



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:45 AM GMT

PDB ID : 2E9Z  
Title : Foot-and-mouth disease virus RNA-polymerase in complex with a template-primer RNA, ATP and UTP  
Authors : Ferrer-Orta, C.; Arias, A.; Perez-Luque, R.; Escarmis, C.; Domingo, E.; Verdaguier, N.  
Deposited on : 2007-01-29  
Resolution : 3.00 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



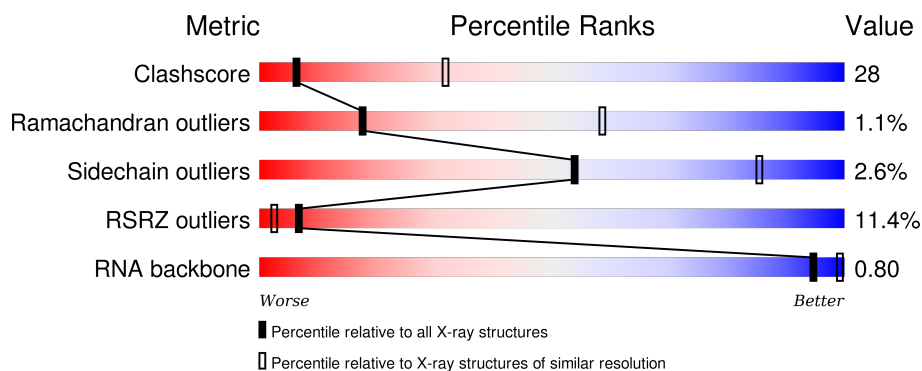
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)
RNA backbone	2183	1036 (3.40-2.60)

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. 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	B	9	<div> <div>100%</div> <div>11% 89%</div> </div>
2	C	7	<div> <div>86%</div> <div>29% 71%</div> </div>
3	A	476	<div> <div>9%</div> <div>51% 46%</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
5	UTP	A	993	-	-	-	X
6	PPV	A	665	-	-	-	X



## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4127 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 RNA chain called 5'-R(\*CP\*AP\*UP\*GP\*GP\*GP\*CP\*CP\*C)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	9	Total	C	N	O	P	0	0	0
			188	85	34	61	8			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	7	Total	C	N	O	P	0	0	0
			148	67	29	46	6			

- Molecule 3 is a protein called RNA-dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	476	Total	C	N	O	S	0	0	0
			3731	2369	652	689	21			

There are 6 discrepancies between the modelled and reference sequences:

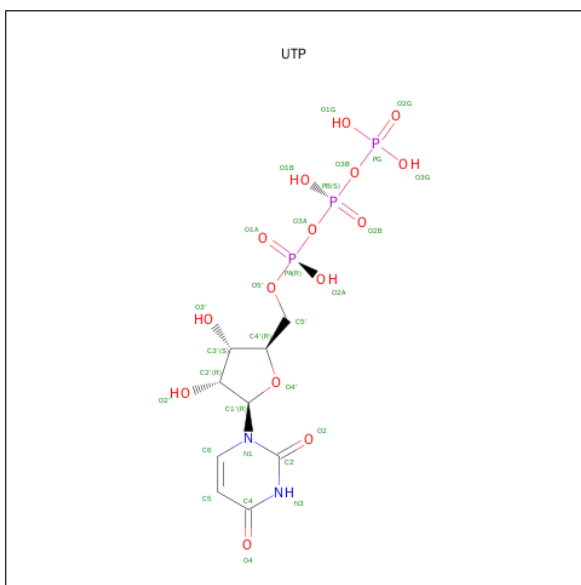
Chain	Residue	Modelled	Actual	Comment	Reference
A	471	ALA	-	CLONING ARTIFACT	UNP Q0QEE1
A	472	ALA	-	CLONING ARTIFACT	UNP Q0QEE1
A	473	LEU	-	CLONING ARTIFACT	UNP Q0QEE1
A	474	GLU	-	CLONING ARTIFACT	UNP Q0QEE1
A	475	HIS	-	CLONING ARTIFACT	UNP Q0QEE1
A	476	HIS	-	CLONING ARTIFACT	UNP Q0QEE1

