



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 5, 2023 – 05:46 AM EDT

PDB ID : 3V4J
Title : First-In-Class Small Molecule Inhibitors of the Single-strand DNA Cytosine Deaminase APOBEC3G
Authors : Shandilya, S.M.D.; Ali, A.; Schiffer, C.A.
Deposited on : 2011-12-15
Resolution : 2.04 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.35
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) : 2.35

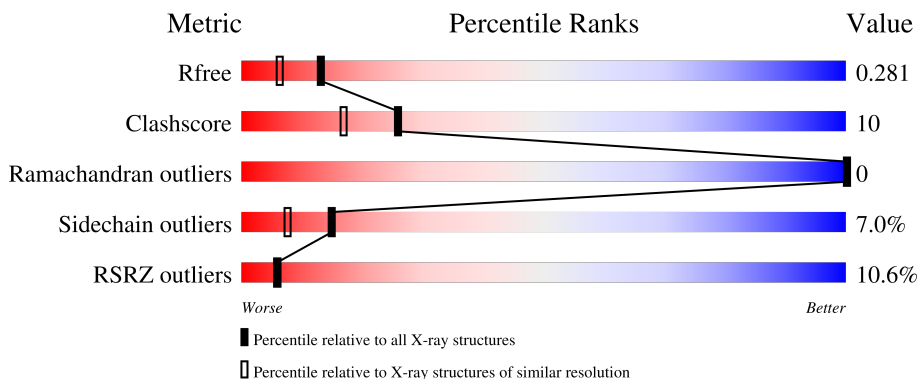
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	207	
1	B	207	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3085 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 DNA dC->dU-editing enzyme APOBEC-3G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	184	1470	937	252	269	12	0	3	0
1	B	185	1433	918	248	255	12	0	2	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	178	GLY	-	expression tag	UNP Q9HC16
A	179	PRO	-	expression tag	UNP Q9HC16
A	180	LEU	-	expression tag	UNP Q9HC16
A	181	GLY	-	expression tag	UNP Q9HC16
A	182	SER	-	expression tag	UNP Q9HC16
A	183	PRO	-	expression tag	UNP Q9HC16
A	184	GLU	-	expression tag	UNP Q9HC16
A	185	PHE	-	expression tag	UNP Q9HC16
A	186	GLU	-	expression tag	UNP Q9HC16
A	187	LEU	-	expression tag	UNP Q9HC16
A	188	GLY	-	expression tag	UNP Q9HC16
A	189	THR	-	expression tag	UNP Q9HC16
A	190	THR	-	expression tag	UNP Q9HC16
A	234	LYS	LEU	engineered mutation	UNP Q9HC16
A	243	ALA	CYS	engineered mutation	UNP Q9HC16
A	310	LYS	PHE	engineered mutation	UNP Q9HC16
A	321	ALA	CYS	engineered mutation	UNP Q9HC16
A	356	ALA	CYS	engineered mutation	UNP Q9HC16
B	178	GLY	-	expression tag	UNP Q9HC16
B	179	PRO	-	expression tag	UNP Q9HC16
B	180	LEU	-	expression tag	UNP Q9HC16
B	181	GLY	-	expression tag	UNP Q9HC16
B	182	SER	-	expression tag	UNP Q9HC16
B	183	PRO	-	expression tag	UNP Q9HC16
B	184	GLU	-	expression tag	UNP Q9HC16

Continued on next page...

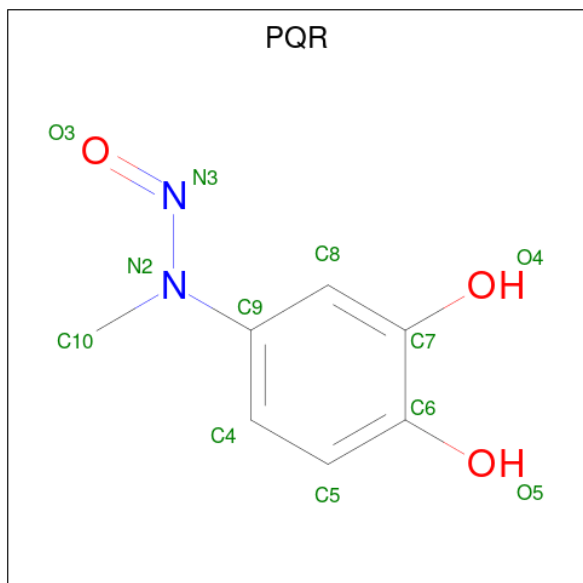
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	185	PHE	-	expression tag	UNP Q9HC16
B	186	GLU	-	expression tag	UNP Q9HC16
B	187	LEU	-	expression tag	UNP Q9HC16
B	188	GLY	-	expression tag	UNP Q9HC16
B	189	THR	-	expression tag	UNP Q9HC16
B	190	THR	-	expression tag	UNP Q9HC16
B	234	LYS	LEU	engineered mutation	UNP Q9HC16
B	243	ALA	CYS	engineered mutation	UNP Q9HC16
B	310	LYS	PHE	engineered mutation	UNP Q9HC16
B	321	ALA	CYS	engineered mutation	UNP Q9HC16
B	356	ALA	CYS	engineered mutation	UNP Q9HC16

