



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 05:59 AM UTC

PDB ID : 1HHI / pdb_00001hhi
Title : THE ANTIGENIC IDENTITY OF PEPTIDE(SLASH)MHC COMPLEXES:
A COMPARISON OF THE CONFORMATION OF FIVE PEPTIDES PRE-
SENTED BY HLA-A2
Authors : Madden, D.R.; Garboczi, D.N.; Wiley, D.C.
Deposited on : 1993-06-30
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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
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

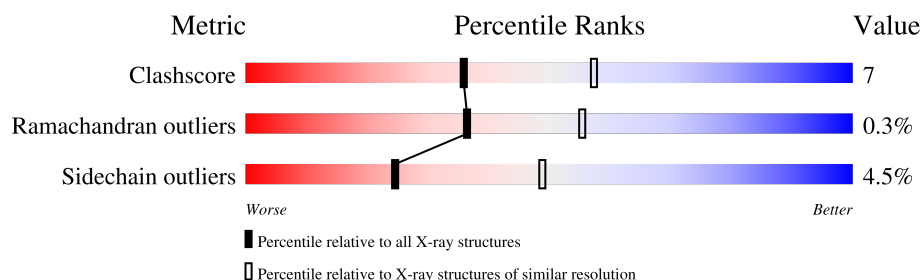
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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	275	
1	D	275	
2	B	100	
2	E	100	
3	C	9	
3	F	9	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6306 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 CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-A*0201) (ALPHA CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	27	0	0
			2247	1403	409	426	9			
1	D	275	Total	C	N	O	S	27	0	0
			2247	1403	409	426	9			

- Molecule 2 is a protein called BETA 2-MICROGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	20	0	0
			837	533	141	159	4			
2	E	100	Total	C	N	O	S	20	0	0
			837	533	141	159	4			

- Molecule 3 is a protein called INFLUENZA A MATRIX PROTEIN M1 (RESIDUES 58-66).

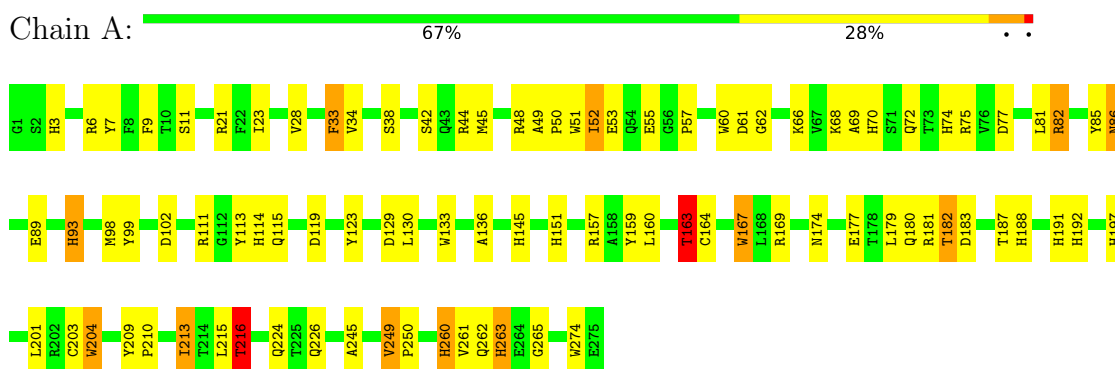
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O		0	0	0
			69	49	9	11				
3	F	9	Total	C	N	O		0	0	0
			69	49	9	11				

3 Residue-property plots [i](#)

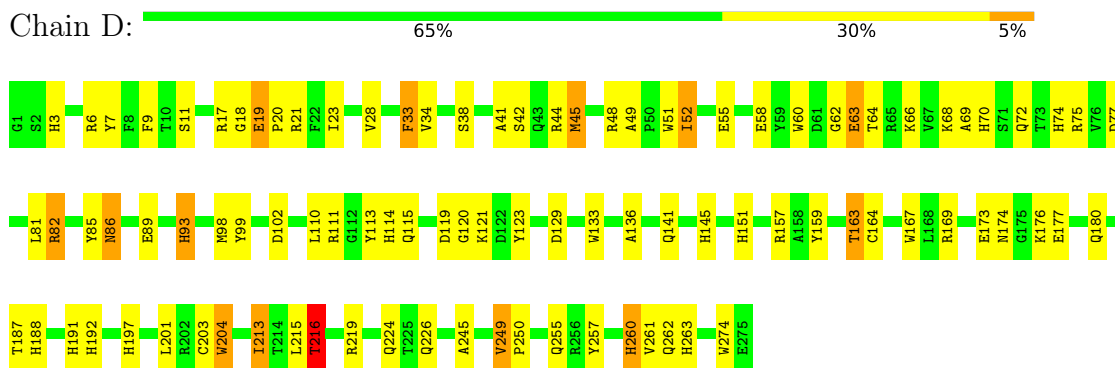
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

