



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 19, 2023 – 01:08 PM EDT

PDB ID : 8SHI  
Title : Valpha3S1 Vbeta13S1 HLA C 0602 VRSRRLRL  
Authors : Littler, D.R.; Anand, S.; Vivian, J.P.; Rossjohn, J.  
Deposited on : 2023-04-14  
Resolution : 2.90 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](mailto: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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.33  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.33

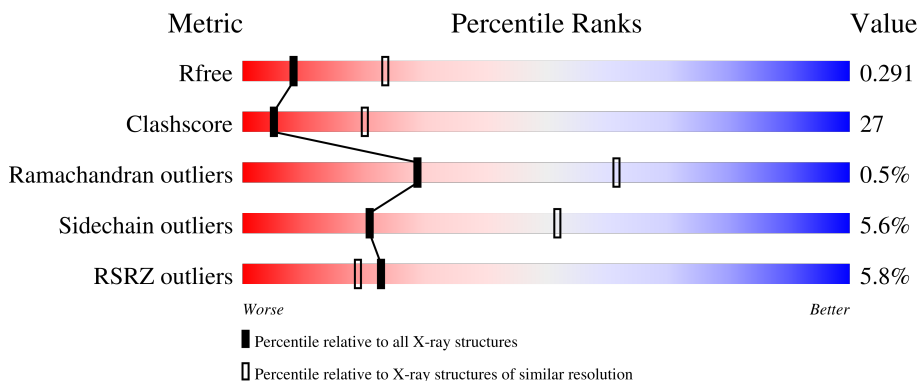
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	277	
1	D	277	
2	B	100	
2	E	100	
3	C	9	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
3	F	9	<p>11% 78% 22%</p>
4	G	196	<p>2% 43% 45% 6% 6%</p>
4	I	196	<p>20% 47% 42% 7% 5%</p>
5	H	242	<p>55% 41% ..</p>
5	J	242	<p>15% 47% 47% 5%</p>

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 12833 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 MHC class I antigen (Fragment).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	273	Total	C	N	O	S	3	0	0
			2217	1383	406	422	6			
1	D	273	Total	C	N	O	S	2	0	0
			2221	1385	406	424	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP F6IQM2
D	0	MET	-	initiating methionine	UNP F6IQM2

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	Total	C	N	O	S	2	0	0
			800	508	135	154	3			
2	E	99	Total	C	N	O	S	0	0	0
			803	511	135	154	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
E	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called VAL-ARG-SER-ARG-ARG-ABA-LEU-ARG-LEU.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	9	Total	C	N	O	0	0	0
			80	48	21	11			
3	F	9	Total	C	N	O	0	0	0
			80	48	21	11			

- Molecule 4 is a protein called T cell receptor alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	G	184	Total 1403	C 865	N 245	O 285	S 8	0	0	0
4	I	187	Total 1436	C 882	N 252	O 294	S 8	0	1	0

- Molecule 5 is a protein called T cell receptor beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	H	240	Total 1896	C 1191	N 327	O 369	S 9	0	0	0
5	J	240	Total 1896	C 1191	N 327	O 369	S 9	0	0	0

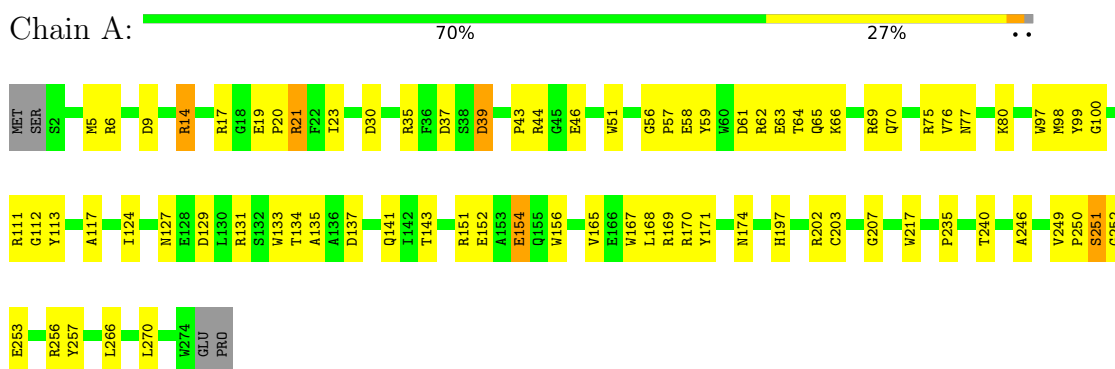
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total 1	O 1	0	0

