



Accessing the ImmPort MHC Sequence Feature Structure Viewer

The screenshot shows the ImmPort homepage with a navigation menu at the top: [About ImmPort](#), [Access Data](#), [Tools](#), [Resources](#), and [News & Events](#). The main content area is divided into three sections: **DATA SOURCES**, **IMMPORT DATABASE**, and **IMMPORT TOOLS**.

About ImmPort section: Describes ImmPort as a one-stop shop for immunologists to access reference and experimental data. It provides advanced information technology support in the production, analysis, archiving, and exchange of scientific data for the diverse community of life science researchers supported by NIAID/DAIT. A link [What is ImmPort](#) is provided.

DATA SOURCES section: Lists **NIAID/DAIT Investigators** (Experimental Data, Clinical Study Data) and **Public Reference Databases** (GenBank, RefSeq, UniProt, etc.).

IMMPORT DATABASE section: Lists **Data Standardization**, **Quality Control**, **Data Curation**, and **Maps to Ontologies**.

IMMPORT TOOLS section: Lists **Search Data**, **Visualization**, and **Data Analysis**.

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

GBrowse: Visualize gene structures and the relative position of SNP locations in the human genome.

Jmol: Visualize MHC protein structures and highlight sequence features, like peptide binding motifs, interchain contact residues, etc.

Cytoscape: Coming Soon!

Sign In section: Includes fields for **User Name:** and **Password:**, a **SIGN IN** button, and a [Forgot Password?](#) link.

Register for ImmPort section: Benefits of Registration:

- Access to data visualization tools
- Compare data sets to other researchers
- Access to data analysis tools

Research Spotlight section:

a Line graph showing **EXTRACTED units per 10⁶ REDUCES** vs **Days post-infection** (0, 5, 10, 15, 20, 25, 30). Two series are shown: **-Rapa** (open circles) and **+Rapa (Day -1 to 30)** (filled circles). P-values are indicated: $P = 0.0180$ and $P = 0.0106$.

b Histograms showing **Day 26 post-infection** for **CD3E7**, **CD3E8**, **KLRF1**, and **B220** markers. The top row shows **-Rapa** and the bottom row shows **+Rapa** (Day -1 to 30).

Callout Box: From the ImmPort homepage, click on the "Visualize Data" tab and select "Jmol"



Selecting the Structure of Interest

Reference Data / MHC Sequence Feature Structure Viewer

[Home](#) | [Genes](#) | [Proteins](#) | [MHC Alleles](#) | [MHC Sequence Feature Structure Viewer](#) | [Pathways](#) | [Protein Networks](#) | [SNPs](#) | [ImmPort Gene Lists](#) ↓ | [Data History](#) ↓ | [Reference Advanced Search](#)

ImmPort's MHC Sequence Feature Structure Viewer highlights the locations of sequence feature on crystal structures of classical class I and class II MHC molecules. Features of the ImmPort MHC Sequence Feature Structure Viewer include:

- ▶ Selection/highlighting of any defined sequence feature on a reference structure for each locus
- ▶ Selection/highlighting of other residues of interest on the MHC molecule, peptide or associated receptor
- ▶ Various display modes, including ball and stick, space fill and ribbons
- ▶ Coloring by charge, residue, structure type, temperature factor or composition
- ▶ Zoom and spin
- ▶ Jmol command line for use of advanced Jmol features
- ▶ Image saving (.jpeg)
- ▶ Save/Restore of the image viewer (zoom, highlighting, orientation, etc)

To run the Jmol viewer, you must first select a Locus and then a PDB ID for that locus

Fields marked with an asterisk * are required.

Jmol Selection Criteria:

Species

Locus*

PDB ID*

Select the species, locus and structure of interest. Note: only *Homo sapiens* is currently supported. Visualization of more crystal structures for each locus is under development.



Accessing the ImmPort MHC Sequence Feature Structure Viewer

Reference Data / Sequence Feature Detailed Report

[Home](#) | [Genes](#) | [Proteins](#) | [MHC Alleles](#) | [MHC Sequence Feature Structure Viewer](#) | [Pathways](#) | [Protein Networks](#) | [SNPs](#) | [ImmPort Gene Lists](#) | [Data History](#) | [Reference Advanced Search](#)

[Back To Feature Search Results](#)

Hsa HLA DRB1 SF128

Locus Name: HLA-DRB1
Sequence Feature Names: Hsa_HLA-DRB1_T cell receptor binding
Hsa_HLA-DRB1_mature protein_T cell receptor binding
Hsa_HLA-DRB1_beta 1 domain_T cell receptor binding
Hsa_HLA-DRB1_full-length protein_T cell receptor binding
Positions: 60..64, 67, 69..71, 73, 76..78, 80..82, 84..85
Allele Alignment: 
Sequence Feature Types: Functional
Structural_Functional Combination
MHC Sequence Structure Viewer: [1FYT](#)

As an alternate point of access, from the Sequence Feature Detailed Report page, select the link under "MHC Sequence Feature Viewer". This will take the user directly to the Sequence Feature Viewer for the selected MHC protein with the indicated SF highlighted in red.

