



wwPDB X-ray Structure Validation Summary Report ⓘ

May 7, 2026 – 08:37 AM EDT

PDB ID : 5QJR / pdb_00005qjr
Title : PanDDA analysis group deposition of models with modelled events (e.g. bound ligands) – Crystal Structure of NUDT5 in complex with Z220816104
Authors : Dubianok, Y.; Collins, P.; Krojer, T.; Wright, N.; Strain-Damerell, C.; Burgess-Brown, N.; Bountra, C.; Arrowsmith, C.H.; Edwards, A.; Huber, K.; von Delft, F.
Deposited on : 2018-10-31
Resolution : 1.62 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

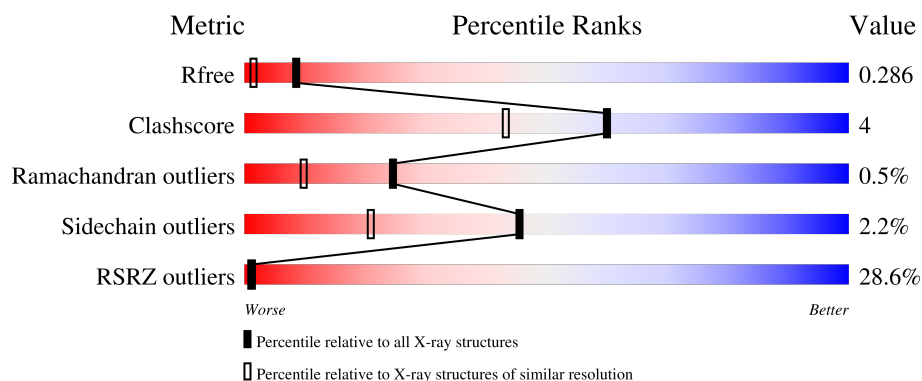
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.62 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}	180053	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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 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	209	
1	B	209	
1	C	209	
1	D	209	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6025 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 ADP-sugar pyrophosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1462	925	245	284	8			
1	B	194	Total	C	N	O	S	0	0	0
			1464	924	244	288	8			
1	C	192	Total	C	N	O	S	0	0	0
			1402	884	234	277	7			
1	D	190	Total	C	N	O	S	0	1	0
			1404	887	235	274	8			

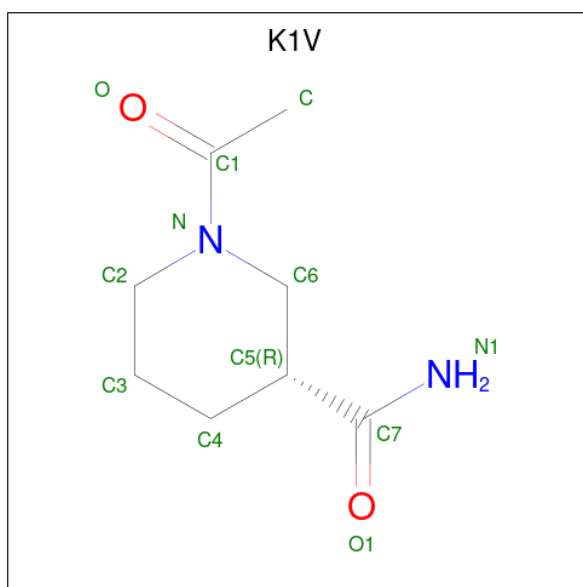
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q9UUKK9
B	0	SER	-	expression tag	UNP Q9UUKK9
C	0	SER	-	expression tag	UNP Q9UUKK9
D	0	SER	-	expression tag	UNP Q9UUKK9

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		
2	C	2	Total	Mg	0	0
			2	2		
2	D	2	Total	Mg	0	0
			2	2		

- Molecule 3 is (3R)-1-acetylpiperidine-3-carboxamide (CCD ID: K1V) (formula: C₈H₁₄N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	8	2	2		
3	A	1	Total	C	N	O	0	0
			12	8	2	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

