



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:06 pm BST

PDB ID : 4L1M  
Title : Structure of the first RCC1-like domain of HERC2  
Authors : Tempel, W.; Khan, M.B.; Dong, A.; Hu, J.; Li, Y.; Bountra, C.; Arrowsmith, C.H.; Edwards, A.M.; Tong, Y.; Structural Genomics Consortium (SGC)  
Deposited on : 2013-06-03  
Resolution : 2.60 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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)	:	2.11

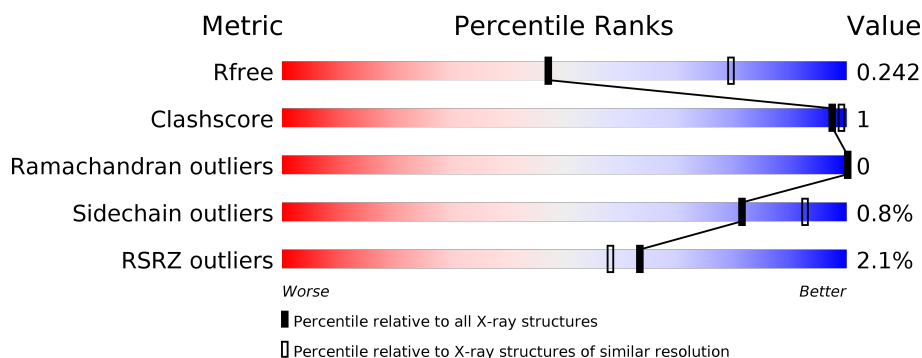
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 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	392	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>9%</div> </div> </div>
1	B	392	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>9%</div> </div> </div>
1	C	392	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>10%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	UNX	A	805	-	-	-	X
3	UNX	A	811	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7981 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 E3 ubiquitin-protein ligase HERC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	3	0
			2637	1659	465	501	12			
1	B	357	Total	C	N	O	S	0	4	0
			2624	1656	455	501	12			
1	C	353	Total	C	N	O	S	0	6	1
			2580	1623	454	491	12			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	399	MET	-	EXPRESSION TAG	UNP O95714
A	400	HIS	-	EXPRESSION TAG	UNP O95714
A	401	HIS	-	EXPRESSION TAG	UNP O95714
A	402	HIS	-	EXPRESSION TAG	UNP O95714
A	403	HIS	-	EXPRESSION TAG	UNP O95714
A	404	HIS	-	EXPRESSION TAG	UNP O95714
A	405	HIS	-	EXPRESSION TAG	UNP O95714
A	406	SER	-	EXPRESSION TAG	UNP O95714
A	407	SER	-	EXPRESSION TAG	UNP O95714
A	408	GLY	-	EXPRESSION TAG	UNP O95714
A	409	ARG	-	EXPRESSION TAG	UNP O95714
A	410	GLU	-	EXPRESSION TAG	UNP O95714
A	411	ASN	-	EXPRESSION TAG	UNP O95714
A	412	LEU	-	EXPRESSION TAG	UNP O95714
A	413	TYR	-	EXPRESSION TAG	UNP O95714
A	414	PHE	-	EXPRESSION TAG	UNP O95714
A	415	GLN	-	EXPRESSION TAG	UNP O95714
A	416	GLY	-	EXPRESSION TAG	UNP O95714
B	399	MET	-	EXPRESSION TAG	UNP O95714
B	400	HIS	-	EXPRESSION TAG	UNP O95714
B	401	HIS	-	EXPRESSION TAG	UNP O95714
B	402	HIS	-	EXPRESSION TAG	UNP O95714
B	403	HIS	-	EXPRESSION TAG	UNP O95714

