Names for ABO (ISBT 001) Blood Group Alleles

General description: The ABO system was discovered as in 1900 and is considered the first and clinically most important system. The *ABO* gene and its 7 coding exons give rise to one of two principally different glycosyltransferases. The A glycosyltransferase (GTA) catalyzes the addition of a donor substrate, UDP-*N*-acetylgalactosamine, to an acceptor substrate known as the H antigen. The B glycosyltransferase (GTB) differs by only four amino-acid substitutions from GTA and performs the same enzymatic reaction but uses UDP-galactose as donor substrate. In this way, genetic polymorphism gives rise to two related antigens in this system. Any polymorphism or mutation that changes the activity or specificity of the encoded enzyme may therefore alter the ABO phenotype. Alterations that completely abolish enzymic activity give rise to the blood group O phenotype, in which the H antigen remains unconverted and no A or B antigen can be detected. If the genetic alteration decreases the activity of the enzyme, or alters its subcellular location and thereby decreases conversion of H to A or B, a weak A or B subgroup phenotype can result. Furthermore, certain polymorphisms result in promiscuous enzymes that can synthesize both A and B antigen, thereby resulting in the so-called cisAB or B(A) phenotypes. The A phenotype is divided into A_1 and A_2. The former is more prevalent in all populations and has approximately 5 times more A epitopes per red cell. The GTA_1 is also better than GTA_2 at synthesizing certain forms of A, .e.g. A type 3 and 4.

In addition to the A and B antigens, two other antigens are included in the ABO system, namely A,B and A1. The former is a joint epitope on A or B antigen and is therefore present in both A, B and AB phenotypes. The exact biochemical nature of the A1 antigen has been more controversial but has been proposed to represent A type 4.

Gene name:	*ABO*
Number of exons:	7
Initiation codon:	Within exon 1
Stop codon:	Within exon 7
Entrez Gene ID:	28
LRG sequence:	NG_006669.1 (genomic) NM_020469.2 (transcript)
Reference allele:	*ABO*A1.01* (shaded)

Molecular bases associated with the A_1, A_2 and weak A phenotypes

Reference allele *ABO*A1.01* encodes A glycosyltransferase that synthesizes A antigen.

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A_1	*ABO*A1.01*			
A_1	*ABO*A1.02*	c.467C>T	7	p.Pro156Leu
A_2	*ABO*A2.01*	c.467C>T; c.1061delC	7	p.Pro156Leu; p.Pro354Argfs*23
A_2	*ABO*A2.02*	c.1054C>T	7	p.Arg352Trp
A_2	*ABO*A2.03*	c.1054C>G	7	p.Arg352Gly
A_2	*ABO*A2.04*	c.297A>G; c.526C>G; c.657C>T; c.703G>A; c.771C>T; c.829G>A	6 7	p.Arg176Gly; p.Gly235Ser; p.Val277Met
A_2	*ABO*A2.05*	c.467C>T; c.1009A>G	7	p.Pro156Leu; p.Arg337Gly
A_2	*ABO*A2.06*	c.1061delC	7	p.Pro354Argfs*23
A_2	*ABO*A2.07*	c.539G>C	7	p.Arg180Pro
A_2	*ABO*A2.08*	c.467C>T; c.539G>C	7	p.Pro156Leu; p.Arg180Pro
A_2	*ABO*A2.09*	c.467C>T; c.527G>A; c.1061delC	7	p.Pro156Leu; p.Arg176His; p.Pro354Argfs*23
A_2	*ABO*A2.10*	c.268T>C; c.467C>T	6 7	p.Trp90Arg; p.Pro156Leu
A_2	*ABO*A2.11*	c.266C>T; c.467C>T	6 7	p.Pro89Leu; p.Pro156Leu
A_2	*ABO*A2.12*	c.190G>A; c.527G>A; c.1061delC	4 7	p.Val64Ile; p.Arg176His; p.Pro354Argfs*23
A_2	*ABO*A2.13*	c.467C>T; c.742C>T	7	p.Pro156Leu; p.Arg248Cys
A_2	*ABO*A2.16*	c.106G>T; c.188G>A; c.189C>T; c.467C>T; c.1061delC	3 4 7	p.Val36Phe; p.Arg63His; p.Pro156Leu; p.Pro354Argfs*23
A_2	*ABO*A2.17*	c.407C>T; c.467C>T	7	p.Thr136Met; p.Pro156Leu
A_2	*ABO*A2.18*	c.467C>T; c.722G>A	7	p.Pro156Leu; p.Arg241Gln
A_2	*ABO*A2.19*	c.467C>T; c.778G>A	7	p.Pro156Leu; p.Glu260Lys

