

# Compatibilità e Alleli NEW

Dott.ssa Mariarosa Battarra  
Laboratorio d'Immunogenetica dei Trapianti  
Dipartimento di Oncoematologia e Terapia Cellulare e Genica  
IRCCS Ospedale Pediatrico Bambino Gesù

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

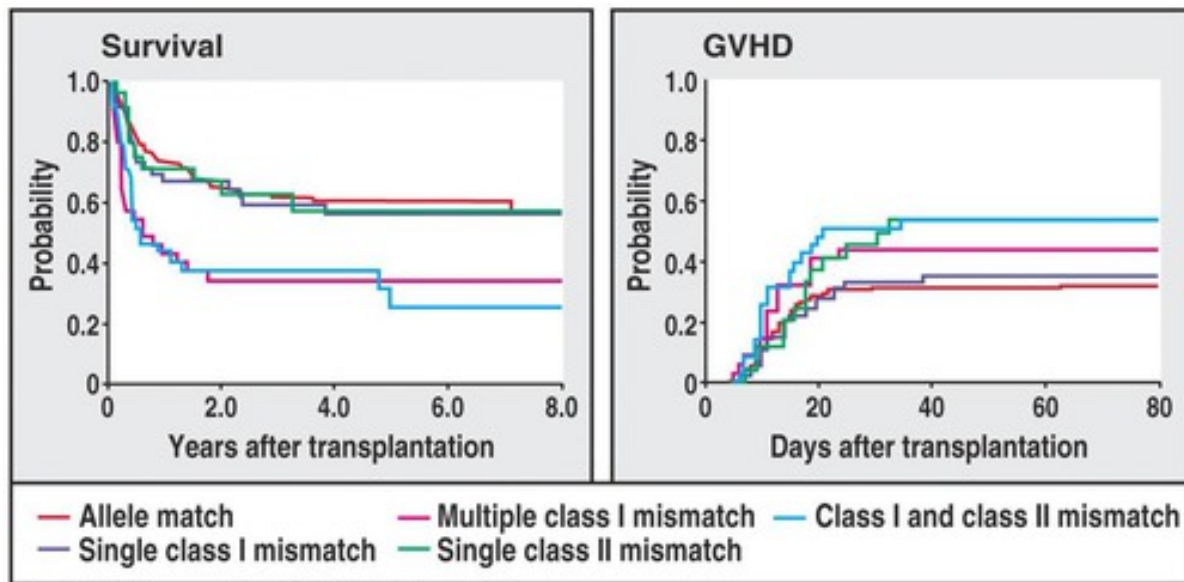
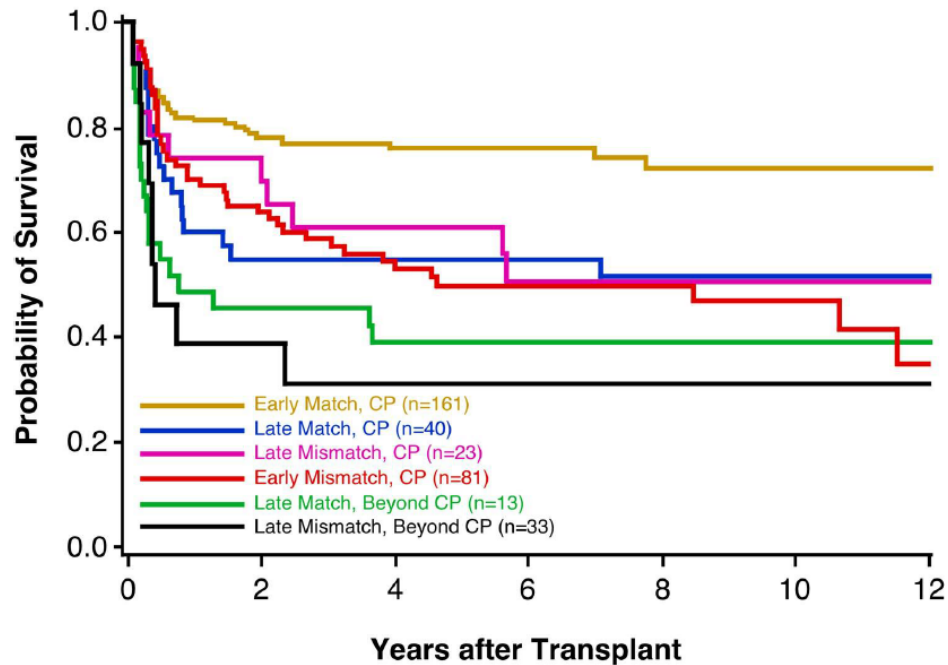



