



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:30 PM UTC

PDB ID : 4OBY / pdb_00004oby
Title : Crystal Structure of E.coli Arginyl-tRNA Synthetase and Ligand Binding Studies Revealed Key Residues in Arginine Recognition
Authors : Bi, K.; Zheng, Y.; Dong, J.; Gao, F.; Wang, J.; Wang, Y.; Gong, W.
Deposited on : 2014-01-08
Resolution : 2.57 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 : 4-5-2 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

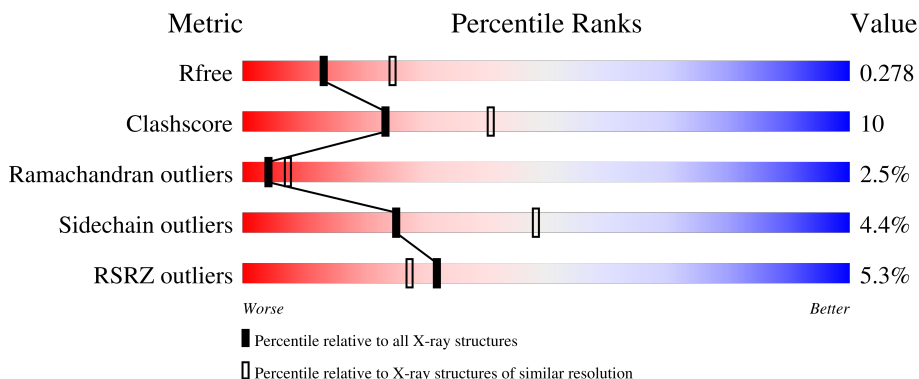
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.57 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	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	578	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4289 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.

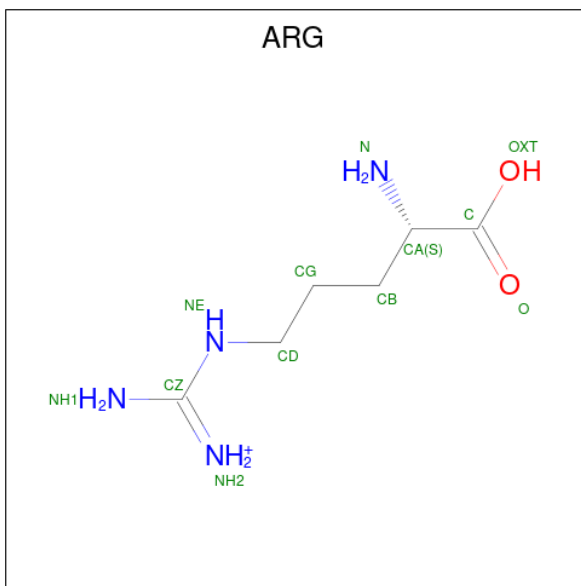
- Molecule 1 is a protein called Arginine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	564	4247	2699	737	788	23	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP P11875

