



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 30, 2023 – 06:06 PM JST

PDB ID : 8IVZ  
Title : Crystal structure of talin R7 in complex with KANK1 KN motif  
Authors : Xu, Y.; Li, K.; Wei, Z.; Cong, Y.  
Deposited on : 2023-03-29  
Resolution : 2.80 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>.

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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) : 1.13  
EDS : 2.36  
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) : 2.36

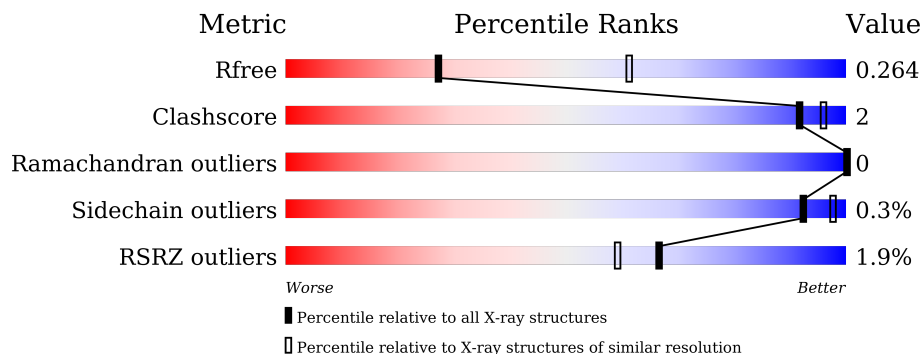
# 1 Overall quality at a glance

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))
$R_{free}$	130704	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (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 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	171	 92% 5%
1	B	171	 3% 92% 5%
2	C	26	 8% 92% 8%
2	D	26	 85% 8% 8%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2869 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 Talin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	165	1229	757	215	248	9	1	2	0
1	B	165	1221	753	216	243	9	1	1	0

There are 268 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1353	HIS	-	expression tag	UNP P26039
A	1354	MET	-	expression tag	UNP P26039
A	1355	GLY	-	expression tag	UNP P26039
A	1356	SER	-	expression tag	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	GLY	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	GLY	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	PRO	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	PHE	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ARG	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ILE	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	MET	deletion	UNP P26039

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	deletion	UNP P26039
A	?	-	CYS	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	GLY	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	PRO	deletion	UNP P26039
A	?	-	GLY	deletion	UNP P26039
A	?	-	CYS	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	ILE	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	LYS	deletion	UNP P26039
A	?	-	HIS	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	CYS	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	CYS	deletion	UNP P26039
A	?	-	ARG	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ARG	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	PRO	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	LYS	deletion	UNP P26039
A	?	-	ARG	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	PHE	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	LYS	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	LYS	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	ILE	deletion	UNP P26039
A	?	-	LYS	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	ASP	deletion	UNP P26039
A	?	-	GLY	deletion	UNP P26039
A	?	-	ASP	deletion	UNP P26039
A	?	-	PHE	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	ARG	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	GLN	deletion	UNP P26039
A	?	-	CYS	deletion	UNP P26039
A	?	-	ARG	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ALA	deletion	UNP P26039
A	?	-	THR	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	PRO	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	ASP	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	LEU	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	PHE	deletion	UNP P26039
A	?	-	ALA	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	ASN	deletion	UNP P26039
A	?	-	PRO	deletion	UNP P26039
A	?	-	GLU	deletion	UNP P26039
A	?	-	PHE	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	SER	deletion	UNP P26039
A	?	-	VAL	deletion	UNP P26039
A	?	-	PRO	deletion	UNP P26039
B	1353	HIS	-	expression tag	UNP P26039
B	1354	MET	-	expression tag	UNP P26039
B	1355	GLY	-	expression tag	UNP P26039
B	1356	SER	-	expression tag	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	GLY	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	GLY	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	GLU	deletion	UNP P26039
B	?	-	PRO	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	PHE	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ARG	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ILE	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	MET	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	CYS	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	GLY	deletion	UNP P26039
B	?	-	GLU	deletion	UNP P26039
B	?	-	PRO	deletion	UNP P26039
B	?	-	GLY	deletion	UNP P26039
B	?	-	CYS	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	ILE	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	LYS	deletion	UNP P26039
B	?	-	HIS	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	CYS	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	CYS	deletion	UNP P26039
B	?	-	ARG	deletion	UNP P26039

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	LEU	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ARG	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	PRO	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	LYS	deletion	UNP P26039
B	?	-	ARG	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	PHE	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	LYS	deletion	UNP P26039
B	?	-	GLU	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	LYS	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	ILE	deletion	UNP P26039
B	?	-	LYS	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	ASP	deletion	UNP P26039
B	?	-	GLY	deletion	UNP P26039
B	?	-	ASP	deletion	UNP P26039
B	?	-	PHE	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	GLU	deletion	UNP P26039

