TOOLS BIOINFORMATICI E RISORSE WEB IN ISTOCOMPATIBILITA'
Ospedale Maggiore Policlinico, Via F. Sforza 35
Milano, 17 Settembre 2018

IMGT/HLA<IPD<EMBL-EBI

Marco Andreani

Laboratorio d'Immunogenetica dei Trapianti - Polo di Ricerca di San Paolo
Dipartimento di Oncoematologia e Terapia Cellulare e Genica
IRCCS Ospedale Pediatrico Bambino Gesù

Bambino Gesù
OSPEDALE PEDIATRICO

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IMGT/HLA < IPD < EMBL-EBI

https://www.ebi.ac.uk/ipd/imgt/hla/ ▾ Traduci questa pagina

The IPD-**IMGT**/**HLA** Database provides a specialist database for sequences of the human major histocompatibility complex (MHC) and includes the official ...

Alleles

The IPD-IMGT/HLA Database allows you to retrieve ...

Releases

The IPD-IMGT/HLA Database provides details of the publicly ...

Align

Help with the Sequence Alignment Tool. Specific sequences are ...

Blast

The EBI provide the only BLAST libraries to use the IPD-IMGT ...

Downloads < IMGT/HLA < IPD ...

The IPD-IMGT/HLA Database provides an FTP site for the ...

Submission tool < IMGT/HLA ...

The IPD-IMGT/HLA Database Submission Tool allows direct ...

Altri risultati in ebi.ac.uk »

HLA Dictionary < IMGT/HLA < IPD < EMBL-EBI

https://www.ebi.ac.uk/cgi-bin/imgt/hla/get_dictionary.cgi ▾ Traduci questa pagina

Further Information. For more information about the database, queries (including website) or to subscribe to the IPD mailing lists please contact IPD Support.

HLA Alleles - HLA Nomenclature @ hla.alleles.org

hla.alleles.org/alleles/index.html ▾ Traduci questa pagina

There are currently 18,955 HLA and related alleles described by the HLA nomenclature and included in the IPD-**IMGT**/**HLA** Database. It is now established ...

Overview | IMGT/HLA | KIR | MHC | NHKIR | HPA | ESTDAB | Contact | Support

Welcome to IPD-IMGT/HLA

Release 3.33.0, 2018-07-11

The IPD-IMGT/HLA Database provides a specialist database for sequences of the human major histocompatibility complex (MHC) and includes the official sequences named by the WHO Nomenclature Committee For Factors of the HLA System. The IPD-IMGT/HLA Database is part of the international ImMunoGeneTics project (IMGT).

The database uses the 2010 naming convention for HLA alleles in all tools herein. To aid in the adoption of the new nomenclature, all search tools can be used with both the current and pre-2010 allele designations. The pre-2010 nomenclature designations are only used where older reports or outputs have been made available for download.

Latest Developments

Recent developments of the IPD database include;

- Online search for SBT - Ambiguous Allele
- Allele reports show source alignments
- HLA-DPB1 T-Cell Epitope Algorithm
- What's new in the latest release

Latest Publications

- Robinson J, Halliwell JA, Hayhurst JH, Flicek P, Parham P, Marsh SGE
  The IPD and IPD-IMGT/HLA Database: allele variant databases
  Nucleic Acids Research (2015) **43**:D423-431
- For further IPD publications, please see our citations page.

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Strumento utile

- Nomenclatura
- Sequenze
- Differenze DPB1
- Alloreattività NK
- B content
- **…….e tanto altro……!**

Immuno Polymorphism Database

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Welcome to IPD

Release 2.0.0, June 2018

IPD was developed in 2003 to provide a centralised system for the study of polymorphism in genes of the immune system. The IPD project was established by the HLA Informatics Group of the Anthony Nolan Research Institute in close collaboration with the European Bioinformatics Institute.

IPD Developers

Development of the IPD Database has been undertaken by the following individuals:

Anthony Nolan Research Institute

- Steven GE Marsh

Latest publications

Please cite the IPD-MHC Database whenever you publish your sequences. For further publications, please see our citations page.

- Robinson J, Halliwell JA, McWilliam H, Lopez R, Marsh SGE

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- Giuseppe Maccari

European Bioinformatics Institute

- Paul Flicek

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- Robinson J, Halliwell JA, McWilliam H, Lopez R, Marsh SGE
  IPD - the Immuno Polymorphism Database
  Nucleic Acids Research (2013) **41**:*D1234-40*
- Robinson J, Halliwell JA, McWilliam H, Lopez R, Parham P, Marsh SGE
  The IMGT/HLA Database
  Nucleic Acids Research (2013) **41**:D1222-7

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IPD—the Immuno Polymorphism Database

James Robinson, Jason A. Halliwell, Hamish McWilliam, Rodrigo Lopez, Steven G. E. Marsh

Nucleic Acids Research, Volume 41, Issue D1, 1 January 2013, Pages D1234–D1240, https://doi.org/10.1093/nar/gks1140
Published: 23 November 2012 **Article history** ▾

Abstract

The Immuno Polymorphism Database (IPD), http://www.ebi.ac.uk/ipd/ is a set of specialist databases related to the study of polymorphic genes in the immune system. The IPD project works with specialist groups or nomenclature committees who provide and curate individual sections before they are submitted to IPD for online publication. The IPD project stores all the data in a set of related databases. IPD currently consists of four databases: IPD-KIR, contains the allelic sequences of killer-cell immunoglobulin-like receptors, IPD-MHC, a database of sequences of the major histocompatibility complex of different species; IPD-HPA, alloantigens expressed only on platelets; and IPD-ESTDAB, which provides access to the European Searchable Tumour Cell-Line Database, a cell bank of immunologically characterized melanoma cell lines. The data is currently available online from the website and FTP directory. This article describes the latest updates and additional tools added to the IPD project.

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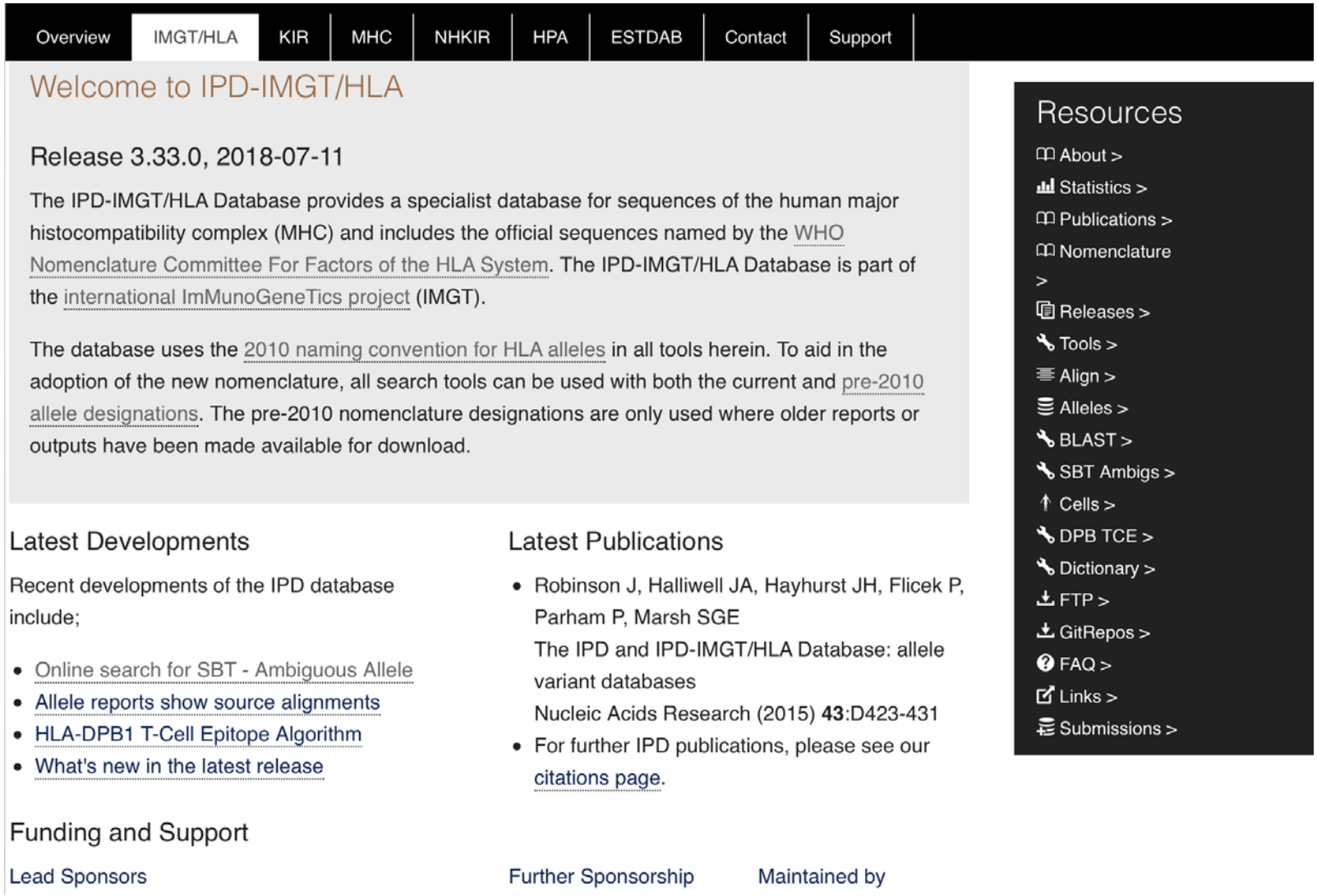
The IMGT/HLA database

James Robinson, Jason A. Halliwell, Hamish McWilliam, Rodrigo Lopez, Peter Parham, Steven G. E. Marsh

Nucleic Acids Research, Volume 41, Issue D1, 1 January 2013, Pages D1222–D1227,
https://doi.org/10.1093/nar/gks949
Published: 17 October 2012 **Article history** ▾

Abstract

It is 14 years since the IMGT/HLA database was first released, providing the HLA community with a searchable repository of highly curated HLA sequences. The HLA complex is located within the 6p21.3 region of human chromosome 6 and contains more than 220 genes of diverse function. Of these, 21 genes encode proteins of the immune system that are highly polymorphic. The naming of these HLA genes and alleles and their quality control is the responsibility of the World Health Organization Nomenclature Committee for Factors of the HLA System. Through the work of the HLA Informatics Group and in collaboration with the European Bioinformatics Institute, we are able to provide public access to these data through the website http://www.ebi.ac.uk/imgt/hla/. Regular updates to the website ensure that new and confirmatory sequences are dispersed to the HLA community and the wider research and clinical communities. This article describes the latest updates and additional tools added to the IMGT/HLA project.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The database uses the 2010 naming convention for HLA alleles in all tools herein. To aid in the adoption of the new nomenclature, all search tools can be used with both the current and pre-2010 allele designations. The pre-2010 nomenclature designations are only used where older reports or outputs have been made available for download.
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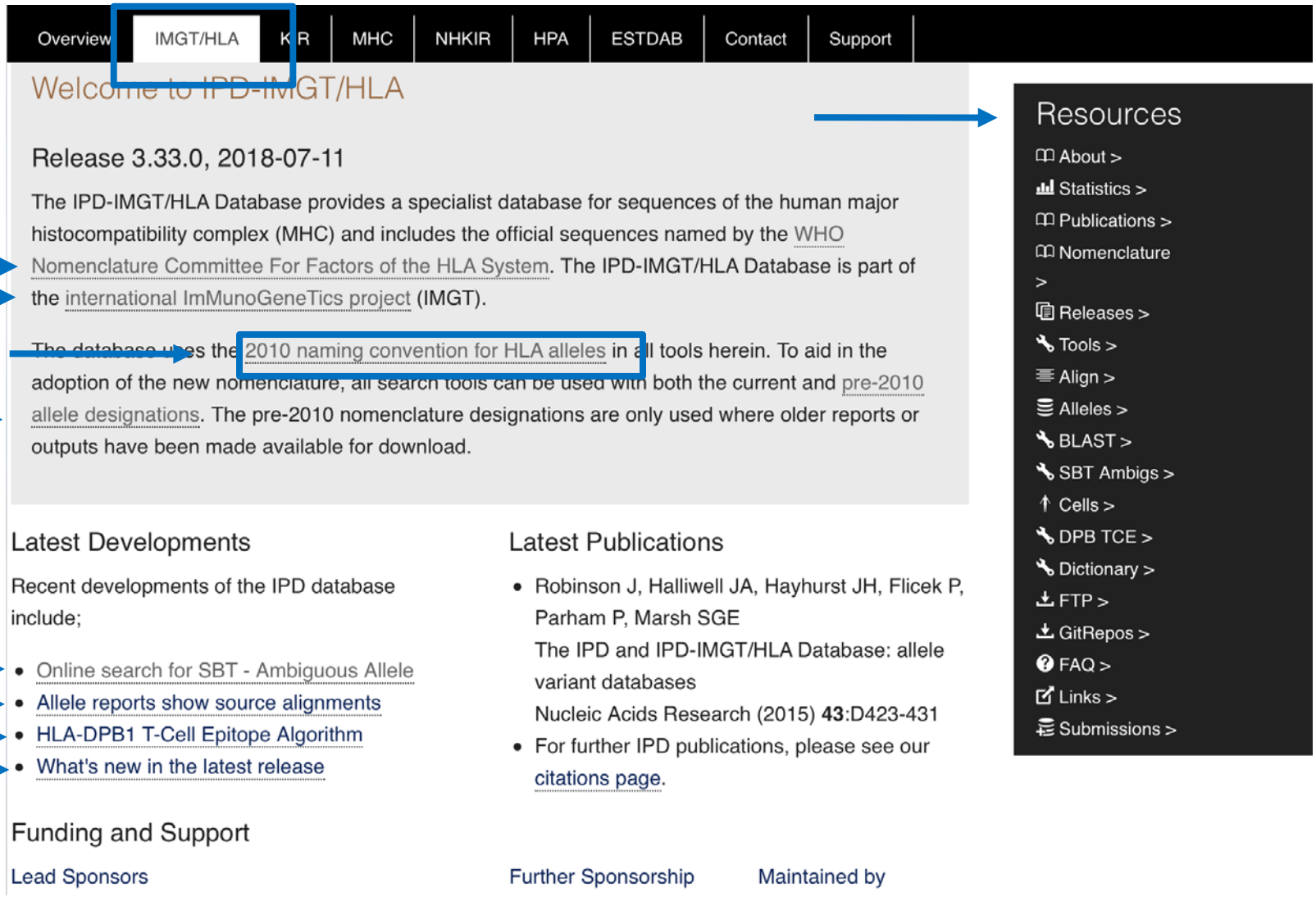
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Nomenclature for Factors of the HLA System

Nomenclature of HLA Alleles

Early in their study, it was recognised that the genes encoding the HLA molecules were highly polymorphic and that there was a need for a systematic nomenclature. The HLA complex is located within the 6p21.3 region on the short arm of human chromosome 6 and contains more than 220 genes of diverse function. Many of the genes encode the proteins of the immune system. The naming of new HLA genes, allele sequences, and their quality control is the responsibility of the WHO Nomenclature Committee for Factors of the HLA System. This commitee first met in 1968 and laid down the criteria for successive meetings. The committee meets regularly to discuss issues of nomenclature and has published 19 major reports documenting the HLA antigens and, more recently, the genes and alleles. The standardisation of HLA antigenic specifications has been controlled by the exchange of typing reagents and cells in the International Histocompatibility Workshops.

