



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 19, 2024 – 12:14 PM JST

PDB ID : 8WFM  
Title : Crystal structure of Omicron BA.1 in complex with a neutralizing antibody scFv T11  
Authors : Terekhov, S.S.; Mokrushina, Y.A.; Zhang, M.; Zhang, N.; Gabibov, A.; Guo, Y.  
Deposited on : 2023-09-19  
Resolution : 2.99 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
Xtriage (Phenix)	:	1.13
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

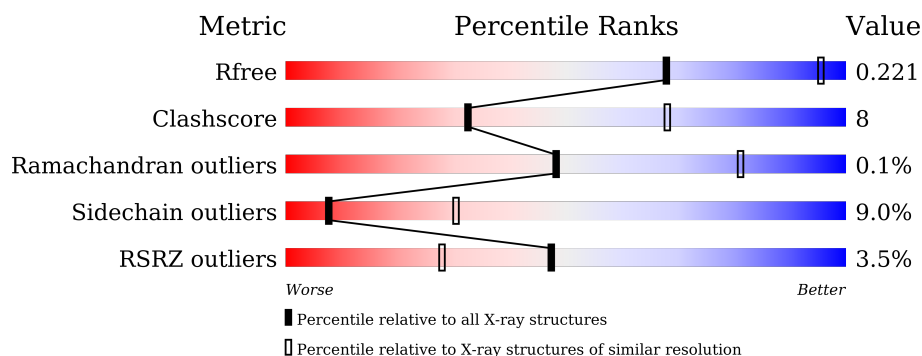
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.99 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))
$R_{free}$	164625	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	255	<div> <div>3%</div> <div>65% 26% 9%</div> </div>
1	C	255	<div> <div>2%</div> <div>73% 16% 9%</div> </div>
1	E	255	<div> <div>5%</div> <div>69% 21% 9%</div> </div>
1	G	255	<div> <div>7%</div> <div>64% 26% 9%</div> </div>
2	B	223	<div> <div>%</div> <div>66% 16% 18%</div> </div>
2	D	223	<div> <div>%</div> <div>62% 20% 18%</div> </div>

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	F	223	<div><div><div>2%</div><div>65%</div><div>14%</div><div>•</div><div>18%</div></div></div>
2	H	223	<div><div><div>3%</div><div>62%</div><div>19%</div><div>•</div><div>18%</div></div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12900 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 T11 scFv.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1741	1100	287	346	8			
1	C	233	Total	C	N	O	S	0	0	0
			1741	1100	287	346	8			
1	E	233	Total	C	N	O	S	0	0	0
			1741	1100	287	346	8			
1	G	233	Total	C	N	O	S	0	0	0
			1741	1100	287	346	8			

- Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	183	Total	C	N	O	S	0	0	0
			1484	957	250	270	7			
2	D	183	Total	C	N	O	S	0	0	0
			1484	957	250	270	7			
2	F	183	Total	C	N	O	S	0	0	0
			1484	957	250	270	7			
2	H	183	Total	C	N	O	S	0	0	0
			1484	957	250	270	7			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	21	ASP	GLY	variant	UNP P0DTC2
B	53	LEU	SER	variant	UNP P0DTC2
B	55	PRO	SER	variant	UNP P0DTC2
B	57	PHE	SER	variant	UNP P0DTC2
B	99	ASN	LYS	variant	UNP P0DTC2
B	122	LYS	ASN	variant	UNP P0DTC2
B	128	SER	GLY	variant	UNP P0DTC2
B	159	ASN	SER	variant	UNP P0DTC2

