



ImmPort MHC Alignment Query

Basic MHC Alignment Query Overview

Search genomic, transcripts or protein sequence alignments for specific or a set of alleles for a MHC locus at a defined region. Searches use allele name, IMGT accession, CWD allele name, G-Code group code, protein and transcript sequence. Or enter specific allele names that conform to the HLA nomenclature. The 'Sequence Type' option below defines that type of sequence to return on the result and can vary from the search sequence used for searching.

For example, A*0202,A*0205, or A0202, A0205, or 0202,0205, or any combination. All searches are case-insensitive. For g-codes, an optional g-suffix can be added. For sequence-based searches, protein or transcript sequences are entered. The 'like' Search Option is a string match operator and not blast-based.

-- CWD alleles and g-codes are described in the paper, "Common and well-documented HLA alleles: report of the Ad-Hoc committee of the American Society for Histocompatibility and Immunogenetics" [[17462507](#)].

-- G-code grouping data was enhanced with ambiguity typing data obtained from Anthony Nolan, [[IMGT/HLA Database](#)].

-- Population data used for generation of allele frequencies was obtained from dbMHC, [[Human Anthropology](#)].

Note: For protein sequence types, "Mature Proteins" are used. For instance, in the HLA-A alleles, the "Mature Proteins" start from 25-100 and so if you search for 0-10 you will get no result (null). If you search for 20-30, you get first five characters of the sequence (25-30) and so on. For the non-HLA-A alleles, the range is from 1-32. Only HLA-A, HLA-B, HLA-C, HLA-DRA start at the 25th amino acid.

Fields marked with an asterisk * are required.

MHC Allele Search - Selected Return Data Type : **Alignment**

Please Choose Query Type: Alignment

General Criteria:

Species: Homo sapiens

Locus*: HLA-A

Allele Criteria:

Search For*: All Alleles

Search Using*: Allele Name

Search Option*: Like

Search Text: A*0102, A_0807, 07, 1611N
(Comma delimited)

Alignment Criteria:

Sequence Type*: genomic

Alignment Span*: All Positions Features

Start: End:

Exon
Intron
5UTR
3UTR
(Multiple)

Results per page: 25

Select Alignment from a list of query types

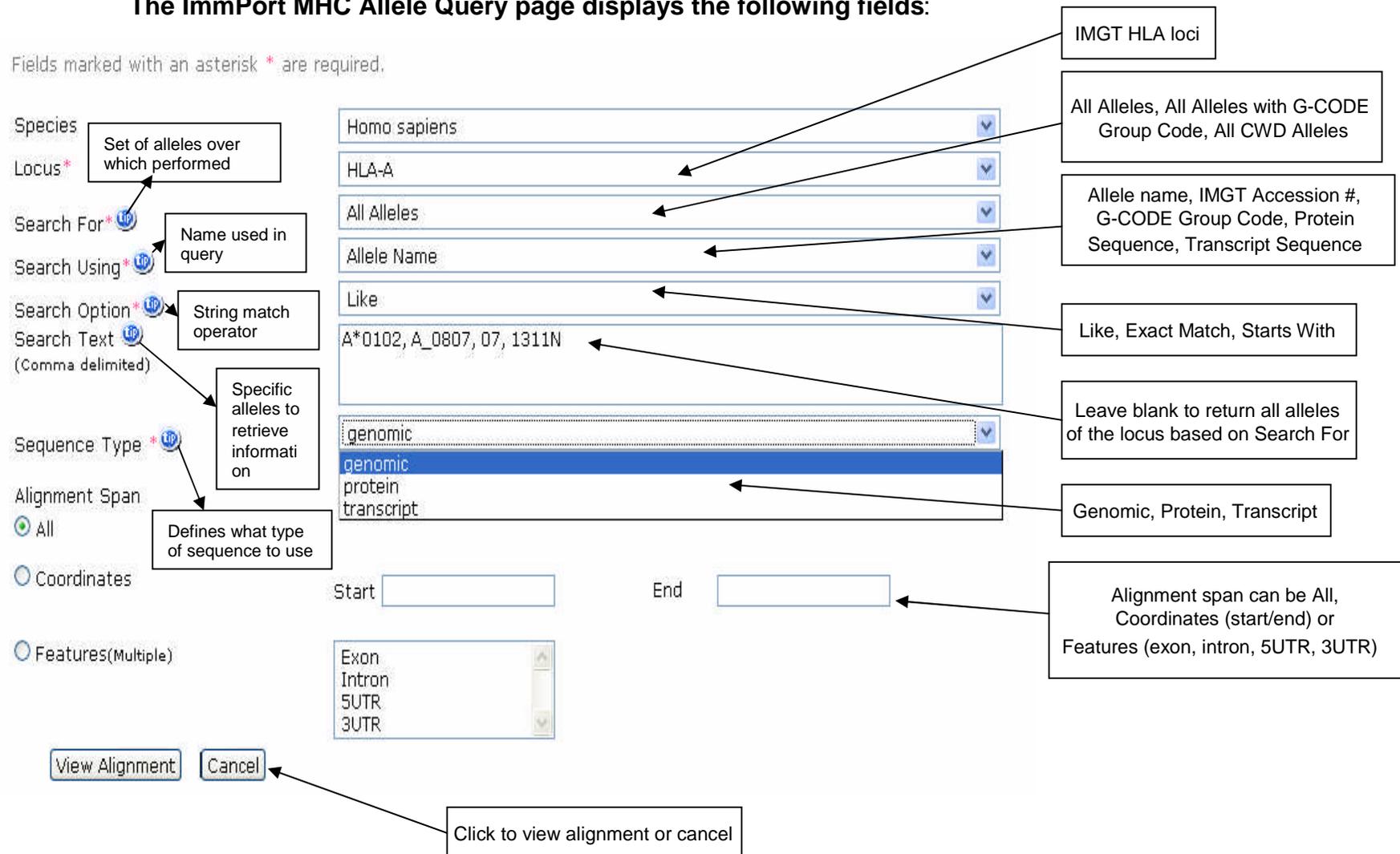
Click here to go back and make to the search page

