



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:32 AM UTC

PDB ID : 3C3V / pdb_00003c3v
Title : Crystal structure of peanut major allergen ara h 3
Authors : Jin, T.; Zhang, Y.
Deposited on : 2008-01-28
Resolution : 1.73 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
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

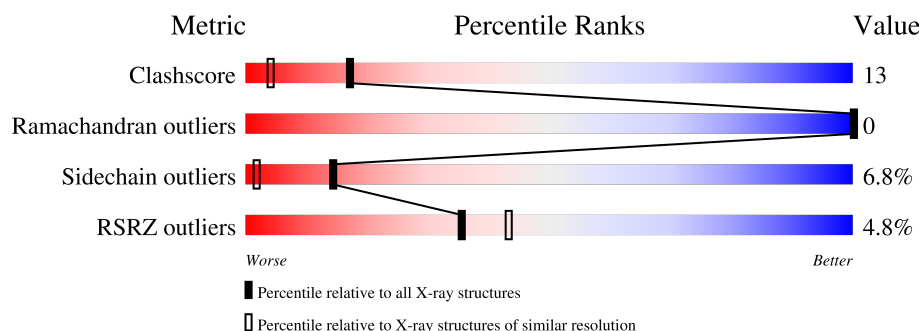
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.73 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))
Clashscore	190562	1207 (1.74-1.74)
Ramachandran outliers	187476	1200 (1.74-1.74)
Sidechain outliers	187428	1200 (1.74-1.74)
RSRZ outliers	180081	1188 (1.74-1.74)

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	510	4% 57% 18% • 22%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3563 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 Arachin Arah3 isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	398	Total	C	N	O	S	0	18	0
			3277	2059	592	622	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	HIS	ASN	SEE REMARK 999	UNP B5TYU1

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		

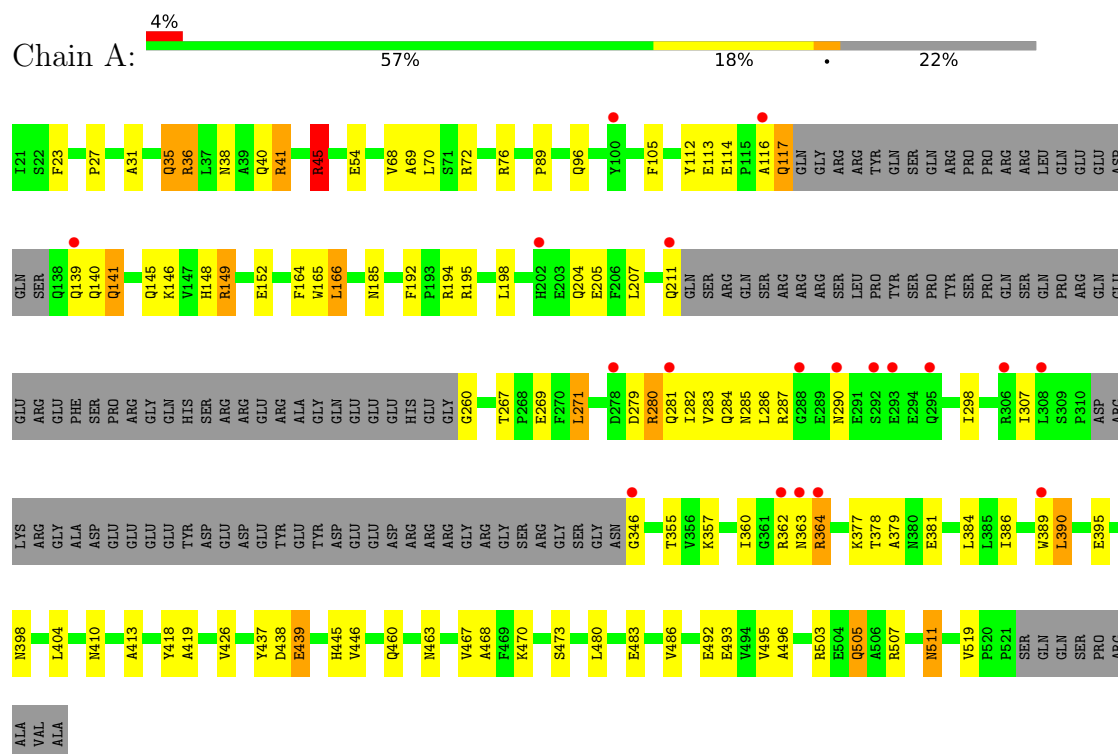
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	285	Total	O	0	0
			285	285		

