



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:43 AM UTC

PDB ID : 2A9G / pdb_00002a9g
Title : Structure of C406A arginine deiminase in complex with L-arginine
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Deposited on : 2005-07-11
Resolution : 2.30 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

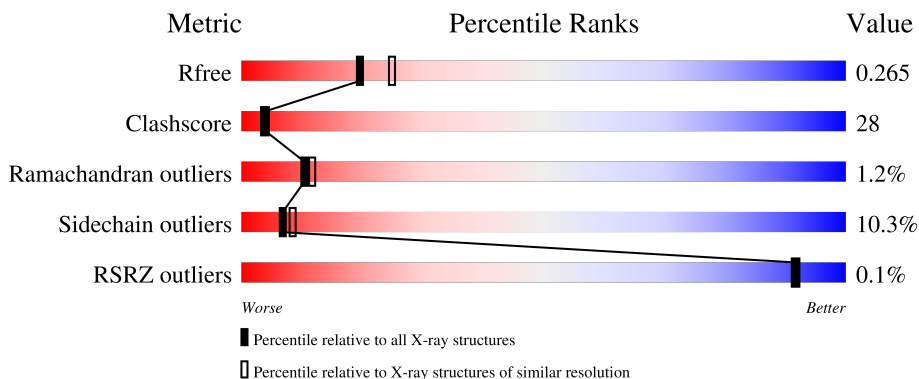
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	418	 45% 41% 10% . .
1	B	418	 54% 35% 7% . .
1	C	418	 54% 33% 9% .
1	D	418	 47% 40% 10% . .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13747 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.

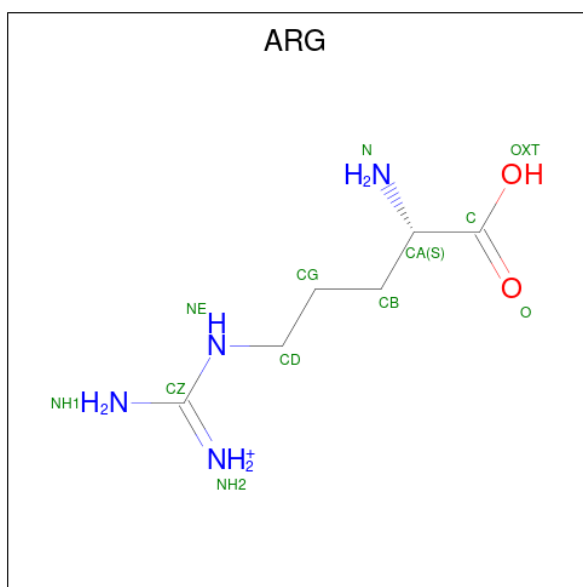
- Molecule 1 is a protein called Arginine deiminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	405	Total	C	N	O	S	0	0	0
			3163	2001	552	594	16			
1	B	405	Total	C	N	O	S	0	0	0
			3164	2002	552	594	16			
1	C	402	Total	C	N	O	S	0	0	0
			3141	1989	546	590	16			
1	D	406	Total	C	N	O	S	0	0	0
			3167	2003	553	595	16			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	406	ALA	CYS	engineered mutation	UNP P13981
B	406	ALA	CYS	engineered mutation	UNP P13981
C	406	ALA	CYS	engineered mutation	UNP P13981
D	406	ALA	CYS	engineered mutation	UNP P13981

- Molecule 2 is ARGININE (CCD ID: ARG) (formula: C₆H₁₅N₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		
2	B	1	Total	C	N	O	0	0
			12	6	4	2		
2	C	1	Total	C	N	O	0	0
			12	6	4	2		
2	D	1	Total	C	N	O	0	0
			12	6	4	2		

