



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:10 am GMT

PDB ID : 1EEY  
Title : Crystal Structure Determination Of HLA A2 Complexed to Peptide GP2 with the substitution (I2L/V5L/L9V)  
Authors : Sharma, A.K.; Kuhns, J.J.; Collins, E.J.  
Deposited on : 2000-02-04  
Resolution : 2.25 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](mailto: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.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

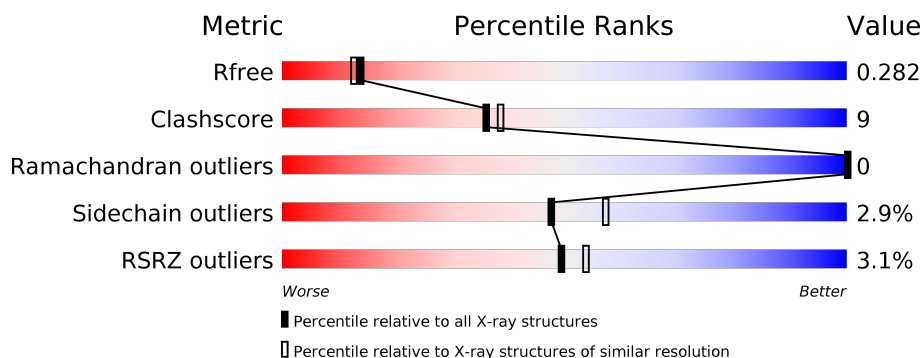
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.25 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))
$R_{free}$	100719	1062 (2.26-2.26)
Clashscore	112137	1178 (2.26-2.26)
Ramachandran outliers	110173	1145 (2.26-2.26)
Sidechain outliers	110143	1146 (2.26-2.26)
RSRZ outliers	101464	1066 (2.26-2.26)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	275	<div> <div>2%</div> <div> <div></div> <div>79%</div> <div>19%</div> <div>.</div> </div> </div>
1	D	275	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>20%</div> <div>.</div> </div> </div>
2	B	100	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>19%</div> <div>.</div> </div> </div>
2	E	100	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>24%</div> <div>.</div> </div> </div>
3	C	9	<div> <div>11%</div> <div> <div></div> <div>78%</div> <div>22%</div> </div> </div>
3	F	9	<div> <div>11%</div> <div> <div></div> <div>67%</div> <div>33%</div> </div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6435 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 HLA-A2.1 MHC CLASS I (HEAVY CHAIN).

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

- Molecule 2 is a protein called BETA-2-MICROGLOBULIN (LIGHT CHAIN).

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	ALA	initiating met	UNP P01884
E	0	MET	ALA	initiating met	UNP P01884

- Molecule 3 is a protein called GP2 PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			62	42	9	11			
3	F	9	Total	C	N	O	0	0	0
			62	42	9	11			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total	O	0	0
			49	49		

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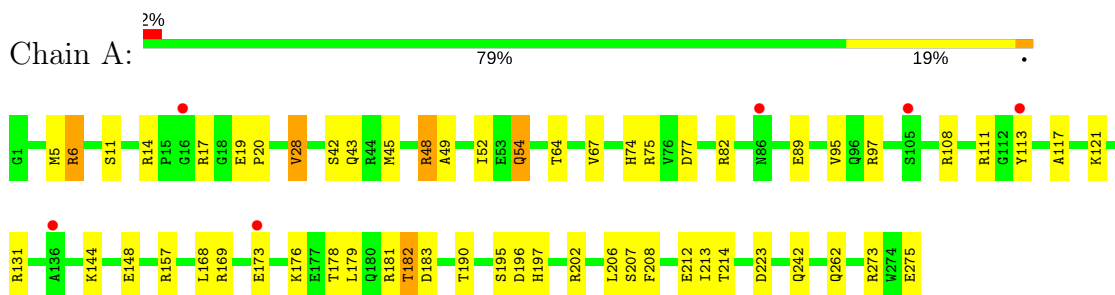
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	31	Total 31	O 31	0	0
4	D	40	Total 40	O 40	1	0
4	E	22	Total 22	O 22	0	0
4	F	1	Total 1	O 1	0	0