Submit the query from selected criteria

Basic MHC Alignment Query Overview

The ImmPort MHC Allele Query page displays the following fields:

Fields marked with an asterisk * are required.



The screenshot shows the following fields and their annotations:

- Species:** Homo sapiens (Annotation: Set of alleles over which performed)
- Locus*:** HLA-A (Annotation: Name used in query)
- Search For*:** All Alleles (Annotation: Allele name, IMGT Accession #, G-CODE Group Code, Protein Sequence, Transcript Sequence)
- Search Using*:** Allele Name (Annotation: Allele name, IMGT Accession #, G-CODE Group Code, Protein Sequence, Transcript Sequence)
- Search Option*:** Like (Annotation: Like, Exact Match, Starts With)
- Search Text*:** A*0102, A_0807, 07, 1311N (Annotation: Leave blank to return all alleles of the locus based on Search For)
- Sequence Type*:** genomic (Annotation: Genomic, Protein, Transcript)
- Alignment Span:** All (Annotation: Defines what type of sequence to use)
- Start/End:** Empty text boxes (Annotation: Alignment span can be All, Coordinates (start/end) or Features (exon, intron, 5UTR, 3UTR))
- Features:** Exon, Intron, 5UTR, 3UTR (Annotation: Alignment span can be All, Coordinates (start/end) or Features (exon, intron, 5UTR, 3UTR))
- Buttons:** View Alignment, Cancel (Annotation: Click to view alignment or cancel)

Basic MHC Alignment Query Species and Locus Fields

MHC Alignment Query

Fields marked with an asterisk * are required.

Species

Homo sapiens

Species: ImmPort currently supports the human species (*Homo sapiens*). Additional species will be added in the future.

Locus

HLA-A

HLA-A

HLA-B

HLA-Cw

HLA-DMA

HLA-DMB

HLA-DOA

HLA-DOB

HLA-DPA1

HLA-DPB1

HLA-DQA1

HLA-DQB1

HLA-DRA

HLA-DRB1

HLA-DRB2

HLA-DRB3

HLA-DRB4

HLA-DRB5

HLA-DRB6

HLA-DRB7

HLA-DRB8

Locus: The ANRI curated list of HLA loci from IMGT is available.

Basic MHC Alignment Query Search Fields

MHC Alignment Query

Search For*

Set of alleles over which performed

Search Using*

Name used in query

Search Option*

Option type in query

Search Text

Specific alleles to retrieve information

Sequence Type*

Defines what type of sequence to use

Alignment Span

All

Coordinates

Features(Multiple)

View Alignment Cancel

Search For: This field is used for allele records for a MHC locus for all alleles, alleles with G-code group code, and all CWD alleles.