- How an allele is named
- HLA Nomenclature Reports
- HLA Nomenclature Updates
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- HLA Workshops

- Sequence alignments and files
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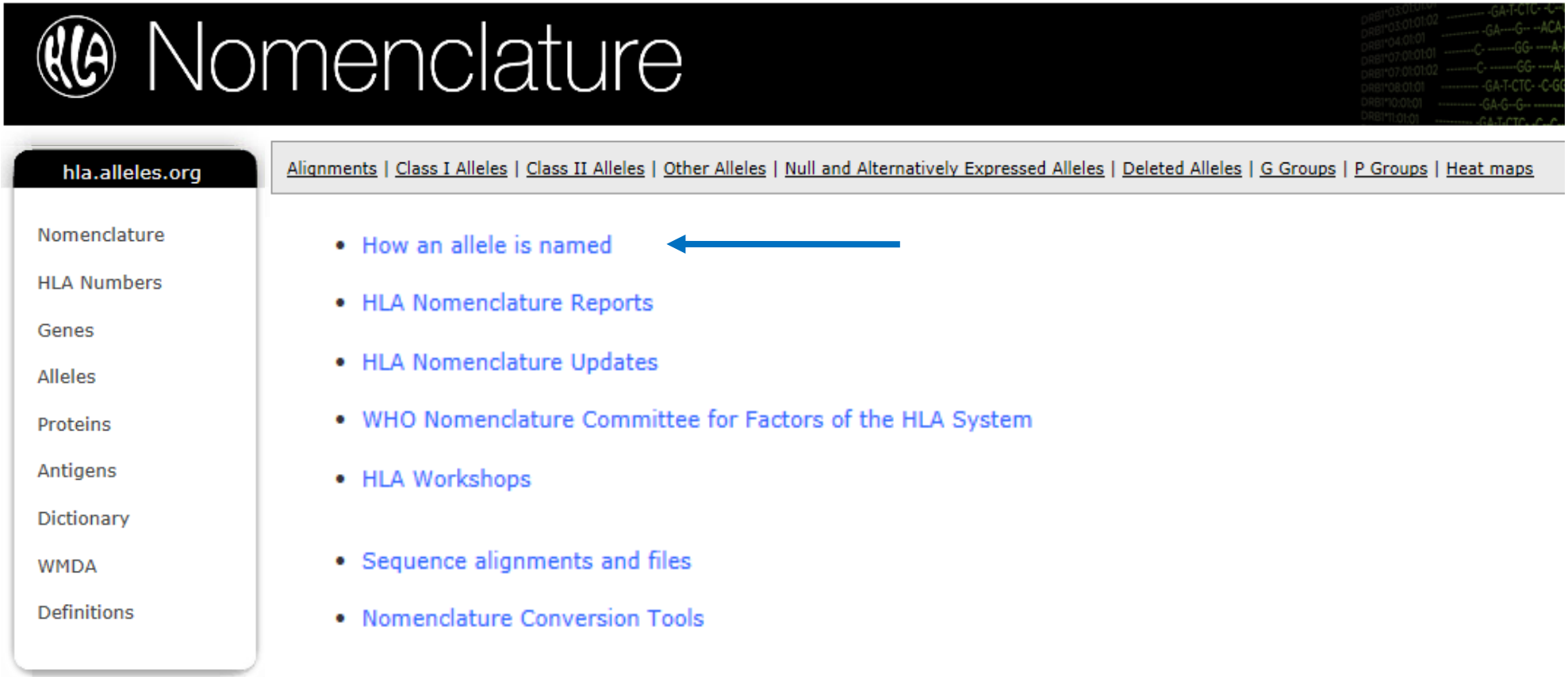
In 1989, a large number of HLA allele sequences were first analysed and named. Since then, the job of curating and maintaining a database of sequences has been of the utmost importance. The dissemination of new allele names and sequences is essential in clinical settings, and through the work of the HLA Informatics Group (in collaboration with the European Bioinformatics Institute) we are able to provide public access to the data through the EBI web site (http://www.ebi.ac.uk/ipd/imgt/hla) and here at http://hla.alleles.org. The IPD-IMGT/HLA Database collects both new and confirmatory sequences that are then expertly analysed and curated before being named by the WHO Nomenclature Committee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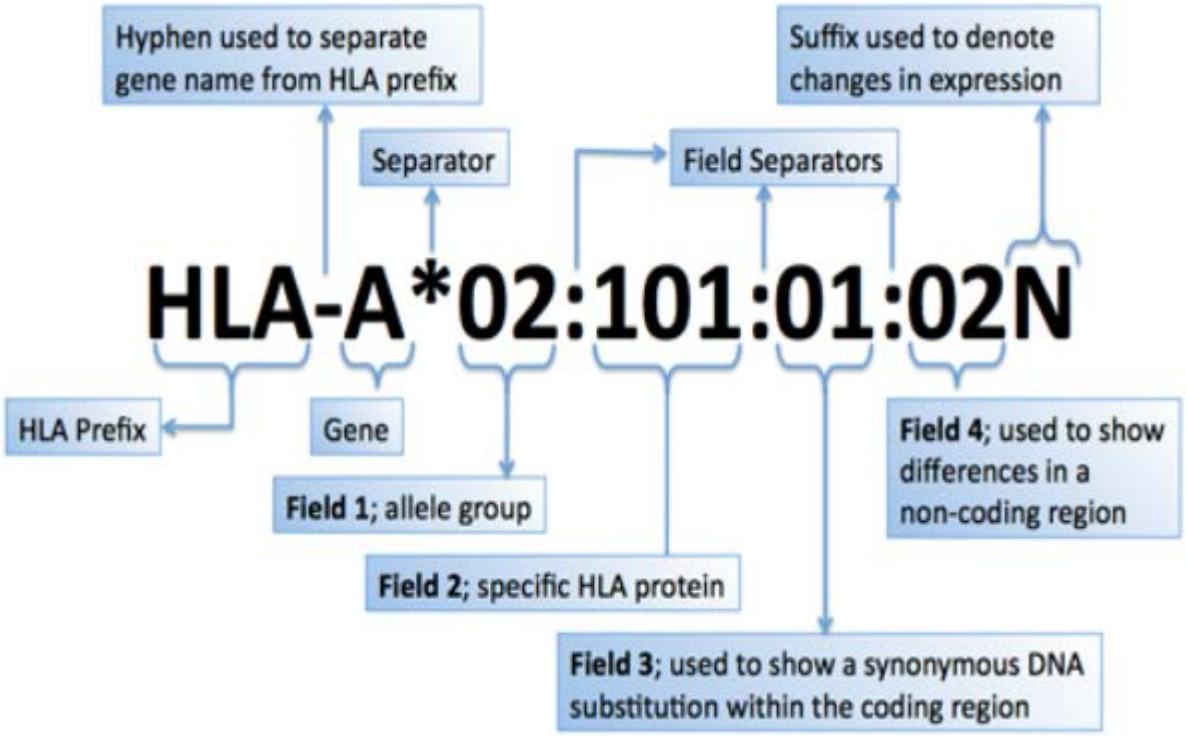
Nomenclature of HLA Alleles

Each HLA allele name has a unique number corresponding to up to four sets of digits separated by colons. The length of the allele designation is dependent on the sequence of the allele and that of its nearest relative. All alleles receive at least a four digit name, which corresponds to the first two sets of digits, longer names are only assigned when necessary.

The digits before the first colon describe the type, which often corresponds to the serological antigen carried by an allotype. The next set of digits are used to list the subtypes, numbers being assigned in the order in which DNA sequences have been determined. Alleles whose numbers differ in the two sets of digits must differ in one or more nucleotide substitutions that change the amino acid sequence of the encoded protein. Alleles that differ only by synonymous nucleotide substitutions (also called silent or non-coding substitutions) within the coding sequence are distinguished by the use of the third set of digits. Alleles that only differ by sequence polymorphisms in the introns, or in the 5' or 3' untranslated regions that flank the exons and introns, are distinguished by the use of the fourth set of digits.

In addition to the unique allele number, there are additional optional suffixes that may be added to an allele to indicate its expression status. Alleles that have been shown not to be expressed - '**N**ull' alleles - have been given the suffix '**N**'. Alleles that have been shown to be alternatively expressed may have the suffix 'L', 'S', 'C', 'A' or 'Q'.

The suffix '**L**' is used to indicate an allele which has been shown to have '**L**ow' cell surface expression when compared to normal levels. The '**S**' suffix is used to denote an allele specifying a protein which is expressed as a soluble, '**S**ecreted' molecule but is not present on the cell surface. The '**C**' suffix is assigned to alleles that produce proteins that are present in the '**C**ytoplasm' and not on the cell surface. An '**A**' suffix indicates an '**A**berrant' expression where there is some doubt as to whether a protein is actually expressed. A '**Q**' suffix is used when the expression of an allele is '**Q**uestionable', given that the mutation seen in the allele has been shown to affect normal expression levels in other alleles.


Hyphen used to separate gene name from HLA prefix
Separator
Field Separators
Suffix used to denote changes in expression
HLA-A*02:101:01:02N
HLA Prefix
Gene
Field 1; allele group
Field 2; specific HLA protein
Field 3; used to show a synonymous DNA substitution within the coding region
Field 4; used to show differences in a non-coding region

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Nomenclature for Factors of the HLA System

HLA Nomenclature Reports

This page details all the previous HLA Nomenclature reports and where possible a link to a freely available PDF of the Tissue Antigens publication has been provided, courtesy of Wiley InterScience, as indicated by the Tissue Antigens cover image. A number of the early reports are also available in PDF format directly from the Bulletin of the World Health Organization website.

Nomenclature for Factors of the HLA System, 2010

SGE Marsh, ED Albert, WF Bodmer, RE Bontrop, B Dupont, HA Erlich, M Fernández-Vina, DE Geraghty, R Holdsworth, CK Hurley, M Lau, KW Lee, B Mach, WR Mayr, M Maiers, CR Müller, P Parham, EW Petersdorf, T Sasazuki, JL Strominger, A Svejgaard, PI Terasaki, JM Tiercy, J Trowsdale

Tissue Antigens 2010 **75**:291-455 (Download PDF)

An Update to HLA Nomenclature, 2010

SGE Marsh, ED Albert, WF Bodmer, RE Bontrop, B Dupont, HA Erlich, M Fernández-Vina, DE Geraghty, R Holdsworth, CK Hurley, M Lau, KW Lee, B Mach, WR Mayr, M Maiers, CR Müller, P Parham, EW Petersdorf, T Sasazuki, JL Strominger, A Svejgaard, PI Terasaki, JM Tiercy, J Trowsdale

Bone Marrow Transplantation 2010 **45**:846-8 (Download PDF)

Nomenclature for Factors of the HLA System, 2004

SGE Marsh, ED Albert, WF Bodmer, RE Bontrop, B Dupont, HA Erlich, DE Geraghty, JA Hansen, CK Hurley, B Mach, WR Mayr, P Parham, EW Petersdorf, T Sasazuki, GMTh Schreuder, JL Strominger, A Svejgaard, PI Terasaki, J Trowsdale

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HLA Nomenclature Updates

Compiled by Steven GE Marsh for the WHO Nomenclature Committee for Factors of the HLA System

These updates are produced on a monthly basis and have been published in the journals Tissue Antigens, Human Immunology and the International Journal of Immunogenet

These updates list all the **New** and **Confirmatory** sequences reported to the Nomenclature Committee, plus information on errors and corrections to sequences. Updates are c

provided for the months following the last full Nomenclature report.

HLA Nomenclature Updates

Year	HLA Nomenclature Updates following the 2010 Nomenclature Report											
2018	January	February	March	April	May	June						
2017	January	February	March	April	May	June	July	August	September	October	November	December
2016	January	February	March	April	May	June	July	August	September	October	November	December
2015	January	February	March	April	May	June	July	August	September	October	November	December
2014	January	February	March	April	May	June	July	August	September	October	November	December
2013	January	February	March	April	May	June	July	August	September	October	November	December
2012	January	February	March	April	May	June	July	August	September	October	November	December
2011	January	February	March	April	May	June	July	August	September	October	November	December
2010				April	May	June	July	August	September	October	November	December
Year	HLA Nomenclature Updates following the 2004 Nomenclature Report											
2010	January	February										

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combinations increases rapidly with the release of novel alleles. For this reason, we would encourage our users to use the XML and Microsoft Excel formats where possible. Please note that Microsoft Office 2010 or later is required to view the files.

