 30284287	KX714950	not found
RH:–2 (C–) (ce in trans)	*RHCE*02N.03* *RHCE*CeN.03*	c.486+1G>A	i3	Splice site	PMID: 30284287	KP334130	rs753832633
RH:–2,–5 (C–e–) RH:–17, inferred	*RHCE*02N.04* *RHCE*CeN.04*	c.93insT	1	p.Thr32Tyrfs*3	PMID: 24020803 (18), Abstract	not found	not found
RH:–2,–5 (C–e–) RH:–17, inferred	*RHCE*02N.05* *RHCE*CeN.05*	c.377C>G	3	p.Ser126Ter	PMID: 26435076	KP136914	not found
RH:–2,–5,–17 (C–e–)	*RHCE*02N.06* *RHCE*CeN.06*	c.148+5G>A	i1	Splice site	PMID: 24020803	not found	rs756955857
RH:–2,–5,–17 (C–e–)	*RHCE*02N.07* *RHCE*CeN.07*	RHD exons 3-8	3-8		PMID: 22686562 PMID: 24020803	not found	NA
RH:–2,–5,–17 (C–e–)	*RHCE*02N.08* *RHCE*CeN.08*	RHD exons 3-9	3-9		PMID: 24020803	not found	NA
RH:–2,–5,–17 (C–e–)	*RHCE*02N.09* *RHCE*CeN.09*	c.938delC	6	p.Pro313Argfs*46	(13), Abstract	not found	not found
RH:–2 (C–) RH:–5 (e–), inferred RH:–17, inferred	*RHCE*02N.10* *RHCE*CeN.10*	c.482insT	3	p.Asn162Glnfs37Ter	(14), Abstract	MK090017	not found
RH:–2,–5 (C–e–) RH:–17, inferred	*RHCE*02N.11* *RHCE*CeN.11*	c.148G>A	1	p.Val50Ile	PMID: 32608521 (14), Abstract	MT210599	not found
RH:–2 (C–) RH:–5 (e–), inferred RH:–17, inferred	*RHCE*02N.12* *RHCE*CeN.12*	c.1059delG	7	p.Trp353Ter	(8), Abstract	MW355846	not found

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:–2 (C–) RH:–5 (e–), inferred	*RHCE*02N.13* *RHCE*CeN.13*	c.635-9G>A	i4	Splice site	(28), Abstract	MZ351768	rs767724106
RH:–2,–5,–17 (C–e–)	*RHCE*02N.14* *RHCE*CeN.14*	c.569_572dupCTCT	4	p.Pro192Serfs*8	PMID: 33270227	MK388216	not found
RH:4 or c RH:3 or E RH:27 or cE	*RHCE*03* or *RHCE*cE*	Reference nucleotides c.307C c.676G>C	 2 5	 p.Pro103 p.Ala226Pro	PMID: 8220426		 rs676785 rs609320
RH:3 (E+ partial, weak to neg) RH:11 (E^{w}+)	*RHCE*03.01* *RHCE*cE.01* *RHCE*cEEW*	c.500T>A	4	p.Met167Lys	PMID: 9827916 PMID: 14996199	not found	rs140421430
RH:3 (E+ partial, weak to neg) RH:4 (c+ weak to neg)	*RHCE*03.02* *RHCE*cE.02* *RHCE*cEKK*	RHD exons 1-3	1-3		PMID: 9827916 PMID: 11724987	AB049753	NA
RH:3 (E+ partial, weak to neg)	*RHCE*03.03* *RHCE*cE.03* *RHCE*cEFM*	c.697C>G c.712A>G	5	p.Gln233Glu p.Met238Val	PMID: 9827916 PMID: 11724987	AB018644	rs142246017 rs144163296
RH:3 (E+ partial, weak to neg)	*RHCE*03.03.02* *RHCE*cE.03.02*	c.697C>G c.712A>G c.733C>G c.744T>C	5	p.Gln233Glu p.Met238Val p.Leu245Val p.Ser248=	(1), Abstract	KY369956	rs142246017 rs144163296 rs1053361 rs149352457
RH:3 (E+ partial, weak to neg)	*RHCE*03.03.03* *RHCE*cE.03.03*	c.697C>G	5	p.Gln233Glu	(12), Abstract	MK934127	rs142246017
RH:3 (E+ partial, weak to neg) RH:4 (c+ weak)	*RHCE*03.04* *RHCE*cE.04* *RHCE*cEIV*	c.602G>C	4	p.Arg201Thr	(15), Abstract	FJ486161	rs141398055
RH:3 (E+ partial, weak to neg) RH:4 (c+ weak to neg)	*RHCE*03.05* *RHCE*cE.05* *RHCE*cEKH*	c.461G>C	3	p.Arg154Thr	PMID: 11724987	AB018645	rs747471048
RH:3 (E+ weak) RH:4 (c+ weak)	*RHCE*03.06* *RHCE*cE.06*	c.28C>T	1	p.Arg10Trp	PMID: 19453980	FJ486155	rs749601047
RH:3 (E+ weak)	*RHCE*03.07* *RHCE*cE.07*	c.344T>C	3	p.Leu115Pro	PMID: 19453979 PMID: 19453980	FJ486156	not found

