

# Compatibilità e Alleli NEW

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IRCCS Ospedale Pediatrico Bambino Gesù

Un alto livello di compatibilità diminuisce il rischio di aGvHD e di mortalità

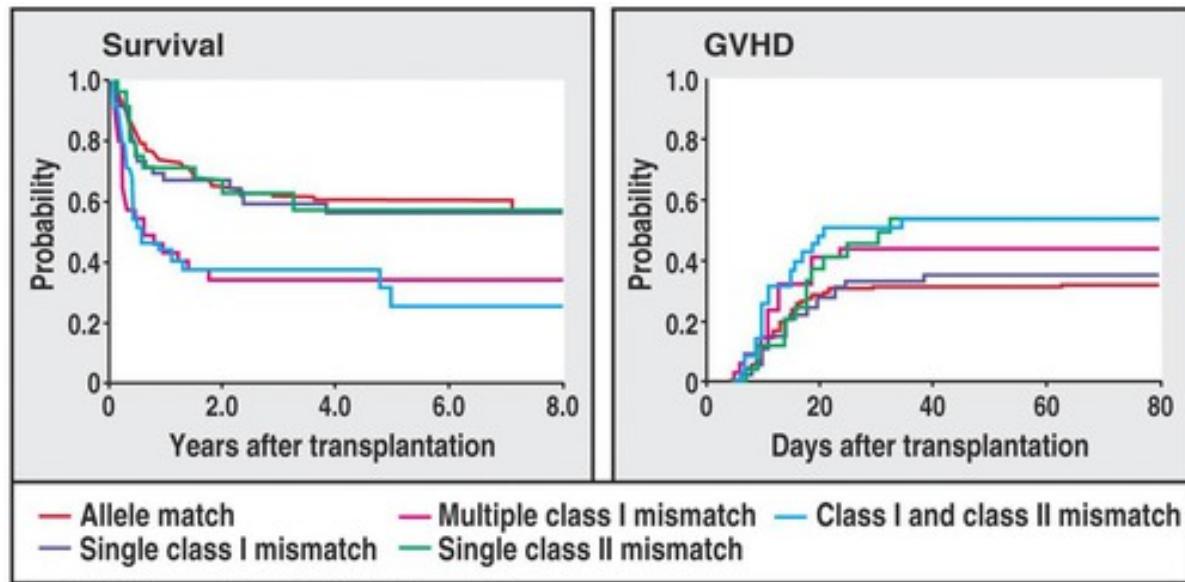
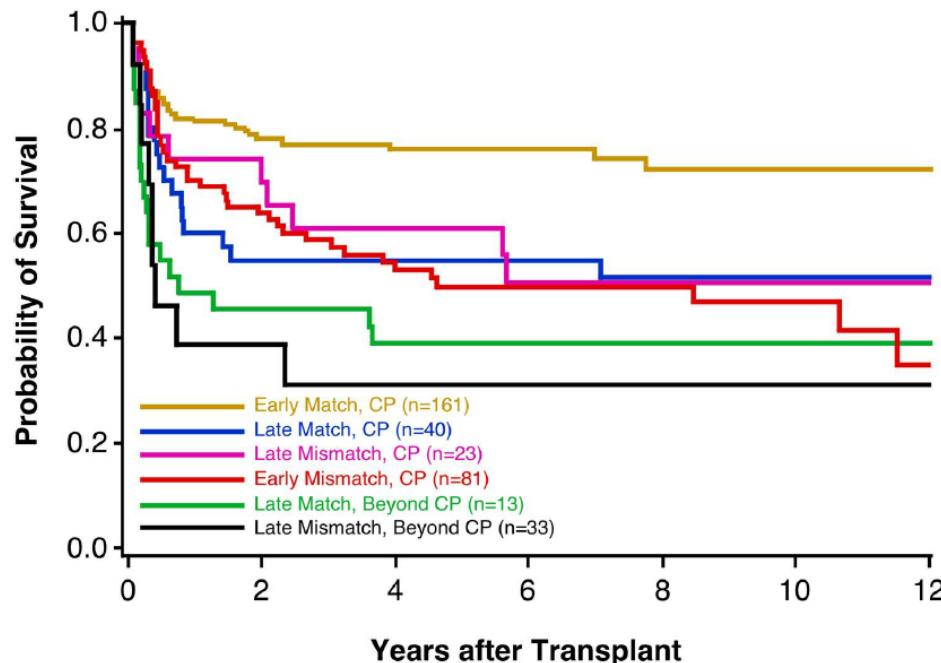


Figure 12-34 The Immune System, 2/e (© Garland Science 2005)

La possibilità di trovare un donatore compatibile entro breve tempo è cruciale per il successo di un trapianto allogenico di CSE



CML patients according to disease phase and presence or absence of a single HLA mismatch.  
EW Petersdorf Blod, 2004 Nov 1;104(9):2976-80.



