



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 09:10 am GMT

PDB ID : 2JLZ  
Title : DENGUE VIRUS 4 NS3 HELICASE IN COMPLEX WITH SSRNA AND ADP  
Authors : Luo, D.H.; Xu, T.; Watson, R.P.; Becker, D.S.; Sampath, A.; Jahnke, W.; Yeong, S.S.; Wang, C.H.; Lim, S.P.; Vasudevan, S.G.; Lescar, J.  
Deposited on : 2008-09-15  
Resolution : 2.20 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

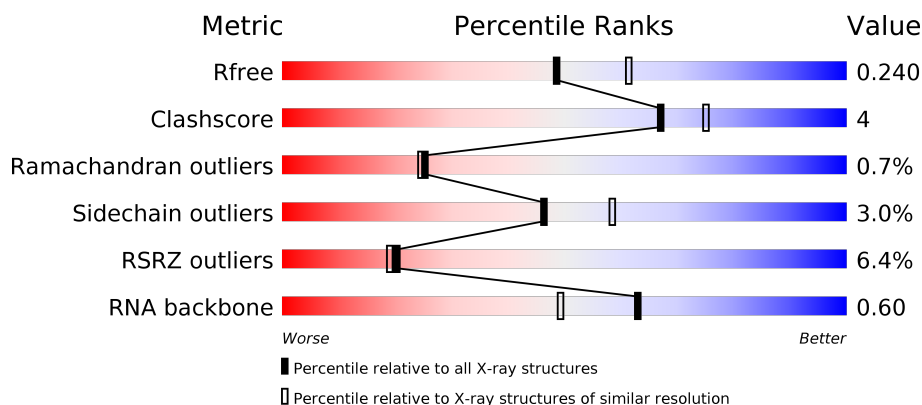
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)
RNA backbone	2435	1007 (2.74-1.66)

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	451	<div> <div>6%</div> <div>87%</div> <div>12%</div> </div>
1	B	451	<div> <div>6%</div> <div>88%</div> <div>11%</div> </div>
2	C	12	<div> <div>17%</div> <div>25%</div> <div>8%</div> <div>25%</div> <div>42%</div> </div>
2	D	12	<div> <div>17%</div> <div>25%</div> <div>25%</div> <div>8%</div> <div>42%</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
6	GOL	A	1622	-	-	X	-

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 7914 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 SERINE PROTEASE SUBUNIT NS3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	451	Total	C	N	O	S	0	0	0
			3609	2274	645	673	17			
1	B	451	Total	C	N	O	S	0	0	0
			3602	2271	642	672	17			

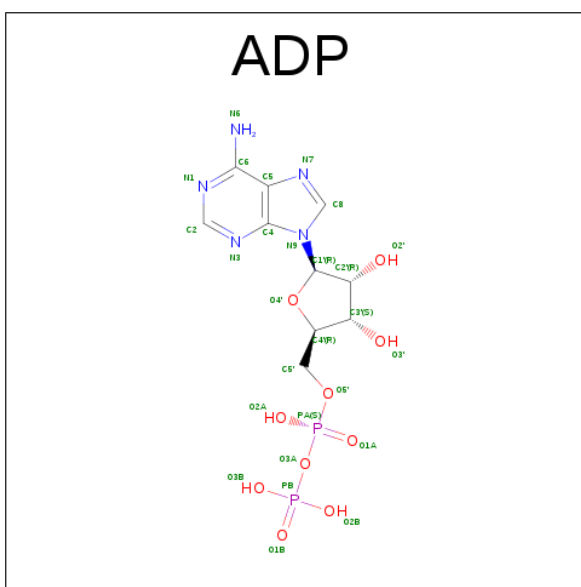
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	250	ASP	GLU	CONFLICT	UNP Q2YHF0
A	292	CYS	SER	CONFLICT	UNP Q2YHF0
A	321	SER	THR	CONFLICT	UNP Q2YHF0
A	322	ILE	THR	CONFLICT	UNP Q2YHF0
A	381	ARG	LYS	CONFLICT	UNP Q2YHF0
A	480	LYS	ARG	CONFLICT	UNP Q2YHF0
B	250	ASP	GLU	CONFLICT	UNP Q2YHF0
B	292	CYS	SER	CONFLICT	UNP Q2YHF0
B	321	SER	THR	CONFLICT	UNP Q2YHF0
B	322	ILE	THR	CONFLICT	UNP Q2YHF0
B	381	ARG	LYS	CONFLICT	UNP Q2YHF0
B	480	LYS	ARG	CONFLICT	UNP Q2YHF0

