



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:54 PM GMT

PDB ID : 1MFR  
Title : CRYSTAL STRUCTURE OF M FERRITIN  
Authors : Ha, Y.; Shi, D.; Allewell, N.M.  
Deposited on : 1998-06-18  
Resolution : 2.80 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.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

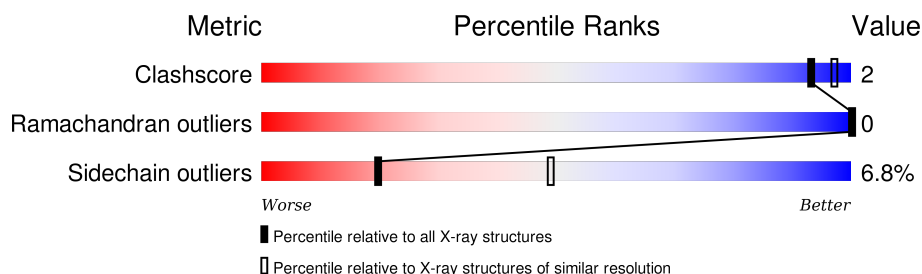
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)


















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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	176	
1	B	176	
1	C	176	
1	D	176	
1	E	176	
1	F	176	
1	G	176	

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Length	Quality of chain
1	H	176	 87% 7% . .
1	I	176	 86% 9% . .
1	J	176	 86% 8% . .
1	K	176	 88% 7% . .
1	L	176	 86% 7% . .
1	M	176	 88% 7% . .
1	N	176	 87% 7% . .
1	O	176	 87% 7% . .
1	P	176	 87% 7% . .
1	Q	176	 86% 8% . .
1	R	176	 88% 7% . .
1	S	176	 87% 7% . .
1	T	176	 88% 7% . .
1	U	176	 88% 7% . .
1	V	176	 88% 7% . .
1	W	176	 87% 7% . .
1	X	176	 86% 8% . .

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34320 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 M FERRITIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	B	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	C	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	D	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	E	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	F	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	G	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	H	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	I	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	J	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	K	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	L	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	M	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	N	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	O	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	P	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	R	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	S	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	T	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	U	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	V	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	W	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			
1	X	171	Total	C	N	O	S	0	0	0
			1373	868	238	260	7			

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	P	2	Total	Mg	0	0
			2	2		
2	K	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		
2	W	2	Total	Mg	0	0
			2	2		
2	N	2	Total	Mg	0	0
			2	2		
2	X	2	Total	Mg	0	0
			2	2		
2	S	2	Total	Mg	0	0
			2	2		
2	J	2	Total	Mg	0	0
			2	2		
2	E	2	Total	Mg	0	0
			2	2		
2	V	2	Total	Mg	0	0
			2	2		
2	A	2	Total	Mg	0	0
			2	2		

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	R	2	Total 2	Mg 2	0	0
2	M	2	Total 2	Mg 2	0	0
2	D	2	Total 2	Mg 2	0	0
2	I	2	Total 2	Mg 2	0	0
2	U	2	Total 2	Mg 2	0	0
2	L	2	Total 2	Mg 2	0	0
2	G	2	Total 2	Mg 2	0	0
2	Q	2	Total 2	Mg 2	0	0
2	H	2	Total 2	Mg 2	0	0
2	C	2	Total 2	Mg 2	0	0
2	T	2	Total 2	Mg 2	0	0
2	O	2	Total 2	Mg 2	0	0
2	F	2	Total 2	Mg 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	54	Total 54	O 54	0	0
3	B	56	Total 56	O 56	0	0
3	C	57	Total 57	O 57	0	0
3	D	55	Total 55	O 55	0	0
3	E	55	Total 55	O 55	0	0
3	F	54	Total 54	O 54	0	0

*Continued on next page...*

*Continued from previous page...*


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	55	Total 55	O 55	0	0
3	H	57	Total 57	O 57	0	0
3	I	55	Total 55	O 55	0	0
3	J	55	Total 55	O 55	0	0
3	K	56	Total 56	O 56	0	0
3	L	53	Total 53	O 53	0	0
3	M	55	Total 55	O 55	0	0
3	N	57	Total 57	O 57	0	0
3	O	55	Total 55	O 55	0	0
3	P	55	Total 55	O 55	0	0
3	Q	54	Total 54	O 54	0	0
3	R	54	Total 54	O 54	0	0
3	S	54	Total 54	O 54	0	0
3	T	58	Total 58	O 58	0	0
3	U	54	Total 54	O 54	0	0
3	V	54	Total 54	O 54	0	0
3	W	53	Total 53	O 53	0	0
3	X	55	Total 55	O 55	0	0

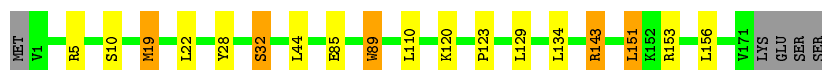
### 3 Residue-property plots [i](#)

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

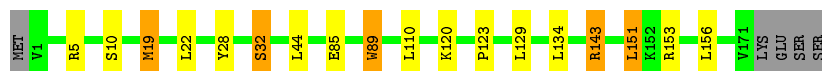
- Molecule 1: M FERRITIN

Chain A: 




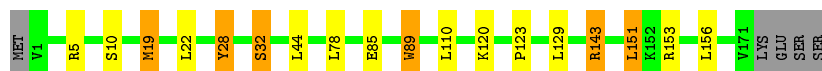
- Molecule 1: M FERRITIN

Chain B: 




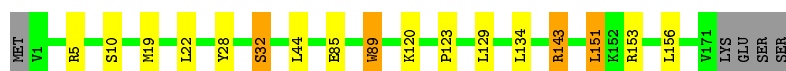
- Molecule 1: M FERRITIN

Chain C: 




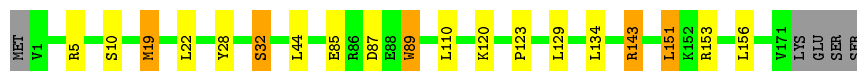
- Molecule 1: M FERRITIN

Chain D: 




- Molecule 1: M FERRITIN

Chain E: 



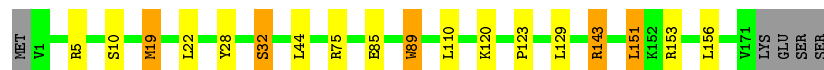
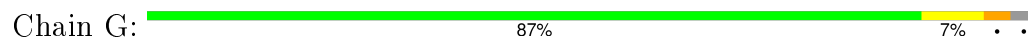
- Molecule 1: M FERRITIN

Chain F: 