Figure 12-34 The Immune System, 2/e (© Garland Science 2005)

# 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 Bllod, 2004Nov 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

## 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

## 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 IMG

# ESEMPIO

---

2052-16 HLA-A\*03 NEW

EX2

GCTCCCACTCCATGAGGTATTTCTTCACATCCGTGTCCCGGCCCGGCCGCGGGGAGCCCCGCTTCATCGCCGTGGGCTA  
CGTGGACGACACGCAGTTCGTGCGGTTTCGACAGCGACGCCGCGAGCCAGAGGATGGAGCCGCGGGCGCCGTGAATAG  
AGCAGGAGGGGGCCGGAGTATTGGGACCAGGAGACACGGAATGTGAAGGCCAGTCACAGACTGACCGAGTGGACCTG  
GGGACCCTGCGCGGCTACTACAACCAGAGCGAGGCCG

INTR 2

NN  
NN  
NN  
NN

EX3

GTTCTCACACCATCCAGATAATGTATGGCTGCGACGTGGGGTTCGGACGGGCGCTTCCTCCGCGGGTACCGGCAGGACG  
CCTACGACGGCAAGGATTACATCGCCCTGAACGAGGACCTGCGCTCTTGACCGCGGCGGACATGGCGGCTCAGATCA  
CCAAGCGCAAGTGGGAGGCGGCCCATGTGGCGGAGCAGCAGAGAGCCTACCTGGATGGCACGTGCGTGGAGTGGCTC  
CGCAGATACCTGGAGAACGGAAGGAGACGCTGCAGCGCACGG



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:

A

Features:

Genomic - Intron 2

### STEP 2 - Specify reference and required sequences

Reference sequence:

03:01:01:01

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

03:01:01:01|

## Resources

About >

Publications >

Releases >

Align >

BLAST >

Cells >

Dictionary >

GitRepos >

Links >

Statistics >

Nomenclature >

Tools >

Alleles >

SBT Ambigs >

DPB TCE >

FTP >

FAQ >

Submissions >

## Sponsors



## 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 would welcome any evidence that helps to maintain the accuracy.

[Please click here to perform further alignments](#)

**241 bp ->241 N**

gDNA	480	490	500	510	520	530	540	550	560	570
A*03:01:01:01	GTGAGTG	ACCCCGGCCG	GGGGCGCAGG	TCAGGACCCC	TCATCCCCCA	CGGACGGGGC	AGGTGCCCCA	CAGTCTCCGG	GTCCGAGATC	CACCCCGAAG
gDNA	580	590	600	610	620	630	640	650	660	670
A*03:01:01:01	CCGCGGGACC	CCGAGACCCT	TGCCCCGGGA	GAGGCCCAGG	CGCCTTTACC	CGGTTTCATT	TTCAGTTTAG	GCCAAAAATC	CCCCCGGGTT	GGTCGGGGCT
gDNA	680	690	700	710						
A*03:01:01:01	GGGCGGGGCT	CGGGGGACTG	GGCTGACCGC	GGGGTCGGGG	CCAG					

