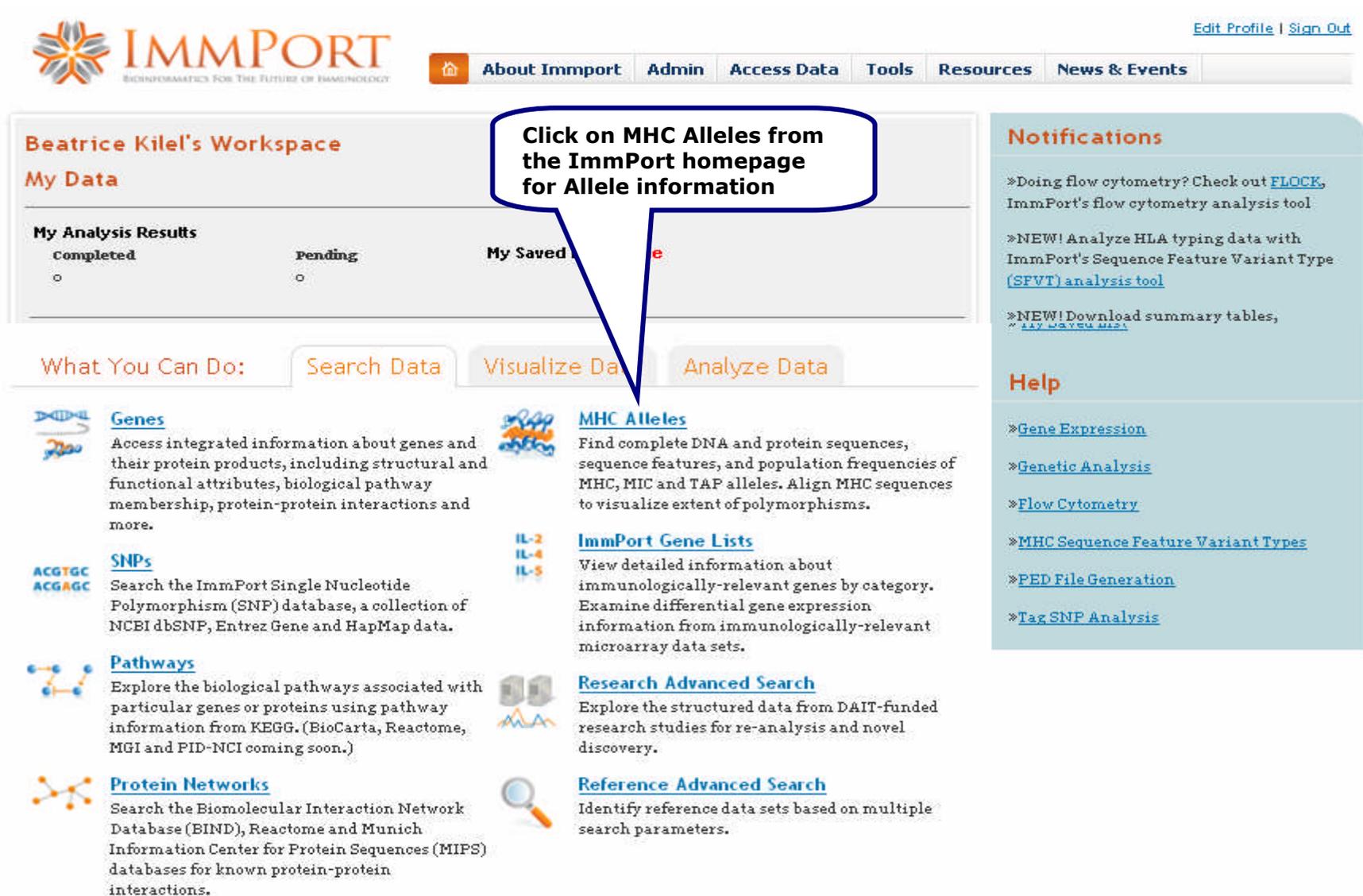


From the ImmPort homepage click MHC Alleles for Allele information.



Beatrice Kilel's Workspace
My Data

My Analysis Results
 completed ○ Pending ○ My Saved ○ e

What You Can Do: [Search Data](#) [Visualize Data](#) [Analyze Data](#)

Genes
 Access integrated information about genes and their protein products, including structural and functional attributes, biological pathway membership, protein-protein interactions and more.