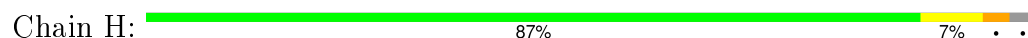




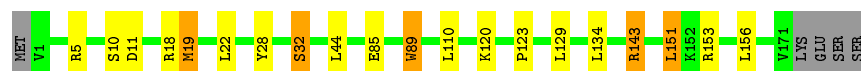
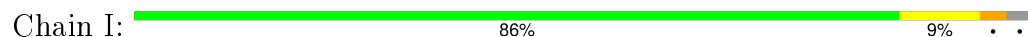
- Molecule 1: M FERRITIN



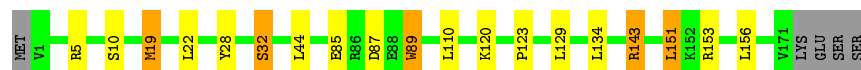
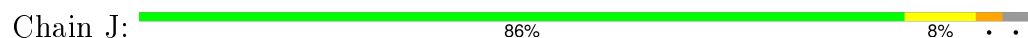
- Molecule 1: M FERRITIN



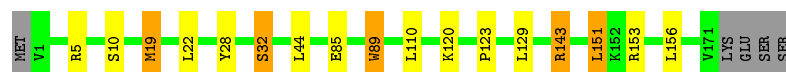
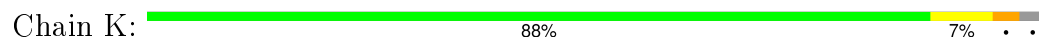
- Molecule 1: M FERRITIN



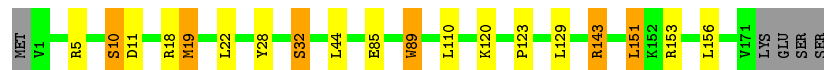
- Molecule 1: M FERRITIN



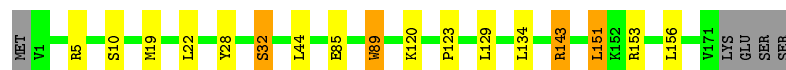
- Molecule 1: M FERRITIN




- Molecule 1: M FERRITIN



- Molecule 1: M FERRITIN




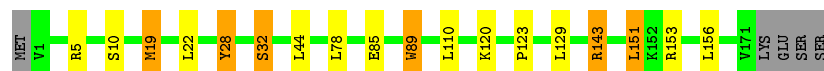
- Molecule 1: M FERRITIN

Chain N:  87% 7% . .




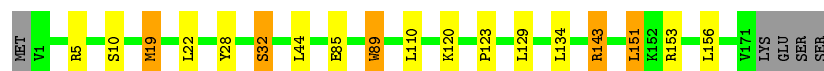
- Molecule 1: M FERRITIN

Chain O:  87% 7% . .




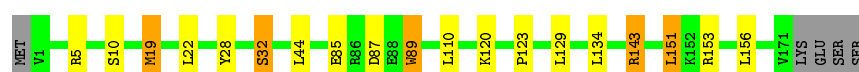
- Molecule 1: M FERRITIN

Chain P:  87% 7% . .




- Molecule 1: M FERRITIN

Chain Q:  86% 8% . .




- Molecule 1: M FERRITIN

Chain R:  88% 7% . .




- Molecule 1: M FERRITIN

Chain S:  87% 7% . .




- Molecule 1: M FERRITIN

Chain T:  88% 7% . .

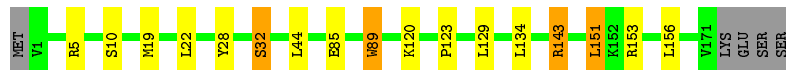
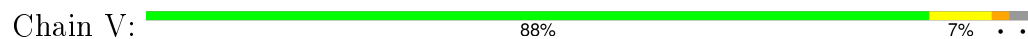


- Molecule 1: M FERRITIN

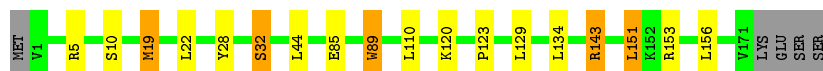
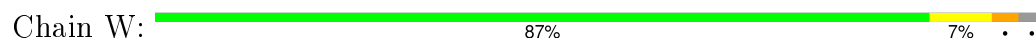
Chain U:  88% 7% . .



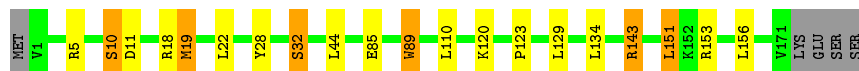
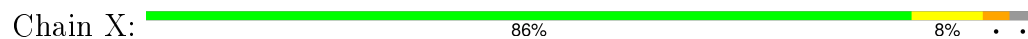
- Molecule 1: M FERRITIN



- Molecule 1: M FERRITIN



- Molecule 1: M FERRITIN



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	210.80 Å   210.80 Å   328.10 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	10.00 – 2.80	Depositor
% Data completeness (in resolution range)	70.0 (10.00-2.80)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	0.08	Depositor
Refinement program	X-PLOR	Depositor
R, $R_{free}$	0.190 , 0.194	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	34320	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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

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	0.75	0/1401	1.21	11/1890 (0.6%)
1	B	0.75	0/1401	1.21	11/1890 (0.6%)
1	C	0.75	0/1401	1.21	11/1890 (0.6%)
1	D	0.75	0/1401	1.21	11/1890 (0.6%)
1	E	0.76	0/1401	1.21	11/1890 (0.6%)
1	F	0.75	0/1401	1.21	11/1890 (0.6%)
1	G	0.75	0/1401	1.21	11/1890 (0.6%)
1	H	0.75	0/1401	1.21	11/1890 (0.6%)
1	I	0.75	0/1401	1.21	11/1890 (0.6%)
1	J	0.75	0/1401	1.21	11/1890 (0.6%)
1	K	0.75	0/1401	1.21	11/1890 (0.6%)
1	L	0.76	0/1401	1.21	11/1890 (0.6%)
1	M	0.76	0/1401	1.21	11/1890 (0.6%)
1	N	0.75	0/1401	1.21	11/1890 (0.6%)
1	O	0.75	0/1401	1.21	11/1890 (0.6%)
1	P	0.76	0/1401	1.21	11/1890 (0.6%)
1	Q	0.76	0/1401	1.21	11/1890 (0.6%)
1	R	0.76	0/1401	1.21	11/1890 (0.6%)
1	S	0.75	0/1401	1.20	11/1890 (0.6%)
1	T	0.75	0/1401	1.21	11/1890 (0.6%)
1	U	0.76	0/1401	1.21	11/1890 (0.6%)
1	V	0.75	0/1401	1.21	11/1890 (0.6%)
1	W	0.75	0/1401	1.21	11/1890 (0.6%)
1	X	0.76	0/1401	1.21	11/1890 (0.6%)
All	All	0.75	0/33624	1.21	264/45360 (0.6%)

There are no bond length outliers.