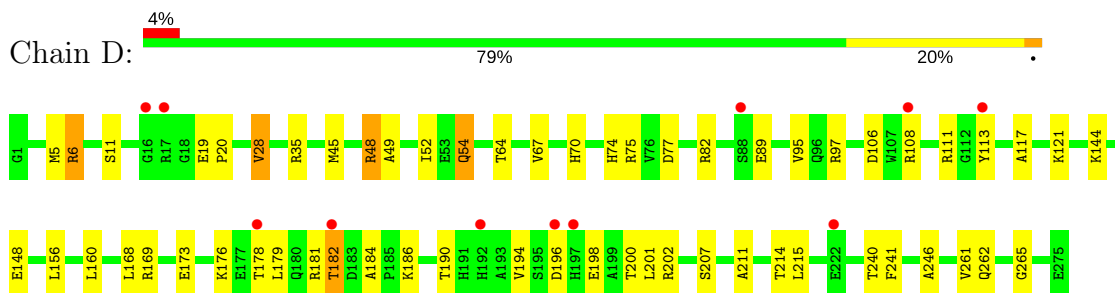
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

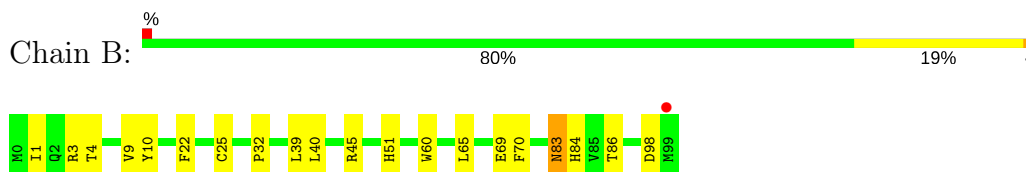
- Molecule 1: HLA-A2.1 MHC CLASS I (HEAVY CHAIN)



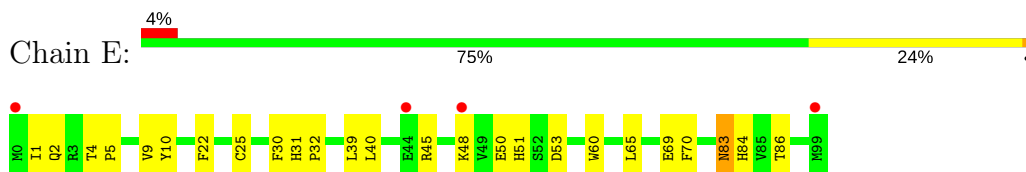
- Molecule 1: HLA-A2.1 MHC CLASS I (HEAVY CHAIN)



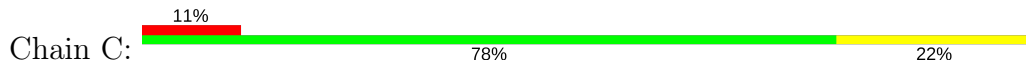
- Molecule 2: BETA-2-MICROGLOBULIN (LIGHT CHAIN)

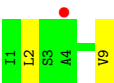


- Molecule 2: BETA-2-MICROGLOBULIN (LIGHT CHAIN)

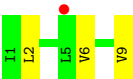


- Molecule 3: GP2 PEPTIDE





● Molecule 3: GP2 PEPTIDE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	49.95Å 62.93Å 74.65Å 82.07° 76.50° 78.04°	Depositor
Resolution (Å)	50.00 – 2.25 49.08 – 2.25	Depositor EDS
% Data completeness (in resolution range)	93.4 (50.00-2.25) 91.7 (49.08-2.25)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.16 (at 2.24Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, $R_{free}$	0.248 , 0.286 0.245 , 0.282	Depositor DCC
$R_{free}$ test set	1907 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.9	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 39.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	6435	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.04% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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	0.39	0/2312	0.63	1/3137 (0.0%)
1	D	0.39	0/2312	0.62	1/3137 (0.0%)
2	B	0.40	0/860	0.64	0/1162
2	E	0.40	0/860	0.63	0/1162
3	C	0.40	0/61	0.68	0/81
3	F	0.43	0/61	0.80	0/81
All	All	0.39	0/6466	0.63	2/8760 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	28	VAL	N-CA-C	-5.32	96.63	111.00
1	D	28	VAL	N-CA-C	-5.17	97.04	111.00

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	2247	0	2096	43	0
1	D	2247	0	2096	43	0
2	B	837	0	805	17	0
2	E	837	0	805	17	0
3	C	62	0	77	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	62	0	77	4	0
4	A	49	0	0	0	0
4	B	31	0	0	2	0
4	D	40	0	0	2	0
4	E	22	0	0	1	0
4	F	1	0	0	0	0
All	All	6435	0	5956	110	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 9.