Categoria: Paziente

		Codice analisi	Data Analisi	
HLA-A	*01:NEW, *02:01;	1	30/08/2017	1,7
HLA-B	*08:01, *51:01P;	1	30/08/2017	1,7
HLA-C	*07:01P, *14:02;	1	25/08/2017	1,7
HLA-DRB1	*01:01, *03:01;	1	25/08/2017	1,7
HLA-DRB3	*01:01,	4	14/09/2017	
HLA-DRB4				
HLA-DRB5				
HLA-DQA1	*01:01P, *05:01;	1	15/09/2017	
HLA-DQB1	*02:01P, *05:01P;	1	25/08/2017	1
HLA-DPB1	*04:01P,	1	12/09/2017	

# Step necessari per la determinazione e inserimento nel database di un new allele

- Accertarsi che sia nuovo
- Isolare la sequenza
- Inserimento in Bankit
- Inserimento in IMGT

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# ESEMPIO

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2052-16 HLA-A\*03 NEW

**EX 2**

GCTCCCACTCCATGAGGTATTCTTACATCCGTGTCCGGCCGCCGGAGCCCCGCTTCATGCCGTGGCTA  
CGTGGACGACACGCAGTCGTGCGGTTGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGCCGTGAATAG  
AGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTG  
GGGACCTGCGCGGCTACTACAACCAGAGCGAGGCCG

**INTR 2**

NN  
NN  
NN  
NN

**EX 3**

GTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGTCGGACGGCGCTCCTCCGCGGGTACCGGCAGGACG  
CCTACGACGGCAAGGATTACATGCCCTGAACGAGGACCTGCGCTTGGACCGCGCGGACATGGCGGCTCAGATCA  
CCAAGCGCAAGTGGAGGCAGGCCATGTGGCGGAGCAGCAGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTC  
CGCAGATACTGGAGAACGGGAAGGAGACGCTGCAGCGCACGG

# ESEMPIO

Overview    IMGT/HLA    KIR    MHC    HPA    ESTDAB    Contact    Support

## 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:

Features:

### STEP 2 - Specify reference and required sequences

Reference sequence:

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

## Resources

- [About >](#)
- [Statistics >](#)
- [Publications >](#)
- [Nomenclature >](#)
- [Releases >](#)
- [Tools >](#)
- [Align >](#)
- [Alleles >](#)
- [BLAST >](#)
- [SBT Ambigs >](#)
- [Cells >](#)
- [DPB TCE >](#)
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## Sponsors



# ESEMPIO



## IPD - IMGT/HLA

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

IPD > IMGT/HLA > Alignments

### 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, where possible, and necessary amendments to published sequences have been incorporated into this alignment. Future sequencing may identify errors which would welcome any evidence that helps to maintain the accuracy.

Please click here to perform further alignments

**241 bp ->241 N**

	480	490	500	510	520	530	540	550	560	570
gDNA										
A*03:01:01:01	GTGAGTG	ACCCCGGCCG	GGGGCGCAGG	TCAGGACCCC	TCATCCCCA	CGGACGGGCC	AGGTCTCCGG	CAGTCTCCGG	GTCCGAGATC	CACCCCGAAG
gDNA	580	590	600	610	620	630	640	650	660	670
A*03:01:01:01	CCGCAGGGACC	CCGAGACCCCT	TGCCCCGGGA	GAGGCCAGG	CGCCTTAC	CGGTTCA	TTCAGTTAG	GCCAAAAATC	CCCCCGGGTT	GTCGGGGCT
gDNA	680	690	700	710						
A*03:01:01:01	GGGGGGGGCT	CGGGGGACTG	GGCTGACCGC	GGGGTGGGGG	CCAG					

# ESEMPIO

INTR 3

## EX 4

ACCCCCCAAGACACATATGACCCACCACCCATCTGACCATGAGGCCACCTGAGGTGCTGGGCCTGGCTCTA  
CCCTCGGGAGATCACACTGACCTGGCAGCGGGATGGGAGGACAGACCCAGGACACGGAGCTCGGAGACCAGGC  
CTGCAGGGGATGGAACCTTCCAGAAAGTGGCGGCTGTGGTGGTCCTCTGGAGAGAGCAGAGATACACCTGCCATG  
TGCAGCATGAGGGTCTGCCAACGCCCTCACCCCTGAGATGGG

