



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:34 AM GMT

PDB ID : 2AWZ  
Title : Hepatitis C Virus NS5b RNA Polymerase in complex with a covalent inhibitor (5h)  
Authors : Powers, J.P.; Piper, D.E.; Li, Y.; Mayorga, V.; Anzola, J.; Chen, J.M.; Jaen, J.C.; Lee, G.; Liu, J.; Peterson, M.G.; Tonn, G.R.; Ye, Q.; Walker, N.P.; Wang, Z.  
Deposited on : 2005-09-02  
Resolution : 2.15 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.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

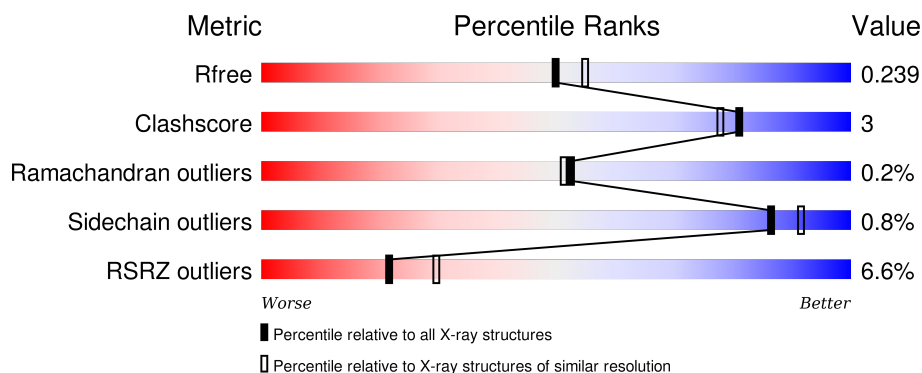
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.15 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))
$R_{free}$	91344	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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.

Mol	Chain	Length	Quality of chain
1	A	580	<div> <div>6%</div> <div>86%</div> <div>10%</div> <div>.</div> </div>
1	B	580	<div> <div>7%</div> <div>89%</div> <div>8%</div> <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
2	SO4	A	904	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9525 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 Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	557	Total	C	N	O	S	0	0	0
			4337	2735	767	804	31			
1	B	562	Total	C	N	O	S	0	0	0
			4370	2755	775	809	31			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	499	ALA	VAL	ENGINEERED	UNP P26663
A	506	ASN	SER	ENGINEERED	UNP P26663
A	514	ARG	GLN	ENGINEERED	UNP P26663
A	520	ILE	THR	ENGINEERED	UNP P26663
A	540	ALA	PRO	ENGINEERED	UNP P26663
A	543	GLY	SER	ENGINEERED	UNP P26663
A	549	SER	GLY	ENGINEERED	UNP P26663
A	552	THR	VAL	ENGINEERED	UNP P26663
A	563	GLY	SER	ENGINEERED	UNP P26663
A	564	VAL	LEU	ENGINEERED	UNP P26663
A	566	HIS	ARG	ENGINEERED	UNP P26663
A	571	HIS	-	EXPRESSION TAG	UNP P26663
A	572	HIS	-	EXPRESSION TAG	UNP P26663
A	573	HIS	-	EXPRESSION TAG	UNP P26663
A	574	HIS	-	EXPRESSION TAG	UNP P26663
A	575	HIS	-	EXPRESSION TAG	UNP P26663
A	576	HIS	-	EXPRESSION TAG	UNP P26663
A	577	HIS	-	EXPRESSION TAG	UNP P26663
A	578	HIS	-	EXPRESSION TAG	UNP P26663
A	579	HIS	-	EXPRESSION TAG	UNP P26663
A	580	HIS	-	EXPRESSION TAG	UNP P26663
B	499	ALA	VAL	ENGINEERED	UNP P26663
B	506	ASN	SER	ENGINEERED	UNP P26663
B	514	ARG	GLN	ENGINEERED	UNP P26663
B	520	ILE	THR	ENGINEERED	UNP P26663

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Chain	Residue	Modelled	Actual	Comment	Reference
B	540	ALA	PRO	ENGINEERED	UNP P26663
B	543	GLY	SER	ENGINEERED	UNP P26663
B	549	SER	GLY	ENGINEERED	UNP P26663
B	552	THR	VAL	ENGINEERED	UNP P26663
B	563	GLY	SER	ENGINEERED	UNP P26663
B	564	VAL	LEU	ENGINEERED	UNP P26663
B	566	HIS	ARG	ENGINEERED	UNP P26663
B	571	HIS	-	EXPRESSION TAG	UNP P26663
B	572	HIS	-	EXPRESSION TAG	UNP P26663
B	573	HIS	-	EXPRESSION TAG	UNP P26663
B	574	HIS	-	EXPRESSION TAG	UNP P26663
B	575	HIS	-	EXPRESSION TAG	UNP P26663
B	576	HIS	-	EXPRESSION TAG	UNP P26663
B	577	HIS	-	EXPRESSION TAG	UNP P26663
B	578	HIS	-	EXPRESSION TAG	UNP P26663
B	579	HIS	-	EXPRESSION TAG	UNP P26663
B	580	HIS	-	EXPRESSION TAG	UNP P26663