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A_2	*ABO*A2.20*	c.467C>T; c.829G>A	7	p.Pro156Leu; p.Val277Met
A_3	*ABO*A3.01*	c.871G>A	7	p.Asp291Asn
A_3	*ABO*A3.02*	c.829G>A; c.1061delC	7	p.Val277Met; p.Pro354Argfs*23
A_3	*ABO*A3.03*	c.838C>T	7	p.Leu280Phe
A_3	*ABO*A3.04*	c.467C>T; c.539G>A; c.1061delC	7	p.Arg180His; p.Pro156Leu; p.Pro354Argfs*23
A_3	*ABO*A3.05*	c.820G>A	7	p.Val274Met
A_3	*ABO*A3.06*	c.467C>T; c.820G>A	7	p.Pro156Leu; p.Val274Met
A_3	*ABO*A3.07*	c.467C>T; c.745C>T	7	p.Pro156Leu; p.Arg249Trp
A_{weak}	*ABO*AW.01*	c.407C>T; c.467C>T; c.1061delC	7	p.Thr136Met; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.02*	c.350G>C; c.467C>T; c.1061delC	6 7	p.Gly117Ala; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.03*	c.203G>C; c.467C>T; c.1061delC	4 7	p.Arg68Thr; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.04*	c.721C>T	7	p.Arg241Trp
A_{weak}	*ABO*AW.05*	c.965A>G	7	p.Glu322Gly
A_{weak}	*ABO*AW.06*	c.502C>G	7	p.Arg168Gly
A_{weak}	*ABO*AW.07*	c.467C>T; c.592C>T; c.1061delC	7	p.Pro156Leu; p.Arg198Trp; p.Pro354Argfs*23
A_{weak}	*ABO*AW.08*	c.220C>T; c.297A>G; c.488C>T; c.526C>G; c.802G>A	5 6 7	p.Pro74Ser; p.Thr163Met; p.Arg176Gly; p.Gly268Arg
A_{weak}	*ABO*AW.09*	c.46G>A; c.106G>T; c.188G>A; c.220C>T; c.467C>T; c.1061delC	2 3 4 5 7	p.Ala16Thr; p.Val36Phe; p.Arg63His; p.Pro74Ser; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.10*	c.784G>A	7	p.Asp262Asn
A_{weak}	*ABO*AW.11*	c.523G>A; c.721C>T	7	p.Val175Met; p.Arg241Trp