Older releases are also available in PDF format, as well as XML and Microsoft Excel.

Release	Date	PDF File	Excel File	XML File
3.33.0	2018-07-11	-	Download Excel	View XML
3.32.0	2018-04-16	-	Download Excel	View XML
3.31.0	2018-01-19	-	Download Excel	View XML
3.30.0	2017-10-27	-	Download Excel	View XML
3.29.0	2017-07-10	-	Download Excel	View XML
3.28.0	2017-04-13	-	Download Excel	View XML
3.27.0	2017-01-20	-	Download Excel	View XML
3.26.0	2016-10-14	-	Download Excel	View XML
3.25.0	2016-07-14	-	Download Excel	View XML
3.24.0	2016-04-15	-	Download Excel	View XML
3.23.0	2016-01-19	-	Download Excel	View XML
3.22.0	2015-10-10	-	Download Excel	View XML
3.21.0	2015-07-06	-	Download Excel	View XML

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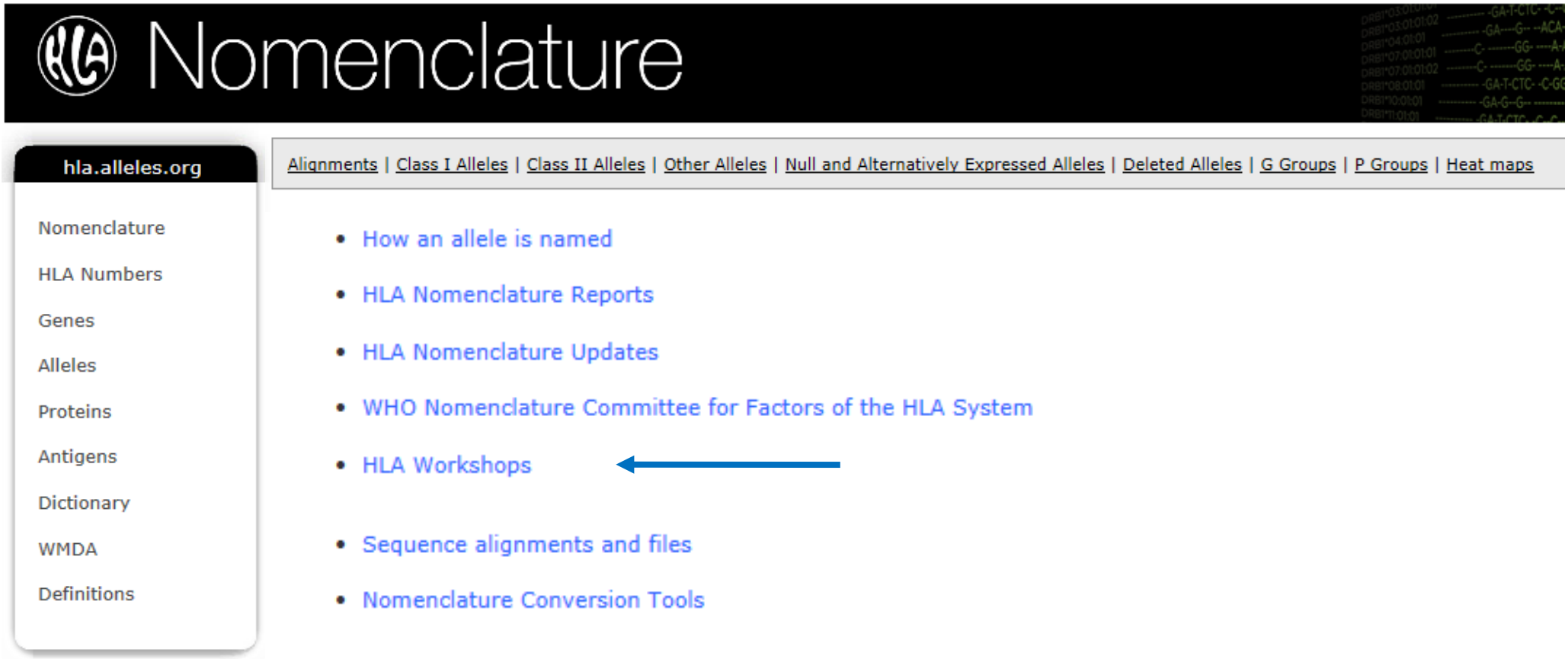
WHO Committee

The WHO Nomenclature Committee for Factors of the HLA System comprises the following individuals:

- Steven G. E. Marsh (*Chair*)
- Ekkehard D. Albert
- Walter F. Bodmer
- Mary N. Carrington
- Henry A. Erlich
- Marcelo Fernández-Vina
- Daniel E. Geraghty
- Rhonda Holdsworth
- Carolyn K. Hurley
- Kyung Wha Lee
- Wolfgang R. Mayr
- Martin Maiers
- Carlheinz R Müller
- Peter Parham
- Effie W. Petersdorf
- James Robinson
- Takehiko Sasazuki
- Jack L. Strominger
- Jean-Marie Tiercy
- John Trowsdale

- Ronald E. Bontrop (*Co-opted Member*)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The Nomenclature Committee has convened at a number of the following International HLA Workshops:

Workshop	Year	Chair	Venue	Advances
1st	1964	DB Amos	Durham, USA	Definition of "Hu-1", "LA" and "Four" antigen specificities
2nd	1965	JJ van Rood	Leiden, The Netherlands	Mixed lymphocyte culture testing
3rd	1967	R Ceppellini	Torino, Italy	Family studies; HLA in renal transplantation
4th	1970	PI Terasaki	Los Angeles, USA	Definition of 27 HLA-A, HLA-B and HLA-C specificities
5th	1972	J Dausset	Evian, France	Worldwide typing of 49 populations
6th	1975	F Kissmeyer-Nielsen	Aarhus, Denmark	Description of Dw specificities
7th	1977	WF Bodmer	Oxford, UK	Definition of DR1-7 specificities; HTC testing
8th	1980	PI Terasaki	Los Angeles, USA	Definition of MB (DQ) and MT (DR52/53); HLA in transplantation and disease
9th	1984	EA Albert/W Mayr	Munich, Germany Vienna, Austria	New class I and II specificities; HLA class II in renal transplantation
10th	1987	B Dupont	Princeton, USA	Establishment of RFLP; T cell clones; HTC methods; Biochemistry – 1D IEF, 2D-gels; Creation of a panel of homozygous cell lines
11th	1991	T Sasazuki/K Tsuji/M Aizawa	Yokohama, Japan	HLA Class II PCR DNA typing; Anthropology
12th	1996	D Charron	St Malo/Paris, France	HLA Class I PCR DNA typing; Anthropology
13th	2002	J Hansen	Victoria, Canada Seattle, USA	Virtual DNA analysis; Identification of SNP markers; Anthropology; Disease association; HSCT
14th	2005	J McCluskey	Melbourne, Australia	MHC and anthropology; Disease; Infection; HSCT; Cancer; KIR; Cytokine genes
15th	2008	M Gerbase de Lima/ME Moraes	Buzios/Rio de Janerio, Brazil	Anthropology; HSCT; Informatics
16th	2012	SGE Marsh/D Middleton	Liverpool, UK	NGS, HSCT
17th	2017	M Fernandez-Viña	Asilomar, USA	NGS, HSCT
18th	2021	S Heidt/E Spierings	Amsterdam, The Netherlands	*To be determined*

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18th	2021	S Heidt/E Spierings	Amsterdam, The Netherlands	*To be determined*

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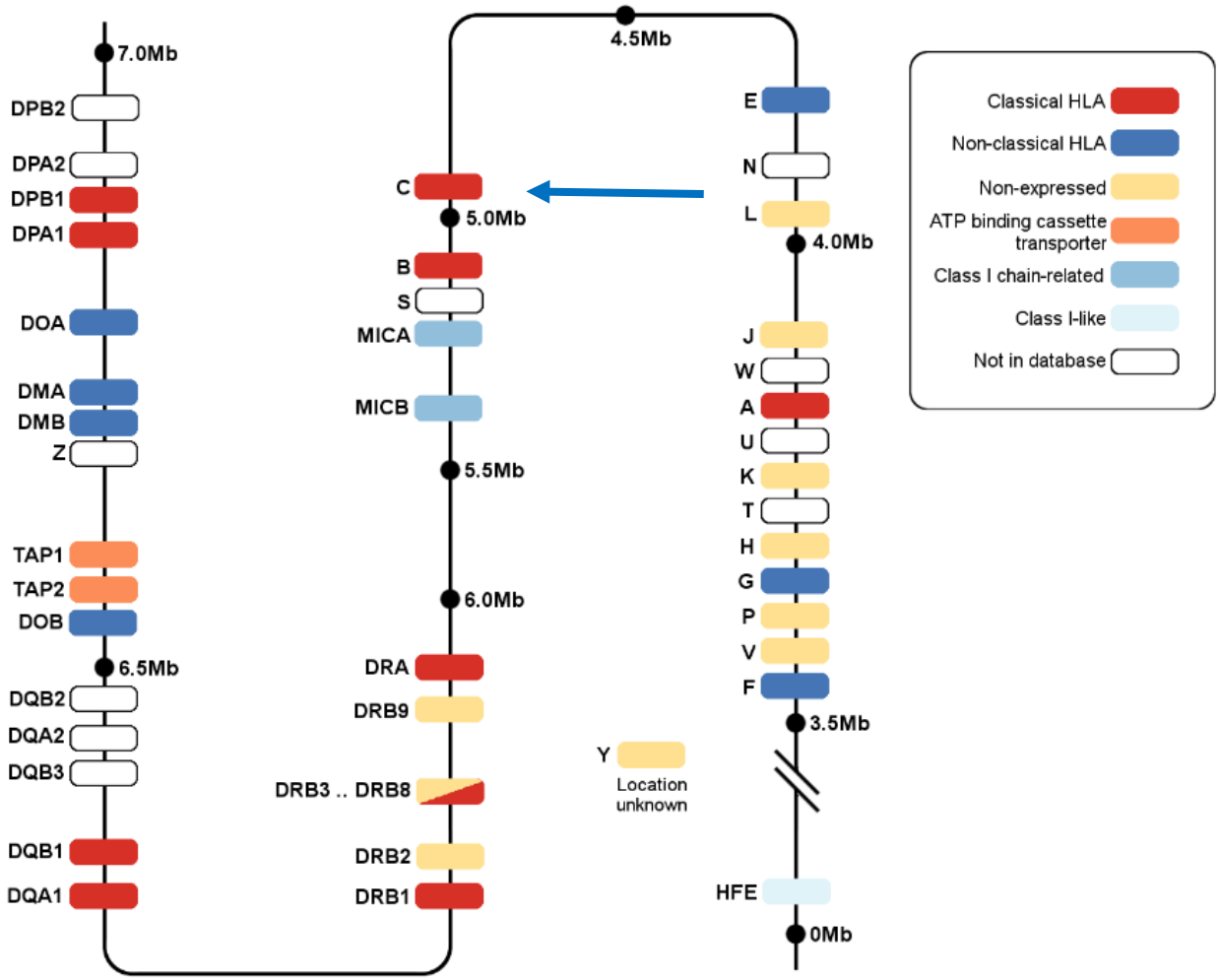
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DQB2
DQA2
DQB3
DQB1
DQA1
4.5Mb
C
5.0Mb
B
S
MICA
MICB
5.5Mb
6.0Mb
DRA
DRB9
DRB3 .. DRB8
DRB2
DRB1
E
N
L
4.0Mb
J
W
A
U
K
T
H
G
P
V
F
3.5Mb
HFE
0Mb
Y
Location unknown
Classical HLA
Non-classical HLA
Non-expressed
ATP binding cassette transporter
Class I chain-related
Class I-like
Not in database

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Release 3.33.0, 11 July 2018

- Nucleotide Sequence (Coding sequences)
- Nucleotide Sequence (Genomic sequences)
- Nucleotide Sequence in PIR format
- Nucleotide Sequence in FASTA format
- Peptide Sequence
- Peptide Sequence in PIR format
- Peptide Sequence in FASTA format
- Reference Information

```
# file: C_nuc.txt
# date: 2018 07 11
# version: IPD-IMGT/HLA 3.33.0
# origin: http://hla.alleles.org/wmda/C_nuc.txt
# repository: https://raw.githubusercontent.com/ANHIG/IMGTHLA/Latest/alignments/C_nuc.txt
# author: WHO, Steven G. E. Marsh (steven.marsh.ac.uk)

 cDNA              1
 AA codon          -24
                   |
 C*01:02:01:01     ATG CGG GTC ATG GCG CCC CGA ACC CTC ATC CTG CTG CTC TCG GGA GCC CTG GCC CTG ACC GAG ACC TGG GCC T|GC
 C*01:02:01:02     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:03     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:04     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:05     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:06     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:07     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:08     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:09     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:01:10     --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:02        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:03        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:04        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:05        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:06        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:07        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:08        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:09        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:10        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:11        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:12        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:13        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:14        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:15        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:16        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:17        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:18        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:19        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:20        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:21        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:22        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:23        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:24        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:25        --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- -|--
 C*01:02:26        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:27        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
 C*01:02:28        *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *** *|--
```

