



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:08 am GMT

PDB ID : 1HSA
Title : THE THREE-DIMENSIONAL STRUCTURE OF HLA-B27 AT 2.1
ANGSTROMS RESOLUTION SUGGESTS A GENERAL MECHANISM
FOR TIGHT PEPTIDE BINDING TO MHC
Authors : Madden, D.R.; Gorga, J.C.; Strominger, J.L.; Wiley, D.C.
Deposited on : 1992-08-11
Resolution : 2.10 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : NOT EXECUTED
EDS : NOT EXECUTED
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

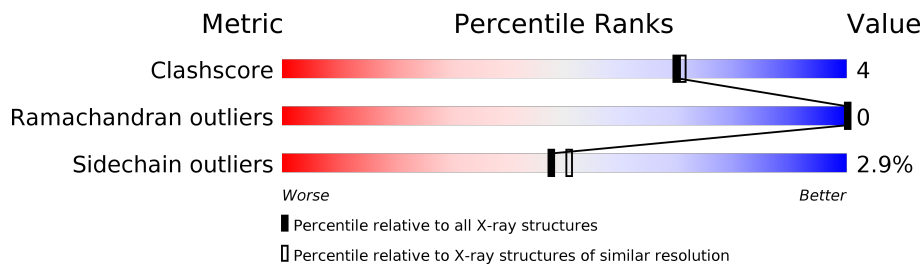
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	276	 78% 21% .
1	D	276	 79% 20% .
2	B	99	 84% 15% .
2	E	99	 85% 13% ..
3	C	9	 100%
3	F	9	 100%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6706 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-B*2705).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	12	0	0
			2252	1401	408	436	7			
1	D	276	Total	C	N	O	S	12	0	0
			2252	1401	408	436	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	5	0	0
			829	528	140	158	3			
2	E	99	Total	C	N	O	S	5	0	0
			829	528	140	158	3			

- Molecule 3 is a protein called MODEL PEPTIDE SEQUENCE - ARAAAAAAA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			52	30	12	10			
3	F	9	Total	C	N	O	0	0	0
			52	30	12	10			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	149	Total	O	0	0
			149	149		
4	B	60	Total	O	0	0
			60	60		
4	C	4	Total	O	0	0
			4	4		
4	D	147	Total	O	0	0
			147	147		

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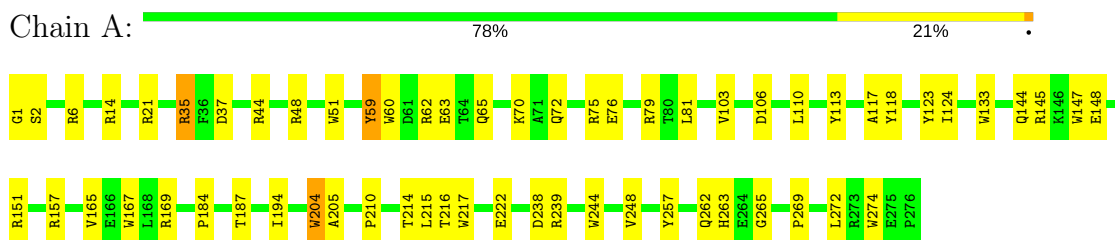
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	75	Total 75	O 75	0	0
4	F	5	Total 5	O 5	0	0

3 Residue-property plots

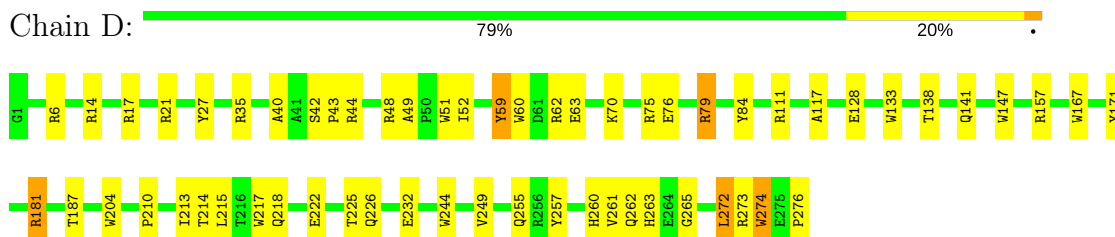
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