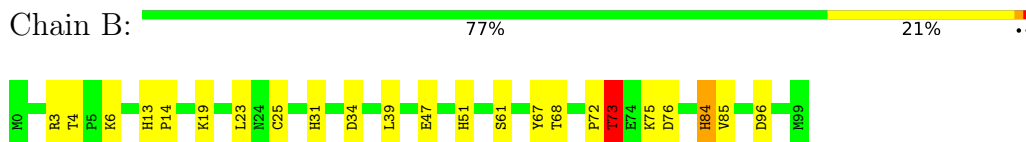
- Molecule 1: CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-A*0201) (ALPHA CHAIN)



- Molecule 1: CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-A*0201) (ALPHA CHAIN)



- Molecule 2: BETA 2-MICROGLOBULIN

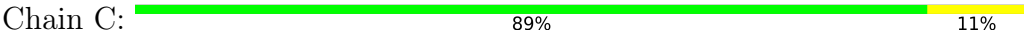


- Molecule 2: BETA 2-MICROGLOBULIN

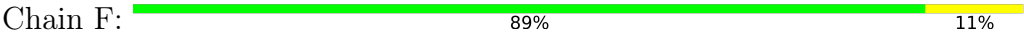




- Molecule 3: INFLUENZA A MATRIX PROTEIN M1 (RESIDUES 58-66)



- Molecule 3: INFLUENZA A MATRIX PROTEIN M1 (RESIDUES 58-66)



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	63.35Å 87.71Å 79.22Å 90.00° 90.10° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.273 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6306	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	1.20	19/2312 (0.8%)	1.85	52/3137 (1.7%)
1	D	1.19	19/2312 (0.8%)	1.83	51/3137 (1.6%)
2	B	1.14	6/860 (0.7%)	1.63	7/1162 (0.6%)
2	E	1.06	5/860 (0.6%)	1.66	9/1162 (0.8%)
3	C	0.67	0/70	1.55	0/92
3	F	0.68	0/70	1.55	0/92
All	All	1.16	49/6484 (0.8%)	1.78	119/8782 (1.4%)