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLU	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	ARG	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	GLN	deletion	UNP P26039
B	?	-	CYS	deletion	UNP P26039
B	?	-	ARG	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	THR	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	PRO	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	GLU	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	ASP	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	LEU	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	PHE	deletion	UNP P26039
B	?	-	ALA	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	ASN	deletion	UNP P26039
B	?	-	PRO	deletion	UNP P26039
B	?	-	GLU	deletion	UNP P26039
B	?	-	PHE	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	SER	deletion	UNP P26039
B	?	-	VAL	deletion	UNP P26039
B	?	-	PRO	deletion	UNP P26039

- Molecule 2 is a protein called KN motif and ankyrin repeat domains 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	24	Total	C	N	O	0	0	0
			209	141	27	41			
2	D	24	Total	C	N	O	0	0	0
			205	138	26	41			

- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
3	A	2	Total O 2 2	0	0
3	B	2	Total O 2 2	0	0
3	C	1	Total O 1 1	0	0

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

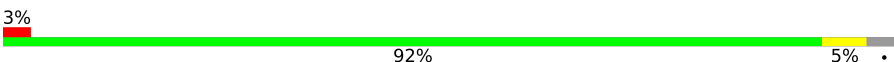
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Talin-1

Chain A:  92% 5% .



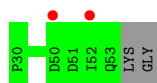
- Molecule 1: Talin-1

Chain B:  3% 92% 5% .




- Molecule 2: KN motif and ankyrin repeat domains 1

Chain C:  8% 92% 8%



- Molecule 2: KN motif and ankyrin repeat domains 1

Chain D:  85% 8% 8%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	40.54Å 46.90Å 261.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.90 – 2.80 46.90 – 2.79	Depositor EDS
% Data completeness (in resolution range)	97.3 (46.90-2.80) 84.6 (46.90-2.79)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.74 (at 2.77Å)	Xtrriage
Refinement program	PHENIX (1.18.2_3874: ???)	Depositor
R, $R_{free}$	0.238 , 0.264 0.238 , 0.264	Depositor DCC
$R_{free}$ test set	643 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.8	Xtrriage
Anisotropy	0.331	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 15.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2869	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	73.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.40% 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	0.23	0/1251	0.37	0/1695
1	B	0.23	0/1241	0.37	0/1681
2	C	0.23	0/216	0.35	0/294
2	D	0.24	0/212	0.36	0/290
All	All	0.23	0/2920	0.37	0/3960

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	1229	0	1225	4	0
1	B	1221	0	1223	5	0
2	C	209	0	191	0	0
2	D	205	0	180	2	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
All	All	2869	0	2819	9	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 2.

The worst 5 of 9 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:B:1415:LYS:HD3	2:D:36:PRO:HG3	1.88	0.54
1:A:1600:VAL:HG12	1:A:1604:LYS:HE2	1.93	0.51
1:B:1404:GLY:HA3	2:D:46:LEU:HD11	1.94	0.49
1:B:1393:LEU:O	1:B:1397:MET:HG2	2.14	0.47
1:B:1432:ALA:O	1:B:1436:PHE:HB2	2.16	0.46

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	165/171 (96%)	164 (99%)	1 (1%)	0	100	100
1	B	164/171 (96%)	162 (99%)	2 (1%)	0	100	100
2	C	22/26 (85%)	22 (100%)	0	0	100	100
2	D	22/26 (85%)	22 (100%)	0	0	100	100
All	All	373/394 (95%)	370 (99%)	3 (1%)	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	133/136 (98%)	132 (99%)	1 (1%)	81	94
1	B	132/136 (97%)	132 (100%)	0	100	100
2	C	23/24 (96%)	23 (100%)	0	100	100
2	D	22/24 (92%)	22 (100%)	0	100	100
All	All	310/320 (97%)	309 (100%)	1 (0%)	92	98

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1591	GLU

Sometimes 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 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	165/171 (96%)	-0.16	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	44, 56, 83, 100	1 (0%)
1	B	165/171 (96%)	-0.01	5 (3%) <span style="border: 1px solid gray; padding: 2px;">50</span> <span style="border: 1px solid gray; padding: 2px;">40</span>	45, 73, 150, 176	2 (1%)
2	C	24/26 (92%)	0.47	2 (8%) <span style="border: 1px solid red; padding: 2px;">11</span> <span style="border: 1px solid red; padding: 2px;">6</span>	56, 71, 123, 139	0
2	D	24/26 (92%)	-0.05	0 <span style="border: 1px solid blue; padding: 2px;">100</span> <span style="border: 1px solid blue; padding: 2px;">100</span>	52, 83, 118, 128	0
All	All	378/394 (95%)	-0.05	7 (1%) <span style="border: 1px solid gray; padding: 2px;">66</span> <span style="border: 1px solid gray; padding: 2px;">59</span>	44, 64, 130, 176	3 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	52	ILE	5.0
2	C	50	ASP	3.2
1	B	1591	GLU	2.9
1	B	1590	PRO	2.7
1	B	1594	ALA	2.6

### 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 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.