# ESEMPIO

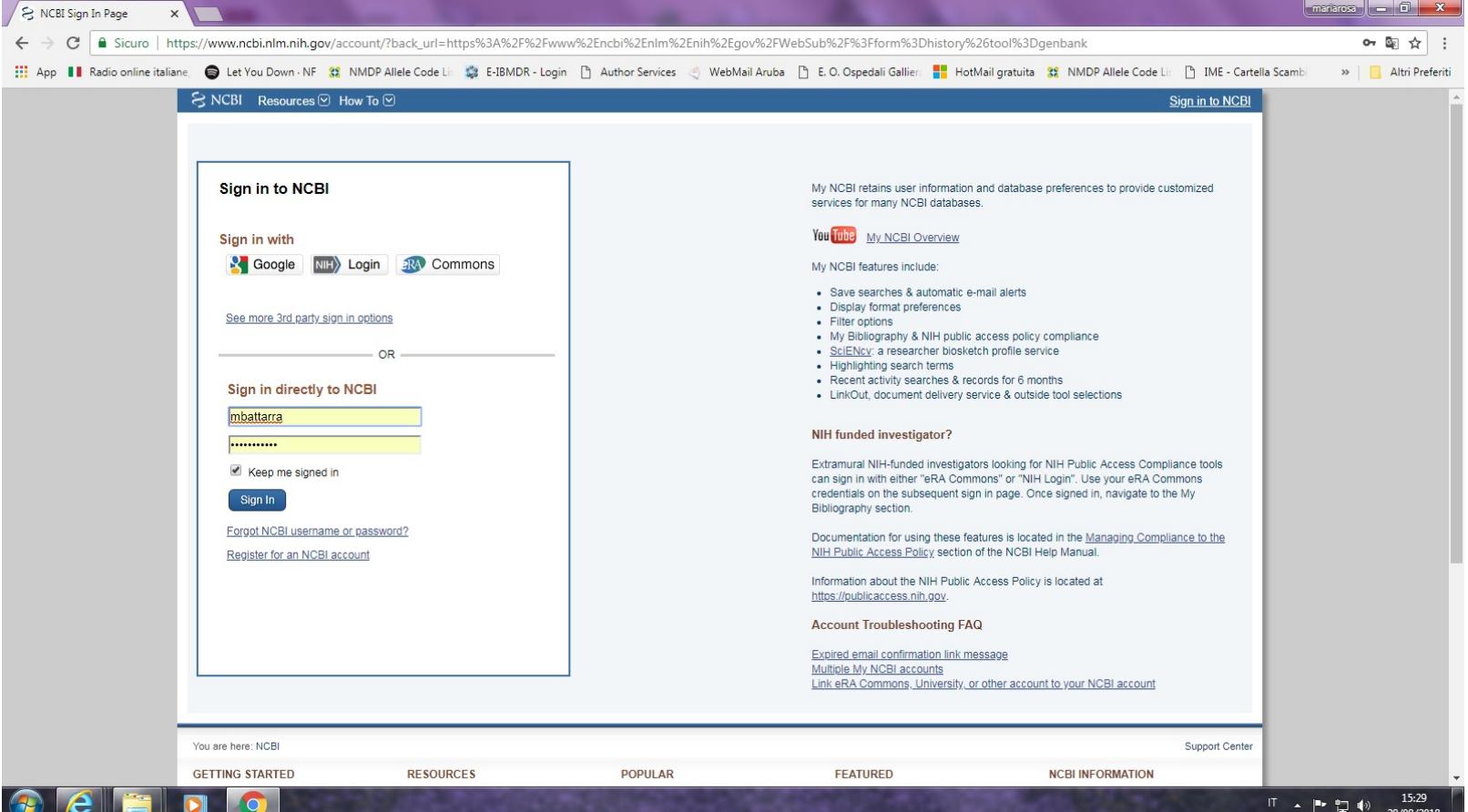
EX 2:	270	1 -	270	(EX2)
INTR2:	241	512 -	787	(EX3)
EX 3:	276	1366 -	1641	(EX4)
INTR3:	578			
EX 4:	276			
TOT:	1641			

MMpos: 225 Base iniziale G → A Base mutata  
 AA: cod 51 codiniale TGG → TGA cod mutato AA iniziale W → STOP AA mutato

## FASTA CON INTRONE

# Inserimento in Bankit

<https://www.ncbi.nlm.nih.gov/account/>



The screenshot shows the NCBI Sign In Page. The main form is titled "Sign in to NCBI". It has two sections: "Sign in with" (Google, NIH Login, eRA Commons) and "Sign in directly to NCBI" (username: mbattarra, password: masked, "Keep me signed in" checked, "Sign In" button). Below these are links for forgot password and register account. To the right, there's a sidebar with "My NCBI retains user information and database preferences to provide customized services for many NCBI databases." It lists "My NCBI features include:" (Save searches & automatic e-mail alerts, Display format preferences, Filter options, My Bibliography & NIH public access policy compliance, SciENcv: a researcher biosketch profile service, Highlighting search terms, Recent activity searches & records for 6 months, LinkOut, document delivery service & outside tool selections), a link to "YouTube My NCBI Overview", and "NIH funded investigator?" information. At the bottom, there are links for account troubleshooting and support.

NCBI Sign In Page

Sicuro | https://www.ncbi.nlm.nih.gov/account/?back\_url=https%3A%2F%2Fwww%2Encbi%2Enlm%2Enih%2Egov%2FWebSub%2F3Form%3Dhistory%26tool%3Dgenbank

App | Radio online italiane | Let You Down - NF | NMDP Allele Code Li | E-IBMDR - Login | Author Services | WebMail Aruba | E. O. Ospedali Galliera | HotMail gratuita | NMDP Allele Code Li | IME - Cartella Scamb | Altri Preferiti

NCBI Resources How To Sign in to NCBI

**Sign in to NCBI**

Sign in with

Google NIH Login eRA Commons

See more 3rd party sign in options

OR

Sign in directly to NCBI

mbattarra

.....

Keep me signed in

Sign In

Forgot NCBI username or password?

Register for an NCBI account

My NCBI retains user information and database preferences to provide customized services for many NCBI databases.

My NCBI features include:

- Save searches & automatic e-mail alerts
- Display format preferences
- Filter options
- My Bibliography & NIH public access policy compliance
- SciENcv: a researcher biosketch profile service
- Highlighting search terms
- Recent activity searches & records for 6 months
- LinkOut, document delivery service & outside tool selections

You Tube My NCBI Overview

NIH funded investigator?

Extramural NIH-funded investigators looking for NIH Public Access Compliance tools can sign in with either "eRA Commons" or "NIH Login". Use your eRA Commons credentials on the subsequent sign in page. Once signed in, navigate to the My Bibliography section.

Documentation for using these features is located in the [Managing Compliance to the NIH Public Access Policy](#) section of the NCBI Help Manual.

Information about the NIH Public Access Policy is located at <https://publicaccess.nih.gov>.

