

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 A₁ and A₂. The former is more prevalent in all populations and has approximately 5 times more A epitopes per red cell. The GTA₁ is also better than GTA₂ 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:	<i>ABO</i>
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:	<i>ABO</i> * <i>A1.01</i> (shaded)

Molecular bases associated with the A₁, A₂ and weak A phenotypesReference allele *ABO*A1.01* encodes A glycosyltransferase that synthesizes A antigen.

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A ₁	<i>ABO*A1.01</i>			
A ₁	<i>ABO*A1.02</i>	c.467C>T	7	p.Pro156Leu
A ₂	<i>ABO*A2.01</i>	c.467C>T; c.1061delC	7	p.Pro156Leu; p.Pro354Argfs*23
A ₂	<i>ABO*A2.02</i>	c.1054C>T	7	p.Arg352Trp
A ₂	<i>ABO*A2.03</i>	c.1054C>G	7	p.Arg352Gly
A ₂	<i>ABO*A2.04</i>	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	<i>ABO*A2.05</i>	c.467C>T; c.1009A>G	7	p.Pro156Leu; p.Arg337Gly
A ₂	<i>ABO*A2.06</i>	c.1061delC	7	p.Pro354Argfs*23
A ₂	<i>ABO*A2.07</i>	c.539G>C	7	p.Arg180Pro
A ₂	<i>ABO*A2.08</i>	c.467C>T; c.539G>C	7	p.Pro156Leu; p.Arg180Pro
A ₂	<i>ABO*A2.09</i>	c.467C>T; c.527G>A; c.1061delC	7	p.Pro156Leu; p.Arg176His; p.Pro354Argfs*23
A ₂	<i>ABO*A2.10</i>	c.268T>C; c.467C>T	6 7	p.Trp90Arg; p.Pro156Leu
A ₂	<i>ABO*A2.11</i>	c.266C>T; c.467C>T	6 7	p.Pro89Leu; p.Pro156Leu
A ₂	<i>ABO*A2.12</i>	c.190G>A; c.527G>A; c.1061delC	4 7	p.Val64Ile; p.Arg176His; p.Pro354Argfs*23
A ₂	<i>ABO*A2.13</i>	c.467C>T; c.742C>T	7	p.Pro156Leu; p.Arg248Cys
A ₂	<i>ABO*A2.16</i>	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	<i>ABO*A2.17</i>	c.407C>T; c.467C>T	7	p.Thr136Met; p.Pro156Leu
A ₂	<i>ABO*A2.18</i>	c.467C>T; c.722G>A	7	p.Pro156Leu; p.Arg241Gln
A ₂	<i>ABO*A2.19</i>	c.467C>T; c.778G>A	7	p.Pro156Leu; p.Glu260Lys

