



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 07:30 AM UTC

PDB ID : 6XV5 / pdb_00006xv5
Title : Crystal structure of penicillin-binding protein 2 from *Yersinia pestis* in complex with ertapenem
Authors : Pankov, G.; Hunter, W.N.; Dawson, A.
Deposited on : 2020-01-21
Resolution : 2.67 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

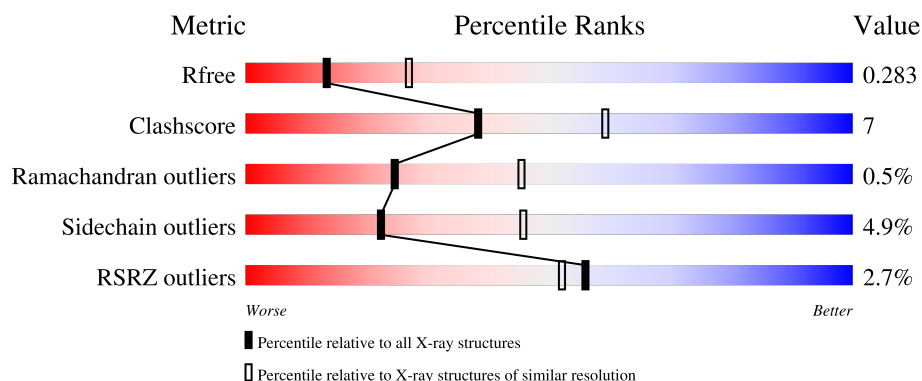
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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 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	AAA	583	3% 76% 15% 7%
1	BBB	583	2% 75% 13% 10%

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
1	O2E	AAA	331	X	-	-	-
1	O2E	BBB	331	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8700 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 Peptidoglycan D,D-transpeptidase MrdA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BBB	526	Total	C	N	O	S	0	3	0
			4205	2683	726	786	10			
1	AAA	543	Total	C	N	O	S	0	1	0
			4336	2761	757	808	10			

There are 36 discrepancies between the modelled and reference sequences:

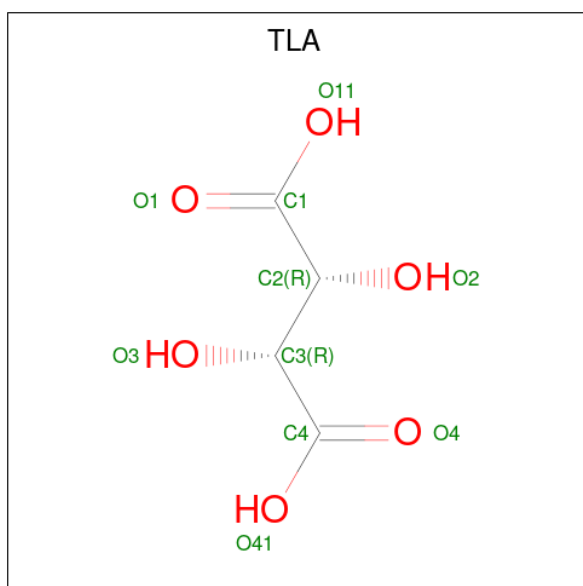
Chain	Residue	Modelled	Actual	Comment	Reference
BBB	31	HIS	-	expression tag	UNP A0A384KFW3
BBB	32	HIS	-	expression tag	UNP A0A384KFW3
BBB	33	HIS	-	expression tag	UNP A0A384KFW3
BBB	34	HIS	-	expression tag	UNP A0A384KFW3
BBB	35	HIS	-	expression tag	UNP A0A384KFW3
BBB	36	HIS	-	expression tag	UNP A0A384KFW3
BBB	37	SER	-	expression tag	UNP A0A384KFW3
BBB	38	SER	-	expression tag	UNP A0A384KFW3
BBB	39	GLY	-	expression tag	UNP A0A384KFW3
BBB	40	GLU	-	expression tag	UNP A0A384KFW3
BBB	41	ASN	-	expression tag	UNP A0A384KFW3
BBB	42	LEU	-	expression tag	UNP A0A384KFW3
BBB	43	TYR	-	expression tag	UNP A0A384KFW3
BBB	44	PHE	-	expression tag	UNP A0A384KFW3
BBB	45	GLN	-	expression tag	UNP A0A384KFW3
BBB	46	GLY	-	expression tag	UNP A0A384KFW3
BBB	47	HIS	-	expression tag	UNP A0A384KFW3
BBB	48	MET	-	expression tag	UNP A0A384KFW3
AAA	31	HIS	-	expression tag	UNP A0A384KFW3
AAA	32	HIS	-	expression tag	UNP A0A384KFW3
AAA	33	HIS	-	expression tag	UNP A0A384KFW3
AAA	34	HIS	-	expression tag	UNP A0A384KFW3
AAA	35	HIS	-	expression tag	UNP A0A384KFW3
AAA	36	HIS	-	expression tag	UNP A0A384KFW3
AAA	37	SER	-	expression tag	UNP A0A384KFW3