SNPs
 Search the ImmPort Single Nucleotide Polymorphism (SNP) database, a collection of NCBI dbSNP, Entrez Gene and HapMap data.

Pathways
 Explore the biological pathways associated with particular genes or proteins using pathway information from KEGG. (BioCarta, Reactome, MGI and PID-NCI coming soon.)

Protein Networks
 Search the Biomolecular Interaction Network Database (BIND), Reactome and Munich Information Center for Protein Sequences (MIPS) databases for known protein-protein interactions.

MHC Alleles
 Find complete DNA and protein sequences, sequence features, and population frequencies of MHC, MIC and TAP alleles. Align MHC sequences to visualize extent of polymorphisms.

ImmPort Gene Lists
 View detailed information about immunologically-relevant genes by category. Examine differential gene expression information from immunologically-relevant microarray data sets.

Research Advanced Search
 Explore the structured data from DAIT-funded research studies for re-analysis and novel discovery.

Reference Advanced Search
 Identify reference data sets based on multiple search parameters.

Notifications

- »Doing flow cytometry? Check out [FLOCK](#), ImmPort's flow cytometry analysis tool.
- »NEW! Analyze HLA typing data with ImmPort's Sequence Feature Variant Type ([SFVT](#)) [analysis tool](#)
- »NEW! Download summary tables, [^ ALL WORKS HERE](#)

Help

- »[Gene Expression](#)
- »[Genetic Analysis](#)
- »[Flow Cytometry](#)
- »[MHC Sequence Feature Variant Types](#)
- »[PED File Generation](#)
- »[Tag SNP Analysis](#)

Callout Box: Click on MHC Alleles from the ImmPort homepage for Allele information



MHC Allele search information

Reference Data / MHC Allele Search

[Home](#) | [Genes](#) | [Proteins](#) | [MHC Alleles](#) | [Pathways](#) | [Protein Networks](#) | [SNPs](#) | [ImmPort Gene Lists](#) | [Immunologically Related Genes](#) | [Download](#) | [Reference Data History](#)

See below for MHC Allele Search information.

Fields marked with an asterisk * are required.

Select the arrow to modify your search criteria

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

Please Choose Query Type : **Allele**

General Criteria:

Species:

Locus * : **HLA-A**

Allele Criteria:

Search For * **All Alleles**

Search Using * **Allele Name**

Search Option * **Like**

Search Text
(Comma delimited)

Query search based on Allele. Indicate results per page and click submit or clear to redefine options