All (110) 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:A:173:GLU:O	1:A:176:LYS:HG3	1.76	0.85
1:D:173:GLU:O	1:D:176:LYS:HG3	1.78	0.83
1:A:11:SER:HB3	1:A:95:VAL:CG2	2.15	0.77
1:D:11:SER:HB3	1:D:95:VAL:CG2	2.15	0.76
1:D:144:LYS:O	1:D:148:GLU:HG3	1.87	0.75
1:A:273:ARG:HD2	1:A:275:GLU:OE1	1.89	0.72
1:A:11:SER:HB3	1:A:95:VAL:HG22	1.71	0.71
1:D:11:SER:HB3	1:D:95:VAL:HG22	1.70	0.71
1:A:48:ARG:HB3	1:A:48:ARG:HH11	1.56	0.70
1:D:48:ARG:HH11	1:D:48:ARG:HB3	1.58	0.68
1:A:144:LYS:O	1:A:148:GLU:HG3	1.94	0.68
1:D:169:ARG:O	1:D:173:GLU:HG3	1.94	0.67
1:D:54:GLN:HE21	1:D:54:GLN:H	1.42	0.67
1:A:169:ARG:O	1:A:173:GLU:HG3	1.96	0.66
1:D:28:VAL:HG11	1:D:179:LEU:HD13	1.79	0.65
1:A:54:GLN:H	1:A:54:GLN:HE21	1.45	0.65
1:D:184:ALA:HB2	1:D:265:GLY:O	1.97	0.65
1:A:111:ARG:HD2	1:A:113:TYR:OH	1.98	0.64
1:D:54:GLN:NE2	1:D:54:GLN:H	1.95	0.64
1:D:111:ARG:HD2	1:D:113:TYR:OH	1.99	0.63
1:A:54:GLN:H	1:A:54:GLN:NE2	1.97	0.62
1:A:28:VAL:HG11	1:A:179:LEU:HD13	1.80	0.62
1:D:49:ALA:O	1:D:52:ILE:HG22	2.01	0.60
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.85	0.59
1:A:49:ALA:O	1:A:52:ILE:HG22	2.03	0.58
1:A:74:HIS:CE1	1:A:97:ARG:HE	2.22	0.58
1:D:77:ASP:OD1	3:F:9:VAL:HG22	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:MET:HB2	1:D:168:LEU:HD13	1.87	0.57
2:B:83:ASN:HD22	2:B:84:HIS:H	1.53	0.56
2:E:83:ASN:HD22	2:E:84:HIS:H	1.53	0.56
1:D:194:VAL:HG22	1:D:198:GLU:O	2.06	0.56
1:D:74:HIS:CE1	1:D:97:ARG:HE	2.24	0.56
1:A:178:THR:O	1:A:181:ARG:HG2	2.06	0.55
1:D:178:THR:O	1:D:181:ARG:HG2	2.05	0.55
1:A:206:LEU:HD23	1:A:242:GLN:HB3	1.89	0.54
1:D:214:THR:HB	1:D:262:GLN:HB2	1.91	0.52
1:D:121:LYS:HE3	2:E:1:ILE:HG13	1.90	0.52
1:D:190:THR:OG1	1:D:202:ARG:HB3	2.10	0.52
1:A:214:THR:HB	1:A:262:GLN:HB2	1.91	0.52
1:A:121:LYS:HZ2	2:B:1:ILE:H	1.56	0.52
1:A:121:LYS:HG2	2:B:1:ILE:HD12	1.91	0.52
1:D:70:HIS:CE1	3:F:6:VAL:HG21	2.46	0.50
1:A:121:LYS:HE3	2:B:1:ILE:HG13	1.93	0.50
1:D:54:GLN:NE2	1:D:54:GLN:N	2.60	0.49
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.47	0.49
2:E:84:HIS:HD2	2:E:86:THR:OG1	1.96	0.49
2:B:22:PHE:CZ	2:B:69:GLU:HG2	2.47	0.49
1:A:121:LYS:NZ	2:B:1:ILE:H	2.10	0.49
2:B:84:HIS:HD2	2:B:86:THR:OG1	1.96	0.49
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.95	0.49
1:D:45:MET:CE	3:F:2:LEU:HD11	2.42	0.49
1:A:48:ARG:CB	1:A:48:ARG:HH11	2.25	0.48
1:D:48:ARG:HH11	1:D:48:ARG:CB	2.27	0.48
2:E:51:HIS:HA	2:E:65:LEU:O	2.14	0.47
2:B:4:THR:HG22	4:B:115:HOH:O	2.13	0.47
2:B:51:HIS:HA	2:B:65:LEU:O	2.15	0.47
1:A:54:GLN:N	1:A:54:GLN:NE2	2.62	0.47
1:A:121:LYS:HG2	2:B:1:ILE:CD1	2.44	0.47
2:B:40:LEU:HD23	2:B:45:ARG:HA	1.97	0.46
2:E:22:PHE:CZ	2:E:69:GLU:HG2	2.50	0.46