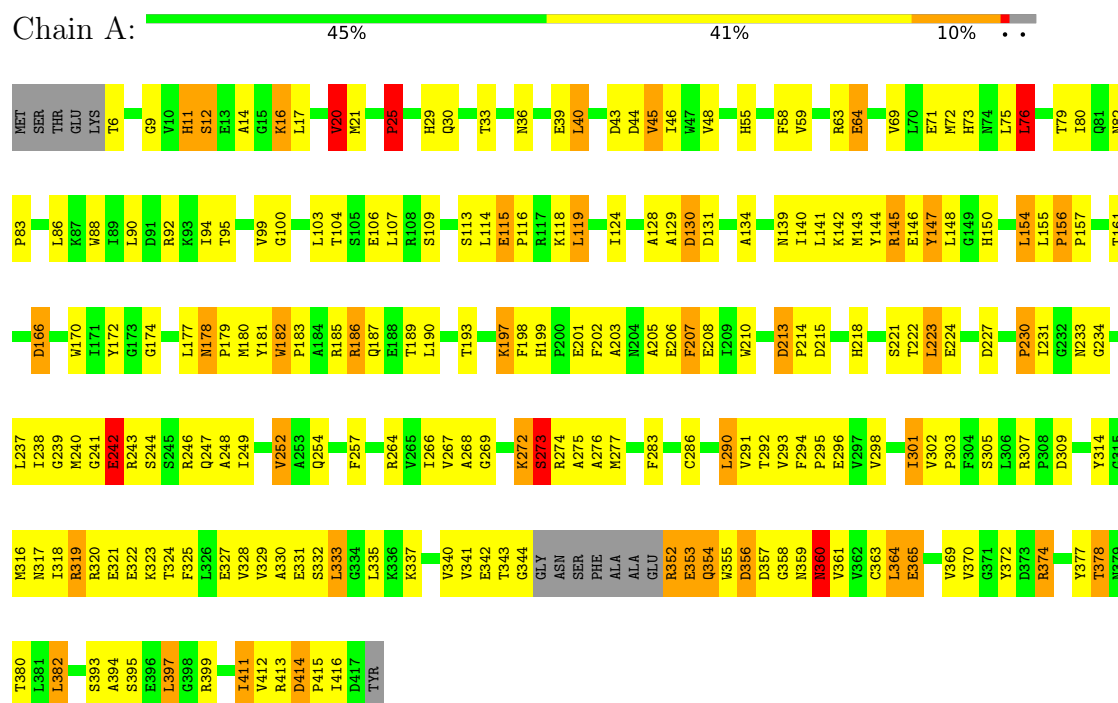
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	223	Total	O	0	0
			223	223		
3	B	277	Total	O	0	0
			277	277		
3	C	309	Total	O	0	0
			309	309		
3	D	255	Total	O	0	0
			255	255		