Account Troubleshooting FAQ

[Expired email confirmation link message](#)  
[Multiple My NCBI accounts](#)  
[Link eRA Commons, University, or other account to your NCBI account](#)

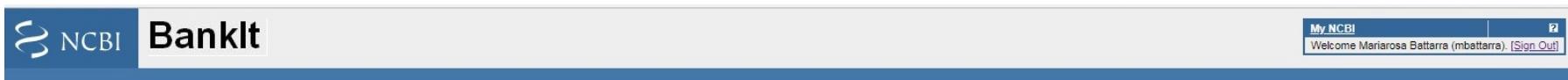
You are here: NCBI

Support Center

GETTING STARTED RESOURCES POPULAR FEATURED NCBI INFORMATION

IT 15:29 28/08/2018

# Inserimento in BankIt



## Welcome BankIt User !

**Attention:** You can receive accessions **faster** if you use [Submission Portal](#) to submit ribosomal RNA (rRNA), rRNA-ITS, or Influenza sequences. Average time for successful submissions to receive accessions is less than a day. Submitting ribosomal RNA (rRNA), rRNA-ITS, or Influenza sequences using BankIt **will delay** processing of your submission.

### Start

[New rRNA or rRNA/ITS Submission](#) (This will redirect you to Submission Portal)

[New Influenza Submission](#) (This will redirect you to Submission Portal)

[New Submission](#) (Submit through BankIt)

### Download your completed submissions

ID	Date	Submitted Record	Title
2086396	09 Feb 2018 05:21:13	<a href="#">Download File (*.gz)</a>	
1998408	08 Mar 2017 03:48:03	<a href="#">Download File (*.gz)</a>	
1997723	06 Mar 2017 06:05:54	<a href="#">Download File (*.gz)</a>	
1973546	05 Dec 2016 03:21:16	<a href="#">Download File (*.gz)</a>	
1972799	01 Dec 2016 03:40:21	<a href="#">Download File (*.gz)</a>	
1961110	17 Oct 2016 06:15:02	<a href="#">Download File (*.gz)</a>	
1957205	29 Sep 2016 09:08:59	<a href="#">Download File (*.gz)</a>	
1955676	23 Sep 2016 05:41:58	<a href="#">Download File (*.gz)</a>	
1953881	16 Sep 2016 06:09:02	<a href="#">Download File (*.qz)</a>	

# Inserimento in BankIt

**BankIt**

Logged in as Mariarosa Battarra (mbattarra) [Log out](#)

The NCBI Submission Portal will be undergoing scheduled maintenance on Thursday, December 1 from 7:00-9:00 AM EST and will be unavailable during this time.

**GenBank Submissions** [Help](#)

Contact Reference Sequencing Technology Nucleotide Submission Category Source Modifiers Features  
Review and Correct

**Submission # 1972799**

**Sequence Authors**

First Name	Middle Initial(s)	Last Name	Suffix	Remove
mariarosa		battarra		X

[Add](#) more sequence authors.

**Reference Information #1**

Please provide the title and relevant publication details (volume, issue, etc.) of a paper that discusses this submission.

**PUBLICATION STATUS**

Unpublished  In-Press  Published

**Reference Title**

A new HLA-A\*03 allele discovered in an Italian Patient

**REFERENCE AUTHORS**

Same As Sequence Authors  
 Specify New Authors

[Add Another Reference](#)

» [Continue](#)

# Inserimento in Bankit

**BankIt**

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**GenBank Submissions** [Help](#)

Contact Reference Sequencing Technology Nucleotide Submission Category Source Modifiers Features Review and Correct

**Submission # 1972799**

**Submission Release Date**

When may we release your sequence record?

Immediately After Processing

Release Date:  Date format is "DD-Mon-YYYY" (example: 20-Feb-2004)

**16S rRNA submissions**

Are the sequences in this submission ONLY 16S ribosomal RNA data?  Yes  No

**Sequence(s) and Definition Line(s)**

Molecule Type:  Topology:  Genomic completeness:

Nucleotide Sequence(s) and Definition Lines

Sequences must be entered in the FASTA format, whether you are submitting a single sequence or multiple sequences. Definition Lines which are used to describe each sequence, should be included in the FASTA format.

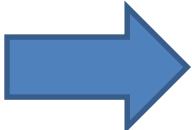
How many nucleotide sequences do you intend to send in this submission?

Paste Sequence(s) →   
CTGAGGTGCTGGGCGCTGGGCTTCTACCTCTGCGGAGATCACACTGACCTGGCA  
GCAGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGGAGACCAGGGCT  
GCAGGGGGATGGGAACCTTCAGAAGTGGCGGCTGTGGTGCTGGAGA  
GGAGCAGAGATAACACCTGCCATGTGCAGCATGAGGGCTGCCAAAGCCCTCAC  
CCTGAGATGGG

Example FASTA nucleotide format:

>Seq1 [organism=genus species] Definition Line for Seq1  
aacggatatacgagagagga....