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A_{weak}	*ABO*AW.12*	c.467C>T; c.556A>G	7	p.Pro156Leu; p.Met186Val
A_{weak}	*ABO*AW.13*	c.2T>C	1	p.Ala2_Met20del
A_{weak}	*ABO*AW.14*	c.467C>T; c.699C>A	7	p.Pro156Leu; p.His233Gln
A_{weak}	*ABO*AW.15*	c.374+4A>T	Intron 6	Altered splicing
A_{weak}	*ABO*AW.16*	c.1A>G; c.467C>T; c.1061delC	1 7	p.Ala2_Met20del; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.17*	c.236C>T; c.467C>T; c.1061delC	5 7	p.Pro79Leu; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.18*	c.347T>C; c.467C>T; c.1061delC	6 7	p.Ile116Thr; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.19*	c.434A>G; c.467C>T; c.1061delC	7	p.His145Arg; p.Pro156Leu; p.Pro354Argfs*23
A_{weak}	*ABO*AW.20*	c.467C>T; c.607G>A; c.1061delC	7	p.Pro156Leu; p.Glu203Lys; p.Pro354Argfs*23
A_{weak}	*ABO*AW.21*	c.467C>T; c.607G>C; c.1061delC	7	p.Pro156Leu; p.Glu203Gln; p.Pro354Argfs*23
A_{weak}	*ABO*AW.22*	c.467C>T; c.634G>A; c.1061delC	7	p.Pro156Leu;Val212Met; p.Pro354Argfs*23
A_{weak}	*ABO*AW.23*	c.467C>T; c.722G>A; c.1061delC	7	p.Pro156Leu; p.Arg241Gln; p.Pro354Argfs*23
A_{weak}	*ABO*AW.24*	c.467C>T; c.742C>T; c.1061delC	7	p.Pro156Leu; p.Arg248Cys; p.Pro354Argfs*23
A_{weak}	*ABO*AW.25*	c.467C>T; c.829G>A; c.1061delC	7	p.Pro156Leu; p.Val277Met; p.Pro354Argfs*23
A_{weak}	*ABO*AW.26*	c.467C>T; c.527G>A; c.1061delC	7	p.Pro156Leu; p.Arg176His; p.Pro354Argfs*23
A_{weak}	*ABO*AW.27*	c.527G>A; c.1061delC	7	p.Arg176His; p.Pro354Argfs*23
A_{weak}	*ABO*AW.28*	c.98+2T>C	Intron 1	Altered splicing
A_{weak}	*ABO*AW.29*	c.311T>A	6	p.Ile104Asn
A_x/A_{weak}	*ABO*AW.30.01*	c.646T>A	7	p.Phe216Ile
A_x/A_{weak}	*ABO*AW.30.02*	c.646T>A; c.681G>A	7	p.Phe216Ile

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A_x/A_{weak}	*ABO*AW.31.01*	c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Phe216Ile; p.Val277Met
A_x/A_{weak}	*ABO*AW31.02-05*	c.646T>A; c.681G>A; c.771C>T; c.829G>A	7	p.Phe216Ile; p.Val277Met
A_x/A_{weak}	*ABO*AW.32*	c.996G>A	7	p.Trp332Ter
A_x/A_{weak}	*ABO*AW.33*	c.467C>T; c.543G>T	7	p.Pro156Leu; p.Trp181Cys
A_x/A_{weak}	*ABO*AW.34*	c.467C>T; c.829G>A; c.1009A>G	7	p.Pro156Leu; p.Val277Met; p.Arg337Gly
A_x/A_{weak}	*ABO*AW.35*	c.467C>T; c.860C>T	7	p.Pro156Leu; p.Ala287Val
A_x/A_{weak}	*ABO*AW.36*	c.607G>A	7	p.Glu203Lys
A_x/A_{weak}	*ABO*AW.37*	c.940A>G	7	p.Lys314Glu
A_x/A_{weak}	*ABO*AW.38*	c.426G>C	7	p.Met142Ile
A_x/A_{weak}	*ABO*AW.39*	c.385T>C	7	p.Phe129Leu
A_x/A_{weak}	*ABO*AW.40*	c.499G>T	7	p.Gly167Cys
A_x/A_{weak}	*ABO*AW.41*	c.370A>G	6	p.Lys124Glu
A_x/A_{weak}	*ABO*AW.42*	c.467C>T; c.905A>G	7	p.Pro156Leu; p.Asp302Gly
A_x/A_{weak}	*ABO*AW.43*	c.467C>T; c.721C>T	7	p.Pro156Leu; p.Arg241Trp
A_{finn}/A_{weak}	*ABO*AW.44*	c.374+4A>G	Intron 6	Altered splicing
A_{bantu}/A_{weak}	*ABO*AW.45*	c.203+1delG; c.467C>T; c.1061delC	Intron 4 7	Altered splicing
A_m	*ABO*AM.01*	c.467C>T; c.761C>T	7	p.Pro156Leu; p.Ala254Val
A_m	*ABO*AM.02*	c.664G>A	7	p.Val222Met
A_{el}	*ABO*AEL.01*	c.804dupG	7	p.Phe269Valfs*124
A_{el}	*ABO*AEL.02*	c.467C>T; c.646T>A; c.681G>A	7	p.Pro156Leu; p.Phe216Ile
A_{el}	*ABO*AEL.03*	c.804delG	7	p.Phe269Serfs*20
A_{el}	*ABO*AEL.04*	c.374+5G>A	Intron 6	Altered splicing
A_{el}	*ABO*AEL.05*	c.467C>T; c.767T>C	7	p.Pro156Leu; p.Ile256Thr
A_{el}	*ABO*AEL.06*	c.425T>C; c.467C>T	7	p.Met142Thr; p.Pro156Leu
A_{el}	*ABO*AEL.07*	c.467C>T; 681G>A; 771C>T; c.829G>A	7	p.Pro156Leu; p.Val277Met