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



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

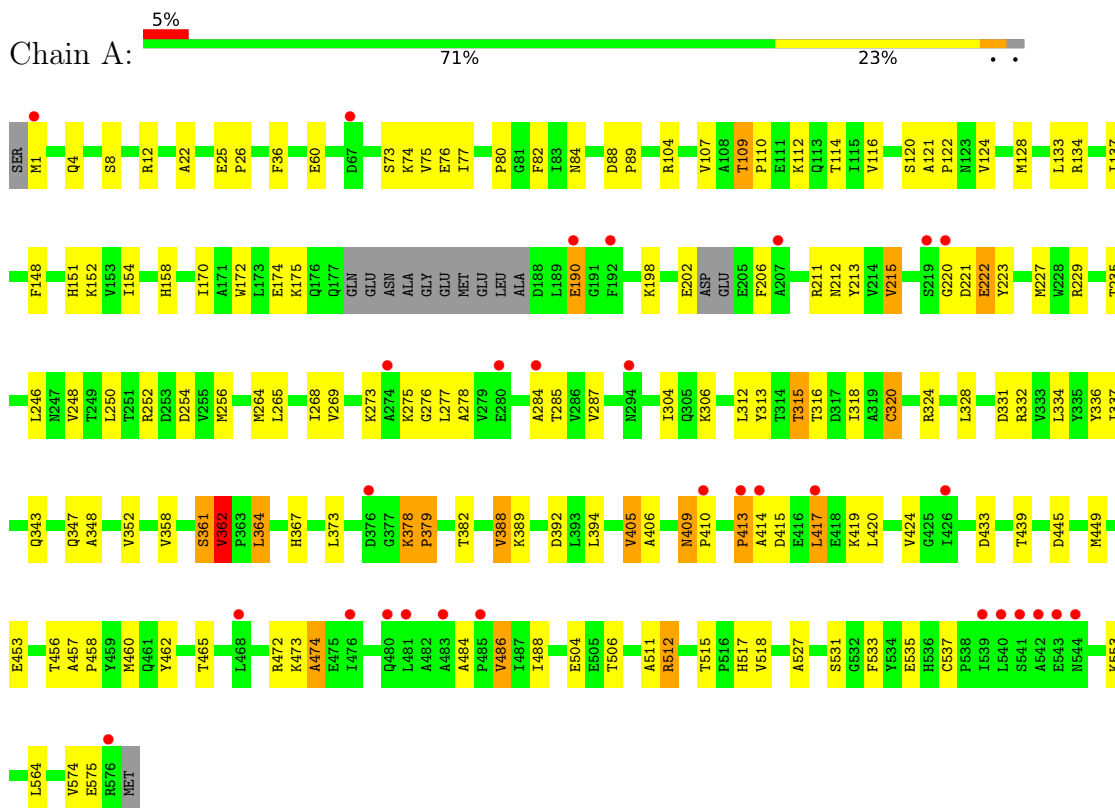
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	30	Total 30	O 30	0	0

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: Arginine-tRNA ligase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	118.60Å 94.14Å 62.72Å 90.00° 110.53° 90.00°	Depositor
Resolution (Å)	35.91 – 2.57 35.91 – 2.57	Depositor EDS
% Data completeness (in resolution range)	98.7 (35.91-2.57) 94.8 (35.91-2.57)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 2.58Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496), CNS	Depositor
R, R_{free}	0.201 , 0.278 0.208 , 0.278	Depositor DCC
R_{free} test set	1046 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	50.7	Xtrriage
Anisotropy	0.409	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4289	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.56% 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](#)

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	0.62	0/4327	0.96	13/5874 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	362	VAL	CA-C-N	7.82	129.61	119.84
1	A	362	VAL	C-N-CA	7.82	129.61	119.84
1	A	484	ALA	CA-C-N	-7.36	110.64	119.84
1	A	484	ALA	C-N-CA	-7.36	110.64	119.84
1	A	378	LYS	CA-C-N	6.92	128.49	119.84
1	A	378	LYS	C-N-CA	6.92	128.49	119.84
1	A	457	ALA	CA-C-N	-6.82	111.42	118.85
1	A	457	ALA	C-N-CA	-6.82	111.42	118.85
1	A	409	ASN	CA-C-N	5.72	126.99	119.84
1	A	409	ASN	C-N-CA	5.72	126.99	119.84
1	A	361	SER	N-CA-C	-5.43	102.96	110.35
1	A	109	THR	CA-C-N	5.29	126.03	120.11
1	A	109	THR	C-N-CA	5.29	126.03	120.11