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:3 (E+ weak)	*RHCE*03.08* *RHCE*cE.08*	c.356G>A	3	p.Ser119Asn	PMID: 19453979	AM295505	rs777819701
RH:3 (E+ weak) RH:4 (c+ weak)	*RHCE*03.09* *RHCE*cE.09*	c.374T>A	3	p.Ile125Asn	PMID: 19453980	FJ486158	not found
RH:3 (E+ weak)	*RHCE*03.10* *RHCE*cE.10*	c.506T>A	4	p.Leu169Gln	PMID: 19453980	FJ486160	not found
RH:3 (E+ weak) RH:4 (c+ weak)	*RHCE*03.11* *RHCE*cE.11*	c.908T>A	6	p.Leu303Gln	PMID: 19453980	FJ486165	not found
RH:3 (E+ weak)	*RHCE*03.12* *RHCE*cE.12*	c.464T>G c.477T>G	3	p.Met155Arg p.Asn159Lys	PMID: 19453979	AM183926	not found not found
RH:3 (E+ weak) RH:4 (c+ weak)	*RHCE*03.13* *RHCE*cE.13*	c.728A>G	5	p.Tyr243Cys	PMID: 21166680	not found	rs555090649
RH:3 (E+ very weak to neg) RH:4 (c+ weak)	*RHCE*03.14* *RHCE*cE.14*	c.734T>C	5	p.Leu245Pro	PMID: 22958092	not found	not found
RH:3 (E+ weak)	*RHCE*03.15.01* *RHCE*cE.15.01* *RHCE*cE BA*	c.380C>T c.383G>A	3	p.Ala127Val p.Gly128Asp	PMID: 21166680	not found	rs1053346 rs1053347
RH:3 (E+ weak)	*RHCE*03.15.02* *RHCE*cE.15.02* *RHCE*cE JU*	c.361A>T c.380C>T c.383G>A	3	p.Met121Leu p.Ala127Val p.Gly128Asp	PMID: 21166680	not found	rs1053345 rs1053346 rs1053347
RH:4 (c+ weak)	*RHCE*03.16* *RHCE*cE.16* *RHCE*cE TA*	c.94A>G	1	p.Thr32Ala	PMID: 26286238	KP271157	rs760999674
RH:3 (E+ partial)	*RHCE*03.17* *RHCE*cE.17*	c.520G>A	4	p.Val174Met	(1), Abstract	KY190221	rs146306079
RH:3 (E+) RH:4 (c+)	*RHCE*03.18* *RHCE*cE.18*	c.48G>C	1	p.Trp16Cys	PMID: 29296782	KY228976	rs586178
RH:3 (E+ weak to neg) RH:4 (c+ weak to neg)	*RHCE*03.19* *RHCE*cE.19*	c.84C>A	1	p.Phe28Leu	PMID: 26435076 (19), Abstract	KP136913 LN554880	not found
RH:3 (E+ weak to neg) RH:4 (c+ weak)	*RHCE*03.20* *RHCE*cE.20*	c.149-1G>A	i1	Splice site	PMID: 19453979	FM866414	not found
RH:3 (E+ weak)	*RHCE*03.21* *RHCE*cE.21*	c.527C>T	4	p.Ala176Val	(5), Abstract	not found	not found