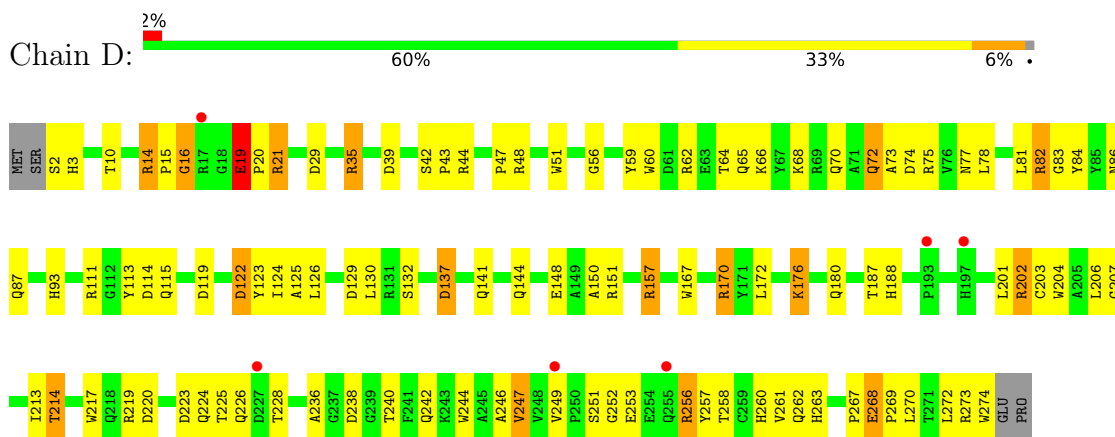
### 3 Residue-property plots [i](#)

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 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.

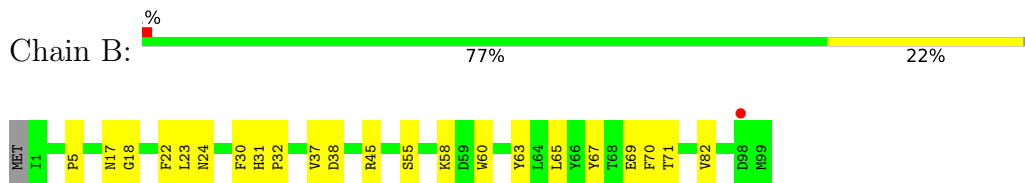
- Molecule 1: MHC class I antigen (Fragment)



- Molecule 1: MHC class I antigen (Fragment)

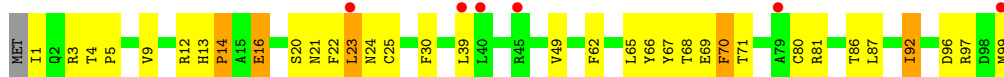


- Molecule 2: Beta-2-microglobulin

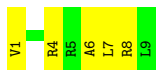


- Molecule 2: Beta-2-microglobulin

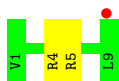
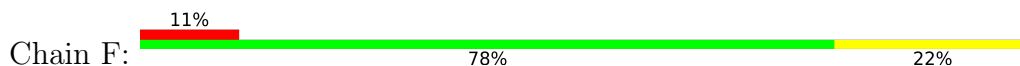