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	164	CYS	N-CA	10.99	1.59	1.46
2	B	84	HIS	CD2-NE2	-8.46	1.28	1.37
1	A	191	HIS	CD2-NE2	-7.74	1.29	1.37
1	D	93	HIS	CD2-NE2	-7.72	1.29	1.37
1	A	93	HIS	CD2-NE2	-7.70	1.29	1.37
1	D	191	HIS	CD2-NE2	-7.64	1.29	1.37
2	B	84	HIS	CG-ND1	-7.56	1.29	1.38
2	E	84	HIS	CD2-NE2	-7.19	1.29	1.37
1	D	3	HIS	CG-ND1	-6.96	1.30	1.38
1	D	151	HIS	CD2-NE2	-6.96	1.30	1.37
1	A	151	HIS	CD2-NE2	-6.95	1.30	1.37
1	D	164	CYS	N-CA	6.90	1.54	1.46
1	D	263	HIS	CD2-NE2	-6.90	1.30	1.37
1	A	74	HIS	CD2-NE2	-6.78	1.30	1.37
1	D	74	HIS	CD2-NE2	-6.75	1.30	1.37
2	B	13	HIS	CD2-NE2	-6.71	1.30	1.37
2	E	51	HIS	CD2-NE2	-6.63	1.30	1.37
1	A	263	HIS	CD2-NE2	-6.62	1.30	1.37
1	D	145	HIS	CD2-NE2	-6.61	1.30	1.37
1	A	145	HIS	CD2-NE2	-6.60	1.30	1.37
2	B	51	HIS	CD2-NE2	-6.60	1.30	1.37
1	A	260	HIS	CD2-NE2	-6.58	1.30	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	260	HIS	CD2-NE2	-6.58	1.30	1.37
2	E	31	HIS	CD2-NE2	-6.58	1.30	1.37
2	B	31	HIS	CD2-NE2	-6.53	1.30	1.37
1	A	192	HIS	CD2-NE2	-6.45	1.30	1.37
1	D	192	HIS	CD2-NE2	-6.43	1.30	1.37
1	D	3	HIS	CD2-NE2	-6.42	1.30	1.37
2	E	13	HIS	CD2-NE2	-6.33	1.30	1.37
1	A	163	THR	CA-C	6.20	1.61	1.52
1	A	70	HIS	CD2-NE2	-6.12	1.31	1.37
1	D	70	HIS	CD2-NE2	-5.96	1.31	1.37
1	D	188	HIS	CD2-NE2	-5.95	1.31	1.37
1	A	188	HIS	CD2-NE2	-5.94	1.31	1.37
1	D	197	HIS	CD2-NE2	-5.92	1.31	1.37
1	A	197	HIS	CD2-NE2	-5.91	1.31	1.37
2	E	84	HIS	CG-ND1	-5.88	1.31	1.38
1	A	3	HIS	CD2-NE2	-5.84	1.31	1.37
1	A	163	THR	C-N	5.76	1.42	1.33
1	A	114	HIS	CD2-NE2	-5.72	1.31	1.37
1	D	114	HIS	CD2-NE2	-5.68	1.31	1.37
1	A	188	HIS	CG-ND1	-5.55	1.32	1.38
1	D	188	HIS	CG-ND1	-5.53	1.32	1.38
1	A	151	HIS	CG-ND1	-5.44	1.32	1.38
1	D	151	HIS	CG-ND1	-5.42	1.32	1.38
1	D	203	CYS	CA-CB	-5.22	1.46	1.53
1	A	203	CYS	CA-CB	-5.19	1.46	1.53
1	D	213	ILE	CA-CB	5.11	1.62	1.55
2	B	85	VAL	CA-CB	5.01	1.61	1.54

