



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 14, 2020 – 04:27 AM BST

PDB ID : 6LRD  
Title : Structure of RecJ complexed with a 5'-P-dSpacer-modified ssDNA  
Authors : Cheng, K.; Hua, Y.  
Deposited on : 2020-01-16  
Resolution : 1.90 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 : 2.14.4.dev1  
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) : 2.14.4.dev1

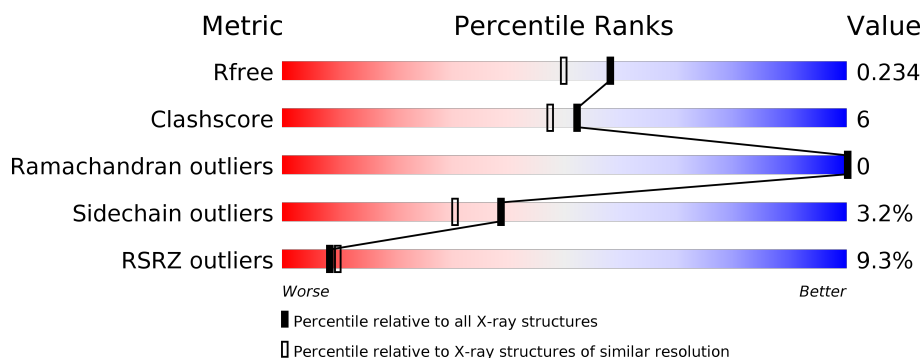
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	705	<div> <div>9%</div> <div>87%</div> <div>11%</div> <div>..</div> </div>
2	C	6	<div> <div>17%</div> <div>67%</div> <div>17%</div> <div>17%</div> </div>
3	B	4	<div> <div>50%</div> <div>100%</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	3DR	C	1	-	-	X	X
5	SO4	A	805	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5922 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 Single-stranded-DNA-specific exonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	698	Total	C	N	O	S	0	3	0
			5303	3348	967	976	12			

- Molecule 2 is a DNA chain called DNA (5'-D(P\*(3DR)P\*TP\*TP\*TP\*TP\*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	P	0	0	0
			112	55	10	41	6			

- Molecule 3 is a protein called ASP-LEU-PRO-PHE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	B	4	Total	C	N	O	0	0	0
			34	24	4	6			

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Mn	0	0
			2	2		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

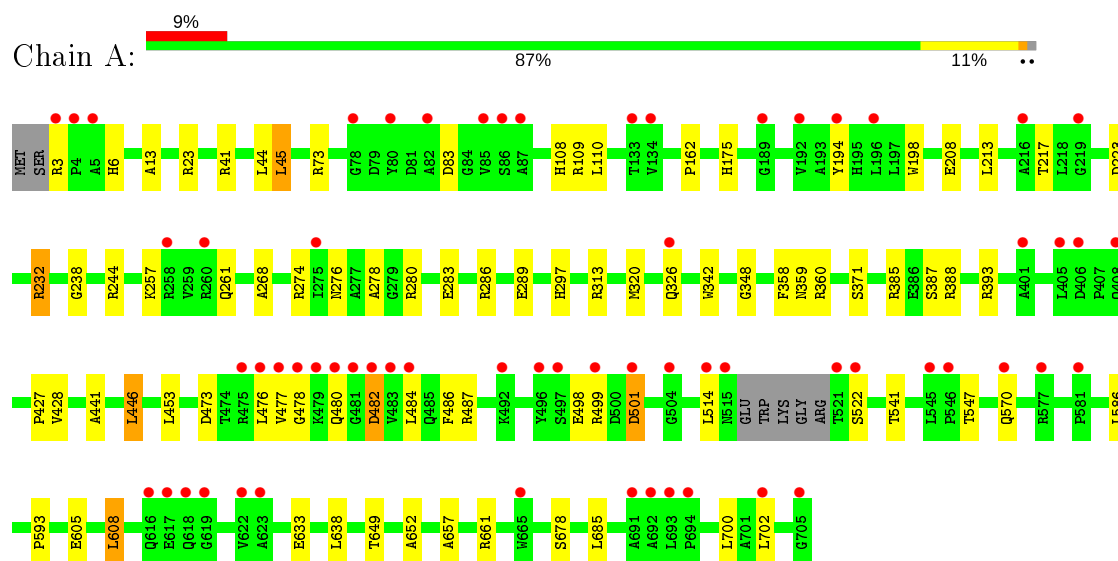
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	441	Total	O	0	0
			441	441		
6	C	8	Total	O	0	0
			8	8		
6	B	2	Total	O	0	0
			2	2		