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:3 (E+ weak)	*RHCE*03.22* *RHCE*cE.22*	c.208C>T	2	p.Arg70Trp	(5), Abstract	not found	rs1239729684
RH:3 (E+ weak)	*RHCE*03.23* *RHCE*cE.23*	c.774T>A c.916A>G	5	p.Leu258= p.Ile306Val	(5), Abstract	not found	not found rs1132765
RH:3 (E+ weak)	*RHCE*03.24* *RHCE*cE.24*	c.1130A>T	8	p.Ala377Val	(5), Abstract	not found	not found
	*RHCE*03.25* *see RHCE*03N.07*						
RH:2 (C+ weak to neg) RH:3 (E+)	*RHCE*03.26* *RHCE*cE.26*	c.48G>C c.307C>T	1 2	p.Trp16Cys p.Pro103Ser	(12), Abstract	MG434498	rs586178 rs676785
Some monoclonal anti-C cross-react	*RHCE*03.27* *RHCE*cE.27*	c.307C>T	2	p.Pro103Ser	(27), Abstract	KX216810	rs676785
RH:3 (E+ weak to neg)	*RHCE*03.28* *RHCE*cE.28*	c.382G>C	3	p.Gly128Arg	PMID: 33694191	MW462131	not found
RH:3 (E+ very weak) RH:4 (c+ weak to neg)	*RHCE*03.29* *RHCE*cE.29*	c.818C>A	6	p.Ala273Glu	(28), Abstract	MZ351767	not found
RH:3 (E+ very weak)	*RHCE*03.30* *RHCE*cE.30*	c.336-2A>G	i2	Splice site	(28), Abstract	MZ351769	not found
RH:3 (E+ very weak to neg) RH:4 (c+ weak to neg) RH:17	*RHCE*03.31* *RHCE*cE.31* *RHCE*cEMI* *(formerly RHCE*03N.01)*	c.350_358delCCATGAGTG	3	p.Arg120_ Ser122del	PMID: 11380457 (20), Abstract	not found	not found
RH:3 (E+ weak to neg)	*RHCE*03.32* *RHCE*cE.32*	c.361A>T c.380C>T c.383G>A c.455C>A	3	p.Met121Leu p.Ala127Val p.Gly128Asp p.Thr152Asn	(26), Abstract	not found	rs1053345 rs1053346 rs1053347 rs35109888
Null phenotypes							
	*RHCE*03N.01* *RHCE*cEN.01* *RHCE*cEMI* *see RHCE*03.31*						
RH:–3,–4,–17 (E–c–)	*RHCE*03N.02* *RHCE*cEN.02*	c.907delC	6	p.Leu303Ter	PMID: 21517889	GU563377	rs747976226

Phenotype †	Allele name	Nucleotide change	Exon Intron	Predicted amino acid change	(Reference No.) PMID	Accession number	rs number
RH:–3,–4 (E–c–) RH:–17, inferred	*RHCE*03N.03* *RHCE*cEN.03*	c.554G>A	4	p.Trp185Ter	(16), Abstract	not found	rs1395012563
RH:–3,–4,–17 (E–c–)	*RHCE*03N.04* *RHCE*cEN.04*	c.486+5G>A	i3	Splice site	PMID: 23252593	not found	not found
RH:–3,–4,–17 (E–c–)	*RHCE*03N.05* *RHCE*cEN.05*	c.221G>A	2	p.Trp74Ter	PMID: 24020803	not found	rs1044945369
RH:–3,–4 (E–c–) RH:–17, inferred	*RHCE*03N.06* *RHCE*cEN.06*	c.200C>A	2	p.Ser67Ter	(10), Abstract	MT374824	not found
RH:–3,–4,–17 (E–c–)	*RHCE*03N.07* *RHCE*cEN.07* *(formerly* *RHCE*03.25)*	c.659G>A	5	p.Trp220Ter	(17), Abstract	not found	not found
RH:2 or C RH:3 or E RH:22 or CE	*RHCE*CE or* *RHCE*04*	Reference nucleotides c.48G>C c.150C>T c.178C>A c.201A>G c.203A>G c.307C>T c.676G>C	 1 2 5	 p.Trp16Cys p.Val50= p.Leu60Ile p.Ser67= p.Asn68Ser p.Pro103Ser p.Ala226Pro	PMID: 8220426		 rs586178 rs200955066 rs181860403 rs1053343 rs1053344 rs676785 rs609320
RH:2 (C+ weak) RH:3 (E+ weak to neg)	*RHCE*04.01* *RHCE*CE.01*	c.722C>T	5	p.Thr241Ile	PMID: 19453980	FJ486163	rs751751505
RH:2 (C+ weak to neg) RH:3 (E+ weak to neg)	*RHCE*04.02* *RHCE*CE.02*	c.380C>A	3	p.Ala127Glu	(14), Abstract	MH807721	rs1053346