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	160	LYS	THR	variant	UNP P0DTC2
B	166	ALA	GLU	variant	UNP P0DTC2
B	175	ARG	GLN	variant	UNP P0DTC2
B	178	SER	GLY	variant	UNP P0DTC2
B	180	ARG	GLN	variant	UNP P0DTC2
B	183	TYR	ASN	variant	UNP P0DTC2
B	187	HIS	TYR	variant	UNP P0DTC2
D	21	ASP	GLY	variant	UNP P0DTC2
D	53	LEU	SER	variant	UNP P0DTC2
D	55	PRO	SER	variant	UNP P0DTC2
D	57	PHE	SER	variant	UNP P0DTC2
D	99	ASN	LYS	variant	UNP P0DTC2
D	122	LYS	ASN	variant	UNP P0DTC2
D	128	SER	GLY	variant	UNP P0DTC2
D	159	ASN	SER	variant	UNP P0DTC2
D	160	LYS	THR	variant	UNP P0DTC2
D	166	ALA	GLU	variant	UNP P0DTC2
D	175	ARG	GLN	variant	UNP P0DTC2
D	178	SER	GLY	variant	UNP P0DTC2
D	180	ARG	GLN	variant	UNP P0DTC2
D	183	TYR	ASN	variant	UNP P0DTC2
D	187	HIS	TYR	variant	UNP P0DTC2
F	21	ASP	GLY	variant	UNP P0DTC2
F	53	LEU	SER	variant	UNP P0DTC2
F	55	PRO	SER	variant	UNP P0DTC2
F	57	PHE	SER	variant	UNP P0DTC2
F	99	ASN	LYS	variant	UNP P0DTC2
F	122	LYS	ASN	variant	UNP P0DTC2
F	128	SER	GLY	variant	UNP P0DTC2
F	159	ASN	SER	variant	UNP P0DTC2
F	160	LYS	THR	variant	UNP P0DTC2
F	166	ALA	GLU	variant	UNP P0DTC2
F	175	ARG	GLN	variant	UNP P0DTC2
F	178	SER	GLY	variant	UNP P0DTC2
F	180	ARG	GLN	variant	UNP P0DTC2
F	183	TYR	ASN	variant	UNP P0DTC2
F	187	HIS	TYR	variant	UNP P0DTC2
H	21	ASP	GLY	variant	UNP P0DTC2
H	53	LEU	SER	variant	UNP P0DTC2
H	55	PRO	SER	variant	UNP P0DTC2
H	57	PHE	SER	variant	UNP P0DTC2
H	99	ASN	LYS	variant	UNP P0DTC2

*Continued on next page...*

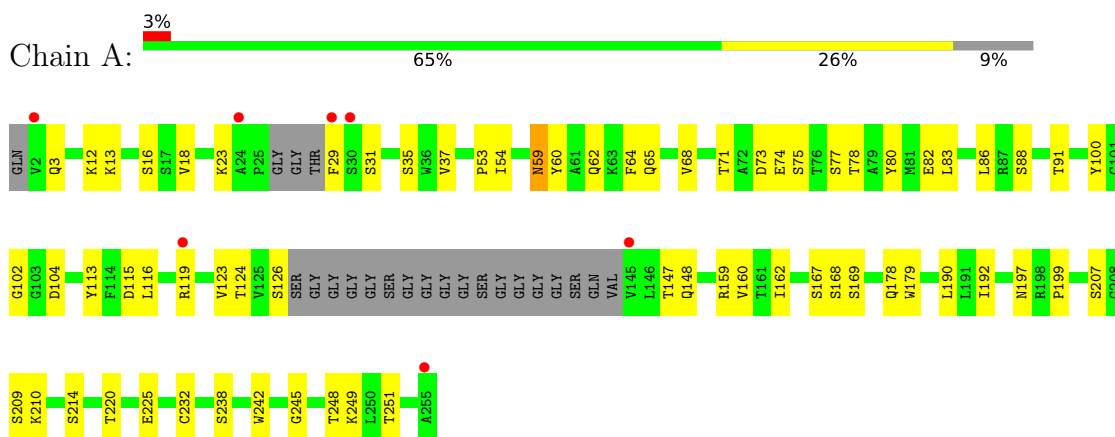
*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
H	122	LYS	ASN	variant	UNP P0DTC2
H	128	SER	GLY	variant	UNP P0DTC2
H	159	ASN	SER	variant	UNP P0DTC2
H	160	LYS	THR	variant	UNP P0DTC2
H	166	ALA	GLU	variant	UNP P0DTC2
H	175	ARG	GLN	variant	UNP P0DTC2
H	178	SER	GLY	variant	UNP P0DTC2
H	180	ARG	GLN	variant	UNP P0DTC2
H	183	TYR	ASN	variant	UNP P0DTC2
H	187	HIS	TYR	variant	UNP P0DTC2

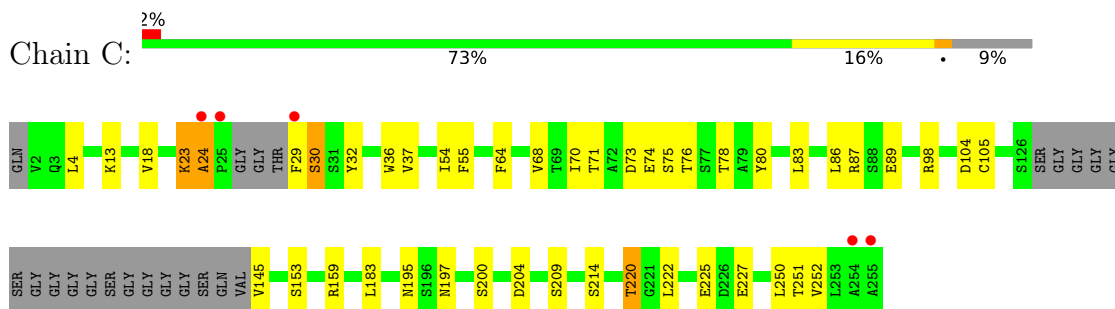
### 3 Residue-property plots [i](#)

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.