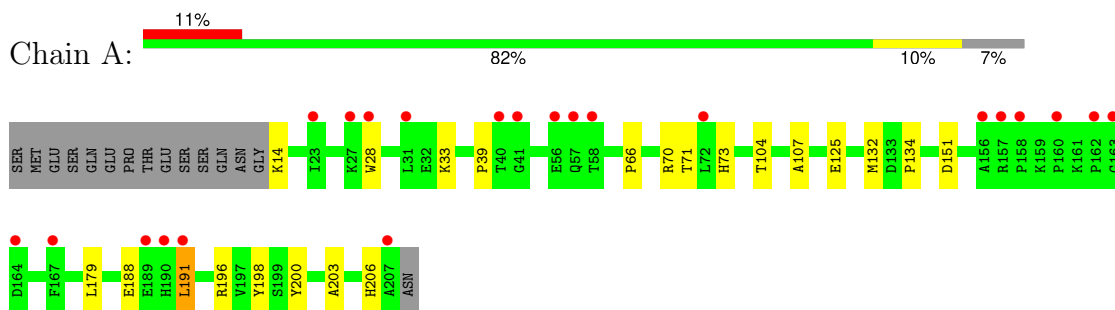
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	74	Total	O	0	0
			74	74		
6	B	72	Total	O	0	0
			72	72		
6	C	69	Total	O	0	0
			69	69		
6	D	29	Total	O	0	0
			29	29		

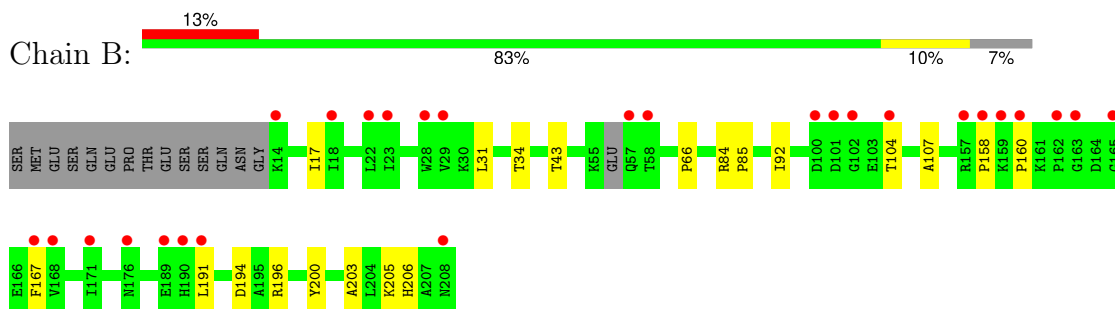
3 Residue-property plots [i](#)

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.