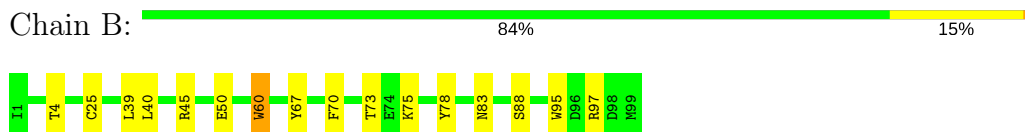
• Molecule 1: CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-B*2705)



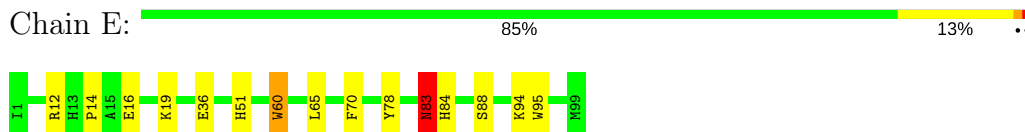
• Molecule 1: CLASS I HISTOCOMPATIBILITY ANTIGEN (HLA-B*2705)



• Molecule 2: BETA 2-MICROGLOBULIN



• Molecule 2: BETA 2-MICROGLOBULIN



• Molecule 3: MODEL PEPTIDE SEQUENCE - ARAAAAAAA



There are no outlier residues recorded for this chain.

- Molecule 3: MODEL PEPTIDE SEQUENCE - ARAAAAAAA

Chain F:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	45.10Å 69.80Å 81.10Å 80.30° 88.60° 89.90°	Depositor
Resolution (Å)	(Not available) – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.203 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6706	wwPDB-VP
Average B, all atoms (Å ²)	24.0	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	0.93	0/2314	1.52	55/3147 (1.7%)
1	D	0.94	0/2314	1.55	48/3147 (1.5%)
2	B	0.91	0/852	1.42	12/1152 (1.0%)
2	E	0.91	0/852	1.44	9/1152 (0.8%)
3	C	0.78	0/51	1.04	0/67
3	F	0.87	0/51	1.16	0/67
All	All	0.93	0/6434	1.50	124/8732 (1.4%)

There are no bond length outliers.