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A_{el}	*ABO*AEL.08*	c.467C>T; c.804dupG	7	p.Pro156Leu; p.Phe269Valfs*124

The *A103-A107* alleles in dbRBC do not give rise to an altered amino acid sequence compared to other alleles, and so are not included here. *A108* and *A109* are listed as unpublished, and had no phenotype registered in dbRBC. *A214* and *A215* represent the same coding sequence as *ABO*A2.01*, but have been registered under other names due to intron polymorphisms. Also, their phenotypes are not given in dbRBC. Some alleles listed above are unpublished, but have been submitted to GenBank/dbRBC.
It is also noteworthy that many of the alleles registered as associated with the rare A_2 phenotype in Asia (e.g. *A2.08, A2.13, A2.17, A2.18* and *A2.20*) cause amino acid substitutions that have been associated with weaker A subgroups in other studies. In the case of *A2.18* and *A2.19*, the phenotype was given as A, not A_2.

Molecular bases associated with the B and weak B phenotypes

The seven B-associated polymorphisms are only shown for the first allele but are present in all the others except *ABO*BEL.04*, which uses *A1.01*. Differences compared to *ABO*B.01*, that encodes B glycosyltransferase, are given.

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
B	*ABO*B.01*	c.297A>G; c.526C>G; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	 p.Arg176Gly; p.Gly235Ser; p.Leu266Met; p.Gly268Ala
B	*ABO*B.02*	c.892G>T	7	p.Ala298Ser
B	*ABO*B.03*	c.559C>T	7	p.Arg187Cys
B_3	*ABO*B3.01*	c.1054C>T	7	p.Arg352Trp
B_3	*ABO*B3.02*	c.646T>A	7	p.Phe216Ile
B_3	*ABO*B3.03*	c.155+5G>A	Intron 3	Altered splicing
B_3	*ABO*B3.04*	c.247G>T	6	p.Asp83Tyr
B_3	*ABO*B3.05*	c.425T>C	7	p.Met142Thr
B_3	*ABO*B3.06*	c.547G>A	7	p.Asp183Asn
B_3	*ABO*B3.07*	c.410C>T	7	p.Ala137Val
B_3	*ABO*B3.08*	c.938A>C	7	p.His313Pro
B_x/B_{weak}	*ABO*BW.01*	c.871G>A	7	p.Asp291Asn
B_{weak}	*ABO*BW.02*	c.873C>G	7	p.Asp291Glu
B_{weak}	*ABO*BW.03*	c.721C>T	7	p.Arg241Trp
B_{weak}	*ABO*BW.04*	c.548A>G	7	p.Asp183Gly
B_{weak}	*ABO*BW.05*	c.539G>A	7	p.Arg180His
B_{weak}	*ABO*BW.06*	c.1036A>G	7	p.Lys346Glu
B_{weak}	*ABO*BW.07*	c.1055G>A	7	p.Arg352Gln
B_{weak}	*ABO*BW.08*	c.863T>G	7	p.Met288Arg
B_{weak}	*ABO*BW.09*	c.1037A>T	7	p.Lys346Met
B_{weak}	*ABO*BW.10*	c.556A>G	7	p.Met186Val
B_{weak}	*ABO*BW.11*	c.695T>C	7	p.Leu232Pro
B_{weak}	*ABO*BW.12*	c.278C>T	6	p.Pro93Leu

