

Names for RH (ISBT 004) Blood Group Alleles

General description: The Rh blood group system consists of 54 antigens carried on two proteins (RhD and RhCE) each consisting of 417 amino acids. Combinations (hybrids) between the two genes are not uncommon. The proteins consist of 12 membrane-spanning domains.

Gene name:	<i>RHD</i>	<i>RHCE</i>
Number of exons:	10	10
Initiation codon:	Beginning of exon 1	same
Stop codon:	middle of exon 10	same
GenBank #:	NG_007494 (gene)	NM_138618
	NM_016124 (mRNA)	NM_020485 (mRNA)
Entrez Gene ID:	6007	6006
Accession number:	L08429	DQ322275 (<i>RHCE*01</i>)
Preferred:	<i>RHD*01</i>	<i>RHCE*01</i> or <i>RHCE*ce</i> <i>RHCE*02</i> or <i>RHCE*Ce</i> <i>RHCE*03</i> or <i>RHCE*cE</i> <i>RHCE*04</i> or <i>RHCE*CE</i>

Common category or name Phenotype(s)	Allele name	Nucleotide	Exon(s)	Amino Acid(s)	Allele Name Detail	Comments Reported as:
D RH:1	<i>RHD*01</i>					
Normal D antigen	<i>RHD*01.01</i>	48G>C	1	Trp16Cys	<i>RHD*48C</i>	DUC-3
DII	<i>RHD*02</i> <i>RHD*DII</i>	1061C>A	7	Ala354Asp	<i>RHD*1061A</i>	
DIIIa RH:54 (DAK+)	<i>RHD*03.01</i> <i>RHD*DIIIa</i>	186G>T 410C>T 455A>C 602C>G 667T>G 819G>A	2,3,4,5	Leu62Phe Ala137Val Asn152Thr Thr201Arg Phe223Val silent	<i>RHD*186T,410T,455C,602G,667G</i>	Also reported as DIIIa type 5 (obsolete) Original DIIIa report missed 186G>T, 410C>T, and 819G>A changes
DIIIb Caucasian RH:54 (DAK+) RH:-12 (G-)	<i>RHD*03.02</i> <i>RHD*DIIIb</i>	150T>C 178A>C 201G>A 203G>A 307T>C	2	silent Ile60Leu silent Ser68Asn Ser103Pro	<i>RHD*D-CE(2)-D</i>	
DIIIc	<i>RHD*03.03</i> <i>RHD*DIIIc</i>	361T>A 380T>C 383A>G 455A>C	3	Leu121Met Val127Ala Asp128Gly Asn152Thr	<i>RHD*D-CE(3)-D</i>	
DIII type 4	<i>RHD*03.04</i> <i>RHD*DIII.04</i>	186G>T 410C>T 455A>C	2, 3	Leu62Phe Ala137Val Asn152Thr	<i>RHD*186T,410T,455C</i>	