† "Weak" and "partial" phenotypes are not mutually exclusive, and for many alleles the associated phenotype(s) have not been extensively investigated or samples have not been informative. All partial antigens may not be indicated.

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	Track of changes		from version	to version
1	**Version**		**v6.0 30-JUN-2021**	**v6.1 23-AUG-2021**
2	Author	created:	Aline Floch, Connie M. Westhoff, June 2021	Aline Floch, Connie M. Westhoff, July 2021
3	Review	reviewed:	Margaret Keller	Christoph Gassner, August 2021
4				
5	General	Allele table		inserted RHCE*01.20.07 because it had been inadvertently skipped
6	Intro	Text		Changed text and number of Antigens to 56.
7	Allele Table	Allele table		RHCE*01.04.0X: removed line
8	Allele Table	Phenotype		RHCE*01.04.02: changed phenotype
9	Allele Table	Phenotype		RHCE*01.04.03: changed phenotype
10	Allele Table	Phenotype Reference		RHCE*01.04.04: changed phenotype, reference
11	Allele Table	Reference		RHCE*01.17: changed reference
12	Allele Table	Phenotype		RHCE*01.20.02.02: changed phenotype
13	Allele Table	Phenotype		RHCE*01.20.04.02: changed phenotype
14	Allele Table	Reference		RHCE*01.20.06.02: added reference
15	Allele Table	Allele		RHCE*01.20.07: added allele
16	Allele Table	Phenotype Reference		RHCE*01.22.01: changed phenotype, reference
17	Allele Table	Phenotype Reference		RHCE*01.22.02: changed phenotype, reference
18	Allele Table	Phenotype Reference		RHCE*01N.11: changed phenotype, splice site
19	Allele Table	Phenotype		RHCE*01N.12: changed phenotype
20	Allele Table	Phenotype Reference		RHCE*01N.13: changed phenotype, reference
21	Allele Table	Phenotype Reference		RHCE*02.08.01: changed reference
22	Allele Table	Text		RHCE*02.10.02: changed text

23	Allele Table	Phenotype Reference		RHCE*02.11: changed phenotype, reference
24	Allele Table	Phenotype Reference		RHCE*02.22: changed phenotype, reference
25	Allele Table	Reference		RHCE*02.39: changed reference
26	Allele Table	Nucleotides Amino acid		RHCE*02.40: corrected nucleotid and amino acid changes
27	Allele Table	Phenotype		RHCE*01.04.02: changed phenotype
28	Allele Table	Phenotype		RHCE*01.04.03: changed phenotype
29	Allele Table	Allele		RHCE*01.04.04 inserted
30	Allele Table	Reference		RHCE*01.17: added reference
31	Allele Table	Reference		RHCE*03.27: added reference
32	Allele Table	Reference		RHCE*03.28: added reference
33	Allele Table	Reference		RHCE*03.29: added reference
34	Allele Table	Reference		RHCE*03.32: added references, rs-numbers
35	**End Version**		**v6.0 30-JUN-2021**	**v6.1 23-AUG-2021**

	Track of changes		from version	to version
1	**Version**		**v5.0 15-JUL-2019**	**v6.0 30-JUN-2021**
2	Author	created:	n.a.	Aline Floch, Connie M. Westhoff, June 2021
3	Review	reviewed:	n.a.	Margaret A. Keller, July 2021
4	General			First Excel map version. Spread-sheets "Intro", "Allele Table", "References", "Versioning" and "Antigens" created.
5	General	Document Title updated	RH (ISBT 004) Blood Group Alleles: *RHCE*	Names for RH (ISBT 004) Blood Group Alleles: *RHCE* Alleles
6	General	File name updated	ISBT004-RHCE-15th_July_2019	(ISBT 004) *RHCE* blood group alleles v6.0