Names for ABO (ISBT 001) blood group alleles v1.1 170123

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
A ₂	<i>ABO*A2.20</i>	c.467C>T; c.829G>A	7	p.Pro156Leu; p.Val277Met
A ₃	<i>ABO*A3.01</i>	c.871G>A	7	p.Asp291Asn
A ₃	<i>ABO*A3.02</i>	c.829G>A; c.1061delC	7	p.Val277Met; p.Pro354Argfs*23
A ₃	<i>ABO*A3.03</i>	c.838C>T	7	p.Leu280Phe
A ₃	<i>ABO*A3.04</i>	c.467C>T; c.539G>A; c.1061delC	7	p.Arg180His; p.Pro156Leu; p.Pro354Argfs*23
A ₃	<i>ABO*A3.05</i>	c.820G>A	7	p.Val274Met
A ₃	<i>ABO*A3.06</i>	c.467C>T; c.820G>A	7	p.Pro156Leu; p.Val274Met
A ₃	<i>ABO*A3.07</i>	c.467C>T; c.745C>T	7	p.Pro156Leu; p.Arg249Trp
A _{weak}	<i>ABO*AW.01</i>	c.407C>T; c.467C>T; c.1061delC	7	p.Thr136Met; p.Pro156Leu; p.Pro354Argfs*23
A _{weak}	<i>ABO*AW.02</i>	c.350G>C; c.467C>T; c.1061delC	6 7	p.Gly117Ala; p.Pro156Leu; p.Pro354Argfs*23
A _{weak}	<i>ABO*AW.03</i>	c.203G>C; c.467C>T; c.1061delC	4 7	p.Arg68Thr; p.Pro156Leu; p.Pro354Argfs*23
A _{weak}	<i>ABO*AW.04</i>	c.721C>T	7	p.Arg241Trp
A _{weak}	<i>ABO*AW.05</i>	c.965A>G	7	p.Glu322Gly
A _{weak}	<i>ABO*AW.06</i>	c.502C>G	7	p.Arg168Gly
A _{weak}	<i>ABO*AW.07</i>	c.467C>T; c.592C>T; c.1061delC	7	p.Pro156Leu; p.Arg198Trp; p.Pro354Argfs*23
A _{weak}	<i>ABO*AW.08</i>	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}	<i>ABO*AW.09</i>	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}	<i>ABO*AW.10</i>	c.784G>A	7	p.Asp262Asn
A _{weak}	<i>ABO*AW.11</i>	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}	<i>ABO*AW.31.01</i>	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}	<i>ABO*AW31.02-05</i>	c.646T>A; c.681G>A; c.771C>T; c.829G>A	7	p.Phe216Ile; p.Val277Met
A _x /A _{weak}	<i>ABO*AW.32</i>	c.996G>A	7	p.Trp332Ter
A _x /A _{weak}	<i>ABO*AW.33</i>	c.467C>T; c.543G>T	7	p.Pro156Leu; p.Trp181Cys
A _x /A _{weak}	<i>ABO*AW.34</i>	c.467C>T; c.829G>A; c.1009A>G	7	p.Pro156Leu; p.Val277Met; p.Arg337Gly
A _x /A _{weak}	<i>ABO*AW.35</i>	c.467C>T; c.860C>T	7	p.Pro156Leu; p.Ala287Val
A _x /A _{weak}	<i>ABO*AW.36</i>	c.607G>A	7	p.Glu203Lys
A _x /A _{weak}	<i>ABO*AW.37</i>	c.940A>G	7	p.Lys314Glu
A _x /A _{weak}	<i>ABO*AW.38</i>	c.426G>C	7	p.Met142Ile
A _x /A _{weak}	<i>ABO*AW.39</i>	c.385T>C	7	p.Phe129Leu
A _x /A _{weak}	<i>ABO*AW.40</i>	c.499G>T	7	p.Gly167Cys
A _x /A _{weak}	<i>ABO*AW.41</i>	c.370A>G	6	p.Lys124Glu
A _x /A _{weak}	<i>ABO*AW.42</i>	c.467C>T; c.905A>G	7	p.Pro156Leu; p.Asp302Gly
A _x /A _{weak}	<i>ABO*AW.43</i>	c.467C>T; c.721C>T	7	p.Pro156Leu; p.Arg241Trp
A _{finn} /A _{weak}	<i>ABO*AW.44</i>	c.374+4A>G	Intron 6	Altered splicing
A _{bantu} /A _{weak}	<i>ABO*AW.45</i>	c.203+1delG; c.467C>T; c.1061delC	Intron 4 7	Altered splicing
A _m	<i>ABO*AM.01</i>	c.467C>T; c.761C>T	7	p.Pro156Leu; p.Ala254Val
A _m	<i>ABO*AM.02</i>	c.664G>A	7	p.Val222Met
A _{el}	<i>ABO*AEL.01</i>	c.804dupG	7	p.Phe269Valfs*124
A _{el}	<i>ABO*AEL.02</i>	c.467C>T; c.646T>A; c.681G>A	7	p.Pro156Leu; p.Phe216Ile
A _{el}	<i>ABO*AEL.03</i>	c.804delG	7	p.Phe269Serfs*20
A _{el}	<i>ABO*AEL.04</i>	c.374+5G>A	Intron 6	Altered splicing
A _{el}	<i>ABO*AEL.05</i>	c.467C>T; c.767T>C	7	p.Pro156Leu; p.Ile256Thr
A _{el}	<i>ABO*AEL.06</i>	c.425T>C; c.467C>T	7	p.Met142Thr; p.Pro156Leu
A _{el}	<i>ABO*AEL.07</i>	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}	<i>ABO*AEL.08</i>	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 A₂ 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 A₂.