- Molecule 2 is a RNA chain called 5'-R(\*AP\*GP\*AP\*CP\*UP\*AP\*AP\*CP\*AP\*AP\*CP\*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	P	0	0	0
			138	63	25	44	6			
2	D	7	Total	C	N	O	P	0	0	0
			138	63	25	44	6			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mn	0	0
			1	1		
4	A	1	Total	Mn	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Cl	0	0
			1	1		
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

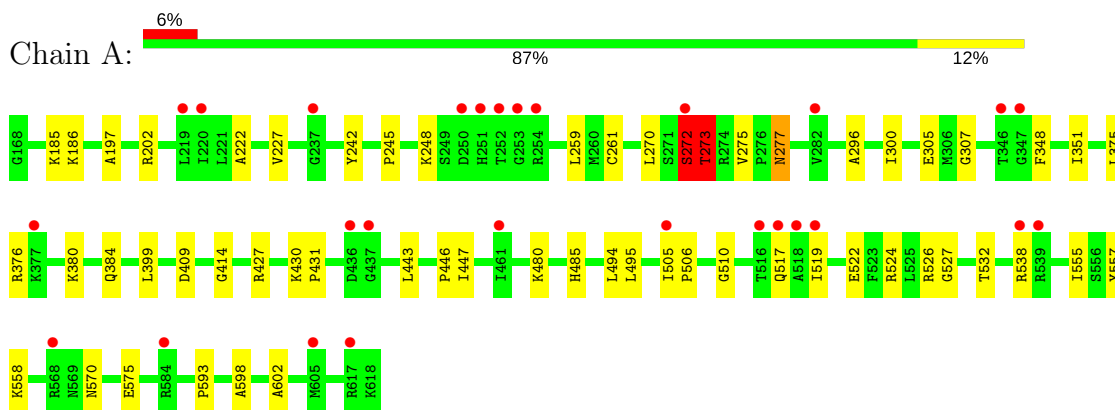
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	174	Total	O	0	0
			174	174		
7	B	166	Total	O	0	0
			166	166		
7	C	6	Total	O	0	0
			6	6		
7	D	11	Total	O	0	0
			11	11		

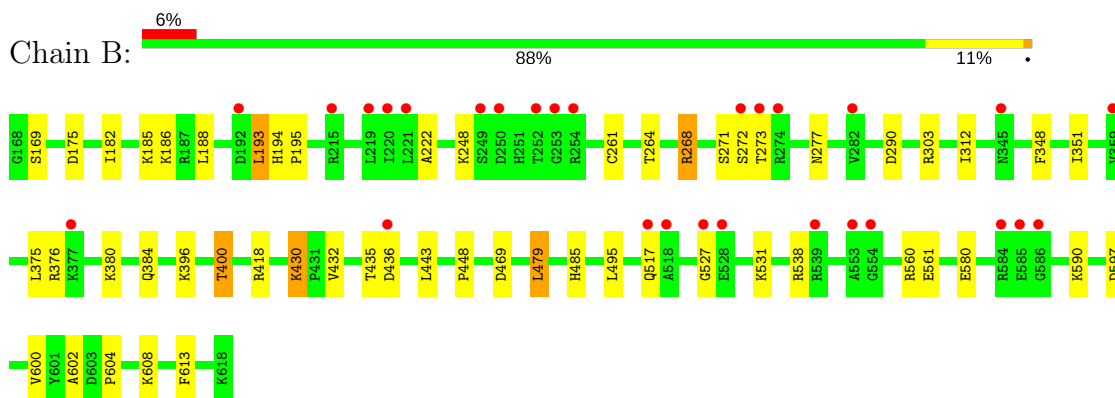
### 3 Residue-property plots [i](#)

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.