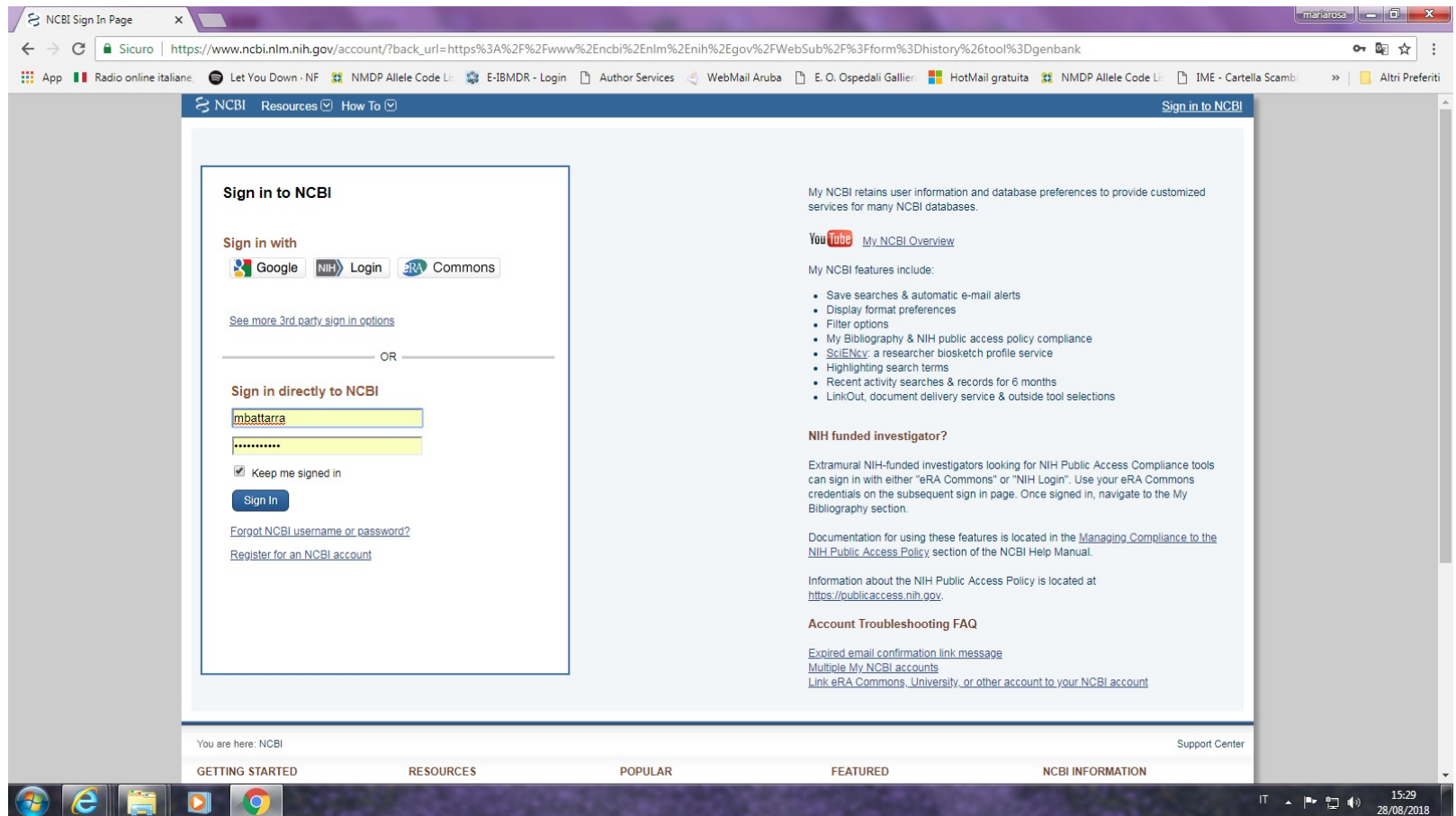
[illegible]

ACCCCCCAAGACACATATGACCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCCTGGGCTTCTA  
CCCTGCGGAGATCACACTGACCTGGCAGCGGGATGGGGAGGACCAGACCCAGGACACGGAGCTCGTGAGACCAGGC  
CTGCAGGGGATGGAACCTTCCAGAAGTGGGCGGCTGTGGTGGTGCCTTCTGGAGAGGAGCAGAGATACACCTGCCATG  
TGCAGCATGAGGGTCTGCCCAAGCCCCTCACCCCTGAGATGGG

12

# Inserimento in Bankit

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



The screenshot shows the NCBI Sign In Page in a web browser. The browser's address bar displays the URL [https://www.ncbi.nlm.nih.gov/account/?back\\_url=https%3A%2F%2Fwww%2Encbi%2Enih%2Egov%2FWebSub%2F%3Fform%3Dhistory%26tool%3Dgenbank](https://www.ncbi.nlm.nih.gov/account/?back_url=https%3A%2F%2Fwww%2Encbi%2Enih%2Egov%2FWebSub%2F%3Fform%3Dhistory%26tool%3Dgenbank). The page features a navigation bar with links to NCBI, Resources, and How To. The main content area is titled "Sign in to NCBI" and includes a "Sign in with" section with buttons for Google, NIH Login, and eRA Commons. Below this is a "Sign in directly to NCBI" section with a username field containing "mbattarra", a password field with masked characters, a "Keep me signed in" checkbox, and a "Sign In" button. Links for "Forgot NCBI username or password?" and "Register for an NCBI account" are also present. To the right, there is a section titled "My NCBI retains user information and database preferences to provide customized services for many NCBI databases." followed by a "YouTube My NCBI Overview" link. Below this, a list of "My NCBI features include:" is provided, including save searches, display format preferences, filter options, My Bibliography, NIH public access policy compliance, SciENcy, highlighting search terms, recent activity searches, and LinkOut. A section titled "NIH funded investigator?" explains that extramural NIH-funded investigators can sign in with either "eRA Commons" or "NIH Login". It also mentions that 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>. A section titled "Account Troubleshooting FAQ" includes links for "Expired email confirmation link message", "Multiple My NCBI accounts", and "Link eRA Commons, University, or other account to your NCBI account". The footer of the page shows the user's location as "You are here: NCBI" and a "Support Center" link. The browser's taskbar at the bottom shows various application icons and the system clock indicating 15:29 on 28/08/2018.

**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**

☒ Keep me signed 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.

**YouTube** [My NCBI Overview](#)

My NCBI features include:

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

**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

# Inserimento in Bankit


**BankIt**

My NCBI  
Welcome Mariarosa Battarra (mbattarra) [\[Sign Out\]](#)

## 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 (*.gz)</a>	

# Inserimento in BankIt

## BankIt

Logged in as Mariarosà 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
mariarosà		battarra		<input type="checkbox"/>

[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

Logged in as Marirosa 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

#### 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?

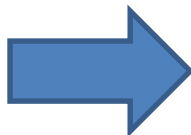
Paste Sequence(s) → [Inserts FASTA from clipboard](#)

```
NNACCCCCCAAGACAGATATGACCCACCACCCCATCTCTGACCATGAGGCCACC
CTGAGGTTGCTGGGCCCCCTGGGGCTTCTACCCCTGCGGAGATCACAAGTACCTGGCA
GCGGGATGGGGAGACACAGACCCAGGACACGAGCTCGTGGAGACCAGGCCT
GCAGGAGATGGGAACCTTCCAGAAAGTGGCGGCTGCTGGTGGTGCCTTCTGGAGA
GGAGCAGAGATACACCTGCCATGTGCAGCATGAGGGTCTGCCCAAGCCCCCTCAC
CCTGAGATGGG
```

Example FASTA nucleotide format:

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

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





17

# Inserimento in Bankit



## BankIt

Logged in as Mariacosa 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](#)
[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	Warning
1	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 CONTINUA