Not tested	RHD*03.04.02 RHD*DIII.04.02	186G>T 307T>C 410C>T 455A>C	2,3	Leu62Phe Ser103Pro Ala137Val Asn152Thr	<i>RHD*186T,307C,</i> <i>410T,455C</i>	<i>In trans</i> to DAR1 2012 Cancun
DIII type 6	RHD*03.06 RHD*DIII.06	410C>T 455A>C 602C>G 667T>G 819G>A	3,4,5	Ala137Val Asn152Thr Thr201Arg Phe223Val silent	<i>RHD*410T,455C,6</i> <i>02G,667G</i>	
DIII type 7 (likely the historically defined DIIIb)	RHD*03.07 RHD*DIII.07	150T>C 178A>C 201G>A 203G>A 307T>C 410C>T, 455A>C 602C>G 667T>G	2,3,4,5	silent Ile60Leu silent Ser68Asn Ser103Pro Ala137Val Asn152Thr Thr201Arg Phe223Val	<i>RHD*D-CE(2)-</i> <i>410T, 455C,</i> <i>602G, 667G-D</i>	
DIVa (DIV type 1) RH30+ (Goa+)	RHD*04.01 RHD*DIVa	186G>T 410C>T 455A>C 1048G>C	2,3,7	Leu62Phe Ala136Val Asn152Thr Asp350His	<i>RHD*186T,410T,</i> <i>455C,1048C</i>	
DIVa type 2 obsolete						original DIVa report missed 410C>T change
DIVa	RHD*04.01.02	186G>T 410C>T 455A>C 667T>G 1048G>C		Leu62Phe Ala136Val Asn152Thr Phe223Val Asp350His		Reported with RHCE*ceTI
DIV type 3	RHD*04.03 RHD* DIV.03	916 G>A 932 A>G 941 G>T 968 C>A 974 G>T 979 A>G 985 G>C 986 G>A 989 A>C 992 A>T 1025 T>C 1048 G>C 1053 C>T 1057 G>T 1059 A>G 1060 G>A 1061 C>A 1063G>T 1170 C>T 1193 A>T	6,7,8,9	Val306Ile Tyr311Cys Gly314Val Pro323His Ser325Ile Ile327Val Gly329His Gly329His Tyr330Ser Asn331Ile Ile343Thr Asp350His silent Gly353Trp Gly353Trp Ala354Asn Ala354Asn silent silent Glu398Val	<i>RHD*D-CE(6-9)-D</i>	
DIV type 4	RHD*04.04 RHD*DIV.04	1048G>C 1053C>T 1057G>T 1059A>G	7	Asp350His silent Gly353Trp Gly353Trp	<i>RHD*1048C,1057</i> <i>T,1059G,1060A,1</i> <i>061A</i>	

		1060G>A 1061C>A		Ala354Asn Ala354Asn		
DIV type 5	RHD*04.05 RHD*DIV.05	916G>A 932A>G 941G>T 968C>A 974G>T 979A>G 985 G>C 986 G>A 989 A>C 992 A>T 1025T>C 1048G>C 1053C>T 1057G>T 1059A>G 1060G>A 1061C>A 1063G>T 1170T>C 1193A>T	7,8,9	Val306Ile Tyr311Cys Gly314Val Pro323His Ser325Ile Ile327Val Gly329His ""Tyr330Ser Asn331Ile Ile342Thr Asp350His silent Gly353Trp Ala354Asn silent silent Glu398Val	<i>RHD*D-CE(7-9)-D</i>	
DIVb	RHD*04.06 RHD*DIVb	1048G>C 1053C>T 1057G>T 1059A>G 1060G>A 1061C>A 1170T>C 1193A>T	7,8,9	Asp350His silent Gly353Trp Gly353Trp Ala354Asn Ala354Asn silent Glu398Val	<i>RHD*D-1048C, 1057T,1059G, 1060A,1061A - CE(8-9)-D</i>	
DV type 1	RHD*05.01 RHD*DV.01	667T>G 697G>C	5	Phe223Val Glu233Gln	<i>RHD*667G, 697C</i>	Kou FK
DV type 2	RHD*05.02 RHD*DV.02	667T>G 697G>C 712G>A 733 G>C 744 C>T 787 G>A 800 A>T	5	Phe223Val Glu233Gln Val238Met Val245Leu silent Gly263Arg Lys267Met	<i>RHD*D-CE(5)-D</i>	Hus
DV type 3	RHD*05.03 RHD*DV.03	667T>G 676G>C 697G>C 712 G>A	5	Phe223Val Ala226Pro Glu233Gln Val238Met	<i>RHD*667G,676C, 697C,712A</i>	Also known as DBS0
DV Type 4 RH:23 (D ^{w+})	RHD*05.04 RHD*DV.4	697G>C	5	Glu233Gln	<i>RHD*697C</i>	SM
DV type 5 RH:-23 (D ^{w-})	RHD*05.05 RHD*DV.05	697G>A	5	Glu233Lys	<i>RHD*697A</i>	DHK, DYO
DV type 6	RHD*05.06 RHD*DV.06	667T>G 697G>C 712G>A	5	Phe223Val Glu233Gln Val238Met	<i>RHD*667G,697C, 712A</i>	Jpn
DV type 7	RHD*05.07 RHD*DV.07	667T>G 697G>C 712G>A 733G>C	5	Phe223Val Glu233Gln Val238Met Val245Leu Gly263Arg	<i>RHD*667G,697C, 712A,733C,787A</i>	DAL