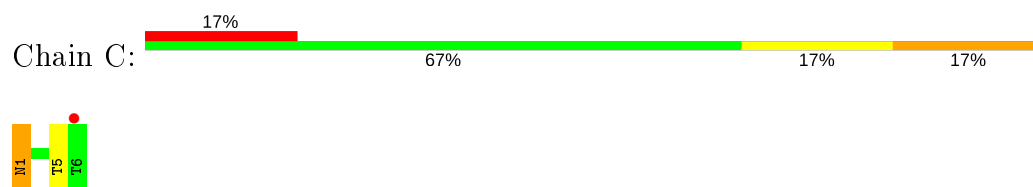
### 3 Residue-property plots

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.

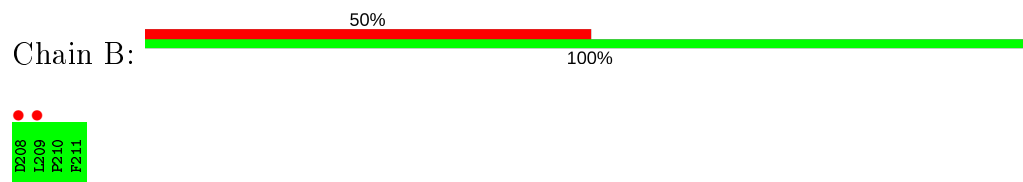
- Molecule 1: Single-stranded-DNA-specific exonuclease



- Molecule 2: DNA (5'-D(P\*(3DR)P\*TP\*TP\*TP\*TP\*T)-3')



- Molecule 3: ASP-LEU-PRO-PHE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.14Å 106.14Å 164.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.35 – 1.90 29.35 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.35-1.90) 98.3 (29.35-1.90)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.87 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, $R_{free}$	0.208 , 0.234 0.208 , 0.234	Depositor DCC
$R_{free}$ test set	4131 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.6	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 53.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5922	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MN, SO4, 3DR

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	0.38	0/5431	0.56	4/7421 (0.1%)
2	C	0.86	0/109	1.42	0/166
3	B	0.40	0/35	0.41	0/47
All	All	0.39	0/5575	0.59	4/7634 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	PRO	C-N-CA	-6.64	108.36	122.30
1	A	313	ARG	NE-CZ-NH1	6.39	123.49	120.30
1	A	313	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	A	232	ARG	NE-CZ-NH2	-5.32	117.64	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	5303	0	5284	59	0
2	C	112	0	69	12	0
3	B	34	0	30	0	0
4	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	20	0	0	5	0
6	A	441	0	0	8	0
6	B	2	0	0	0	0
6	C	8	0	0	0	0
All	All	5922	0	5383	60	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 6.