Search Using: This field is used to record the allele name, IMGT accession, G-code group code, protein and transcript sequence, CWD allele names that conform to the HLA nomenclature.

Search Option: The Search Option supports either the "Starts With" or "Exact Match" option. ...in the search text. For the "Exact" option all digits and suffixes in the allele names or all digits in IMGT Accessions need to be intact to find the match. For the "start with" option, the search returns all the matches to a partial input but aligned from the beginning of the names (e.g. if input is '0101' of HLA-A, it will return A*01010102N and A*01010101 ..., but not A*02010101).

Search Text: This field supports a comma delimited list of allele names (exact or partial) and returns all the matches. The Search function accepts many variants on allele name prefixes including A*, A, HLA-A, HLA_A.

Sequence Type: Selecting "genomic" will include all features like UTRs, coding and non-coding exons, and introns. Selecting "transcript" will return exon features.

Alignment Span: 'All' will display the sequence alignment from the beginning to end of an available sequence. The 'Coordinates' allows you to specify a region in gene using the Start and End boxes. The coordinates are based on the locus reference sequences from IMGT/HLA. The 'Features' with exon, intron, 5UTR and 3UTR are multi-selectable by holding CTRL key while clicking the features.

All Alleles

All Alleles

All Alleles with G-CODE Group Code

All CWD Alleles

Allele Name

Allele Name

IMGT Accession#

G-CODE Group Code

Protein Sequence

Transcript Sequence

Like

Like

Exact Match

Starts With

A*0102, A_0807, 07, 1611N

genomic

genomic

protein

transcript

Start

End

Exon

Intron

5UTR

3UTR

Allele Alignment

The aligned allele features are based on the query input options. The alignment reference sequence is based on the ANRI/IMGT reference. The scroll bar is used to view the entire matrix of the sequence alignment while maintaining the reference sequence at the top of the viewer. To modify the parameters selected, click Modify Search. The Alignment span can be All, Coordinates (start/end) or Features (exon, intron, 5UTR, 3UTR).

Alignment Viewer Legend:
 - denotes the same sequence as the reference
 * denotes not sequenced
 . denotes gaps

NOTE: If the alignment viewer coordinates and letters are not aligned, use the following correction path: Firefox > Tools > Options > Content > Select Fonts & Colors from the middle of pop-up page > Click Advanced > In the middle of the pop-up page, put a check on "Allow pages to choose their own fonts, instead of my selections above"

Reference Data / Allele Alignment Results

Home | Genes | Proteins | MHC Alleles | Pathways | Protein Networks | SNPs | ImmPort Gene Lists | Immunologically Related Genes | Download | Data History

[\(Modify Search\)](#)

Click to go back and modify search

Allele Search Criteria

Locus Name: HLA-A
Search For: All Alleles
Search Using: Allele Name
Search Option: Like **Text:** A*0102, A_0807, 07, 1611N

Alignment Specific Criteria

Sequence genomic

Type:

Alignment Span: ALL

Types:

Alignment Span coordinates

IMGT reference sequence

To view a detailed Allele summary, click Allele ID

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Allele ID	1	10	20	30	40	50	60	70	80
A*01010101 (Ref)	C	A	G	G	A	G	C	A	G
A*0207	*	*	*	*	*	*	*	*	*
A*2407	*	*	*	*	*	*	*	*	*
A*3307	*	*	*	*	*	*	*	*	*

A*0101, A*0201 alignment

HLA Nomenclature

The HLA allele names are curated by the WHO nomenclature committee (see <http://www.ebi.ac.uk/imgt/hla/nomenclature/index.html> and <http://www.anthonynolan.org.uk/HIG/lists/nomenlist.html>).

The allele names are in the format of

- Gene/locus,
- Asterisk,
- Allele family (the serological antigen),
- Allelic Subtype (Amino acid difference),
- Non-coding (synonymous) polymorphism, intron 3'or 5' polymorphism
- Optional suffix in single letter suffix 'N', 'L', 'S', 'C', 'A' or 'Q'
(N = Null expression, L = Low expression, Aberrant expression S = Secreted, C = Cytoplasm, Q = Questionable) .

The IMGT Accession is a sequence ID generated by IMGT (<http://www.ebi.ac.uk/imgt/hla/nomenclature/alignments.html>).