		787G>A				
DV type 8	RHD*05.08 RHD*DV.08	667T>G 697G>C 712G>A 733G>C	5	Phe223Val Glu233Gln Val238Met Val245Leu		TT
DV type 9	RHD*05.09 RHD*DV.9	697G>C 712G>A	5	Glu233Gln Val238Met	<i>RHD*697C, 712A</i>	TO
DVI type 1 RH:—52 (BARC—)	RHD*06.01 RHD*DVI.01	505A>C 509T>G 514A>T 544T>A 577G>A 594A>T 602C>G 667T>G 697G>C 712G>A 733G>C 744C>T 787G>A 800A>T	4,5	Met169Leu Met170Arg Ile172Phe Ser182Thr Glu193Lys Lys198Asn Thr201Arg Phe223Val Glu233Gln Val238Met Val254Leu silent Gly263Arg Lys267Met	<i>RHD*D-CE(4-5)-D</i>	linked to <i>RHCE*cE</i>
DVI type 2 RH:52 (BARC+)	RHD*06.02 RHD*DVI.02	505A>C 509T>G 514A>T 544T>A 577G>A 594A>T 602C>G 667T>G 697G>C 712G>A 733G>C 744C>T 787G>A 800A>T 916G>A 932A>G	4,5,6	Met169Leu Met170Arg Ile172Phe Ser182Thr Glu193Lys Lys198Asn Thr201Arg Phe223Val Glu233Gln Val238Met Val254Leu silent Gly263Arg Lys267Met Val306Ile Tyr311Cys	<i>RHD*D-CE(4-6)-D</i>	linked to <i>RHCE*Ce</i>
DVI type 3 RH:52 (BARC+)	RHD*06.03.01 RHD*DVI.03.01	361T>A 380T>C 383A>G 455A>C 505A>C 509T>G 514A>T 544T>A 577G>A 594A>T 602C>G 667T>G 697G>C 712G>A 733G>C 744C>T 787G>A 800A>T 916G>A 932A>G	3,4,5,6	Leu121Met Val127Ala Asp128Gly Asn152Thr Met169Leu Met170Arg Ile172Phe Ser182Thr Glu193Lys Lys198Asn Thr201Arg Phe223Val Glu233Gln Val238Met Val254Leu silent Gly263Arg Lys267Met Val306Ile Tyr311Cys	<i>RHD*D-CE(3-6)-D</i>	linked to <i>RHCE*Ce</i>