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
B_{weak}	*ABO*BW.14*	c.523G>A	7	p.Val175Met
B_{weak}	*ABO*BW.15*	c.565A>G	7	p.Met189Val
B_{weak}	*ABO*BW.16*	c.575T>C	7	p.Ile192Thr
B_{weak}	*ABO*BW.17*	c.784G>A	7	p.Asp262Asn
B_{weak}	*ABO*BW.18*	c.802G>A	7	p.Gly268Thr
B_{weak}	*ABO*BW.19*	c.646T>A; c.681G>A	7	p.Phe216Ile
B_{weak}	*ABO*BW.20*	c.815_816insG	7	p.Ser273Valfs*?
B_{weak}	*ABO*BW.21*	c.688G>C	7	p.Gly230Arg
B_{weak}	*ABO*BW.22*	c.503G>T	7	p.Arg168Leu
B_{weak}	*ABO*BW.23*	c.743G>C	7	p.Arg248Pro
B_{weak}	*ABO*BW.24*	c.558G>T	7	p.Met186Ile
B_{weak}	*ABO*BW.25*	c.103G>A; c.619C>G	3 7	p.Gly35Arg; p.Leu207Val
B_{weak}	*ABO*BW.26*	c.53G>T	2	p.Arg18Leu
B_{weak}	*ABO*BW.27*	c.905A>G	7	p.Asp302Gly
B_{weak}	*ABO*BW.28*	c.541T>C	7	p.Trp181Arg
B_{weak}	*ABO*BW.29*	c.588C>G	7	p.Cys196Trp
B_{weak}	*ABO*BW.30*	c.976G>T	7	p.Asp326Tyr
B_{weak}	*ABO*BW.31*	c.900G>C	7	p.Trp300Cys
B_{weak}	*ABO*BW.32*	c.808T>A	7	p.Phe270Ile
B_{weak}	*ABO*BW.33*	c.550G>A	7	p.Val184Met
B_{weak}	*ABO*BW.34*	c.889G>A	7	p.Glu297Lys
B_{el}	*ABO*BEL.01*	c.641T>G	7	p.Met214Arg
B_{el}	*ABO*BEL.02*	c.669G>T	7	p.Glu223Asp
B_{el}	*ABO*BEL.03*	c.502C>T	7	p.Arg168Trp
B_{el}	*ABO*BEL.05*	c.952G>A	7	p.Val318Met
B_{el}	*ABO*BEL.04*	c.467C>T; c.646T>A; c.681G>A; c.771C>T; c.796C>A; c.803G>C; c.829G>A	7	p.Pro156Leu; p.Phe216Ile; p.Leu266Met; p.Gly268Ala; p.Val277Met

Other variants of *B* alleles exist, but the ones listed in dbRBC are either based on: 1) lack of one

of the silent A vs. B SNPs (e.g. *B102* has 930G; *B103* has 657C); 2) silent mutations (B109 has 498C>T); 3) intron SNPs (e.g. *B107, B113, B114, B116*); 4) a sequence identical to a proven B_{weak}; 5) unpublished (*B113-B116*).

Molecular bases associated with cisAB and B(A) phenotypes

Differences compared to *ABO*A1.01* are given.