Click submit on the selected criteria or clear to reset the parameters

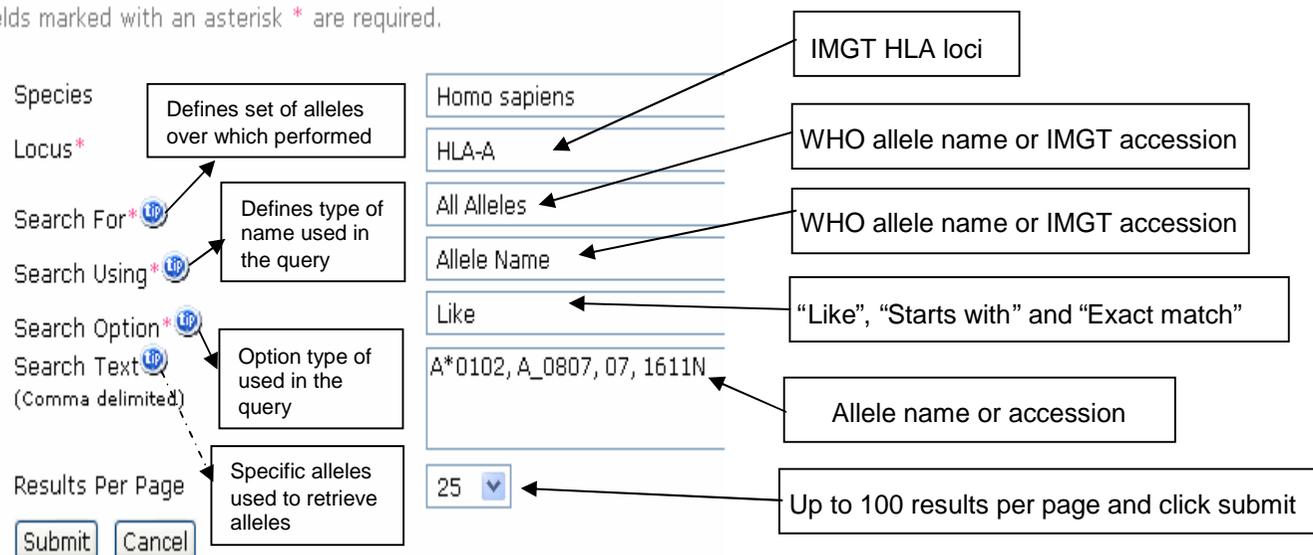
Basic MHC Allele Query Overview

The human leukocyte antigen system (HLA) is the name of the human major histocompatibility complex (MHC). Data obtained from IMGT/HLA database (<http://www.ebi.ac.uk/imgt/hla/>) maintained by the Anthony Nolan Research Institute (ANRI) includes accession, allele name, version, ethnic origin, cell source, gene structure, protein sequence, and genomic sequence. Search for allele records for a MHC locus using the 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. 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].

The ImmPort MHC Allele Query page displays the following fields:

Fields marked with an asterisk * are required.



The form contains the following fields and callouts:

- Species:** Homo sapiens (Callout: Defines set of alleles over which performed)
- Locus*:** HLA-A (Callout: IMGT HLA loci)
- Search For*:** All Alleles (Callout: WHO allele name or IMGT accession)
- Search Using*:** Allele Name (Callout: WHO allele name or IMGT accession)
- Search Option*:** Like (Callout: "Like", "Starts with" and "Exact match")
- Search Text* (Comma delimited):** A*0102, A_0807, 07, 1611N (Callout: Allele name or accession)
- Results Per Page:** 25 (Callout: Up to 100 results per page and click submit)
- Buttons:** Submit, Cancel

Note: To see alleles for a locus, please leave the Search Text field blank.



IMMPORT
BIOINFORMATICS FOR THE FUTURE OF IMMUNOLOGY

ImmPort MHC Allele 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.

Basic MHC Allele Query Species and Locus Fields

MHC Allele Query

Fields marked with an asterisk * are required.

Species

Locus*

Homo sapiens

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

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

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

Basic MHC Allele Query Search Fields

Allele Criteria:

Fields marked with an asterisk * are required.

Species

Locus*

Search For* 

Defines the set of alleles over which the search is performed

Search Using* 

Defines type of name used in the query - allele names exact search option for deleted and changed names list.- G-code group search type on group code names with optional g-suffix in search options - Transcript and protein sequence type

Search Option* 

This is a string match operator and not blast-based

Search Text 

(Comma delimited)

Enter A*01010102N for specific allele or just A*0101 to retrieve A*01010102N, A*01010101. Blank retrieves all alleles of locus based on Search For

Results Per Page

Submit

Cancel

Homo sapiens 

HLA-A

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 Sequenc-

Like 

Like

Exact Match

Starts With

A*0102, A_0807, 07, 1611N

25 

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: This field supports either the Starts With or Exact Match option. ... in the search text. For the 'Exact' option, all digits and suffixes in 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 matches to a partial input but aligned from the beginning of the name (e.g. if the 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.

Basic MHC Allele Query Search Fields

Sequence Feature Criteria:

Feature Type 

All Types
Structural
Functional
Sequence Alteration
Structural - Complete protein
Structural - Domain
Structural - Secondary structure motif
Structural - Cleaved peptide region
Sequence Alteration - Single amino acid variation
Sequence Alteration - Insertions and Deletions
Structural_Functional Combination
Structural_Sequence Alteration Combination
Functional_Sequence Alteration Combination

Feature Type is based on functional or structural characteristics or amino acid positions

Feature Names 
(Comma delimited)

A*0207

Allele Name can be comma-delimited combination

Feature Locations 
(Comma delimited)

-24

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)

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

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.

Start End

Exon

Intron

5UTR

3UTR

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.



Allele Query Results

The aligned allele features are based on the query input options. The alignment reference sequence is based on the ANRI/IMGT reference. To modify the parameters selected, click Modify Search. A summary of the search criteria is displayed. The results show the allele name/CWD, Sequence Features and Allele Features which can be sorted. Click each feature and more detailed information will be displayed.