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```
# file: C_gen.txt
# date: 2018 07 11
# version: IPD-IMGT/HLA 3.33.0
# origin: http://hla.alleles.org/wmda/C_gen.txt
# repository: https://raw.githubusercontent.com/ANHIG/IMGTHLA/Latest/alignments/C_gen.txt
# author: WHO, Steven G. E. Marsh (steven.marsh.ac.uk)

 gDNA             -283
                  |
 C*01:02:01:01    TTATTTTGCT GGATGTAGTT TAATATTACC TGAGGTAAGG TAAGGC.... .AAAGAGTGG GAGGCAGGGA GTCCAGTTCA GGGACGGGGA TTCCAGGAG.
 C*01:02:01:02    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:03    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:04    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:05    ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:02:01:06    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:07    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:08    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:09    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:01:10    ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:03       ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:02:04       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:11       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:16       ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:02:18       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:29       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:30       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:36       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:37       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:39       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:40       ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:02:41       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:42       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:43       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:44       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:02:45       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:03          ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:04          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:05          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:06          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:07:02       ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:08          ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:13          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:14          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:17          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:21          ********** ********** ********** ********** ********** ********** ********** ********** ********** **********
 C*01:27          ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
 C*01:30          ---------- ---------- ---------- ---------- ------.... .--------- ---------- ---------- ---------- ---------.
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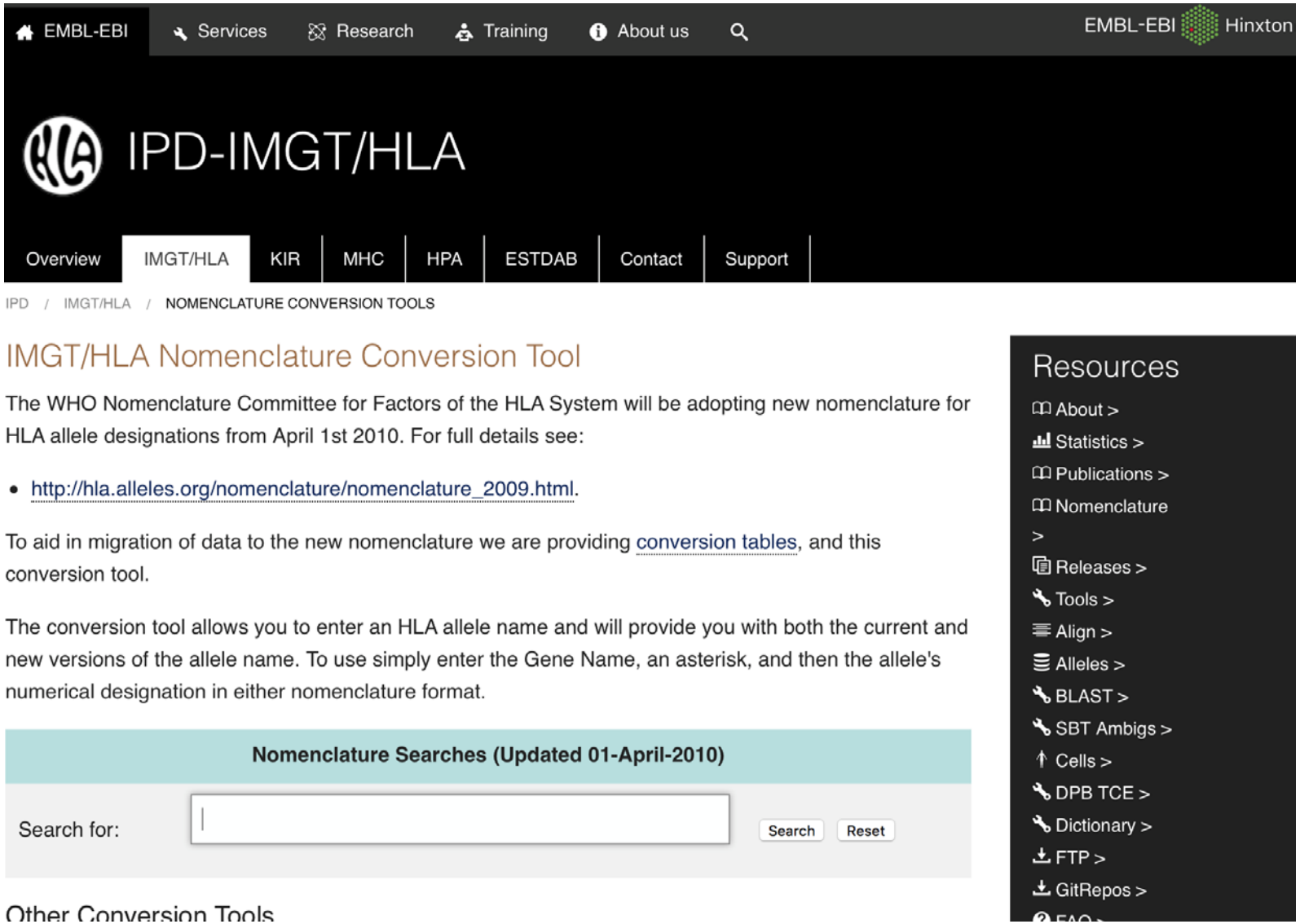
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The WHO Nomenclature Committee for Factors of the HLA System will be adopting new nomenclature for HLA allele designations from April 1st 2010. For full details see:
http://hla.alleles.org/nomenclature/nomenclature_2009.html.
To aid in migration of data to the new nomenclature we are providing conversion tables, and this conversion tool.
The conversion tool allows you to enter an HLA allele name and will provide you with both the current and new versions of the allele name. To use simply enter the Gene Name, an asterisk, and then the allele's numerical designation in either nomenclature format.
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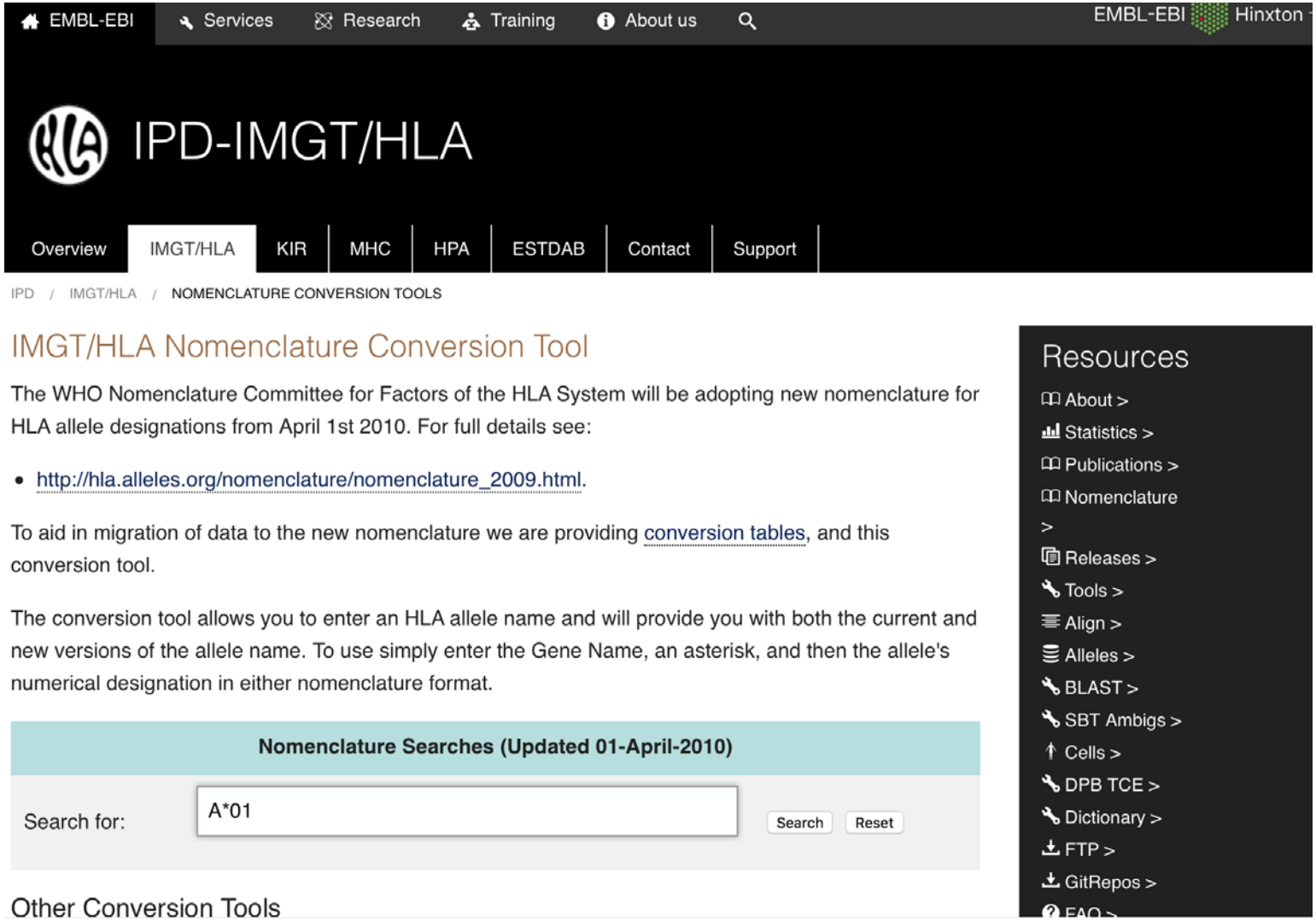
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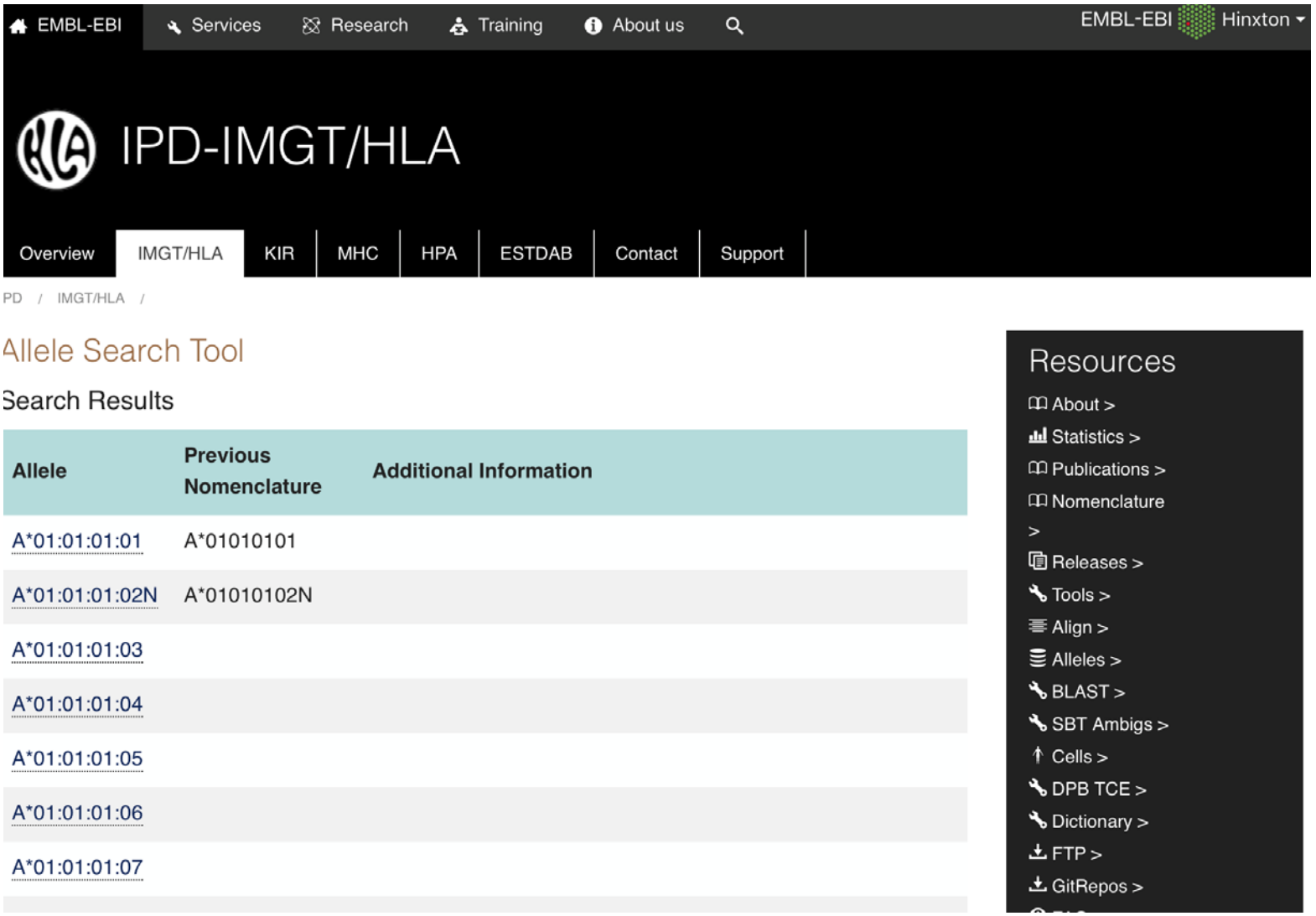
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A*01:01:01:02N
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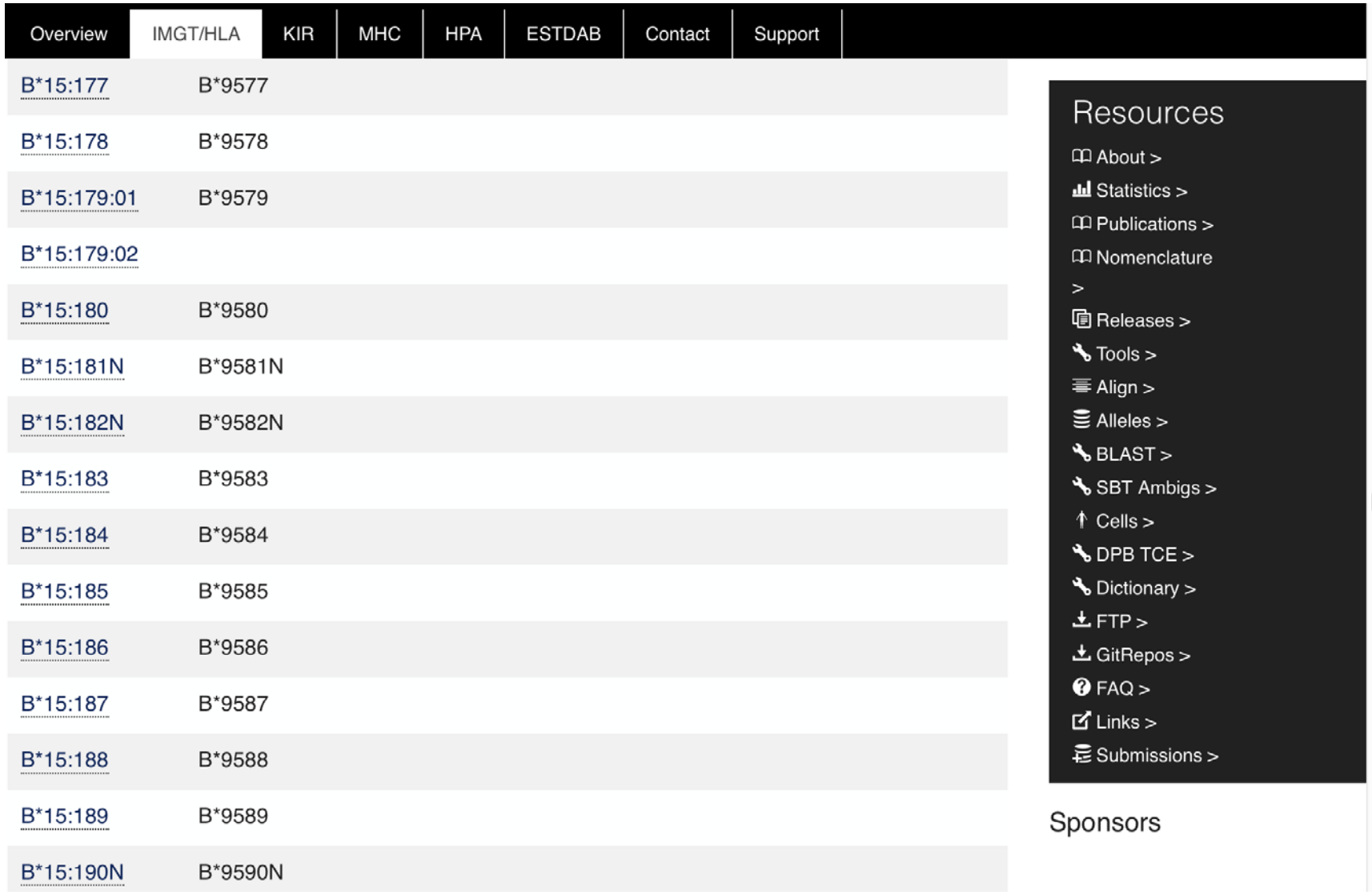
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B*15:179:01 B*9579
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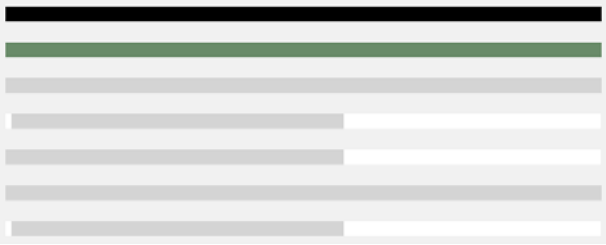
Allele Report for B*15:01:01:01

