



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:28 PM GMT

PDB ID : 4LQ3
Title : Crystal structure of human norovirus RNA-dependent RNA-polymerase bound to the inhibitor PPNDs
Authors : Milani, M.; Tarantino, D.; Mastrangelo, E.; Croci, R.
Deposited on : 2013-07-17
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
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 (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

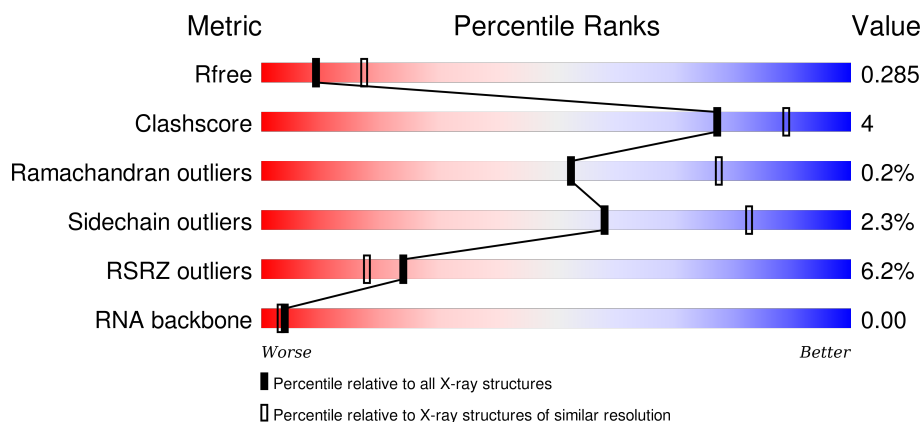
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


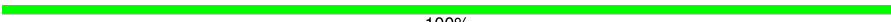
The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)
RNA backbone	2183	1022 (3.00-2.20)

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 ≥ 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	526	 6% 86% 7% • 6%
2	R	2	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4215 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 RNA-dependent RNA-polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	495	Total	C	N	O	S	0	0	0
			3880	2463	664	731	22			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	EXPRESSION TAG	UNP Q2N379
A	1	GLY	-	EXPRESSION TAG	UNP Q2N379
A	2	GLY	-	EXPRESSION TAG	UNP Q2N379
A	153	GLY	GLU	CONFLICT	UNP Q2N379
A	511	VAL	-	EXPRESSION TAG	UNP Q2N379
A	512	ASP	-	EXPRESSION TAG	UNP Q2N379
A	513	LYS	-	EXPRESSION TAG	UNP Q2N379
A	514	LEU	-	EXPRESSION TAG	UNP Q2N379
A	515	ALA	-	EXPRESSION TAG	UNP Q2N379
A	516	ALA	-	EXPRESSION TAG	UNP Q2N379
A	517	ALA	-	EXPRESSION TAG	UNP Q2N379
A	518	LEU	-	EXPRESSION TAG	UNP Q2N379
A	519	GLU	-	EXPRESSION TAG	UNP Q2N379
A	520	HIS	-	EXPRESSION TAG	UNP Q2N379
A	521	HIS	-	EXPRESSION TAG	UNP Q2N379
A	522	HIS	-	EXPRESSION TAG	UNP Q2N379
A	523	HIS	-	EXPRESSION TAG	UNP Q2N379
A	524	HIS	-	EXPRESSION TAG	UNP Q2N379
A	525	HIS	-	EXPRESSION TAG	UNP Q2N379

- Molecule 2 is a RNA chain called 5'-R(P*GP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	R	2	Total	C	N	O	P	0	0	0
			46	20	10	14	2			

- 20V
-
- The image displays a complex organic molecule, likely a derivative of a heterocyclic compound, featuring a central benzene ring substituted with various functional groups and labeled atoms. The structure includes a central benzene ring with substituents at the 1, 2, and 4 positions. The 1-position is substituted with a nitro group (NO₂) and a sulfonate group (SO₃⁻). The 2-position is substituted with a sulfonate group (SO₃⁻) and a sulfonate group (SO₃⁻). The 4-position is substituted with a sulfonate group (SO₃⁻) and a sulfonate group (SO₃⁻). The molecule also features a pyridine ring substituted with a sulfonate group (SO₃⁻) and a sulfonate group (SO₃⁻). The structure is labeled with various atoms and groups, including N, O, S, and P, and is associated with a 20V potential.