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Chain	Residue	Modelled	Actual	Comment	Reference
B	404	HIS	-	EXPRESSION TAG	UNP O95714
B	405	HIS	-	EXPRESSION TAG	UNP O95714
B	406	SER	-	EXPRESSION TAG	UNP O95714
B	407	SER	-	EXPRESSION TAG	UNP O95714
B	408	GLY	-	EXPRESSION TAG	UNP O95714
B	409	ARG	-	EXPRESSION TAG	UNP O95714
B	410	GLU	-	EXPRESSION TAG	UNP O95714
B	411	ASN	-	EXPRESSION TAG	UNP O95714
B	412	LEU	-	EXPRESSION TAG	UNP O95714
B	413	TYR	-	EXPRESSION TAG	UNP O95714
B	414	PHE	-	EXPRESSION TAG	UNP O95714
B	415	GLN	-	EXPRESSION TAG	UNP O95714
B	416	GLY	-	EXPRESSION TAG	UNP O95714
C	399	MET	-	EXPRESSION TAG	UNP O95714
C	400	HIS	-	EXPRESSION TAG	UNP O95714
C	401	HIS	-	EXPRESSION TAG	UNP O95714
C	402	HIS	-	EXPRESSION TAG	UNP O95714
C	403	HIS	-	EXPRESSION TAG	UNP O95714
C	404	HIS	-	EXPRESSION TAG	UNP O95714
C	405	HIS	-	EXPRESSION TAG	UNP O95714
C	406	SER	-	EXPRESSION TAG	UNP O95714
C	407	SER	-	EXPRESSION TAG	UNP O95714
C	408	GLY	-	EXPRESSION TAG	UNP O95714
C	409	ARG	-	EXPRESSION TAG	UNP O95714
C	410	GLU	-	EXPRESSION TAG	UNP O95714
C	411	ASN	-	EXPRESSION TAG	UNP O95714
C	412	LEU	-	EXPRESSION TAG	UNP O95714
C	413	TYR	-	EXPRESSION TAG	UNP O95714
C	414	PHE	-	EXPRESSION TAG	UNP O95714
C	415	GLN	-	EXPRESSION TAG	UNP O95714
C	416	GLY	-	EXPRESSION TAG	UNP O95714

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	12	Total	X	0	0
			12	12		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	X	0	0
			9	9		
3	C	13	Total	X	0	0
			13	13		

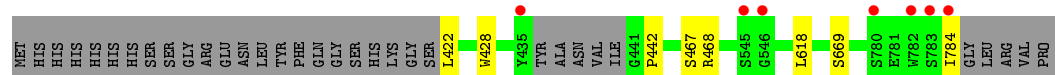
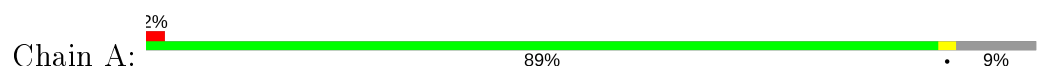
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	17	Total	O	0	0
			17	17		
4	B	25	Total	O	0	0
			25	25		
4	C	9	Total	O	0	0
			9	9		

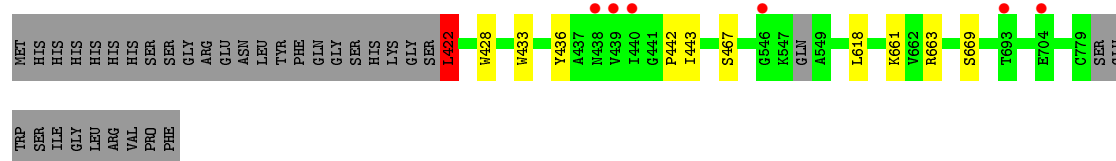
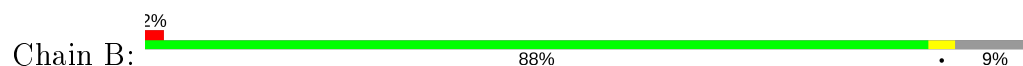
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

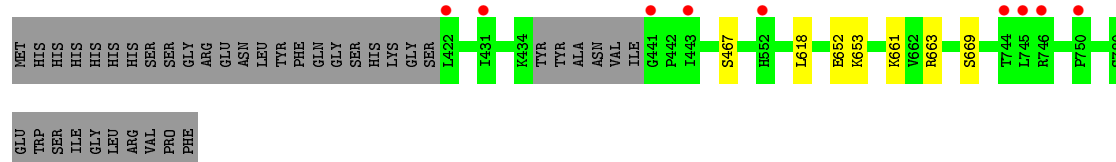
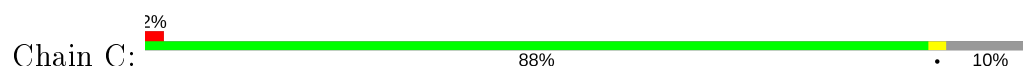
- Molecule 1: E3 ubiquitin-protein ligase HERC2



- Molecule 1: E3 ubiquitin-protein ligase HERC2



- Molecule 1: E3 ubiquitin-protein ligase HERC2





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.16 Å 94.16 Å 281.89 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 2.60 39.17 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (40.00-2.60) 100.0 (39.17-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.61 Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.199 , 0.238 0.208 , 0.242	Depositor DCC
$R_{free}$ test set	2500 reflections (5.48%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.5	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 46.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7981	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.09 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.1247e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: UNX, SO4

