



wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 09:06 AM GMT

PDB ID : 1SEB
Title : COMPLEX OF THE HUMAN MHC CLASS II GLYCOPROTEIN HLA-DR1
AND THE BACTERIAL SUPERANTIGEN SEB
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Deposited on : 1995-11-26
Resolution : 2.70 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

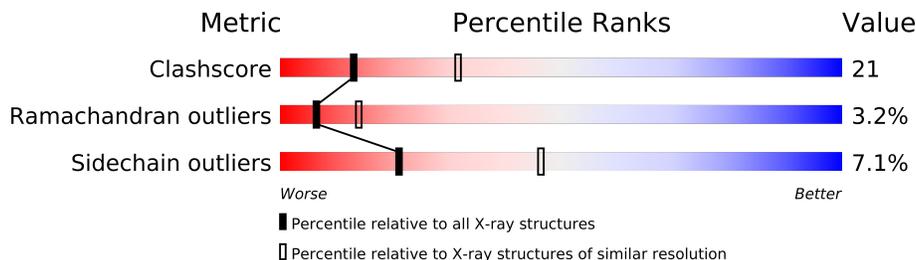
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	181	
1	E	181	
2	B	192	
2	F	192	
3	C	13	
3	G	13	
4	D	234	
4	H	234	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9396 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called HLA CLASS II HISTOCOMPATIBILITY ANTIGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	181	1483	960	241	277	5	0	0	0
1	E	181	1483	960	241	277	5	0	0	0

- Molecule 2 is a protein called HLA CLASS II HISTOCOMPATIBILITY ANTIGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	192	1556	980	277	293	6	0	0	0
2	F	192	1556	980	277	293	6	0	0	0

- Molecule 3 is a protein called ENDOGENOUS PEPTIDE MODEL, POLY-ALA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	13	65	39	13	13	0	0	0
3	G	13	65	39	13	13	0	0	0

- Molecule 4 is a protein called ENTEROTOXIN TYPE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	206	1594	1024	249	311	10	0	0	0
4	H	206	1594	1024	249	311	10	0	0	0

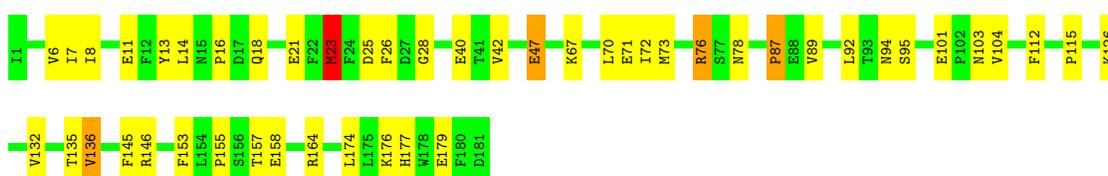
3 Residue-property plots i

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

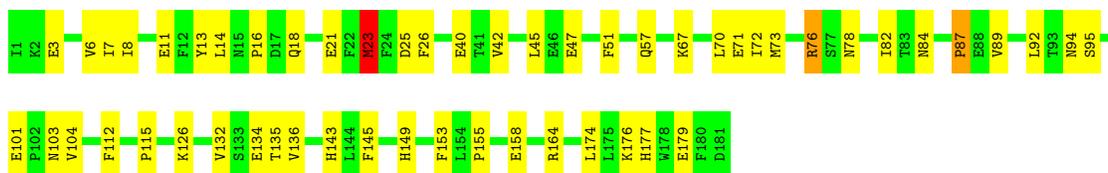
- Molecule 1: HLA CLASS II HISTOCOMPATIBILITY ANTIGEN

Chain A:



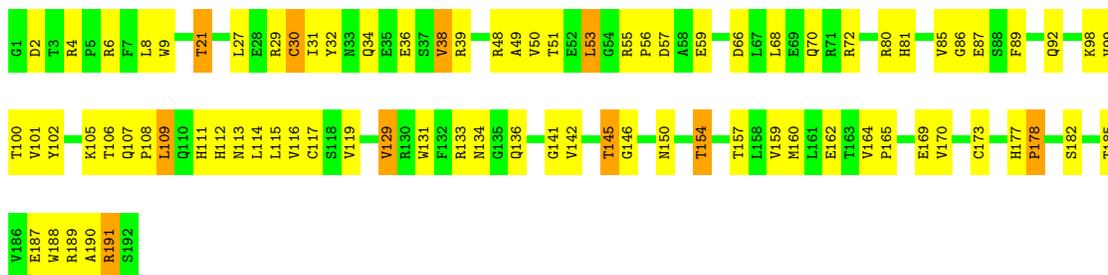
- Molecule 1: HLA CLASS II HISTOCOMPATIBILITY ANTIGEN