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	38	SER	-	expression tag	UNP A0A384KFW3
AAA	39	GLY	-	expression tag	UNP A0A384KFW3
AAA	40	GLU	-	expression tag	UNP A0A384KFW3
AAA	41	ASN	-	expression tag	UNP A0A384KFW3
AAA	42	LEU	-	expression tag	UNP A0A384KFW3
AAA	43	TYR	-	expression tag	UNP A0A384KFW3
AAA	44	PHE	-	expression tag	UNP A0A384KFW3
AAA	45	GLN	-	expression tag	UNP A0A384KFW3
AAA	46	GLY	-	expression tag	UNP A0A384KFW3
AAA	47	HIS	-	expression tag	UNP A0A384KFW3
AAA	48	MET	-	expression tag	UNP A0A384KFW3

- Molecule 2 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: $C_4H_6O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	AAA	1	Total C O 10 4 6	0	0

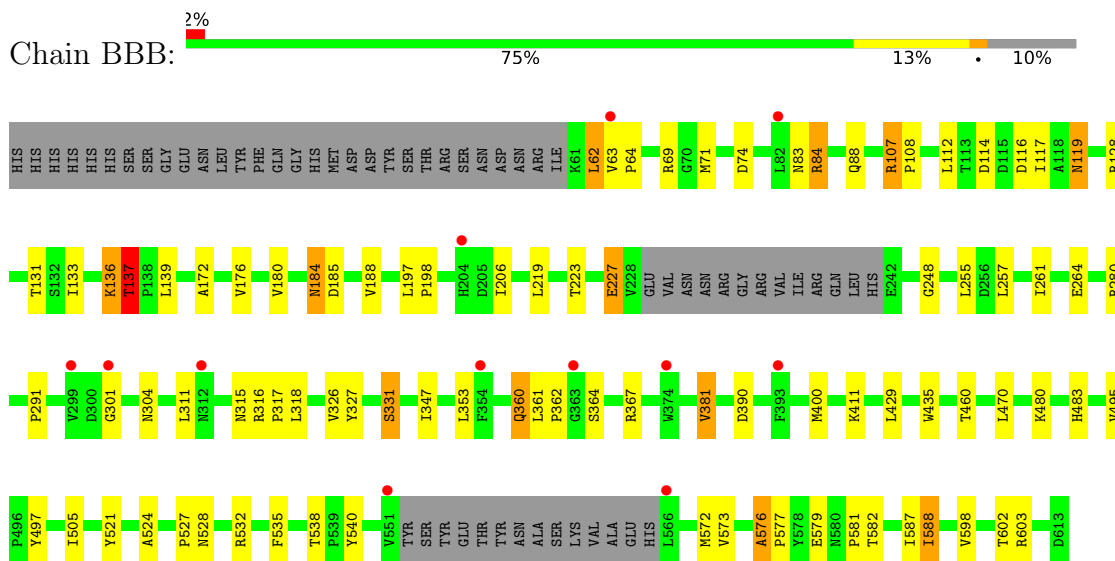
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	BBB	88	Total O 88 88	0	0
3	AAA	61	Total O 61 61	0	0