Allele Query Results

[\(Modify Search\)](#)

Allele Search Criteria

Locus Name: HLA-A
Search For: All Alleles
Search Using: Allele Name
Search Option: Like

Text: A*0101

Click on Modify Search to go back to the MHC Allele search page

Click on Sequence and Allele Features for detailed information.
See next 3 slides

Selected items: A*01010101, A*01010102N, A*010102

Page 1 of 1 | View Details | Export | Displaying 1 - 6 of 6

<input type="checkbox"/>	Allele Name/CWD	Sequence Features	Allele Frequency
<input checked="" type="checkbox"/>	A*01010101 CWD		
<input checked="" type="checkbox"/>	A*01010102N		
<input checked="" type="checkbox"/>	A*010102		
<input type="checkbox"/>	A*010103		
<input type="checkbox"/>	A*010104		
<input type="checkbox"/>	A*010105		

Sort Ascending
Sort Descending
Columns

- Allele Name/CWD
- Sequence Features
- Allele Frequency

Select any or all boxes for detailed view or export the output file for further analysis



Allele Variant Sequence Features for **A*01010101**

Locus Name: **HLA-A**

Page 1 of 1 | Displaying 1 - 312 of 312

Variant Type	Sequence Feature Names	Sequence Feature Types	Positions	Sequence Motif
A*0101	Hsa_HLA-A_allele	Structural - Complete protei		
Hsa HLA-A SF2 UT1	Hsa_HLA-A_full-length prot	Structural - Complete protei	-24..341	-24M -23A -22V -21M -20A
Hsa HLA-A SF3 UT1	Hsa_HLA-A_signal peptide	Structural - Cleaved peptide	-24..-1	-24M -23A -22V -21M -20A
Hsa HLA-A SF4 UT1	Hsa_HLA-A_mature protein	Structural - Complete protei	1..341	1G 2S 3H 4S 5M 6R 7Y 8F
Hsa HLA-A SF5 UT1	Hsa_HLA-A_alpha 1 domai	Structural - Domain	1..90	1G 2S 3H 4S 5M 6R 7Y 8F
Hsa HLA-A SF6 UT1	Hsa_HLA-A_alpha 2 domai	Structural - Domain	91..182	91G 92S 93H 94T 95I 96Q
Hsa HLA-A SF7 UT1	Hsa_HLA-A_alpha 3 domai	Structural - Domain	183..274	183D 184P 185P 186K 187T
Hsa HLA-A SF8 UT1	Hsa_HLA-A_alpha 3 domai	Structural - Domain	275..284	275E 276L 277S 278S 279Q
Hsa HLA-A SF9 UT1	Hsa_HLA-A_putative transm	Structural - Domain	285..308	285V 286G 287I 288I 289A
Hsa HLA-A SF10 UT1	Hsa_HLA-A_putative cytopl.	Structural - Domain	309..341	309R 310R 311K 312S 313S
Hsa HLA-A SF11 UT1	Hsa_HLA-A_N-terminus seq	Structural - Secondary struct	1..2	1G 2S
Hsa HLA-A SF12 UT1	Hsa_HLA-A_beta-strand 1	Structural - Secondary struct	3..14	3H 4S 5M 6R 7Y 8F 9F 10T
Hsa HLA-A SF13 UT1	Hsa_HLA-A_loop between t	Structural - Secondary struct	15..17	15P 16G 17R
Hsa HLA-A SF14 UT1	Hsa_HLA-A_beta-strand 2	Structural - Secondary struct	18..28	18G 19E 20P 21R 22F 23I
Hsa HLA-A SF15 UT1	Hsa_HLA-A_loop between t	Structural - Secondary struct	29..30	29D 30D
Hsa HLA-A SF16 UT1	Hsa_HLA-A_beta-strand 3	Structural - Secondary struct	31..37	31T 32Q 33F 34V 35R 36F
Hsa HLA-A SF17 UT1	Hsa_HLA-A_loop between t	Structural - Secondary struct	38..45	38S 39D 40A 41A 42S 43Q
Hsa HLA-A SF18 UT1	Hsa_HLA-A_beta-strand 4	Structural - Secondary struct	46..47	46E 47P
Hsa HLA-A SF19 UT1	Hsa_HLA-A_loop between t	Structural - Secondary struct	48..49	48R 49A
Hsa HLA-A SF20 UT1	Hsa_HLA-A_alpha-helix 1	Structural - Secondary struct	50..54	50P 51W 52I 53E 54Q
Hsa HLA-A SF21 UT1	Hsa_HLA-A_loop between :	Structural - Secondary struct	55..56	55E 56G
Hsa HLA-A SF22 UT1	Hsa_HLA-A_alpha-helix 2	Structural - Secondary struct	57..84	57P 58E 59Y 60W 61D 62Q
Hsa HLA-A SF23 UT1	Hsa_HLA-A_loop between :	Structural - Secondary struct	85..93	85Y 86N 87Q 88S 89E 90D
Hsa HLA-A SF24 UT1	Hsa_HLA-A_beta-strand 5	Structural - Secondary struct	94..103	94T 95I 96Q 97I 98M 99Y