All (119) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	42	SER	N-CA-C	8.86	121.02	111.36
1	A	42	SER	N-CA-C	8.81	120.96	111.36
1	A	226	GLN	CA-CB-CG	-8.45	97.20	114.10
1	D	226	GLN	CA-CB-CG	-8.43	97.25	114.10
2	E	47	GLU	N-CA-C	7.78	119.84	111.36
2	B	47	GLU	N-CA-C	7.42	119.15	111.14
1	A	28	VAL	N-CA-C	-7.16	98.14	108.17
1	D	28	VAL	N-CA-C	-7.16	98.15	108.17
1	A	129	ASP	CA-CB-CG	7.13	119.73	112.60
1	D	129	ASP	CA-CB-CG	7.05	119.65	112.60
1	D	255	GLN	OE1-CD-NE2	-6.86	115.74	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	6	LYS	N-CA-C	-6.86	100.33	110.48
2	B	6	LYS	N-CA-C	-6.84	100.35	110.48
2	E	13	HIS	CB-CG-CD2	-6.84	122.31	131.20
2	B	13	HIS	CB-CG-CD2	-6.78	122.39	131.20
1	A	93	HIS	CB-CG-CD2	-6.52	122.72	131.20
1	D	93	HIS	CB-CG-CD2	-6.50	122.74	131.20
1	A	86	ASN	CA-CB-CG	-6.24	106.36	112.60
1	A	61	ASP	CA-CB-CG	6.22	118.82	112.60
2	E	85	VAL	CB-CA-C	-6.15	102.62	112.16
1	D	86	ASN	CA-CB-CG	-6.13	106.47	112.60
1	D	33	PHE	CA-CB-CG	6.08	119.88	113.80
1	A	33	PHE	CA-CB-CG	6.08	119.88	113.80
1	A	262	GLN	OE1-CD-NE2	-6.06	116.54	122.60
1	A	191	HIS	CB-CG-CD2	-6.00	123.41	131.20
1	D	191	HIS	CB-CG-CD2	-5.98	123.43	131.20
1	D	262	GLN	OE1-CD-NE2	-5.96	116.64	122.60
1	A	174	ASN	OD1-CG-ND2	-5.93	116.67	122.60
1	A	167	TRP	CG-CD2-CE3	5.93	139.83	133.90
1	A	74	HIS	CB-CG-CD2	-5.92	123.51	131.20
1	A	55	GLU	N-CA-C	-5.90	103.15	110.41
1	A	197	HIS	CB-CG-CD2	-5.89	123.54	131.20
1	D	74	HIS	CB-CG-CD2	-5.89	123.55	131.20
1	D	167	TRP	CG-CD2-CE3	5.88	139.78	133.90
1	D	197	HIS	CB-CG-CD2	-5.86	123.59	131.20
2	E	31	HIS	CB-CG-CD2	-5.82	123.64	131.20
2	B	31	HIS	CB-CG-CD2	-5.81	123.64	131.20
1	A	93	HIS	CA-CB-CG	-5.75	108.05	113.80
1	D	93	HIS	CA-CB-CG	-5.75	108.05	113.80
1	D	133	TRP	CG-CD2-CE3	5.74	139.64	133.90
1	A	133	TRP	CG-CD2-CE3	5.71	139.61	133.90
1	D	173	GLU	CA-CB-CG	5.71	125.51	114.10
1	D	70	HIS	CB-CG-CD2	-5.67	123.83	131.20
1	D	204	TRP	CE2-CD2-CG	-5.66	100.41	107.20
1	A	3	HIS	CB-CG-CD2	-5.65	123.85	131.20
1	A	70	HIS	CB-CG-CD2	-5.65	123.86	131.20
1	A	204	TRP	CE2-CD2-CG	-5.64	100.43	107.20
1	D	69	ALA	N-CA-C	-5.64	104.75	111.69
1	D	141	GLN	OE1-CD-NE2	-5.62	116.98	122.60
1	D	41	ALA	N-CA-C	5.62	117.86	111.11
1	A	69	ALA	N-CA-C	-5.61	104.79	111.69
1	D	260	HIS	CB-CG-CD2	-5.55	123.98	131.20
1	A	260	HIS	CB-CG-CD2	-5.53	124.01	131.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	73	THR	N-CA-CB	-5.52	101.94	111.55
2	E	73	THR	N-CA-CB	-5.52	101.94	111.55
1	D	52	ILE	N-CA-CB	-5.50	106.16	112.21
1	A	52	ILE	N-CA-CB	-5.49	106.17	112.21
1	A	180	GLN	OE1-CD-NE2	-5.49	117.11	122.60