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Zn 2 2	0	0
2	B	2	Total Zn 2 2	0	0

- Molecule 3 is 4-[methyl(nitroso)amino]benzene-1,2-diol (three-letter code: PQR) (formula: C₇H₈N₂O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 12 7 2 3	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	B	1	12	7	2	3	0	0

- Molecule 4 is water.

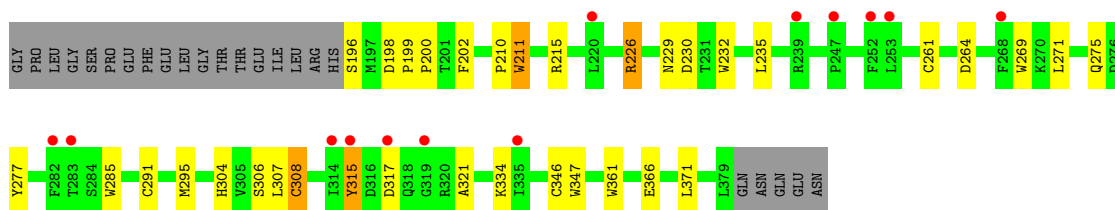
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	94	Total	O	0	0
			94	94		
4	B	60	Total	O	0	0
			60	60		

3 Residue-property plots [i](#)

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.

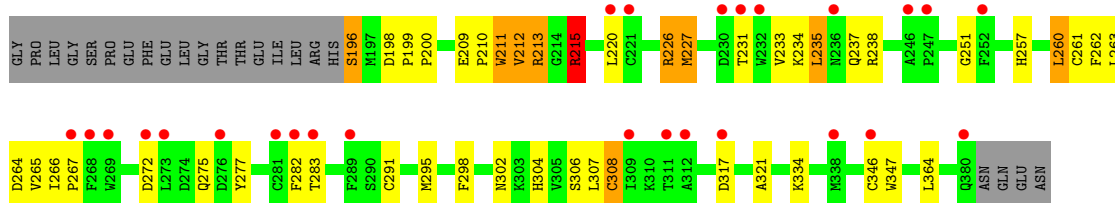
- Molecule 1: DNA dC->dU-editing enzyme APOBEC-3G

Chain A: 



- Molecule 1: DNA dC->dU-editing enzyme APOBEC-3G

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.08Å 67.76Å 64.47Å 90.00° 107.38° 90.00°	Depositor
Resolution (Å)	28.01 – 2.04 28.01 – 2.04	Depositor EDS
% Data completeness (in resolution range)	96.0 (28.01-2.04) 96.1 (28.01-2.04)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.49 (at 2.04Å)	Xtrriage
Refinement program	REFMAC refmac_5.6.0081	Depositor
R, R_{free}	0.228 , 0.276 0.233 , 0.281	Depositor DCC
R_{free} test set	1335 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtrriage
Anisotropy	0.154	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3085	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.26% 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, 0.333 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: PQR, ZN

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	0.77	8/1526 (0.5%)	0.77	0/2079
1	B	0.78	4/1486 (0.3%)	0.75	1/2027 (0.0%)
All	All	0.77	12/3012 (0.4%)	0.76	1/4106 (0.0%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	307	LEU	C-N	10.53	1.58	1.34
1	A	308	CYS	C-N	7.76	1.51	1.34
1	B	308	CYS	C-N	7.22	1.50	1.34
1	A	347	TRP	CD2-CE2	6.25	1.48	1.41
1	B	347	TRP	CD2-CE2	5.97	1.48	1.41
1	A	307	LEU	C-N	5.70	1.47	1.34
1	B	211	TRP	CD2-CE2	5.55	1.48	1.41
1	A	269	TRP	CD2-CE2	5.50	1.48	1.41
1	A	285	TRP	CD2-CE2	5.47	1.48	1.41
1	A	232	TRP	CD2-CE2	5.42	1.47	1.41
1	A	211	TRP	CD2-CE2	5.28	1.47	1.41
1	A	361	TRP	CD2-CE2	5.26	1.47	1.41