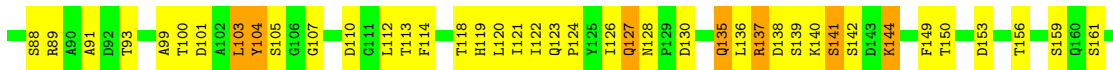
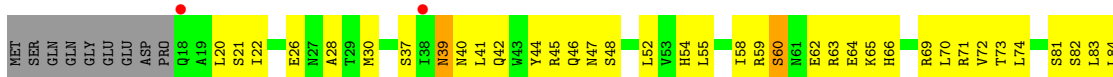
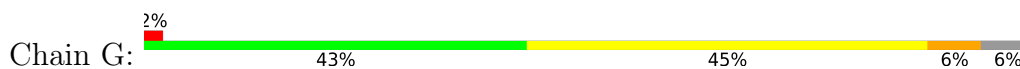
- Molecule 3: VAL-ARG-SER-ARG-ARG-ABA-LEU-ARG-LEU



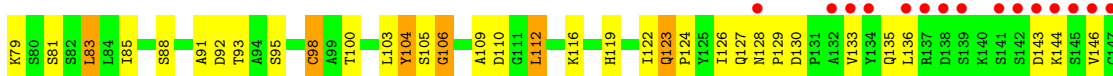
- Molecule 3: VAL-ARG-SER-ARG-ARG-ABA-LEU-ARG-LEU



- Molecule 4: T cell receptor alpha

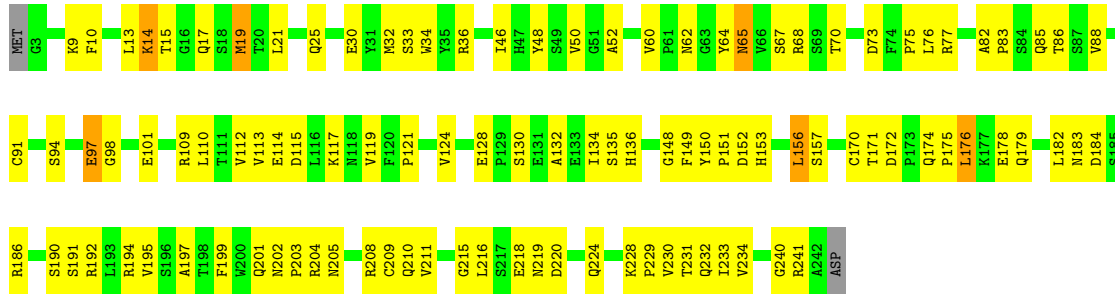


- Molecule 4: T cell receptor alpha

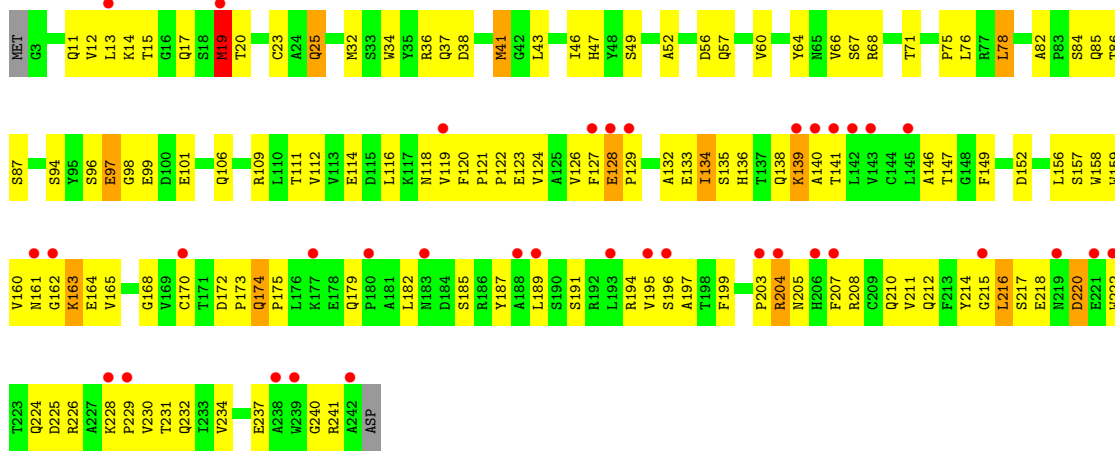


- Molecule 5: T cell receptor beta





• Molecule 5: T cell receptor beta





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.00Å 192.96Å 211.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.20 – 2.90 48.79 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.20-2.90) 100.0 (48.79-2.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 2.91Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, $R_{free}$	0.235 , 0.291 0.235 , 0.291	Depositor DCC
$R_{free}$ test set	2419 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.0	Xtrriage
Anisotropy	0.020	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 34.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	12833	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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