All (264) bond angle outliers are listed below:

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
-----	-------	-----	------	-------	---	-------------	----------

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	153	ARG	NE-CZ-NH2	-9.34	115.63	120.30
1	N	153	ARG	NE-CZ-NH2	-9.31	115.65	120.30
1	L	153	ARG	NE-CZ-NH2	-9.30	115.65	120.30
1	M	153	ARG	NE-CZ-NH2	-9.30	115.65	120.30
1	X	153	ARG	NE-CZ-NH2	-9.29	115.66	120.30
1	P	153	ARG	NE-CZ-NH2	-9.28	115.66	120.30
1	J	153	ARG	NE-CZ-NH2	-9.27	115.66	120.30
1	U	153	ARG	NE-CZ-NH2	-9.26	115.67	120.30
1	G	153	ARG	NE-CZ-NH2	-9.26	115.67	120.30
1	C	153	ARG	NE-CZ-NH2	-9.25	115.67	120.30
1	S	153	ARG	NE-CZ-NH2	-9.25	115.67	120.30
1	A	153	ARG	NE-CZ-NH2	-9.22	115.69	120.30
1	E	153	ARG	NE-CZ-NH2	-9.22	115.69	120.30
1	R	153	ARG	NE-CZ-NH2	-9.21	115.69	120.30
1	B	153	ARG	NE-CZ-NH2	-9.20	115.70	120.30
1	W	153	ARG	NE-CZ-NH2	-9.20	115.70	120.30
1	I	153	ARG	NE-CZ-NH2	-9.19	115.70	120.30
1	D	153	ARG	NE-CZ-NH2	-9.18	115.71	120.30
1	H	153	ARG	NE-CZ-NH2	-9.18	115.71	120.30
1	Q	153	ARG	NE-CZ-NH2	-9.18	115.71	120.30
1	F	153	ARG	NE-CZ-NH2	-9.17	115.71	120.30
1	V	153	ARG	NE-CZ-NH2	-9.16	115.72	120.30
1	O	153	ARG	NE-CZ-NH2	-9.13	115.74	120.30
1	K	153	ARG	NE-CZ-NH2	-9.11	115.75	120.30
1	D	143	ARG	NE-CZ-NH1	8.62	124.61	120.30
1	K	143	ARG	NE-CZ-NH1	8.60	124.60	120.30
1	I	143	ARG	NE-CZ-NH1	8.59	124.59	120.30
1	J	143	ARG	NE-CZ-NH1	8.59	124.59	120.30
1	G	143	ARG	NE-CZ-NH1	8.55	124.58	120.30
1	F	143	ARG	NE-CZ-NH1	8.55	124.57	120.30
1	E	143	ARG	NE-CZ-NH1	8.54	124.57	120.30
1	N	143	ARG	NE-CZ-NH1	8.54	124.57	120.30
1	M	143	ARG	NE-CZ-NH1	8.54	124.57	120.30
1	Q	143	ARG	NE-CZ-NH1	8.53	124.57	120.30
1	O	143	ARG	NE-CZ-NH1	8.53	124.57	120.30
1	B	143	ARG	NE-CZ-NH1	8.52	124.56	120.30
1	A	143	ARG	NE-CZ-NH1	8.52	124.56	120.30
1	T	143	ARG	NE-CZ-NH1	8.51	124.56	120.30
1	R	143	ARG	NE-CZ-NH1	8.51	124.55	120.30
1	X	143	ARG	NE-CZ-NH1	8.50	124.55	120.30
1	V	143	ARG	NE-CZ-NH1	8.49	124.54	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	143	ARG	NE-CZ-NH1	8.47	124.53	120.30
1	L	143	ARG	NE-CZ-NH1	8.46	124.53	120.30
1	U	143	ARG	NE-CZ-NH1	8.45	124.53	120.30
1	S	143	ARG	NE-CZ-NH1	8.44	124.52	120.30
1	W	143	ARG	NE-CZ-NH1	8.44	124.52	120.30
1	C	143	ARG	NE-CZ-NH1	8.43	124.51	120.30
1	P	143	ARG	NE-CZ-NH1	8.41	124.51	120.30
1	I	5	ARG	NE-CZ-NH2	-8.30	116.15	120.30
1	M	5	ARG	NE-CZ-NH2	-8.28	116.16	120.30
1	M	5	ARG	NE-CZ-NH1	8.24	124.42	120.30
1	H	5	ARG	NE-CZ-NH1	8.24	124.42	120.30
1	H	5	ARG	NE-CZ-NH2	-8.23	116.18	120.30
1	U	5	ARG	NE-CZ-NH1	8.23	124.42	120.30
1	I	5	ARG	NE-CZ-NH1	8.23	124.42	120.30
1	R	5	ARG	NE-CZ-NH2	-8.23	116.19	120.30
1	N	5	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	B	5	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	U	5	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	W	5	ARG	NE-CZ-NH2	-8.22	116.19	120.30
1	L	5	ARG	NE-CZ-NH2	-8.21	116.20	120.30
1	D	5	ARG	NE-CZ-NH1	8.21	124.40	120.30
1	N	5	ARG	NE-CZ-NH2	-8.20	116.20	120.30
1	G	5	ARG	NE-CZ-NH2	-8.19	116.20	120.30
1	X	5	ARG	NE-CZ-NH2	-8.19	116.20	120.30
1	E	5	ARG	NE-CZ-NH2	-8.19	116.20	120.30
1	K	5	ARG	NE-CZ-NH2	-8.19	116.21	120.30
1	A	5	ARG	NE-CZ-NH2	-8.18	116.21	120.30
1	C	5	ARG	NE-CZ-NH2	-8.17	116.22	120.30
1	F	5	ARG	NE-CZ-NH2	-8.17	116.21	120.30
1	P	5	ARG	NE-CZ-NH2	-8.17	116.22	120.30
1	O	5	ARG	NE-CZ-NH2	-8.17	116.22	120.30
1	L	5	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	V	5	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	S	5	ARG	NE-CZ-NH1	8.16	124.38	120.30
1	V	5	ARG	NE-CZ-NH2	-8.16	116.22	120.30
1	E	5	ARG	NE-CZ-NH1	8.15	124.38	120.30
1	J	5	ARG	NE-CZ-NH2	-8.14	116.23	120.30
1	D	5	ARG	NE-CZ-NH2	-8.14	116.23	120.30
1	T	5	ARG	NE-CZ-NH2	-8.13	116.23	120.30
1	K	5	ARG	NE-CZ-NH1	8.13	124.37	120.30
1	A	5	ARG	NE-CZ-NH1	8.13	124.36	120.30
1	W	5	ARG	NE-CZ-NH1	8.13	124.36	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	5	ARG	NE-CZ-NH1	8.11	124.36	120.30
1	P	5	ARG	NE-CZ-NH1	8.11	124.36	120.30
1	X	5	ARG	NE-CZ-NH1	8.11	124.36	120.30
1	O	5	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	S	5	ARG	NE-CZ-NH2	-8.10	116.25	120.30
1	Q	5	ARG	NE-CZ-NH2	-8.10	116.25	120.30
1	B	5	ARG	NE-CZ-NH1	8.09	124.34	120.30
1	R	5	ARG	NE-CZ-NH1	8.09	124.34	120.30
1	G	5	ARG	NE-CZ-NH1	8.07	124.34	120.30
1	Q	5	ARG	NE-CZ-NH1	8.06	124.33	120.30
1	C	5	ARG	NE-CZ-NH1	8.05	124.33	120.30
1	J	5	ARG	NE-CZ-NH1	8.05	124.33	120.30
1	T	5	ARG	NE-CZ-NH1	7.99	124.30	120.30
1	P	89	TRP	CD1-CG-CD2	7.81	112.55	106.30
1	K	89	TRP	CE2-CD2-CG	-7.80	101.06	107.30
1	G	89	TRP	CE2-CD2-CG	-7.80	101.06	107.30
1	P	89	TRP	CE2-CD2-CG	-7.79	101.07	107.30
1	E	89	TRP	CE2-CD2-CG	-7.77	101.08	107.30
1	G	89	TRP	CD1-CG-CD2	7.77	112.52	106.30
1	C	89	TRP	CE2-CD2-CG	-7.77	101.08	107.30
1	L	89	TRP	CE2-CD2-CG	-7.77	101.08	107.30
1	H	89	TRP	CE2-CD2-CG	-7.77	101.08	107.30
1	D	89	TRP	CD1-CG-CD2	7.77	112.51	106.30
1	L	89	TRP	CD1-CG-CD2	7.77	112.51	106.30
1	N	89	TRP	CE2-CD2-CG	-7.77	101.09	107.30
1	D	89	TRP	CE2-CD2-CG	-7.76	101.09	107.30
1	J	89	TRP	CE2-CD2-CG	-7.76	101.09	107.30
1	N	89	TRP	CD1-CG-CD2	7.76	112.51	106.30
1	O	89	TRP	CD1-CG-CD2	7.76	112.51	106.30
1	B	89	TRP	CD1-CG-CD2	7.76	112.51	106.30
1	Q	89	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	J	89	TRP	CD1-CG-CD2	7.75	112.50	106.30
1	K	89	TRP	CD1-CG-CD2	7.75	112.50	106.30
1	O	89	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	Q	89	TRP	CD1-CG-CD2	7.75	112.50	106.30
1	A	89	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	X	89	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	B	89	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	M	89	TRP	CE2-CD2-CG	-7.75	101.10	107.30
1	E	89	TRP	CD1-CG-CD2	7.74	112.50	106.30
1	R	89	TRP	CE2-CD2-CG	-7.74	101.11	107.30
1	W	89	TRP	CE2-CD2-CG	-7.74	101.10	107.30