1:A:77:ASP:OD1	3:C:9:VAL:HG22	2.15	0.46
2:E:32:PRO:O	2:E:84:HIS:HE1	1.98	0.46
2:B:32:PRO:O	2:B:84:HIS:HE1	1.99	0.46
1:D:19:GLU:OE2	1:D:75:ARG:CZ	2.64	0.46
1:A:131:ARG:NE	1:A:157:ARG:HH12	2.14	0.45
1:A:182:THR:OG1	1:A:182:THR:O	2.32	0.45
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.51	0.45
1:D:64:THR:O	1:D:67:VAL:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:LEU:O	1:D:246:ALA:HA	2.17	0.45
2:E:10:TYR:N	2:E:10:TYR:CD1	2.85	0.44
2:E:25:CYS:HB2	2:E:39:LEU:HD21	1.98	0.44
1:D:106:ASP:OD2	1:D:108:ARG:NH1	2.48	0.44
2:E:40:LEU:HD23	2:E:45:ARG:HA	1.99	0.44
1:A:19:GLU:OE2	1:A:75:ARG:CZ	2.66	0.44
2:B:98:ASP:HB3	4:B:106:HOH:O	2.18	0.44
1:D:169:ARG:NH2	4:D:294:HOH:O	2.50	0.44
2:B:10:TYR:N	2:B:10:TYR:CD1	2.85	0.43
2:E:9:VAL:O	2:E:9:VAL:HG13	2.17	0.43
1:A:64:THR:O	1:A:67:VAL:HG12	2.17	0.43
1:D:211:ALA:HB2	1:D:241:PHE:CE2	2.53	0.43
1:D:6:ARG:HG2	4:D:314:HOH:O	2.18	0.43
1:A:195:SER:HG	1:A:197:HIS:CE1	2.36	0.43
1:A:6:ARG:HB3	1:A:6:ARG:HE	1.66	0.43
2:E:4:THR:HG22	4:E:102:HOH:O	2.19	0.43
1:D:215:LEU:HD12	1:D:261:VAL:HG22	2.00	0.43
1:D:182:THR:O	1:D:182:THR:OG1	2.34	0.42
1:D:19:GLU:HG3	1:D:20:PRO:HD2	2.01	0.42
1:D:207:SER:HA	1:D:240:THR:HB	2.00	0.42
1:D:6:ARG:HE	1:D:6:ARG:HB3	1.66	0.42
1:A:14:ARG:HB3	1:A:17:ARG:HB2	2.01	0.42
1:A:190:THR:OG1	1:A:202:ARG:HB3	2.19	0.42
1:D:156:LEU:O	1:D:160:LEU:HG	2.20	0.42
1:D:19:GLU:HA	1:D:20:PRO:HD3	1.93	0.42
1:D:45:MET:HE1	3:F:2:LEU:HD11	2.02	0.42
1:A:108:ARG:HB2	1:A:108:ARG:HH11	1.85	0.41
1:A:213:ILE:HG13	1:A:262:GLN:O	2.19	0.41
1:D:82:ARG:CZ	1:D:89:GLU:HG3	2.49	0.41
1:A:19:GLU:HG3	1:A:20:PRO:HD2	2.03	0.41
1:A:212:GLU:OE2	1:A:212:GLU:HA	2.19	0.41
1:D:121:LYS:NZ	2:E:1:ILE:H	2.17	0.41
1:A:42:SER:O	1:A:43:GLN:HB2	2.21	0.41
1:A:45:MET:HE1	3:C:2:LEU:HD11	2.02	0.41
1:A:45:MET:CE	3:C:2:LEU:HD11	2.51	0.41
2:B:9:VAL:HG13	2:B:9:VAL:O	2.20	0.41
2:E:5:PRO:HB3	2:E:30:PHE:HB3	2.02	0.41
1:A:82:ARG:CZ	1:A:89:GLU:HG3	2.51	0.41
2:E:48:LYS:NZ	2:E:50:GLU:OE2	2.53	0.40
1:A:183:ASP:O	1:A:208:PHE:HA	2.21	0.40
2:E:2:GLN:HA	2:E:31:HIS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:35:ARG:HD3	2:E:53:ASP:OD2	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 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	273/275 (99%)	263 (96%)	10 (4%)	0	100	100
1	D	273/275 (99%)	263 (96%)	10 (4%)	0	100	100
2	B	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
2	E	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
3	C	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	756/768 (98%)	727 (96%)	29 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	231/231 (100%)	224 (97%)	7 (3%)	46	56
1	D	231/231 (100%)	224 (97%)	7 (3%)	46	56