Allele Frequencies for A*01010101

(1) Ordered by Data Type and Population Area

(2) Population data acquired from the 13th International Histocompatibility Workshop and Congress 2003

(3) Serological pairs (A*02, A*92) and (B*15, B*95) are identical

Allele Name	Data Type	Population Area	Allele Freq	Allele Count	Total Alleles Examined
A*0101	sequencing	Australia	0.0222	18	810
A*0101	sequencing	Europe	0.1641	600	3656
A*0101	sequencing	North Africa	0.1367	38	278
A*0101	sequencing	North America	0.0352	47	1337
A*0101	sequencing	North-East Asia	0.0586	62	1058
A*0101	sequencing	Oceania	0.0101	10	994
A*0101	sequencing	Other	0.0718	78	1087
A*0101	sequencing	South America	0.0021	1	479
A*0101	sequencing	South-East Asia	0.0072	42	5847
A*0101	sequencing	South-West Asia	0.0991	113	1140
A*0101	sequencing	Sub-Saharan Africa	0.0526	185	3516
A*01	serological	Australia	0.0222	18	810
A*01	serological	Europe	0.1641	600	3656
A*01	serological	North Africa	0.1403	39	278
A*01	serological	North America	0.0351	47	1338
A*01	serological	North-East Asia	0.0595	63	1058
A*01	serological	Oceania	0.0101	10	994
A*01	serological	Other	0.0753	82	1089

Alternatively, Click on 'View Details' for the Allele Detailed Report indicating the Allele Summary, Allele Frequencies, PubMed Publications, and Sequences.

Allele Detailed Report

A*010102
A*01010102N
A*01010101

Collapse All: Expand All:

Allele Summary

Allele Name:	A*010102
IMGT/HLA Acc:	HLA01244
Sequence Features:	
CWD Allele:	No
Entrez Gene ID:	3105 [Details Build_36.1, hg18] [Details Build_35, hg17]
Assigned Date:	2000-05-18
Last Update:	2003-02-04
Reference Sequence Sources:	AF248059, AF248060,
Reference Cell Lines:	GN00348,
Aliases:	A*01012 (changed),

Allele Frequencies

Allele Frequencies for A*010102

(1) Ordered by Data Type and Population Area
 (2) Population data acquired from the 13th International Histocompatibility Workshop and Congress 2003
 (3) Serological pairs (A*02, A*92) and (B*15, B*95) are identical

Allele Name	Data Type	Population Area	Allele Freq	Allele Count	Total Alleles Examined
A*0101	sequencing	Australia	0.0222	18	810
A*0101	sequencing	Europe	0.1641	600	3656
A*0101	sequencing	North Africa	0.1367	38	278
A*0101	sequencing	North America	0.0352	47	1337
A*0101	sequencing	North-East Asia	0.0586	62	1058
A*0101	sequencing	Oceania	0.0101	10	994
A*0101	sequencing	Other	0.0718	78	1087
A*0101	sequencing	South America	0.0021	1	479
A*0101	sequencing	South-East Asia	0.0072	42	5847
A*0101	sequencing	South-West Asia	0.0991	113	1140
A*0101	sequencing	Sub-Saharan Africa	0.0526	185	3516
A*01	serological	Australia	0.0222	18	810
A*01	serological	Europe	0.1641	600	3656
A*01	serological	North Africa	0.1403	39	278
A*01	serological	North America	0.0351	47	1338
A*01	serological	North-East Asia	0.0595	63	1058
A*01	serological	Oceania	0.0101	10	994
A*01	serological	Other	0.0753	82	1089
A*01	serological	South America	0.0021	1	480
A*01	serological	South-East Asia	0.0072	42	5847
A*01	serological	South-West Asia	0.1044	119	1140
A*01	serological	Sub-Saharan Africa	0.0628	221	3517

PubMed Publications

References:

PubMed ID	Title
[12135434]	Novel HLA-A locus alleles including A*01012, A*0306, A*0308, A*2616, A*2617, A*3009, A*3206, A*3403, A*3602 and A*6604.