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	T	89	TRP	CE2-CD2-CG	-7.74	101.11	107.30
1	A	89	TRP	CD1-CG-CD2	7.74	112.49	106.30
1	H	89	TRP	CD1-CG-CD2	7.74	112.49	106.30
1	C	89	TRP	CD1-CG-CD2	7.73	112.48	106.30
1	T	89	TRP	CD1-CG-CD2	7.73	112.48	106.30
1	F	89	TRP	CE2-CD2-CG	-7.73	101.12	107.30
1	W	89	TRP	CD1-CG-CD2	7.72	112.48	106.30
1	M	89	TRP	CD1-CG-CD2	7.72	112.48	106.30
1	X	89	TRP	CD1-CG-CD2	7.72	112.48	106.30
1	I	89	TRP	CD1-CG-CD2	7.72	112.48	106.30
1	S	89	TRP	CE2-CD2-CG	-7.72	101.13	107.30
1	I	89	TRP	CE2-CD2-CG	-7.71	101.13	107.30
1	R	89	TRP	CD1-CG-CD2	7.71	112.47	106.30
1	F	89	TRP	CD1-CG-CD2	7.71	112.47	106.30
1	S	89	TRP	CD1-CG-CD2	7.71	112.47	106.30
1	V	89	TRP	CE2-CD2-CG	-7.71	101.13	107.30
1	U	89	TRP	CD1-CG-CD2	7.70	112.46	106.30
1	U	89	TRP	CE2-CD2-CG	-7.68	101.15	107.30
1	V	89	TRP	CD1-CG-CD2	7.67	112.44	106.30
1	D	143	ARG	NE-CZ-NH2	-7.38	116.61	120.30
1	E	143	ARG	NE-CZ-NH2	-7.35	116.63	120.30
1	G	143	ARG	NE-CZ-NH2	-7.35	116.63	120.30
1	R	19	MET	CG-SD-CE	-7.34	88.45	100.20
1	M	19	MET	CG-SD-CE	-7.34	88.46	100.20
1	N	143	ARG	NE-CZ-NH2	-7.34	116.63	120.30
1	F	19	MET	CG-SD-CE	-7.33	88.47	100.20
1	X	143	ARG	NE-CZ-NH2	-7.33	116.64	120.30
1	X	19	MET	CG-SD-CE	-7.33	88.48	100.20
1	R	143	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	F	143	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	C	19	MET	CG-SD-CE	-7.32	88.49	100.20
1	N	19	MET	CG-SD-CE	-7.32	88.49	100.20
1	A	19	MET	CG-SD-CE	-7.32	88.49	100.20
1	D	19	MET	CG-SD-CE	-7.32	88.49	100.20
1	O	143	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	Q	143	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	H	19	MET	CG-SD-CE	-7.31	88.50	100.20
1	I	19	MET	CG-SD-CE	-7.31	88.50	100.20
1	L	19	MET	CG-SD-CE	-7.31	88.50	100.20
1	I	143	ARG	NE-CZ-NH2	-7.31	116.64	120.30
1	J	143	ARG	NE-CZ-NH2	-7.31	116.64	120.30
1	T	19	MET	CG-SD-CE	-7.31	88.50	100.20