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: Arachin Arah3 isoform



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	144.93Å 144.93Å 86.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.63 – 1.73 41.63 – 1.73	Depositor EDS
% Data completeness (in resolution range)	92.8 (41.63-1.73) 92.7 (41.63-1.73)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 1.73Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.186 , 0.248 0.183 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3563	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% 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:
NA

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	1.42	11/3394 (0.3%)	1.21	7/4605 (0.2%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	496	ALA	N-CA	6.46	1.54	1.46
1	A	426	VAL	CA-CB	6.14	1.62	1.54
1	A	69	ALA	N-CA	5.80	1.53	1.45
1	A	419	ALA	CA-CB	5.60	1.61	1.53
1	A	165	TRP	N-CA	5.48	1.52	1.45
1	A	112	TYR	N-CA	5.34	1.52	1.46
1	A	23	PHE	C-O	5.34	1.30	1.24
1	A	467	VAL	N-CA	5.25	1.52	1.46
1	A	68	VAL	CA-CB	5.10	1.62	1.54
1	A	486	VAL	C-O	-5.04	1.18	1.24
1	A	298	ILE	CA-CB	5.00	1.60	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	45	ARG	NE-CZ-NH2	-6.08	113.72	119.20
1	A	114	GLU	CA-C-N	6.07	126.02	119.76
1	A	114	GLU	C-N-CA	6.07	126.02	119.76
1	A	439	GLU	N-CA-C	5.84	116.11	107.88
1	A	495	VAL	N-CA-C	-5.83	104.83	110.72
1	A	389	TRP	CA-CB-CG	-5.65	102.86	113.60
1	A	511	ASN	N-CA-C	5.22	120.65	113.97

There are no chirality outliers.

There are no planarity outliers.

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	3277	0	3161	81	0
2	A	1	0	0	0	0
3	A	285	0	0	14	2
All	All	3563	0	3161	81	2

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 13.