All (60) 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:348:GLY:H	2:C:1:3DR:H1'2	1.15	1.06
1:A:109:ARG:HE	2:C:1:3DR:H4'1	1.31	0.94
1:A:286:ARG:NH2	1:A:289:GLU:OE1	2.10	0.82
1:A:348:GLY:H	2:C:1:3DR:C1'	1.95	0.78
1:A:348:GLY:N	2:C:1:3DR:H1'2	1.96	0.77
1:A:482:ASP:OD1	1:A:499:ARG:NH2	2.20	0.73
1:A:109:ARG:NE	2:C:1:3DR:H4'1	2.02	0.72
1:A:73[B]:ARG:NH2	6:A:902:HOH:O	2.24	0.70
1:A:649:THR:HG23	1:A:652:ALA:H	1.58	0.68
1:A:477:VAL:HG12	1:A:478:GLY:H	1.60	0.66
1:A:326:GLN:NE2	6:A:906:HOH:O	2.30	0.64
1:A:484:LEU:HD12	1:A:498:GLU:HG2	1.81	0.62
1:A:257:LYS:HE3	1:A:274:ARG:NH2	2.17	0.59
1:A:198:TRP:NE1	1:A:208:GLU:HG2	2.18	0.58
1:A:261:GLN:NE2	6:A:916:HOH:O	2.40	0.55
1:A:232:ARG:NH2	1:A:453:LEU:O	2.39	0.55
1:A:268:ALA:HB1	2:C:5:DT:H72	1.87	0.55
1:A:605:GLU:OE2	1:A:661:ARG:NH1	2.40	0.55
1:A:441:ALA:HB1	1:A:446:LEU:HD13	1.88	0.55
1:A:388:ARG:NH2	5:A:805:SO4:S	2.76	0.54
1:A:393:ARG:NH1	6:A:909:HOH:O	2.35	0.54
1:A:73[B]:ARG:NH1	6:A:917:HOH:O	2.40	0.54
1:A:276:ASN:O	1:A:280:ARG:HG3	2.08	0.54
1:A:194:TYR:CZ	1:A:213:LEU:HD13	2.43	0.53
1:A:109:ARG:HH21	2:C:1:3DR:H4'1	1.73	0.52
1:A:13:ALA:O	1:A:661:ARG:NH2	2.39	0.52
1:A:547:THR:HB	1:A:678:SER:OG	2.10	0.52
1:A:6[B]:HIS:CE1	1:A:428:VAL:HG11	2.44	0.52
1:A:388:ARG:NH2	5:A:805:SO4:O2	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:ASN:O	1:A:427:PRO:HB2	2.10	0.51
1:A:385:ARG:NH1	5:A:805:SO4:O1	2.45	0.50
1:A:482:ASP:HB3	6:A:1016:HOH:O	2.10	0.50
1:A:476:LEU:CD1	1:A:501:ASP:HB3	2.41	0.49
1:A:608:LEU:HD13	1:A:685:LEU:HD11	1.94	0.49
1:A:320:MET:HG2	1:A:342:TRP:CD1	2.48	0.49
1:A:586:LEU:HD11	1:A:593:PRO:HD3	1.95	0.48
1:A:480:GLN:HG2	1:A:499:ARG:NH2	2.28	0.48
1:A:23:ARG:NH1	6:A:923:HOH:O	2.46	0.47
1:A:371:SER:OG	2:C:1:3DR:H2'	2.16	0.46
1:A:657:ALA:O	1:A:661:ARG:HG3	2.16	0.46
1:A:108:HIS:CE1	1:A:110:LEU:HB2	2.51	0.46
1:A:109:ARG:NH2	2:C:1:3DR:H4'1	2.30	0.45
1:A:109:ARG:HE	2:C:1:3DR:C4'	2.16	0.45
2:C:1:3DR:H3'	2:C:1:3DR:OP3	2.17	0.45
1:A:484:LEU:HD22	1:A:486:PHE:HD2	1.82	0.45
1:A:108:HIS:HE1	1:A:110:LEU:HB2	1.82	0.44
1:A:41:ARG:HH21	1:A:44:LEU:HD11	1.83	0.44
1:A:257:LYS:HA	1:A:257:LYS:HD3	1.70	0.44
1:A:6[B]:HIS:ND1	1:A:428:VAL:HG11	2.32	0.44
1:A:480:GLN:HG2	1:A:499:ARG:HH22	1.81	0.44
1:A:83:ASP:HB3	6:A:928:HOH:O	2.18	0.44
1:A:388:ARG:NH2	5:A:805:SO4:O3	2.48	0.43
1:A:297:HIS:ND1	5:A:803:SO4:O1	2.52	0.43
1:A:109:ARG:CZ	2:C:1:3DR:H4'1	2.48	0.43
1:A:217:THR:OG1	1:A:238:GLY:HA3	2.18	0.43
1:A:473:ASP:OD2	1:A:487:ARG:HD3	2.20	0.41
1:A:358:PHE:HB3	1:A:360:ARG:HD2	2.02	0.41
1:A:514:LEU:HA	1:A:514:LEU:HD23	1.85	0.41
1:A:45:LEU:HD12	1:A:45:LEU:HA	1.92	0.41
1:A:278:ALA:HB1	1:A:283:GLU:O	2.21	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	697/705 (99%)	689 (99%)	8 (1%)	0	100	100
3	B	2/4 (50%)	2 (100%)	0	0	100	100
All	All	699/709 (99%)	691 (99%)	8 (1%)	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	536/543 (99%)	519 (97%)	17 (3%)	39	30
3	B	4/4 (100%)	4 (100%)	0	100	100
All	All	540/547 (99%)	523 (97%)	17 (3%)	39	32

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	45	LEU
1	A	175	HIS
1	A	223	ASP
1	A	244	ARG
1	A	387	SER
1	A	446	LEU
1	A	482	ASP
1	A	501	ASP
1	A	522	SER
1	A	541	THR
1	A	570	GLN
1	A	608	LEU
1	A	633	GLU
1	A	638	LEU

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Mol	Chain	Res	Type
1	A	700	LEU
1	A	702	LEU

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

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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
2	3DR	C	1	2	12,12,12	0.60	0	16,17,17	2.13	6 (37%)