1/2

# Inserimento in Bankit

## BankIt

Logged in as Mariarosa Battarra (mbattarra) [Logout](#)

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'

**Strand?** ☒ 5' ☐ 3'

**Partial?** ☒ 1 ☐ 2 ☐ 3

If partial at 5' end, indicate reading frame: ☐ Yes ☒ No

Is this a Pseudogene? ☐ Yes ☒ No

Is this an intronless gene? ☐ Yes ☒ No

**Nucleotide Interval Spans:**  
☒ Entire Sequence *→ scegliete questa opzione quando si sequenzia un solo esone (come nel DBA1)*  
☐ Specific Spans - specify nucleotide numbers within your sequence. (Use this if your sequences contain introns)

Start	Stop	Strand
1	270	Plus ▼
512	787	Plus ▼
1366	1641	Plus ▼

[Add](#) more intervals

**Protein Information**  
**Protein Name**   
**Protein Description**   
**EC Number**

# Inserimento in Bankit

---

**BankIt**

Logged in as Merlarosa 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

### 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 [gh-admin@ncbi.nlm.nih.gov](mailto:gh-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](#)

---

[Contact](#) | [Copyright](#) | [Disclaimer](#) | [Privacy](#) | [Accessibility](#)  
National Center for Biotechnology Information, US National Library of Medicine  
8800 Rockville Pike, Bethesda, MD USA 20894

## 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
<p><b>Search</b> Search tool for generating probe and primer hit tables.</p>							
<p><b>Sequence Alignments</b> Interactive sequence alignment tool with <a href="#">help page</a> available.</p> <p>Static text version of the sequence alignments are available from <a href="http://hla.alleles.org/">http://hla.alleles.org/</a> provided by the <a href="#">HLA Informatics Group</a>.</p>							
<p><b>Search Determinants</b> A comparison of search determinants used by different registries (2007)</p>							
<p><b>Submission Tools</b></p> <p><b>Sequence Submission Tool</b> Online submission of sequences to the WHO Nomenclature Committee for Factors of the HLA System.</p>							
<p><b>Other EBI Search Tools</b></p> <p><b>BLAST Search Tool</b> The EBI's BLAST search engine for nucleotide and protein searches.</p> <p><b>FASTA Protein Search Tool</b> The EBI's FASTA search engine for protein sequence searches.</p>							
<p><b>Phylogenetic Analysis</b></p>							

## Resources

- About >
- Publications >
- Repositories >
- Align >
- BLAST >
- Cells >
- Dictionary >
- GitRepos >
- Links >
- Statistics >
- Nomenclature >
- Tools >
- Alleles >
- SBT Ambigs >
- DPB TCE >
- FTP >
- FAQ >
- Submissions >

Sponsors

GENDX

# Inserimento in IMGT

Overview
IMGTHLA
KIR
MHC
HPA
ESTDAB
Contact
Support

IPD / IMGTHLA / 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 <b>both directions</b> ?	<input checked="" type="checkbox"/>
Has the novel allele been <b>sequenced in isolation</b> from the second allele?	<input checked="" type="checkbox"/>
Has the primers sequence used to amplify an allele been removed from the sequence being submitting?	<input checked="" type="checkbox"/>
Has an EMBL, GenBank or DDBJ <b>accession number</b> been obtained? If not the sequence must be submitted to one of these databases at the following addresses: EMBL: <a href="http://embl/Submission/index.html">/embl/Submission/index.html</a> GenBank: <a href="http://www.ncbi.nlm.nih.gov/Genbank/submit.html">http://www.ncbi.nlm.nih.gov/Genbank/submit.html</a> DDBJ: <a href="http://www.ddbj.nig.ac.jp/submission-e.html">http://www.ddbj.nig.ac.jp/submission-e.html</a>	<input checked="" type="checkbox"/>
Does your sequence meet the <b>minimum requirements</b> 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?	<input checked="" type="checkbox"/>
Have you provided the HLA typing for the A, B and DRB1 genes of the source individual?	<input checked="" type="checkbox"/>