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	19	MET	CG-SD-CE	-7.31	88.51	100.20
1	O	19	MET	CG-SD-CE	-7.31	88.50	100.20
1	Q	19	MET	CG-SD-CE	-7.31	88.51	100.20
1	V	19	MET	CG-SD-CE	-7.31	88.51	100.20
1	S	19	MET	CG-SD-CE	-7.31	88.51	100.20
1	B	19	MET	CG-SD-CE	-7.30	88.51	100.20
1	J	19	MET	CG-SD-CE	-7.30	88.51	100.20
1	W	19	MET	CG-SD-CE	-7.30	88.51	100.20
1	C	143	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	U	143	ARG	NE-CZ-NH2	-7.30	116.65	120.30
1	E	19	MET	CG-SD-CE	-7.30	88.52	100.20
1	P	19	MET	CG-SD-CE	-7.30	88.53	100.20
1	U	19	MET	CG-SD-CE	-7.29	88.53	100.20
1	K	19	MET	CG-SD-CE	-7.29	88.53	100.20
1	A	143	ARG	NE-CZ-NH2	-7.29	116.66	120.30
1	B	143	ARG	NE-CZ-NH2	-7.28	116.66	120.30
1	H	143	ARG	NE-CZ-NH2	-7.27	116.66	120.30
1	T	143	ARG	NE-CZ-NH2	-7.26	116.67	120.30
1	W	143	ARG	NE-CZ-NH2	-7.25	116.67	120.30
1	M	143	ARG	NE-CZ-NH2	-7.24	116.68	120.30
1	K	143	ARG	NE-CZ-NH2	-7.23	116.68	120.30
1	P	143	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	V	143	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	L	143	ARG	NE-CZ-NH2	-7.19	116.71	120.30
1	S	143	ARG	NE-CZ-NH2	-7.18	116.71	120.30
1	X	153	ARG	NE-CZ-NH1	6.05	123.32	120.30
1	C	153	ARG	NE-CZ-NH1	6.03	123.31	120.30
1	M	153	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	N	153	ARG	NE-CZ-NH1	6.01	123.30	120.30
1	P	153	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	R	153	ARG	NE-CZ-NH1	5.99	123.30	120.30
1	E	153	ARG	NE-CZ-NH1	5.99	123.30	120.30
1	D	153	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	S	153	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	Q	153	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	L	153	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	W	153	ARG	NE-CZ-NH1	5.95	123.28	120.30
1	J	153	ARG	NE-CZ-NH1	5.95	123.28	120.30
1	I	153	ARG	NE-CZ-NH1	5.95	123.27	120.30
1	T	153	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	153	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	V	153	ARG	NE-CZ-NH1	5.93	123.26	120.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	153	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	B	153	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	K	153	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	U	153	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	H	153	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	O	153	ARG	NE-CZ-NH1	5.86	123.23	120.30
1	F	153	ARG	NE-CZ-NH1	5.84	123.22	120.30
1	P	89	TRP	CG-CD2-CE3	5.75	139.07	133.90
1	J	89	TRP	CG-CD2-CE3	5.74	139.07	133.90
1	R	89	TRP	CG-CD2-CE3	5.74	139.07	133.90
1	B	89	TRP	CG-CD2-CE3	5.74	139.06	133.90
1	O	89	TRP	CG-CD2-CE3	5.73	139.06	133.90
1	G	89	TRP	CG-CD2-CE3	5.73	139.05	133.90
1	D	89	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	Q	89	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	T	89	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	W	89	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	X	89	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	K	89	TRP	CG-CD2-CE3	5.72	139.05	133.90
1	A	89	TRP	CG-CD2-CE3	5.71	139.04	133.90
1	H	89	TRP	CG-CD2-CE3	5.71	139.04	133.90
1	L	89	TRP	CG-CD2-CE3	5.71	139.04	133.90
1	C	89	TRP	CG-CD2-CE3	5.71	139.04	133.90
1	E	89	TRP	CG-CD2-CE3	5.70	139.03	133.90
1	I	89	TRP	CG-CD2-CE3	5.70	139.03	133.90
1	S	89	TRP	CG-CD2-CE3	5.69	139.02	133.90
1	F	89	TRP	CG-CD2-CE3	5.69	139.02	133.90
1	N	89	TRP	CG-CD2-CE3	5.68	139.02	133.90
1	M	89	TRP	CG-CD2-CE3	5.68	139.01	133.90
1	V	89	TRP	CG-CD2-CE3	5.67	139.01	133.90
1	U	89	TRP	CG-CD2-CE3	5.67	139.00	133.90
1	P	89	TRP	CB-CG-CD1	-5.09	120.38	127.00
1	S	89	TRP	CB-CG-CD1	-5.08	120.40	127.00
1	D	89	TRP	CB-CG-CD1	-5.08	120.40	127.00
1	N	89	TRP	CB-CG-CD1	-5.08	120.40	127.00
1	G	89	TRP	CB-CG-CD1	-5.07	120.41	127.00
1	Q	89	TRP	CB-CG-CD1	-5.07	120.40	127.00
1	U	89	TRP	CB-CG-CD1	-5.07	120.40	127.00
1	K	89	TRP	CB-CG-CD1	-5.07	120.41	127.00
1	L	89	TRP	CB-CG-CD1	-5.07	120.41	127.00
1	J	89	TRP	CB-CG-CD1	-5.07	120.42	127.00
1	A	89	TRP	CB-CG-CD1	-5.06	120.42	127.00

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	89	TRP	CB-CG-CD1	-5.06	120.42	127.00
1	W	89	TRP	CB-CG-CD1	-5.06	120.42	127.00
1	M	89	TRP	CB-CG-CD1	-5.06	120.42	127.00
1	T	89	TRP	CB-CG-CD1	-5.06	120.42	127.00
1	F	89	TRP	CB-CG-CD1	-5.05	120.43	127.00
1	I	89	TRP	CB-CG-CD1	-5.05	120.43	127.00
1	O	89	TRP	CB-CG-CD1	-5.05	120.43	127.00
1	R	89	TRP	CB-CG-CD1	-5.05	120.43	127.00
1	E	89	TRP	CB-CG-CD1	-5.05	120.44	127.00
1	X	89	TRP	CB-CG-CD1	-5.05	120.44	127.00
1	B	89	TRP	CB-CG-CD1	-5.04	120.44	127.00
1	H	89	TRP	CB-CG-CD1	-5.04	120.44	127.00
1	V	89	TRP	CB-CG-CD1	-5.04	120.45	127.00