DVI type 3.2 BARC not tested	RHD*06.03.02 RHD*DVI.03.02	As above and 1195G>A	3, 4, 5, 6, 9	As above and Ala399Thr	RHD*D-CE(3-6)-D 1195A	
DVI type 4 RH:52 (BARC+)	RHD*06.04 RHD*DVI.04	361T>A 380T>C 383A>G 455A>C 505A>C 509T>G 514A>T 544T>A 577G>A 594A>T 602C>G 667T>G 697G>C 712G>A 733G>C 744C>T 787G>A 800A>T	3,4,5	Leu121Met Val127Ala Asp128Gly Asn152Thr Met169Leu Met170Arg Ile172Phe Ser182Thr Glu193Lys Lys198Asn Thr201Arg Phe223Val Glu233Gln Val238Met Val254Leu silent Gly263Arg Lys267Met	RHD*D-CE(3-5)-D	linked to <i>RHCE*</i> Ce
DVII RH:40 (Tar+)	RHD*07.01 RHD*DVII.01	329T>C	2	Leu110Pro	RHD*329C	
DVII type 2	RHD*07.02 RHD*DVII.02	307T>C 329T>C	2	Ser103Pro Leu110Pro	RHD*307C,329C	
DFV	RHD*08.01 RHD*DFV	667T>G	5	Phe223Val	RHD*667G	
DAR1 (weak D 4.2)	RHD*09.01.00 RHD*DAR1.00	602C>G 667T>G 1025T>C	4,5,7	Thr201Arg Phe223Val Ile342Thr	RHD*602G,667G, 1025C	
DAR1.1 (weak D 4.2.1)	RHD*09.01.01 RHD*DAR1.01	602C>G 667T>G 957G>A 1025T>C	4,5,7	Thr201Arg Phe223Val silent Ile342Thr	RHD*602G,667G, 1025C	
DAR1.2 (weak D 4.2.2)	RHD*09.01.02 RHD*DAR1.02	602C>G 667T>G 744C>T 957G>A 1025T>C	4,5,7	Thr201Arg Phe223Val silent silent Ile342Thr	RHD*602G,667G, 1025C	
DAR1.3 (weak D 4.2.3)	RHD*09.01.03 RHD*DAR1.03	602C>G 667T>G 744C>T 1025T>C	4,5,7	Thr201Arg Phe223Val silent Ile342Thr	RHD*602G,667G, 1025C	
DAR2 (DARE)	RHD*09.02.00 RHD*DAR2.00	602C>G 667T>G 697G>C 957G>A 1025 T>C	4,5,7	Thr201Arg Phe223Val Glu233Gln silent Ile342Thr	RHD*602G,667G, 697C,1025C	Reported as DAR-E
DAR2.1	RHD*09.02.01 RHD*DAR2.01	602C>G 667T>G 697G>C 744C>T 957G>A 1025 T>C	4,5,7	Thr201Arg Phe223Val Glu233Gln silent silent Ile342Thr		

DAR3 (weak partial D 4.0.1)	RHD*09.03 RHD*DAR3	602C>G 667T>G	4, 5	Thr201Arg Phe223Val	<i>RHD*602G,667G</i>	
DAR3.1 (weak partial D 4.0)	RHD*09.03.01 RHD*DAR3.01	602C>G 667T>G 819G>A	4, 5, 6	Thr201Arg Phe223Val silent	<i>RHD*602G,667G</i>	
DAR4 (weak D 4.1)	RHD*09.04 RHD*DAR4	48G>C 602C>G 667T>G 819G>A	1,4,5,6	Trp16Cys Thr201Arg Phe223Val silent	<i>RHD*48C,602G, 667G</i>	
DAR5 (weak D 4.3 or Del)	RHD*09.05 RHD*DAR5	602C>G 667T>G 819G>A 872C>G	4,5,6	Thr201Arg Phe223Val silent Pro291Arg	<i>RHD*602G, 667G, 872G</i>	
DAU0	RHD*10.00 RHD*DAU0	1136C>T	8	Thr379Met	<i>RHD*1136T</i>	
DAU0.01	RHD*10.00.01	1136C>T 579G>A	8 4	Thr370Met silent	<i>RHD*1136T,579A</i>	
DAU0.02	RHD*10.00.02	1136C>T 150T>C	8 2	Thr370Met silent(common)	<i>RHD*1136T,150C</i>	
DAU1	RHD*10.01 RHD*DAU1	689G>T 1136C>T	5,8	Ser230Ile Thr379Met	<i>RHD*689T,1136T</i>	
DAU2	RHD*10.02 RHD*DAU2	209G>A 998G>A 1136C>T	2,7,8	Arg70Gln Ser333Asn Thr379Met	<i>RHD*209A,998A, 1136T</i>	
DAU3	RHD*10.03 RHD*DAU3	835G>A 1136C>T	6, 8	Val279Met Thr379Met	<i>RHD*835A,1136T</i>	
DAU4	RHD*10.04 RHD*DAU4	697G>A 1136C>T	5, 8	Glu233Lys Thr379Met	<i>RHD*697A,1136T</i>	
DAU5	RHD*10.05 RHD*DAU5	667T>G 697G>C 1136C>T	5, 8	Phe223Val Glu233Gln Thr379Met	<i>RHD*667G,697C, 1136T</i>	
DAU6	RHD*10.06 RHD*DAU6	998G>A 1136C>T	7, 8	Ser333Asn Thr379Met	<i>RHD*998A,1136T</i>	
DAU7	RHD*10.07 RHD*DAU7	835G>A 998G>A 1136C>T	6,7,8	Val279Met Ser333Asn Thr379Met	<i>RHD*835A,998A,1 136T</i>	
weak partial 11 or Del	RHD*11 RHD*weak partial 11	885G>T	6	Met295Ile	<i>RHD*885T</i>	allo-anti-D reported Del phenotype when with <i>RHCE*Ce</i>
DOL1 RH:54(DAK+)	RHD*12.01 RHD*DOL1	509T>C 667T>G	4,5	Met170Thr Phe223Val	<i>RHD*509C,667G</i>	
DOL2 RH:54(DAK+)	RHD*12.02 RHD*DOL2	509T>C 667T>G 1132C>G	4,5,8	Met170Thr Phe223Val Leu378Val	<i>RHD*509C,667G, 1132G</i>	
DOL3	RHD*12.03 RHD*DOL3	410C>T 509T>C 667T>G	3,4,5	Ala137Val Met170Thr Phe223Val	<i>RHD*410T,509C,6 67G</i>	
DBS1	RHD*13.01 RHD*DBS1	667T>G 676G>C 697G>C 712G>A 733G>C	5	Phe223Val Ala226Pro Glu233Gln Val238Met Val245Leu	<i>RHD*D-cE(5)-D</i>	