B*15:01:01:01			View HGVS Report
Pre-2010 Nomenclature:	B*15010101	Local Names:	B*1501101, B*1501
IMGT/HLA Acc No:	HLA00162	OMIM Entry:	*142830
Assigned:	1989-08-01	Sequence Last Modified:	1998-12-16
Source Entries:	AF436090 , AJ295140 , CR759828 , D50292 , DQ249177 , EF203076 , HG794370 , HM370045 , HM543708 , HM543709 , KU319236 , L48400 , L79939 , LT575607 , M28203 , M83193 , U03859		



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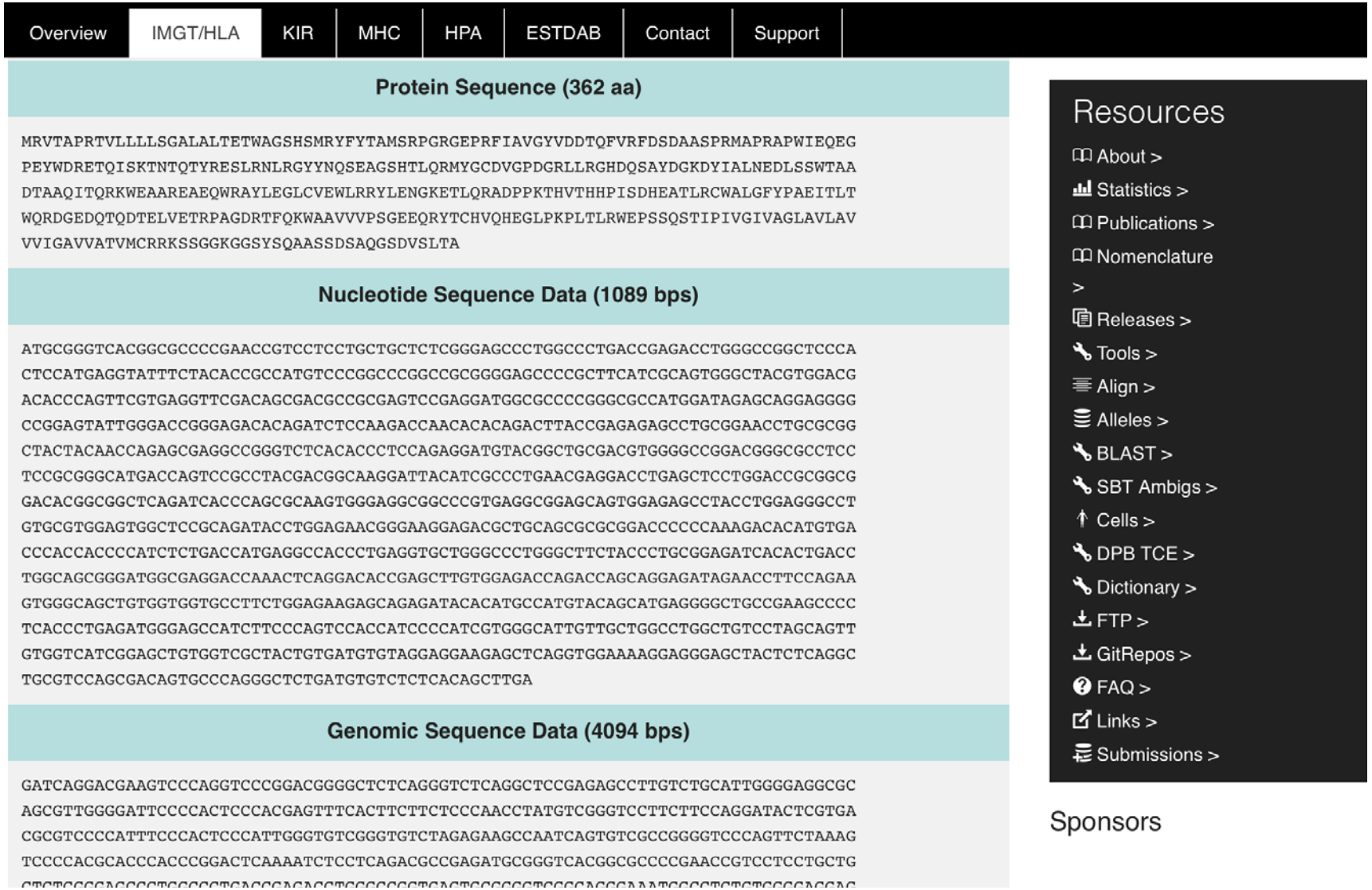
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PEYWDRETQISKTNTQTYRESLRNLRGYYNQSEAGSHTLQRMYGCDVGPDGRLLRGHDQSAYDGKDYIALNEDLSSWTAA
DTAAQITQRKWEAAREAEQWRAYLEGLCVEWLRRYLENGKETLQRADPPKTHVTHHPISDHEATLRCWALGFYPAEITLT
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VVIGAVVATVMCRRKSSGGKGGSYSQAASSDSAQGSDVSLTA
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CTCCATGAGGTATTTCTACACCGCCATGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCAGTGGGCTACGTGGACG
ACACCCAGTTCGTGAGGTTCGACAGCGACGCCGCGAGTCCGAGGATGGCGCCCCGGGCGCCATGGATAGAGCAGGAGGGG
CCGGAGTATTGGGACCGGGAGACACAGATCTCCAAGACCAACACACAGACTTACCGAGAGAGCCTGCGGAACCTGCGCGG
CTACTACAACCAGAGCGAGGCCGGGTCTCACACCCTCCAGAGGATGTACGGCTGCGACGTGGGGCCGGACGGGCGCCTCC
TCCGCGGGCATGACCAGTCCGCCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGAGCTCCTGGACCGCGGCG
GACACGGCGGCTCAGATCACCCAGCGCAAGTGGGAGGCGGCCCGTGAGGCGGAGCAGTGGAGAGCCTACCTGGAGGGCCT
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CCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACACTGACC
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GTGGGCAGCTGTGGTGGTGCCTTCTGGAGAAGAGCAGAGATACACATGCCATGTACAGCATGAGGGGCTGCCGAAGCCCC
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Genomic Sequence Data (4094 bps)
GATCAGGACGAAGTCCCAGGTCCCGGACGGGGCTCTCAGGGTCTCAGGCTCCGAGAGCCTTGTCTGCATTGGGGAGGCGC
AGCGTTGGGGATTCCCCACTCCCACGAGTTTCACTTCTTCTCCCAACCTATGTCGGGTCCTTCTTCCAGGATACTCGTGA
CGCGTCCCCATTTCCCACTCCCATTGGGTGTCGGGTGTCTAGAGAAGCCAATCAGTGTCGCCGGGGTCCCAGTTCTAAAG
TCCCCACGCACCCACCCGGACTCAAAATCTCCTCAGACGCCGAGATGCGGGTCACGGCGCCCCGAACCGTCCTCCTGCTG
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Nomenclature for Factors of the HLA System

Nomenclature of HLA Alleles

Early in their study, it was recognised that the genes encoding the HLA molecules were highly polymorphic and that there was a need for a systematic nomenclature. The HLA complex is located within the 6p21.3 region on the short arm of human chromosome 6 and contains more than 220 genes of diverse function. Many of the genes encode the proteins of the immune system. The naming of new HLA genes, allele sequences, and their quality control is the responsibility of the WHO Nomenclature Committee for Factors of the HLA System. This commitee first met in 1968 and laid down the criteria for successive meetings. The committee meets regularly to discuss issues of nomenclature and has published 19 major reports documenting the HLA antigens and, more recently, the genes and alleles. The standardisation of HLA antigenic specifications has been controlled by the exchange of typing reagents and cells in the International Histocompatibility Workshops.

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Full List of HLA Class I Alleles

Assigned as of June 2018

HLA-A	HLA-B	HLA-C	HLA-E	HLA-F	HLA-G
A*01:01:01:01	B*07:02:01:01	C*01:02:01:01	E*01:01:01:01	F*01:01:01:01	G*01:01:01:01
A*01:01:01:02N	B*07:02:01:02	C*01:02:01:02	E*01:01:01:02	F*01:01:01:02	G*01:01:01:02
A*01:01:01:03	B*07:02:01:03	C*01:02:01:03	E*01:01:01:03	F*01:01:01:03	G*01:01:01:03
A*01:01:01:04	B*07:02:01:04	C*01:02:01:04	E*01:01:01:04	F*01:01:01:04	G*01:01:01:04
A*01:01:01:05	B*07:02:01:05	C*01:02:01:05	E*01:01:01:05	F*01:01:01:05	G*01:01:01:05
A*01:01:01:06	B*07:02:01:06	C*01:02:01:06	E*01:01:01:06	F*01:01:01:06	G*01:01:01:06
A*01:01:01:07	B*07:02:01:07	C*01:02:01:07	E*01:01:01:07	F*01:01:01:07	G*01:01:01:07
A*01:01:01:08	B*07:02:01:08	C*01:02:01:08	E*01:01:01:08	F*01:01:01:08	G*01:01:01:08
A*01:01:01:09	B*07:02:01:09	C*01:02:01:09	E*01:01:01:09	F*01:01:01:09	G*01:01:02:01
A*01:01:01:10	B*07:02:02	C*01:02:01:10	E*01:01:01:10	F*01:01:01:10	G*01:01:02:02
A*01:01:01:11	B*07:02:03	C*01:02:02	E*01:01:02	F*01:01:01:11	G*01:01:03:01
A*01:01:01:12	B*07:02:04	C*01:02:03	E*01:03:01:01	F*01:01:01:12	G*01:01:03:02

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Nomenclature for Factors of the HLA System

Nomenclature of HLA Alleles

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Deleted Alleles

Assigned as of June 2018

The following list details all the allele names that have been deleted from the official WHO HLA Nomenclature, up to and including the latest database release. The list provides the allele name and the reason for the deletion. Please note that deleted alleles have not received new allele designations.

Allele	Reason for deletion
A*0105N	Sequence shown to be identical to *A*01:04N* (July 2001)
A*01:34N	Sequence shown to be expressed at low levels and renamed *A*01:01:38L* (March 2011)
A*020116	Sequence named in error and renamed *A*02:134* (September 2007)
A*020120	Sequence named in error = *A*02:01:18* (March 2008)
A*0223	Sequence identical to *A*02:22:01* (August 1997)
A*0298	Sequence named in error = *A*02:96* (August 2006)
A*02:01:82	Sequence shown to contain errors and be identical to *A*02:01:84* (September 2012)
A*02:100	Name never assigned
A*03:194	Sequence shown to contain errors and be identical to *A*03:213* (July 2015)

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Nomenclature for Factors of the HLA System

P Codes For Reporting of Ambiguous Allele Typings

This file contains details of all HLA Sequences having the same antigen binding domains. This analysis is performed on the protein sequence, and for HLA Class I alleles, identity in the 'antigen binding domains' is based on identical protein sequences as encoded by exons 2 and 3. For HLA Class II alleles this is based on identical protein sequences as encoded by exon 2. HLA alleles having nucleotide sequences that encode the same protein sequence for the peptide binding domains (exon 2 and 3 for HLA class I and exon 2 only for HLA class II alleles) will be designated by an upper case 'P' which follows the 2 field allele designation of the lowest numbered allele in the group. The group designation will contain a minimum of four digits. A computer readable file of these codes, hla_nom_p.txt, is available to download, please see the WMDA section for further details.

