



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.

Reference Data / Allele Query Results

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([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, 1

Selected items: A*0102, A*0107, A*020107, A*0207

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<input type="checkbox"/>	Allele Name/CWD	Sequence Features	Allele Frequency
<input checked="" type="checkbox"/>	A*0102 CWD		
<input checked="" type="checkbox"/>	A*0107		
<input checked="" type="checkbox"/>	A*020107		
<input checked="" type="checkbox"/>	A*0207 CWD		
<input type="checkbox"/>	A*030107		
<input type="checkbox"/>	A*0307		
<input type="checkbox"/>	A*110107		
<input type="checkbox"/>	A*1107		
<input type="checkbox"/>	A*2307N		
<input type="checkbox"/>	A*240207		
<input type="checkbox"/>	A*2407 CWD		
<input type="checkbox"/>	A*2507		
<input type="checkbox"/>	A*260107		

Annotations:

- Click on [Modify Search](#) to go back to the MHC Allele search page
- Click on the arrow on Allele name, Sequence and Allele frequency detailed information to view the columns available. This can be selected or deselected per user requirements. See next 3 slides
- Click on the arrow to sort the items ascending/descending
- 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

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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



ImmPort Allele Detailed Report

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

Reference Data / Allele Detailed Report

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A*9207

A*0102

A*6807

A*7407

Collapse All: Expand All:

Allele Summary

Allele Name:	A*9207
IMGT/HLA Acc:	HLA02711
Sequence Features:	
CWD Allele:	No
Entrez Gene ID:	3105 [Details Build 36.1, hg18] [Details Build 35, hg17]
Assigned Date:	2006-11-30
Last Update:	2007-01-12
Reference Sequence Sources:	EF088206,
Reference Cell Lines:	VTIS138774,
Aliases:	
HLA Allele References:	hla.allele.org references for HLA-A

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

Expand the blocks to view the details

Allele Frequencies

PubMed Publications

Sequences

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

Export



ImmPort Sequence Feature Query

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](#))

MHC Allele Search

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 : Sequence Feature

Please Choose Query Type : **Sequence Feature** Results per page : 25

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): A*0101

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 Names (Comma delimited):

Feature Locations (Comma delimited):

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

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

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>).