		744 C>T 787G>A 800 A>T		silent Gly263Arg Lys267Met		
DBS2	RHD*13.02 RHD*DBS2	667T>G 676G>C 697G>C	5	Phe223Val Ala226Pro Glu233Gln	<i>RHD*667G,676C, 697C</i>	
DBT1	RHD*14.01 RHD*DBT1	667T>G 697G>C 712 G>A 733G>C 744C>T 787G>A 800A>T 916G>A 932A>G 941G>T 968C>A 974G>T 979A>G 985 G>C 986 G>A 989 A>C 992 A>T 1025T>C 1048G>C 1053C>T 1057G>T 1059A>G 1060G>A 1061C>A	5,6,7	Phe223Val Glu233Gln Val238Met Val254Leu silent Gly263Arg Lys267Met Val306Ile Tyr311Cys Gly314Val Pro323His Ser325Ile Ile327Val Gly329His Tyr330Ser Asn331Ile Ile342Thr Asp350His silent Gly353Trp Ala354Asn	<i>RHD*D-CE(5-7)-D</i>	
DBT2	RHD*14.02 RHD*DBT2	667T>G 697G>C 712G>A 733G>C 744C>T 787G>A 800A>T 916G>A 932A>G 941G>T 968C>A 974G>T 979A>G 985G>C 986G>A 989A>C 992A>T 1025T>C 1048G>C 1053C>T 1057G>T 1059A>G 1060G>A 1061C>A 1170C>T 1193 A>T	5,6,7,8, 9	Phe223Val Glu233Gln Val238Met Val254Leu silent Gly263Arg Lys267Met Val306Ile Tyr311Cys Gly314Val Pro323His Ser325Ile Ile327Val Gly329His Tyr330Ser Asn331Ile Ile342Thr Asp350His silent Gly353Trp Ala354Asn silent Glu398Val	<i>RHD*D-CE(5-9)-D</i>	