7	Intro	Intro moved from Allele Table to Intro and updated:	The Rh blood group system consists of 55 antigens, many of which are encode at the RHCE locus and also include a number encoded by hybrid RHCE with RHD. Commonly encountered antigens include C, E, c, e, f, Ce, Cw, Cx, V, VS, cE, and CE. The less common include hrS, hrB, Ew, Hr0, Hr, CG, Rh26 c-like, hrH, Rh32, Rh33, Rh35, Bea, Rh39, Rh41, Rh42, Crawford, Nou, Riv, Sec, Dav, JAL, STEM, MAR, JAHK , LOCR, CENR, CEST, CELO, CEAG, PARG and CEVF. Antigens encoded from either RHCE or RHD loci include G, FPTT, BARC, DAK, Rh29, HrB and CEWA. The protein consists of 12 membrane-spanning domains and 417 amino acids.	General description The Rh blood group system consists of 55 antigens. Many are encoded at the *RHCE* locus and a number are encoded by hybrid alleles with both *RHCE* and *RHD* sequences. The RhCE protein (CD240CE) consists of 12 membrane-spanning domains and 417 amino acids. The amino and carboxyl termini are predicted to be intracellular, and the initial methionine is cleaved post-translationally. The expression of Rh proteins requires functional RhAG proteins, predicted to form heterotrimers with Rh. Antigens commonly typed for include RH2 (C), RH3 (E), RH4 (c), RH5 (e), RH8 (C^w), RH9 (C^x), RH10 (V) and RH20 (VS). The less common include RH11 (E^w), RH17 (Hr_0), RH18 (Hr), RH19 (hr^S), RH21 (CG), RH26 (c-like), RH28 (hr^H), RH31 (hr^B), RH32, RH33, RH34 (Hr^B), RH35, RH36 (Be^a), RH39, RH41, RH42, RH43 (Crawford), RH44 (Nou), RH45 (Riv), RH46 (Sec), RH47 (Dav), RH48 (JAL), RH49 (STEM), RH51 (MAR), RH53 (JAHK), RH55 (LOCR), RH56 (CENR), RH57 (CEST), RH58 (CELO), RH59 (CEAG), RH60 (PARG), RH61 (CEVF) and RH63 (CETW). Compound antigens include RH6 (f), RH7 (Ce), RH22 (CE) and RH27 (cE). Antigens encoded from either *RHCE* or *RHD* loci include RH12 (G), RH50 (FPTT), RH52 (BARC), RH54 (DAK), RH29 and CEWA (RH62).
8	Intro	LRG sequence: line renamed and comments added	NCBI RefSeq: NG_009208 (gene) NM_020485 (mRNA) NP_065231 (protein)	LRG sequence: NG_009208.3 (genomic) (This NG Ref Seq corresponds to a *RHCE*01* allele) NM_020485.8 (mRNA transcript) (This NM Ref Seq corresponds to a *RHCE*01* allele) NP_065231.4 (protein) (This NP Ref Seq corresponds to a *RHCE*01* allele)

9	Intro	Reference allele line moved from Allele Table to Intro and updated:	n.a.	Reference allele: Preferred: *RHCE*01* (shaded) Acceptable: *RHCE*C, RHCE*c, RHCE*E* or *RHCE*e* when only testing for the specific polymorphism(s) associated with expression of that antigen. Reference allele RHCE*01 encodes: RH4, RH5, RH6, RH17, RH18, RH19, RH26, RH29, RH31, RH34, RH44, RH46, RH47, RH51, RH57, RH58, RH59, RH61
10	Intro	Antithetical Antigens line created in Intro:	n.a.	[RH2 RH4] [RH3 RH5] [RH8/RH9 RH52] [RH26 RH55] [RH32 RH46] [RH43 RH58] [RH48 RH57]
11	Allele Table	Table column and header modifications	Table columns were: Phenotype Allele name (*ce=01 *Ce=02 *cE=03 *CE=04) Nucleotide Exon Amino Acid Antigen frequency Clinical significance Reference, PubMed ID (PMID) GenBank# rs number# Allele detail Reported as Or Linked to	Columns were removed from the ISBT table Antigen frequency Clinical significance Allele detail Reported as Or Linked to These columns and data are available online: https://www.bloodgroupgenomics.org/rhce/rhce-table/ Columns were renamed: Phenotype Allele name Nucleotide change Exon Predicted amino acid change (Reference No.) PMID Accession number rs number