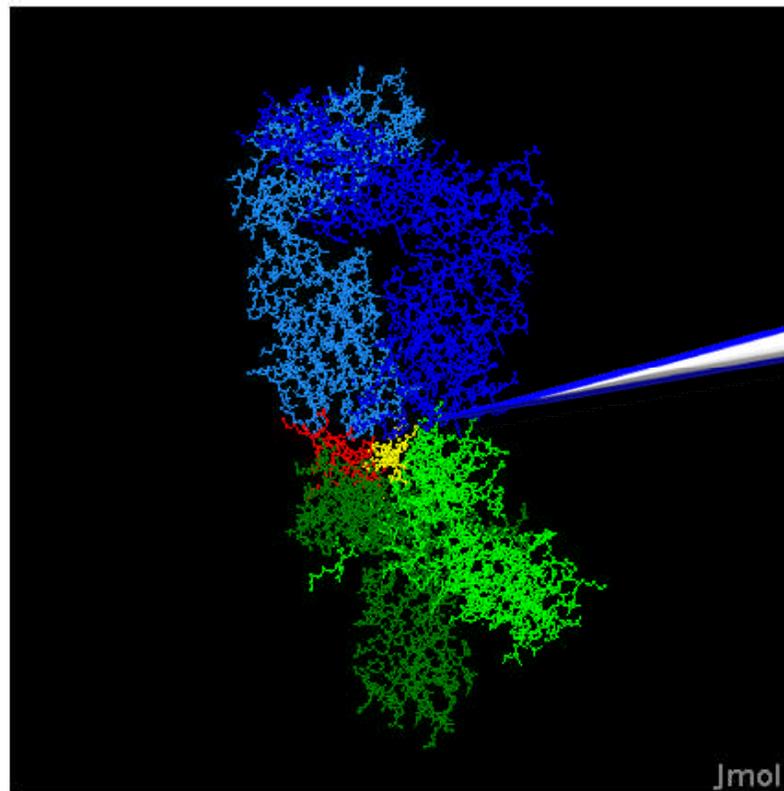
Allele Grouping

Page 1 of 1 |  | Displaying 1 - 83 of 83

No of Alleles (All Alleles for Locus)	Variant Type	Variant Motif
627	Hsa_HLA-DRB1_SF128_VT1	YQKDLEQRADTYRHNGV
82	Hsa_HLA-DRB1_SF128_VT1	-----
7	Hsa_HLA-DRB1_SF128_VT2	-----A
58	Hsa_HLA-DRB1_SF128_VT3	----I-DE-----
5	Hsa_HLA-DRB1_SF128_VT4	-----N-----
5	Hsa_HLA-DRB1_SF128_VT5	-----



Accessing the ImmPort MHC Sequence Feature Structure Viewer



Reset View

Save View As Image

Information
Protein (PDB):
Description: CRYSTAL STRUCTURE OF A COMPLEX OF A HUMAN ALPHA/BETA-T CELL RECEPTOR-INFLUENZA HA ANTIGEN

Collapse All: [-] Expand All: [+]

Display Options

Sequence Features

Highlight sequence features from a list. The feature type(s) from a list. The

- All Types
- Structural
- Functional
- Sequence Alteration
- Structural - Domain
- Structural - Secondary structure motif
- Structural - Cleaved peptide region
- Sequence Alteration - Single amino acid
- Sequence Alteration - Insertions and

Display selected features from PDB protein structure and sequence feature table

Clear selected features from PDB protein structure and sequence feature table

Selected items: Hsa_HLA-DRB1_SF128

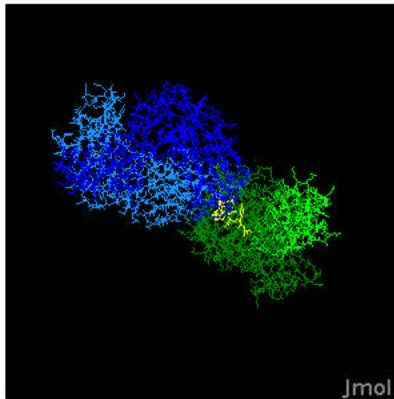
<input type="checkbox"/>	Sequence Feature Number	Sequence F...	Sequence F...	Positions
<input type="checkbox"/>	Hsa_HLA-DRB1_SF2	Hsa_HLA-DRB1_full-length protein	Structural - Complete protein	-29..237
<input type="checkbox"/>	Hsa_HLA-DRB1_SF4	Hsa_HLA-DRB1_mature protein	Structural - Complete protein	1..237
<input type="checkbox"/>	Hsa_HLA-DRB1_SF5	Hsa_HLA-DRB1_beta 1 domain	Structural - Domain	1..95

The MHC Sequence Feature Structure Viewer will automatically highlight the sequence feature from the Sequence Feature Detailed Report page in red



MHC Sequence Feature Structure Viewer Display Options

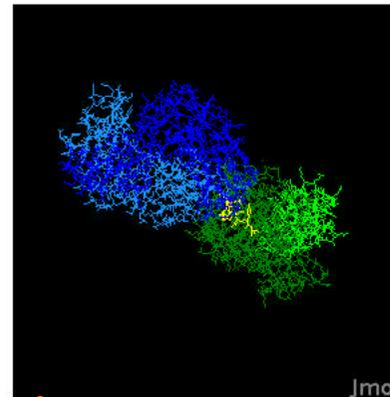
Blocks of visualization tools can be expanded or collapsed as preferred.



- Reset View
- Save View As Image
- Information
- Allele to PDB Mapping
- Save Restore
- Jmol Command Line

Jmol is an open-source Java viewer for chemical structures in 3D

- Collapse All: [] Expand All: []
- Display Options
- Sequence Features
- Highlight/Label Features



Reset View Save View As Image

Information

Protein (PDB):
Description: THE COMPLEX BETWEEN TCR A6 AND HUMAN CLASS I MHC HLA-A2 WITH THE BOUND TEL1P PEPTIDE

PDB Link: [3H95](#)

MHC Protein: HLA-A2

Peptide:

Feature (ImmPort):
Locus Name: HLA-A
Reference: A*02010101
Allele:

PDB Molecule Color Map:

Molecule	Color
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA	Green
MHC CLASS I ANTIGEN A*2	Yellow
BETA-2-MICROGLOBULIN	Blue
A6 TCR ALPHA CHAIN	Red
TRBV6-5 PROTEIN	Orange

Allele to PDB Mapping

You can view the locations of residues on the reference allele A*02010101 using IMGT/HLA coordinates onto the PDB structure 3H95 above. Input IMGT/HLA coordinates (for example, 10-30, 50, 70-150) on the allele and click **Highlight in gold** to view the location(s) on the PDB structure. To clear the coordinates, click **Clear**. The table below specifies the mapping of the reference allele to PDB structure chain coordinates.