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

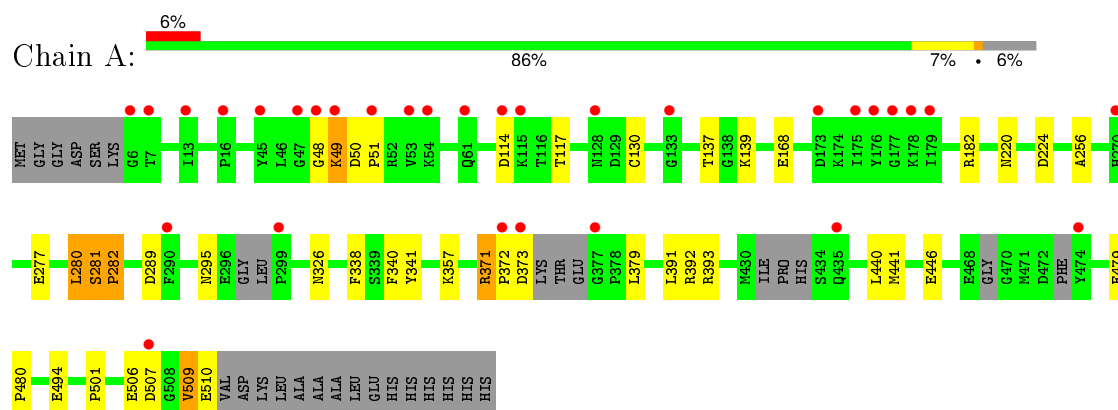
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	129	Total O 129 129	0	0
5	R	3	Total O 3 3	0	0

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 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: RNA-dependent RNA-polymerase



• Molecule 2: 5'-R(P*GP*G)-3'



There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	85.75Å 116.10Å 122.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.40 – 2.60 38.41 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.40-2.60) 99.7 (38.41-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.220 , 0.285 0.222 , 0.285	Depositor DCC
R_{free} test set	985 reflections (5.45%)	DCC
Wilson B-factor (Å ²)	58.0	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.1	EDS
Estimated twinning fraction	0.015 for -h,-l,-k	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 19046 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4215	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: MG, 20V

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	0.41	2/3974 (0.1%)	0.57	2/5381 (0.0%)
2	R	0.22	0/51	0.61	0/78
All	All	0.41	2/4025 (0.0%)	0.57	2/5459 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	51	PRO	N-CD	5.22	1.55	1.47
1	A	282	PRO	N-CD	5.13	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	50	ASP	C-N-CD	5.67	140.31	128.40
1	A	281	SER	C-N-CD	5.64	140.25	128.40

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	3880	0	3850	28	0
2	R	46	0	23	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	156	0	57	6	0
4	A	1	0	0	0	0
5	A	129	0	0	0	0
5	R	3	0	0	0	0
All	All	4215	0	3930	30	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 (30) 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:509:VAL:HA	1:A:510:GLU:C	2.09	0.72
1:A:393:ARG:NH2	1:A:446:GLU:OE1	2.30	0.64
3:A:602:20V:OAM	3:A:602:20V:H12	1.98	0.63
3:A:602:20V:OAG	3:A:602:20V:H10	2.01	0.60
1:A:256:ALA:HA	1:A:280:LEU:HD21	1.84	0.60
1:A:391:LEU:C	1:A:392:ARG:HG3	2.21	0.60
1:A:282:PRO:HB3	1:A:295:ASN:HA	1.85	0.59
1:A:506:GLU:HG3	1:A:507:ASP:N	2.19	0.56
1:A:277:GLU:O	1:A:281:SER:OG	2.27	0.53
1:A:441:MET:HB3	1:A:501:PRO:HB3	1.91	0.52
1:A:393:ARG:HH22	1:A:446:GLU:CD	2.13	0.51
1:A:220:ASN:O	1:A:224:ASP:HB2	2.12	0.50
1:A:371:ARG:HB3	1:A:372:PRO:HD2	1.93	0.49
1:A:392:ARG:NH1	3:A:603:20V:H13	2.28	0.49
1:A:357:LYS:NZ	3:A:602:20V:OAB	2.45	0.48
1:A:392:ARG:NH1	3:A:603:20V:OAM	2.46	0.48
1:A:371:ARG:HB3	1:A:372:PRO:CD	2.44	0.48
1:A:48:GLY:O	1:A:49:LYS:HB2	2.14	0.47
1:A:114:ASP:O	1:A:117:THR:HG22	2.15	0.46
1:A:357:LYS:CE	3:A:602:20V:OAB	2.65	0.45
1:A:130:CYS:HB3	1:A:137:THR:HB	1.99	0.44
1:A:168:GLU:OE2	1:A:182:ARG:HD2	2.17	0.43
1:A:509:VAL:CA	1:A:510:GLU:C	2.85	0.43
1:A:479:GLU:HB2	1:A:480:PRO:HD3	2.02	0.42
1:A:338:PHE:HB3	1:A:340:PHE:CZ	2.55	0.42
1:A:48:GLY:O	1:A:49:LYS:CB	2.68	0.41
1:A:280:LEU:HA	1:A:280:LEU:HD12	1.87	0.41
1:A:371:ARG:CB	1:A:372:PRO:CD	2.98	0.40
1:A:506:GLU:CG	1:A:507:ASP:N	2.83	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:LEU:HD12	1:A:379:LEU:C	2.41	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	483/526 (92%)	475 (98%)	7 (1%)	1 (0%)	52 77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	371	ARG