Weak partial Type 15	RHD*15 RHD*weak partial 15	845G>A	6	Gly282Asp	RHD*845A	allo anti-D reported
DCS1	RHD*16.01 RHD*DCS1	667G>T 676G>C	5	Phe223Val Ala226Pro	RHD*667T,676C	
DCS2	RHD*16.02 RHD*DCS2	676G>C	5	Ala226Pro	RHD*676C	
DFR1	RHD*17.01 RHD*DFR1	505A>C 509T>G 514A>T	4	Met169Leu Met170Arg Ile172Phe	RHD*505C,509G,514T	
DFR2	RHD*17.02 RHD*DFR2	505A>C 509T>G 514A>T 544T>A 577G>A 594A>T 602C>G	4	Met169Leu Met170Arg Ile172Phe Ser182Thr Glu193Lys Lys198Asn Thr201Arg	RHD*D-CE(4)-D	
DFR3	RHD*17.03 RHD*DFR3	505A>C 509T>G 514A>T 539G>C	4	Met169Leu Met170Arg Ile172Phe Gly180Ala	RHD*505C,509G,514T,539C	
DFR4	RHD*17.04 RHD*DFR4	505A>C 509T>G	4	Met169Leu Met170Arg	RHD*505C,509G	
DFR5	RHD*17.05 RHD*DFR5	361 T>A 380 T>C 383 A>G 455 A>C 505 A>C 509 T>G 514 A>T 544 T>A 577 G>A 594 A>T 602 C>G	3,4	Leu121Met Val127Ala Asp128G, Asn152Thr Met169Leu Met170Arg Ile172Phe Ser182Thr Glu193Lys Lys198Asn Thr201Arg	RHD*D-CE(3-4)-D	
DFW	RHD*18 RHD*DFW	497A>C	4	His166Pro	RHD*497C	
DHMi	RHD*19 RHD*DHMi	848C>T	6	Thr283Ile	RHD*848T	
DHO	RHD*20 RHD*DHO	704A>C	5	Lys235Thr	RHD*704C	
Weak partial Type 21	RHD*21 RHD*weak partial D 21	938C>T	6	Pro313Leu	RHD*938T	allo-anti-D reported
DHR	RHD*22 RHD*DHR	686G>A	5	Arg229Lys	RHD*686A	
DMH	RHD*23 RHD*DMH	161T>C	2	Leu54Pro	RHD*161C	
DNAK	RHD*24 RHD*DNAK	1070G>A	7	Gly357Asp	RHD*1070A	
DNB	RHD*25 RHD*DNB	1063G>A	7	Gly355Ser	RHD*1063A	

DNU	RHD*26 RHD*DNU	1057G>A	7	Gly353Arg	RHD*1057A	
DDE	RHD*27 RHD*DDE	120T>A	1	Asp40Glu	RHD*120A	
DFL	RHD*28 RHD*DFL	494A>G	4	Tyr165Cys	RHD*494G	
DYU (DQC)	RHD*29 RHD*DYU	700A>T	5	Arg234Trp	RHD*700T	
DTO	RHD*30 RHD*DTO	667T>G 674C>T	5	Phe223Val Ser225Phe	RHD*667G,674T	
DVL1	RHD*31 RHD*DVL1	deletion 684 to 686 GAG	5	deletion of Arg at position 229 Arg229del	RHD*del684-686	
DVL2	RHD*32 RHD*DVL2	deletion 705 to 707 GAA	5	deletion of Lys at position 235 Lys235del	RHD*del705-707	
DWI (DWLLE)	RHD*33 RHD*DWI	1073T>C	7	Met358Thr	RHD*1073C	
DIM (DlleM)	RHD*34 RHD*DIM	854G>A	6	Cys285Tyr	RHD*854A	
DMA	RHD*35 RHD*DMA	621G>C	5	Leu207Phe	RHD*621C	
DLO	RHD*36 RHD*DLO	851C>T	6	Ser284Leu	RHD*851T	
DUC2	RHD*37 RHD*DUC2	733G>C	5	Val245Leu	RHD*733C	
DNT	RHD*38	455A>C	3	Asn152Thr	RHD*455C	
RH:–12 (G–)	RHD*39	307T>C	2	Ser103Pro	RHD*307C	Linked to RHCE*cE