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	4247	0	4065	85	0
2	A	12	0	12	1	0
3	A	30	0	0	1	0
All	All	4289	0	4077	85	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 (85) 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:273:LYS:HG2	1:A:277:LEU:HD12	1.56	0.85
1:A:12:ARG:NH1	1:A:22:ALA:O	2.11	0.82
1:A:277:LEU:HD11	1:A:285:THR:HB	1.65	0.78
1:A:104:ARG:NH2	1:A:148:PHE:O	2.22	0.71
1:A:256:MET:HE1	1:A:328:LEU:HD11	1.72	0.71
1:A:275:LYS:HB2	1:A:276:GLY:HA3	1.73	0.70
1:A:122:PRO:HB3	1:A:128:MET:HG3	1.77	0.66
1:A:36:PHE:O	1:A:84:ASN:ND2	2.29	0.65
1:A:413:PRO:HA	1:A:417:LEU:HB2	1.79	0.65
1:A:306:LYS:HD3	1:A:312:LEU:HD21	1.79	0.64
1:A:343:GLN:HE21	1:A:347:GLN:HE21	1.45	0.64
1:A:277:LEU:HD23	1:A:287:VAL:HG22	1.81	0.63
1:A:248:VAL:HG12	1:A:250:LEU:H	1.64	0.62
1:A:134:ARG:HG2	1:A:433:ASP:OD2	2.01	0.61
1:A:273:LYS:HA	1:A:277:LEU:HB3	1.83	0.60
1:A:107:VAL:HG13	1:A:504:GLU:HG3	1.84	0.60
1:A:304:ILE:O	1:A:315:THR:OG1	2.20	0.58
1:A:124:VAL:HA	1:A:235:THR:HG21	1.85	0.58
1:A:512:ARG:HD3	3:A:714:HOH:O	2.03	0.58
1:A:531:SER:O	1:A:535:GLU:HG3	2.05	0.56
1:A:486:VAL:HG13	1:A:553:LYS:HE3	1.88	0.56
1:A:114:THR:HG22	1:A:152:LYS:HD3	1.88	0.56
1:A:74:LYS:NZ	1:A:76:GLU:OE1	2.39	0.56
1:A:318:ILE:HG23	1:A:352:VAL:HG22	1.89	0.54
1:A:198:LYS:O	1:A:202:GLU:HG2	2.07	0.54
1:A:420:LEU:HD13	1:A:574:VAL:HG11	1.90	0.52
1:A:313:TYR:O	1:A:316:THR:HG22	2.09	0.52
1:A:73:SER:HB3	1:A:88:ASP:HA	1.91	0.52
1:A:533:PHE:O	1:A:537:CYS:HB3	2.09	0.52
1:A:515:THR:HB	1:A:517:HIS:CE1	2.45	0.51
1:A:456:THR:HB	1:A:458:PRO:HD2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LEU:HD13	1:A:278:ALA:N	2.26	0.50
1:A:275:LYS:HB2	1:A:276:GLY:CA	2.41	0.50
1:A:334:LEU:HG	1:A:367:HIS:CE1	2.47	0.49
1:A:424:VAL:HG13	1:A:458:PRO:HG3	1.93	0.49
1:A:133:LEU:O	1:A:137:ILE:HG12	2.11	0.49
1:A:212:ASN:O	1:A:215:VAL:HG22	2.13	0.49
1:A:112:LYS:HG2	1:A:151:HIS:HA	1.95	0.49
1:A:211:ARG:O	1:A:215:VAL:HG13	2.12	0.49
1:A:121:ALA:O	2:A:601:ARG:N	2.46	0.48
1:A:89:PRO:HB3	1:A:488:ILE:HB	1.95	0.48
1:A:174:GLU:OE1	1:A:213:TYR:OH	2.26	0.48
1:A:4:GLN:O	1:A:8:SER:HB2	2.14	0.48
1:A:331:ASP:O	1:A:362:VAL:HA	2.14	0.47
1:A:389:LYS:O	1:A:392:ASP:HB3	2.15	0.46
1:A:269:VAL:HG22	1:A:304:ILE:HD12	1.97	0.46
1:A:405:VAL:HG21	1:A:420:LEU:HG	1.96	0.46
1:A:223:TYR:O	1:A:227:MET:HG3	2.16	0.46
1:A:406:ALA:O	1:A:409:ASN:HB3	2.16	0.45
1:A:413:PRO:O	1:A:415:ASP:N	2.50	0.45
1:A:158:HIS:HA	1:A:256:MET:O	2.17	0.45
1:A:265:LEU:HD22	1:A:315:THR:HG22	1.98	0.45
1:A:36:PHE:HB3	1:A:84:ASN:ND2	2.32	0.44
1:A:222:GLU:OE1	1:A:229:ARG:NH2	2.51	0.44
1:A:122:PRO:HB3	1:A:128:MET:CG	2.45	0.44
1:A:190:GLU:H	1:A:190:GLU:HG2	1.54	0.44
1:A:564:LEU:HD23	1:A:564:LEU:HA	1.72	0.44
1:A:462:TYR:O	1:A:465:THR:OG1	2.28	0.43
1:A:472:ARG:O	1:A:474:ALA:N	2.51	0.43
1:A:172:TRP:HE3	1:A:206:PHE:CZ	2.37	0.43
1:A:336:TYR:C	1:A:337:ILE:HD13	2.44	0.43
1:A:415:ASP:HB2	1:A:419:LYS:NZ	2.33	0.43
1:A:332:ARG:NH2	1:A:511:ALA:O	2.44	0.42
1:A:264:MET:O	1:A:268:ILE:HG13	2.19	0.42
1:A:75:VAL:O	1:A:75:VAL:HG13	2.19	0.42
1:A:277:LEU:HD23	1:A:287:VAL:CG2	2.48	0.42
1:A:246:LEU:HD21	1:A:394:LEU:HD11	2.02	0.42
1:A:348:ALA:O	1:A:352:VAL:HG23	2.19	0.42
1:A:378:LYS:HA	1:A:379:PRO:HD3	1.86	0.42
1:A:60:GLU:OE1	1:A:77:ILE:HD12	2.20	0.42
1:A:80:PRO:HD2	1:A:82:PHE:CE2	2.55	0.42
1:A:506:THR:HG23	1:A:518:VAL:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:LEU:HD23	1:A:246:LEU:HA	1.86	0.41
1:A:316:THR:O	1:A:320:CYS:HB3	2.19	0.41
1:A:116:VAL:HG11	1:A:324:ARG:HD3	2.03	0.41
1:A:382:THR:HG23	1:A:388:VAL:HG13	2.02	0.41
1:A:277:LEU:HD11	1:A:285:THR:CB	2.45	0.41
1:A:116:VAL:HG22	1:A:154:ILE:HB	2.03	0.41
1:A:109:THR:HA	1:A:110:PRO:HD2	1.82	0.41
1:A:445:ASP:H	1:A:449:MET:HE3	1.86	0.41
1:A:25:GLU:HA	1:A:26:PRO:HD2	1.91	0.41
1:A:361:SER:O	1:A:362:VAL:HB	2.21	0.41
1:A:472:ARG:HH12	1:A:575:GLU:CD	2.29	0.40
1:A:343:GLN:HE21	1:A:347:GLN:NE2	2.15	0.40
1:A:460:MET:HE1	1:A:527:ALA:HB3	2.03	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	558/578 (96%)	511 (92%)	33 (6%)	14 (2%)	4 7