<https://www.ncbi.nlm.nih.gov/WebSub?form=orgseq&id=1972799&tool=genbank>



# ESEMPIO

EX 2:	270	1 - 270 (EX2)
INTR2:	241	512 - 787 (EX3)
EX 3:	276	1366 - 1641 (EX4)
INTR3:	578	
EX 4:	276	
TOT:	1641	

MMpos: 225 Base iniziale G  A Base mutata  
 AA: cod 51 codiniale TGG  TGA cod mutato AA iniziale W  STOP AA mutato

## FASTA CON INTRONE

```

GCTCCCACCTCCATGAGGTATTCTCACATCCGTCTCGGCCGCCGCCGGGGAGCCCCGCTCATGCCGTGGCTA
CGTGGACGACACGAGTCGTGCGGTTGACAGCGACGCCGCAGCCAGAGGATGGAGGCCGCGGCCGTGAATAG
AGCAGGAGGGGCCGGAGTATTGGGACCAGGAGACCGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTG
GGGACCTGCGCGGCTACTACAACCAGAGCGAGGCCGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
GTATGGCTGCGACGTGGGTCGGACGGCGCTTCCGCGGGTACCGGCAGGACGCCACGACGGCAAGGATTACAT
CGCCCTGAACGAGGACCTGCGCTTGGACCGCGGGACATGGCGGCTCAGATCACCAGCGCAAGTGGAGGGCGGC
CCATGTGGCGGAGCAGCAGAGACCTAACCTGGATGGCACGTGCGTGGAGTGGCTCCGCAGATACTGGAGAACGGGA
AGGAGACGCTGCGACGCCAGGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
NNNNNNNACCCCCCAAGACACATGACCCACCCCATCTCTGACCATGAGGCCACCCCTGAGGTGCTGGCCCTGG
GCTTCTACCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGAGGACAGACCCAGGGACACGGAGCTCGTGGAG
ACCAGGCCTGAGGGATGGAACCTCCAGAAGTGGCGGCTGTGGTGGCCTCTGGAGAGGGAGCAGAGATAACACC
TGCCATGTGCAGCATGAGGGCTGCCAAGCCCTCACCTGAGATGGG

```

# Inserimento in Bankit

**BankIt**

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The NCBI Submission Portal will be undergoing scheduled maintenance on Thursday, December 1 from 7:00-9:00 AM EST and will be unavailable during this time.

**GenBank Submissions** [Help](#)

Contact Reference Sequencing Technology Nucleotide Organism Submission Category Source Modifiers Features Review and Correct

**Submission # 1972799**

Warning: We found the following problems while reading your FASTA sequences. Please upload a corrected FASTA (see help page) or click Continue.

Line num:	1	Warning
FASTA-Reader: First data line in seq is about 49% ambiguous nucleotides (shouldn't be over 40%)		

Warning: There are one or more significant strings of NNNs (length >10). Please explain what the strings of internal NNNs represent

A region of estimated length between the sequenced regions based on an alignment to similar sequences or genome

A region of unknown length between the sequenced regions

Note: You have chosen to submit a single sequence. BankIt allows you to submit multiple sequences and add modifier and feature annotation for all of them in one submission. See [FASTA documentation](#) on how to submit more than one sequence. If single sequence is correct, please press 'Continue'.

**Submission Release Date**

When may we release your sequence record?

Immediately After Processing

Release Date:  Date format is 'DD-Mon-YYYY' (example: 20-Feb-2004)

**16S rRNA submissions**

Are the sequences in this submission ONLY 16S ribosomal RNA data?  Yes  No

**Sequence(s) and Definition Line(s)**

Molecule Type:

Topology:

Genomic completeness:

**Nucleotide Sequence(s) and Definition Lines**

<https://www.ncbi.nlm.nih.gov/WebSub/>

[Clicca su CONTINUAR](#) 

# Inserimento in Bankit

## BankIt

Logged in as Marilaura Battarra (imbatterra) Local

The NCBI Submission Portal will be undergoing scheduled maintenance on Thursday, December 1 from 7:00-9:00 AM EST and will be unavailable during this time.

### GenBank Submissions

Contact Reference Sequencing Technology Nucleotide Organism Submission Category Source Modifiers  
Features Review and Correct

#### Submission # 1972799

##### Features (Detail)

**Adding Feature 'CDS'**

<b>Strand?</b>	Information on Coding Sequences (Pick strand for each span below)		
<b>Partial?</b>	<input checked="" type="checkbox"/> 5' <input type="checkbox"/> 3' <input type="checkbox"/>		
If partial at 5' end, indicate reading frame:	<input type="radio"/> 1 <input type="radio"/> 2 <input type="radio"/> 3		
<b>Is this a Pseudogene?</b>	<input type="radio"/> Yes <input checked="" type="radio"/> No		
<b>Is this an intronless gene?</b>	<input type="radio"/> Yes <input checked="" type="radio"/> No		
<b>Nucleotide Interval Spans:</b> Selezionate queste opzioni secondo le sequenze in solo esone (come è nel DnaS1)			
<input type="radio"/> Entire Sequence <input checked="" type="radio"/> Specific Spans - specify nucleotide numbers within your sequence. (Use this if your sequences contain introns)			
<b>Start</b>	<b>Stop</b>	<b>Strand</b>	
1	270	Plus	<input type="button" value="▼"/>
512	787	Plus	<input type="button" value="▼"/>
1366	1641	Plus	<input type="button" value="▼"/>
<b>Add more intervals</b>			
<b>Protein Information</b>			
<b>Protein Name</b>	HLA-A Antigen		
<b>Protein Description</b>			
<b>EC Number</b>	<input type="text"/> 2.6.1.1		



# Inserimento in Bankit

## Bankit

Logged in as Marlarosa Battarre (mbattarre) [Log out](#)

The NCBI Submission Portal will be undergoing scheduled maintenance on Thursday, December 1 from 7:00-9:00 AM EST and will be unavailable during this time.

### GenBank Submissions

#### Submission # 1972799

#### Submission Completed

Thank you for using the GenBank Submissions Tool.

You have requested that your sequence data be released immediately after processing.

Your Submission ID is 1972799. This is not an accession number. GenBank accession numbers will be assigned to your submissions and sent to you by email within two working days, unless there are issues with your submission that we must ask you to explain first. If you have any questions or corrections regarding your submissions before you receive these, be sure to refer this Submission ID in your email.