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

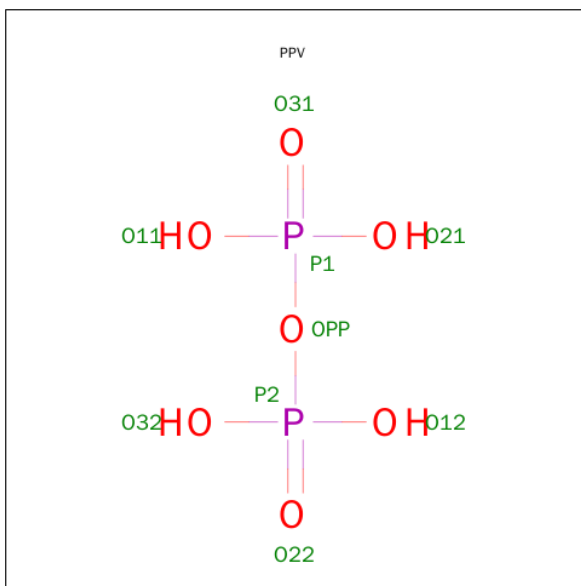
- Molecule 5 is URIDINE 5'-TRIPHOSPHATE (three-letter code: UTP) (formula: C<sub>9</sub>H<sub>15</sub>N<sub>2</sub>O<sub>15</sub>P<sub>3</sub>).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			29	9	2	15	3		

- Molecule 6 is PYROPHOSPHATE (three-letter code: PPV) (formula:  $\text{H}_4\text{O}_7\text{P}_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			9	7	2		

- Molecule 7 is water.



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	15	Total 15	O 15	0	0
7	B	2	Total 2	O 2	0	0
7	C	3	Total 3	O 3	0	0



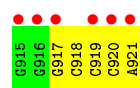
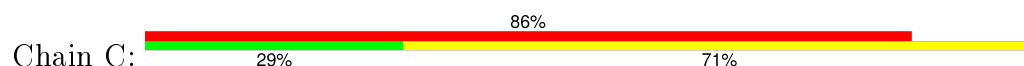
### 3 Residue-property plots

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.

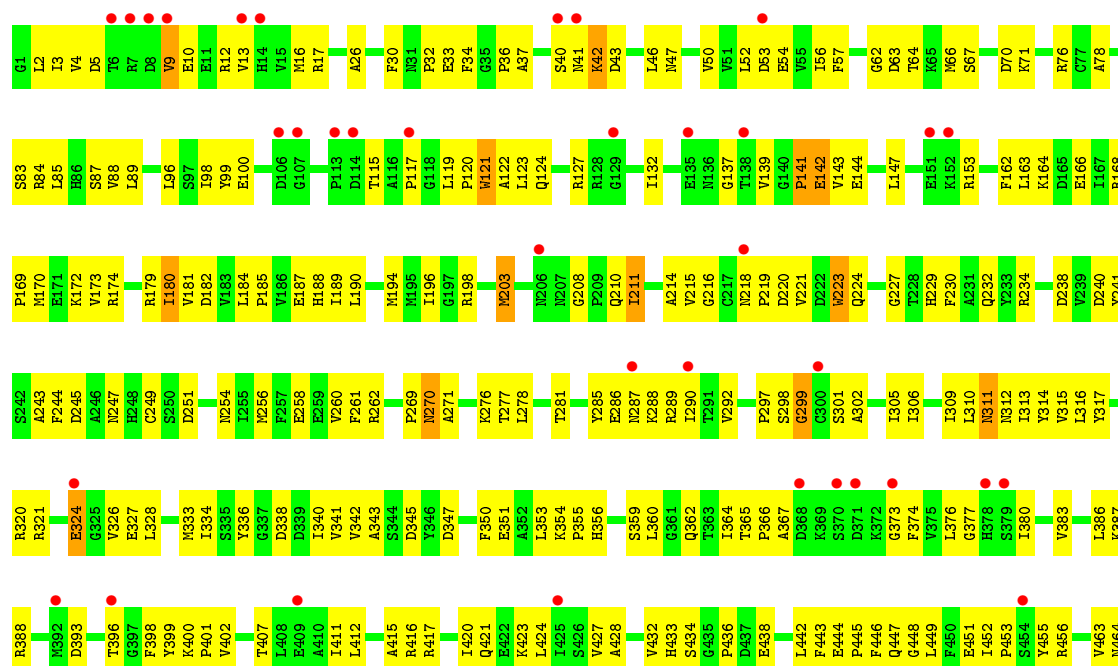
- Molecule 1: 5'-R(\*CP\*AP\*UP\*GP\*GP\*GP\*CP\*CP\*C)-3'



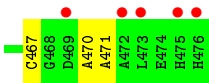
- Molecule 2: 5'-R(\*GP\*GP\*GP\*CP\*CP\*CP\*A)-3'