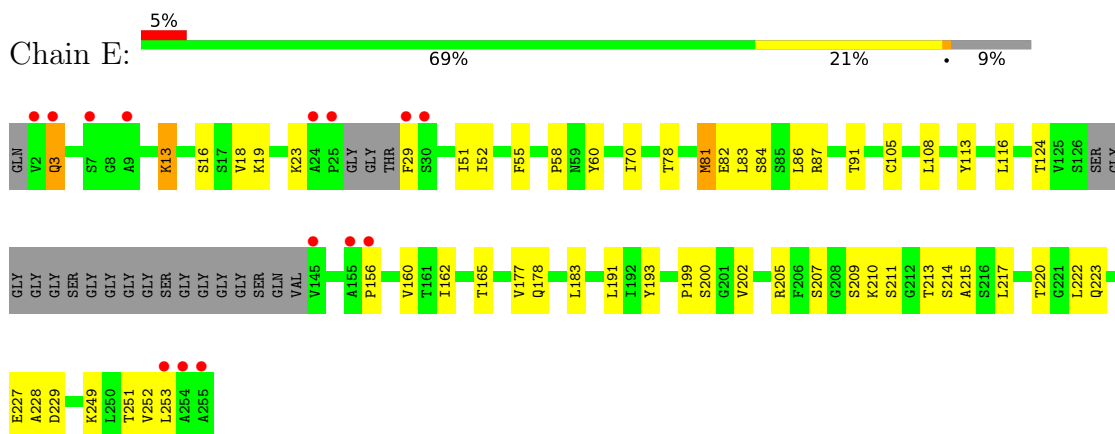
#### • Molecule 1: T11 scFv



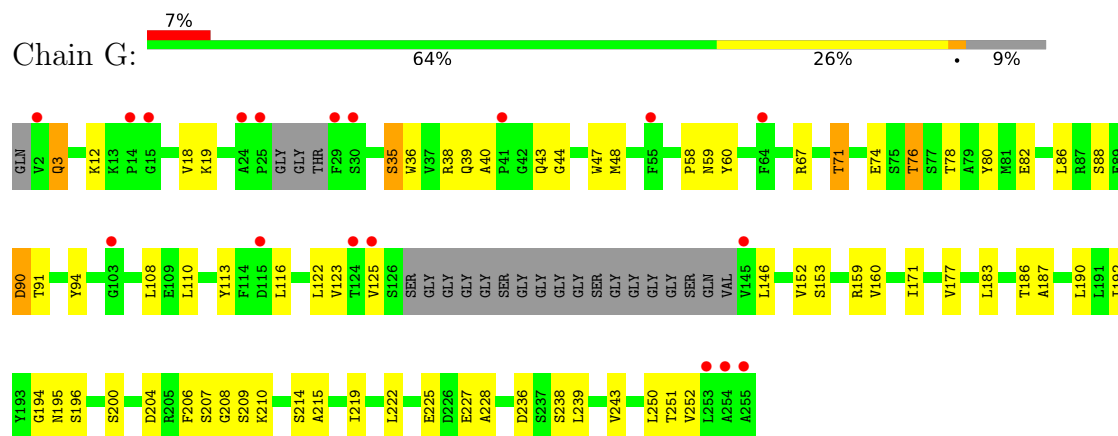
#### • Molecule 1: T11 scFv



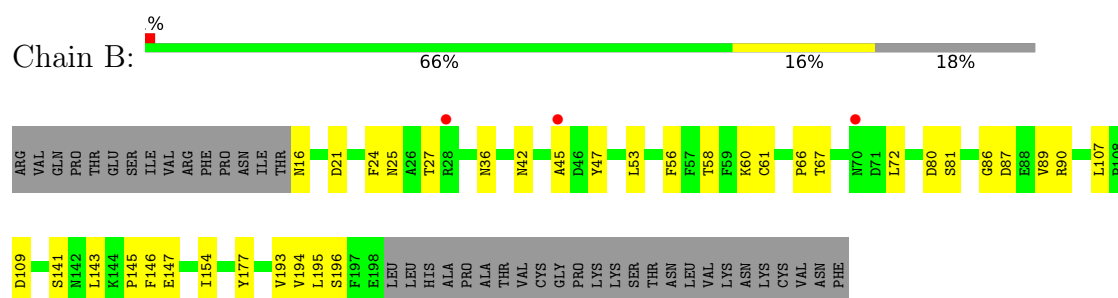
#### • Molecule 1: T11 scFv



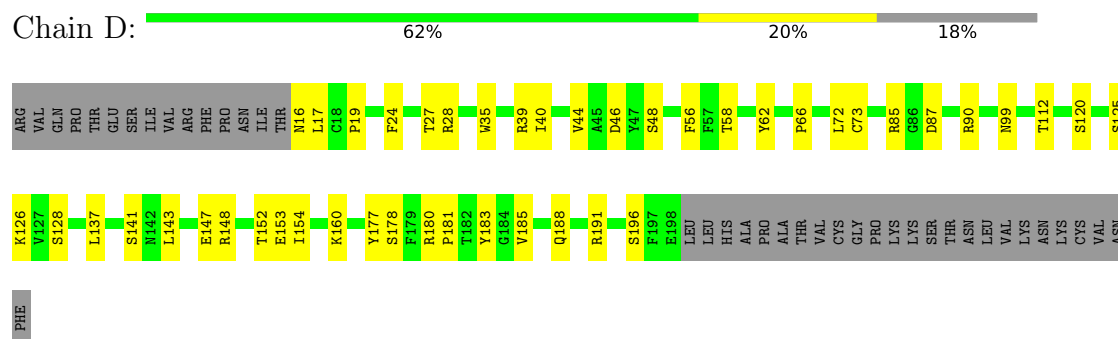
- Molecule 1: T11 scFv



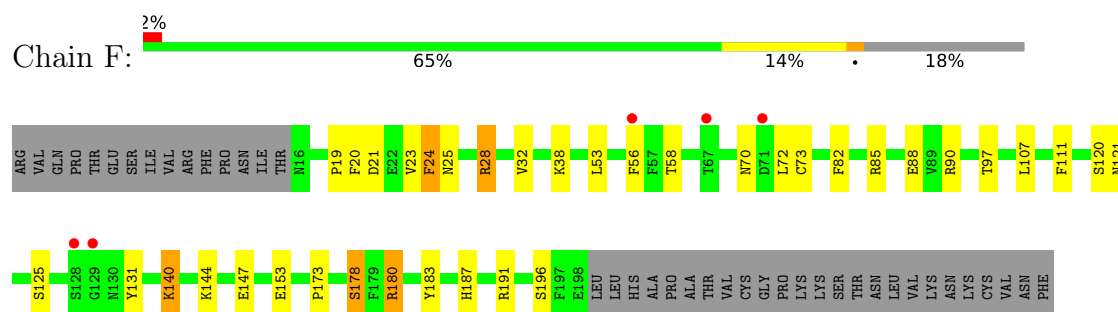
- Molecule 2: Spike protein S1



- Molecule 2: Spike protein S1

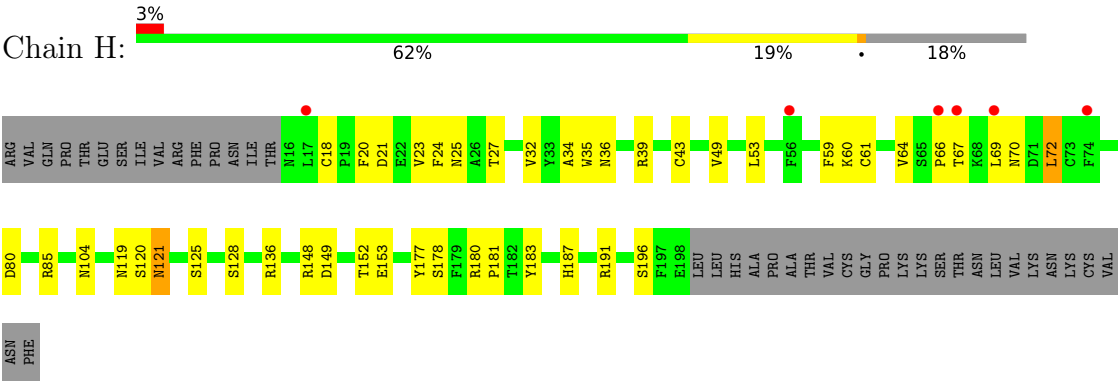


- Molecule 2: Spike protein S1



- Molecule 2: Spike protein S1





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.41Å 172.49Å 487.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	64.61 – 2.99 64.61 – 2.99	Depositor EDS
% Data completeness (in resolution range)	99.9 (64.61-2.99) 90.7 (64.61-2.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 3.01Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, $R_{free}$	0.215 , 0.265 0.217 , 0.221	Depositor DCC
$R_{free}$ test set	2478 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	51.9	Xtriage
Anisotropy	0.395	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 29.8	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	0.91	EDS
Total number of atoms	12900	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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	0.55	0/1782	0.71	0/2424
1	C	0.53	0/1782	0.72	0/2424
1	E	0.47	0/1782	0.64	0/2424
1	G	0.44	0/1782	0.64	0/2424
2	B	0.51	0/1528	0.70	0/2077
2	D	0.50	0/1528	0.67	0/2077
2	F	0.47	0/1528	0.65	0/2077