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	<i>ABO*B.01</i>	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	<i>ABO*B.02</i>	c.892G>T	7	p.Ala298Ser
B	<i>ABO*B.03</i>	c.559C>T	7	p.Arg187Cys
B ₃	<i>ABO*B3.01</i>	c.1054C>T	7	p.Arg352Trp
B ₃	<i>ABO*B3.02</i>	c.646T>A	7	p.Phe216Ile
B ₃	<i>ABO*B3.03</i>	c.155+5G>A	Intron 3	Altered splicing
B ₃	<i>ABO*B3.04</i>	c.247G>T	6	p.Asp83Tyr
B ₃	<i>ABO*B3.05</i>	c.425T>C	7	p.Met142Thr
B ₃	<i>ABO*B3.06</i>	c.547G>A	7	p.Asp183Asn
B ₃	<i>ABO*B3.07</i>	c.410C>T	7	p.Ala137Val
B ₃	<i>ABO*B3.08</i>	c.938A>C	7	p.His313Pro
B _x /B _{weak}	<i>ABO*BW.01</i>	c.871G>A	7	p.Asp291Asn
B _{weak}	<i>ABO*BW.02</i>	c.873C>G	7	p.Asp291Glu
B _{weak}	<i>ABO*BW.03</i>	c.721C>T	7	p.Arg241Trp
B _{weak}	<i>ABO*BW.04</i>	c.548A>G	7	p.Asp183Gly
B _{weak}	<i>ABO*BW.05</i>	c.539G>A	7	p.Arg180His
B _{weak}	<i>ABO*BW.06</i>	c.1036A>G	7	p.Lys346Glu
B _{weak}	<i>ABO*BW.07</i>	c.1055G>A	7	p.Arg352Gln
B _{weak}	<i>ABO*BW.08</i>	c.863T>G	7	p.Met288Arg
B _{weak}	<i>ABO*BW.09</i>	c.1037A>T	7	p.Lys346Met
B _{weak}	<i>ABO*BW.10</i>	c.556A>G	7	p.Met186Val
B _{weak}	<i>ABO*BW.11</i>	c.695T>C	7	p.Leu232Pro
B _{weak}	<i>ABO*BW.12</i>	c.278C>T	6	p.Pro93Leu