All (124) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	48	ARG	NE-CZ-NH1	9.72	125.16	120.30
1	A	151	ARG	NE-CZ-NH2	-9.43	115.59	120.30
1	D	75	ARG	NE-CZ-NH2	-9.37	115.61	120.30
1	D	6	ARG	NE-CZ-NH1	9.36	124.98	120.30
1	A	51	TRP	CD1-CG-CD2	9.21	113.67	106.30
1	A	133	TRP	CD1-CG-CD2	9.05	113.54	106.30
2	B	60	TRP	CD1-CG-CD2	8.80	113.34	106.30
1	D	133	TRP	CD1-CG-CD2	8.57	113.16	106.30
2	E	60	TRP	CD1-CG-CD2	8.50	113.10	106.30
1	D	204	TRP	CD1-CG-CD2	8.44	113.05	106.30
1	D	167	TRP	CD1-CG-CD2	8.39	113.01	106.30
1	D	6	ARG	NE-CZ-NH2	-8.34	116.13	120.30
1	D	274	TRP	CD1-CG-CD2	8.24	112.89	106.30
1	A	51	TRP	CE2-CD2-CG	-8.14	100.79	107.30
1	D	79	ARG	NE-CZ-NH1	8.05	124.33	120.30
1	D	181	ARG	NE-CZ-NH1	8.02	124.31	120.30
1	A	204	TRP	CD1-CG-CD2	7.99	112.69	106.30
1	D	60	TRP	CD1-CG-CD2	7.93	112.64	106.30
1	A	274	TRP	CD1-CG-CD2	7.90	112.62	106.30
1	D	244	TRP	CE2-CD2-CG	-7.79	101.06	107.30
1	D	217	TRP	CD1-CG-CD2	7.73	112.49	106.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	244	TRP	CE2-CD2-CG	-7.70	101.14	107.30
1	A	60	TRP	CE2-CD2-CG	-7.70	101.14	107.30
2	B	60	TRP	CE2-CD2-CG	-7.67	101.17	107.30
1	A	60	TRP	CD1-CG-CD2	7.63	112.40	106.30
1	D	274	TRP	CE2-CD2-CG	-7.53	101.27	107.30
1	A	244	TRP	CD1-CG-CD2	7.51	112.31	106.30
1	D	21	ARG	NE-CZ-NH1	7.51	124.05	120.30
1	D	51	TRP	CD1-CG-CD2	7.48	112.28	106.30
1	D	60	TRP	CE2-CD2-CG	-7.32	101.44	107.30
1	A	157	ARG	NE-CZ-NH1	7.29	123.94	120.30
1	D	167	TRP	CE2-CD2-CG	-7.16	101.57	107.30
1	A	14	ARG	NE-CZ-NH2	-7.11	116.75	120.30
1	D	244	TRP	CG-CD2-CE3	7.01	140.21	133.90
1	D	217	TRP	CE2-CD2-CG	-7.00	101.70	107.30
1	A	274	TRP	CE2-CD2-CG	-6.99	101.71	107.30
1	D	204	TRP	CE2-CD2-CG	-6.96	101.73	107.30
1	A	44	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	D	157	ARG	NE-CZ-NH1	6.89	123.74	120.30
1	D	244	TRP	CD1-CG-CD2	6.81	111.75	106.30
2	B	95	TRP	CD1-CG-CD2	6.80	111.74	106.30
1	A	217	TRP	CD1-CG-CD2	6.80	111.74	106.30
1	D	14	ARG	NE-CZ-NH1	6.78	123.69	120.30
1	D	51	TRP	CE2-CD2-CG	-6.77	101.89	107.30
2	E	60	TRP	CE2-CD2-CG	-6.75	101.90	107.30
1	A	204	TRP	CE2-CD2-CG	-6.71	101.93	107.30
1	A	133	TRP	CE2-CD2-CG	-6.57	102.05	107.30
2	E	12	ARG	NE-CZ-NH1	6.56	123.58	120.30
2	E	95	TRP	CE2-CD2-CG	-6.55	102.06	107.30
2	E	95	TRP	CD1-CG-CD2	6.54	111.53	106.30
1	A	217	TRP	CE2-CD2-CG	-6.53	102.08	107.30
1	A	147	TRP	CE2-CD2-CG	-6.50	102.10	107.30
1	D	48	ARG	NE-CZ-NH2	-6.50	117.05	120.30
1	D	133	TRP	CE2-CD2-CG	-6.50	102.10	107.30
2	B	95	TRP	CE2-CD2-CG	-6.48	102.11	107.30
1	A	274	TRP	CG-CD2-CE3	6.46	139.71	133.90
1	A	167	TRP	CD1-CG-CD2	6.45	111.46	106.30
2	E	60	TRP	CG-CD1-NE1	-6.43	103.67	110.10
1	A	147	TRP	CD1-CG-CD2	6.40	111.42	106.30
1	A	14	ARG	NE-CZ-NH1	6.37	123.48	120.30
1	D	62	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	A	106	ASP	CB-CG-OD1	6.31	123.98	118.30