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
2	3DR	C	1	2	-	4/6/16/16	0/1/1/1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	3DR	OP2-P-O5'	-4.27	95.38	106.73
2	C	1	3DR	O3'-C3'-C4'	3.87	124.89	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	3DR	OP3-P-OP2	2.94	118.87	107.64
2	C	1	3DR	C1'-C2'-C3'	2.86	106.44	103.20
2	C	1	3DR	P-O5'-C5'	-2.73	110.77	118.30
2	C	1	3DR	O3'-C3'-C2'	-2.01	106.75	111.54

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	3DR	C5'-O5'-P-OP3
2	C	1	3DR	O4'-C4'-C5'-O5'
2	C	1	3DR	C5'-O5'-P-OP1
2	C	1	3DR	C5'-O5'-P-OP2

There are no ring outliers.

1 monomer is involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	3DR	11	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z  > 2$
5	SO4	A	804	-	4,4,4	0.14	0	6,6,6	0.27	0
5	SO4	A	805	-	4,4,4	0.16	0	6,6,6	0.07	0
5	SO4	A	803	-	4,4,4	0.14	0	6,6,6	0.16	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
5	SO4	A	806	-	4,4,4	0.15	0	6,6,6	0.05	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.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	805	SO4	4	0
5	A	803	SO4	1	0

## 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	698/705 (99%)	0.44	63 (9%)	9 10	25, 41, 71, 88	0
2	C	5/6 (83%)	0.29	1 (20%)	1 1	38, 39, 42, 78	0
3	B	4/4 (100%)	2.40	2 (50%)	0 0	47, 51, 55, 65	0
All	All	707/715 (98%)	0.45	66 (9%)	8 10	25, 41, 71, 88	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	692	ALA	9.4
1	A	693	LEU	7.3
1	A	521	THR	7.1
1	A	691	ALA	6.6
1	A	476	LEU	6.2
1	A	477	VAL	6.0
1	A	479	LYS	5.7
1	A	4	PRO	5.2
1	A	481	GLY	5.2
1	A	478	GLY	5.1
1	A	496	TYR	4.8
1	A	3	ARG	4.7
1	A	480	GLN	4.7
1	A	694	PRO	4.7
1	A	545	LEU	4.5
1	A	546	PRO	4.5
3	B	208	ASP	4.3
1	A	482	ASP	4.2
1	A	617	GLU	3.7
1	A	515	ASN	3.6
1	A	408	GLN	3.4
1	A	616	GLN	3.4
1	A	260	ARG	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	581	PRO	3.2
1	A	499	ARG	3.1
3	B	209	LEU	3.1
1	A	570	GLN	3.1
1	A	85	VAL	3.1
1	A	619	GLY	3.0
1	A	497	SER	3.0
1	A	492	LYS	2.9
1	A	618	GLN	2.8
1	A	192	VAL	2.8
1	A	326	GLN	2.8
2	C	6	DT	2.8
1	A	258	ARG	2.7
1	A	483	VAL	2.7
1	A	514	LEU	2.7
1	A	406	ASP	2.7
1	A	705	GLY	2.7
1	A	702	LEU	2.7
1	A	275	ILE	2.6
1	A	522	SER	2.6
1	A	623	ALA	2.6
1	A	87	ALA	2.6
1	A	189	GLY	2.5
1	A	475	ARG	2.5
1	A	82	ALA	2.4
1	A	665	TRP	2.4
1	A	405	LEU	2.4
1	A	501	ASP	2.4
1	A	216	ALA	2.3
1	A	401	ALA	2.3
1	A	133	THR	2.3
1	A	484	LEU	2.3
1	A	622	VAL	2.2
1	A	219	GLY	2.2
1	A	577	ARG	2.2
1	A	80	TYR	2.1
1	A	134	VAL	2.1
1	A	504	GLY	2.1
1	A	196	LEU	2.0
1	A	194	TYR	2.0
1	A	5	ALA	2.0
1	A	78	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	86[A]	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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(Å <sup>2</sup> )	Q<0.9
2	3DR	C	1	12/12	0.68	0.46	35,47,62,68	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides 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(Å <sup>2</sup> )	Q<0.9
5	SO4	A	803	5/5	0.91	0.27	61,63,74,79	0
5	SO4	A	806	5/5	0.91	0.12	117,119,124,129	0
5	SO4	A	805	5/5	0.94	0.10	104,108,111,111	0
5	SO4	A	804	5/5	0.97	0.09	66,67,71,72	0
4	MN	A	802	1/1	0.98	0.07	41,41,41,41	0
4	MN	A	801	1/1	1.00	0.19	37,37,37,37	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.