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	1373	0	1302	5	0
1	B	1373	0	1302	5	0
1	C	1373	0	1302	7	0
1	D	1373	0	1302	4	0
1	E	1373	0	1302	5	2
1	F	1373	0	1302	5	0
1	G	1373	0	1302	6	0
1	H	1373	0	1302	5	0
1	I	1373	0	1302	5	3
1	J	1373	0	1302	5	1
1	K	1373	0	1302	5	0
1	L	1373	0	1302	5	7
1	M	1373	0	1302	4	0
1	N	1373	0	1302	5	0
1	O	1373	0	1302	7	0
1	P	1373	0	1302	5	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	1373	0	1302	5	2
1	R	1373	0	1302	5	0
1	S	1373	0	1302	5	0
1	T	1373	0	1302	5	0
1	U	1373	0	1302	5	0
1	V	1373	0	1302	4	0
1	W	1373	0	1302	5	0
1	X	1373	0	1302	5	5
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
2	M	2	0	0	0	0
2	N	2	0	0	0	0
2	O	2	0	0	0	0
2	P	2	0	0	0	0
2	Q	2	0	0	0	0
2	R	2	0	0	0	0
2	S	2	0	0	0	0
2	T	2	0	0	0	0
2	U	2	0	0	0	0
2	V	2	0	0	0	0
2	W	2	0	0	0	0
2	X	2	0	0	0	0
3	A	54	0	0	2	0
3	B	56	0	0	2	0
3	C	57	0	0	2	0
3	D	55	0	0	2	0
3	E	55	0	0	2	2
3	F	54	0	0	2	0
3	G	55	0	0	2	0
3	H	57	0	0	2	0
3	I	55	0	0	2	3
3	J	55	0	0	2	2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	56	0	0	2	0
3	L	53	0	0	2	1
3	M	55	0	0	2	0
3	N	57	0	0	2	0
3	O	55	0	0	2	0
3	P	55	0	0	2	0
3	Q	54	0	0	2	4
3	R	54	0	0	2	0
3	S	54	0	0	2	0
3	T	58	0	0	2	0
3	U	54	0	0	2	2
3	V	54	0	0	2	0
3	W	53	0	0	2	0
3	X	55	0	0	2	2
All	All	34320	0	31248	120	18

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 2.

All (120) 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:W:151:LEU:HD12	1:W:156:LEU:HD13	1.82	0.62
1:K:151:LEU:HD12	1:K:156:LEU:HD13	1.82	0.62
1:N:151:LEU:HD12	1:N:156:LEU:HD13	1.82	0.62
1:D:151:LEU:HD12	1:D:156:LEU:HD13	1.82	0.61
1:E:151:LEU:HD12	1:E:156:LEU:HD13	1.82	0.61
1:S:151:LEU:HD12	1:S:156:LEU:HD13	1.82	0.61
1:H:151:LEU:HD12	1:H:156:LEU:HD13	1.82	0.61
1:U:151:LEU:HD12	1:U:156:LEU:HD13	1.82	0.61
1:O:151:LEU:HD12	1:O:156:LEU:HD13	1.82	0.61
1:X:151:LEU:HD12	1:X:156:LEU:HD13	1.82	0.61
1:J:151:LEU:HD12	1:J:156:LEU:HD13	1.82	0.61
1:G:151:LEU:HD12	1:G:156:LEU:HD13	1.82	0.61
1:F:151:LEU:HD12	1:F:156:LEU:HD13	1.82	0.61
1:L:151:LEU:HD12	1:L:156:LEU:HD13	1.82	0.61
1:C:151:LEU:HD12	1:C:156:LEU:HD13	1.82	0.61
1:Q:151:LEU:HD12	1:Q:156:LEU:HD13	1.82	0.60
1:B:151:LEU:HD12	1:B:156:LEU:HD13	1.82	0.60
1:I:151:LEU:HD12	1:I:156:LEU:HD13	1.82	0.60
1:V:151:LEU:HD12	1:V:156:LEU:HD13	1.82	0.60

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:151:LEU:HD12	1:P:156:LEU:HD13	1.82	0.60
1:T:151:LEU:HD12	1:T:156:LEU:HD13	1.82	0.60
1:A:151:LEU:HD12	1:A:156:LEU:HD13	1.82	0.60
1:M:151:LEU:HD12	1:M:156:LEU:HD13	1.82	0.60
1:R:151:LEU:HD12	1:R:156:LEU:HD13	1.82	0.59
1:D:32:SER:HB3	1:D:89:TRP:HE1	1.72	0.55
1:R:32:SER:HB3	1:R:89:TRP:HE1	1.72	0.55
1:P:32:SER:HB3	1:P:89:TRP:HE1	1.72	0.55
1:T:32:SER:HB3	1:T:89:TRP:HE1	1.72	0.54
1:Q:32:SER:HB3	1:Q:89:TRP:HE1	1.72	0.54
1:H:32:SER:HB3	1:H:89:TRP:HE1	1.72	0.54
1:F:32:SER:HB3	1:F:89:TRP:HE1	1.72	0.54
1:G:32:SER:HB3	1:G:89:TRP:HE1	1.72	0.54
1:J:32:SER:HB3	1:J:89:TRP:HE1	1.72	0.54
1:S:32:SER:HB3	1:S:89:TRP:HE1	1.72	0.54
1:U:32:SER:HB3	1:U:89:TRP:HE1	1.72	0.54
1:M:32:SER:HB3	1:M:89:TRP:HE1	1.72	0.54
1:A:32:SER:HB3	1:A:89:TRP:HE1	1.72	0.54
1:L:32:SER:HB3	1:L:89:TRP:HE1	1.72	0.54
1:C:32:SER:HB3	1:C:89:TRP:HE1	1.72	0.54
1:W:32:SER:HB3	1:W:89:TRP:HE1	1.72	0.54
1:O:32:SER:HB3	1:O:89:TRP:HE1	1.72	0.53
1:E:32:SER:HB3	1:E:89:TRP:HE1	1.72	0.53
1:X:32:SER:HB3	1:X:89:TRP:HE1	1.72	0.53
1:N:32:SER:HB3	1:N:89:TRP:HE1	1.72	0.53
1:K:32:SER:HB3	1:K:89:TRP:HE1	1.72	0.53
1:B:32:SER:HB3	1:B:89:TRP:HE1	1.72	0.53
1:V:32:SER:HB3	1:V:89:TRP:HE1	1.72	0.52
1:I:32:SER:HB3	1:I:89:TRP:HE1	1.72	0.52
1:X:143:ARG:HD3	3:X:231:HOH:O	2.11	0.51
1:B:143:ARG:HD3	3:B:223:HOH:O	2.11	0.51
1:P:143:ARG:HD3	3:P:227:HOH:O	2.11	0.51
1:E:143:ARG:HD3	3:E:223:HOH:O	2.11	0.51
1:S:143:ARG:HD3	3:S:230:HOH:O	2.11	0.51
1:L:143:ARG:HD3	3:L:222:HOH:O	2.11	0.50
1:C:143:ARG:HD3	3:C:224:HOH:O	2.11	0.50
1:Q:143:ARG:HD3	3:Q:226:HOH:O	2.11	0.50
1:H:143:ARG:HD3	3:H:231:HOH:O	2.11	0.50
1:O:143:ARG:HD3	3:O:230:HOH:O	2.11	0.50
1:F:143:ARG:HD3	3:F:226:HOH:O	2.11	0.50
1:I:143:ARG:HD3	3:I:230:HOH:O	2.11	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:143:ARG:HD3	3:J:224:HOH:O	2.11	0.50
1:K:143:ARG:HD3	3:K:223:HOH:O	2.11	0.50
1:M:143:ARG:HD3	3:M:226:HOH:O	2.11	0.49
1:W:143:ARG:HD3	3:W:229:HOH:O	2.11	0.49
1:V:143:ARG:HD3	3:V:230:HOH:O	2.11	0.49
1:N:143:ARG:HD3	3:N:224:HOH:O	2.11	0.49
1:D:143:ARG:HD3	3:D:223:HOH:O	2.11	0.49
1:G:143:ARG:HD3	3:G:230:HOH:O	2.11	0.49
1:U:143:ARG:HD3	3:U:230:HOH:O	2.11	0.49
1:A:143:ARG:HD3	3:A:222:HOH:O	2.11	0.49
1:T:143:ARG:HD3	3:T:233:HOH:O	2.11	0.48
1:R:143:ARG:HD3	3:R:229:HOH:O	2.11	0.48
1:R:19:MET:HE3	1:R:110:LEU:HA	1.97	0.47
1:U:19:MET:HE3	1:U:110:LEU:HA	1.97	0.47
1:G:19:MET:HE3	1:G:110:LEU:HA	1.98	0.46
1:S:19:MET:HE3	1:S:110:LEU:HA	1.98	0.46
1:N:19:MET:HE3	1:N:110:LEU:HA	1.98	0.46
1:I:19:MET:HE3	1:I:110:LEU:HA	1.98	0.46
1:E:19:MET:HE3	1:E:110:LEU:HA	1.98	0.46
1:L:19:MET:HE3	1:L:110:LEU:HA	1.97	0.46
1:K:19:MET:HE3	1:K:110:LEU:HA	1.99	0.45
1:C:19:MET:HE3	1:C:110:LEU:HA	1.97	0.45
1:H:19:MET:HE3	1:H:110:LEU:HA	1.97	0.45
1:P:19:MET:HE3	1:P:110:LEU:HA	1.98	0.45
1:F:19:MET:HE3	1:F:110:LEU:HA	1.98	0.45
1:X:19:MET:HE1	1:X:110:LEU:HA	1.99	0.45
1:T:19:MET:HE3	1:T:110:LEU:HA	1.99	0.45
1:W:19:MET:HE1	1:W:110:LEU:HA	1.98	0.44
1:J:19:MET:HE1	1:J:110:LEU:HA	2.00	0.44
1:A:19:MET:HE1	1:A:110:LEU:HA	2.00	0.43
1:F:123:PRO:HD2	3:F:183:HOH:O	2.19	0.43
1:P:123:PRO:HD2	3:P:183:HOH:O	2.19	0.43
1:L:123:PRO:HD2	3:L:179:HOH:O	2.19	0.42
1:O:123:PRO:HD2	3:O:187:HOH:O	2.19	0.42
1:V:123:PRO:HD2	3:V:187:HOH:O	2.19	0.42
1:Q:123:PRO:HD2	3:Q:184:HOH:O	2.19	0.42
1:X:123:PRO:HD2	3:X:187:HOH:O	2.19	0.42
1:M:123:PRO:HD2	3:M:182:HOH:O	2.19	0.42
1:N:123:PRO:HD2	3:N:180:HOH:O	2.19	0.42
1:S:123:PRO:HD2	3:S:187:HOH:O	2.19	0.42
1:B:19:MET:HE3	1:B:110:LEU:HA	2.00	0.42