IMGT/HLA Coordinate Interval	PDB Chain Coordinate Interval	PDB Molecule
[-24, -1]	--	--
[1, 275]	1-275:8	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA
[276, 341]	--	--

Display Options

These options control the general appearance of the protein structure viewer.

Display Type: Ball & Stick

Zoom: 100%

Spin:

Details

Sequence Features

Highlight sequence features on the structure in red. First select a sequence feature type(s) from a list. Then check the sequence features to highlight.

All Types: Structural, Functional, Sequence Alteration, Structural - Complete protein, Structural - Domain, Structural - Secondary structure motif, Structural - Cleaved peptide region, Sequence Alteration - Single amino acid, Sequence Alteration - Insertions and Deletions

Display: Display selected features from table into PDB protein structure

Clear: Clear selected features from PDB protein structure and sequence feature table

Page 1 of 29 | Displaying 1 - 10 of 296

Sequence Feature	Sequence Feature	Sequence Feature	Positions
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_full-length protein	Structural - Complete protein	-24..341
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_mature protein	Structural - Complete protein	1..341
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_alpha 1 domain	Structural - Domain	1..90
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_alpha 2 domain	Structural - Domain	91..182
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_alpha 3 domain	Structural - Domain	183..274
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_alpha 3 domain-	Structural - Domain	275..284

Highlight/Label Features

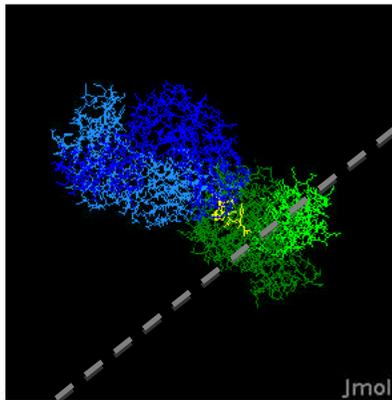
These options color, highlight or label certain features of the structure.

Color Structure By: []

Label: []



Information Section



Reset View Save View As Image

Information

Protein (PDB):

Description: THE COMPLEX BETWEEN TCR A6 AND HUMAN CLASS I MHC HLA-A2 WITH THE BOUND TEL1P PEPTIDE

PDB Link: [3H95](#)

MHC Protein: HLA-A2

Peptide:

Feature (ImmPort):

Locus Name: HLA-A

Reference Allele: A*02010101

Allele:

PDB Molecule Color Map:

Molecule	Color
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA	
MHC CLASS I ANTIGEN A*2	
BETA-2-MICROGLOBULIN	
A6 TCR ALPHA CHAIN	
TRBV6-5 PROTEIN	

Align to PDB Mapping

You can view the locations of residues on the reference allele A*02010101 using IMG/HLA coordinates onto the PDB structure 3H95 above. Input IMG/HLA coordinates (for example, 10-30, 50, 70-150) on the allele and click **Highlight in gold** to view the location(s) on the PDB structure. To clear the coordinates, click **Clear**. The table below specifies the mapping of the reference allele to PDB structure chain coordinates.

IMG/HLA Coordinate Interval	PDB Chain Coordinate Interval	PDB Molecule
[-24, -1]	--	--
[1, 275]	1..275:A	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA
[276, 341]	--	--

Display Options

These options control the general the general structure viewer.

Display Type: Ball & Stick

Zoom: 100%

Spin:

Sequence Features

Highlight sequence features on the structure (sequence feature type(s) from a list. Then click highlight.

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

Display: Display selected features from table

Clear: Clear selected features from PDB protein feature table

Page 1 of 29

Sequence Fe...	Sequence Fe...	Seque
<input type="checkbox"/> Hsa_HLA-A...	Hsa_HLA-A_full-length protein	Structural - Complete protein
<input type="checkbox"/> Hsa_HLA-A...	Hsa_HLA-A_mature protein	Structural - Complete protein
<input type="checkbox"/> Hsa_HLA-A...	Hsa_HLA-A_alpha 1 domain	Structural - Domain 1..90
<input type="checkbox"/> Hsa_HLA-A...	Hsa_HLA-A_alpha 2 domain	Structural - Domain 91..182
<input type="checkbox"/> Hsa_HLA-A...	Hsa_HLA-A_alpha 3 domain	Structural - Domain 183..274
<input type="checkbox"/> Hsa_HLA-A...	Hsa_HLA-A_alpha 3 domain	Structural - Domain 275..284

Highlight/Label Features

These options color, highlight or label certain features of the structure.

Color Structure By:

Label:

Information

Protein (PDB):

Description: THE COMPLEX BETWEEN TCR A6 AND HUMAN CLASS I MHC HLA-A2 WITH THE BOUND TEL1P PEPTIDE

PDB Link: [3H95](#)

MHC Protein: HLA-A2

Peptide:

Feature (ImmPort):

Locus Name: HLA-A

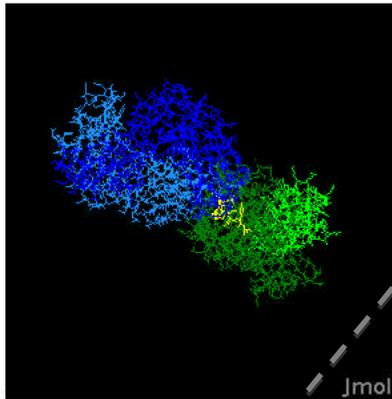
Reference Allele: A*0201

PDB Molecule Color Map:

Molecule	Color
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA	
BETA-2-MICROGLOBULIN	
TEL1P PEPTIDE	
A6 TCR ALPHA CHAIN	
TRBV6-5 PROTEIN	

The information section displays key information about the structure, including the color map for the default chain view and the link to the PDB page for that structure.