Your submission data have been sent to GenBank. For each complete sequence submission, you will receive the following at the email address you provided:

1. an automatic reply confirming our receipt of your submissions;
2. GenBank accession numbers (within two working days); and
3. the final GenBank records, processed by the GenBank Annotation staff and incorporating the information you have provided for you to review before they are released to the public database.

If you do not receive this information from us by email within the time frame indicated, please send an inquiry to [gb-admin@ncbi.nlm.nih.gov](mailto:gb-admin@ncbi.nlm.nih.gov) and be sure to include the Submission ID and the email address used in your submission.

[Start a New Submission](#)

# Step necessari per la determinazione e inserimento nel database di un new allele

- Accertarsi che sia nuovo
- Isolare la sequenza
- Inserimento in Bankit
- Inserimento in IMGT

# Inserimento in IMGT

<https://www.ebi.ac.uk/ipd/imgt/hla/access.html>

Overview    **IMGT/HLA**    KIR    MHC    HPA    ESTDAB    Contact    Support

Search tool for generating probe and primer hit tables.

Search

Interactive sequence alignment tool with [help page](#) available.

Sequence Alignments

Static text version of the sequence alignments are available from <http://hla.alleles.org/> provided by the [HLA Informatics Group](#).

Search Determinants

A comparison of search determinants used by different registries (2007)

Submission Tools

Sequence Submission Tool

Online submission of sequences to the WHO Nomenclature Committee for Factors of the HLA System.

Other EBI Search Tools

BLAST Search Tool

The EBI's BLAST search engine for nucleotide and protein searches.

FASTA Protein Search Tool

The EBI's FASTA search engine for protein sequence searches.

Phylogenetic Analysis

**Resources**

- [About >](#)
- [Publications >](#)
- [R](#) 
- [Align >](#)
- [BLAST >](#)
- [Cells >](#)
- [Dictionary >](#)
- [GitRepos >](#)
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- [Statistics >](#)
- [Nomenclature](#)
- [Tools >](#)
- [Alleles >](#)
- [SBT Ambigs >](#)
- [DPB TCE >](#)
- [FTP >](#)
- [FAQ >](#)
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Sponsors



# Inserimento in IMGT

[Overview](#)[IMGT/HLA](#)[KIR](#)[MHC](#)[HPA](#)[ESTDAB](#)[Contact](#)[Support](#)

IPD / IMGT/HLA / SUBMISSION CHECKLIST

## Submission Checklist

Please read through and complete the following checklist before starting your submission. If you cannot meet all these points please do not submit your sequences as it will not be named until all these conditions are met.

### Checklist

Has sequencing been performed in **both directions?**

Has the novel allele been **sequenced in isolation** from the second allele?

Has the primers sequence used to amplify an allele been removed from the sequence being submitting?

Has an EMBL, GenBank or DDBJ **accession number** been obtained? If not the sequence must be submitted to one of these databases at the following addresses:

EMBL: </embl/Submission/index.html>

GenBank: <http://www.ncbi.nlm.nih.gov/Genbank/submit.html>

DDBJ: <http://www.ddbj.nig.ac.jp/submission-e.html>

Does your sequence meet the **minimum requirements** for sequence length?

Have exons 2 and 3 been sequenced at minimum for an HLA class I sequence? Or exon 2 at minimum for an HLA class II sequence?

Have you provided the HLA typing for the A, B and DRB1 genes of the source individual?

[Proceed to next step](#)

## Resources

- [!\[\]\(127d4a3e36ea604f52f4aa43782b3bc2\_img.jpg\) About >](#)
- [!\[\]\(7c8d466228a8bf5b49a0ba20858effa4\_img.jpg\) Statistics >](#)
- [!\[\]\(62f04c21d236587e834b549b6fe89fd1\_img.jpg\) Publications >](#)
- [!\[\]\(a75e4f4918e3588d18c38aac8bcebd59\_img.jpg\) Nomenclature >](#)
- [!\[\]\(45f82ab053adf6d225efa8c82a52317f\_img.jpg\) Releases >](#)
- [!\[\]\(69ece484ee9fc43a2b769c26f7b78896\_img.jpg\) Tools >](#)
- [!\[\]\(68c032fdebbb467db5cfc5c6047c9a45\_img.jpg\) Align >](#)
- [!\[\]\(37b2fd0e7312f68e50a2732e58fd60a0\_img.jpg\) Alleles >](#)
- [!\[\]\(9fd58ffedcba3a323a9d00d0bd69e64e\_img.jpg\) BLAST >](#)
- [!\[\]\(b3394a7f3721a28d35215cedc52b17b1\_img.jpg\) SBT Ambigs >](#)
- [!\[\]\(7f4cf229436b61a218a1c848ca73a225\_img.jpg\) Cells >](#)
- [!\[\]\(7ce3b75a88711935f3a3f115cb26ad61\_img.jpg\) DPB TCE >](#)
- [!\[\]\(c0d8fba4b9c81ad5b2f2f7d8e78c3e7b\_img.jpg\) Dictionary >](#)
- [!\[\]\(10c9360906b5596d7695fa93076677c9\_img.jpg\) FTP >](#)
- [!\[\]\(6984ac007add7a08addd04570216ced2\_img.jpg\) GitRepos >](#)
- [!\[\]\(e09ed1124d4663f839a12114ae26872d\_img.jpg\) FAQ >](#)
- [!\[\]\(ae8d40695305d7811d1eb60d44420e65\_img.jpg\) Links >](#)
- [!\[\]\(3c2f7b79c05e4f46fad2943d916f0a19\_img.jpg\) Submissions >](#)