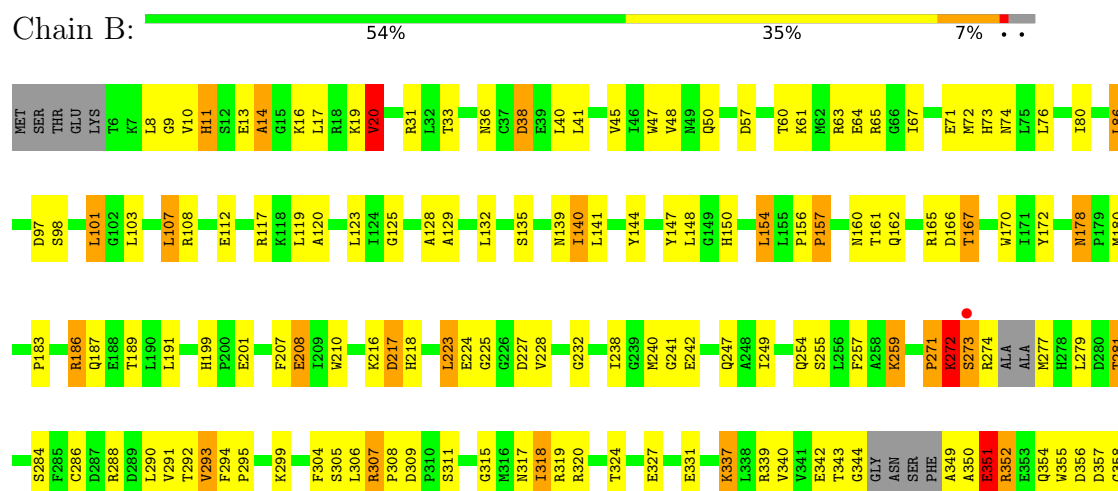
3 Residue-property plots

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: Arginine deiminase



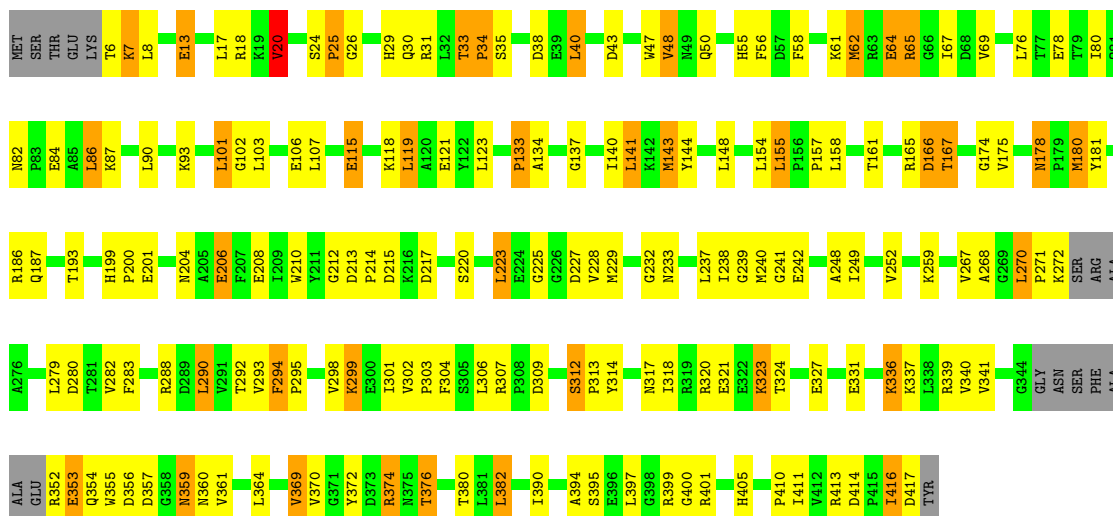
• Molecule 1: Arginine deiminase





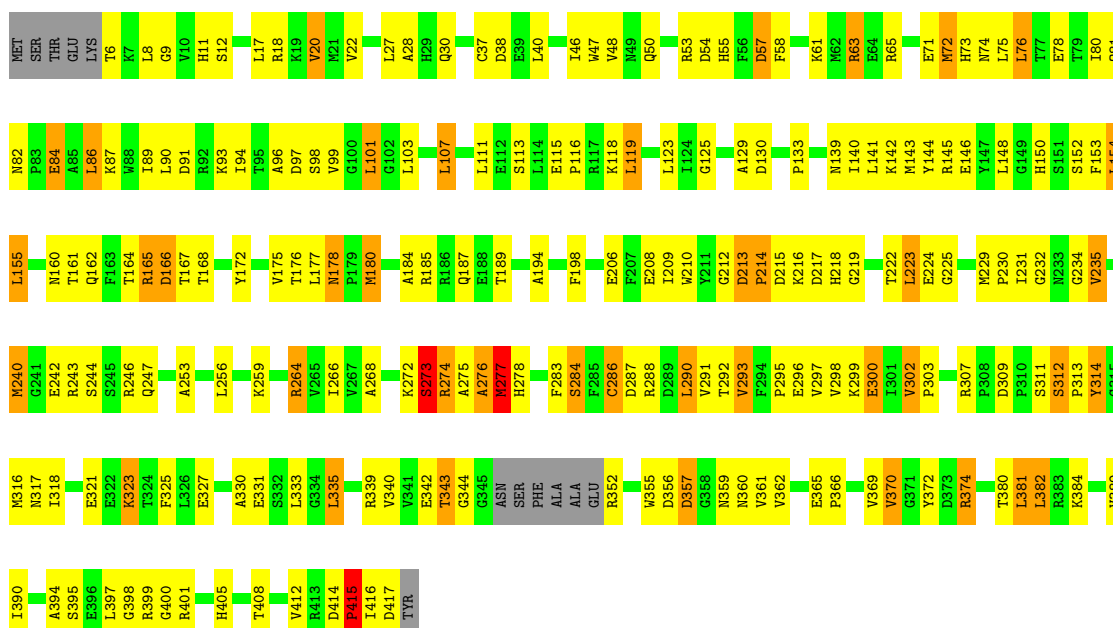
• Molecule 1: Arginine deiminase

Chain C: 54% 33% 9%



• Molecule 1: Arginine deiminase

Chain D: 47% 40% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.10Å 120.70Å 151.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.30) 99.0 (20.00-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.99 (at 2.30Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.199 , 0.267 0.199 , 0.265	Depositor DCC
R_{free} test set	2001 reflections (2.71%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13747	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 14.75% 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

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	0.78	0/3230	1.30	42/4381 (1.0%)
1	B	0.86	3/3230 (0.1%)	1.36	43/4379 (1.0%)
1	C	0.84	1/3207 (0.0%)	1.28	33/4349 (0.8%)
1	D	0.82	2/3234 (0.1%)	1.26	31/4386 (0.7%)
All	All	0.82	6/12901 (0.0%)	1.30	149/17495 (0.9%)