Allele to PDB Mapping Submenu



Information

Protein (PDB):
Description: THE COMPLEX BETWEEN TCR A6 AND HUMAN CLASS I MHC HLA-A2 WITH THE BOUND TEL1P PEPTIDE

PDB Link: [3H9S](#)

MHC Protein: HLA-A2

Peptide:

Feature (ImmPort):
Locus Name: HLA-A
Reference: A*02010101
Allele:

PDB Molecule Color Map:

Molecule	Color
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA	Green
MHC CLASS I ANTIGEN A*2	Yellow
BETA-2-MICROGLOBULIN	Blue
A6 TCR ALPHA CHAIN	Red
TRBV6-5 PROTEIN	Orange

Display Options

These options control the general appearance of the structure viewer.

Display Type: Ball & Stick

Zoom:

Spin:

Sequence Features

Highlight sequence features on the structure in red. Select one or more sequence feature type(s) from a list. Then check the highlight checkbox.

All Types

- Structural
- Functional
- Sequence Alteration
- Structural - Complete protein
- Structural - Domain
- Structural - Secondary structure motif
- Structural - Cleaved peptide region
- Sequence Alteration - Single amino acid
- Sequence Alteration - Insertions and Deletions

Display: Display selected features from table into structure

Clear: Clear selected features from PDB protein feature table

Page 1 of 29

Sequence Fe...	Sequence Fe...	Sequence F...
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_full-length protein	Structural - Complete protein
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_mature protein	Structural - Complete protein
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_alpha 1 domain	Structural - Domain
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A_alpha 2 domain	Structural - Domain
<input type="checkbox"/> Hsa_HLA-A_...	Hsa_HLA-A...	Structural - ...

Highlight/Label Feature

These options control the color and label of the structure.

Color Structure By:

Label:

Allele to PDB Mapping

You can view the locations of residues on the reference allele A*0201 using IMGT/HLA coordinates onto the PDB structure 3H9S above. Input IMGT/HLA coordinates (for example, 10-30, 50, 70-150) on the allele and click Highlight in gold to view the location(s) on the PDB structure. To clear the coordinates, click Clear. The table below specifies the mapping of the reference allele to PDB structure chain coordinates.

IMGT/HLA Coordinate Interval	PDB Chain Coordinate Interval	PDB Molecule
[-24, -1]	--	--
[1, 275]	1-275:8	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA
[276, 341]	--	--

Highlight: Highlight the allele coordinates onto the PDB structure

Clear: Clear the selected allele coordinates from the PDB structure

IMGT/HLA Coords:

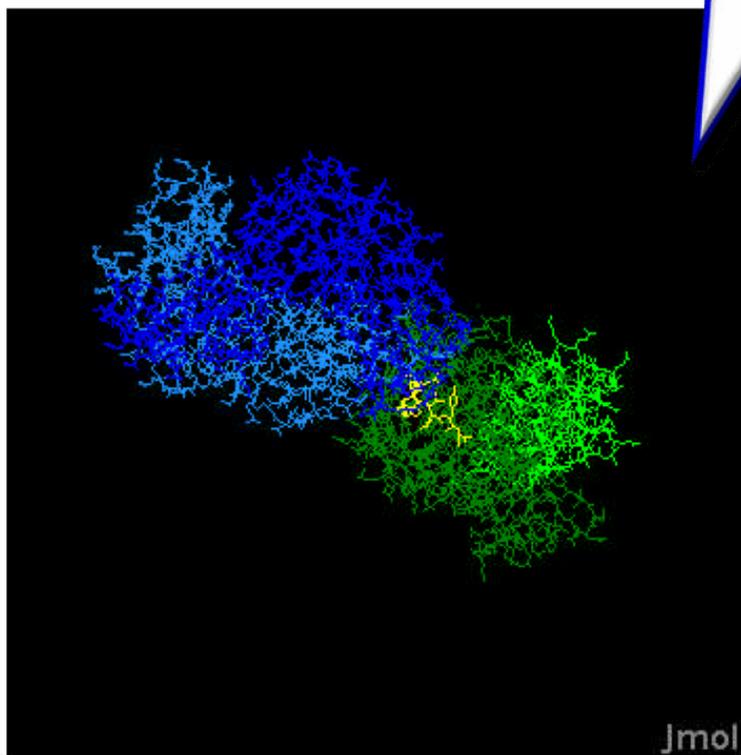
Use this section to highlight particular residues of interest in the indicated HLA heavy chain in yellow.

PDB Chain Coordinate Intervals indicate which residues are represented in the structure. In this example, residues -29 - 2 in the IMGT/HLA Coordinate System cannot be highlighted because they are in the HLA-A leader peptide and are not part of the mature protein that is displayed here.



Display Options Submenu

Click and drag the cursor arrow in the Jmol display box to orient the structure as desired.



Display Options

These options control the general viewer.

