



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:29 AM UTC

PDB ID : 1F3J / pdb_00001f3j
Title : HISTOCOMPATIBILITY ANTIGEN I-AG7
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Deposited on : 2000-06-04
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

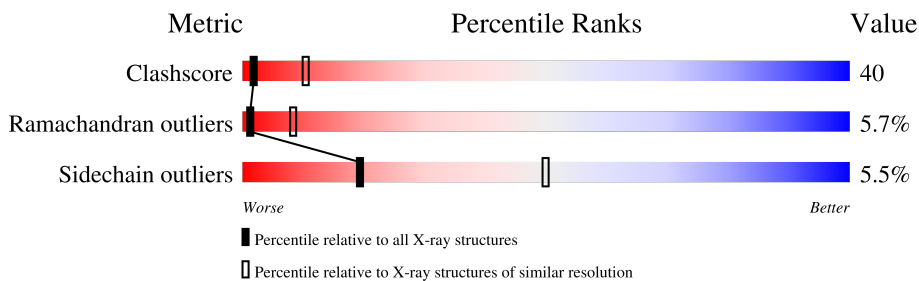
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	182	36% 56% 8%
1	D	182	34% 56% 9% .
2	B	187	41% 49% 10%
2	E	187	40% 52% 8% .
3	P	14	71% 29%
3	Q	14	64% 36%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6464 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1474	954	238	280	2			
1	D	182	Total	C	N	O	S	0	0	0
			1474	954	238	280	2			

- Molecule 2 is a protein called MHC CLASS II NOD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	187	Total	C	N	O	S	0	0	0
			1563	978	285	294	6			
2	E	187	Total	C	N	O	S	0	0	0
			1563	978	285	294	6			

- Molecule 3 is a protein called LYSOZYME C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	P	14	Total	C	N	O	S	0	0	0
			117	71	24	21	1			
3	Q	14	Total	C	N	O	S	0	0	0
			117	71	24	21	1			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is water.

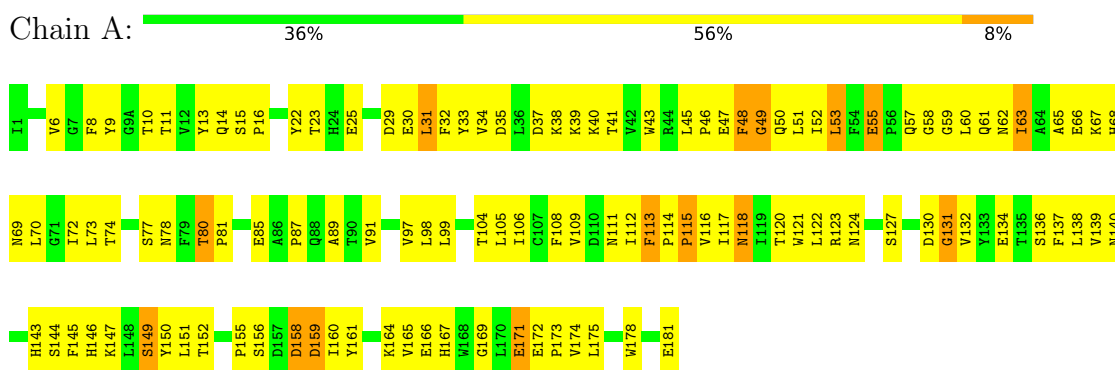
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	19	Total	O	0	0
			19	19		
5	B	26	Total	O	0	0
			26	26		
5	P	2	Total	O	0	0
			2	2		
5	D	12	Total	O	0	0
			12	12		
5	E	11	Total	O	0	0
			11	11		
5	Q	2	Total	O	0	0
			2	2		

3 Residue-property plots

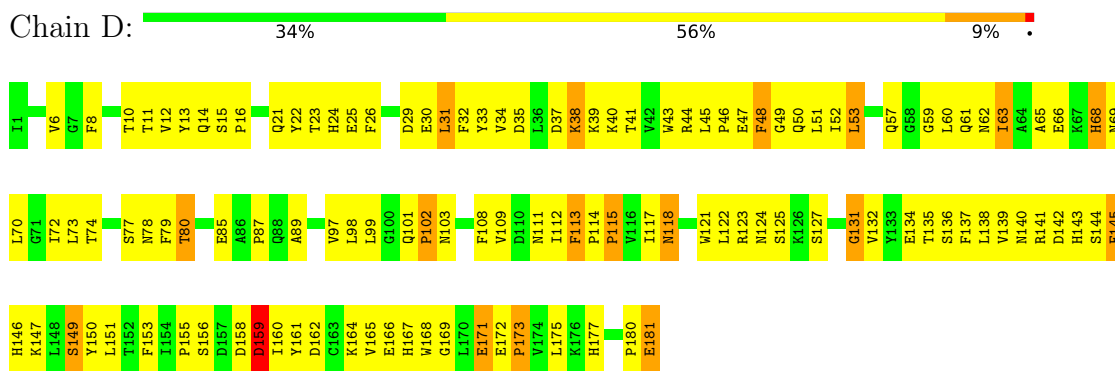
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