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
cisAB	*ABO*cisAB.01*	c.467C>T; c.803G>C	7	p.Pro156Leu; p.Gly268Ala
cisAB	*ABO*cisAB.02*	c.526C>G; c.657C>T; c.703G>A; c.803G>C	7	p.Arg176Gly; p.Gly235Ser; p.Gly268Ala
cisAB	*ABO*cisAB.03*	c.297A>G; c.526C>G; c.657C>T; c.700C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	p.Arg176Gly; p.Pro234Ser; p.Gly235Ser; p.Leu266Met; p.Gly268Ala
cisAB	*ABO*cisAB.04*	c.467C>T; c.796C>A	7	p.Pro156Leu; p.Leu266Met
cisAB	*ABO*cisAB.05*	c.297A>G; c.526C>G; c.657C>T; c.703G>A; c.796C>A; c.930G>A	6 7	p.Arg176Gly; p.Gly235Ser; p.Leu266Met
cisAB	*ABO*cisAB.06*	c.297A>G; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	p.Gly235Ser; p.Leu266Met; p.Gly268Ala
B(A)	*ABO*BA.01*	c.297A>G; c.526C>G; c.796C>A; c.803G>C; c.930G>A	6 7	p.Arg176Gly; p.Leu266Met; p.Gly268Ala
B(A)	*ABO*BA.02*	c.297A>G; c.526C>G; c.657C>T; c.700C>G; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	p.Arg176Gly; p.Pro234Ala; p.Gly235Ser; p.Leu266Met; p.Gly268Ala
B(A)	*ABO*BA.03*	c.297A>G; c.526C>G; c.657C>T; c.796C>A; c.803G>C; c.930G>A	6 7	p.Arg176Gly; p.Leu266Met; p.Gly268Ala
B(A)	*ABO*BA.04*	c.297A>G; c.526C>G; c.640A>G; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	p.Arg176Gly; p.Met214Val; p.Gly235Ser; p.Leu266Met; p.Gly268Ala

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
B(A)	*ABO*BA.05*	c.297A>G; c.526C>G; c.641T>C; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	p.Arg176Gly; p.Met214Thr; p.Gly235Ser; p.Leu266Met; p.Gly268Ala
B(A)	*ABO*BA.06*	c.297A>G; c.526C>G; c.657C>T; c.703G>A; c.796C>A; c.930G>A	6 7	p.Arg176Gly; p.Gly235Ser; p.Leu266Met

Molecular bases associated with O (null) phenotype

Differences compared to *ABO*A1.01* are given.

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	*ABO*O.01.01*	O01 (*O*^{1})	c.261delG	6	p.Thr88Profs*31
O	*ABO*O.01.02*	O02 (*O*^{1v})	c.106G>T; c.188G>A; c.189C>T; c.220C>T; c.261delG; c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	3 4 5 6 7	p.Val36Phe; p.Arg63His; p.Pro74Ser; p.Thr88Profs*31
O	*ABO*O.01.04*	O04	c.261delG; c.579T>C	6	p.Thr88Profs*31
O	*ABO*O.01.05*	O05	c.261delG; c.297A>G	6	p.Thr88Profs*31
O	*ABO*O.01.06*	O06, O30	c.261delG; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.07*	O07	c.261delG; c.297A>G; c.646T>A; c.681G>A; c.721C>T; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.09*	O09	c.261delG; c.318C>T; c.467C>T	6 7	p.Thr88Profs*31
O	*ABO*O.01.10*	O10	c.261delG; 657C>T	6 7	p.Thr88Profs*31
O	*ABO*O.01.11*	O11	c.261delG; c.297A>G; c.542G>A; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.12*	O12	c.261delG; c.297A>G; c.595C>T; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.13*	O13	c.261delG; c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.22*	O22	c.261delG c.467C>T; c.1061delC	6 7	p.Thr88Profs*31