In most genes the exon borders fall within an amino acid codon, with the first base often belonging to one exon and the final two bases to the next. In the P group analysis these incomplete codons are excluded from our analysis. For example, the HLA-A analysis does not include codons 1 and 183, which span the borders of exon 1 and 2 and 3 and 4 respectively.

Alleles that are un-sequenced for a part of the region analysed are still included in the analysis, which is based on the protein sequence present.

Group Designation	Alleles Within Group
A*01:01P	*A*01:01:01:01/A*01:01:01:03/A*01:01:01:04/A*01:01:01:05/A*01:01:01:06/A*01:01:01:07/A*01:01:01:08/A*01:01:01:09/A*01:01:01:10/A*01:01:01:11/A*01:01:01:12/ A*01:01:01:13/A*01:01:01:14/A*01:01:01:15/A*01:01:01:16/A*01:01:01:17/A*01:01:01:18/A*01:01:02/A*01:01:03/A*01:01:04/A*01:01:05/A*01:01:06/A*01:01:07/ A*01:01:08/A*01:01:09/A*01:01:10/A*01:01:11/A*01:01:12/A*01:01:13/A*01:01:14/A*01:01:15/A*01:01:16/A*01:01:17/A*01:01:18/A*01:01:19/A*01:01:20/A*01:01:21/ A*01:01:22/A*01:01:23/A*01:01:24/A*01:01:25/A*01:01:26/A*01:01:27/A*01:01:28/A*01:01:29/A*01:01:30/A*01:01:31/A*01:01:32/A*01:01:33/A*01:01:34/A*01:01:35/ A*01:01:36/A*01:01:37/A*01:01:38L/A*01:01:39/A*01:01:40/A*01:01:41/A*01:01:42/A*01:01:43/A*01:01:44/A*01:01:45/A*01:01:46/A*01:01:47/A*01:01:48/A*01:01:49/ A*01:01:50/A*01:01:51/A*01:01:52/A*01:01:53/A*01:01:54/A*01:01:55/A*01:01:56/A*01:01:57/A*01:01:58/A*01:01:59/A*01:01:60/A*01:01:61/A*01:01:62/A*01:01:63/*

A*02:79P	*A*02:79:01/A*02:79:02*
A*02:81P	*A*02:81/A*02:124*
A*02:86P	*A*02:86:01/A*02:86:02*
A*02:93P	*A*02:93:01/A*02:93:02*
A*02:101P	*A*02:101:01/A*02:101:02*
A*02:153P	*A*02:153:01/A*02:153:02*
A*02:157P	*A*02:157:01/A*02:157:02*
A*02:164P	*A*02:164:01/A*02:164:02*
A*02:171P	*A*02:171:01/A*02:171:02*
A*02:197P	*A*02:197:01/A*02:197:02*
A*02:211P	*A*02:211:01/A*02:211:02*
A*02:217P	*A*02:217:01/A*02:217:02*
A*02:243P	*A*02:243:01/A*02:243:02/A*02:243:03*
A*02:289P	*A*02:289:01/A*02:289:02*
A*02:419P	*A*02:419:01/A*02:419:02*
A*02:524P	*A*02:524:01/A*02:524:02*
A*02:528P	*A*02:528:01/A*02:528:02*
A*02:591P	*A*02:591:01/A*02:591:02*
A*02:610P	*A*02:610:01/A*02:610:02*

Select Page: 1/18 Select Page Size (Rows): 50

Group Designation	Alleles Within Group
DRB1*11:147P	*DRB1*11:147:01/DRB1*11:147:02*
DRB1*11:193P	*DRB1*11:193:01/DRB1*11:193:02*
DRB1*12:01P	*DRB1*12:01:01:01/DRB1*12:01:01:02/DRB1*12:01:01:03/DRB1*12:01:01:04/DRB1*12:01:01:05/DRB1*12:01:01:06/DRB1*12:01:02/DRB1*12:01:03/DRB1*12:01:04/DRB1*12:01:05/ DRB1*12:01:06/DRB1*12:01:07/DRB1*12:01:08/DRB1*12:01:09/DRB1*12:06/DRB1*12:10/DRB1*12:17/DRB1*12:68*
DRB1*12:02P	*DRB1*12:02:01:01/DRB1*12:02:01:02/DRB1*12:02:01:03/DRB1*12:02:01:04/DRB1*12:02:02/DRB1*12:02:03/DRB1*12:02:04/DRB1*12:02:05/DRB1*12:02:06/DRB1*12:02:07/ DRB1*12:02:08/DRB1*12:69*
DRB1*12:03P	*DRB1*12:03:02/DRB1*12:03:03*
DRB1*12:16P	*DRB1*12:16:01/DRB1*12:16:02/DRB1*12:16:03*
DRB1*13:01P	*DRB1*13:01:01:01/DRB1*13:01:01:02/DRB1*13:01:02/DRB1*13:01:03/DRB1*13:01:04/DRB1*13:01:05/DRB1*13:01:06/DRB1*13:01:07/DRB1*13:01:08/DRB1*13:01:09/DRB1*13:01:10/ DRB1*13:01:11/DRB1*13:01:12/DRB1*13:01:13/DRB1*13:01:14/DRB1*13:01:15/DRB1*13:01:16/DRB1*13:01:17/DRB1*13:01:18/DRB1*13:01:19/DRB1*13:01:20/DRB1*13:01:21/ DRB1*13:01:22/DRB1*13:117/DRB1*13:190/DRB1*13:215/DRB1*13:233/DRB1*13:238/DRB1*13:251/DRB1*13:256/DRB1*13:261*
DRB1*13:02P	*DRB1*13:02:01:01/DRB1*13:02:01:02/DRB1*13:02:01:03/DRB1*13:02:02/DRB1*13:02:03/DRB1*13:02:04/DRB1*13:02:05/DRB1*13:02:06/DRB1*13:02:07/DRB1*13:02:08/ DRB1*13:02:09/DRB1*13:02:10/DRB1*13:02:11/DRB1*13:02:12/DRB1*13:02:13/DRB1*13:02:14/DRB1*13:02:15/DRB1*13:208/DRB1*13:236/DRB1*13:239*

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G Codes For Reporting of Ambiguous Allele Typings

HLA alleles that have identical nucleotide sequences across the exons encoding the peptide binding domains (exon 2 and 3 for HLA class I and exon 2 only for HLA class II alleles), will be designated by an upper case 'G' which follows the first 3 fields of the allele designation of the lowest numbered allele in the group. The group designation will contain a minimum of six digits. A computer readable file of these codes, hla_nom_g.txt, is available to download, please see the WMDA section for further details.

The algorithm used to generate the G groups does include alleles which contain unsequenced regions. For the alleles in question, the sequence of an alternate allele has been used to extend the sequence over this region. Where possible a genomic or silent variant of the unsequenced allele are used, when this is not possible an alternate allele from within the same first field groupis used and only used when there is a high probability that the sequence used would be shown to be correct if the region was fully sequenced. The list of alleles containing unsequenced regions and the alternate alleles used to infer the missing sequence are detailed in the Ambiguous Typing files available at from the IMGT/HLA Database.

Following the modification or deletion of an allele sequence a G group may contain only a single allele. In these cases the G group is retained and can refer to single allele, the G group may expand at a later date if new alleles are shown to have an identical nucleotide sequences across the exons encoding the peptide binding domains.

In the case of unsequenced regions that cannot be accurately be inferred from known sequences with a high level of confidence the allele has been omitted from the analysis.

We recognise that future sequencing of unsequenced regions may reveal disparity between the predicted sequence and the newly sequenced region. We therefore welcome any further information which will help improve analysis of these regions.

Group Designation	Alleles Within Group
A*01:01:01G	*01:01:01:01/01:01:01:02N/01:01:01:03/01:01:01:04/01:01:01:05/01:01:01:06/01:01:01:07/01:01:01:08/01:01:01:09/01:01:01:10/01:01:01:11/01:01:01:12/01:01:01:13/ 01:01:01:14/01:01:01:15/01:01:01:16/01:01:01:17/01:01:01:18/01:01:38L/01:01:51/01:01:83/01:01:84/01:04:01:01N/01:04:01:02N/01:22N/01:32/01:37/01:45/01:56N/ 01:81/01:87N/01:103/01:107/01:109/01:132/01:141/01:142/01:155/01:177/01:212/01:217/01:234/01:237/01:246/01:248Q/01:249/01:251/01:252/01:253/01:261*
A*01:03:01G	*01:03:01:01/01:03:01:02*


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Welcome to IPD-IMGT/HLA
Release 3.33.0, 2018-07-11
The IPD-IMGT/HLA Database provides a specialist database for sequences of the human major histocompatibility complex (MHC) and includes the official sequences named by the WHO Nomenclature Committee For Factors of the HLA System. The IPD-IMGT/HLA Database is part of the international ImMunoGeneTics project (IMGT).
The database uses the 2010 naming convention for HLA alleles in all tools herein. To aid in the adoption of the new nomenclature, all search tools can be used with both the current and pre-2010 allele designations. The pre-2010 nomenclature designations are only used where older reports or outputs have been made available for download.
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Allele reports show source alignments
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What's new in the latest release
Latest Publications
Robinson J, Halliwell JA, Hayhurst JH, Flicek P, Parham P, Marsh SGE
The IPD and IPD-IMGT/HLA Database: allele variant databases
Nucleic Acids Research (2015) 43:D423-431
For further IPD publications, please see our citations page.
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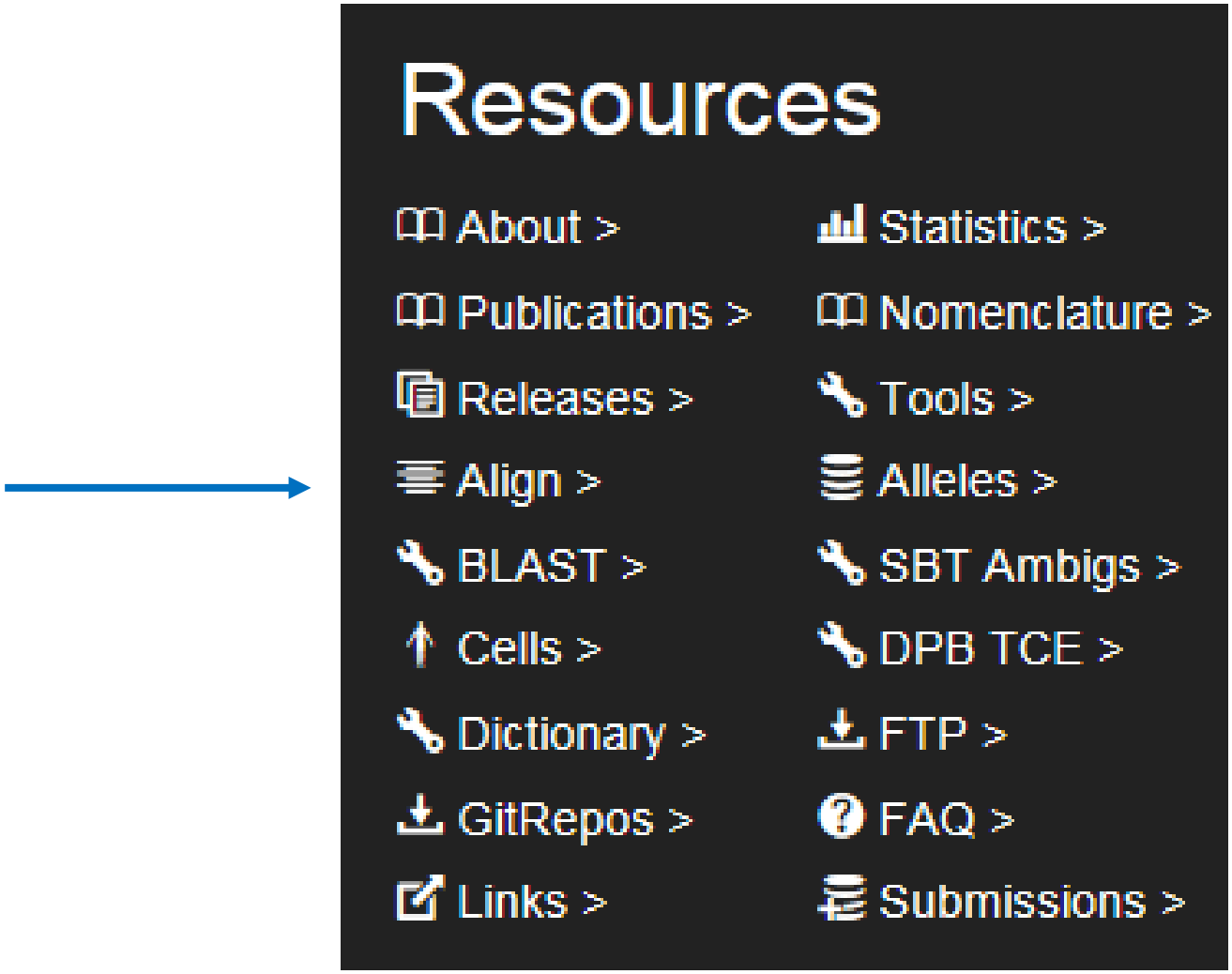
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Sequence Alignment Tool

The latest version of the alignment tool now includes genomic sequences as well alignments of commonly sequenced regions (*e.g.* specific exons and introns).