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

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	0/2281	0.83	3/3104 (0.1%)
1	D	0.59	1/2285 (0.0%)	0.88	11/3109 (0.4%)
2	B	0.61	0/823	0.83	0/1120
2	E	0.48	0/826	0.81	2/1124 (0.2%)
3	C	0.51	0/72	0.98	0/90
3	F	0.83	0/72	0.80	0/90
4	G	0.55	0/1426	0.81	2/1929 (0.1%)
4	I	0.56	2/1462 (0.1%)	0.87	3/1977 (0.2%)
5	H	0.58	1/1947 (0.1%)	0.79	1/2652 (0.0%)
5	J	0.66	0/1947	0.99	9/2652 (0.3%)
All	All	0.59	4/13141 (0.0%)	0.86	31/17847 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	I	32	CYS	CB-SG	-5.91	1.72	1.81
5	H	228	LYS	C-N	5.48	1.44	1.34
1	D	247	VAL	CB-CG2	-5.26	1.41	1.52
4	I	98	CYS	CB-SG	-5.07	1.73	1.81

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	216	LEU	CB-CG-CD2	-13.63	87.82	111.00
5	J	134	ILE	CG1-CB-CG2	-10.52	88.26	111.40
5	J	139	LYS	N-CA-C	-9.39	85.64	111.00
1	D	16	GLY	N-CA-C	8.94	135.45	113.10
1	D	176	LYS	CD-CE-NZ	-8.87	91.29	111.70

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	2217	0	2047	80	0
1	D	2221	0	2047	113	0
2	B	800	0	726	14	0
2	E	803	0	735	27	0
3	C	80	0	96	12	0
3	F	80	0	96	0	0
4	G	1403	0	1332	91	0
4	I	1436	0	1366	125	3
5	H	1896	0	1786	90	0
5	J	1896	0	1786	172	1
6	A	1	0	0	0	0
All	All	12833	0	12017	666	3

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 27.

The worst 5 of 666 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:81:LEU:O	1:D:84:TYR:HB2	1.45	1.12
1:D:82:ARG:NH1	1:D:93:HIS:CG	2.22	1.06
1:A:19:GLU:HG2	1:A:20:PRO:HD2	1.38	1.05
5:J:222:TRP:CZ2	5:J:229:PRO:HD3	1.92	1.04
4:I:104:TYR:CE1	4:I:106:GLY:HA3	1.94	1.03

All (3) 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)
4:I:178:SER:O	4:I:178:SER:O[3_454]	0.55	1.65
4:I:178:SER:C	4:I:178:SER:O[3_454]	1.53	0.67

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:179:MET:SD	5:J:196:SER:OG[3_454]	2.14	0.06

## 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	271/277 (98%)	254 (94%)	17 (6%)	0	100	100
1	D	271/277 (98%)	255 (94%)	13 (5%)	3 (1%)	14	42
2	B	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
2	E	97/100 (97%)	93 (96%)	4 (4%)	0	100	100
3	C	6/9 (67%)	6 (100%)	0	0	100	100
3	F	6/9 (67%)	6 (100%)	0	0	100	100
4	G	182/196 (93%)	156 (86%)	25 (14%)	1 (0%)	29	61
4	I	186/196 (95%)	160 (86%)	22 (12%)	4 (2%)	6	24
5	H	238/242 (98%)	219 (92%)	19 (8%)	0	100	100
5	J	238/242 (98%)	216 (91%)	22 (9%)	0	100	100
All	All	1592/1648 (97%)	1458 (92%)	126 (8%)	8 (0%)	29	61

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	19	GLU
4	G	107	GLY
1	D	267	PRO
4	I	51	GLY
4	I	128	ASN