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	427/451 (95%)	417 (98%)	10 (2%)	58 83

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

Mol	Chain	Res	Type
1	A	49	LYS
1	A	139	LYS

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Mol	Chain	Res	Type
1	A	280	LEU
1	A	289	ASP
1	A	326	ASN
1	A	341	TYR
1	A	373	ASP
1	A	440	LEU
1	A	494	GLU
1	A	509	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	143	GLN
1	A	148	ASN
1	A	326	ASN
1	A	423	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	R	1/2 (50%)	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 [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is 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	20V	A	601	-	39,41,41	2.70	14 (35%)	48,64,64	1.76	13 (27%)
3	20V	A	602	-	39,41,41	2.62	14 (35%)	48,64,64	1.97	9 (18%)
3	20V	A	603	-	39,41,41	2.88	14 (35%)	48,64,64	1.66	13 (27%)
3	20V	A	604	-	39,41,41	3.19	13 (33%)	48,64,64	1.58	10 (20%)

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	20V	A	601	-	-	0/28/29/29	0/3/3/3
3	20V	A	602	-	-	0/28/29/29	0/3/3/3
3	20V	A	603	-	-	0/28/29/29	0/3/3/3
3	20V	A	604	-	-	2/28/29/29	0/3/3/3

All (55) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	603	20V	CBD-NAV	-5.87	1.33	1.41
3	A	602	20V	CAT-CBE	-5.59	1.40	1.51
3	A	601	20V	CAA-CAY	-5.43	1.39	1.50
3	A	604	20V	CBD-NAV	-5.37	1.34	1.41
3	A	602	20V	CBD-NAV	-5.33	1.34	1.41
3	A	604	20V	CAA-CAY	-5.32	1.39	1.50
3	A	601	20V	CBD-NAV	-5.08	1.34	1.41
3	A	602	20V	CAA-CAY	-5.06	1.40	1.50
3	A	602	20V	CBG-SBM	-5.03	1.71	1.78
3	A	604	20V	CAT-CBE	-4.98	1.41	1.51
3	A	603	20V	CAA-CAY	-4.97	1.40	1.50
3	A	601	20V	CAT-CBE	-4.94	1.41	1.51
3	A	603	20V	CAT-CBE	-4.66	1.42	1.51
3	A	602	20V	CBC-CAO	-3.29	1.38	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	603	20V	CBC-CAO	-3.01	1.39	1.46
3	A	604	20V	CBC-CAO	-2.80	1.40	1.46
3	A	601	20V	CBC-CAO	-2.76	1.40	1.46
3	A	603	20V	CBG-SBM	-2.74	1.74	1.78
3	A	602	20V	CBA-CAY	-2.65	1.38	1.40
3	A	601	20V	CAZ-NAU	-2.56	1.33	1.44
3	A	604	20V	CAZ-NAU	-2.54	1.33	1.44
3	A	602	20V	CAZ-NAU	-2.54	1.33	1.44
3	A	604	20V	CBG-SBM	-2.50	1.75	1.78
3	A	603	20V	CAZ-NAU	-2.46	1.34	1.44
3	A	602	20V	CBG-CBH	-2.33	1.39	1.43
3	A	602	20V	CBF-CBI	-2.27	1.40	1.43
3	A	601	20V	CBA-CAY	-2.07	1.39	1.40
3	A	604	20V	NAV-NAU	-2.00	1.15	1.24
3	A	602	20V	OAG-SBM	2.00	1.53	1.43
3	A	604	20V	OAM-SBL	2.01	1.53	1.43
3	A	603	20V	OAD-SBL	2.01	1.53	1.43
3	A	601	20V	OAD-SBL	2.01	1.53	1.43
3	A	602	20V	OAD-SBL	2.03	1.53	1.43
3	A	601	20V	OAF-SBM	2.03	1.53	1.43
3	A	603	20V	OAF-SBM	2.03	1.53	1.43
3	A	604	20V	OAD-SBL	2.08	1.53	1.43
3	A	604	20V	PBK-OAK	2.08	1.62	1.54
3	A	601	20V	PBK-OAK	2.09	1.62	1.54
3	A	603	20V	OAM-SBL	2.09	1.53	1.43
3	A	603	20V	OAG-SBM	2.11	1.53	1.43
3	A	603	20V	CAR-CAZ	2.28	1.39	1.37
3	A	601	20V	OAG-SBM	2.28	1.54	1.43
3	A	602	20V	PBK-OAK	2.34	1.63	1.54
3	A	603	20V	PBK-OAK	2.45	1.63	1.54
3	A	604	20V	CAR-CAZ	2.52	1.39	1.37
3	A	601	20V	CBG-SBM	2.90	1.83	1.78
3	A	601	20V	CAR-CAZ	3.07	1.40	1.37
3	A	601	20V	PBK-OAL	3.24	1.61	1.51
3	A	604	20V	PBK-OAL	3.27	1.61	1.51
3	A	603	20V	PBK-OAL	3.37	1.62	1.51
3	A	602	20V	PBK-OAL	3.59	1.63	1.51
3	A	602	20V	OAI-NBJ	8.02	1.38	1.22
3	A	601	20V	OAI-NBJ	10.34	1.43	1.22
3	A	603	20V	OAI-NBJ	12.24	1.47	1.22
3	A	604	20V	OAI-NBJ	14.98	1.52	1.22