12		Common allele names	Common names for the alleles were in the column "Reported as Or Linked to"	The most common names have been moved to "Allele name" column. The column "Reported as Or Linked to" is available online: https://www.bloodgroupgenomics.org/rhce/rhce-table/
13	Allele Table	Allele nomenclature update	*RHCE*c, RHCE*C, RHCE*E, RHCE*e* were in the allele name column for the 4 main alleles *RHCE*01, RHCE*02, RHCE*03, RHCE*04*	Removed from the Allele Table sheet. Commented on the Intro sheet: "Acceptable: *RHCE*C, RHCE*c, RHCE*E* or *RHCE*e* when only testing for the specific polymorphism(s) associated with expression of that antigen."
14	Allele Table	Phenotypes	n.a.	Phenotypes updated for most alleles
15	Allele Table	Phenotypes	*RHCE*01.20.09,* RH10 (V) phenotype	Updated: RH:10 (V+)
16	Allele Table	Phenotypes	n.a.	Warning added as a footnote: † "Weak" and "partial" phenotypes are not mutually exclusive, and for many alleles the associated phenotype(s) have not been extensively investigated or samples have not been informative. All partial antigens may not be indicated.
17	Allele Table	Alleles added	n.a.	Alleles added: *RHCE*01.17; RHCE*01.18* *RHCE*01.20.02.02* (thus *RHCE*01.20.02* becomes *RHCE*01.20.02.01); RHCE*01.20.06.02; RHCE*01.20.12; RHCE*01.20.13* *RHCE*01.43; RHCE*01.44* *RHCE*01N.11; RHCE*01N.12* *RHCE*02.38; RHCE*02.39* *RHCE*02N.11; RHCE*02N.12; RHCE*02N.13* *RHCE*03.27; RHCE*03.28; RHCE*03.29; RHCE*03.30* *RHCE*03N.06*
18	Allele Table	Allele updated	*RHCE*ceSL*	separated into 2 entries: *RHCE*ceSL.01.01* and *RHCE*ceSL.01.02* differing by the silent c.105C>T change

19	Allele Table	Allele updated	*RHCE*03N.01* *RHCE*cEN.01* *RHCE*cEMI*	Updated pohenotype information leads to renumbering the allele *RHCE*03.31* *RHCE*cE.31* *RHCE*cEMI*
20	Allele Table	Nomenclature update	Nomenclature of silent changes	Updated to follow HGVS recommendation
21	Allele Table	PMIDs added	n.a.	PMIDs added for existing alleles: 32196693 for *RHCE*01.05.02* 11380457 and 23772606 for *RHCE*01.07.01* 20609196 for *RHCE*01.20.06* 29296782 for *RHCE*03.18* and for new entries
22	Allele Table	Abstracts aded	n.a.	Abstract~~s~~ references added for existing alleles: *RHCE*02.10.01; RHCE*02.27* *RHCE*02N.04; RHCE*02N.11* *RHCE*cEMI* and for new entries
23	Allele Table	rs numbers added	n.a.	one or more rs numbers added for existing entries: *RHCE*01.13* *RHCE*01.21.01* and *RHCE*01.21.02* *RHCE*01.25; RHCE*01.27* *RHCE*02* *RHCE*02.10.01* and *RHCE*02.10.02* *RHCE*02N.06* *RHCE*03* *RHCE*03.22; RHCE*03N.03* *RHCE*04* and for new entries
24	Allele Table	rs numbers removed	n.a.	rs609320 removed for *RHCE*01N.04*