- Molecule 3: RNA-dependent RNA polymerase









## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.11Å 94.11Å 99.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 3.00 29.42 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.00) 100.0 (29.42-3.00)	Depositor EDS
$R_{merge}$	0.80	Depositor
$R_{sym}$	0.56	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.32 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.227 , 0.290 0.350 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	68.7	Xtriage
Anisotropy	0.243	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 57.8	EDS
Estimated twinning fraction	0.037 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 10549 reflections	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	4127	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UTP, MG, PPV

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	B	0.15	0/209	0.61	0/324
2	C	0.15	0/165	0.61	0/256
3	A	0.25	0/3820	0.43	0/5174
All	All	0.24	0/4194	0.45	0/5754

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

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	B	188	0	100	13	3
2	C	148	0	79	12	0
3	A	3731	0	3646	214	14
4	A	2	0	0	0	0
5	A	29	0	11	1	0
6	A	9	0	0	0	0
7	A	15	0	0	2	0
7	B	2	0	0	0	0
7	C	3	0	0	0	0
All	All	4127	0	3836	221	14



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 28.

All (221) 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)
3:A:388:ARG:HD3	3:A:401:PRO:HB3	1.45	0.97
3:A:189:ILE:HG23	3:A:301:SER:HB2	1.46	0.94
3:A:12:ARG:HG2	3:A:287:ASN:HB3	1.48	0.92
3:A:89:LEU:HD11	3:A:203:MET:HE3	1.52	0.90
3:A:180:ILE:H	3:A:180:ILE:HD13	1.34	0.90
3:A:230:PHE:HB2	3:A:380:ILE:HD12	1.61	0.83
3:A:172:LYS:HA	3:A:172:LYS:HE2	1.61	0.82
3:A:78:ALA:HA	3:A:313:ILE:HD12	1.62	0.82
2:C:920:C:H5''	3:A:387:LYS:HG3	1.64	0.79
3:A:37:ALA:HA	3:A:173:VAL:HG13	1.65	0.79
3:A:443:PHE:HB3	3:A:452:ILE:HD13	1.65	0.77
3:A:153:ARG:HH12	3:A:270:ASN:HA	1.52	0.75
3:A:98:ILE:HD11	3:A:139:VAL:HG13	1.69	0.72
3:A:281:THR:HG21	3:A:297:PRO:HG3	1.73	0.70
3:A:290:ILE:H	3:A:290:ILE:HD12	1.58	0.69
1:B:906:G:H4'	3:A:216:GLY:HA2	1.75	0.69
3:A:350:PHE:HA	3:A:353:LEU:HD12	1.75	0.69
3:A:354:LYS:HB2	3:A:355:PRO:HD3	1.73	0.68
3:A:43:ASP:HB3	3:A:46:LEU:HG	1.74	0.68
3:A:96:LEU:HD11	3:A:198:ARG:N	2.09	0.67
3:A:96:LEU:HD11	3:A:198:ARG:H	1.60	0.66
1:B:902:C:H5'	3:A:17:ARG:HH22	1.58	0.66
3:A:314:TYR:CD1	3:A:360:LEU:HD13	2.31	0.66
3:A:163:LEU:HD23	3:A:180:ILE:HG22	1.77	0.66
3:A:234:ARG:HB3	3:A:234:ARG:NH1	2.11	0.66
3:A:185:PRO:HB2	3:A:187:GLU:OE1	1.97	0.65
3:A:85:LEU:HD11	3:A:203:MET:HE1	1.79	0.63
3:A:9:VAL:HG12	3:A:10:GLU:H	1.64	0.63
3:A:444:GLU:HB3	3:A:445:PRO:HD3	1.81	0.63
1:B:903:A:H5'	3:A:115:THR:HB	1.79	0.63