- Display Type:
 - Ball & Stick
 - Line
 - Stick
 - Space
- Sequence:
 - Composition of Protein, Water, Solvent, etc
 - Charge View
- Highlight:
 - Primary Structure in Residue Color
 - Primary Structure in Rainbow
 - Secondary Structure in Cartoon
 - Secondary Structure in Rocket

Line, Stick, Spacefill, and Ball&Stick Views

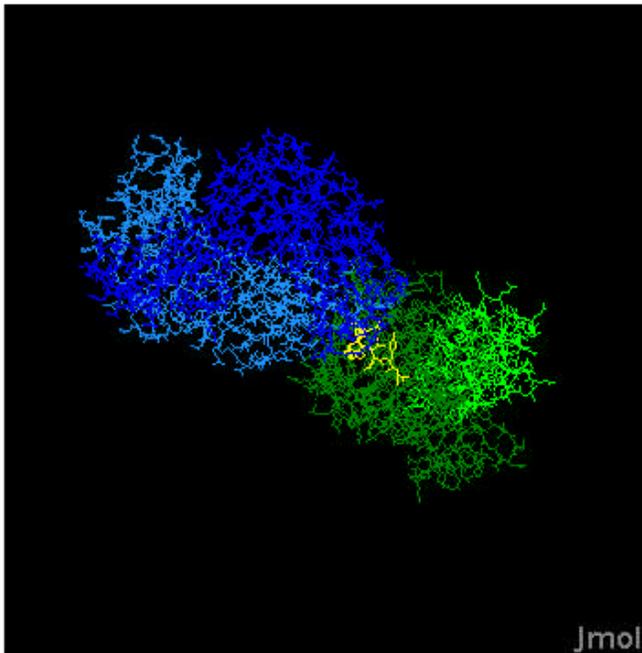
These four display styles are basic views and use the molecule coloring schema which means different molecules have different colors: HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR, Alpha Chain ■, HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1, Beta Chain ■, HEMAGGLUTININ HA1 PEPTIDE CHAIN ■, T-CELL RECEPTOR ALPHA CHAIN ■, T-CELL RECEPTOR BETA CHAIN ■. The ball&stick view is combo view from line/stick and spacefill.

Choose from a variety of display options by selecting a display type.

Mouse over the "Details" box for information about the meaning of colors and shapes used in the selected display type.



Sequence Features Submenu



Reset View Save View As Image

- Information +
- Allele to PDB Mapping +
- Save Restore +
- Jmol Command Line +

Jmol is an open-source Java viewer for chemical structures in 3D

Collapse All: Expand All:

Sequence Features

Highlight sequence features on the structure in red. First select a sequence feature type(s) from a list. Then check the sequence features to highlight.

All Types

- Structural
- Functional
- Sequence Alteration
- Structural - Complete protein
- Structural - Domain
- Structural - Secondary structure motif
- Structural - Cleaved peptide region
- Sequence Alteration - Single amino acid var...
- Sequence Alteration - Insertions and Deletio...

Load feature types into sequence feature table below

Display selected features from table into PDB protein structure

Clear selected features from PDB protein structure and sequence feature table

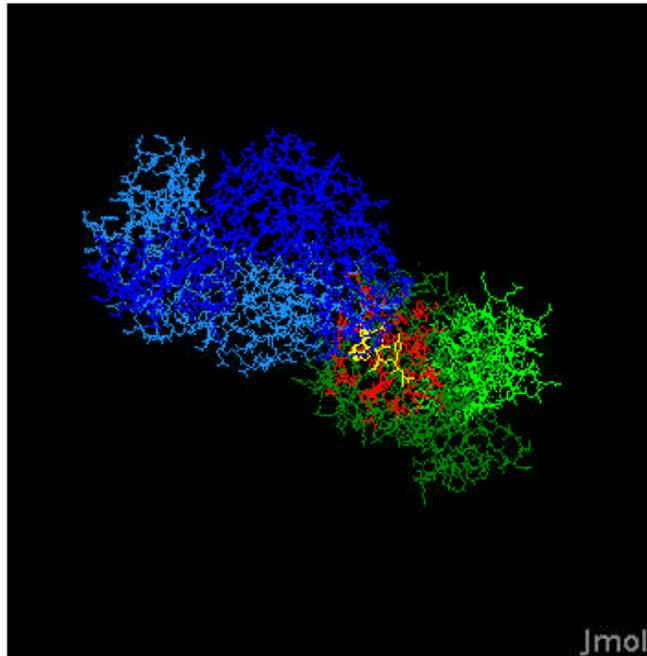
Select the sequence feature type you are interested in displaying, and hit "Load" to see a list of these feature types in the table below

Page 1 of 29 Displaying 1 - 10 of 290

<input type="checkbox"/>	Sequence Feat...	Sequence Feat...	Sequence Feat...	Positions
<input type="checkbox"/>	Hsa_HLA-A_SF2	Hsa_HLA-A_full-length protein	Structural - Complete protein	-24..341
<input type="checkbox"/>	Hsa_HLA-A_SF4	Hsa_HLA-A_mature protein	Structural - Complete protein	1..341
<input type="checkbox"/>	Hsa_HLA-A_SF5	Hsa_HLA-A_alpha 1 domain	Structural - Domain	1..90
<input type="checkbox"/>	Hsa_HLA-A_SF6	Hsa_HLA-A_alpha 2 domain	Structural - Domain	91..182
<input type="checkbox"/>	Hsa_HLA-A_SF7	Hsa_HLA-A_alpha 3 domain	Structural - Domain	183..274
<input type="checkbox"/>	Hsa_HLA-A_SF8	Hsa_HLA-A_alpha 3 domain-transmembrane connecting peptide	Structural - Domain	275..284
<input type="checkbox"/>	Hsa_HLA-A_SF11	Hsa_HLA-A_N-terminus sequence	Structural - Secondary structure motif	1..2
<input type="checkbox"/>	Hsa_HLA-A_SF12	Hsa_HLA-A_beta...	Structural -	3..14



Sequence Features Submenu



Reset View Save View As Image

Information

Allele to PDB Mapping

Save Restore

Jmol Command Line

Jmol is an open-source Java viewer for chemical structures in 3D

Display Options Collapse All: [-] Expand All: [+]

Sequence Features

Highlight sequence features on the structure in red. First select a sequence feature type(s) from a list. Then check the sequence features to highlight.

All Types

Structural

Functional

Sequence Alteration

Structural - Complete protein

Structural - Domain

Structural - Secondary structure motif

Structural - Cleaved peptide region

Sequence Alteration - Single amino acid var...