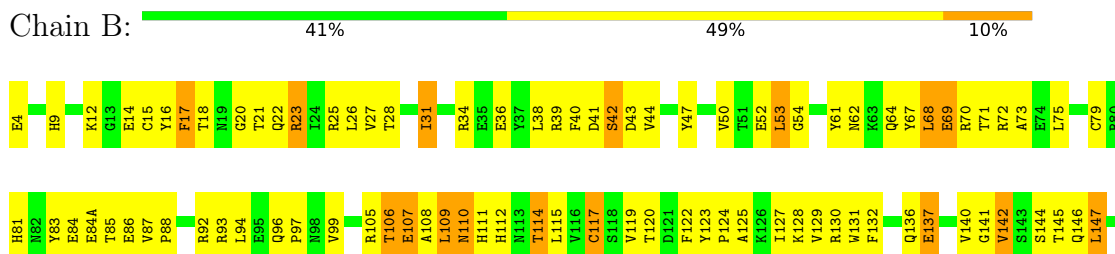
• Molecule 1: H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN



• Molecule 1: H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN



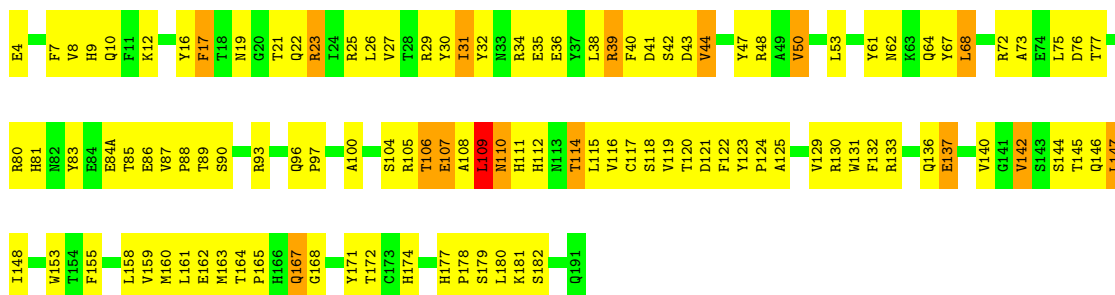
• Molecule 2: MHC CLASS II NOD





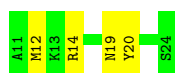
• Molecule 2: MHC CLASS II NOD

Chain E: 40% 52% 8%



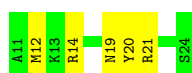
• Molecule 3: LYSOZYME C

Chain P: 71% 29%



• Molecule 3: LYSOZYME C

Chain Q: 64% 36%



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	109.54Å 109.54Å 176.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.82 – 3.10	Depositor
% Data completeness (in resolution range)	80.2 (19.82-3.10)	Depositor
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.221 , 0.299	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6464	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

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	0.61	0/1520	1.11	10/2074 (0.5%)
1	D	0.56	0/1520	1.11	10/2074 (0.5%)
2	B	0.62	0/1601	1.07	6/2170 (0.3%)
2	E	0.62	0/1601	1.07	9/2170 (0.4%)
3	P	0.53	0/119	0.78	0/155
3	Q	0.49	0/119	0.73	0/155
All	All	0.60	0/6480	1.08	35/8798 (0.4%)

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	131	GLY	N-CA-C	-12.93	97.32	115.30
1	A	131	GLY	N-CA-C	-10.87	100.10	115.43
2	B	166	HIS	N-CA-C	-7.77	101.30	108.75
1	A	80	THR	CA-C-N	7.21	127.78	120.14
1	A	80	THR	C-N-CA	7.21	127.78	120.14

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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 hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1474	0	1407	136	0
1	D	1474	0	1407	150	1
2	B	1563	0	1491	114	0
2	E	1563	0	1490	126	0
3	P	117	0	109	9	0
3	Q	117	0	109	10	0
4	A	28	0	26	8	0
4	B	14	0	13	0	0
4	D	28	0	26	5	0
4	E	14	0	13	1	0
5	A	19	0	0	4	0
5	B	26	0	0	2	0
5	D	12	0	0	4	0
5	E	11	0	0	4	0
5	P	2	0	0	1	0
5	Q	2	0	0	1	0
All	All	6464	0	6091	498	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 40.