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	215	ARG	NE-CZ-NH1	5.31	122.96	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	1470	0	1324	19	0
1	B	1433	0	1269	39	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	12	0	5	1	0
3	B	12	0	5	1	0
4	A	94	0	0	2	0
4	B	60	0	0	2	0
All	All	3085	0	2603	58	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (58) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:PHE:O	1:B:302:ASN:ND2	2.13	0.80
1:A:317:ASP:HB3	1:A:321:ALA:HB2	1.64	0.79
1:B:210:PRO:HD2	1:B:211:TRP:CE3	2.18	0.78
1:B:226:ARG:HB2	1:B:235:LEU:HD21	1.69	0.75
1:B:227:MET:CE	1:B:231:THR:C	2.60	0.70
1:A:334:LYS:NZ	4:A:514:HOH:O	2.30	0.65
1:A:317:ASP:CB	1:A:321:ALA:HB2	2.29	0.63
1:A:202:PHE:HE1	1:A:346[A]:CYS:HG	1.46	0.63
1:B:272:ASP:HB3	1:B:275:GLN:HG2	1.82	0.61
1:B:317:ASP:HB3	1:B:321:ALA:HB2	1.83	0.60
1:B:308:CYS:SG	3:B:403:PQR:N3	2.75	0.60
1:A:199:PRO:HB2	1:A:200:PRO:HD3	1.84	0.59
1:B:227:MET:HE2	1:B:231:THR:O	2.03	0.59
1:B:211:TRP:CD1	1:B:212:VAL:N	2.71	0.58
1:B:199:PRO:HB2	1:B:200:PRO:HD3	1.85	0.57
1:A:210:PRO:HD2	1:A:211:TRP:CE3	2.41	0.55
1:B:251:GLY:HA2	4:B:508:HOH:O	2.05	0.55
1:B:209:GLU:O	1:B:215:ARG:NH2	2.41	0.53
1:A:226:ARG:CZ	1:A:275:GLN:HG3	2.38	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:227:MET:HE3	1:B:227:MET:HA	1.91	0.52
1:B:272:ASP:HB3	1:B:275:GLN:CG	2.39	0.52
1:B:266:ILE:N	1:B:267:PRO:HD2	2.25	0.52
1:A:275:GLN:O	1:A:304:HIS:HB2	2.11	0.50
1:B:227:MET:HE1	1:B:231:THR:C	2.32	0.50
1:B:317:ASP:CB	1:B:321:ALA:HB2	2.41	0.49
1:B:261:CYS:O	1:B:264:ASP:HB2	2.13	0.48
1:B:235:LEU:O	1:B:237:GLN:O	2.31	0.48
1:A:226:ARG:HG3	1:A:277:TYR:CE2	2.49	0.48
1:B:227:MET:HE1	1:B:231:THR:CA	2.44	0.48
1:B:227:MET:CE	1:B:231:THR:O	2.60	0.47
1:B:262:PHE:O	1:B:265:VAL:HG22	2.14	0.47
1:B:226:ARG:HG3	1:B:277:TYR:CE1	2.50	0.47
1:B:196:SER:HB3	4:B:550:HOH:O	2.15	0.46
1:B:364:LEU:C	1:B:364:LEU:HD23	2.35	0.46
1:A:229:ASN:O	1:A:230:ASP:HB2	2.15	0.46
1:B:198:ASP:OD2	1:B:200:PRO:HD2	2.16	0.46
1:B:275:GLN:O	1:B:304:HIS:HB2	2.16	0.46
1:A:315[B]:TYR:CE2	1:A:317:ASP:HB2	2.51	0.46
1:A:308:CYS:SG	3:A:403:PQR:N3	2.89	0.45
1:A:261:CYS:O	1:A:264:ASP:HB2	2.17	0.44
1:B:227:MET:HE2	1:B:231:THR:C	2.36	0.43
1:B:291:CYS:O	1:B:295:MET:HG3	2.18	0.43
1:B:213:ARG:HD3	1:B:213:ARG:HA	1.83	0.43
1:A:291:CYS:O	1:A:295:MET:HG3	2.19	0.42
1:B:257:HIS:HB2	1:B:260:LEU:HD22	2.01	0.42
1:B:282:PHE:CG	1:B:346[B]:CYS:SG	3.13	0.42
1:B:227:MET:CE	1:B:231:THR:N	2.83	0.42
1:B:237:GLN:O	1:B:238:ARG:CB	2.68	0.42
1:B:266:ILE:HB	1:B:267:PRO:CD	2.49	0.42
1:A:198:ASP:OD1	1:A:199:PRO:HD2	2.20	0.42
1:A:226:ARG:NH2	1:A:275:GLN:HG3	2.36	0.41
1:A:371:LEU:HD21	4:A:509:HOH:O	2.19	0.41
1:A:202:PHE:HE1	1:A:346[A]:CYS:SG	2.44	0.41
1:B:227:MET:CE	1:B:227:MET:HA	2.51	0.41
1:B:235:LEU:N	1:B:235:LEU:HD13	2.36	0.41
1:B:220:LEU:HG	1:B:283:THR:HG22	2.03	0.41
1:B:302:ASN:ND2	1:B:302:ASN:N	2.69	0.40
1:A:271:LEU:HD22	1:A:277:TYR:CE2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	185/207 (89%)	178 (96%)	7 (4%)	0	100	100
1	B	185/207 (89%)	179 (97%)	6 (3%)	0	100	100
All	All	370/414 (89%)	357 (96%)	13 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	151/182 (83%)	143 (95%)	8 (5%)	22	14
1	B	140/182 (77%)	127 (91%)	13 (9%)	9	3
All	All	291/364 (80%)	270 (93%)	21 (7%)	15	7