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	0.59	0/2707	0.66	0/3679
1	B	4.92	4/2692 (0.1%)	1.93	6/3658 (0.2%)
1	C	0.57	0/2648	0.65	0/3597
All	All	2.89	4/8047 (0.0%)	1.24	6/10934 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	422[A]	LEU	CG-CD2	140.53	6.71	1.51
1	B	422[B]	LEU	CG-CD2	140.53	6.71	1.51
1	B	422[A]	LEU	CG-CD1	111.39	5.63	1.51
1	B	422[B]	LEU	CG-CD1	111.39	5.63	1.51

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	422[A]	LEU	CB-CG-CD1	-56.53	14.89	111.00
1	B	422[B]	LEU	CB-CG-CD1	-56.53	14.89	111.00
1	B	422[A]	LEU	CB-CG-CD2	-44.44	35.46	111.00
1	B	422[B]	LEU	CB-CG-CD2	-44.44	35.46	111.00
1	B	422[A]	LEU	CD1-CG-CD2	-29.76	21.22	110.50
1	B	422[B]	LEU	CD1-CG-CD2	-29.76	21.22	110.50

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	2637	0	2516	4	0
1	B	2624	0	2496	6	0
1	C	2580	0	2443	3	0
2	A	20	0	0	0	0
2	B	20	0	0	0	0
2	C	15	0	0	0	0
3	A	9	0	0	0	0
3	B	12	0	0	0	0
3	C	13	0	0	0	0
4	A	17	0	0	0	0
4	B	25	0	0	0	0
4	C	9	0	0	0	0
All	All	7981	0	7455	13	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 1.

All (13) 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:422[B]:LEU:HB2	1:A:784:ILE:HD13	1.82	0.62
1:A:422[B]:LEU:HB3	1:A:784:ILE:HG21	1.86	0.58
1:B:436:TYR:HD2	1:B:443:ILE:HG21	1.76	0.50
1:C:661:LYS:HD3	1:C:663:ARG:HH22	1.77	0.50
1:B:661:LYS:HD3	1:B:663:ARG:HH22	1.77	0.47
1:C:618:LEU:HD11	1:C:669:SER:HB3	1.99	0.44
1:B:618:LEU:HD11	1:B:669:SER:HB3	1.99	0.43
1:A:618:LEU:HD11	1:A:669:SER:HB3	2.02	0.42
1:B:436:TYR:CD2	1:B:443:ILE:HG21	2.55	0.42
1:B:428:TRP:HB3	1:B:442:PRO:HA	2.03	0.41
1:C:652:GLU:OE1	1:C:653:LYS:HE2	2.21	0.41
1:A:428:TRP:HB3	1:A:442:PRO:HA	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	356/392 (91%)	350 (98%)	6 (2%)	0	100	100
1	B	356/392 (91%)	350 (98%)	6 (2%)	0	100	100
1	C	353/392 (90%)	348 (99%)	5 (1%)	0	100	100
All	All	1065/1176 (91%)	1048 (98%)	17 (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	262/306 (86%)	259 (99%)	3 (1%)	73	88
1	B	257/306 (84%)	252 (98%)	5 (2%)	57	79
1	C	252/306 (82%)	250 (99%)	2 (1%)	81	92
All	All	771/918 (84%)	761 (99%)	10 (1%)	81	86

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	467[A]	SER
1	A	467[B]	SER
1	A	468	ARG
1	B	422[A]	LEU
1	B	422[B]	LEU

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Mol	Chain	Res	Type
1	B	433	TRP
1	B	467[A]	SER
1	B	467[B]	SER
1	C	467[A]	SER
1	C	467[B]	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	455	GLN
1	A	555	HIS
1	C	687	GLN

### 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 45 ligands modelled in this entry, 34 are unknown - leaving 11 for Mogul analysis.

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	$\# Z  > 2$
2	SO4	C	801	-	4,4,4	0.46	0	6,6,6	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	B	803	-	4,4,4	0.39	0	6,6,6	0.66	0
2	SO4	B	804	-	4,4,4	0.44	0	6,6,6	0.45	0
2	SO4	A	801	-	4,4,4	0.51	0	6,6,6	0.20	0
2	SO4	C	802	-	4,4,4	0.16	0	6,6,6	0.51	0
2	SO4	A	802	-	4,4,4	0.45	0	6,6,6	0.59	0
2	SO4	B	802	-	4,4,4	0.48	0	6,6,6	0.84	0
2	SO4	A	803	-	4,4,4	0.28	0	6,6,6	0.50	0
2	SO4	B	801	-	4,4,4	0.40	0	6,6,6	0.43	0
2	SO4	C	803	-	4,4,4	0.49	0	6,6,6	0.09	0
2	SO4	A	804	-	4,4,4	0.43	0	6,6,6	0.19	0