The worst 5 of 498 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:167:GLN:HE21	2:B:167:GLN:HA	1.25	1.00
2:B:142:VAL:HB	2:E:146:GLN:CG	1.91	1.00
2:E:167:GLN:HA	2:E:167:GLN:HE21	1.24	1.00
2:E:109:LEU:H	2:E:109:LEU:HD12	1.26	0.99
2:B:142:VAL:HB	2:E:146:GLN:HG3	1.00	0.99

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:123:ARG:NH2	1:D:123:ARG:NH2[8_555]	1.70	0.50

5.3 Torsion angles

5.3.1 Protein backbone

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	180/182 (99%)	141 (78%)	28 (16%)	11 (6%)	1	7
1	D	180/182 (99%)	141 (78%)	27 (15%)	12 (7%)	1	6
2	B	185/187 (99%)	150 (81%)	24 (13%)	11 (6%)	1	8
2	E	185/187 (99%)	149 (80%)	27 (15%)	9 (5%)	1	11
3	P	12/14 (86%)	12 (100%)	0	0	100	100
3	Q	12/14 (86%)	12 (100%)	0	0	100	100
All	All	754/766 (98%)	605 (80%)	106 (14%)	43 (6%)	1	8

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	GLU
1	A	51	LEU
1	A	113	PHE
1	A	159	ASP
2	B	23	ARG

5.3.2 Protein sidechains

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	164/164 (100%)	158 (96%)	6 (4%)	30	61
1	D	164/164 (100%)	157 (96%)	7 (4%)	26	57
2	B	171/171 (100%)	158 (92%)	13 (8%)	12	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	171/171 (100%)	159 (93%)	12 (7%)	14	41
3	P	11/11 (100%)	11 (100%)	0	100	100
3	Q	11/11 (100%)	11 (100%)	0	100	100
All	All	692/692 (100%)	654 (94%)	38 (6%)	19	50

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	50	VAL
2	E	167	GLN
2	E	104	SER
2	E	137	GLU
2	E	182	SER

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

Mol	Chain	Res	Type
1	D	140	ASN
2	E	110	ASN
2	E	167	GLN
2	E	136	GLN
2	E	6	HIS

5.3.3 RNA ⓘ

There are no RNA molecules 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 oligosaccharides in this entry.

5.6 Ligand geometry

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	E	1003	2	14,14,15	1.31	2 (14%)	17,19,21	1.30	1 (5%)
4	NAG	A	1002	1	14,14,15	0.70	0	17,19,21	0.57	0
4	NAG	D	1001	1	14,14,15	0.64	0	17,19,21	0.59	0
4	NAG	A	1001	1	14,14,15	0.91	1 (7%)	17,19,21	0.67	0
4	NAG	D	1002	1	14,14,15	0.51	0	17,19,21	0.88	0
4	NAG	B	1003	2	14,14,15	1.36	2 (14%)	17,19,21	1.15	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	E	1003	2	-	4/6/23/26	0/1/1/1
4	NAG	A	1002	1	-	3/6/23/26	0/1/1/1
4	NAG	D	1001	1	-	6/6/23/26	0/1/1/1
4	NAG	A	1001	1	-	3/6/23/26	0/1/1/1
4	NAG	D	1002	1	-	3/6/23/26	0/1/1/1
4	NAG	B	1003	2	-	3/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1003	NAG	C1-C2	3.67	1.57	1.52
4	E	1003	NAG	C1-C2	3.40	1.57	1.52
4	B	1003	NAG	C3-C2	3.03	1.58	1.52
4	A	1001	NAG	C1-C2	2.73	1.56	1.52
4	E	1003	NAG	C3-C2	2.36	1.57	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1003	NAG	C4-C3-C2	4.54	117.67	111.02
4	B	1003	NAG	C4-C3-C2	3.20	115.70	111.02

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1001	NAG	C1-C2-N2-C7
4	A	1001	NAG	C8-C7-N2-C2
4	A	1001	NAG	O7-C7-N2-C2
4	A	1002	NAG	C3-C2-N2-C7
4	A	1002	NAG	C8-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1003	NAG	1	0
4	A	1002	NAG	6	0
4	D	1001	NAG	1	0
4	A	1001	NAG	2	0
4	D	1002	NAG	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.