STEP 1 - Select the locus and features to align

Locus:

A

Features:

Nucleotide - Exon 2

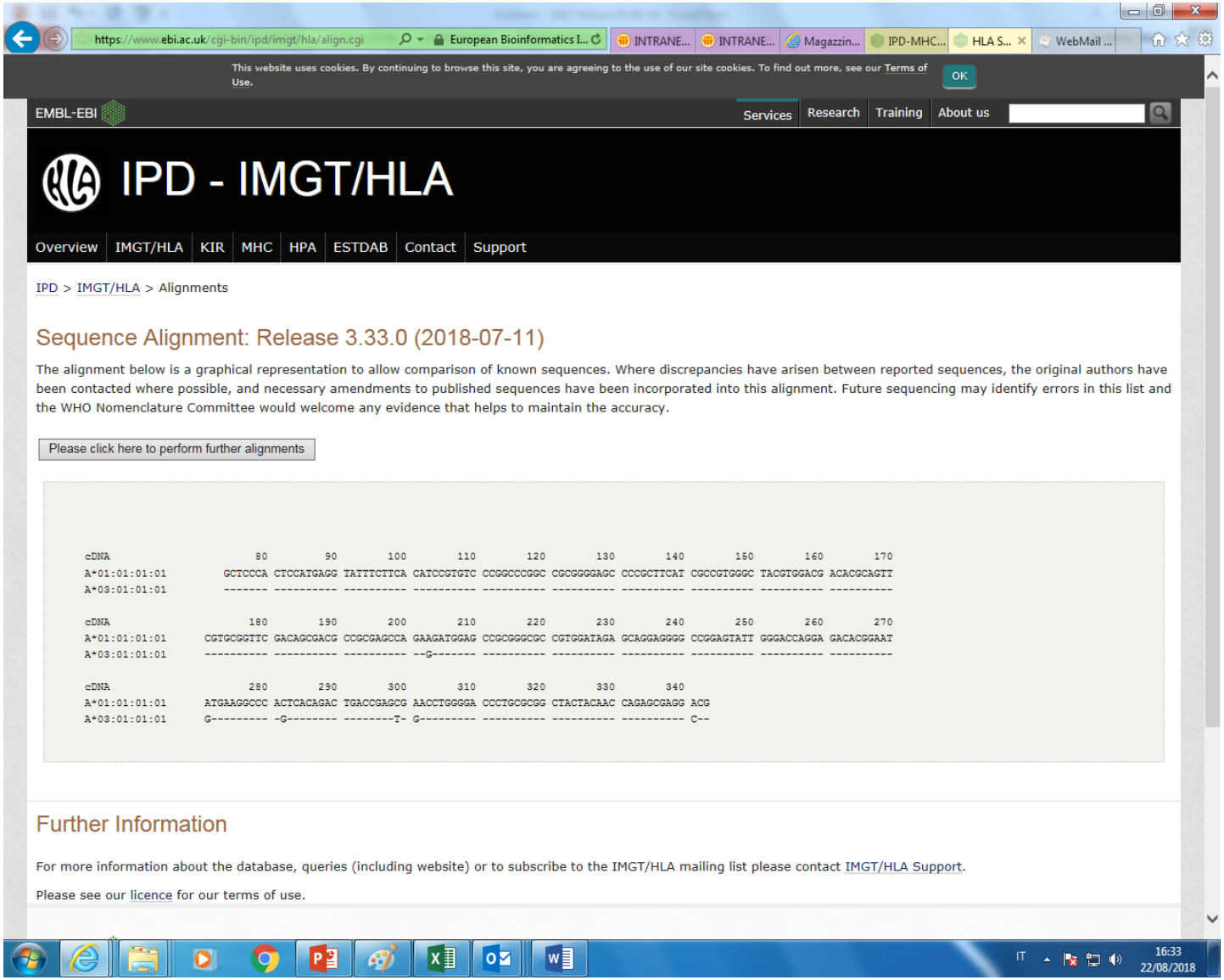
STEP 2 - Specify reference and required sequences

Reference sequence:

01:01:01:01

Specific sequences required (separated by a new line or a comma):

03:01:01:01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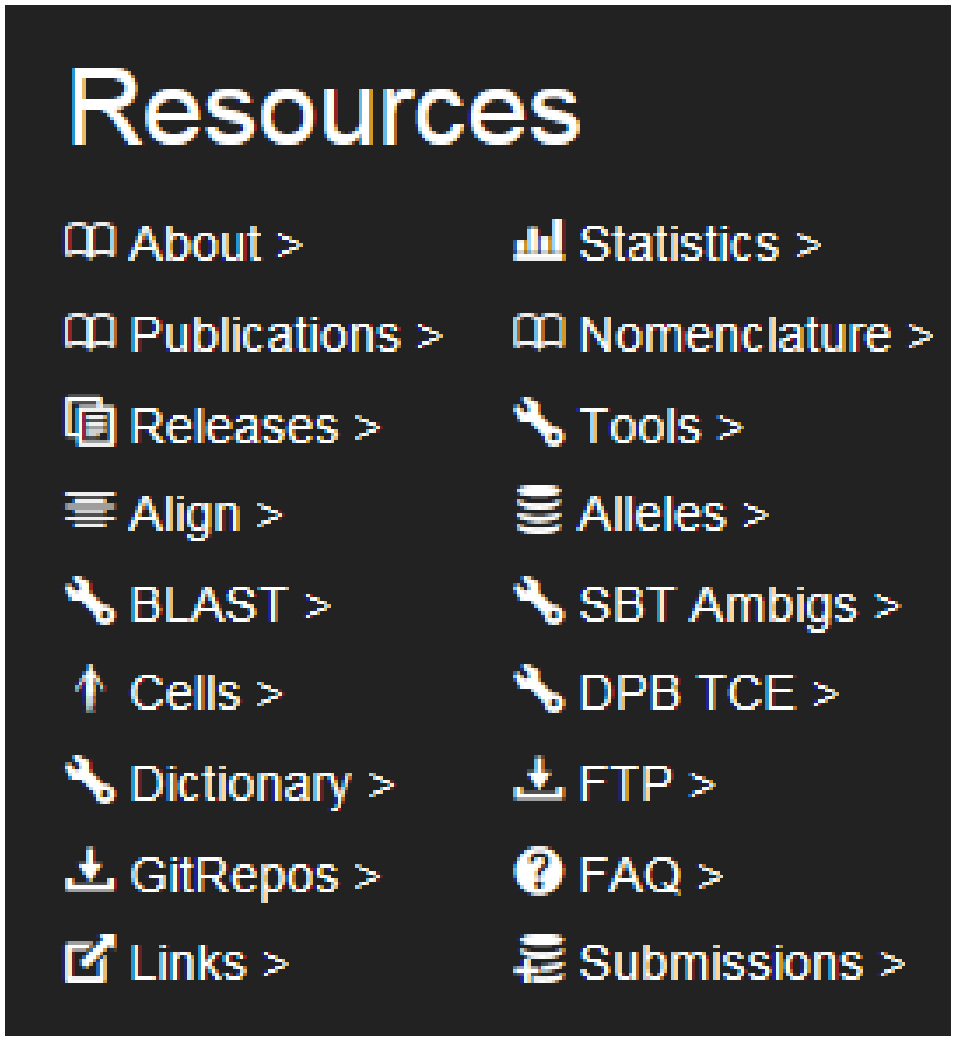
Sequence Alignment: Release 3.33.0 (2018-07-11)
The alignment below is a graphical representation to allow comparison of known sequences. Where discrepancies have arisen between reported sequences, the original authors have been contacted where possible, and necessary amendments to published sequences have been incorporated into this alignment. Future sequencing may identify errors in this list and the WHO Nomenclature Committee would welcome any evidence that helps to maintain the accuracy.
Please click here to perform further alignments
cDNA 80 90 100 110 120 130 140 150 160 170
A*01:01:01:01 GCTCCCA CTCCATGAGG TATTTCTTCA CATCCGTGTC CCGGCCCGGC CGCGGGGAGC CCCGCTTCAT CGCCGTGGGC TACGTGGACG ACACGCAGTT
A*03:01:01:01 ------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------
cDNA 180 190 200 210 220 230 240 250 260 270
A*01:01:01:01 CGTGCGGTTC GACAGCGACG CCGCGAGCCA GAAGATGGAG CCGCGGGCGC CGTGGATAGA GCAGGAGGGG CCGGAGTATT GGGACCAGGA GACACGGAAT
A*03:01:01:01 ---------- ---------- ---------- --G------- ---------- ---------- ---------- ---------- ---------- ----------
cDNA 280 290 300 310 320 330 340
A*01:01:01:01 ATGAAGGCCC ACTCACAGAC TGACCGAGCG AACCTGGGGA CCCTGCGCGG CTACTACAAC CAGAGCGAGG ACG
A*03:01:01:01 G--------- -G-------- --------T- G--------- ---------- ---------- ---------- C--
Further Information
For more information about the database, queries (including website) or to subscribe to the IMGT/HLA mailing list please contact IMGT/HLA Support.
Please see our licence for our terms of use.
IT
16:33
22/08/2018

```
cDNA                    80         90        100        110        120        130        140        150        160        170
A*01:01:01:01       GCTCCCA CTCCATGAGG TATTTCTTCA CATCCGTGTC CCGGCCCGGC CGCGGGGAGC CCCGCTTCAT CGCCGTGGGC TACGTGGACG ACACGCAGTT
A*03:01:01:01       ------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ---------- ----------

cDNA                   180        190        200        210        220        230        240        250        260        270
A*01:01:01:01     CGTGCGGTTC GACAGCGACG CCGCGAGCCA GAAGATGGAG CCGCGGGCGC CGTGGATAGA GCAGGAGGGG CCGGAGTATT GGGACCAGGA GACACGGAAT
A*03:01:01:01     ---------- ---------- ---------- --G------- ---------- ---------- ---------- ---------- ---------- ----------

cDNA                   280        290        300        310        320        330        340
A*01:01:01:01     ATGAAGGCCC ACTCACAGAC TGACCGAGCG AACCTGGGGA CCCTGCGCGG CTACTACAAC CAGAGCGAGG ACG
A*03:01:01:01     G--------- -G-------- --------T- G--------- ---------- ---------- ---------- C--
```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DPB1 T-Cell Epitope Algorithms

Classification of HLA-DPB1 mismatches based on T-cell-epitope Groups (TCE-Groups) has been shown to identify mismatches that might be tolerated (permissive) and those that would increase risks (non-permissive) after unrelated-donor haematopoietic stem cell transplantation (HSCT). These calculators allows you to enter the HLA-DPB1 typing of a patient and donor and view the predicted T-Cell epitopes and resulting prediction of the effect of mismatching when selecting appropriate donors for HSCT recipients.

The implementations of the DPB1 T-Cell Epitope tools has been written in collaboration with Katharina Fleischhauer, University Hospital Essen, Germany and Bronwen Shaw, CIBMTR, USA.

There are currently two versions of the tool, please click on the appropriate link for the version you require:

- Version 1.0 of the tool was originally added to the IPD-IMGT/HLA site in 2012. This tool has been extensively used and validated in a number of studies (1-7). To faciliate ongoing studies which continue to use this algorithm, the first version of this tool will remain online.
- Version 2.0 of the tool has been updated following the recent publication by Crivello et al (8). This update uses a new methodology for assessing the TCE group, and some predicted groups differ to the first version of the tool. At the current time there are no further studies published using the new algorithm.

TCE Group Lists

The FTP and Github repositories provide a listing of the HLA-DPB1 T-Cell Epitope Group Assignments for DPB1 proteins. The assignments are taken from the algorithms used for the online tools provided on this page. The file formart is as follows;

- DPB1 allele, DPB1 protein, Version 1 Assignment, Version 2 Assignment, Comments

Alleles which have yet to be assigned a TCE group using either version are left blank.

References

1. Zino E, Frumento G, Marktel S, *et al.*
A T-cell epitope encoded by a subset of HLA-DPB1 alleles determines nonpermissive mismatches for hematologic stem cell transplantation.

Prospective HLA-DPB1 Typing

Prospective Patient 1	DPB1*	DPB1*
Prospective Donor 1	DPB1*	DPB1*

⊞ Add Further Donors

Predict!

Reset the form!

Prospective HLA-DPB1 Typing

Prospective Patient 1	DPB1* 04:01	DPB1* 14:01
Prospective Donor 1	DPB1* 09:01	DPB1* 02:01

Add Further Donors

Predict!

Reset the form!