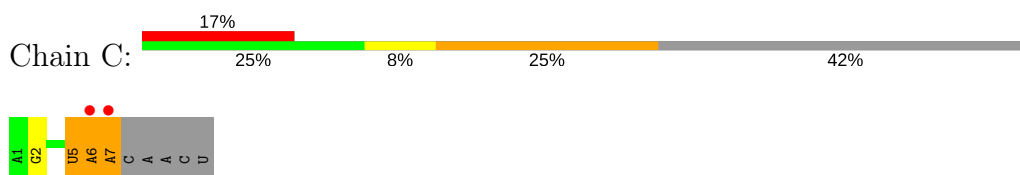
#### • Molecule 1: SERINE PROTEASE SUBUNIT NS3



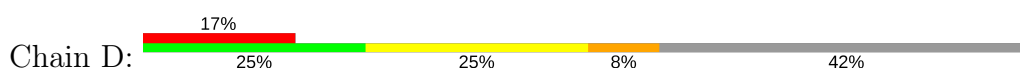
#### • Molecule 1: SERINE PROTEASE SUBUNIT NS3

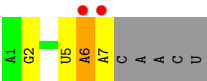


#### • Molecule 2: 5'-R(\*AP\*GP\*AP\*CP\*UP\*AP\*AP\*CP\*AP\*AP\*CP\*U)-3'



#### • Molecule 2: 5'-R(\*AP\*GP\*AP\*CP\*UP\*AP\*AP\*CP\*AP\*AP\*CP\*U)-3'







## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	133.02Å 104.79Å 72.97Å 90.00° 115.91° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 19.94 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.20) 100.0 (19.94-2.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.17 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.192 , 0.238 0.192 , 0.240	Depositor DCC
$R_{free}$ test set	2304 reflections (5.32%)	DCC
Wilson B-factor (Å <sup>2</sup> )	35.9	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7914	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, MN, ADP, CL

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	0.42	0/3690	0.59	2/4994 (0.0%)
1	B	0.43	0/3683	0.58	1/4987 (0.0%)
2	C	0.82	0/154	1.32	1/238 (0.4%)
2	D	0.79	0/154	1.27	0/238
All	All	0.44	0/7681	0.63	4/10457 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	5	U	P-O3'-C3'	7.59	128.81	119.70
1	A	272	SER	C-N-CA	6.38	137.66	121.70
1	A	273	THR	N-CA-CB	5.45	120.65	110.30
1	B	193	LEU	CA-CB-CG	5.38	127.67	115.30

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	3609	0	3600	36	0
1	B	3602	0	3589	31	0
2	C	138	0	73	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	138	0	73	2	0
3	A	27	0	12	0	0
3	B	27	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	6	0	8	5	0
6	B	6	0	8	2	0
7	A	174	0	0	1	0
7	B	166	0	0	1	0
7	C	6	0	0	0	0
7	D	11	0	0	0	0
All	All	7914	0	7375	67	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 4.