25	Allele Table	Accession numbers added	n.a.	Genbank accession numbers added for: *RHCE*02.26*
26	Allele Table	Genbank accession	n.a.	Updated to show only the Genbank accession number
27	Allele Table	Allele name update	*RHCE*03.25*	*RHCE*03N.07*
28	Allele Table	Nucleotide change numbering update to the most 3' position possible	*RHCE*01.13* c.685_687delAGA	*RHCE*01.13* c.687_689delAGA
29	Allele Table	Nucleotide change numbering update	*RHCE*02N.04* c.93_94insT	*RHCE*02N.04* c.93insT
30	Allele Table	Nucleotide change numbering update	*RHCE*02N.10* Ce482_483insT	*RHCE*02N.10* c.482insT
31	Allele Table	Correction of a truncated nucleotide change	*RHCE*01N.09* c.1044_1050dupGCT	*RHCE*01N.09* c.1044_1050dupGCTTCAT
32	Allele Table	Correction of a typographical error	*RHCE*01.20.04.02* c.744C>T	*RHCE*01.20.04.02* c.744T>C

33	Allele Table	Correction of a typographical error	*RHCE*01N893.10* *RHCE*ceN.10*	*RHCE*01N.10* *RHCE*ceN.10*
34	Allele Table	Correction of a typographical error	*RHCE*04N.04* *RHCE*cE N.04*	*RHCE*03N.04*
35	Allele Table	Correction of a typographical error	*RHCE*04N.05* *RHCE*cE N.05*	*RHCE*03N.05*
36	Allele Table	Reference sheet created	PMID numbers and brief references for the abstracts were in the Allele Table	Detailed references listed for the first time
37	Allele Table	Reference not carried over	n.a.	Reference to abstract Silvy et al. (Vox Sanguinis, abstract) not carried over because redundant with PMID 22958092
38	**End Version**		**v5.0 15th July 2019**	**v6.0 30-JUN-2021**

ISBT	Common names (others or obsolete)	Prevalence	Antithetical Ag
RH1	D		
RH2	C		RH4
RH3	E		RH5
RH4	c (hr')		RH2
RH5	e (hr'')		RH3
RH6	ce, f		
RH7	Ce (rhi)		
RH8	C^W (Willis; rh^W)	Low	RH51
RH9	C^X (rh^X)	Low	RH51
RH10	V (ces; hr^V)	Low	
RH11	E^W (rh^{W_2})	Low	
RH12	G		
RH17	Hr_0	High	
RH18	Hr (Hr^S; Shabalala)	High	
RH19	hr^S (Shabalala; e-like)	High	
RH20	VS (e^s)	Low	
RH21	C^G		
RH22	CE		
RH23	D^W (Weil)	Low	
RH26	(Deal; c-like)	High	RH55
RH27	cE		
RH28	hr^H	Low	
RH29	(Total Rh)	High	
RH30	Goa (Gonzales; DCor)	Low	
RH31	hr^B (Bastiaan; e-like)	High	
RH32	(R^N_{-})	Low	RH46
RH33	R_0Har (Har; DHar)	Low	
RH34	Hr^B (Bastiaan; Bas)	High	
RH35	1114	Low	
RH36	Be^a (Berrens)	Low	
RH37	Evans	Low	
RH39	(C-like)	High	
RH40	Tar	Low	
RH41	(Ce-like)		
RH42	(Ce^S; Cce^S; rh^S; Thornton)	Low	
RH43	Crawford	Low	RH58
RH44	Nou	High	
RH45	Riv	Low	
RH46	Sec	High	RH32
RH47	Dav	High	
RH48	JAL (S.Allen; J.Allen)	Low	RH57

ISBT	Common names (others or obsolete)	Prevalence	Antithetical Ag
RH49	STEM (Stemper)	Low	
RH50	FPTT (700048; Mol)	Low	
RH51	MAR	High	RH8 and RH9
RH52	BARC	Low	
RH53	JAHK	Low	
RH54	DAK	Low	
RH55	LOCR (700053)	Low	RH26
RH56	CENR	Low	
RH57	CEST	High	RH48
RH58	CELO	High	RH43
RH59	CEAG	High	
RH60	PARG	Low	
RH61	CEVF	High	
RH62	CEWA	High	
RH63	CETW	Low	