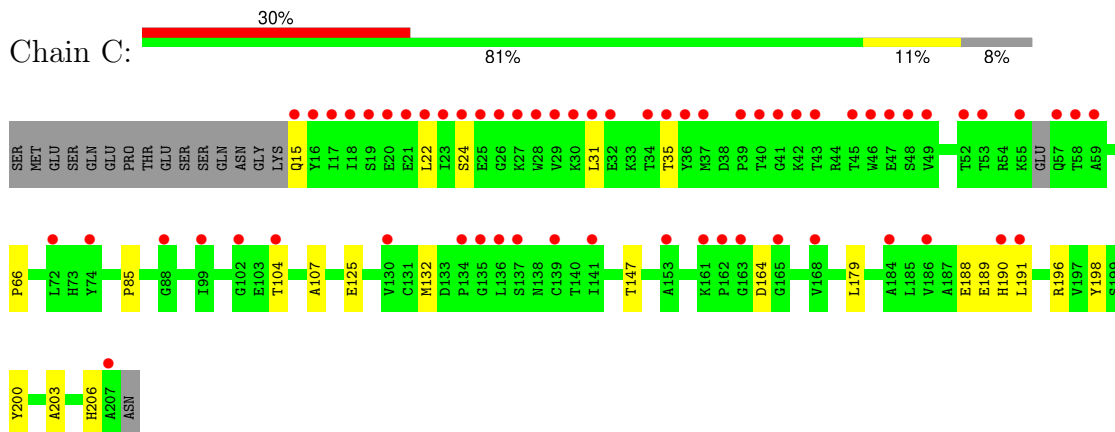
- Molecule 1: ADP-sugar pyrophosphatase



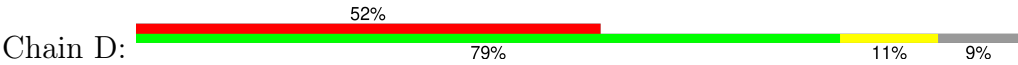
- Molecule 1: ADP-sugar pyrophosphatase



- Molecule 1: ADP-sugar pyrophosphatase



- Molecule 1: ADP-sugar pyrophosphatase



SER	MEI	GLU	SER	GLN	GLN	GLU	PRO	THR	GLU	SER	SER	GLN	ASN	GLY	K14	Q15	Y16	I17	I18	L22	I23	S24	E25	G26	K27	W28	V29	K30	L31	T34	P39	T40	G41	K42	T43	W46	V49	K50	R51	T52	T53	ARG	LYS	GLU	GLN	THR	A59	V62	A63	V64	I65	P66	V67	L68		
Q69	R70	T71	L72	H73	Y74	E75	C76	I77	V78	L79	V80	K81	Q82	F83	R84	P85	P86	M87	G88	G89	Y90	C91	I92	E93	F94	P95	A96	V97	K98	L98	I99	D100	D101	G102	E103	T104	P105	E106	A107	A108	A109	L110	R111	E112	L113	T117	G118	Y119	K120	G121	D122	I123	A124	L136	C139	V146
T147	I148	N149	G150	D151	D152	A153	E154	N155	A156	R157	P158	K159	P160	K161	P162	G163	D164	G165	E166	F167	V168	E169	V170	I171	S172	L173	P174	K175	N176	D177	L178	L179	Q180	R181	L182	V186	A187	E188	E189	H190	L191	T192	V193	R196	V197	Y200	A203	H206	A207	N208						

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.54Å 60.03Å 79.99Å 79.25° 81.06° 75.33°	Depositor
Resolution (Å)	78.08 – 1.62 78.08 – 1.62	Depositor EDS
% Data completeness (in resolution range)	96.3 (78.08-1.62) 96.3 (78.08-1.62)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.62Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.242 , 0.277 0.254 , 0.286	Depositor DCC
R_{free} test set	5590 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	27.9	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 27.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6025	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% 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: MG, CL, EDO, K1V

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	1.12	0/1490	1.04	1/2032 (0.0%)
1	B	1.05	1/1492 (0.1%)	1.04	0/2035
1	C	1.12	1/1429 (0.1%)	1.09	2/1958 (0.1%)
1	D	1.09	1/1430 (0.1%)	1.09	7/1954 (0.4%)
All	All	1.09	3/5841 (0.1%)	1.07	10/7979 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	84	ARG	C-O	-7.55	1.18	1.25
1	C	147	THR	N-CA	5.77	1.53	1.46
1	B	85	PRO	CA-C	5.08	1.56	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	94	PHE	CA-C-N	-6.50	112.81	119.83
1	D	94	PHE	C-N-CA	-6.50	112.81	119.83
1	C	190	HIS	N-CA-CB	6.19	119.96	109.87
1	D	188	GLU	N-CA-C	6.15	121.84	113.97
1	C	85	PRO	N-CA-C	6.12	118.17	110.70

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	1462	0	1433	16	0
1	B	1464	0	1414	13	0
1	C	1402	0	1298	13	0
1	D	1404	0	1338	21	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	24	0	0	1	0
4	A	4	0	6	0	0
4	B	8	0	12	0	0
4	C	4	0	6	0	0
5	B	1	0	0	0	0
6	A	74	0	0	0	0
6	B	72	0	0	0	0
6	C	69	0	0	3	0
6	D	29	0	0	0	0
All	All	6025	0	5507	49	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.

The worst 5 of 49 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:D:196[B]:ARG:HH21	1:D:196[B]:ARG:CG	1.44	1.23
1:D:196[B]:ARG:HG3	1:D:196[B]:ARG:NH2	1.38	1.10
1:D:196[B]:ARG:CG	1:D:196[B]:ARG:NH2	2.16	0.80
1:C:125:GLU:OE1	6:C:401:HOH:O	2.12	0.68
1:A:203:ALA:HB3	1:B:203:ALA:HB3	1.77	0.65

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	192/209 (92%)	188 (98%)	3 (2%)	1 (0%)	24	10
1	B	190/209 (91%)	185 (97%)	4 (2%)	1 (0%)	24	10
1	C	188/209 (90%)	180 (96%)	6 (3%)	2 (1%)	11	2
1	D	187/209 (90%)	176 (94%)	11 (6%)	0	100	100
All	All	757/836 (91%)	729 (96%)	24 (3%)	4 (0%)	24	10

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	24	SER
1	A	66	PRO
1	C	66	PRO
1	B	66	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	154/179 (86%)	150 (97%)	4 (3%)	40	16
1	B	154/179 (86%)	151 (98%)	3 (2%)	50	26
1	C	139/179 (78%)	135 (97%)	4 (3%)	37	13
1	D	143/179 (80%)	141 (99%)	2 (1%)	59	37
All	All	590/716 (82%)	577 (98%)	13 (2%)	45	21