All (67) 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:272:SER:HB3	1:A:273:THR:HG23	1.34	1.06
1:A:272:SER:CB	1:A:273:THR:HG23	1.96	0.94
1:A:376:ARG:HH22	1:A:384:GLN:HE21	1.24	0.81
1:A:598:ALA:HB1	6:A:1622:GOL:H32	1.64	0.80
1:B:376:ARG:HH22	1:B:384:GLN:HE21	1.30	0.79
1:A:186:LYS:HG3	1:A:307:GLY:HA2	1.73	0.69
1:B:185:LYS:O	1:B:186:LYS:HB2	1.94	0.68
1:B:448:PRO:HB2	1:B:479:LEU:HB2	1.75	0.67
1:A:443:LEU:HB2	6:A:1622:GOL:H31	1.78	0.66
1:A:272:SER:HB3	1:A:273:THR:CG2	2.22	0.63
1:B:396:LYS:O	1:B:400:THR:HB	1.99	0.62
1:B:430:LYS:HB3	7:B:2095:HOH:O	1.99	0.62
1:A:222:ALA:O	1:A:261:CYS:HA	2.00	0.60
1:A:185:LYS:O	1:A:186:LYS:HB2	2.02	0.59
1:A:598:ALA:CB	6:A:1622:GOL:H32	2.33	0.58
1:B:375:LEU:O	1:B:380:LYS:HB2	2.04	0.57
1:A:270:LEU:HD11	1:A:494:LEU:HD22	1.86	0.56
1:B:222:ALA:O	1:B:261:CYS:HA	2.04	0.56
1:A:376:ARG:HH22	1:A:384:GLN:NE2	1.99	0.55
1:A:485:HIS:HE1	7:A:2106:HOH:O	1.90	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:ARG:NH1	1:B:268:ARG:HG2	2.21	0.55
1:A:277:ASN:C	1:A:277:ASN:HD22	2.09	0.54
2:C:6:A:H2'	2:C:7:A:H5''	1.91	0.53
1:A:245:PRO:O	1:B:248:LYS:HD3	2.10	0.51
1:A:495:LEU:HD11	1:A:506:PRO:HB2	1.93	0.51
1:B:268:ARG:HH11	1:B:268:ARG:HG2	1.74	0.51
1:B:348:PHE:HB3	1:B:351:ILE:HD12	1.94	0.49
1:A:532:THR:HG21	1:A:555:ILE:O	2.12	0.49
1:B:418:ARG:HH11	1:B:418:ARG:HG2	1.78	0.49
1:B:169:SER:HB3	1:B:175:ASP:HA	1.94	0.49
1:A:348:PHE:HB3	1:A:351:ILE:HD12	1.94	0.49
1:A:197:ALA:O	1:A:202:ARG:NH1	2.46	0.49
1:A:430:LYS:HG2	1:A:485:HIS:CE1	2.47	0.48
1:B:580:GLU:HG2	1:B:590:LYS:HG2	1.96	0.48
1:A:524:ARG:HD2	1:A:526:ARG:HH12	1.78	0.48
1:B:182:ILE:HD12	1:B:312:ILE:HD11	1.95	0.47
1:A:227:VAL:HG22	1:A:414:GLY:HA3	1.95	0.47
1:B:271:SER:O	1:B:273:THR:N	2.47	0.47
1:A:519:ILE:O	1:A:522:GLU:HG2	2.15	0.46
1:B:430:LYS:HD2	1:B:432:VAL:CG2	2.46	0.46
1:A:296:ALA:O	1:A:300:ILE:HG13	2.16	0.45
1:A:602:ALA:HB2	6:A:1622:GOL:H11	1.99	0.45
1:B:268:ARG:CG	1:B:268:ARG:HH11	2.30	0.45
1:B:538:ARG:HD3	1:B:538:ARG:HA	1.78	0.45
1:A:272:SER:HB2	1:A:273:THR:HG23	1.93	0.44
1:B:602:ALA:HB2	6:B:1622:GOL:H32	2.00	0.44
1:A:375:LEU:O	1:A:380:LYS:HB2	2.18	0.44
1:B:430:LYS:NZ	1:B:485:HIS:HD2	2.15	0.44
1:B:469:ASP:OD1	1:B:469:ASP:N	2.50	0.44
1:A:427:ARG:NH2	1:A:446:PRO:O	2.50	0.44
1:B:560:ARG:HD2	1:B:613:PHE:O	2.17	0.44
1:B:194:HIS:HD2	1:B:195:PRO:O	2.00	0.44
1:B:597:ASP:O	1:B:600:VAL:HG22	2.17	0.44
1:B:264:THR:CG2	2:D:6:A:H1'	2.48	0.43
1:A:430:LYS:HB2	1:A:447:ILE:HD11	1.99	0.43
1:B:290:ASP:OD1	2:D:2:G:N2	2.51	0.43
1:A:480:LYS:HE2	1:A:480:LYS:HB3	1.88	0.43
1:A:602:ALA:CB	6:A:1622:GOL:H11	2.49	0.42
1:B:443:LEU:H	6:B:1622:GOL:C1	2.32	0.42
1:A:570:ASN:O	1:A:593:PRO:HD2	2.19	0.42
1:B:430:LYS:HD2	1:B:432:VAL:HG22	2.02	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:303:ARG:HA	1:B:303:ARG:HD2	1.76	0.42
1:A:557:TYR:CE2	1:A:558:LYS:HE3	2.55	0.42
1:A:242:TYR:CE2	1:A:259:LEU:HD13	2.56	0.41
1:A:430:LYS:HA	1:A:431:PRO:HD3	1.91	0.40
1:B:604:PRO:O	1:B:608:LYS:HG2	2.21	0.40
1:A:409:ASP:HB2	2:C:2:G:O2'	2.21	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	449/451 (100%)	429 (96%)	16 (4%)	4 (1%)	20	18
1	B	449/451 (100%)	431 (96%)	16 (4%)	2 (0%)	38	41
All	All	898/902 (100%)	860 (96%)	32 (4%)	6 (1%)	25	24