All (81) 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:410[B]:ASN:ND2	1:A:413:ALA:HB3	1.70	1.04
1:A:410[B]:ASN:HD21	1:A:413:ALA:HB3	1.26	1.00
1:A:164:PHE:CE2	1:A:166:LEU:HD12	1.97	0.99
1:A:492:GLU:OE2	1:A:507:ARG:HG2	1.68	0.94
1:A:364[A]:ARG:H	1:A:364[A]:ARG:HE	1.18	0.87
1:A:503:ARG:HD2	1:A:507:ARG:HH21	1.43	0.84
1:A:96:GLN:HA	1:A:152:GLU:CG	2.13	0.78
1:A:164:PHE:HE2	1:A:166:LEU:HD12	1.49	0.76
1:A:404:LEU:HB3	1:A:519[A]:VAL:HG12	1.67	0.75
1:A:503:ARG:HH11	1:A:507:ARG:HE	1.35	0.73
1:A:267:THR:O	1:A:271[B]:LEU:HD12	1.88	0.72
1:A:492:GLU:OE2	1:A:507:ARG:CG	2.39	0.71
1:A:205[B]:GLU:H	1:A:205[B]:GLU:CD	1.94	0.70
1:A:76:ARG:HD2	3:A:663:HOH:O	1.93	0.68
1:A:164:PHE:CZ	1:A:166:LEU:HD12	2.30	0.67
1:A:363:ASN:CB	1:A:377:LYS:HE2	2.24	0.66
1:A:96:GLN:HA	1:A:152:GLU:HG2	1.76	0.66
1:A:116:ALA:HA	1:A:141:GLN:HB2	1.78	0.66
1:A:194:ARG:HA	1:A:204:GLN:HE22	1.61	0.65
1:A:149:ARG:O	1:A:357:LYS:HE2	1.97	0.64
1:A:40:GLN:HE21	1:A:40:GLN:HA	1.62	0.64
1:A:395[B]:GLU:HG2	1:A:470:LYS:HE3	1.81	0.63
1:A:195:ARG:H	1:A:204:GLN:NE2	1.98	0.61
1:A:185[A]:ASN:HB3	3:A:871:HOH:O	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:395[B]:GLU:HG3	1:A:468:ALA:HB3	1.84	0.59
1:A:105:PHE:H	1:A:145:GLN:HE22	1.51	0.58
1:A:364[A]:ARG:H	1:A:364[A]:ARG:NE	1.96	0.58
1:A:260:GLY:HA3	3:A:744:HOH:O	2.04	0.57
1:A:378:THR:HG23	3:A:855:HOH:O	2.05	0.56
1:A:503:ARG:HH11	1:A:507:ARG:NE	2.03	0.56
1:A:362:ARG:NH2	3:A:633:HOH:O	2.40	0.54
1:A:41:ARG:NH2	1:A:72[B]:ARG:HH22	2.08	0.52
1:A:281:GLN:O	1:A:281:GLN:HG3	2.09	0.52
1:A:211:GLN:HG2	3:A:803:HOH:O	2.08	0.52
1:A:503:ARG:NH1	1:A:507:ARG:HE	2.05	0.51
1:A:364[A]:ARG:NH2	3:A:884:HOH:O	2.44	0.51
1:A:41:ARG:HG3	1:A:445:HIS:CD2	2.46	0.51
1:A:116:ALA:HA	1:A:141:GLN:HE21	1.76	0.51
1:A:355:THR:HG22	1:A:384:LEU:CD1	2.41	0.50
1:A:45:ARG:HD2	1:A:54:GLU:HG2	1.94	0.50
1:A:439:GLU:HB2	3:A:813:HOH:O	2.12	0.49
1:A:40:GLN:HA	1:A:40:GLN:NE2	2.28	0.48
1:A:418:TYR:HD1	1:A:446:VAL:HG22	1.78	0.48
1:A:381:GLU:OE1	1:A:473:SER:OG	2.28	0.48
1:A:139:GLN:HB3	3:A:847:HOH:O	2.13	0.47
1:A:146:LYS:HE2	1:A:148:HIS:CD2	2.49	0.47
1:A:505:GLN:HG2	3:A:726:HOH:O	2.14	0.47
1:A:438:ASP:O	1:A:439:GLU:HB3	2.14	0.47
1:A:390:LEU:HD23	1:A:390:LEU:N	2.30	0.47
1:A:398:ASN:HB3	1:A:463:ASN:HD21	1.81	0.46
1:A:45:ARG:HD2	1:A:54:GLU:CG	2.46	0.46
1:A:194:ARG:HA	1:A:204:GLN:NE2	2.27	0.46
1:A:360:ILE:HG21	1:A:379:ALA:HB2	1.98	0.45
1:A:195:ARG:H	1:A:204:GLN:HE21	1.64	0.45
1:A:346:GLY:N	3:A:725:HOH:O	2.49	0.45
1:A:35[A]:GLN:NE2	3:A:863:HOH:O	2.50	0.44
1:A:70:LEU:CD2	1:A:446:VAL:HG21	2.48	0.44
1:A:141:GLN:HB2	1:A:141:GLN:HE21	1.62	0.44
1:A:271[B]:LEU:HD23	1:A:286[B]:LEU:HD13	1.99	0.43
1:A:27:PRO:HB2	1:A:31:ALA:HB3	2.00	0.43
1:A:164:PHE:CZ	1:A:166:LEU:CD1	3.00	0.43
1:A:364[A]:ARG:HE	1:A:364[A]:ARG:N	2.00	0.43
1:A:279:ASP:HB3	1:A:282:ILE:HD12	2.00	0.43
1:A:117:GLN:HB2	3:A:777:HOH:O	2.18	0.43
1:A:437:TYR:CZ	1:A:439:GLU:HG2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:271[A]:LEU:HD23	1:A:287:ARG:HD3	2.01	0.43
1:A:36:ARG:CD	1:A:38:ASN:HD21	2.32	0.43
1:A:70:LEU:HD23	1:A:446:VAL:HG21	2.01	0.42
1:A:507:ARG:O	1:A:511:ASN:ND2	2.52	0.42
1:A:280:ARG:O	1:A:284:GLN:HG3	2.20	0.42
1:A:113:GLU:OE1	1:A:140:GLN:NE2	2.53	0.42
1:A:283:VAL:O	1:A:287:ARG:HG3	2.19	0.42
1:A:89:PRO:HB3	1:A:390:LEU:HD13	2.01	0.42
1:A:117:GLN:H	1:A:141:GLN:NE2	2.19	0.41
1:A:378:THR:CG2	3:A:855:HOH:O	2.67	0.41
1:A:36:ARG:NE	1:A:38:ASN:HD21	2.19	0.41
1:A:117:GLN:HE21	1:A:117:GLN:HB3	1.56	0.40
1:A:204:GLN:HA	1:A:205[B]:GLU:OE1	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:846:HOH:O	3:A:868:HOH:O[2_545]	2.09	0.11
3:A:867:HOH:O	3:A:869:HOH:O[9_555]	2.14	0.06