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	410	PRO
1	A	414	ALA
1	A	486	VAL
1	A	221	ASP
1	A	220	GLY
1	A	364	LEU
1	A	379	PRO
1	A	473	LYS

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Mol	Chain	Res	Type
1	A	474	ALA
1	A	120	SER
1	A	388	VAL
1	A	284	ALA
1	A	362	VAL
1	A	413	PRO

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	407/473 (86%)	389 (96%)	18 (4%)	25 48

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	170	ILE
1	A	175	LYS
1	A	190	GLU
1	A	215	VAL
1	A	222	GLU
1	A	252	ARG
1	A	254	ASP
1	A	315	THR
1	A	320	CYS
1	A	358	VAL
1	A	364	LEU
1	A	373	LEU
1	A	405	VAL
1	A	417	LEU
1	A	439	THR
1	A	453	GLU
1	A	512	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	HIS
1	A	98	GLN
1	A	113	GLN
1	A	343	GLN
1	A	536	HIS
1	A	556	GLN

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](#)

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	ARG	A	601	-	10,11,11	0.68	0	9,13,13	1.27	2 (22%)

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	A	601	-	-	0/11/11/11	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	ARG	OXT-C-O	-2.60	118.19	124.08
2	A	601	ARG	CG-CD-NE	2.31	118.68	112.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	ARG	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	564/578 (97%)	0.53	30 (5%) 32 27	33, 62, 106, 153	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	541	SER	3.6
1	A	539	ILE	3.3
1	A	280	GLU	3.2
1	A	481	LEU	3.0
1	A	192	PHE	2.9
1	A	480	GLN	2.9
1	A	376	ASP	2.8
1	A	476	ILE	2.8
1	A	540	LEU	2.7
1	A	485	PRO	2.7
1	A	207	ALA	2.6
1	A	417	LEU	2.6
1	A	219	SER	2.6
1	A	414	ALA	2.6
1	A	410	PRO	2.5
1	A	190	GLU	2.5
1	A	544	ASN	2.5
1	A	294	ASN	2.4
1	A	542	ALA	2.4
1	A	220	GLY	2.4
1	A	67	ASP	2.3
1	A	468	LEU	2.3
1	A	274	ALA	2.2
1	A	284	ALA	2.2
1	A	413	PRO	2.2
1	A	483	ALA	2.1
1	A	1	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	576	ARG	2.1
1	A	543	GLU	2.1
1	A	426	ILE	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 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	A	601	12/12	0.96	0.08	30,42,53,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.