Sequence Alteration - Insertions and Deletions

Load Load feature types into sequence feature table below

Display Display selected features from table into PDB protein structure

Clear Clear selected features from PDB protein structure and sequence feature table

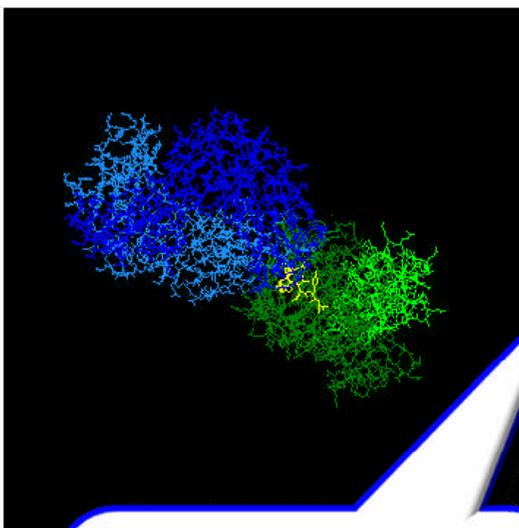
Selected items: Hsa_HLA-A_SF220

Sequence Feature	Sequence Feature	Sequence Feature	Positions
<input checked="" type="checkbox"/>	Hsa_HLA-A_SF...	Hsa_HLA-A_peptide antigen binding; Hsa_HLA-A_mature protein_peptide antigen binding; Hsa_HLA-A_full-length protein_peptide antigen binding	Functional; Structural_Func... Combination 5, 7, 9, 22, 24...
<input type="checkbox"/>	Hsa_HLA-A_SF...	Hsa_HLA-A_T cell receptor binding; Hsa_HLA-A_mature protein_T cell receptor binding; Hsa_HLA-A_full-length protein_T cell receptor binding	Functional; Structural_Func... Combination 57..58, 61..62, ...
<input type="checkbox"/>	Hsa_HLA-A_SF...	Hsa_HLA-A_peptide antigen	Functional; Structural_Func... 58, 62, 146, 15...

Choose one or more sequence features to visualize on the crystal structure, and hit "Display" to see them highlighted in red. Hit "Clear" to remove all red highlighting



Highlight/Label Features Submenu



In order to highlight backbone or sidechain portions of the structure's component amino acids or particular chains in the structure, select "Molecule" under the Highlight/Label Features menu.

Display Options Collapse All: Expand All: +

Sequence Features

Highlight/Label Features These options color, highlight or label certain features of the structure.

Color: Structure Type: Temperature Factor

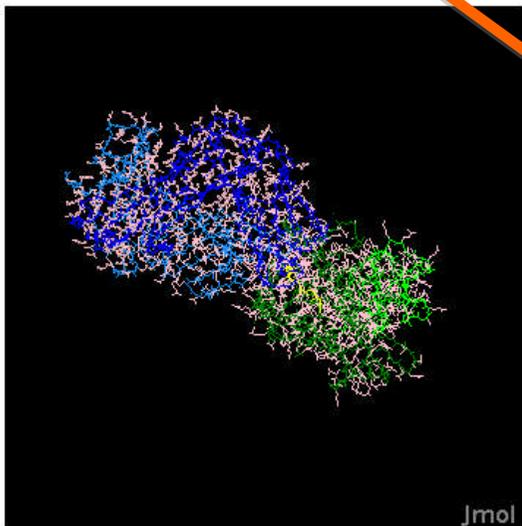
By: Molecule (checked) Amino Acid Residue Structure Type Temperature Factor

Highlight in Pink: Label:

Save Restore

Jmol Command Line

Once "Molecule" has been selected, a second selection box will appear. Here, choose the desired portion of the structure to highlight in pink. If particular sequence features have been selected for display in red, the red highlighting will not change to pink when using this feature.



Display Options Collapse All: Expand All: +

Sequence Features

Highlight/Label Features These options color, highlight or label certain features of the structure.

Color: Structure Type: Temperature Factor

By: Sidechain (checked) Backbone HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 ALPHA MHC CLASS I ANTIGEN A*2 BETA-2-MICROGLOBULIN A6 TCR ALPHA CHAIN TRBV6-5 PROTEIN

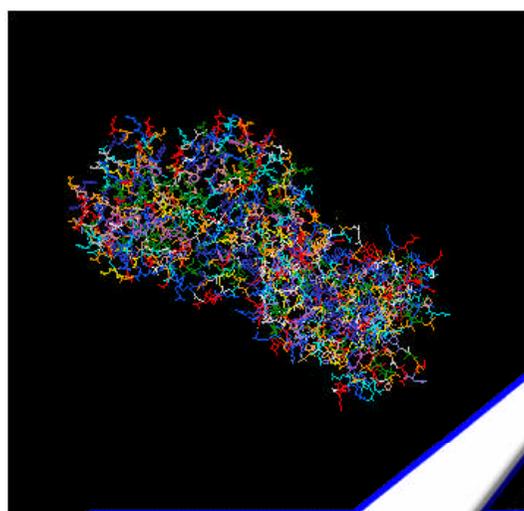
Highlight in Pink: Label:

Save Restore

Jmol Command Line



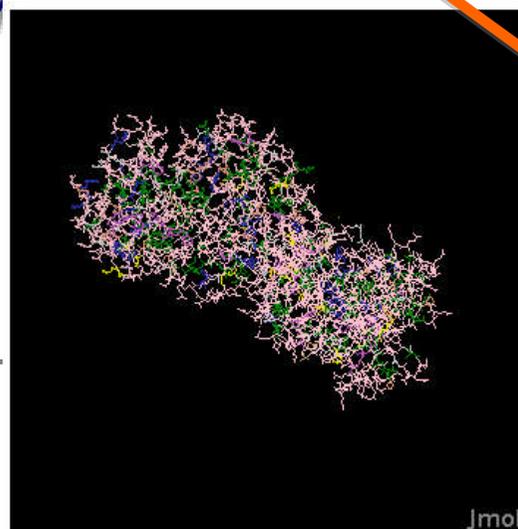
Highlight/Label Features Submenu



To visualize the use of particular amino acids and amino acid types in a structure, under "Color Structure By:" select "Amino Acid Residue".