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	SER
1	A	215	ARG
1	A	226	ARG
1	A	235	LEU
1	A	306	SER
1	A	315[A]	TYR
1	A	315[B]	TYR
1	A	366	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	196	SER
1	B	212	VAL
1	B	213	ARG
1	B	215	ARG
1	B	226	ARG
1	B	227	MET
1	B	233	VAL
1	B	234	LYS
1	B	235	LEU
1	B	260	LEU
1	B	263	LEU
1	B	306	SER
1	B	334	LYS

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 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
3	PQR	B	403	1	12,12,12	3.75	5 (41%)	14,16,16	1.36	1 (7%)
3	PQR	A	403	1	12,12,12	3.58	5 (41%)	14,16,16	1.15	1 (7%)

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	PQR	B	403	1	-	1/6/6/6	0/1/1/1
3	PQR	A	403	1	-	0/6/6/6	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	403	PQR	C4-C9	6.12	1.51	1.39
3	B	403	PQR	C4-C9	6.08	1.51	1.39
3	B	403	PQR	O5-C6	-5.87	1.24	1.36
3	B	403	PQR	O4-C7	-5.63	1.24	1.36
3	B	403	PQR	O3-N3	5.55	1.41	1.23
3	A	403	PQR	O5-C6	-5.47	1.25	1.36
3	B	403	PQR	C7-C6	5.44	1.48	1.40
3	A	403	PQR	O3-N3	5.41	1.40	1.23
3	A	403	PQR	O4-C7	-5.31	1.25	1.36
3	A	403	PQR	C7-C6	5.18	1.48	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	403	PQR	O3-N3-N2	3.41	123.67	114.71
3	A	403	PQR	C4-C9-N2	2.41	123.52	120.59

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	403	PQR	C9-N2-N3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	403	PQR	1	0
3	A	403	PQR	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, 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	184/207 (88%)	0.41	13 (7%) 16 17	42, 55, 72, 97	2 (1%)
1	B	185/207 (89%)	0.53	26 (14%) 2 2	44, 61, 76, 87	2 (1%)
All	All	369/414 (89%)	0.47	39 (10%) 6 6	42, 57, 76, 97	4 (1%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	317	ASP	5.0
1	A	335	ILE	4.8
1	A	315[A]	TYR	4.3
1	A	252	PHE	4.0
1	B	272	ASP	3.1
1	A	314	ILE	3.1
1	B	252	PHE	3.1
1	B	312	ALA	3.0
1	B	267	PRO	3.0
1	B	317	ASP	3.0
1	B	380	GLN	2.9
1	A	319	GLY	2.9
1	B	246	ALA	2.9
1	A	253	LEU	2.8
1	B	268	PHE	2.8
1	B	232	TRP	2.8
1	B	247	PRO	2.7
1	B	231	THR	2.7
1	A	268	PHE	2.6
1	B	346[A]	CYS	2.6
1	B	309	ILE	2.5
1	B	230	ASP	2.5
1	B	276	ASP	2.5
1	B	282	PHE	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	311	THR	2.4
1	A	220	LEU	2.4
1	B	281	CYS	2.3
1	B	338	MET	2.2
1	A	282	PHE	2.2
1	A	247	PRO	2.2
1	B	273	LEU	2.2
1	B	289	PHE	2.2
1	B	283	THR	2.2
1	B	220	LEU	2.1
1	A	239	ARG	2.1
1	A	283	THR	2.1
1	B	221	CYS	2.1
1	B	236	ASN	2.0
1	B	269	TRP	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 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, 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	B-factors(Å ²)	Q<0.9
3	PQR	B	403	12/12	0.78	0.22	70,77,83,90	0
3	PQR	A	403	12/12	0.90	0.17	63,69,75,77	0
2	ZN	A	402	1/1	0.97	0.05	57,57,57,57	0
2	ZN	B	401	1/1	0.98	0.05	57,57,57,57	0
2	ZN	B	402	1/1	0.98	0.03	60,60,60,60	0
2	ZN	A	401	1/1	0.99	0.03	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.