1	A	245	ALA	O-C-N	-5.48	116.78	123.30
1	A	204	TRP	CG-CD1-NE1	-5.47	103.09	110.20
1	D	204	TRP	CG-CD1-NE1	-5.46	103.10	110.20
1	D	245	ALA	O-C-N	-5.46	116.80	123.30
1	D	204	TRP	CG-CD2-CE3	5.46	139.36	133.90
1	A	114	HIS	CA-CB-CG	-5.46	108.34	113.80
1	A	204	TRP	CG-CD2-CE3	5.45	139.35	133.90
1	A	181	ARG	NE-CZ-NH2	-5.44	114.31	119.20
1	D	18	GLY	O-C-N	5.42	127.38	122.88
1	D	114	HIS	CA-CB-CG	-5.42	108.38	113.80
1	A	167	TRP	CE2-CD2-CG	-5.41	100.71	107.20
1	D	255	GLN	N-CA-C	5.41	118.98	112.38
2	E	51	HIS	CB-CG-CD2	-5.39	124.20	131.20
2	B	51	HIS	CB-CG-CD2	-5.37	124.22	131.20
1	D	167	TRP	CE2-CD2-CG	-5.34	100.79	107.20
1	A	57	PRO	CA-C-N	5.29	127.36	120.28
1	A	57	PRO	C-N-CA	5.29	127.36	120.28
1	D	136	ALA	N-CA-C	5.28	116.73	110.97
1	D	174	ASN	OD1-CG-ND2	-5.28	117.32	122.60
1	A	204	TRP	CD1-CG-CD2	5.28	114.75	106.30
1	D	204	TRP	CD1-CG-CD2	5.28	114.75	106.30
2	E	96	ASP	CA-CB-CG	5.28	117.88	112.60
1	A	61	ASP	CA-C-N	5.25	125.77	119.94
1	A	61	ASP	C-N-CA	5.25	125.77	119.94
1	D	55	GLU	N-CA-C	-5.25	103.75	110.53
1	A	136	ALA	N-CA-C	5.25	116.69	110.97
1	D	63	GLU	CA-C-N	5.24	127.31	120.28
1	D	63	GLU	C-N-CA	5.24	127.31	120.28
2	B	96	ASP	CA-CB-CG	5.24	117.84	112.60
1	A	188	HIS	CB-CG-CD2	-5.24	124.39	131.20
1	A	182	THR	CB-CA-C	-5.24	103.10	111.17
1	A	133	TRP	CE2-CD2-CG	-5.24	100.92	107.20
1	D	169	ARG	CB-CG-CD	-5.23	99.28	111.30
1	D	133	TRP	CE2-CD2-CG	-5.23	100.93	107.20
1	D	82	ARG	N-CA-C	-5.22	105.59	111.28
1	A	249	VAL	N-CA-CB	-5.21	104.59	111.21
1	A	169	ARG	CB-CG-CD	-5.21	99.31	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	ARG	N-CA-C	-5.21	105.60	111.28
1	D	45	MET	N-CA-C	-5.21	101.48	109.76
1	D	188	HIS	CB-CG-CD2	-5.20	124.44	131.20
1	A	274	TRP	CE2-CD2-CG	-5.20	100.96	107.20
1	D	274	TRP	CE2-CD2-CG	-5.19	100.97	107.20
1	D	249	VAL	N-CA-CB	-5.18	104.63	111.21
1	D	58	GLU	N-CA-CB	-5.18	102.50	110.01
1	D	263	HIS	CB-CG-CD2	-5.18	124.47	131.20
1	D	167	TRP	CB-CG-CD1	-5.17	119.15	126.90
1	A	45	MET	N-CA-C	-5.16	101.55	109.76
1	A	51	TRP	CE2-CD2-CG	-5.16	101.01	107.20
1	A	179	LEU	N-CA-C	5.14	116.97	111.36
1	D	51	TRP	CE2-CD2-CG	-5.14	101.03	107.20
1	A	216	THR	N-CA-CB	-5.14	102.11	110.59
1	D	274	TRP	CG-CD2-CE3	5.14	139.04	133.90
1	A	167	TRP	CB-CG-CD1	-5.14	119.19	126.90
2	E	84	HIS	CB-CG-CD2	-5.12	124.54	131.20
1	D	216	THR	N-CA-CB	-5.12	102.14	110.59
1	A	274	TRP	CG-CD2-CE3	5.11	139.01	133.90
1	A	23	ILE	N-CA-C	-5.02	100.89	108.12
1	A	192	HIS	CB-CG-CD2	-5.02	124.68	131.20
1	D	70	HIS	CB-CG-ND1	5.02	130.23	122.70
1	A	70	HIS	CB-CG-ND1	5.01	130.22	122.70
1	D	23	ILE	N-CA-C	-5.01	100.91	108.12