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 ⓘ

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	358/392 (91%)	-0.07	7 (1%) 65 60	32, 48, 75, 98	1 (0%)
1	B	357/392 (91%)	-0.16	6 (1%) 70 66	32, 45, 73, 90	1 (0%)
1	C	353/392 (90%)	-0.10	9 (2%) 57 51	34, 52, 83, 99	1 (0%)
All	All	1068/1176 (90%)	-0.11	22 (2%) 63 58	32, 48, 78, 99	3 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	422	LEU	5.6
1	A	784	ILE	4.3
1	A	782	TRP	3.9
1	B	440	ILE	3.5
1	B	438	ASN	3.2
1	A	435	TYR	2.9
1	C	746	ARG	2.8
1	A	783	SER	2.8
1	A	546	GLY	2.8
1	B	693	THR	2.6
1	B	439	VAL	2.5
1	C	750	PRO	2.5
1	C	431	ILE	2.3
1	C	744	THR	2.3
1	A	545	SER	2.2
1	A	780	SER	2.2
1	B	704	GLU	2.1
1	C	441	GLY	2.1
1	B	546	GLY	2.0
1	C	443	ILE	2.0
1	C	745	LEU	2.0
1	C	552	HIS	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

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	UNX	A	807	1/1	0.57	0.29	42,42,42,42	0
3	UNX	B	814	1/1	0.58	0.31	33,33,33,33	0
3	UNX	C	805	1/1	0.59	0.38	40,40,40,40	0
3	UNX	C	806	1/1	0.74	0.38	30,30,30,30	0
3	UNX	A	805	1/1	0.75	0.51	35,35,35,35	0
3	UNX	B	812	1/1	0.78	0.39	31,31,31,31	0
3	UNX	A	811	1/1	0.80	1.17	33,33,33,33	0
3	UNX	B	809	1/1	0.80	0.46	33,33,33,33	0
3	UNX	C	808	1/1	0.81	0.55	37,37,37,37	0
2	SO4	A	804	5/5	0.81	0.27	97,101,115,121	0
3	UNX	B	808	1/1	0.81	0.20	39,39,39,39	0
3	UNX	C	810	1/1	0.81	0.53	30,30,30,30	0
3	UNX	C	816	1/1	0.83	0.26	35,35,35,35	0
2	SO4	B	804	5/5	0.83	0.20	86,88,103,103	0
3	UNX	B	813	1/1	0.85	0.27	29,29,29,29	0
3	UNX	A	812	1/1	0.85	0.15	36,36,36,36	0
3	UNX	C	809	1/1	0.85	0.38	39,39,39,39	0
3	UNX	B	815	1/1	0.85	0.37	43,43,43,43	0
3	UNX	A	810	1/1	0.86	0.53	33,33,33,33	0
3	UNX	B	806	1/1	0.86	0.31	29,29,29,29	0
3	UNX	A	813	1/1	0.86	0.17	33,33,33,33	0
3	UNX	C	812	1/1	0.88	0.25	32,32,32,32	0
3	UNX	C	804	1/1	0.90	0.14	50,50,50,50	0
2	SO4	C	803	5/5	0.90	0.15	94,94,108,108	0
3	UNX	C	807	1/1	0.90	0.49	36,36,36,36	0
2	SO4	A	801	5/5	0.91	0.35	83,85,91,93	0
3	UNX	B	805	1/1	0.91	0.19	30,30,30,30	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	UNX	A	809	1/1	0.92	0.25	31,31,31,31	0
2	SO4	A	802	5/5	0.92	0.15	61,63,71,72	0
3	UNX	C	814	1/1	0.92	0.21	29,29,29,29	0
3	UNX	C	811	1/1	0.92	0.35	31,31,31,31	0
3	UNX	B	807	1/1	0.93	0.24	11,11,11,11	0
3	UNX	C	815	1/1	0.93	0.23	28,28,28,28	0
3	UNX	C	813	1/1	0.93	0.41	35,35,35,35	0
3	UNX	B	811	1/1	0.94	0.21	33,33,33,33	0
2	SO4	C	801	5/5	0.95	0.13	52,62,67,67	0
3	UNX	B	810	1/1	0.95	0.66	25,25,25,25	0
3	UNX	A	806	1/1	0.95	0.18	36,36,36,36	0
3	UNX	A	808	1/1	0.95	0.33	34,34,34,34	0
2	SO4	B	803	5/5	0.96	0.19	54,60,66,68	0
3	UNX	B	816	1/1	0.97	0.53	20,20,20,20	1
2	SO4	B	802	5/5	0.97	0.12	48,53,57,59	0
2	SO4	A	803	5/5	0.98	0.10	59,60,62,64	0
2	SO4	C	802	5/5	0.98	0.09	53,54,60,64	0
2	SO4	B	801	5/5	0.98	0.34	67,67,68,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.