3:A:436:PRO:HG3	3:A:455:TYR:CE2	2.34	0.62
3:A:256:MET:HG3	3:A:310:LEU:HD23	1.82	0.62
3:A:290:ILE:HD12	3:A:290:ILE:N	2.14	0.61
3:A:52:LEU:O	3:A:56:ILE:HD13	2.00	0.61
3:A:227:GLY:HA2	3:A:380:ILE:HD13	1.82	0.61
3:A:12:ARG:HB3	3:A:12:ARG:NH1	2.15	0.61
3:A:9:VAL:HG12	3:A:10:GLU:N	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:84:ARG:HG2	3:A:84:ARG:HH11	1.67	0.59
3:A:276:LYS:C	3:A:278:LEU:H	2.07	0.58
3:A:85:LEU:HD11	3:A:203:MET:CE	2.34	0.58
3:A:208:GLY:N	3:A:211:ILE:HD11	2.18	0.58
3:A:351:GLU:HG2	3:A:374:PHE:HB2	1.86	0.57
3:A:211:ILE:H	3:A:211:ILE:HD13	1.70	0.57
3:A:463:VAL:HG12	3:A:471:ALA:HB2	1.86	0.57
3:A:123:LEU:HD12	3:A:124:GLN:HG3	1.87	0.57
3:A:305:ILE:O	3:A:309:ILE:HG13	2.05	0.57
3:A:144:GLU:HA	3:A:147:LEU:HD23	1.85	0.57
3:A:229:HIS:O	3:A:232:GLN:HG2	2.04	0.57
3:A:321:ARG:HH11	3:A:356:HIS:HA	1.69	0.57
3:A:316:LEU:HD22	3:A:328:LEU:HD21	1.87	0.57
3:A:420:ILE:HG22	3:A:424:LEU:HD11	1.87	0.56
1:B:903:A:N3	3:A:299:GLY:HA2	2.20	0.56
3:A:43:ASP:H	3:A:46:LEU:HD12	1.69	0.56
3:A:238:ASP:HB2	3:A:383:VAL:HG12	1.88	0.56
1:B:902:C:N3	3:A:164:LYS:HE2	2.21	0.56
3:A:432:VAL:HG13	3:A:433:HIS:CD2	2.41	0.55
3:A:141:PRO:HG2	3:A:142:GLU:H	1.71	0.55
3:A:71:LYS:HE2	3:A:251:ASP:OD2	2.06	0.55
3:A:184:LEU:HD23	3:A:188:HIS:CD2	2.42	0.55
3:A:376:LEU:HD12	3:A:376:LEU:N	2.21	0.55
3:A:214:ALA:HB2	3:A:334:ILE:HG12	1.89	0.54
3:A:180:ILE:N	3:A:180:ILE:HD13	2.13	0.54
3:A:3:ILE:HD13	3:A:292:VAL:HG22	1.89	0.54
3:A:2:LEU:HD13	3:A:62:GLY:HA2	1.90	0.53
3:A:56:ILE:HG22	3:A:57:PHE:CD1	2.44	0.53
3:A:211:ILE:N	3:A:211:ILE:HD13	2.23	0.53
3:A:211:ILE:CD1	3:A:211:ILE:H	2.21	0.53
3:A:36:PRO:HA	3:A:166:GLU:O	2.09	0.53
3:A:119:LEU:HD23	3:A:122:ALA:HB3	1.90	0.53
3:A:64:THR:O	3:A:249:CYS:HB2	2.08	0.53
3:A:184:LEU:HB3	3:A:185:PRO:HD2	1.91	0.52
3:A:219:PRO:O	3:A:223:TRP:HB2	2.09	0.52
3:A:311:ASN:O	3:A:315:VAL:HG23	2.09	0.52
3:A:240:ASP:HB2	3:A:365:THR:HG23	1.90	0.52
3:A:456:ARG:HH11	3:A:456:ARG:HG3	1.75	0.52
3:A:13:VAL:O	3:A:286:GLU:HG2	2.09	0.52
3:A:99:TYR:CD1	3:A:137:GLY:HA3	2.45	0.52
3:A:340:ILE:HG12	3:A:341:VAL:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:288:LYS:N	3:A:288:LYS:HD2	2.25	0.52
3:A:2:LEU:HB2	3:A:63:ASP:N	2.26	0.51
3:A:121:TRP:CH2	3:A:142:GLU:HB3	2.45	0.51
3:A:141:PRO:HG2	3:A:142:GLU:OE1	2.11	0.51
3:A:88:VAL:HG21	3:A:210:GLN:HE21	1.76	0.51
3:A:386:LEU:O	3:A:388:ARG:HG3	2.09	0.51
3:A:153:ARG:HH11	3:A:153:ARG:HG2	1.75	0.51
3:A:290:ILE:CD1	3:A:290:ILE:H	2.24	0.51
3:A:350:PHE:HA	3:A:353:LEU:CD1	2.41	0.51
2:C:918:C:H2'	2:C:919:C:C6	2.46	0.50
1:B:908:C:H2'	1:B:909:C:C6	2.45	0.50
1:B:903:A:H62	3:A:164:LYS:NZ	2.09	0.50
3:A:420:ILE:O	3:A:424:LEU:HG	2.12	0.50
3:A:84:ARG:HG2	3:A:84:ARG:NH1	2.26	0.50
3:A:190:LEU:O	3:A:194:MET:HG3	2.11	0.50