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	22	LEU
1	C	31	LEU
1	D	72	LEU

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Mol	Chain	Res	Type
1	C	164	ASP
1	D	43	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	206	HIS
1	D	15	GLN
1	D	206	HIS
1	D	82	GLN
1	D	155	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 9 are monoatomic - leaving 6 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	K1V	A	304	-	12,12,12	1.39	2 (16%)	15,16,16	1.35	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	B	305	-	3,3,3	0.46	0	2,2,2	0.34	0
4	EDO	C	301	-	3,3,3	0.47	0	2,2,2	0.26	0
3	K1V	A	303	-	12,12,12	1.25	2 (16%)	15,16,16	1.26	2 (13%)
4	EDO	A	305	-	3,3,3	0.46	0	2,2,2	0.67	0
4	EDO	B	302	-	3,3,3	0.52	0	2,2,2	0.37	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	K1V	A	304	-	-	4/8/18/18	0/1/1/1
4	EDO	B	305	-	-	0/1/1/1	-
4	EDO	C	301	-	-	1/1/1/1	-
3	K1V	A	303	-	-	2/8/18/18	0/1/1/1
4	EDO	A	305	-	-	0/1/1/1	-
4	EDO	B	302	-	-	0/1/1/1	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	304	K1V	C1-N	2.80	1.43	1.35
3	A	303	K1V	C2-N	2.75	1.52	1.47
3	A	304	K1V	C7-N1	2.22	1.38	1.32
3	A	303	K1V	C1-N	2.12	1.41	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	304	K1V	C6-C5-C7	-3.06	104.33	110.07
3	A	303	K1V	C6-C5-C7	-3.05	104.35	110.07
3	A	304	K1V	C4-C3-C2	-2.28	107.76	110.75
3	A	303	K1V	O1-C7-N1	-2.08	119.37	123.04
3	A	304	K1V	O1-C7-N1	-2.02	119.47	123.04

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	K1V	C4-C5-C7-N1

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Mol	Chain	Res	Type	Atoms
3	A	303	K1V	C4-C5-C7-O1
3	A	304	K1V	C4-C5-C7-N1
3	A	304	K1V	C4-C5-C7-O1
3	A	304	K1V	C-C1-N-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	K1V	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	194/209 (92%)	0.76	22 (11%)	10 10	19, 28, 50, 63	7 (3%)
1	B	194/209 (92%)	1.01	27 (13%)	6 6	20, 32, 54, 72	4 (2%)
1	C	192/209 (91%)	1.68	62 (32%)	1 1	20, 35, 61, 74	4 (2%)
1	D	190/209 (90%)	2.55	109 (57%)	0 0	8, 42, 64, 77	9 (4%)
All	All	770/836 (92%)	1.49	220 (28%)	1 1	8, 34, 60, 77	24 (3%)

The worst 5 of 220 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	23	ILE	17.1
1	C	22	LEU	15.7
1	D	156	ALA	12.4
1	C	24	SER	11.4
1	B	191	LEU	10.5

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	K1V	A	304	12/12	0.73	0.27	43,49,53,54	12
4	EDO	B	305	4/4	0.76	0.19	50,51,51,54	0
2	MG	B	304	1/1	0.82	0.14	73,73,73,73	0
2	MG	C	302	1/1	0.82	0.15	59,59,59,59	0
4	EDO	C	301	4/4	0.82	0.17	39,52,55,59	0
3	K1V	A	303	12/12	0.83	0.21	33,36,38,40	12
5	CL	B	301	1/1	0.84	0.17	67,67,67,67	0
2	MG	A	302	1/1	0.85	0.10	59,59,59,59	0
4	EDO	B	302	4/4	0.89	0.12	41,43,43,45	0
2	MG	D	301	1/1	0.90	0.08	38,38,38,38	0
2	MG	D	302	1/1	0.94	0.19	40,40,40,40	0
4	EDO	A	305	4/4	0.94	0.08	26,27,28,29	0
2	MG	A	301	1/1	0.99	0.03	26,26,26,26	0
2	MG	B	303	1/1	0.99	0.02	27,27,27,27	0
2	MG	C	303	1/1	0.99	0.04	35,35,35,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.