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2247	0	2096	37	0
1	D	2247	0	2096	37	0
2	B	837	0	803	7	0
2	E	837	0	803	10	0
3	C	69	0	75	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	69	0	75	2	0
All	All	6306	0	5948	88	0

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 7.

All (88) 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:E:73:THR:HG22	2:E:76:ASP:H	1.48	0.77
2:B:73:THR:HG22	2:B:76:ASP:H	1.48	0.77
1:D:77:ASP:HB3	3:F:9:LEU:HD12	1.70	0.74
1:A:77:ASP:HB3	3:C:9:LEU:HD12	1.70	0.74
2:E:3:ARG:HH11	2:E:61:SER:HB3	1.61	0.65
2:B:3:ARG:HH11	2:B:61:SER:HB3	1.61	0.65
1:A:159:TYR:HA	1:A:163:THR:HG23	1.81	0.63
2:B:19:LYS:O	2:B:72:PRO:HD2	1.99	0.63
1:D:159:TYR:CD1	1:D:163:THR:HG23	2.36	0.61
2:E:19:LYS:O	2:E:72:PRO:HD2	2.03	0.59
1:A:213:ILE:HD12	1:A:263:HIS:HB2	1.85	0.59
1:D:19:GLU:HG3	1:D:20:PRO:HD2	1.85	0.58
1:D:159:TYR:HA	1:D:163:THR:CG2	2.34	0.58
1:D:62:GLY:O	1:D:66:LYS:HG3	2.03	0.57
1:D:93:HIS:HD2	1:D:119:ASP:OD2	1.88	0.57
1:A:93:HIS:HD2	1:A:119:ASP:OD2	1.88	0.56
1:D:215:LEU:HD12	1:D:261:VAL:HG22	1.89	0.55
1:D:44:ARG:HA	1:D:64:THR:HG23	1.88	0.55
1:A:215:LEU:HD12	1:A:261:VAL:HG22	1.89	0.54
1:D:176:LYS:HG3	1:D:180:GLN:OE1	2.07	0.54
1:A:159:TYR:HA	1:A:163:THR:CG2	2.38	0.54
2:E:25:CYS:HB2	2:E:39:LEU:HD21	1.90	0.53
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.90	0.53
1:A:210:PRO:O	1:A:263:HIS:HE1	1.92	0.51
1:A:123:TYR:CE2	3:C:9:LEU:HD22	2.45	0.51
1:D:123:TYR:CE2	3:F:9:LEU:HD22	2.45	0.51
1:A:163:THR:O	1:A:167:TRP:CD1	2.64	0.51
1:A:72:GLN:HE22	1:A:75:ARG:HD3	1.77	0.50
1:A:44:ARG:HH21	1:A:60:TRP:HB3	1.76	0.50
1:D:72:GLN:HE22	1:D:75:ARG:HD3	1.77	0.50
1:D:187:THR:HA	1:D:204:TRP:O	2.13	0.49
1:A:187:THR:HA	1:A:204:TRP:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ALA:O	1:A:52:ILE:HG22	2.13	0.49
1:A:50:PRO:HA	1:A:53:GLU:OE1	2.13	0.49
1:D:49:ALA:O	1:D:52:ILE:HG22	2.13	0.49
1:A:21:ARG:HD2	1:A:38:SER:OG	2.13	0.48
1:D:21:ARG:HD2	1:D:38:SER:OG	2.13	0.48
1:D:44:ARG:HH21	1:D:60:TRP:HB3	1.78	0.48
1:D:121:LYS:HG2	2:E:1:ILE:HD11	1.94	0.48
1:A:82:ARG:HE	1:A:89:GLU:HA	1.79	0.48
2:B:34:ASP:O	2:B:84:HIS:HD2	1.97	0.48
1:D:82:ARG:HE	1:D:89:GLU:HA	1.80	0.47
1:D:45:MET:HG2	1:D:63:GLU:HB3	1.97	0.47
1:A:81:LEU:O	1:A:85:TYR:HD2	1.99	0.46
1:D:216:THR:HG22	1:D:260:HIS:HB2	1.98	0.46
1:A:9:PHE:HE2	1:A:99:TYR:CE2	2.34	0.45
1:A:216:THR:HG22	1:A:260:HIS:HB2	1.98	0.45
1:D:81:LEU:O	1:D:85:TYR:HD2	1.99	0.45
2:B:23:LEU:O	2:B:67:TYR:HA	2.17	0.45
1:D:9:PHE:HE2	1:D:99:TYR:CE2	2.34	0.45
1:A:111:ARG:HD2	1:A:113:TYR:OH	2.17	0.45
1:A:263:HIS:HD2	1:A:265:GLY:H	1.64	0.45
2:E:34:ASP:O	2:E:84:HIS:HD2	1.99	0.44
1:A:249:VAL:HA	1:A:250:PRO:HD3	1.89	0.44
1:D:93:HIS:NE2	2:E:0:MET:HE1	2.32	0.44
1:D:98:MET:C	1:D:98:MET:SD	3.00	0.44
1:A:98:MET:SD	1:A:98:MET:C	3.00	0.44
1:A:183:ASP:HB2	1:A:209:TYR:N	2.33	0.44
1:A:201:LEU:HD22	1:A:249:VAL:HG21	1.99	0.44
2:E:23:LEU:O	2:E:67:TYR:HA	2.18	0.44
2:B:34:ASP:O	2:B:84:HIS:CD2	2.71	0.43
1:A:62:GLY:O	1:A:66:LYS:HG3	2.18	0.43
1:D:48:ARG:HA	1:D:48:ARG:HD2	1.82	0.43
1:D:201:LEU:HD22	1:D:249:VAL:HG21	1.99	0.43
1:D:159:TYR:HA	1:D:163:THR:HG22	1.99	0.43
1:D:249:VAL:HA	1:D:250:PRO:HD3	1.90	0.43
1:A:48:ARG:HA	1:A:48:ARG:HD2	1.82	0.43
1:A:7:TYR:O	1:A:98:MET:HA	2.19	0.43
1:D:7:TYR:O	1:D:98:MET:HA	2.19	0.43
1:D:120:GLY:O	2:E:3:ARG:NH2	2.52	0.42
2:E:34:ASP:O	2:E:84:HIS:CD2	2.73	0.42
1:A:82:ARG:HH21	1:A:89:GLU:HB2	1.84	0.42
1:A:263:HIS:CD2	1:A:265:GLY:H	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:GLN:NE2	1:A:75:ARG:HD3	2.34	0.42
1:D:72:GLN:NE2	1:D:75:ARG:HD3	2.34	0.42
1:A:130:LEU:HD22	1:A:160:LEU:HD12	2.01	0.41
1:D:159:TYR:HD1	1:D:163:THR:HG23	1.82	0.41
1:D:219:ARG:HD3	1:D:257:TYR:OH	2.19	0.41
1:A:163:THR:O	1:A:167:TRP:HD1	2.04	0.41
1:A:6:ARG:NH2	1:A:102:ASP:OD1	2.54	0.41
1:D:6:ARG:NH2	1:D:102:ASP:OD1	2.54	0.41
1:D:110:LEU:HD12	1:D:110:LEU:HA	1.86	0.41
1:A:9:PHE:CE2	1:A:99:TYR:CE2	3.09	0.41
1:D:111:ARG:HD2	1:D:113:TYR:OH	2.21	0.41
1:A:182:THR:HG21	1:A:265:GLY:CA	2.50	0.40
1:A:33:PHE:CD2	1:A:34:VAL:HG13	2.57	0.40
1:D:9:PHE:CE2	1:D:99:TYR:CE2	3.09	0.40
1:D:33:PHE:CD2	1:D:34:VAL:HG13	2.57	0.40