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:PRO:HD2	3:B:179:HOH:O	2.19	0.42
1:G:123:PRO:HD2	3:G:186:HOH:O	2.19	0.42
1:K:123:PRO:HD2	3:K:179:HOH:O	2.19	0.42
1:J:123:PRO:HD2	3:J:180:HOH:O	2.19	0.42
1:D:123:PRO:HD2	3:D:179:HOH:O	2.19	0.42
1:Q:19:MET:HE1	1:Q:110:LEU:HA	2.01	0.41
1:A:123:PRO:HD2	3:A:179:HOH:O	2.19	0.41
1:E:123:PRO:HD2	3:E:180:HOH:O	2.19	0.41
1:T:123:PRO:HD2	3:T:188:HOH:O	2.19	0.41
1:H:123:PRO:HD2	3:H:186:HOH:O	2.19	0.41
1:O:19:MET:HE3	1:O:110:LEU:HA	2.03	0.41
1:R:123:PRO:HD2	3:R:186:HOH:O	2.19	0.41
1:I:123:PRO:HD2	3:I:187:HOH:O	2.19	0.41
1:C:123:PRO:HD2	3:C:179:HOH:O	2.19	0.41
1:U:123:PRO:HD2	3:U:187:HOH:O	2.19	0.40
1:C:28:TYR:CE1	1:O:78:LEU:HD13	2.56	0.40
1:C:78:LEU:HD13	1:O:28:TYR:CE1	2.57	0.40
1:G:75:ARG:HH11	1:G:75:ARG:HD3	1.79	0.40
1:W:123:PRO:HD2	3:W:186:HOH:O	2.19	0.40

All (18) 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)
1:L:18:ARG:NH1	1:Q:87:ASP:OD2[4_566]	0.93	1.27
1:L:11:ASP:CG	3:Q:224:HOH:O[4_566]	1.31	0.89
1:L:11:ASP:OD1	3:Q:224:HOH:O[4_566]	1.50	0.70
1:E:87:ASP:OD2	1:X:18:ARG:NH1[5_665]	1.53	0.67
1:X:11:ASP:OD1	3:E:221:HOH:O[5_565]	1.56	0.64
3:I:225:HOH:O	3:X:189:HOH:O[5_665]	1.61	0.59
1:L:18:ARG:NH1	1:Q:87:ASP:CG[4_566]	1.68	0.52
1:I:11:ASP:OD1	3:J:222:HOH:O[5_665]	1.72	0.48
1:X:11:ASP:CG	3:E:221:HOH:O[5_565]	1.74	0.46
1:I:18:ARG:NH1	1:J:87:ASP:OD2[5_665]	1.74	0.46
3:L:181:HOH:O	3:U:225:HOH:O[4_566]	1.84	0.36
3:I:189:HOH:O	3:X:226:HOH:O[5_665]	1.93	0.27
1:L:11:ASP:OD2	3:Q:224:HOH:O[4_566]	1.94	0.26
1:I:11:ASP:CG	3:J:222:HOH:O[5_665]	2.09	0.11
1:X:10:SER:OG	3:I:199:HOH:O[5_565]	2.11	0.09
1:L:11:ASP:CB	3:Q:224:HOH:O[4_566]	2.14	0.06

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:87:ASP:CG	1:X:18:ARG:NH1[5_665]	2.18	0.02
1:L:10:SER:OG	3:U:199:HOH:O[4_566]	2.19	0.01