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B _{weak}	<i>ABO*BW.14</i>	c.523G>A	7	p.Val175Met
B _{weak}	<i>ABO*BW.15</i>	c.565A>G	7	p.Met189Val
B _{weak}	<i>ABO*BW.16</i>	c.575T>C	7	p.Ile192Thr
B _{weak}	<i>ABO*BW.17</i>	c.784G>A	7	p.Asp262Asn
B _{weak}	<i>ABO*BW.18</i>	c.802G>A	7	p.Gly268Thr
B _{weak}	<i>ABO*BW.19</i>	c.646T>A; c.681G>A	7	p.Phe216Ile
B _{weak}	<i>ABO*BW.20</i>	c.815_816insG	7	p.Ser273Valfs*?
B _{weak}	<i>ABO*BW.21</i>	c.688G>C	7	p.Gly230Arg
B _{weak}	<i>ABO*BW.22</i>	c.503G>T	7	p.Arg168Leu
B _{weak}	<i>ABO*BW.23</i>	c.743G>C	7	p.Arg248Pro
B _{weak}	<i>ABO*BW.24</i>	c.558G>T	7	p.Met186Ile
B _{weak}	<i>ABO*BW.25</i>	c.103G>A; c.619C>G	3 7	p.Gly35Arg; p.Leu207Val
B _{weak}	<i>ABO*BW.26</i>	c.53G>T	2	p.Arg18Leu
B _{weak}	<i>ABO*BW.27</i>	c.905A>G	7	p.Asp302Gly
B _{weak}	<i>ABO*BW.28</i>	c.541T>C	7	p.Trp181Arg
B _{weak}	<i>ABO*BW.29</i>	c.588C>G	7	p.Cys196Trp
B _{weak}	<i>ABO*BW.30</i>	c.976G>T	7	p.Asp326Tyr
B _{weak}	<i>ABO*BW.31</i>	c.900G>C	7	p.Trp300Cys
B _{weak}	<i>ABO*BW.32</i>	c.808T>A	7	p.Phe270Ile
B _{weak}	<i>ABO*BW.33</i>	c.550G>A	7	p.Val184Met
B _{weak}	<i>ABO*BW.34</i>	c.889G>A	7	p.Glu297Lys
B _{el}	<i>ABO*BEL.01</i>	c.641T>G	7	p.Met214Arg
B _{el}	<i>ABO*BEL.02</i>	c.669G>T	7	p.Glu223Asp
B _{el}	<i>ABO*BEL.03</i>	c.502C>T	7	p.Arg168Trp
B _{el}	<i>ABO*BEL.05</i>	c.952G>A	7	p.Val318Met
B _{el}	<i>ABO*BEL.04</i>	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) phenotypesDifferences compared to *ABO*AI.01* are given.

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
cisAB	<i>ABO*cisAB.01</i>	c.467C>T; c.803G>C	7	p.Pro156Leu; p.Gly268Ala
cisAB	<i>ABO*cisAB.02</i>	c.526C>G; c.657C>T; c.703G>A; c.803G>C	7	p.Arg176Gly; p.Gly235Ser; p.Gly268Ala
cisAB	<i>ABO*cisAB.03</i>	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	<i>ABO*cisAB.04</i>	c.467C>T; c.796C>A	7	p.Pro156Leu; p.Leu266Met
cisAB	<i>ABO*cisAB.05</i>	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	<i>ABO*cisAB.06</i>	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)	<i>ABO*BA.01</i>	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)	<i>ABO*BA.02</i>	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)	<i>ABO*BA.03</i>	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)	<i>ABO*BA.04</i>	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

Names for ABO (ISBT 001) blood group alleles v1.1 170123

Phenotype	Allele name	Nucleotide change	Exon	Predicted amino acid change
B(A)	<i>ABO*BA.05</i>	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)	<i>ABO*BA.06</i>	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) phenotypeDifferences compared to *ABO*A1.01* are given.

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	<i>ABO*O.01.01</i>	O01 (O ¹)	c.261delG	6	p.Thr88Profs*31
O	<i>ABO*O.01.02</i>	O02 (O ^{1'})	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	<i>ABO*O.01.04</i>	O04	c.261delG; c.579T>C	6	p.Thr88Profs*31
O	<i>ABO*O.01.05</i>	O05	c.261delG; c.297A>G	6	p.Thr88Profs*31
O	<i>ABO*O.01.06</i>	O06, O30	c.261delG; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.07</i>	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	<i>ABO*O.01.09</i>	O09	c.261delG; c.318C>T; c.467C>T	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.10</i>	O10	c.261delG; 657C>T	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.11</i>	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	<i>ABO*O.01.12</i>	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	<i>ABO*O.01.13</i>	O13	c.261delG; c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.22</i>	O22	c.261delG c.467C>T; c.1061delC	6 7	p.Thr88Profs*31