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	THR
1	B	272	SER
1	B	527	GLY
1	A	272	SER
1	A	527	GLY
1	A	510	GLY

### 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	388/388 (100%)	378 (97%)	10 (3%)	51	64
1	B	387/388 (100%)	374 (97%)	13 (3%)	42	53
All	All	775/776 (100%)	752 (97%)	23 (3%)	46	58

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	248	LYS
1	A	272	SER
1	A	275	VAL
1	A	277	ASN
1	A	305	GLU
1	A	399	LEU
1	A	505	ILE
1	A	517	GLN
1	A	538	ARG
1	A	575	GLU
1	B	188	LEU
1	B	193	LEU
1	B	268	ARG
1	B	277	ASN
1	B	400	THR
1	B	430	LYS
1	B	435	THR
1	B	436	ASP
1	B	479	LEU
1	B	495	LEU
1	B	517	GLN
1	B	531	LYS
1	B	561	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	HIS
1	A	277	ASN
1	A	384	GLN
1	A	529	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	194	HIS
1	B	279	ASN
1	B	384	GLN
1	B	485	HIS
1	B	529	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	6/12 (50%)	3 (50%)	0
2	D	6/12 (50%)	3 (50%)	0
All	All	12/24 (50%)	6 (50%)	0

All (6) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	5	U
2	C	6	A
2	C	7	A
2	D	5	U
2	D	6	A
2	D	7	A

There are no RNA pucker outliers to report.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 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
3	ADP	A	1619	4	25,29,29	1.05	1 (4%)	24,45,45	1.61	2 (8%)
6	GOL	A	1622	-	5,5,5	0.41	0	5,5,5	0.51	0
3	ADP	B	1619	4	25,29,29	1.07	2 (8%)	24,45,45	1.60	3 (12%)
6	GOL	B	1622	-	5,5,5	0.32	0	5,5,5	0.24	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	ADP	A	1619	4	-	0/12/32/32	0/3/3/3
6	GOL	A	1622	-	-	0/4/4/4	0/0/0/0
3	ADP	B	1619	4	-	0/12/32/32	0/3/3/3
6	GOL	B	1622	-	-	0/4/4/4	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1619	ADP	C2-N3	2.02	1.35	1.32
3	A	1619	ADP	C5-C4	3.27	1.47	1.40
3	B	1619	ADP	C5-C4	3.31	1.48	1.40

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1619	ADP	N3-C2-N1	-6.30	123.38	128.86
3	B	1619	ADP	N3-C2-N1	-6.15	123.50	128.86
3	B	1619	ADP	C4-C5-N7	-2.35	107.14	109.41
3	A	1619	ADP	C4-C5-N7	-2.31	107.17	109.41
3	B	1619	ADP	O3B-PB-O2B	2.14	116.26	107.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.