Display Options Collapse All: [-] Expand All: [+]
Sequence Features [-]
Highlight/Label Features [-]
These options color, highlight or label the structure.
Color Structure By: Amino Acid Residue (checked) Structure Type Temperature Factor
Highlight in Pink:
Label:
Save Restore [+]
Jmol Command Line [+]

Use the second selection box to highlight particular residues or residue types in pink.

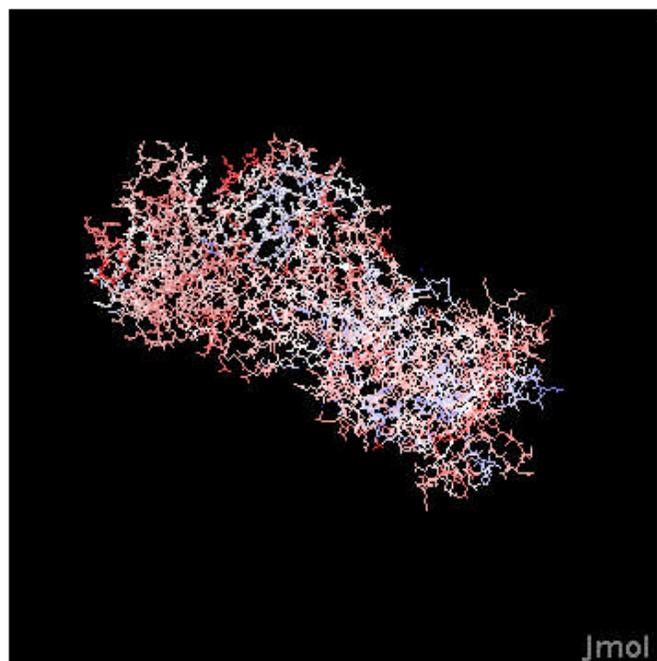


Display Options Collapse All: [-] Expand All: [+]
Sequence Features [-]
Highlight/Label Features [-]
These options color, highlight or label the structure.
Color Structure By: Hydrophobic Residues Polar Residues (checked) Pos. Charged Residues Neg. Charged Residues Proline Glycine Histidine
Highlight in Pink:
Label:
Save Restore [+]
Jmol Command Line [+]

Reset View Save View As Image



Highlight/Label Features Submenu



Reset View Save View As Image

Information

Allele to PDB Mapping

Jmol is an open-source Java viewer for chemical structures in 3D

Collapse All: [-] Expand All: [+]

Display Options [+]

Sequence Features [+]

Highlight/Label Features [-]
These options color, highlight
Color Structure By: [+]
Label: [+]

- Molecule
- Amino Acid Residue
- Structure Type
- Temperature Factor

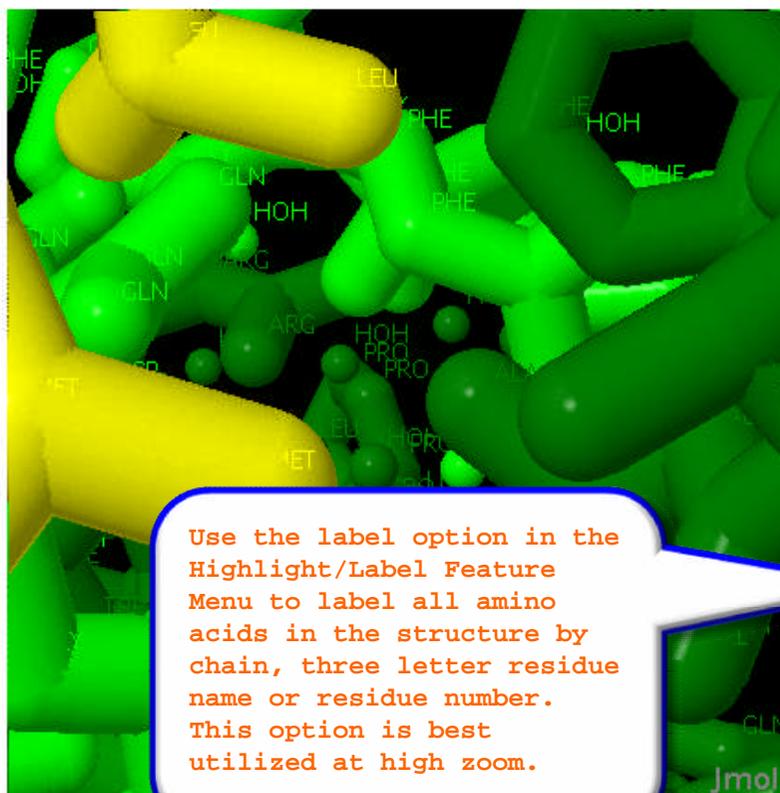
Save Restore [+]

Jmol Command Line [+]

Other types of feature highlighting include coloring of residues by structure type or temperature factor.



Highlight/Label Features Submenu



Reset View Save View As Image

Collapse All: [-] Expand All: [+]

Display Options

These options control the general the general appearance of the protein structure viewer.

Display Type:

Zoom:

Spin:



[Details](#)

Sequence Features

Highlight/Label Features

These options color, highlight or label certain features of the structure.