## Sponsors

# Inserimento in IMGT



## IPD - IMGT/HLA

[IPD](#) > [IMGT/HLA](#) > Submissions

### Stage 3 - Basic Sequence Information

Please complete all sections

Local Name:

JME 956-16

Sequence Type:

Class II - Partial CDS

Source Entries

1. All submissions must contain a valid EMBL/GenBank/DDBJ accession number.

2. Multiple accession numbers should be separated by a comma (,).

Accession Number(s):

KY003228

→ numero BankIt



IMGT/HLA Database Release Policy

The IMGT/HLA Database will not release confidential sequences until the date you specify, upto a maximum of six months. If sequences are publically available in EMBL/Genbank/DDBJ or published in a journal, we will make these public in the following release of the database.

Release Date:

19

Oct 2016

Continue

Clear Form

# Inserimento in IMGT



**IPD - IMGT/HLA**

[IPD](#) > [IMGT/HLA](#) > Submissions

## Stage 5 - Submit Nucleotide Sequence and Sequence Features

### Sequence Alignment

Launch BLAST server - You can use the BLAST server to provide the name of the closest matching HLA sequence and also to check for vector contamination using the [EMVEC Database](#).

Please Select Locus:

Closest known HLA Allele eg: 'A\*01:01:01:01'

HLA-DQA	▼
DQA1*01:03:01:01	



### Written Description

You must include a full written description indicating how your sequence differs from the closest known HLA allele you have listed above, as well as any additional features such as inserts or deletions. Sequence descriptions should be numbered according to the HLA alignments and not numbered from the first base of your sequence.

e.g. B\*07:01 has 1nt change from B\*07:02:01 at nt 131 where C>T (codon 20 CCC>CTC) resulting in a coding change, 20P is changed to L.

DQA1\*01 new has 1nt change from DQA1\*01:03:01:01 at nt212 where G >A(codon 48 TGG>TAG) resulting in a coding change, 48W is changed to Y (Stop codon)



### Entering sequence features (co-ordinates)

#### Exon only (CDS) Submissions

If you are submitting a single exon (class II only) or exons 2+3 (class I), you can skip the sequence features section. Please note that if your sequence does contain non-coding regions and you use this option, the processing time of your submission will be greatly increased.

#### Manual Submission of Features

If you are submitting a sequence which has non-coding regions, please use the manual features option. This is the same as the previous version and lets you annotate all sequence features.

For more information see the [sequence feature help page](#).

#### Assigning sequence features with 'automatic' detection

If you are submitting the **complete genomic sequence** for a **class I allele**, the exon and intron co-ordinates can be detected semi-automatically. It is possible for some features to be incorrectly identified and so care should be made to check that the co-ordinates returned correlate with those you expect.

Note - If the gene of interest is not supported, you will have to revert to manual sequence feature labelling.

# Inserimento in IMGT

Input Sequence Features:

Exon Sequence (No Features)

Number of Features:

→ Se si hanno + BX

## Nucleotide Sequence Features

Please enter the nucleotide sequence here, do not include numbering or any annotation in the sequence.

```
CTGACCATGTTGCTCTTGTGGTAAACCTTGACCAAGTTTAACGGTCCCTCTGCCAGTTAACCC  
CATGAATTGATGGAGATGAGCAGTTCTACGTGGACCTGGAGAAGAAGGAGACTGCGTGGCGG  
TAGCGTGGAGTTCAAGCAAATTGGAGGTTTGACCGCGAGGGTGCAGTGAGAAAATGGCTGTG  
GCAAAACACAACATTGAAACATCATGATTAAACCGTACAACCTAACCGCTGCTACCAATGAGGTTCC  
TGAGGTACAGTGTTCAGTCTCCCGTGACAGCTGGGTGAGGCGAACACCGCTCATCTGTCTT  
GTGGACAAACATCTTCCCTCTGTGGTCAACATCACATGGCTGAGCAATGGGCAOGCAGTCACAG  
AAGGTGTTCTGAGACCGAGCTTCTCTGAGAAGTGTGATCATTCCTCTCAAGATCAAGTACCTC  
ACCTTCCCTCCCTCTGCTGATGAGATTATGACTGCAAGGTGGAGCACTGGGGCCTGGACAGC  
CTCTTCTGAAACACTGGG
```

No N  
Solo CDS

Continue

Clear Form

PD-IMGT/HLA

# Inserimento in IMGT



[IPD](#) > [IMGT/HLA](#) > Submissions

## Stage 7 - Information on the Source Cell or Individual

This form allows you to enter details of the cell/individual from which the sequence originates. The IMGT/HLA Database requires details of the source cell/individual in order for the sequence to be submitted.

For help on any section of the cell details, click [here to open the Cell Help Page](#) in a separate window.

We would like to encourage all submitters to provide ethnic origin information when possible. This information is of great interest to the HLA community.