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	20V	OAB-CAO-CBC	-3.07	118.90	125.11
3	A	604	20V	CAS-CBI-CBF	-2.70	120.12	123.23
3	A	601	20V	CBA-CBC-CBE	-2.68	117.65	120.02
3	A	601	20V	CAS-CBI-CBF	-2.58	120.25	123.23
3	A	602	20V	CBA-CAY-NAW	-2.58	117.48	120.71
3	A	603	20V	OAB-CAO-CBC	-2.42	120.22	125.11
3	A	603	20V	CBA-CAY-NAW	-2.23	117.92	120.71
3	A	602	20V	CAS-CBI-CBF	-2.22	120.67	123.23
3	A	602	20V	CAR-CBH-CBG	-2.11	120.80	123.23
3	A	601	20V	OAK-PBK-OAL	-2.07	103.91	110.58
3	A	603	20V	CAS-CBI-CBF	-2.05	120.87	123.23
3	A	604	20V	CBA-CBC-CBE	-2.00	118.25	120.02
3	A	601	20V	OAF-SBM-CBG	2.04	108.52	106.20
3	A	603	20V	CBF-CBI-CBH	2.06	119.87	117.78
3	A	604	20V	CBF-CBI-CBH	2.15	119.97	117.78
3	A	603	20V	CAA-CAY-NAW	2.17	119.77	116.34
3	A	601	20V	CBB-CAS-CBI	2.33	121.02	119.33
3	A	604	20V	CAA-CAY-NAW	2.34	120.04	116.34
3	A	601	20V	CBF-CBI-CBH	2.38	120.20	117.78
3	A	602	20V	CAS-CBB-NBJ	2.53	121.02	118.80
3	A	603	20V	OAF-SBM-CBG	2.55	109.09	106.20
3	A	604	20V	OAC-PBK-OAX	2.65	114.18	106.56
3	A	601	20V	CBD-NAV-NAU	2.68	116.83	113.27
3	A	603	20V	CAS-CBB-NBJ	2.71	121.18	118.80
3	A	603	20V	CBB-CAS-CBI	2.77	121.33	119.33
3	A	603	20V	OAC-PBK-OAX	2.83	114.71	106.56
3	A	601	20V	CAA-CAY-NAW	2.90	120.92	116.34
3	A	602	20V	OAC-PBK-OAX	2.91	114.93	106.56
3	A	601	20V	OAC-PBK-OAX	2.97	115.11	106.56
3	A	602	20V	CAA-CAY-NAW	3.12	121.28	116.34
3	A	603	20V	OAM-SBL-CBF	3.19	109.82	106.20
3	A	604	20V	OAD-SBL-CBF	3.20	109.83	106.20
3	A	604	20V	OAF-SBM-CBG	3.25	109.88	106.20
3	A	603	20V	OAD-SBL-CBF	3.32	109.96	106.20
3	A	603	20V	OAG-SBM-CBG	3.36	110.00	106.20
3	A	604	20V	OAG-SBM-CBG	3.38	110.04	106.20
3	A	601	20V	OAD-SBL-CBF	3.38	110.04	106.20
3	A	604	20V	OAM-SBL-CBF	3.41	110.06	106.20
3	A	601	20V	CAQ-CBB-NBJ	3.57	121.93	118.80
3	A	604	20V	CBD-NAV-NAU	3.96	118.53	113.27