Chain E:



- Molecule 2: HLA CLASS II HISTOCOMPATIBILITY ANTIGEN

Chain B:



- Molecule 2: HLA CLASS II HISTOCOMPATIBILITY ANTIGEN

Chain F:





• Molecule 3: ENDOGENOUS PEPTIDE MODEL, POLY-ALA

Chain C:



• Molecule 3: ENDOGENOUS PEPTIDE MODEL, POLY-ALA

Chain G:



• Molecule 4: ENTEROTOXIN TYPE B

Chain D:



• Molecule 4: ENTEROTOXIN TYPE B

Chain H:



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.00Å 114.70Å 149.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.70)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.257 , 0.327	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	9396	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.92	0/1528	1.05	2/2084 (0.1%)
1	E	0.93	1/1528 (0.1%)	1.06	2/2084 (0.1%)
2	B	0.87	2/1596 (0.1%)	1.04	4/2170 (0.2%)
2	F	0.89	3/1596 (0.2%)	1.19	7/2170 (0.3%)
4	D	0.69	0/1627	0.92	2/2206 (0.1%)
4	H	0.78	1/1627 (0.1%)	0.92	2/2206 (0.1%)
All	All	0.85	7/9502 (0.1%)	1.03	19/12920 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	F	0	1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	19	GLY	C-N	14.42	1.67	1.34
2	F	93	ARG	C-N	8.46	1.53	1.34
2	F	129	VAL	CB-CG2	-6.10	1.40	1.52
2	B	129	VAL	CB-CG2	-6.09	1.40	1.52
1	E	84	ASN	C-N	-5.83	1.20	1.34

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	93	ARG	O-C-N	-19.70	91.19	122.70
2	F	93	ARG	CA-C-N	13.94	147.87	117.20
2	F	93	ARG	C-N-CA	11.14	149.56	121.70
2	F	38	VAL	CB-CA-C	-6.21	99.60	111.40
2	B	38	VAL	CB-CA-C	-6.20	99.61	111.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	93	ARG	Mainchain

5.2 Close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1483	0	1414	40	0
1	E	1483	0	1414	40	0
2	B	1556	0	1475	67	0
2	F	1556	0	1475	75	0
3	C	65	0	15	2	0
3	G	65	0	15	2	0
4	D	1594	0	1407	90	0
4	H	1594	0	1407	92	0
All	All	9396	0	8622	371	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 21.

The worst 5 of 371 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:82:VAL:HG11	4:D:118:VAL:HB	1.27	1.12
4:H:82:VAL:HG11	4:H:118:VAL:HB	1.27	1.09
1:A:157:THR:O	2:F:112:HIS:HE1	1.41	1.02
4:D:203:ALA:HB1	4:D:204:PRO:HD2	1.44	1.00
2:B:51:THR:CA	2:F:52:GLU:OE2	2.11	0.98

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone i

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	179/181 (99%)	176 (98%)	3 (2%)	0	100	100
1	E	179/181 (99%)	176 (98%)	3 (2%)	0	100	100
2	B	190/192 (99%)	178 (94%)	7 (4%)	5 (3%)	8	20
2	F	190/192 (99%)	178 (94%)	7 (4%)	5 (3%)	8	20
4	D	196/234 (84%)	163 (83%)	20 (10%)	13 (7%)	2	2
4	H	196/234 (84%)	163 (83%)	20 (10%)	13 (7%)	2	2
All	All	1130/1214 (93%)	1034 (92%)	60 (5%)	36 (3%)	6	14

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	62	ASP
4	D	136	VAL
4	D	153	LYS
4	H	62	ASP
4	H	136	VAL

5.3.2 Protein sidechains i

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	164/166 (99%)	151 (92%)	13 (8%)	18	39
1	E	164/166 (99%)	151 (92%)	13 (8%)	18	39
2	B	169/173 (98%)	160 (95%)	9 (5%)	32	62
2	F	169/173 (98%)	160 (95%)	9 (5%)	32	62
4	D	159/220 (72%)	146 (92%)	13 (8%)	17	36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	159/220 (72%)	146 (92%)	13 (8%)	17	36
All	All	984/1118 (88%)	914 (93%)	70 (7%)	21	46

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	200	MET
1	E	76	ARG
4	H	143	LEU
4	D	201	MET
1	E	23	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	43	GLN
1	E	143	HIS
2	F	150	ASN
2	B	156	GLN
2	F	156	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.