## 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	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	B	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	C	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	D	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	E	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	F	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	G	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	H	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	I	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	J	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	K	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	L	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	M	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	N	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	O	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	P	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	Q	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	R	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	S	169/176 (96%)	165 (98%)	4 (2%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	U	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	V	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	W	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
1	X	169/176 (96%)	165 (98%)	4 (2%)	0	100	100
All	All	4056/4224 (96%)	3960 (98%)	96 (2%)	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	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	B	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	C	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	D	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	E	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	F	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	G	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	H	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	I	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	J	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	K	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	L	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	M	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	N	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	O	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	P	142/157 (90%)	132 (93%)	10 (7%)	19	47

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Q	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	R	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	S	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	T	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	U	142/157 (90%)	133 (94%)	9 (6%)	22	53
1	V	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	W	142/157 (90%)	132 (93%)	10 (7%)	19	47
1	X	142/157 (90%)	132 (93%)	10 (7%)	19	47
All	All	3408/3768 (90%)	3176 (93%)	232 (7%)	20	49

All (232) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	22	LEU
1	A	28	TYR
1	A	32	SER
1	A	44	LEU
1	A	85	GLU
1	A	120	LYS
1	A	129	LEU
1	A	134	LEU
1	A	151	LEU
1	B	10	SER
1	B	22	LEU
1	B	28	TYR
1	B	32	SER
1	B	44	LEU
1	B	85	GLU
1	B	120	LYS
1	B	129	LEU
1	B	134	LEU
1	B	151	LEU
1	C	10	SER
1	C	22	LEU
1	C	28	TYR
1	C	32	SER
1	C	44	LEU
1	C	85	GLU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	120	LYS
1	C	129	LEU
1	C	151	LEU
1	D	10	SER
1	D	22	LEU
1	D	28	TYR
1	D	32	SER
1	D	44	LEU
1	D	85	GLU
1	D	120	LYS
1	D	129	LEU
1	D	134	LEU
1	D	151	LEU
1	E	10	SER
1	E	22	LEU
1	E	28	TYR
1	E	32	SER
1	E	44	LEU
1	E	85	GLU
1	E	120	LYS
1	E	129	LEU
1	E	134	LEU
1	E	151	LEU
1	F	10	SER
1	F	22	LEU
1	F	28	TYR
1	F	32	SER
1	F	44	LEU
1	F	85	GLU
1	F	120	LYS
1	F	129	LEU
1	F	134	LEU
1	F	151	LEU
1	G	10	SER
1	G	22	LEU
1	G	28	TYR
1	G	32	SER
1	G	44	LEU
1	G	85	GLU
1	G	120	LYS
1	G	129	LEU
1	G	151	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	H	10	SER
1	H	22	LEU
1	H	28	TYR
1	H	32	SER
1	H	44	LEU
1	H	85	GLU
1	H	120	LYS
1	H	129	LEU
1	H	134	LEU
1	H	151	LEU
1	I	10	SER
1	I	22	LEU
1	I	28	TYR
1	I	32	SER
1	I	44	LEU
1	I	85	GLU
1	I	120	LYS
1	I	129	LEU
1	I	134	LEU
1	I	151	LEU
1	J	10	SER
1	J	22	LEU
1	J	28	TYR
1	J	32	SER
1	J	44	LEU
1	J	85	GLU
1	J	120	LYS
1	J	129	LEU
1	J	134	LEU
1	J	151	LEU
1	K	10	SER
1	K	22	LEU
1	K	28	TYR
1	K	32	SER
1	K	44	LEU
1	K	85	GLU
1	K	120	LYS
1	K	129	LEU
1	K	151	LEU
1	L	10	SER
1	L	22	LEU
1	L	28	TYR

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	L	32	SER
1	L	44	LEU
1	L	85	GLU
1	L	120	LYS
1	L	129	LEU
1	L	151	LEU
1	M	10	SER
1	M	22	LEU
1	M	28	TYR
1	M	32	SER
1	M	44	LEU
1	M	85	GLU
1	M	120	LYS
1	M	129	LEU
1	M	134	LEU
1	M	151	LEU
1	N	10	SER
1	N	22	LEU
1	N	28	TYR
1	N	32	SER
1	N	44	LEU
1	N	85	GLU
1	N	120	LYS
1	N	129	LEU
1	N	134	LEU
1	N	151	LEU
1	O	10	SER
1	O	22	LEU
1	O	28	TYR
1	O	32	SER
1	O	44	LEU
1	O	85	GLU
1	O	120	LYS
1	O	129	LEU
1	O	151	LEU
1	P	10	SER
1	P	22	LEU
1	P	28	TYR
1	P	32	SER
1	P	44	LEU
1	P	85	GLU
1	P	120	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	P	129	LEU
1	P	134	LEU
1	P	151	LEU
1	Q	10	SER
1	Q	22	LEU
1	Q	28	TYR
1	Q	32	SER
1	Q	44	LEU
1	Q	85	GLU
1	Q	120	LYS
1	Q	129	LEU
1	Q	134	LEU
1	Q	151	LEU
1	R	10	SER
1	R	22	LEU
1	R	28	TYR
1	R	32	SER
1	R	44	LEU
1	R	85	GLU
1	R	120	LYS
1	R	129	LEU
1	R	151	LEU
1	S	10	SER
1	S	22	LEU
1	S	28	TYR
1	S	32	SER
1	S	44	LEU
1	S	85	GLU
1	S	120	LYS
1	S	129	LEU
1	S	134	LEU
1	S	151	LEU
1	T	10	SER
1	T	22	LEU
1	T	28	TYR
1	T	32	SER
1	T	44	LEU
1	T	85	GLU
1	T	120	LYS
1	T	129	LEU
1	T	151	LEU
1	U	10	SER

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type
1	U	22	LEU
1	U	28	TYR
1	U	32	SER
1	U	44	LEU
1	U	85	GLU
1	U	120	LYS
1	U	129	LEU
1	U	151	LEU
1	V	10	SER
1	V	22	LEU
1	V	28	TYR
1	V	32	SER
1	V	44	LEU
1	V	85	GLU
1	V	120	LYS
1	V	129	LEU
1	V	134	LEU
1	V	151	LEU
1	W	10	SER
1	W	22	LEU
1	W	28	TYR
1	W	32	SER
1	W	44	LEU
1	W	85	GLU
1	W	120	LYS
1	W	129	LEU
1	W	134	LEU
1	W	151	LEU
1	X	10	SER
1	X	22	LEU
1	X	28	TYR
1	X	32	SER
1	X	44	LEU
1	X	85	GLU
1	X	120	LYS
1	X	129	LEU
1	X	134	LEU
1	X	151	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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](#)

Of 48 ligands modelled in this entry, 48 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.