2	H	0.48	0/1528	0.65	0/2077
All	All	0.49	0/13240	0.67	0/18004

There are no bond length outliers.

There are no bond angle outliers.

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	1741	0	1670	36	0
1	C	1741	0	1670	22	0
1	E	1741	0	1670	28	0
1	G	1741	0	1670	38	0
2	B	1484	0	1412	16	0
2	D	1484	0	1412	18	0
2	F	1484	0	1412	21	0
2	H	1484	0	1412	32	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	12900	0	12328	196	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 8.

The worst 5 of 196 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:54:ILE:HD11	1:A:74:GLU:HB2	1.52	0.90
2:B:60:LYS:HG2	2:H:60:LYS:HG2	1.54	0.88
1:G:35:SER:HG	1:G:47:TRP:HE1	1.17	0.87
2:B:66:PRO:HB2	2:H:66:PRO:HB2	1.60	0.83
1:C:71:THR:HG22	1:C:80:TYR:HB2	1.64	0.80

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	227/255 (89%)	219 (96%)	8 (4%)	0	100	100
1	C	227/255 (89%)	212 (93%)	14 (6%)	1 (0%)	30	66
1	E	227/255 (89%)	211 (93%)	15 (7%)	1 (0%)	30	66
1	G	227/255 (89%)	209 (92%)	18 (8%)	0	100	100
2	B	181/223 (81%)	172 (95%)	9 (5%)	0	100	100
2	D	181/223 (81%)	164 (91%)	17 (9%)	0	100	100
2	F	181/223 (81%)	170 (94%)	11 (6%)	0	100	100
2	H	181/223 (81%)	170 (94%)	11 (6%)	0	100	100
All	All	1632/1912 (85%)	1527 (94%)	103 (6%)	2 (0%)	48	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	253	LEU
1	C	24	ALA

### 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	187/195 (96%)	167 (89%)	20 (11%)	5	22
1	C	187/195 (96%)	168 (90%)	19 (10%)	6	24
1	E	187/195 (96%)	173 (92%)	14 (8%)	11	38