3:A:99:TYR:HD1	3:A:137:GLY:HA3	1.77	0.49
3:A:132:ILE:HD11	3:A:143:VAL:HG11	1.95	0.49
3:A:447:GLN:NE2	3:A:447:GLN:HA	2.27	0.49
3:A:117:PRO:HB3	3:A:127:ARG:HA	1.95	0.49
3:A:215:VAL:HA	3:A:336:TYR:CE1	2.47	0.49
1:B:906:G:H2'	1:B:907:G:C8	2.48	0.49
3:A:467:CYS:HB3	3:A:470:ALA:HB2	1.94	0.49
2:C:918:C:O3'	3:A:423:LYS:HE2	2.13	0.49
3:A:40:SER:C	3:A:52:LEU:HD22	2.33	0.49
3:A:302:ALA:O	3:A:306:ILE:HG12	2.12	0.49
3:A:66:MET:O	3:A:71:LYS:HE3	2.12	0.48
2:C:918:C:H5''	3:A:423:LYS:HE3	1.94	0.48
3:A:184:LEU:N	3:A:184:LEU:HD12	2.28	0.48
3:A:223:TRP:CG	3:A:401:PRO:HG3	2.48	0.48
3:A:132:ILE:CG1	3:A:143:VAL:HG21	2.43	0.48
3:A:434:SER:O	3:A:438:GLU:HB2	2.14	0.48
3:A:227:GLY:HA2	3:A:380:ILE:CD1	2.43	0.48
2:C:921:A:O3'	3:A:338:ASP:OD1	2.32	0.48
3:A:449:LEU:HD12	3:A:449:LEU:N	2.29	0.48
3:A:9:VAL:CG1	3:A:10:GLU:H	2.25	0.47
3:A:40:SER:OG	3:A:42:LYS:HD2	2.14	0.47
3:A:98:ILE:HD11	3:A:139:VAL:HG22	1.96	0.47
3:A:96:LEU:N	3:A:96:LEU:HD12	2.28	0.47
3:A:245:ASP:HB2	5:A:993:UTP:O2'	2.14	0.47
3:A:53:ASP:OD1	3:A:285:TYR:HE2	1.98	0.47
3:A:386:LEU:HD23	7:A:1034:HOH:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:920:C:H5''	3:A:387:LYS:CG	2.40	0.47
3:A:180:ILE:H	3:A:180:ILE:CD1	2.16	0.47
3:A:185:PRO:HG2	3:A:188:HIS:HB2	1.95	0.47
3:A:407:THR:O	3:A:411:ILE:HG13	2.15	0.47
3:A:342:VAL:HG12	3:A:343:ALA:N	2.30	0.47
3:A:47:ASN:O	3:A:50:VAL:HG12	2.15	0.47
3:A:324:GLU:OE1	3:A:324:GLU:N	2.43	0.47
3:A:386:LEU:HA	7:A:1034:HOH:O	2.15	0.47
3:A:234:ARG:HB2	3:A:345:ASP:HA	1.97	0.47
3:A:366:PRO:HD3	3:A:374:PHE:CE1	2.50	0.47
3:A:320:ARG:HG2	3:A:326:VAL:HB	1.98	0.46
3:A:447:GLN:CD	3:A:452:ILE:HD12	2.36	0.46
3:A:354:LYS:HG2	3:A:364:ILE:HG13	1.98	0.46
3:A:33:GLU:C	3:A:170:MET:HG2	2.36	0.46
2:C:918:C:OP1	3:A:416:ARG:HG2	2.16	0.46
3:A:309:ILE:O	3:A:313:ILE:HG12	2.15	0.46
3:A:88:VAL:CG2	3:A:210:GLN:HE21	2.29	0.46
3:A:448:GLY:C	3:A:449:LEU:HD12	2.36	0.46
3:A:4:VAL:HG23	3:A:5:ASP:N	2.32	0.46
3:A:321:ARG:NH1	3:A:359:SER:HB3	2.31	0.45
3:A:16:MET:HA	3:A:163:LEU:HD12	1.98	0.45
3:A:351:GLU:OE1	3:A:373:GLY:HA2	2.16	0.45
3:A:415:ALA:HB3	3:A:420:ILE:HD13	1.97	0.45
3:A:241:TYR:HB3	3:A:244:PHE:HB2	1.97	0.45
3:A:244:PHE:HA	3:A:362:GLN:HE22	1.81	0.45
3:A:132:ILE:HD13	3:A:139:VAL:HG12	1.99	0.45
1:B:903:A:C2	3:A:299:GLY:HA2	2.52	0.45
2:C:918:C:H5''	3:A:423:LYS:CE	2.46	0.45
3:A:256:MET:O	3:A:260:VAL:HG23	2.16	0.45
3:A:401:PRO:HD2	3:A:433:HIS:CE1	2.52	0.45
3:A:432:VAL:O	3:A:455:TYR:HE1	1.99	0.45
1:B:903:A:H1'	3:A:181:VAL:HG11	1.97	0.45
3:A:123:LEU:HD12	3:A:124:GLN:N	2.32	0.45
3:A:241:TYR:CB	3:A:244:PHE:HB2	2.46	0.45
3:A:56:ILE:CG2	3:A:180:ILE:HG21	2.47	0.44
3:A:185:PRO:HB2	3:A:187:GLU:CD	2.37	0.44
3:A:182:ASP:HB2	3:A:298:SER:N	2.32	0.44
3:A:26:ALA:HB1	3:A:30:PHE:CE2	2.53	0.44
3:A:396:THR:HG1	3:A:398:PHE:HD2	1.62	0.44