Proceed to next step

## Resources

- About >
- Publications >
- Releases >
- Align >
- BLAST >
- Cells >
- Dictionary >
- GitRepos >
- Links >
- Statistics >
- Nomenclature >
- Tools >
- Alleles >
- SBT Ambigs >
- DPB TCE >
- FTP >
- FAQ >
- Submissions >

## Sponsors

# Inserimento in IMGT



## IPD - IMGT/HLA

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

### Stage 3 - Basic Sequence Information

Please complete all sections

Local Name:

IME 956-16

Sequence Type:

Class II - Partial CDS

Source Entries

1. All submissions **must** contain a valid EMBL/GenBank/DBJ accession number.
2. Multiple accession numbers should be separated by a comma (,).

Accession Number(s):

KY003228

→ *nona 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/DBJ 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](#) > 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.

eg: B\*07:new 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 you 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 may 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 IMG

Input Sequence Features:

Exon Sequence (No Features)

→ se si hanno + EX

Number of Features:

Nucleotide Sequence Features

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

```
CTGAACATGTTGCCTCTTGTGGTGTAACTTGTACCAAGTTTACGGTCCCTCTGGCCAGTTCAGC
CATGAATTTGATGGAGATGAGCAGTTCTACGTGGACCTGGAGAAGAAGGAGACTGCCTGGCGG
TAGCCTGAGTTCAGCAAATTTGGAGGTTTTGACCCGCGAGGGTGCAGTGGAGAAACATGGCTGTG
GCAAAACACAACCTTGAACATCATGATTAAACGCTACAACCTCTACCGCTGCTACCAATGAGGTTCC
TGAGGTGACAGTGTTCCTCAAGTCTCCCGTGACACTGGGTGAGCCCAACACCCCTCATCTGTCTT
GTGGACAACATCTTCCTCCTGTGGTCAACATCAGATGGCTGAGCAATGGGCAAGCAGTCACAG
AAGGTGTTTCTGAGACCAGCTTCCTCTCCAAGAGTGATCATTCCTTCTTCAAGATCAGTTACCTC
ACCTTCCTCCCTTCTGCTGATGAGATTTATGACTGCAAGGTGGAGCACTGGGGCCTGGACCAGC
CTCTTCTGAAACACTGGG
```

NO N  
Solo CDS

Continue

Clear Form

PD-IMG/HLA

1. ANALISI DI SEQUENZE

# 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:	IME 956-16
Other names:	Important Note: Please do not use a person's name for this fields
Ethnic origin:	Caucasoid - Italy, Europe ▼
Sex of donor:	Female ▼
Consanguineous:	Unknown ▼
Homozygous:	No ▼
Comments:	
Contact Information	
Lab of Origin:	IME foundation
Lab Contact:	mariorosa.bettarra
Cell Availability	
Material Available:	DNA ▼
Cell Bank:	Not Available ▼
Cell Workshop Details	
IHW No:	
7th Workshop:	
8th Workshop:	
9th Workshop:	
10th Workshop:	
Other Workshops:	

# 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:

Direct sequencing of PCR product from DNA (SBT) ▼

Secondary Sequencing:

Direct sequencing of PCR product from DNA (SBT) ▼

Types of PCR primers:

Both allele and locus specific ▼

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:

Yes ▼

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	GenDX locus HLA-DQA1
Primer 2	GenDX locus HLA-DQA1 EX2 DQA1*01
Primer 3	GenDX locus HLA-DQA1 EX2 DQA1*05
Primer 4	GenDX locus HLA-DQA1 EX3 FW
Primer 5	GenDX locus HLA-DQA1 EX3 Rv
Primer 6	
Primer 7	
Primer 8	

No. Clones sequenced:

6

No. PCR reactions:

6

Sequencing Direction:

Both ▼

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"/> 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 mariorosa 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;

# GRAZIE PER L'ATTENZIONE