1	A	6	ARG	NE-CZ-NH2	-6.31	117.15	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	TRP	CG-CD1-NE1	-6.27	103.83	110.10
1	A	147	TRP	CG-CD2-CE3	6.21	139.49	133.90
1	A	51	TRP	CG-CD1-NE1	-6.16	103.94	110.10
1	D	44	ARG	NE-CZ-NH2	-6.05	117.28	120.30
1	A	113	TYR	CB-CG-CD1	-6.04	117.38	121.00
2	B	50	GLU	CA-CB-CG	-5.99	100.22	113.40
1	A	167	TRP	CE2-CD2-CG	-5.98	102.52	107.30
1	D	21	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	D	244	TRP	CB-CG-CD1	-5.92	119.30	127.00
1	A	257	TYR	CB-CG-CD2	-5.90	117.46	121.00
1	D	27	TYR	CB-CG-CD2	-5.89	117.46	121.00
1	A	6	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	D	75	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	145	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	D	167	TRP	CG-CD2-CE3	5.83	139.15	133.90
1	A	65	GLN	CA-CB-CG	5.81	126.19	113.40
1	A	238	ASP	CB-CG-OD1	5.77	123.50	118.30
2	B	67	TYR	CB-CG-CD2	-5.74	117.56	121.00
1	A	60	TRP	CG-CD2-CE3	5.73	139.06	133.90
2	B	60	TRP	CB-CG-CD1	-5.73	119.55	127.00
1	A	145	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	239	ARG	NE-CZ-NH1	5.69	123.14	120.30
1	A	48	ARG	NE-CZ-NH2	-5.67	117.47	120.30
1	D	59	TYR	CB-CG-CD2	-5.60	117.64	121.00
2	B	78	TYR	CB-CG-CD2	-5.56	117.66	121.00
1	D	249	VAL	CG1-CB-CG2	-5.55	102.01	110.90
1	D	204	TRP	CG-CD1-NE1	-5.53	104.57	110.10
1	A	169	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	D	167	TRP	CB-CG-CD1	-5.52	119.82	127.00
1	A	244	TRP	CB-CG-CD1	-5.51	119.83	127.00
1	D	274	TRP	CG-CD2-CE3	5.49	138.84	133.90
1	D	133	TRP	CG-CD1-NE1	-5.47	104.63	110.10
1	A	51	TRP	CB-CG-CD1	-5.47	119.89	127.00
1	A	35	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	37	ASP	CB-CG-OD1	5.46	123.21	118.30
1	D	171	TYR	CB-CG-CD2	-5.42	117.75	121.00
1	D	147	TRP	CE2-CD2-CG	-5.39	102.99	107.30
1	A	60	TRP	CB-CG-CD1	-5.38	120.00	127.00
1	A	244	TRP	CG-CD1-NE1	-5.32	104.78	110.10
1	D	84	TYR	CB-CG-CD2	-5.31	117.81	121.00
2	B	60	TRP	CG-CD1-NE1	-5.28	104.82	110.10
1	D	274	TRP	CG-CD1-NE1	-5.24	104.86	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	ARG	NE-CZ-NH1	5.23	122.92	120.30
1	D	167	TRP	CG-CD1-NE1	-5.23	104.87	110.10
2	E	60	TRP	CB-CG-CD1	-5.21	120.22	127.00
1	A	274	TRP	CG-CD1-NE1	-5.20	104.90	110.10
2	E	78	TYR	CB-CG-CD1	-5.17	117.90	121.00
1	A	59	TYR	CB-CG-CD1	-5.14	117.92	121.00
1	D	147	TRP	CD1-CG-CD2	5.11	110.39	106.30
2	E	83	ASN	CB-CG-ND2	5.11	128.97	116.70
1	A	167	TRP	CB-CG-CD1	-5.08	120.39	127.00
1	D	60	TRP	CG-CD1-NE1	-5.08	105.02	110.10
2	B	60	TRP	CG-CD2-CE3	5.06	138.46	133.90
2	B	95	TRP	CG-CD1-NE1	-5.05	105.05	110.10
1	A	204	TRP	CG-CD1-NE1	-5.02	105.08	110.10
2	B	97	ARG	NE-CZ-NH1	5.02	122.81	120.30
1	A	21	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	A	157	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	A	48	ARG	NE-CZ-NH1	5.01	122.81	120.30
1	D	51	TRP	CB-CG-CD1	-5.01	120.49	127.00
1	A	51	TRP	CG-CD2-CE3	5.01	138.41	133.90