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	*ABO*O.01.23*	O23	c.261delG; c.297A>G; c.646T>A; c.771C>T; c.829G>A; 1054C>T	6 7	p.Thr88Profs*31
O	*ABO*O.01.24*	O24	c.106G>T; c.188G>A; c.189C>T; c.261delG; c.297A>G; c.526C>G; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	3 4 6 7	p.Val36Phe; p.Arg63His; p.Thr88Profs*31
O	*ABO*O.01.25*	O25	c.261delG; c.454T>C	6 7	p.Thr88Profs*31
O	*ABO*O.01.26*	O26	c.261delG; c.768C>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.27*	O27	c.261delG; c.318C>T; c.467C>T; c.729C>T	6 7	p.Thr88Profs*31
O	*ABO*O.01.28*	O28	c.261delG; c.926A>G	6 7	p.Thr88Profs*31
O	*ABO*O.01.29*	O29	c.261delG; c.318C>T	6	p.Thr88Profs*31
O	*ABO*O.01.31*	O31	c.261delG; c.297A>G; c.529G>A; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.32*	O32	c.261delG; c.297A>G; c.538C>T; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.33*	O33	c.261delG; c.297A>G; c.498C>T; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.34*	O34	c.261delG; c.297A>G; c.351G>A; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	*ABO*O.01.35*	O35	c.106G>T; c.188G>A; c.189C>T; c.220C>T; c.261delG; c.297A>G; c.681G>A; c.771C>T; c.829G>A	3 4 5 6 7	p.Val36Phe; p.Arg63His; p.Pro74Ser; p.Thr88Profs*31
O	*ABO*O.01.36*	O36	c.106G>T; c.188G>A; c.189C>T; c.220C>T; c.261delG; c.297A>G; c.646T>A; c.681G>A; c.829G>A	3 4 5 6 7	p.Val36Phe; p.Arg63His; p.Pro74Ser; p.Thr88Profs*31
O	*ABO*O.01.39*	O39	c.220C>T; c.261delG; c.297A>G; c.681G>A; c.771C>T; c.829G>A	5 6 7	p.Pro74Ser; p.Thr88Profs*31
O	*ABO*O.01.40*	O40	c.106G>T; c.188G>A; c.189C>T; c.261delG; c.297A>G; c.646T>A; c.681G>A; c.829G>A	3 4 6 7	p.Val36Phe; p.Arg63His; p.Thr88Profs*31
O	*ABO*O.01.41*	O41	c.261delG; c.297A>G; c.526C>G; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.44*	O44	c.261delG; c.297A>G; c.646T>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.45*	O45	c.261delG; c.646T>A; c.771C>T	6 7	p.Thr88Profs*31
O	*ABO*O.01.46*	O46	c.261delG; c.646T>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.56*	O56; O70	c.261delG; c.496delA	6 7	p.Thr88Profs*31
O	*ABO*O.01.57*	O57	c.261delG; c.802G>A	6 7	p.Thr88Profs*31

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	*ABO*O.01.58*	O58	c.261delG; c.297A>G; c.646T>A; c.681G>A; c.687C>T; 771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.61*	O61	c.261delG; c.743G>C	6 7	p.Thr88Profs*31
O	*ABO*O.01.67*	O67	c.103G>A; c.106G>T; c.188G>A; c.189C>T; c.220C>T; c.261delG; c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	3 4 5 6 7	p.Gly35Arg; p.Val36Phe; p.Arg63His; p.Pro74Ser; p.Thr88Profs*31
O	*ABO*O.01.68*	O68	c.106G>T; c.188G>A; c.189C>T; c.261delG; c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	3 4 6 7	p.Val36Phe; p.Arg63His; p.Thr88Profs*31
O	*ABO*O.01.71*	O71	c.261delG; c.829G>A	6 7	p.Thr88Profs*31
O	*ABO*O.01.75*	O75	c.106G>T; c.188G>A; c.189C>T; c.220C>T; c.261delG; c.297A>G; c.542G>A; c.646T>A; c.681G>A; c.771C>T; c.829G>A	3 4 5 6 7	p.Val36Phe; p.Arg63His; p.Pro74Ser; p.Thr88Profs*31
O	*ABO*O.01.76*	O76	c.261delG; c.579T>C; c.1046_1048delAGG	6 7	p.Thr88Profs*31
O	*ABO*O.01.82*		c.190G>A; c.261delG	4 6	p.Val64Ile; p.Thr88Profs*31
O	*ABO*O.01.83*		c.106G>T; c.188G>A; c.261delG; c.297A>G	3 4 6	p.Val36Phe; p.Arg63His; p.Thr88Profs*31
O	*ABO*O.02.01*	O03 (O^2)	c.53G>T; c.220C>T; c.297A>G; c.526C>G; c.802G>A	2 5 6 7	p.Arg18Leu; p.Pro74Ser; p.Arg176Gly; p.Gly268Arg