Sequences

Gene UTR and Exon Sequence:

5'UTR Sequence data not available

3'UTR Sequence data not available

Protein Sequence: [View Complete Sequence](#)

Genomic Sequence: [View Complete Sequence](#)

CDS Sequence: [View Complete Sequence](#)

Click on each tab to see the detailed information of each allele

Click on Export to open or save an output file for further analysis

Choose the query type as Sequence Feature and enter the search options from the different criteria. (See the Sequence Feature Detailed Report from set options)

Reference Data / MHC Allele Search

Home | Genes | Proteins | MHC Alleles | Pathways | Protein Networks | SNPs | ImmPort Gene Lists | Data History | Reference Advanced Search

The MHC data is provided by the [IMGT/HLA Database](#) and [hla.allele.org](#) databases:

- Robinson J, Waller MJ, Fail SC, McWilliam H, Lopez R, Parham P, Marsh SGEL: The IMGT/HLA database, Nucleic Acids Research (2009), 37:D1013-7
- Robinson J, Malik A, Parham P, Bodmer JG, Marsh SGE: IMGT/HLA - a sequence database for the human major histocompatibility complex, Tissue Antigens (2000), 55:280-287

Fields marked with an asterisk * are required.

MHC Allele Search - Selected Return Data Type : Sequence Feature

Please Choose Query Type: **Sequence Feature**

General Criteria:

Species: Homo sapiens

Locus*: HLA-A

Allele Criteria:

Search For*: All Alleles

Search Using*: Allele Name

Search Option*: Like

Search Text: (Comma delimited)

Sequence Feature Criteria:

Feature Type*: All Types

- Structural
- Functional
- Sequence Alteration
- Structural - Complete protein
- Structural - Domain
- Structural - Secondary structure motif
- Structural - Cleaved peptide region
- Sequence Alteration - Single amino acid v
- Sequence Alteration - Insertions and Dele
- Structural_Functional Combination
- Structural_Sequence Alteration Combinat
- Functional_Sequence Alteration Combinat

Feature Names: (Comma delimited)

Feature Locations: (Comma delimited)

Submit Clear Results per page: 25

Callout 1: Select the arrow to modify your search criteria

Callout 2: Query search based on Sequence Feature. Indicate results per page and click submit or clear to redefine options

Callout 3: Click submit on the selected criteria or clear to reset the parameters



ImmPort Sequence Feature Results

Choose the query type as Sequence Feature and enter the search options from the different criteria.

[\(Modify Search\)](#)

Click modify search to make changes on the search query

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

Sequence Feature Specific Criteria

Feature Types:
Feature Names:
Feature Locations:

Click on the sequence feature number to 'view details' or 'export' file for further analysis

Select/deselect the sequence feature from the list of features available. These can sorted ascending/descending

Selected items: Hsa_HLA-A_SF3, Hsa_HLA-A_SF4, Hsa_HLA-A_SF5

The screenshot shows a table of search results with the following columns: Sequence Feature Number, Sequence Feature Names, Sequence Feature Types, and Positions. The first three columns are selected. A context menu is open over the 'Positions' column, showing options for 'Sort Ascending' and 'Sort Descending'. To the right of the table is a list of checkboxes for column selection: Sequence Feature Number, Sequence Feature Names, Sequence Feature Types, Positions, and Comments. The first three are checked.

Sequence Feature Number	Sequence Feature Names	Sequence Feature Types	Positions
<input checked="" type="checkbox"/> Hsa_HLA-A_SF3	Hsa_HLA-A_signal peptide	Structural - Cleaved peptide	
<input checked="" type="checkbox"/> Hsa_HLA-A_SF4	Hsa_HLA-A_mature protein	Structural - Complete protein	
<input checked="" type="checkbox"/> Hsa_HLA-A_SF5	Hsa_HLA-A_alpha 1 domain	Structural - Domain	
<input type="checkbox"/> Hsa_HLA-A_SF6	Hsa_HLA-A_alpha 2 domain	Structural - Domain	
<input type="checkbox"/> Hsa_HLA-A_SF7	Hsa_HLA-A_alpha 3 domain	Structural - Domain	

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>).