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	408/510 (80%)	390 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	355/441 (80%)	328 (92%)	27 (8%)	12 1

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35[A]	GLN
1	A	35[B]	GLN
1	A	36	ARG
1	A	41	ARG
1	A	45	ARG
1	A	117	GLN
1	A	141	GLN
1	A	149	ARG
1	A	166	LEU
1	A	192	PHE
1	A	198	LEU
1	A	207	LEU
1	A	269	GLU
1	A	271[A]	LEU
1	A	271[B]	LEU
1	A	280	ARG
1	A	290[A]	ASN
1	A	290[B]	ASN
1	A	307	ILE
1	A	364[A]	ARG
1	A	364[B]	ARG
1	A	390	LEU
1	A	460	GLN
1	A	480	LEU
1	A	483	GLU
1	A	493	GLU
1	A	505	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	30	ASN
1	A	38	ASN
1	A	40	GLN
1	A	44	ASN
1	A	60	ASN
1	A	117	GLN
1	A	140	GLN
1	A	141	GLN
1	A	145	GLN
1	A	148	HIS
1	A	151	ASN
1	A	191	GLN
1	A	204	GLN
1	A	210	GLN
1	A	211	GLN
1	A	276	GLN
1	A	398	ASN
1	A	460	GLN
1	A	463	ASN
1	A	484	ASN
1	A	512	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 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	398/510 (78%)	0.39	19 (4%)	35 43	13, 32, 53, 81	18 (4%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	364[A]	ARG	5.7
1	A	295[A]	GLN	4.4
1	A	308	LEU	3.7
1	A	389	TRP	3.5
1	A	290[A]	ASN	3.2
1	A	292	SER	3.1
1	A	281	GLN	2.9
1	A	116	ALA	2.9
1	A	363	ASN	2.8
1	A	202	HIS	2.7
1	A	346	GLY	2.5
1	A	362	ARG	2.4
1	A	288	GLY	2.4
1	A	211	GLN	2.2
1	A	293	GLU	2.2
1	A	278	ASP	2.1
1	A	139	GLN	2.0
1	A	306	ARG	2.0
1	A	100	TYR	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($\text{\AA}^2$)	Q<0.9
2	NA	A	1	1/1	0.98	0.05	29,29,29,29	0

6.5 Other polymers [i](#)

There are no such residues in this entry.