3	A	601	20V	OAM-SBL-CBF	4.18	110.94	106.20
3	A	601	20V	OAG-SBM-CBG	4.42	111.21	106.20
3	A	603	20V	CBD-NAV-NAU	4.82	119.67	113.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	20V	OAM-SBL-CBF	6.75	113.86	106.20
3	A	602	20V	OAG-SBM-CBG	7.01	114.15	106.20

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	604	20V	CAQ-CBB-NBJ-OAI
3	A	604	20V	CAS-CBB-NBJ-OAI

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	602	20V	4	0
3	A	603	20V	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, 95th 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 ²)	Q<0.9
1	A	495/526 (94%)	0.14	31 (6%) 23 17	26, 53, 82, 107	5 (1%)
2	R	2/2 (100%)	1.26	0 100 100	93, 93, 93, 106	0
All	All	497/528 (94%)	0.15	31 (6%) 24 18	26, 53, 83, 107	5 (1%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	6	GLY	5.6
1	A	54	LYS	4.1
1	A	48	GLY	4.1
1	A	474	TYR	4.1
1	A	7	THR	3.6
1	A	51	PRO	3.6
1	A	178	LYS	3.5
1	A	47	GLY	3.4
1	A	45	TYR	3.4
1	A	115	LYS	3.3
1	A	507	ASP	3.3
1	A	128	ASN	3.3
1	A	377	GLY	3.2
1	A	299	PRO	3.0
1	A	372	PRO	3.0
1	A	53	VAL	3.0
1	A	13	ILE	2.9
1	A	16	PRO	2.8
1	A	49	LYS	2.7
1	A	133	GLY	2.7
1	A	177	GLY	2.7
1	A	175	ILE	2.7
1	A	173	ASP	2.5
1	A	373	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	179	ILE	2.3
1	A	290	PHE	2.3
1	A	176	TYR	2.3
1	A	435	GLN	2.2
1	A	114	ASP	2.0
1	A	61	GLN	2.0
1	A	270	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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, 95th 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 ²)	Q<0.9
3	20V	A	603	39/39	0.87	0.21	0.55	70,82,89,92	0
4	MG	A	605	1/1	0.77	0.20	0.48	45,45,45,45	0
3	20V	A	604	39/39	0.86	0.22	-0.13	91,101,111,112	0
3	20V	A	602	39/39	0.93	0.14	-0.44	49,59,70,75	0
3	20V	A	601	39/39	0.95	0.13	-1.38	42,53,72,81	0

6.5 Other polymers [i](#)

There are no such residues in this entry.