2:C:917:G:O2'	2:C:918:C:H5'	2.17	0.44
3:A:120:PRO:O	3:A:123:LEU:HG	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:67:SER:O	3:A:71:LYS:HG3	2.17	0.44
3:A:168:ARG:NH1	3:A:179:ARG:HG3	2.33	0.44
3:A:421:GLN:HA	3:A:424:LEU:HD12	2.00	0.44
3:A:218:ASN:HD22	3:A:221:VAL:HG22	1.83	0.44
3:A:400:LYS:O	3:A:402:VAL:HG23	2.17	0.44
3:A:256:MET:HG3	3:A:310:LEU:CD2	2.47	0.44
3:A:132:ILE:HG13	3:A:143:VAL:HG21	2.00	0.43
3:A:47:ASN:OD1	3:A:174:ARG:HG2	2.18	0.43
3:A:412:LEU:HD21	3:A:427:VAL:HG11	2.00	0.43
3:A:123:LEU:CD1	3:A:124:GLN:HG3	2.48	0.43
3:A:412:LEU:O	3:A:446:PHE:HZ	2.02	0.43
3:A:26:ALA:HB2	3:A:446:PHE:CE1	2.53	0.43
3:A:289:ARG:HH11	3:A:289:ARG:HG2	1.84	0.43
2:C:920:C:O2'	3:A:386:LEU:HD22	2.19	0.43
3:A:456:ARG:HG3	3:A:456:ARG:NH1	2.33	0.43
3:A:312:ASN:HA	3:A:333:MET:HE1	2.00	0.43
3:A:143:VAL:HG12	3:A:147:LEU:HD21	2.00	0.43
2:C:919:C:H2'	2:C:920:C:C6	2.54	0.42
3:A:243:ALA:HB3	3:A:247:ASN:ND2	2.34	0.42
3:A:417:ARG:HH21	3:A:417:ARG:HG3	1.85	0.42
3:A:447:GLN:HE21	3:A:447:GLN:HA	1.85	0.42
3:A:321:ARG:HD3	3:A:356:HIS:CD2	2.55	0.42
1:B:905:G:N2	2:C:920:C:O2	2.52	0.42
3:A:16:MET:SD	3:A:41:ASN:ND2	2.92	0.42
3:A:276:LYS:C	3:A:278:LEU:N	2.71	0.42
3:A:42:LYS:HD2	3:A:42:LYS:H	1.83	0.42
3:A:162:PHE:HB2	3:A:181:VAL:HB	2.02	0.42
3:A:215:VAL:HG22	3:A:336:TYR:CD1	2.55	0.42
3:A:393:ASP:HB2	3:A:400:LYS:HD3	2.01	0.42
3:A:56:ILE:HG23	3:A:180:ILE:HG21	2.01	0.42
3:A:3:ILE:CD1	3:A:292:VAL:HG22	2.50	0.42
3:A:240:ASP:OD1	3:A:367:ALA:HB2	2.20	0.42
3:A:52:LEU:C	3:A:54:GLU:H	2.23	0.41
3:A:340:ILE:CG1	3:A:341:VAL:N	2.82	0.41
3:A:234:ARG:HH11	3:A:234:ARG:HB3	1.84	0.41
3:A:240:ASP:HB2	3:A:365:THR:O	2.20	0.41
3:A:288:LYS:H	3:A:288:LYS:HD2	1.84	0.41
3:A:254:ASN:O	3:A:258:GLU:HG3	2.21	0.41
3:A:190:LEU:C	3:A:190:LEU:HD13	2.41	0.41
3:A:224:GLN:HA	3:A:399:TYR:HB2	2.02	0.41
3:A:278:LEU:O	3:A:281:THR:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:906:G:H2'	1:B:907:G:O4'	2.19	0.41
3:A:32:PRO:C	3:A:34:PHE:H	2.23	0.41
3:A:142:GLU:OE1	3:A:142:GLU:N	2.54	0.41
3:A:243:ALA:HB3	3:A:247:ASN:HD21	1.85	0.41
3:A:70:ASP:HB3	3:A:317:TYR:OH	2.21	0.41
3:A:12:ARG:HH11	3:A:12:ARG:CB	2.33	0.41
3:A:143:VAL:HG12	3:A:147:LEU:CD2	2.51	0.41
3:A:3:ILE:HD12	3:A:290:ILE:CG2	2.51	0.41
3:A:119:LEU:CD2	3:A:122:ALA:HB3	2.50	0.41
3:A:172:LYS:CA	3:A:172:LYS:HE2	2.40	0.41
3:A:208:GLY:H	3:A:211:ILE:HD11	1.85	0.41
3:A:182:ASP:HB2	3:A:298:SER:H	1.86	0.40
3:A:196:ILE:HG21	3:A:261:PHE:CD2	2.56	0.40
3:A:428:ALA:HA	3:A:443:PHE:CZ	2.55	0.40
1:B:903:A:N6	3:A:164:LYS:HZ2	2.20	0.40
3:A:438:GLU:O	3:A:442:LEU:HG	2.20	0.40
3:A:234:ARG:HH11	3:A:234:ARG:CB	2.34	0.40
3:A:347:ASP:HB3	3:A:376:LEU:CD2	2.51	0.40
3:A:269:PRO:C	3:A:271:ALA:H	2.25	0.40
3:A:34:PHE:CE2	3:A:169:PRO:HG3	2.57	0.40

