## ORIGINAL PAPER

C. A. Garcia · J. Robinson · L. A. Guethlein ·
P. Parham · J. A. Madrigal · S. G. E. Marsh

# Human KIR sequences 2003

**Abstract** We have compiled the nucleotide sequences and their amino acid translations from a total of 89 Killer Immunoglobulin-like Receptor (KIR) alleles, derived from 17 different KIR genes. The alignments use the KIR3DL2*001 allele as a reference sequence. Each of the KIR sequences included in these alignments has been checked and where discrepancies have arisen between reported sequences, the original authors have been contacted where possible, and necessary amendments to published sequences have been incorporated into this alignment. Future sequencing may identify errors in this list and we would welcome any evidence that helps to maintain the accuracy of this compilation.

The sequences included in this compilation are taken from the publications listed in the Killer Immunoglobulin-like Receptor (KIR) Nomenclature Committee Report (Marsh et al. 2003). The KIR Nomenclature Committee has officially assigned the names to all the sequences included in these sequence alignments with the exception of two. Details of the officially named sequences including accession numbers and publication details can be found in the accompanying Nomenclature Report (Marsh et al. 2003). The two sequences listed under the names KIR2DL5(KIR2DLXa) (AF271607) and KIR2DL5(KIR2DLXb) (AF271608) have not yet been assigned official names as it is unclear whether they represent alleles of the KIR2DL5A or KIR2DL5B genes.

Each of the KIR sequences included in these alignments has been checked and where discrepancies have arisen between reported sequences, the original authors have been contacted where possible, and necessary amendments to published sequences have been incorporated into this alignment. Future sequencing may identify errors in this list and we would welcome any evidence that helps to maintain the accuracy of this compilation.

In the nucleotide (Fig. 1) and amino acid (Fig. 2) sequence alignments, a total of 89 sequences comprising 14 KIR genes and three pseudogenes have been aligned to the KIR3DL2*001 sequence. The KIR3DL2*001 sequence was used as a reference sequence as it provided a sufficiently long reference sequence which also possessed a high level of nucleotide identity and structural homology to the majority of the other KIR genes. The KIR sequences were retrieved from the EMBL Nucleotide Sequence Database or GenBank by means of the accession numbers given in the KIR Nomenclature Report (Marsh et al. 2003). Criteria used for the grouping of these sequences into genes is based on the number of immunoglobulin domains, the length of the cytoplasmic tail and sequence homology as proposed in previous publications (Long et al. 1996; Steffens et al. 1998; Vilches and Parham 2002). The sequence comparison was done by using a combination of Clustal (Thompson et al. 1994) and manual analysis after which sequence alignments were subjected to a reformatting tool available in house, which allowed us to show identity to a reference sequence and translate the nucleotide sequences into their corresponding protein sequences (Fig. 2).

In the alignments, exon intron boundaries and protein domains have been marked with a pipe (|), asterisks (*) indicate positions where sequence is unavailable, periods (.) indicate an insertion or deletion. Identity to the reference sequence KIR3DL2*001 is shown by a hyphen

C. A. Garcia · J. Robinson · J. A. Madrigal · S. G. E. Marsh (✉)
Anthony Nolan Research Institute,
Royal Free Hospital,
Pond Street, London, NW3 2QG, UK
e-mail: marsh@ebi.ac.uk
Tel.: +44-20-72848321
Fax: +44-20-72848331

C. A. Garcia · J. A. Madrigal · S. G. E. Marsh
Department of Haematology,
Royal Free Hospital,
Pond Street, London, NW3 2QG, UK