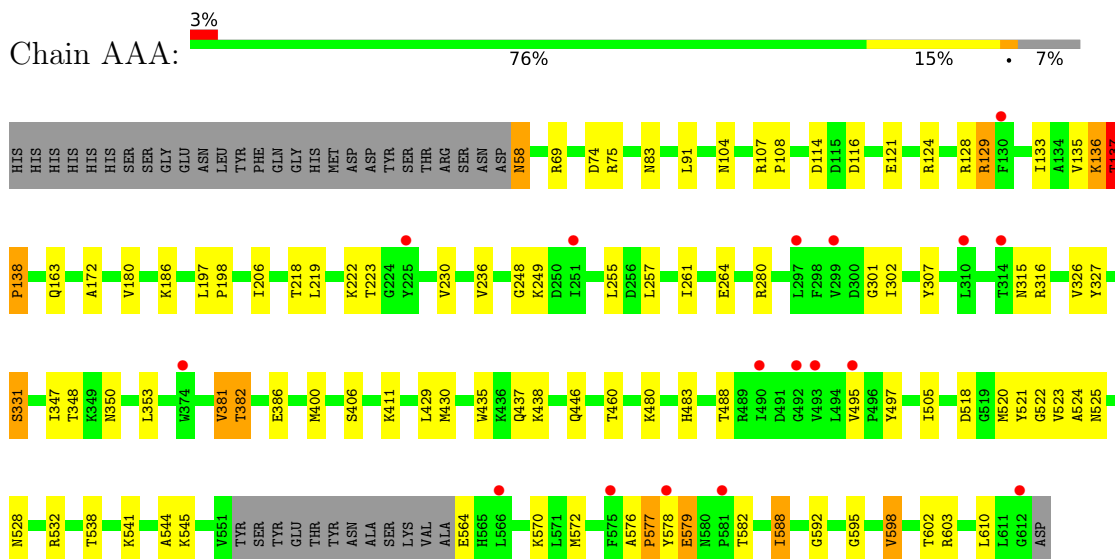
3 Residue-property plots

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: Peptidoglycan D,D-transpeptidase MrdA



- Molecule 1: Peptidoglycan D,D-transpeptidase MrdA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.27Å 147.77Å 164.52Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	109.94 – 2.67 109.94 – 2.67	Depositor EDS
% Data completeness (in resolution range)	77.2 (109.94-2.67) 77.3 (109.94-2.67)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.213 , 0.285 0.216 , 0.283	Depositor DCC
R_{free} test set	1485 reflections (3.74%)	wwPDB-VP
Wilson B-factor (Å ²)	75.1	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8700	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: O2E, TLA

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	AAA	0.99	0/4396	1.42	4/5963 (0.1%)
1	BBB	0.98	0/4266	1.43	3/5787 (0.1%)
All	All	0.99	0/8662	1.42	7/11750 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AAA	1	2
1	BBB	1	2
All	All	2	4

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	137	THR	CB-CA-C	7.79	120.94	108.87
1	BBB	137	THR	CB-CA-C	6.21	118.66	109.22
1	AAA	382	THR	CB-CA-C	5.59	120.35	110.85
1	AAA	528	ASN	CA-C-N	5.43	125.13	119.92
1	AAA	528	ASN	C-N-CA	5.43	125.13	119.92

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	BBB	331	O2E	C11
1	AAA	331	O2E	C11

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	137	THR	Peptide
1	AAA	576	ALA	Peptide
1	BBB	137	THR	Peptide
1	BBB	576	ALA	Peptide

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	AAA	4336	0	4295	57	0
1	BBB	4205	0	4159	61	0
2	AAA	10	0	4	0	0
3	AAA	61	0	0	0	0
3	BBB	88	0	0	2	0
All	All	8700	0	8458	117	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 7.