Names for ABO (ISBT 001) blood group alleles v1.1 170123

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	<i>ABO</i> *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	<i>ABO</i> *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	<i>ABO</i> *O.01.25	O25	c.261delG; c.454T>C	6 7	p.Thr88Profs*31
O	<i>ABO</i> *O.01.26	O26	c.261delG; c.768C>A	6 7	p.Thr88Profs*31
O	<i>ABO</i> *O.01.27	O27	c.261delG; c.318C>T; c.467C>T; c.729C>T	6 7	p.Thr88Profs*31
O	<i>ABO</i> *O.01.28	O28	c.261delG; c.926A>G	6 7	p.Thr88Profs*31
O	<i>ABO</i> *O.01.29	O29	c.261delG; c.318C>T	6	p.Thr88Profs*31
O	<i>ABO</i> *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	<i>ABO</i> *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	<i>ABO</i> *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	<i>ABO</i> *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	<i>ABO*O.01.35</i>	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	<i>ABO*O.01.36</i>	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	<i>ABO*O.01.39</i>	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	<i>ABO*O.01.40</i>	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	<i>ABO*O.01.41</i>	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	<i>ABO*O.01.44</i>	O44	c.261delG; c.297A>G; c.646T>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.45</i>	O45	c.261delG; c.646T>A; c.771C>T	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.46</i>	O46	c.261delG; c.646T>A; c.771C>T; c.829G>A	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.56</i>	O56; O70	c.261delG; c.496delA	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.57</i>	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	<i>ABO*O.01.58</i>	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	<i>ABO*O.01.61</i>	O61	c.261delG; c.743G>C	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.67</i>	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	<i>ABO*O.01.68</i>	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	<i>ABO*O.01.71</i>	O71	c.261delG; c.829G>A	6 7	p.Thr88Profs*31
O	<i>ABO*O.01.75</i>	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	<i>ABO*O.01.76</i>	O76	c.261delG; c.579T>C; c.1046_1048delAGG	6 7	p.Thr88Profs*31
O	<i>ABO*O.02.01</i>	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
O	<i>ABO*O.02.02</i>	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

Names for ABO (ISBT 001) blood group alleles v1.1 170123

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	<i>ABO*O.02.03</i>	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	<i>ABO*O.02.04</i>	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	<i>ABO*O.03</i>	O08 (O ³)	c.467C>T; c.804dupG; c.1061delC	7	p.Pro156Leu; p.Phe269Valfs*87
O	<i>ABO*O.04.01</i>	O41 (O ⁴)	c.87_88insG	2	p.Val30Glyfs*27
O	<i>ABO*O.04.02</i>	O21 (O ⁴)	c.87_88insG; c.261delG; c.467C>T	2 6 7	p.Val30Glyfs*27
O	<i>ABO*O.05</i>	O52 (O ⁵)	c.322C>T	6	p.Gln108Ter
O	<i>ABO*O.06</i>	O53 (O ⁶)	c.542G>A	7	p.Trp181Ter
O	<i>ABO*O.07</i>	O14 (O301)	c.467C>T; c.893C>T	7	p.Pro156Leu; p.Ala298Val
O	<i>ABO*O.08</i>	O15 (O302)	c.927C>A	7	p.Tyr309Ter
O	<i>ABO*O.09.01</i>	O19 (R102)	c.646T>A; c.681G>A; c.771C>T; c.829G>A	7	p.Phe216Ile; p.Val277Met
O	<i>ABO*O.09.02</i>	O20 (R103)	c.297A>G; c.646T>A; c.681G>A; c.771C>T; c.829G>A	6 7	p.Phe216Ile; p.Val277Met
O	<i>ABO*O.10</i>	O72	c.66_67insG	2	p.Phe23Valfs*34
O	<i>ABO*O.11</i>	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

Phenotype	Allele name	dbRBC (alt.) name	Nucleotide change	Exon	Predicted amino acid change
O	<i>ABO</i> * <i>O.12</i>	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	<i>ABO</i> * <i>O.13</i>	O78	c.452T>G	7	p.Val151Gly
O	<i>ABO</i> * <i>O.14</i>	O79	c.635T>A	7	p.Val212Glu
O	<i>ABO</i> * <i>O.15</i>	O81	c.793T>C	7	p.Tyr265His

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.