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	*ABO*O.02.02*	O48 (*O^2-2*)	c.53G>T; c.220C>T; c.297A>G; c.526C>G; c.649C>T; c.689G>A; c.802G>A	2 5 6 7	p.Arg18Leu; p.Pro74Ser; p.Arg176Gly; p.Arg217Cys; p.Gly230Asp; p.Gly268Arg
O	*ABO*O.02.03*	O49 (*O^2-2*)	c.53G>T; c.220C>T; c.297A>G; c.526C>G; c.689G>A; c.802G>A	2 5 6 7	p.Arg18Leu; p.Pro74Ser; p.Arg176Gly; p.Gly230Asp; p.Gly268Arg
O	*ABO*O.02.04*	O50 (*O^2-4*)	c.53G>T; c.220C>T; c.297A>G; c.488C>T; c.526C>G; c.802G>A	2 5 6 7	p.Arg18Leu; p.Pro74Ser; p.Thr163Met; p.Arg176Gly; p.Gly268Arg
O	*ABO*O.03*	O08 (*O^3*)	c.467C>T; c.804dupG; c.1061delC	7	p.Pro156Leu; p.Phe269Valfs*87
O	*ABO*O.04.01*	O41 (*O^4*)	c.87_88insG	2	p.Val30Glyfs*27
O	*ABO*O.04.02*	O21 (*O^4*)	c.87_88insG; c.261delG; c.467C>T	2 6 7	p.Val30Glyfs*27
O	*ABO*O.05*	O52 (*O^5*)	c.322C>T	6	p.Gln108Ter
O	*ABO*O.06*	O53 (*O^6*)	c.542G>A	7	p.Trp181Ter
O	*ABO*O.07*	O14 (*O301*)	c.467C>T; c.893C>T	7	p.Pro156Leu; p.Ala298Val
O	*ABO*O.08*	O15 (*O302*)	c.927C>A	7	p.Tyr309Ter
O	*ABO*O.09.01*	O19 (*R102*)	c.646T>A; c.681G>A; c.771C>T; c.829G>A	7	p.Phe216Ile; p.Val277Met
O	*ABO*O.09.02*	O20 (*R103*)	c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Phe216Ile; p.Val277Met
O	*ABO*O.10*	O72	c.66_67insG	2	p.Phe23Valfs*34

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	*ABO*O.11*	O74	c.297A>G; c.505_507delCAG; c.526C>G; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	 p.Gln169del; p.Arg176Gly; p.Gly235Ser; p.Leu266Met; p.Gly268Ala
O	*ABO*O.12*	O77	c.297A>G; c.526C>G; c.563G>A; c.657C>T; c.703G>A; c.796C>A; c.803G>C; c.930G>A	6 7	 p.Arg176Gly; Arg188His; p.Gly235Ser; p.Leu266Met; p.Gly268Ala
O	*ABO*O.13*	O78	c.452T>G	7	p.Val151Gly
O	*ABO*O.14*	O79	c.635T>A	7	p.Val212Glu
O	*ABO*O.15*	O81	c.793T>C	7	p.Tyr265His
O	*ABO*O.16*		c.106G>T; c.188G>A; Deletion of exons 5-7	3 4 5-7	p.?

All alleles in which c.261delG occurs are numbered *ABO*O.01.XX*. Those *O* alleles that arise from a molecular basis other than c.261delG have been assigned independent *ABO*O.XX* numbers.