The worst 5 of 117 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:BBB:84[B]:ARG:HH21	1:BBB:84[B]:ARG:HG2	1.11	1.12
1:BBB:62:LEU:HD21	1:BBB:227:GLU:OE1	1.46	1.12
1:BBB:84[B]:ARG:HH21	1:BBB:84[B]:ARG:CG	1.82	0.93
1:BBB:131:THR:O	1:BBB:133:ILE:HD12	1.68	0.92
1:BBB:62:LEU:HD21	1:BBB:227:GLU:CD	1.98	0.89

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	AAA	539/583 (92%)	514 (95%)	22 (4%)	3 (1%)	21	41
1	BBB	522/583 (90%)	499 (96%)	21 (4%)	2 (0%)	30	51
All	All	1061/1166 (91%)	1013 (96%)	43 (4%)	5 (0%)	24	45

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	301	GLY
1	BBB	577	PRO
1	AAA	577	PRO
1	AAA	301	GLY
1	AAA	595	GLY

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	AAA	458/493 (93%)	434 (95%)	24 (5%)	21	43
1	BBB	444/493 (90%)	423 (95%)	21 (5%)	23	47
All	All	902/986 (92%)	857 (95%)	45 (5%)	22	45

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	186	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	AAA	437	GLN
1	AAA	222	LYS
1	AAA	381	VAL
1	AAA	446	GLN

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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$
1	O2E	BBB	331	1	38,41,41	1.81	6 (15%)	32,58,58	1.27	5 (15%)
1	O2E	AAA	331	1	38,41,41	1.76	6 (15%)	32,58,58	1.23	6 (18%)

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
1	O2E	BBB	331	1	1/1/13/16	29/35/64/64	0/3/3/3
1	O2E	AAA	331	1	1/1/13/16	26/35/64/64	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	331	O2E	C11-C24	-6.74	1.50	1.55
1	BBB	331	O2E	C11-C24	-6.46	1.50	1.55
1	BBB	331	O2E	C9-N2	6.00	1.33	1.28
1	AAA	331	O2E	C9-N2	4.84	1.32	1.28
1	BBB	331	O2E	C11-S1	-4.18	1.74	1.84

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	331	O2E	O5-C10-C9	-3.31	116.67	121.13
1	BBB	331	O2E	C23-C14-N3	-3.01	100.40	106.20
1	BBB	331	O2E	O8-C19-C18	2.78	121.97	114.84
1	AAA	331	O2E	O8-C19-C18	2.78	121.97	114.84
1	AAA	331	O2E	O5-C10-C9	-2.72	117.46	121.13

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	BBB	331	O2E	C11
1	AAA	331	O2E	C11

5 of 55 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	BBB	331	O2E	C24-C11-S1-C12
1	BBB	331	O2E	CA-C2-O2-C1
1	BBB	331	O2E	O2-C2-CA-C
1	BBB	331	O2E	C14-C15-N4-C16
1	BBB	331	O2E	O9-C15-N4-C16

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	BBB	331	O2E	3	0
1	AAA	331	O2E	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

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
2	TLA	AAA	701	-	9,9,9	1.13	0	12,12,12	0.97	1 (8%)

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
2	TLA	AAA	701	-	-	10/12/12/12	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	701	TLA	O11-C1-C2	2.03	118.95	113.31

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	701	TLA	C1-C2-C3-O3
2	AAA	701	TLA	O2-C2-C3-O3
2	AAA	701	TLA	O2-C2-C3-C4
2	AAA	701	TLA	C1-C2-C3-C4
2	AAA	701	TLA	O3-C3-C4-O4

There are no ring outliers.

No monomer is involved in short contacts.

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	AAA	542/583 (92%)	0.41	17 (3%)	51 47	46, 85, 126, 151	1 (0%)
1	BBB	525/583 (90%)	0.20	12 (2%)	61 57	32, 73, 124, 148	3 (0%)
All	All	1067/1166 (91%)	0.31	29 (2%)	56 52	32, 79, 126, 151	4 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	493	VAL	3.7
1	AAA	225[A]	TYR	3.6
1	AAA	310	LEU	3.0
1	AAA	566	LEU	2.9
1	BBB	82	LEU	2.8

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	O2E	BBB	331	39/39	0.87	0.12	56,99,136,138	0
1	O2E	AAA	331	39/39	0.89	0.11	56,96,164,165	0

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
2	TLA	AAA	701	10/10	0.64	0.10	111,122,126,127	0

6.5 Other polymers [i](#)

There are no such residues in this entry.