1	G	187/195 (96%)	169 (90%)	18 (10%)	7	27
2	B	161/198 (81%)	147 (91%)	14 (9%)	8	32
2	D	161/198 (81%)	143 (89%)	18 (11%)	5	21
2	F	161/198 (81%)	148 (92%)	13 (8%)	9	34
2	H	161/198 (81%)	152 (94%)	9 (6%)	17	49
All	All	1392/1572 (88%)	1267 (91%)	125 (9%)	8	30

5 of 125 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	72	LEU
1	G	207	SER
1	E	3	GLN
1	G	204	ASP
2	H	59	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	70	ASN
1	G	223	GLN
2	H	121	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	H	119	ASN
2	D	121	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 oligosaccharides 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	233/255 (91%)	-0.18	7 (3%) 52 31	28, 43, 74, 88	0
1	C	233/255 (91%)	-0.09	5 (2%) 63 41	32, 47, 79, 98	0
1	E	233/255 (91%)	0.44	14 (6%) 29 16	50, 66, 96, 114	0
1	G	233/255 (91%)	0.63	18 (7%) 21 12	52, 73, 98, 115	0
2	B	183/223 (82%)	-0.06	3 (1%) 70 49	28, 46, 78, 89	0
2	D	183/223 (82%)	-0.15	0 100 100	30, 45, 84, 97	0
2	F	183/223 (82%)	0.12	5 (2%) 56 34	42, 55, 82, 92	0
2	H	183/223 (82%)	0.18	6 (3%) 49 29	43, 58, 89, 104	0
All	All	1664/1912 (87%)	0.12	58 (3%) 47 28	28, 56, 87, 115	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	66	PRO	7.2
1	E	29	PHE	4.7
1	E	255	ALA	4.4
1	C	25	PRO	4.3
1	E	254	ALA	4.2

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

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

### 6.3 Carbohydrates ⓘ

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.