All (14) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:910:C:OP2	3:A:327:GLU:OE1[6_665]	1.56	0.64
1:B:910:C:OP2	3:A:327:GLU:CD[6_665]	1.69	0.51
3:A:83:SER:OG	3:A:453:PRO:CA[6_655]	1.72	0.48
3:A:87:SER:OG	3:A:451:GLU:CA[6_655]	1.75	0.45
3:A:377:GLY:O	3:A:417:ARG:NH1[5_665]	1.76	0.44
3:A:100:GLU:CD	3:A:100:GLU:CD[4_556]	1.77	0.43
3:A:100:GLU:OE1	3:A:100:GLU:OE1[4_556]	2.00	0.20
1:B:910:C:C5'	3:A:327:GLU:CG[6_665]	2.02	0.18
3:A:76:ARG:NH2	3:A:464:ASN:ND2[6_655]	2.06	0.14
3:A:100:GLU:CG	3:A:100:GLU:OE2[4_556]	2.10	0.10
3:A:100:GLU:CD	3:A:100:GLU:OE2[4_556]	2.13	0.07
3:A:84:ARG:CD	3:A:451:GLU:OE1[6_655]	2.17	0.03
3:A:100:GLU:CD	3:A:100:GLU:OE1[4_556]	2.17	0.03
3:A:262:ARG:CZ	3:A:456:ARG:CD[6_655]	2.18	0.02