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



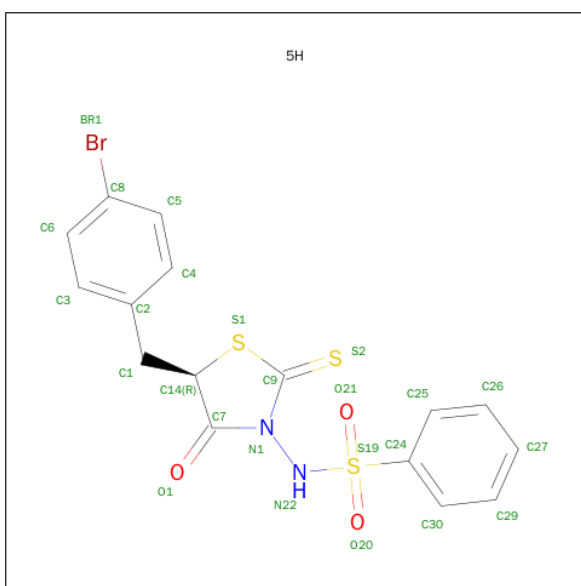
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 3 is 5R-(4-BROMOPHENYLMETHYL)-3-(BENZENESULFONYLAMINO)-4-O XO-2-THIONOTHIAZOLIDINE (three-letter code: 5H) (formula:  $C_{16}H_{13}BrN_2O_3S_3$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total 25	Br 1	C 16	N 2	O 3	S 3	0	0
3	B	1	Total 25	Br 1	C 16	N 2	O 3	S 3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	364	Total O 364 364	0	0
4	B	374	Total O 374 374	0	0

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.

Chain A:

[illegible]

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.09Å 87.02Å 162.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.15 24.98 – 2.16	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.15) 96.5 (24.98-2.16)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.81 (at 2.15Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.205 , 0.243 0.201 , 0.239	Depositor DCC
$R_{free}$ test set	6552 reflections (11.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	27.0	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 53.2	EDS
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 65077 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9525	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 5H, 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	0.33	0/4431	0.57	1/6010 (0.0%)
1	B	0.32	0/4465	0.56	1/6057 (0.0%)
All	All	0.32	0/8896	0.56	2/12067 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	LEU	CA-CB-CG	5.89	128.84	115.30
1	B	56	ARG	NE-CZ-NH2	-5.17	117.72	120.30

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	4337	0	4355	33	0
1	B	4370	0	4393	25	0
2	A	20	0	0	0	0
2	B	10	0	0	0	0
3	A	25	0	12	0	0
3	B	25	0	12	0	0
4	A	364	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	374	0	0	0	0
All	All	9525	0	8772	58	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 3.

