Instructions for Authors | New Blood Group Allele Reports

A. For describing an allele that has not been described in a peer-reviewed publication and for which an allele name or provisional allele name has been assigned by the ISBT Working Party on Blood Group Allele Terminology (http://www.isbtweb.org/working-parties/red-cell-immunogenetics-and-blood-group-terminology/blood-group-terminology/blood-group-allele-terminology/)

B. Preparation

1. Title: Allele Name (Allele Detail)

   ex. *RHCE*01.01 (RHCE*ce48C)*

2. Author Names (initials and last name of each [no degrees, ALL CAPS])

C. Text

1. Case Report
   i. Clinical and immunohematologic data
   ii. Race/ethnicity and country of origin of proband, if known
2. Materials and Methods

   Description of appropriate controls, procedures, methods, equipment, reagents, etc. Equipment and reagents should be identified in parentheses by model or lot and manufacturer's name, city, and state. Do not use patient names or hospital numbers.
3. Results

   Complete the Table Below:

Phenotype	Allele Name	Nucleotide(s)	Exon(s)	Amino Acid(s)	Allele Detail	References
e weak	*RHCE*01.01*	48G>C	1	Trp16Cys	*RHCE*ce48C*	1

   Column 1: Describe the immunohematologic phenotype (ex. weak or negative for an antigen).

   Column 2: List the allele name or provisional allele name.

   Column 3: List the nucleotide number and the change, using the reference sequence (see ISBT Blood Group Allele Terminology Pages for reference sequence ID).

   Column 4: List the exons where changes in nucleotide sequence were detected.

   Column 5: List the amino acids that are predicted to be changed, using the three-letter amino acid code.

   Column 6: List the non-consensus nucleotides after the gene name and asterisk.

   Column 7: If this allele was described in a meeting abstract, please assign a reference number and list in the References section.
4. Additional Information
   i. Indicate whether the variant is listed in the dbSNP database (http://www.ncbi.nlm.nih.gov/snp/); if so, provide rs number and any population frequency information, if available.
   ii. Indicate whether the authors performed any population screening and, if so, what the allele and genotype frequencies were.
   iii. Indicate whether the authors developed a genotyping assay to screen for this variant and, if so, describe in detail here.
   iv. Indicate whether this variant was found associated with other variants already reported (ex. *RHCE*ce48C,1025T* is often linked to *RHD*DIVa-2*).

D. Acknowledgments

E. References

F. Author Information

List first name, middle initial, last name, highest degree, position held, institution and department, and complete address (including ZIP code) for all authors. List country when applicable.