2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1622	GOL	5	0
6	B	1622	GOL	2	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	451/451 (100%)	0.23	27 (5%)	23 22	26, 34, 44, 54	1 (0%)
1	B	451/451 (100%)	0.25	28 (6%)	21 20	26, 34, 44, 54	1 (0%)
2	C	7/12 (58%)	0.68	2 (28%)	1 0	28, 31, 46, 47	0
2	D	7/12 (58%)	0.58	2 (28%)	1 0	28, 30, 56, 59	0
All	All	916/926 (98%)	0.25	59 (6%)	20 19	26, 34, 44, 59	2 (0%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	274	ARG	5.2
1	B	585	GLU	5.2
1	B	584	ARG	4.6
1	B	272	SER	4.6
1	A	272	SER	4.5
1	A	519	ILE	4.5
1	A	517	GLN	4.2
1	B	517	GLN	4.2
1	B	586	GLY	4.1
1	B	252	THR	4.0
1	A	518	ALA	4.0
2	D	7	A	3.9
1	B	436	ASP	3.8
2	C	7	A	3.8
1	A	346	THR	3.7
1	A	254	ARG	3.6
1	B	219	LEU	3.5
1	A	252	THR	3.4
2	D	6	A	3.3
1	A	584	ARG	3.3
1	B	254	ARG	3.3

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	436	ASP	3.1
1	A	219	LEU	3.0
1	B	192	ASP	3.0
2	C	6	A	3.0
1	A	237	GLY	3.0
1	B	528	GLU	2.9
1	B	249	SER	2.9
1	A	220	ILE	2.9
1	B	539	ARG	2.9
1	B	553	ALA	2.9
1	A	253	GLY	2.8
1	B	250	ASP	2.8
1	A	516	THR	2.8
1	B	345	ASN	2.7
1	B	253	GLY	2.7
1	B	377	LYS	2.6
1	B	518	ALA	2.6
1	A	251	HIS	2.6
1	B	273	THR	2.6
1	A	538	ARG	2.6
1	A	461	ILE	2.6
1	B	282	VAL	2.5
1	A	437	GLY	2.5
1	B	220	ILE	2.4
1	B	554	GLY	2.3
1	A	282	VAL	2.3
1	A	377	LYS	2.2
1	B	527	GLY	2.2
1	A	617	ARG	2.2
1	A	250	ASP	2.2
1	A	539	ARG	2.1
1	A	568	ARG	2.1
1	B	359	VAL	2.1
1	B	221	LEU	2.1
1	A	347	GLY	2.1
1	A	505	ILE	2.0
1	A	605	MET	2.0
1	B	215	ARG	2.0

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

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( $\text{\AA}^2$ )	Q<0.9
3	ADP	B	1619	27/27	0.95	0.12	-0.38	25,37,41,41	0
6	GOL	A	1622	6/6	0.94	0.11	-0.60	41,43,44,44	0
3	ADP	A	1619	27/27	0.95	0.12	-0.79	26,34,39,39	0
6	GOL	B	1622	6/6	0.93	0.12	-1.24	41,41,41,42	0
5	CL	B	1621	1/1	0.97	0.09	-1.80	32,32,32,32	0
5	CL	A	1621	1/1	1.00	0.02	-3.33	27,27,27,27	0
4	MN	A	1620	1/1	0.99	0.01	-5.04	27,27,27,27	0
4	MN	B	1620	1/1	0.99	0.02	-	25,25,25,25	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.