## 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
3	A	474/476 (100%)	410 (86%)	59 (12%)	5 (1%)	17 58

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	9	VAL
3	A	299	GLY
3	A	141	PRO
3	A	270	ASN
3	A	277	THR

### 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
3	A	392/399 (98%)	382 (97%)	10 (3%)	54 85

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

Mol	Chain	Res	Type
3	A	42	LYS
3	A	121	TRP
3	A	142	GLU
3	A	180	ILE
3	A	203	MET
3	A	211	ILE

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Mol	Chain	Res	Type
3	A	220	ASP
3	A	223	TRP
3	A	311	ASN
3	A	324	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	31	ASN
3	A	124	GLN
3	A	160	GLN
3	A	188	HIS
3	A	210	GLN
3	A	247	ASN
3	A	311	ASN
3	A	356	HIS
3	A	362	GLN
3	A	447	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	8/9 (88%)	0	0
2	C	6/7 (85%)	0	0
All	All	14/16 (87%)	0	0

There are no RNA backbone outliers to report.

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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$
6	PPV	A	665	-	6,8,8	1.68	1 (16%)	11,13,13	1.03	1 (9%)
5	UTP	A	993	4	20,30,30	2.03	4 (20%)	30,47,47	4.22	11 (36%)

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
6	PPV	A	665	-	-	0/6/6/6	0/0/0/0
5	UTP	A	993	4	-	0/18/38/38	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	993	UTP	PA-O1A	2.07	1.58	1.51
5	A	993	UTP	O4'-C1'	2.80	1.44	1.41
6	A	665	PPV	P1-O31	3.33	1.62	1.51
5	A	993	UTP	C4-N3	4.94	1.42	1.33
5	A	993	UTP	C6-N1	5.63	1.43	1.35

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	993	UTP	O2A-PA-O5'	-5.93	78.54	108.46
5	A	993	UTP	PB-O3A-PA	-3.94	121.66	132.73
5	A	993	UTP	C5-C4-N3	-3.15	115.05	123.12
5	A	993	UTP	O5'-PA-O1A	-2.44	100.13	109.62
6	A	665	PPV	O12-P2-O22	-2.34	103.04	110.58
5	A	993	UTP	O3G-PG-O2G	2.03	117.12	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	993	UTP	O4'-C4'-C3'	2.92	111.04	105.15
5	A	993	UTP	O2A-PA-O1A	3.10	129.31	112.53
5	A	993	UTP	O1B-PB-O3B	3.19	119.55	105.09
5	A	993	UTP	O3'-C3'-C2'	3.85	124.36	111.83
5	A	993	UTP	C4-N3-C2	13.18	127.19	114.14
5	A	993	UTP	O3A-PA-O5'	15.21	143.29	102.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	993	UTP	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	B	9/9 (100%)	3.69	9 (100%) 0 0	68, 75, 103, 112	9 (100%)
2	C	7/7 (100%)	3.48	6 (85%) 0 0	55, 65, 97, 104	7 (100%)
3	A	476/476 (100%)	0.80	41 (8%) 13 4	26, 56, 93, 111	0
All	All	492/492 (100%)	0.89	56 (11%) 7 2	26, 56, 95, 112	16 (3%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	910	C	7.6
3	A	370	SER	6.6
1	B	902	C	6.5
2	C	916	G	5.5
2	C	915	G	5.1
3	A	9	VAL	4.9
3	A	476	HIS	4.6
3	A	371	ASP	4.5
3	A	472	ALA	4.5
3	A	473	LEU	4.2
2	C	917	G	4.1
1	B	906	G	3.9
3	A	373	GLY	3.7
3	A	475	HIS	3.5
3	A	106	ASP	3.4
1	B	903	A	3.4
2	C	921	A	3.3
3	A	135	GLU	3.3
3	A	129	GLY	3.0
3	A	113	PRO	2.9
3	A	14	HIS	2.8
3	A	117	PRO	2.8
3	A	300	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
3	A	107	GLY	2.7
3	A	392	MET	2.7
3	A	469	ASP	2.7
3	A	287	ASN	2.6
1	B	908	C	2.6
3	A	290	ILE	2.6
3	A	8	ASP	2.5
3	A	379	SER	2.4
3	A	396	THR	2.4
2	C	920	C	2.4
3	A	114	ASP	2.4
3	A	152	LYS	2.4
3	A	151	GLU	2.4
1	B	905	G	2.4
1	B	907	G	2.4
1	B	909	C	2.3
3	A	40	SER	2.3
3	A	378	HIS	2.3
3	A	454	SER	2.2
3	A	324	GLU	2.2
3	A	53	ASP	2.2
1	B	904	U	2.2
3	A	6	THR	2.2
3	A	7	ARG	2.2
3	A	13	VAL	2.2
3	A	218	ASN	2.1
3	A	368	ASP	2.1
2	C	919	C	2.1
3	A	409	GLU	2.1
3	A	138	THR	2.0
3	A	425	ILE	2.0
3	A	206	ASN	2.0
3	A	41	ASN	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 ⓘ

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
5	UTP	A	993	29/29	0.42	0.82	7.58	94,98,100,101	29
6	PPV	A	665	9/9	0.56	0.54	3.24	60,60,61,61	9
4	MG	A	1030	1/1	0.71	0.30	-0.57	27,27,27,27	0
4	MG	A	1031	1/1	0.78	0.73	-	73,73,73,73	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.