There are no symmetry-related clashes.

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	273/275 (99%)	262 (96%)	11 (4%)	0	100	100
1	D	273/275 (99%)	261 (96%)	12 (4%)	0	100	100
2	B	98/100 (98%)	93 (95%)	4 (4%)	1 (1%)	12	24
2	E	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	12	24
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	756/768 (98%)	720 (95%)	34 (4%)	2 (0%)	36	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	14	PRO
2	E	14	PRO

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	231/231 (100%)	221 (96%)	10 (4%)	26	51
1	D	231/231 (100%)	219 (95%)	12 (5%)	21	42
2	B	95/95 (100%)	91 (96%)	4 (4%)	26	52
2	E	95/95 (100%)	91 (96%)	4 (4%)	26	52
3	C	7/7 (100%)	7 (100%)	0	100	100
3	F	7/7 (100%)	7 (100%)	0	100	100
All	All	666/666 (100%)	636 (96%)	30 (4%)	24	49

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	68	LYS
1	A	86	ASN
1	A	115	GLN
1	A	157	ARG
1	A	163	THR
1	A	177	GLU
1	A	213	ILE
1	A	216	THR
1	A	224	GLN
2	B	4	THR
2	B	68	THR
2	B	73	THR
2	B	75	LYS
1	D	11	SER
1	D	17	ARG
1	D	19	GLU

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Mol	Chain	Res	Type
1	D	68	LYS
1	D	86	ASN
1	D	115	GLN
1	D	157	ARG
1	D	163	THR
1	D	177	GLU
1	D	213	ILE
1	D	216	THR
1	D	224	GLN
2	E	4	THR
2	E	68	THR
2	E	73	THR
2	E	75	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	GLN
1	A	72	GLN
1	A	93	HIS
1	A	114	HIS
1	A	174	ASN
1	A	263	HIS
1	D	72	GLN
1	D	114	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

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.