Patient Typings: PROSPECTIVEPATIENT1

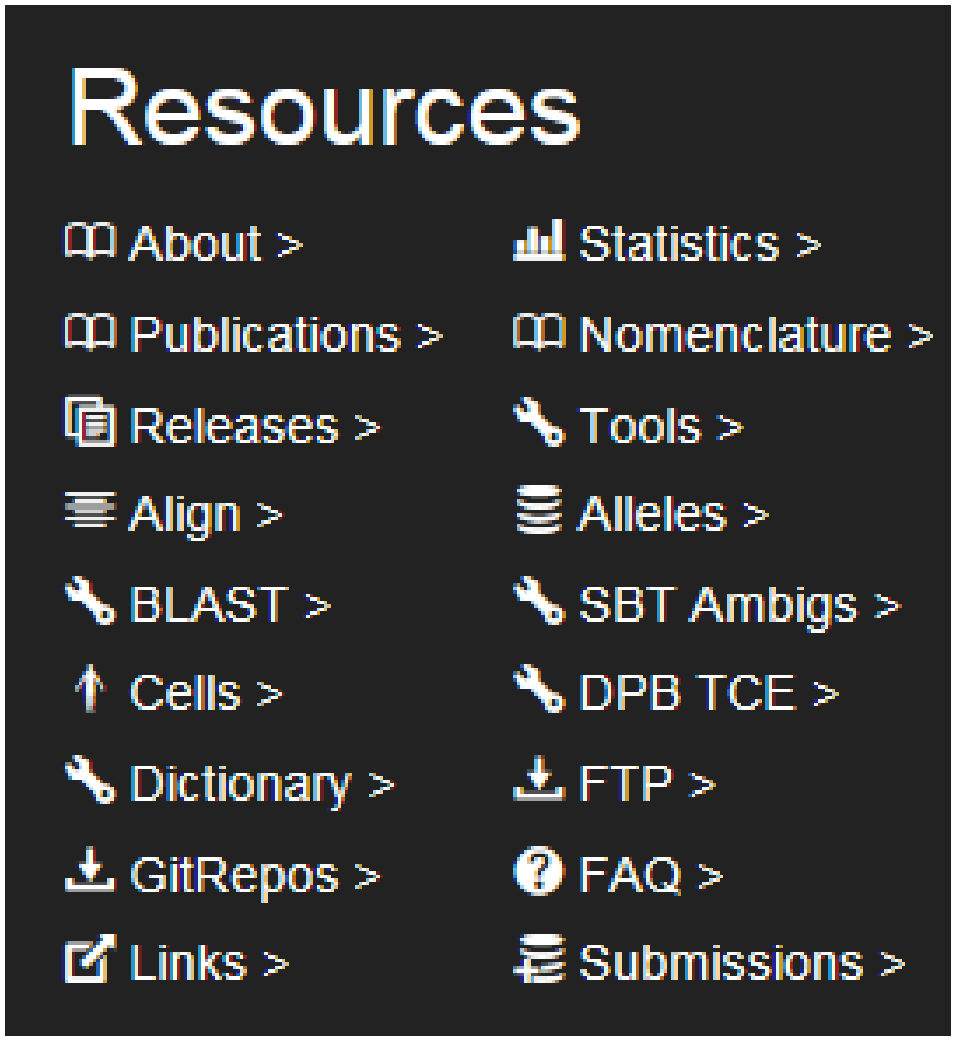
Allele	TCE Group	Predicted Immunogenicity	Comments
DPB1*04:01	3	Low	
DPB1*14:01	2	Intermediate	

Donor Typings: PROSPECTIVEDONOR1

Allele	TCE Group	Predicted Immunogenicity	Comments
DPB1*09:01	1	High	
DPB1*02:01	3	Low	

Prediction

Results
The predicted immunogenecity of the DPB1 matching for this pair is: **Non-Permissive HvG**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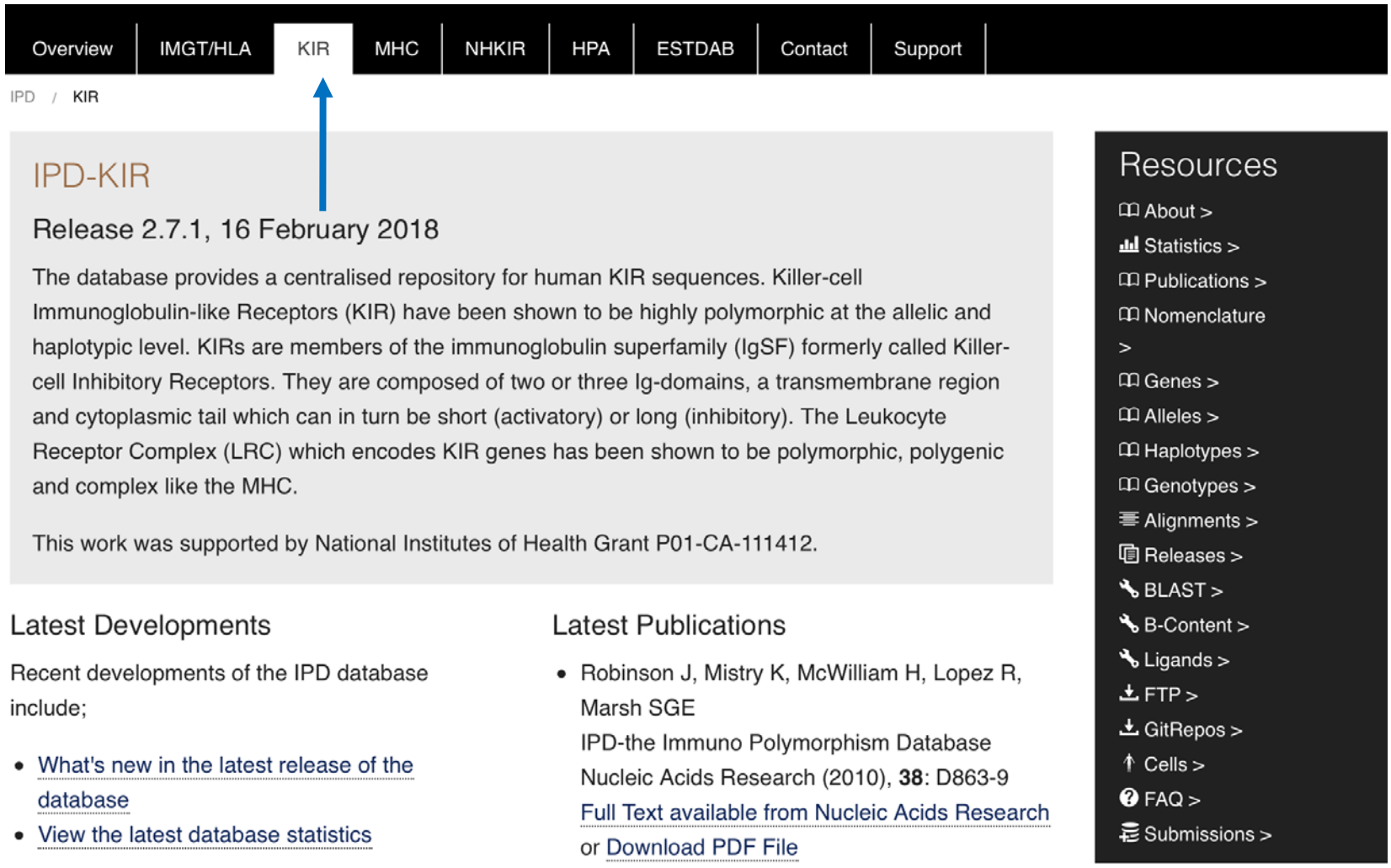
Query Tools	
Allele Query Form	Search tool for retrieving information on any allele in the IPD-IMGT/HLA Database.
Allele Status Checker	Allows users to determine which alleles contain only partial sequences and which alleles have not been independently confirmed.
Cell Queries	Search tool which allows complex queries on source cells.
Conversion Tools	Tool for converting allele names to the new nomenclature
Deleted Alleles	List of deleted allele names, with reason for deletion
Ethnic Origins	Search tool which displays the known ethnic origins for HLA Alleles.
HL7 OIDs for HLA alleles	All HLA alleles and antigen specificities have now received ISO standard HL7 Registered IDs.
KIR Ligand Calculator	Defines HLA-B and HLA-C ligand motifs associated with NK cell alloreactivity.
Polymorphism Search Tool	Search tool to identify polymorphic positions in HLA sequences.
Probe and Primer Search	Search tool for generating probe and primer hit tables.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IPD-KIR
Release 2.7.1, 16 February 2018
The database provides a centralised repository for human KIR sequences. Killer-cell Immunoglobulin-like Receptors (KIR) have been shown to be highly polymorphic at the allelic and haplotypic level. KIRs are members of the immunoglobulin superfamily (IgSF) formerly called Killer-cell Inhibitory Receptors. They are composed of two or three Ig-domains, a transmembrane region and cytoplasmic tail which can in turn be short (activatory) or long (inhibitory). The Leukocyte Receptor Complex (LRC) which encodes KIR genes has been shown to be polymorphic, polygenic and complex like the MHC.
This work was supported by National Institutes of Health Grant P01-CA-111412.
Latest Developments
Recent developments of the IPD database include;
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Latest Publications
Robinson J, Mistry K, McWilliam H, Lopez R, Marsh SGE
IPD-the Immuno Polymorphism Database
Nucleic Acids Research (2010), 38: D863-9
Full Text available from Nucleic Acids Research
or Download PDF File
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KIR Ligand Calculator

Recent transplant strategies based on KIR-ligand mismatch to predict NK cell alloreactivity have resulted in less relapse, less GvHD and better overall survival in patients with Acute Myeloid Leukaemia (AML) (1). KIR-ligands are HLA molecules that can be grouped into three major categories based on the amino acid sequence determining the KIR-binding epitope in HLA-C and HLA-B molecules. All expressed HLA-C alleles are of the C1 or C2 group (2) and most HLA-B alleles can be classified as either Bw4 or Bw6 (3). The grid below shows how the tool defines these groups. Killer-immunoglobin receptors KIR2DL1, KIR2DL2 and KIR3DL1 bind KIR-ligand C2, C1 and Bw4 respectively, resulting in inhibition of NK cell mediated lysis.

Locus	Motif	77	80
HLA-B	Bw4	N (Asparagine)	I (Isoleucine)
HLA-B	Bw4	N (Asparagine)	T (Threonine)
HLA-B	Bw4	D (Aspartic acid)	T (Threonine)
HLA-B	Bw4	S (Serine)	T (Threonine)
HLA-B	Bw6	G (Glycine)	N (Asparagine)
HLA-B	Bw6	S (Serine)	N (Asparagine)
HLA-C	C1		N (Asparagine)
HLA-C	C2		K (Lysine)

Search for Mismatches Between KIR Ligands

Patient	HLA-B*
	HLA-B*
	HLA-C*
	HLA-C*
Donor	HLA-B*
	HLA-B*
	HLA-C*
	HLA-C*
	Submit Typings Reset the form

Search for Mismatches Between KIR Ligands	
Patient	HLA-B* 07:02 HLA-B* 35:01 HLA-C* 07:01 HLA-C* 04:01
Donor	HLA-B* 07:02 HLA-B* 35:01 HLA-C* 07:01 HLA-C* 04:01
	Submit Typings Reset the form

Predicted Ligands for Patient				
Typing	B*07:02	B*35:01	C*07:01	C*04:01
Alleles	Allele listing	Allele listing	Allele listing	Allele listing
Ligand	Bw6	Bw6	C1	C2
Exceptions				
Predicted Ligands for Donor				
Typing	B*07:02	B*35:01	C*07:01	C*04:01
Alleles	Allele listing	Allele listing	Allele listing	Allele listing
Ligand	Bw6	Bw6	C1	C2
Exceptions				
Mismatching in the GvH Direction				
HLA-B	KIR ligands are matched			
HLA-C	KIR ligands are matched			
Mismatching in the HvG Direction				
HLA-B	KIR ligands are matched			
HLA-C	KIR ligands are matched			

In summary, these ligands will be matched in the GvH direction and matched in the HvG direction.

Search for Mismatches Between KIR Ligands	
Patient	HLA-B*: 07:02 HLA-B*: 08:01 HLA-C*: 07:01 HLA-C*: 07:01
Donor	HLA-B*: 07:02 HLA-B*: 35:01 HLA-C*: 07:01 HLA-C*: 04:01
	Submit Typings / Reset the form

Predicted Ligands for Patient				
Typing	B*07:02	B*08:01	C*07:01	C*07:01
Alleles	Allele listing	Allele listing	Allele listing	Allele listing
Ligand	Bw6	Bw6	C1	C1
Exceptions				
Predicted Ligands for Donor				
Typing	B*07:02	B*35:01	C*07:01	C*04:01
Alleles	Allele listing	Allele listing	Allele listing	Allele listing
Ligand	Bw6	Bw6	C1	C2
Exceptions				
Mismatching in the GvH Direction				
HLA-B	KIR ligands are matched			
HLA-C	KIR ligands are (mis)matched in the GvH Direction (C2)			
Mismatching in the HvG Direction				
HLA-B	KIR ligands are matched			
HLA-C	KIR ligands are matched			

In summary, these ligands will be (mis)matched in the GvH direction and matched in the HvG direction.

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IPD / KIR

IPD-KIR

Release 2.7.1, 16 February 2018

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- For further IPD publications, please see our

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Prospective Donor KIR Typing

Prospective Patient ID

Prospective Donor 1

CEN genes					TEL genes				CEN or TEL genes			Framework genes			
2DS2	2DL2	2DL3	2DP1	2DL1	3DL1	2DS4	3DS1	2DS1	2DL5	2DS3	2DS5	3DL3	3DP1	2DL4	3DL2
☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☑	☑	☑	☑

Prospective Donor 2

CEN genes					TEL genes				CEN or TEL genes			Framework genes			
2DS2	2DL2	2DL3	2DP1	2DL1	3DL1	2DS4	3DS1	2DS1	2DL5	2DS3	2DS5	3DL3	3DP1	2DL4	3DL2
☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☐	☑	☑	☑	☑

GRAZIE

Dipartimento di:

Bambino Gesù
OSPEDALE PEDIATRICO

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HLA-B	Bw6	G (Glycine)	N (Asparagine)
HLA-B	Bw6	S (Serine)	N (Asparagine)

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Donor KIR B-content group calculator

Killer-cell Immunoglobulin-like Receptor (KIR) genes form a diverse, immunogenetic system unlinked to HLA. Group A and B KIR haplotypes have distinctive centromeric (Cen) and telomeric (Tel) gene-content motifs. With the goal of developing a donor selection strategy to improve transplant outcome, Cooley *et al.*, compared the contribution of these motifs to the clinical benefit conferred by B haplotype donors. Donor KIR genotype influenced transplantation outcome for AML, but not ALL, after HLA-matched or mismatched T-cell replete unrelated donor transplants. Compared to A haplotype motifs, centromeric and telomeric B motifs both contributed to relapse protection and improved survival, but Cen-B homozygosity had the strongest independent effect. KIR genotyping several best HLA-matched potential donors should substantially increase the frequency of transplants using unrelated donor grafts with favorable KIR gene content. Adopting this practice could result in superior disease-free survival for patients transplanted for AML.

Disclaimer - This research tool is being offered as a tool to predict donor KIR B-content groups assignments as reported in:

S Cooley, DJ Weisdorf, LA Guethlein, JP Klein, T Wang, CT Le, SGE Marsh, D Geraghty, S Spellman, MD Haagenson, M Ladner, E Trachtenberg, P Parham and JS Miller.
Donor selection for natural killer cell receptor genes leads to superior survival after unrelated transplantation for acute myelogenous leukemia.
Blood (2010) 116:2411-9.

No information entered into this tool is collected or stored on our servers.

This calculator allows you to enter the genotypes for up to five prospective donors, and receive their assignments to one of 3 groups based on KIR B-content. The groups, "Neutral", "Better", "Best", refer to

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