L. A. Guethlein · P. Parham
Department of Structural Biology
and Microbiology & Immunology,
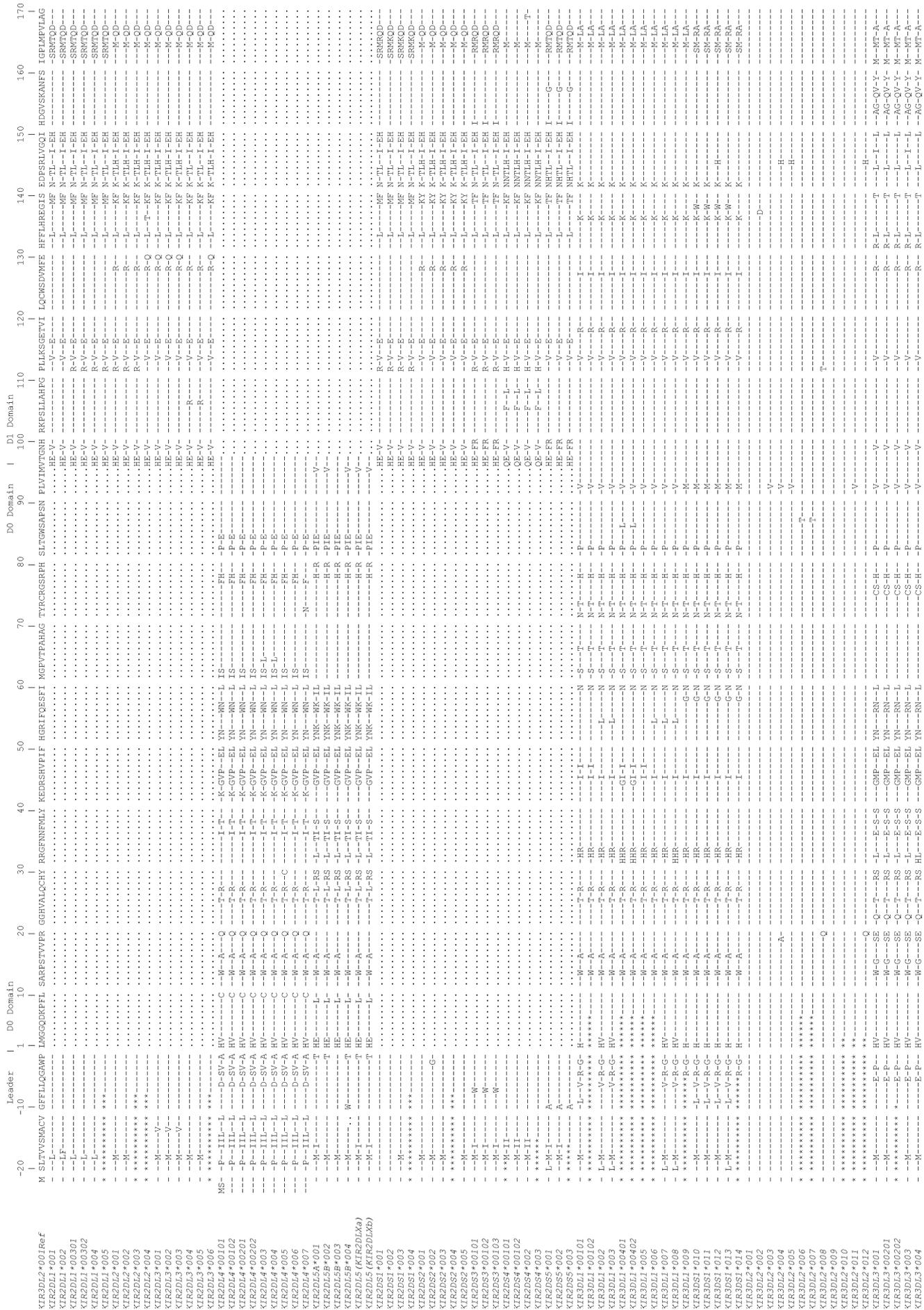Stanford University,
California, USA

**Fig. 1** Alignment of KIR nucleotide sequences

**Fig. 1** (continued)

**Fig. 1** (continued)

**Fig. 1** (continued)

**Fig. 1** (continued)

Exon 5 | Exon 6

**Fig. 1** (continued)

**Fig. 1** (continued)

**Fig. 1** (continued)

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**Fig. 1** (continued)

**Fig. 2** Alignment of KIR amino acid sequences

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                     D1 Domain                                                    D2 Domain            D2 Domain
           180        190        200        210        220        230        240        250        260        270        280        290        300
           |          |          |          |          |          |          |          |          |          |          |          |          |
                    TYRCYGSVPH SPYQLSAPSD PLDIVITGLY EKPSLSAQPG PTVQAGENVT LSCSSWSSYD IYHLSREGEA HERRLRAVPK VNRTFQADFP LGPATHGGTY RCFGSFRALP CWNSNSSDPL LVSVTGNPSS