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	2252	0	2109	19	0
1	D	2252	0	2109	23	0
2	B	829	0	794	5	0
2	E	829	0	794	6	0
3	C	52	0	55	0	0
3	F	52	0	55	0	0
4	A	149	0	0	1	0
4	B	60	0	0	1	0
4	C	4	0	0	0	0
4	D	147	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	75	0	0	2	0
4	F	5	0	0	0	0
All	All	6706	0	5916	51	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 4.

All (51) 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)
1:D:76:GLU:HG2	1:D:79:ARG:HH21	1.53	0.73
1:D:111:ARG:HD2	4:D:787:HOH:O	1.97	0.65
1:A:144:GLN:O	1:A:148:GLU:HG3	2.00	0.61
1:D:111:ARG:NE	1:D:128:GLU:HG2	2.21	0.56
1:D:274:TRP:O	1:D:276:PRO:HD3	2.06	0.55
1:A:262:GLN:HG2	1:A:269:PRO:HB3	1.87	0.55
1:D:263:HIS:CD2	1:D:265:GLY:H	2.25	0.54
1:A:1:GLY:HA3	1:A:110:LEU:CD1	2.38	0.54
1:A:70:LYS:HE2	4:A:509:HOH:O	2.08	0.53
1:D:76:GLU:HG2	1:D:79:ARG:NH2	2.23	0.53
2:B:4:THR:HG22	4:B:606:HOH:O	2.09	0.52
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.43	0.52
1:A:210:PRO:O	1:A:263:HIS:HE1	1.93	0.51
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.47	0.50
1:A:1:GLY:HA3	1:A:110:LEU:HD12	1.94	0.49
1:D:111:ARG:CD	1:D:128:GLU:HG2	2.42	0.49
1:D:49:ALA:O	1:D:52:ILE:HG22	2.11	0.49
1:A:205:ALA:HB2	1:A:215:LEU:HD21	1.95	0.49
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.94	0.48
1:A:76:GLU:HG2	1:A:79:ARG:HH21	1.79	0.47
2:E:83:ASN:HD22	2:E:84:HIS:H	1.61	0.47
2:E:16:GLU:CD	2:E:19:LYS:HG3	2.35	0.47
1:D:40:ALA:O	1:D:43:PRO:HD3	2.15	0.47
1:D:255:GLN:O	1:D:273:ARG:NH1	2.47	0.46
1:D:187:THR:HB	1:D:272:LEU:HD21	1.98	0.46
1:A:214:THR:HB	1:A:262:GLN:HB2	1.99	0.45
1:D:218:GLN:O	1:D:257:TYR:HA	2.16	0.45
1:A:103:VAL:HG11	1:A:165:VAL:HG13	1.99	0.45
1:D:138:THR:O	1:D:141:GLN:HB2	2.16	0.45
2:E:94:LYS:HB3	4:E:825:HOH:O	2.17	0.45
2:E:36:GLU:HA	4:E:779:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:213:ILE:HG13	1:D:263:HIS:HB2	1.99	0.44
1:D:59:TYR:O	1:D:63:GLU:HG2	2.18	0.44
1:D:210:PRO:O	1:D:263:HIS:HE1	2.00	0.44
1:D:214:THR:HB	1:D:262:GLN:HB2	1.99	0.44
1:A:187:THR:HA	1:A:204:TRP:O	2.18	0.43
1:A:184:PRO:HB3	1:A:265:GLY:O	2.19	0.43
1:D:17:ARG:HH11	1:D:17:ARG:HD2	1.69	0.43
1:D:70:LYS:HE2	4:D:524:HOH:O	2.19	0.43
1:A:59:TYR:O	1:A:63:GLU:HG2	2.19	0.42
1:A:81:LEU:HD23	1:A:118:TYR:CD1	2.54	0.42
1:D:218:GLN:OE1	1:D:260:HIS:NE2	2.52	0.42
2:E:51:HIS:HA	2:E:65:LEU:O	2.19	0.42
2:B:73:THR:OG1	2:B:75:LYS:HG3	2.20	0.42
1:A:194:ILE:HD12	1:A:248:VAL:HG13	2.03	0.41
2:B:40:LEU:HD23	2:B:45:ARG:HA	2.01	0.41
1:D:111:ARG:HA	4:D:787:HOH:O	2.20	0.41
1:A:187:THR:HB	1:A:272:LEU:HD21	2.02	0.41
1:A:72:GLN:OE1	1:A:75:ARG:NH1	2.54	0.40
1:D:215:LEU:HD22	1:D:261:VAL:HG22	2.03	0.40
1:A:123:TYR:HD2	1:A:124:ILE:HG22	1.86	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	274/276 (99%)	264 (96%)	10 (4%)	0	100	100
1	D	274/276 (99%)	265 (97%)	9 (3%)	0	100	100
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
2	E	97/99 (98%)	97 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	7/9 (78%)	7 (100%)	0	0	100	100
3	F	7/9 (78%)	7 (100%)	0	0	100	100
All	All	756/768 (98%)	734 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	235/235 (100%)	231 (98%)	4 (2%)	66	72
1	D	235/235 (100%)	227 (97%)	8 (3%)	42	43
2	B	94/94 (100%)	91 (97%)	3 (3%)	44	46
2	E	94/94 (100%)	90 (96%)	4 (4%)	33	32
3	C	1/1 (100%)	1 (100%)	0	100	100
3	F	1/1 (100%)	1 (100%)	0	100	100
All	All	660/660 (100%)	641 (97%)	19 (3%)	48	51

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	35	ARG
1	A	216	THR
1	A	222	GLU
2	B	70	PHE
2	B	83	ASN
2	B	88	SER
1	D	35	ARG
1	D	42	SER
1	D	181	ARG
1	D	222	GLU
1	D	225	THR

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Mol	Chain	Res	Type
1	D	226	GLN
1	D	232	GLU
1	D	272	LEU
2	E	14	PRO
2	E	70	PHE
2	E	83	ASN
2	E	88	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	197	HIS
1	A	263	HIS
2	B	83	ASN
1	D	54	GLN
1	D	174	ASN
1	D	188	HIS
1	D	197	HIS
1	D	263	HIS
2	E	83	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

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.