Color Structure:

By:

Highlight in Pink:

Label: Residue Name

Chain

Residue Number

Save Restore

Jmol Command Line

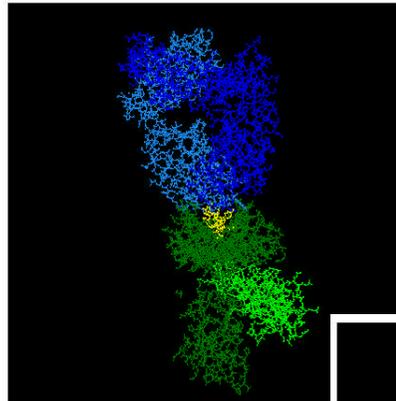
Information

Allele to PDB Mapping

Jmol is an open-source Java viewer for chemical structures in 3D



Save Restore Submenu



Reset View Save

Collapse All: Expand All:

Display Options
These options control the general appearance of the protein structure viewer.

Display Type: Ball & Stick

Zoom: 100%

Spin:

Sequence Features

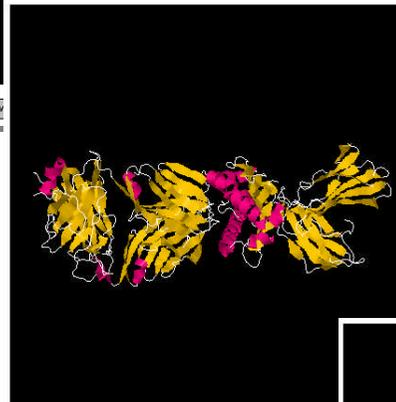
Highlight/Label Features

Save Restore
The state of the viewer (highlighting, zooming, etc) can be saved at any time and then retrieved later. Choose the view you want to save, then restore it later when you are ready.

Save View: Orientation

Restore View:

1) Save the state, selection or orientation of the viewer. (Here, the orientation is saved).



Reset View Save

Collapse All: Expand All:

Display Options
These options control the general appearance of the protein structure viewer.

Display Type: Secondary Structure

Zoom: 100%

Spin:

Sequence Features

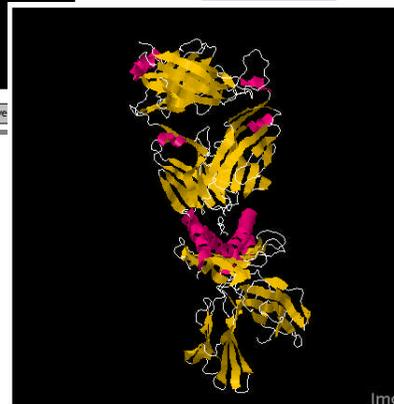
Highlight/Label Features

Save Restore
The state of the viewer (highlighting, zooming, etc) can be saved at any time and then retrieved later. Choose the view you want to save, then restore it later when you are ready.

Save View:

Restore View:

2) Alter the orientation and any other view of the molecule. (Here, the orientation and display type are altered.)



Reset View Save View As Image

Collapse All: Expand All:

Display Options
These options control the general appearance of the protein structure viewer.

Display Type: Secondary Structure

Zoom: 100%

Spin:

Sequence Features

Highlight/Label Features

Save Restore
The state of the viewer (highlighting, zooming, etc) can be saved at any time and then retrieved later. Choose the view you want to save, then restore it later when you are ready.

Save View:

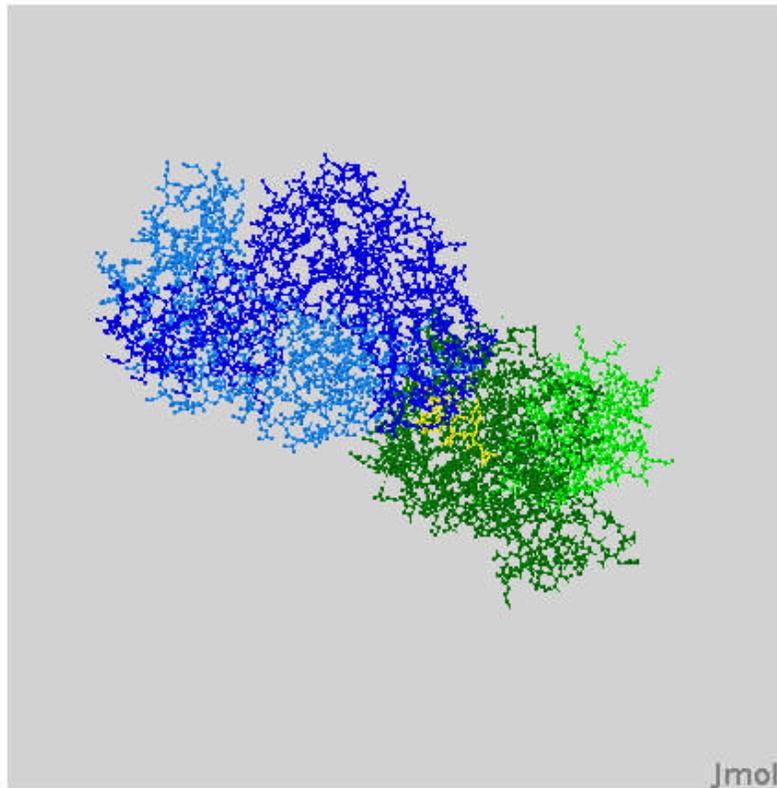
Restore View: Orientation

Jmol Command Line

3) Select "Restore View: Orientation", and the orientation that was saved in step one, but not the new display type, is restored.



Jmol Command Line Submenu



Reset View Save View As Image

Collapse All: Expand All:

- Display Options
- Sequence Features
- Highlight/Label Features
- Save Restore
- Jmol Command Line

Advanced users can enter a Jmol command directly using [Jmol Interactive Script](#)

Jmol commands can be executed here to further personalize the MHC Sequence Feature Structure Viewer



Reset View and Save View As Image Buttons

Click on the "Reset View" button to return all of the visualization settings to default (i.e. the display type, zoom, sequence feature selection, etc that was on display in this browser window before user manipulation).

Click on the "Save View As Image" button to save a .jpeg file of the current state of the viewer to your local hard drive.