Cell/Individual Details	
Cell/Individual ID/Code:	<input type="text" value="IME 956-16"/> <small>Important Note: Please do not use a person's name for this field</small>
Other names:	<input type="text"/>
Ethnic origin:	<input type="text" value="Caucasoid - Italy, Europe"/>
Sex of donor:	<input type="text" value="Female"/>
Consanguineous:	<input type="text" value="Unknown"/>
Homozygous:	<input type="text" value="No"/>
Comments:	<input type="text"/>
Contact Information	
Lab of Origin:	<input type="text" value="IME foundation"/>
Lab Contact:	<input type="text" value="marianna.bettarini"/>
Cell Availability	
Material Available:	<input type="text" value="DNA"/>
Cell Bank:	<input type="text" value="Not Available"/>
Cell Workshop Details	
IHW No:	<input type="text"/>
7th Workshop:	<input type="text"/>
8th Workshop:	<input type="text"/>
9th Workshop:	<input type="text"/>
10th Workshop:	<input type="text"/>
Other Workshops:	<input type="text"/>

[Continue](#) | [Clear Form](#)

# Inserimento in IMGT



## IPD - IMGT/HLA

[IPD](#) > [IMGT/HLA](#) > Submissions

### Stage 8 - Source Sample Typing Profile

Information on the HLA typing or serology of the sample aids analysis and the eventual assignment of an official name. Whilst it is not a requirement to fully type a sample before submission, the IMGT/HLA database encourages submitters to provide as much information on the source of the sample as possible.

For each gene please enter any serological typing data and any DNA typing data in the appropriate box and separate serological subtypes and alleles by a comma. Whilst DNA typing is not mandatory the inclusion of HLA-A, B, C and DRB1 typing may speed up the processing of your submission.

For DNA-typing enter the allele names in the boxes provided.  
e.g.: A cell DNA typed as HLA-A\*02:01, 24:01 would be entered as 02:01, 24:01 in the HLA-A\* box of the HLA DNA Typing section. Where possible do not use NMDP Ambiguity codes to replace allele names.

For serological data please enter the highest subtype specificity. If you have not performed serological typing, please do not infer serology typing from DNA typing methods, leave the boxes blank.  
e.g.: A cell typed serologically as A2, A24(9) would be entered as 2, 24 in the HLA-A box.

#### Source Sample Profile - HLA DNA Typing

DNA typing data should be entered for each gene using the current nomenclature. DNA Typing includes entering your local allele designation in the appropriate box. HLA-A, B and DRB1 typing is mandatory.

HLA-A*	03, 24	HLA-DRB6*	
HLA-C*	04, 12	HLA-DRB7*	
HLA-B*	35, 38	HLA-DRB8*	
HLA-DRA*		HLA-DRB9*	
HLA-DRB1*	11, 13	HLA-DQA1*	01NEW, 05:05
HLA-DRB3*		HLA-DQB1*	03, 06
HLA-DRB4*		HLA-DPA1*	
HLA-DRB5*		HLA-DPB1*	

#### Source Sample Profile - Serology

If you have not performed serological typing, please do not infer serology typing from DNA typing methods, leave the boxes blank.

HLA-A		HLA-DR51	
HLA-C		HLA-DR52	
HLA-B		HLA-DR53	
HLA-Bw4/w6		HLA-DQ	
HLA-DR		HLA-DP	

[Continue](#)

[Clear Form](#)

# Inserimento in IMGT



**IPD - IMGT/HLA**

[IPD](#) > [IMGT/HLA](#) > Submissions

## Return to Stage 7 - Submissions from Multiple Cells/Sources

If your sequence comes from multiple sources you may now add these to your submission. To add further sources please click the "New Source" button and repeat the procedure for entering a cell line. You may enter as many sources as you require. Once you have completed all entries please move to the section below.

[New Source](#)

## Stage 9 - Methods

Once all cell entries are complete please enter method data below. Please complete all sections.

### Methods

Primary Sequencing:

Secondary Sequencing:

Types of PCR primers:

Please confirm that your novel allele has been sequenced in isolation from any second allele of the same locus in a heterozygous DNA sample and that this allele has not only been determined by Sequencing Based Typing (SBT).

Sequenced in isolation:

Primers Used

Please provide details of all primers used in the amplification and sequencing for this submission.

For each primer, provide its sequence, name and the location it binds.

Primer 1

Primer 2

Primer 3

Primer 4

Primer 5

Primer 6

Primer 7

Primer 8

No. Clones sequenced:

8

No. PCR reactions:

Sequencing Direction:

It is mandatory to sequence in both directions. If sequencing has been performed in only one direction, your submission will be held until such a time as the work is completed.

Confirmation Methods

<input type="checkbox"/> PCR-SSO	<input type="checkbox"/> PCR-SSP	<input type="checkbox"/> PCR-RFLP	<input type="checkbox"/>
<input type="checkbox"/> Reverse-SSOP	<input checked="" type="checkbox"/> SBT	<input type="checkbox"/> NGS	<input type="checkbox"/> None

Other Comments i.e. analysis software,, phasing methods

# Inserimento in IMGT



## IPD - IMGT/HLA

[IPD](#) > [IMGT/HLA](#) > Submissions

FINE !

### Submission Process Completed

Submission HWS10027015, by mariarosa battarra is now complete

Please write down the ID number for use in any further communications and print this page.

Your submission will now be processed and you will be contacted shortly regarding the official name or for further information. Every effort will be made to process your submission in a timely manner, however in the unlikely situation that you do not hear anything from us after three months, please [contact us](#). Once processed your submission will be entered into the IMGT/HLA Database and also included in the next monthly update of HLA sequences published in *Tissue Antigens*, *Human Immunology* and the *International Journal of Immunogenetics*.

Your completed submission is shown below, please print this for your records;



Bambino Gesù  
OSPEDALE PEDIATRICO

# GRAZIE PER L'ATTENZIONE