All (58) 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:517:ARG:HH11	1:A:517:ARG:HG3	1.40	0.86
1:A:83:LEU:HB2	1:A:173:MET:HA	1.68	0.74
1:B:233:ILE:HD13	1:B:262:ILE:HA	1.69	0.73
1:B:83:LEU:HB2	1:B:173:MET:HA	1.72	0.70
1:B:336:LEU:HD22	1:B:356:PRO:HG3	1.75	0.69
1:A:445:CYS:SG	1:A:454:ILE:HD12	2.33	0.69
1:A:241:GLN:OE1	1:A:250:ARG:HG3	1.92	0.69
1:A:18:GLU:HG2	1:A:401:ARG:CZ	2.25	0.66
1:B:150:GLU:O	1:B:152:GLY:N	2.29	0.64
1:A:506:ASN:HD21	1:A:510:ARG:HH11	1.49	0.61
1:A:336:LEU:HD22	1:A:356:PRO:HG3	1.84	0.59
1:B:313:MET:HG2	1:B:322:VAL:HG22	1.84	0.59
1:A:455:GLU:HB3	4:A:1033:HOH:O	2.03	0.59
1:A:280:ARG:HD2	1:A:291:ASN:OD1	2.03	0.58
1:A:308:LEU:HB2	1:A:311:CYS:SG	2.46	0.55
1:B:346:TYR:O	1:B:347:SER:HB3	2.07	0.55
1:A:517:ARG:NH1	1:A:517:ARG:HG3	2.16	0.55
1:A:119:ILE:HD13	1:A:169:VAL:HG11	1.89	0.54
1:B:172:LYS:HE3	1:B:560:ILE:HD13	1.90	0.53
1:B:361:GLU:OE1	1:B:372:VAL:HG23	2.09	0.53
1:B:309:GLN:HG3	1:B:325:GLU:HB2	1.91	0.52
1:A:34:HIS:HB3	4:A:1244:HOH:O	2.10	0.52
1:B:308:LEU:HB2	1:B:311:CYS:SG	2.50	0.51
1:B:115:ALA:O	1:B:119:ILE:HG13	2.11	0.51
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.93	0.51
1:A:346:TYR:O	1:A:347:SER:HB3	2.12	0.50
1:B:56:ARG:NH2	1:B:279:CYS:HB3	2.26	0.50
1:B:183:PRO:HG3	1:B:289:CYS:SG	2.52	0.49
1:A:419:LEU:HD11	1:A:485:VAL:HG11	1.94	0.49
1:A:51:LYS:HG3	1:A:222:ARG:NH2	2.28	0.48
1:A:18:GLU:HG2	1:A:401:ARG:NH2	2.29	0.48
1:B:237:GLU:OE2	1:B:254:LYS:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:ILE:HD13	1:A:261:TYR:O	2.15	0.47
1:A:160:ILE:HA	1:A:282:SER:OG	2.16	0.46
1:A:308:LEU:CB	1:A:311:CYS:SG	3.03	0.46
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.56	0.46
1:B:515:GLY:HA2	1:B:519:ALA:HB2	1.98	0.45
1:A:390:THR:HB	1:A:391:PRO:HD3	1.98	0.45
1:A:485:VAL:O	1:A:489:LEU:HG	2.17	0.45
1:B:390:THR:HB	1:B:391:PRO:HD3	1.99	0.44
1:B:355:GLN:HA	1:B:356:PRO:HD3	1.90	0.44
1:B:334:ALA:HA	1:B:337:ARG:HH11	1.83	0.43
1:B:429:PHE:O	1:B:433:LEU:HG	2.18	0.43
1:A:257:THR:HA	1:A:261:TYR:HB2	2.01	0.43
1:A:511:LEU:HB3	1:A:518:ALA:O	2.19	0.42
1:A:76:SER:HA	1:A:242:CYS:O	2.18	0.42
1:A:21:LEU:HD12	1:A:22:PRO:HD2	2.02	0.42
1:B:149:PRO:O	1:B:150:GLU:O	2.38	0.42
1:A:100:LYS:HB3	1:A:100:LYS:HE2	1.86	0.42
1:B:309:GLN:H	1:B:309:GLN:HG2	1.73	0.41
1:A:406:ASN:ND2	1:A:443:LEU:HB3	2.35	0.41
1:A:423:MET:HA	1:A:528:TRP:CZ2	2.55	0.41
1:B:423:MET:HA	1:B:528:TRP:CZ2	2.55	0.41
1:B:56:ARG:NH2	1:B:228:VAL:O	2.54	0.41
1:A:309:GLN:HB2	1:A:325:GLU:HB2	2.02	0.41
1:B:216:GLY:HA2	1:B:322:VAL:O	2.21	0.40
1:A:314:LEU:HB3	1:A:321:VAL:CG1	2.51	0.40
1:A:123:TRP:CH2	1:A:174:ALA:HB2	2.57	0.40

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	553/580 (95%)	544 (98%)	9 (2%)	0	100	100
1	B	560/580 (97%)	551 (98%)	7 (1%)	2 (0%)	39	34
All	All	1113/1160 (96%)	1095 (98%)	16 (1%)	2 (0%)	52	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	151	LYS
1	B	150	GLU

### 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	474/492 (96%)	470 (99%)	4 (1%)	86	91
1	B	476/492 (97%)	472 (99%)	4 (1%)	86	91
All	All	950/984 (96%)	942 (99%)	8 (1%)	86	91

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	220	ASP
1	A	366	CYS
1	A	461	GLN
1	A	517	ARG
1	B	56	ARG
1	B	150	GLU
1	B	366	CYS
1	B	498	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN

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Mol	Chain	Res	Type
1	A	35	ASN
1	A	184	GLN
1	A	206	ASN
1	A	213	ASN
1	A	309	GLN
1	A	461	GLN
1	A	506	ASN
1	B	35	ASN
1	B	49	GLN
1	B	184	GLN
1	B	273	ASN
1	B	330	GLN
1	B	506	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
3	5H	A	801	1	24,27,27	1.55	2 (8%)	30,39,39	1.11	2 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	A	901	-	4,4,4	1.07	0	6,6,6	0.06	0
2	SO4	A	902	-	4,4,4	0.94	0	6,6,6	0.07	0
2	SO4	A	903	-	4,4,4	1.05	0	6,6,6	0.10	0
2	SO4	A	904	-	4,4,4	1.10	0	6,6,6	0.10	0
3	5H	B	802	1	24,27,27	1.64	2 (8%)	30,39,39	1.03	2 (6%)
2	SO4	B	905	-	4,4,4	1.12	0	6,6,6	0.11	0
2	SO4	B	906	-	4,4,4	1.15	0	6,6,6	0.08	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	5H	A	801	1	-	0/13/31/31	0/3/3/3
2	SO4	A	901	-	-	0/0/0/0	0/0/0/0
2	SO4	A	902	-	-	0/0/0/0	0/0/0/0
2	SO4	A	903	-	-	0/0/0/0	0/0/0/0
2	SO4	A	904	-	-	0/0/0/0	0/0/0/0
3	5H	B	802	1	-	0/13/31/31	0/3/3/3
2	SO4	B	905	-	-	0/0/0/0	0/0/0/0
2	SO4	B	906	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	802	5H	C14-S1	-3.50	1.75	1.82
3	A	801	5H	C14-S1	-2.61	1.77	1.82
3	A	801	5H	S19-N22	4.42	1.74	1.65
3	B	802	5H	S19-N22	4.63	1.75	1.65

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	801	5H	C7-C14-S1	-3.82	102.38	105.99
3	B	802	5H	C7-C14-S1	-2.81	103.34	105.99
3	A	801	5H	O1-C7-N1	-2.80	121.30	124.33
3	B	802	5H	O1-C7-N1	-2.72	121.40	124.33

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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	557/580 (96%)	0.24	32 (5%) 27 37	14, 25, 44, 64	0
1	B	562/580 (96%)	0.35	42 (7%) 17 23	12, 26, 45, 57	0
All	All	1119/1160 (96%)	0.30	74 (6%) 22 30	12, 26, 44, 64	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	149	PRO	6.0
1	B	425	LEU	5.1
1	B	421	ALA	5.0
1	B	412	ILE	4.9
1	A	546	ASP	4.8
1	B	402	HIS	4.8
1	B	150	GLU	4.6
1	A	402	HIS	4.6
1	B	531	LYS	4.5
1	A	548	SER	4.4
1	A	412	ILE	4.0
1	B	376	ALA	3.9
1	B	544	ARG	3.9
1	A	421	ALA	3.8
1	B	16	ALA	3.7
1	B	15	ALA	3.6
1	B	498	ARG	3.5
1	B	424	ILE	3.4
1	B	14	CYS	3.3
1	B	76	SER	3.3
1	A	379	LYS	3.2
1	B	322	VAL	3.2
1	B	404	PRO	3.2
1	A	540	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	535	LYS	3.1
1	B	247	PRO	3.1
1	B	403	THR	3.1
1	B	420	TRP	3.0
1	A	15	ALA	3.0
1	B	102	GLY	2.9
1	A	426	MET	2.9
1	A	14	CYS	2.8
1	B	106	LYS	2.8
1	A	101	PHE	2.8
1	A	547	LEU	2.8
1	A	376	ALA	2.7
1	A	128	GLU	2.7
1	B	101	PHE	2.7
1	B	151	LYS	2.7
1	A	110	ASN	2.7
1	B	30	LEU	2.6
1	B	405	VAL	2.6
1	A	416	ALA	2.6
1	A	377	SER	2.6
1	B	418	THR	2.6
1	B	18	GLU	2.6
1	A	284	VAL	2.6
1	B	321	VAL	2.6
1	A	465	ARG	2.5
1	A	404	PRO	2.5
1	B	111	LEU	2.5
1	A	425	LEU	2.4
1	B	501	ARG	2.4
1	B	95	HIS	2.4
1	A	261	TYR	2.4
1	B	90	LYS	2.4
1	B	113	SER	2.4
1	B	148	GLN	2.3
1	B	530	VAL	2.3
1	A	100	LYS	2.3
1	B	476	SER	2.3
1	A	260	LEU	2.2
1	A	502	HIS	2.2
1	B	543	GLY	2.2
1	A	247	PRO	2.2
1	B	561	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	86	GLU	2.2
1	A	285	LEU	2.2
1	A	286	THR	2.1
1	A	418	THR	2.1
1	B	77	THR	2.1
1	A	463	ILE	2.1
1	B	246	ALA	2.1
1	A	262	ILE	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	SO4	A	904	5/5	0.91	0.15	3.11	41,42,43,43	0
3	5H	A	801	25/25	0.92	0.17	1.31	46,51,52,56	0
3	5H	B	802	25/25	0.90	0.16	0.74	47,49,51,55	0
2	SO4	B	905	5/5	0.98	0.14	0.32	32,33,33,34	0
2	SO4	A	903	5/5	0.94	0.20	0.17	48,48,49,49	0
2	SO4	B	906	5/5	0.90	0.22	-0.23	73,73,73,73	0
2	SO4	A	902	5/5	0.98	0.07	-1.11	40,40,41,42	0
2	SO4	A	901	5/5	0.98	0.08	-1.53	30,30,31,31	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.