### 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	224/234 (96%)	218 (97%)	6 (3%)	44 77
1	D	225/234 (96%)	211 (94%)	14 (6%)	18 47
2	B	86/95 (90%)	84 (98%)	2 (2%)	50 80
2	E	87/95 (92%)	83 (95%)	4 (5%)	27 60
3	C	8/8 (100%)	8 (100%)	0	100 100
3	F	8/8 (100%)	6 (75%)	2 (25%)	0 2
4	G	154/170 (91%)	134 (87%)	20 (13%)	4 12
4	I	160/170 (94%)	147 (92%)	13 (8%)	11 33
5	H	207/209 (99%)	199 (96%)	8 (4%)	32 66
5	J	207/209 (99%)	199 (96%)	8 (4%)	32 66
All	All	1366/1432 (95%)	1289 (94%)	77 (6%)	21 52

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	I	37	SER
5	J	56	ASP
4	I	50	ARG
4	I	123	GLN
5	J	204	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
5	H	219	ASN
5	J	11	GLN
5	J	224	GLN
4	I	42	GLN
4	G	39	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](#)

2 non-standard protein/DNA/RNA residues 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
3	ABA	F	6	3	4,5,6	0.86	0	1,5,7	0.53	0
3	ABA	C	6	3	4,5,6	0.78	0	1,5,7	0.36	0

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
3	ABA	F	6	3	-	0/3/4/6	-
3	ABA	C	6	3	-	2/3/4/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	6	ABA	N-CA-CB-CG
3	C	6	ABA	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	6	ABA	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides 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 [i](#)

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

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	273/277 (98%)	-0.08	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	37, 58, 86, 119	2 (0%)
1	D	273/277 (98%)	0.24	6 (2%) <span style="border: 1px solid blue; padding: 2px;">62</span> <span style="border: 1px solid blue; padding: 2px;">59</span>	52, 77, 123, 156	1 (0%)
2	B	99/100 (99%)	-0.04	1 (1%) <span style="border: 1px solid blue; padding: 2px;">82</span> <span style="border: 1px solid blue; padding: 2px;">82</span>	37, 55, 85, 110	1 (1%)
2	E	99/100 (99%)	0.51	6 (6%) <span style="border: 1px solid red; padding: 2px;">21</span> <span style="border: 1px solid red; padding: 2px;">17</span>	63, 88, 123, 139	1 (1%)
3	C	8/9 (88%)	0.40	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	45, 52, 56, 66	0
3	F	8/9 (88%)	0.27	1 (12%) <span style="border: 1px solid red; padding: 2px;">3</span> <span style="border: 1px solid red; padding: 2px;">3</span>	54, 67, 80, 86	0
4	G	184/196 (93%)	0.14	3 (1%) <span style="border: 1px solid blue; padding: 2px;">72</span> <span style="border: 1px solid blue; padding: 2px;">71</span>	46, 73, 115, 135	0
4	I	187/196 (95%)	1.07	40 (21%) <span style="border: 1px solid red; padding: 2px;">0</span> <span style="border: 1px solid red; padding: 2px;">0</span>	47, 87, 200, 228	0
5	H	240/242 (99%)	0.05	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	39, 59, 100, 120	0
5	J	240/242 (99%)	0.79	36 (15%) <span style="border: 1px solid red; padding: 2px;">2</span> <span style="border: 1px solid red; padding: 2px;">1</span>	52, 102, 178, 205	0
All	All	1611/1648 (97%)	0.33	93 (5%) <span style="border: 1px solid red; padding: 2px;">23</span> <span style="border: 1px solid red; padding: 2px;">19</span>	37, 71, 157, 228	5 (0%)

The worst 5 of 93 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	J	239	TRP	9.8
4	I	195	PHE	9.0
4	I	189	TRP	8.9
4	I	166	VAL	7.6
4	I	128	ASN	7.2

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ABA	C	6	6/7	0.91	0.37	49,57,70,72	0
3	ABA	F	6	6/7	0.93	0.28	65,69,78,85	0

### 6.3 Carbohydrates [i](#)

There are no monosaccharides 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.