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	95/95 (100%)	92 (97%)	3 (3%)	44	54
2	E	95/95 (100%)	93 (98%)	2 (2%)	59	68
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%)	647 (97%)	19 (3%)	48	57

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

Mol	Chain	Res	Type
1	A	6	ARG
1	A	48	ARG
1	A	54	GLN
1	A	182	THR
1	A	196	ASP
1	A	207	SER
1	A	223	ASP
2	B	3	ARG
2	B	70	PHE
2	B	83	ASN
1	D	6	ARG
1	D	48	ARG
1	D	54	GLN
1	D	182	THR
1	D	186	LYS
1	D	196	ASP
1	D	200	THR
2	E	70	PHE
2	E	83	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	A	141	GLN
1	A	155	GLN
1	A	192	HIS
2	B	83	ASN
2	B	84	HIS
1	D	54	GLN
1	D	141	GLN

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Mol	Chain	Res	Type
1	D	155	GLN
2	E	83	ASN
2	E	84	HIS

### 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 ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	275/275 (100%)	0.36	6 (2%) 62 65	9, 18, 26, 31	0
1	D	275/275 (100%)	0.39	11 (4%) 39 42	11, 20, 28, 32	0
2	B	100/100 (100%)	0.26	1 (1%) 82 84	11, 17, 26, 31	0
2	E	100/100 (100%)	0.34	4 (4%) 39 42	12, 18, 26, 31	0
3	C	9/9 (100%)	1.08	1 (11%) 6 6	20, 21, 26, 27	0
3	F	9/9 (100%)	0.59	1 (11%) 6 6	18, 21, 26, 26	0
All	All	768/768 (100%)	0.37	24 (3%) 49 54	9, 19, 27, 32	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	136	ALA	4.5
1	D	88	SER	4.0
1	D	16	GLY	2.9
3	C	4	ALA	2.9
1	D	192	HIS	2.8
1	D	182	THR	2.8
2	E	0	MET	2.6
1	A	113	TYR	2.5
1	D	108	ARG	2.5
2	E	44	GLU	2.5
1	A	105	SER	2.4
1	A	16	GLY	2.3
2	E	99	MET	2.3
1	D	222	GLU	2.3
2	B	99	MET	2.2
1	D	113	TYR	2.2
1	A	173	GLU	2.2
2	E	48	LYS	2.1
3	F	5	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	197	HIS	2.1
1	D	178	THR	2.1
1	D	196	ASP	2.1
1	D	17	ARG	2.0
1	A	86	ASN	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.