                                               Stem                  Transmembrane              Cytoplasmic Domain
           310        320        330        340        350        360
           |          |          |          |          |          |
                    SWPSPTEPSS KSGICRHLHV LIGTSVVIFL FILLLFFLLY RWCSNKKNAA VMDQEPAGDR
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KIR2DL2*001Ref
KIR2DL1*001
KIR2DL1*002
KIR2DL1*00301
KIR2DL1*00302
KIR2DL1*004
KIR2DL1*005
KIR2DL2*001
KIR2DL2*002
KIR2DL2*003
KIR2DL2*004
KIR2DL3*001
KIR2DL3*002
KIR2DL3*003
KIR2DL3*004
KIR2DL3*005
KIR2DL3*006
KIR2DL4*00101
KIR2DL4*00102
KIR2DL4*00201
KIR2DL4*00202
KIR2DL4*003
KIR2DL4*004
KIR2DL4*005
KIR2DL4*006
KIR2DL4*007
KIR2DL5A*001
KIR2DL5B*001
KIR2DL5B*002
KIR2DL5B*003
KIR2DL5B*004
KIR2DL5 (KIR2DLXa)
KIR2DL5 (KIR2DLXb)
KIR2DS1*001
KIR2DS1*002
KIR2DS1*003
KIR2DS1*004
KIR2DS2*001
KIR2DS2*002
KIR2DS2*003
KIR2DS2*004
KIR2DS2*005
KIR2DS3*00101
KIR2DS3*00102
KIR2DS3*00103
KIR2DS4*00101
KIR2DS4*00102
KIR2DS4*002
KIR2DS4*003
KIR2DS5*001
KIR2DS5*002
KIR2DS5*003
KIR3DL1*00101
KIR3DL1*00102
KIR3DL1*002
KIR3DL1*003
KIR3DL1*00401
KIR3DL1*00402
KIR3DL1*005
KIR3DL1*006
KIR3DL1*007
KIR3DL1*008
KIR3DL1*009
KIR3DS1*010
KIR3DL1*011
KIR3DS1*012
KIR3DL2*013
KIR3DS1*014
KIR3DL2*001
KIR3DL2*002
KIR3DL2*003
KIR3DL2*004
KIR3DL2*005
KIR3DL2*006
KIR3DL2*007
KIR3DL2*008
KIR3DL2*009
KIR3DL2*010
KIR3DL2*011
KIR3DL2*012
KIR3DL3*001
KIR3DL3*00201
KIR3DL3*00202
KIR3DL3*003
KIR3DL3*004

(-). In the amino acid alignment, stop codons are indicated by an X. Minimum gaps in the sequence, indicated by a period (.), have been inserted to maintain the alignment between alleles of differing length, in such a way as to maintain the reading frame. The pseudo-exon 3 sequences for type I KIR2Ds have been included in the nucleotide alignment where available. The nucleotides are numbered starting at 1 for the first nucleotide of the codon for the initiation methionine. The numbering of the codons of the mature protein, after cleavage of the signal sequence, begins at +1, while the signal sequence is numbered backwards from −1. These alignments include KIR genes and alleles for which complete cDNA sequences or full genomic sequences are available, alternative splice variants escape the scope of this publication and partial cDNA sequences are not being included until further information for them is made available.

These sequences are also available from the IPD/KIR Database, http://www.ebi.ac.uk/ipd/kir. The database provides an online repository for the KIR sequences officially named by the KIR Nomenclature Committee. The IPD/KIR Database provides online versions of the sequence alignments and the nomenclature reports. In time it is envisaged that the website will also provide tools for the submission of new and confirmatory KIR sequences to the KIR Nomenclature Committee. The IPD/KIR Database is part of the Immuno Polymorphism Database (IPD), which provides a suite of tools, and databases for the study of polymorphisms in the immune system.

## References

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**Fig. 2** (continued)