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	A	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	13	GLU	N-CA	6.14	1.53	1.46
1	D	297	VAL	N-CA	5.66	1.52	1.45
1	C	13	GLU	N-CA	5.50	1.53	1.46
1	D	370	VAL	CA-CB	-5.35	1.47	1.54
1	B	366	PRO	N-CA	5.09	1.53	1.47

The worst 5 of 149 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	273	SER	N-CA-C	17.42	131.79	110.19
1	C	48	VAL	N-CA-C	10.55	120.54	110.42
1	A	234	GLY	N-CA-C	-10.51	100.61	115.43
1	C	178	ASN	N-CA-C	9.91	122.14	109.65
1	B	354	GLN	OE1-CD-NE2	-9.71	112.89	122.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	147	TYR	Sidechain

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	A	3163	0	3151	209	0
1	B	3164	0	3152	155	0
1	C	3141	0	3127	169	0
1	D	3167	0	3154	194	0
2	A	12	0	12	0	0
2	B	12	0	12	2	0
2	C	12	0	12	0	0
2	D	12	0	12	0	0
3	A	223	0	0	53	0
3	B	277	0	0	32	0
3	C	309	0	0	46	0
3	D	255	0	0	46	0
All	All	13747	0	12632	703	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 28.

The worst 5 of 703 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:14:ALA:O	1:B:366:PRO:HD3	1.34	1.22
1:D:276:ALA:HA	3:D:4622:HOH:O	1.42	1.19
1:B:242:GLU:OE2	1:B:273:SER:HB3	1.42	1.19
1:A:247:GLN:HG2	3:D:4733:HOH:O	1.42	1.16
1:B:73:HIS:HB3	1:B:117:ARG:HH12	1.04	1.14

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	401/418 (96%)	366 (91%)	27 (7%)	8 (2%)	6	5
1	B	399/418 (96%)	367 (92%)	30 (8%)	2 (0%)	24	31
1	C	396/418 (95%)	368 (93%)	26 (7%)	2 (0%)	24	31
1	D	402/418 (96%)	363 (90%)	32 (8%)	7 (2%)	7	7
All	All	1598/1672 (96%)	1464 (92%)	115 (7%)	19 (1%)	10	12

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	242	GLU
1	B	352	ARG
1	A	273	SER
1	A	353	GLU
1	B	351	GLU

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	344/354 (97%)	309 (90%)	35 (10%)	7	8
1	B	344/354 (97%)	312 (91%)	32 (9%)	8	11
1	C	342/354 (97%)	304 (89%)	38 (11%)	6	7
1	D	344/354 (97%)	307 (89%)	37 (11%)	6	7
All	All	1374/1416 (97%)	1232 (90%)	142 (10%)	7	8

5 of 142 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	116	PRO
1	D	165	ARG
1	D	293	VAL
1	B	247	GLN
1	B	223	LEU

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	199	HIS
1	C	354	GLN
1	D	199	HIS
1	D	30	GLN
1	D	139	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](#)

4 ligands 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
2	ARG	D	4500	-	10,11,11	0.80	0	9,13,13	0.26	0
2	ARG	C	3500	-	10,11,11	0.77	0	9,13,13	0.74	0
2	ARG	B	2500	-	10,11,11	0.66	0	9,13,13	0.75	0
2	ARG	A	1500	-	10,11,11	0.72	0	9,13,13	0.88	1 (11%)

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	ARG	D	4500	-	-	0/11/11/11	-
2	ARG	C	3500	-	-	0/11/11/11	-
2	ARG	B	2500	-	-	1/11/11/11	-
2	ARG	A	1500	-	-	0/11/11/11	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1500	ARG	OXT-C-O	-2.00	119.54	124.08

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2500	ARG	OXT-C-CA-N

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2500	ARG	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	405/418 (96%)	-0.46	0 100 100	21, 38, 63, 78	0
1	B	405/418 (96%)	-0.67	1 (0%) 91 91	18, 30, 54, 78	0
1	C	402/418 (96%)	-0.68	0 100 100	18, 30, 54, 74	0
1	D	406/418 (97%)	-0.48	0 100 100	20, 36, 62, 79	0
All	All	1618/1672 (96%)	-0.57	1 (0%) 92 91	18, 33, 60, 79	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	273	SER	2.3

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(Å ²)	Q<0.9
2	ARG	D	4500	12/12	0.96	0.05	16,28,37,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ARG	B	2500	12/12	0.97	0.04	16,23,26,32	0
2	ARG	C	3500	12/12	0.97	0.05	16,21,29,33	0
2	ARG	A	1500	12/12	0.97	0.05	16,28,39,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.