



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:54 AM UTC

PDB ID : 5G5S / pdb_00005g5s
Title : Structure of the Argonaute protein from Methanocaldococcus janaschii
Authors : Schneider, S.; Oellig, C.A.; Keegan, R.; Grohmann, D.; Zander, A.; Willkomm, S.
Deposited on : 2016-06-03
Resolution : 2.29 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

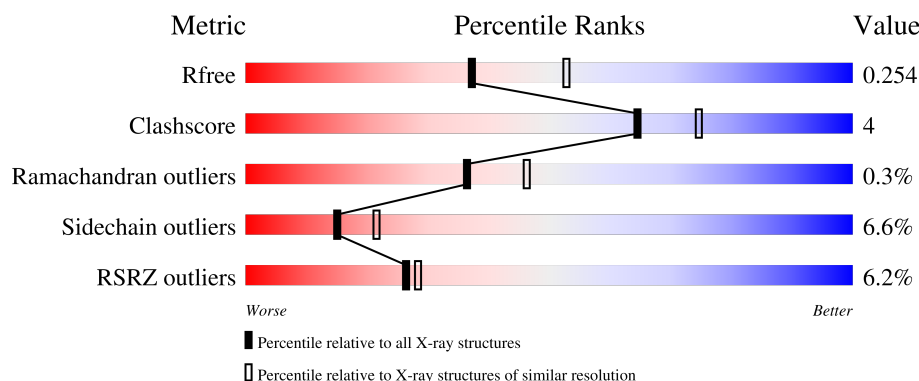
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	715	6% 81% 15% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5570 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 ARGONAUTE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	692	Total	C	N	O	S	0	3	0
			5559	3629	892	1019	19			

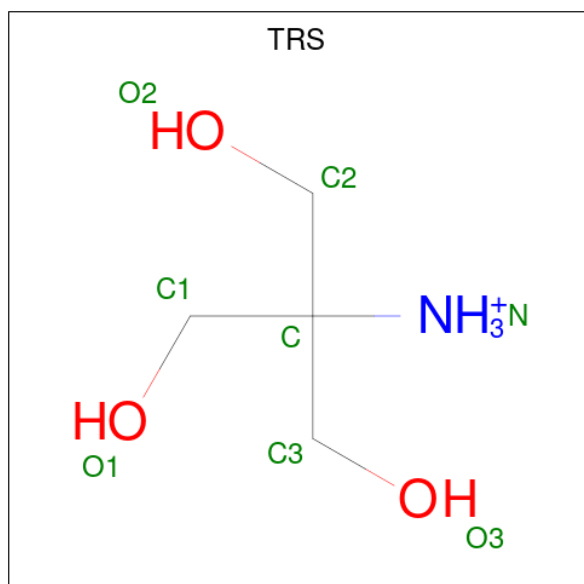
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	PHE	-	expression tag	UNP Q58717
A	0	THR	-	expression tag	UNP Q58717

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

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

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			8	4	1	3		

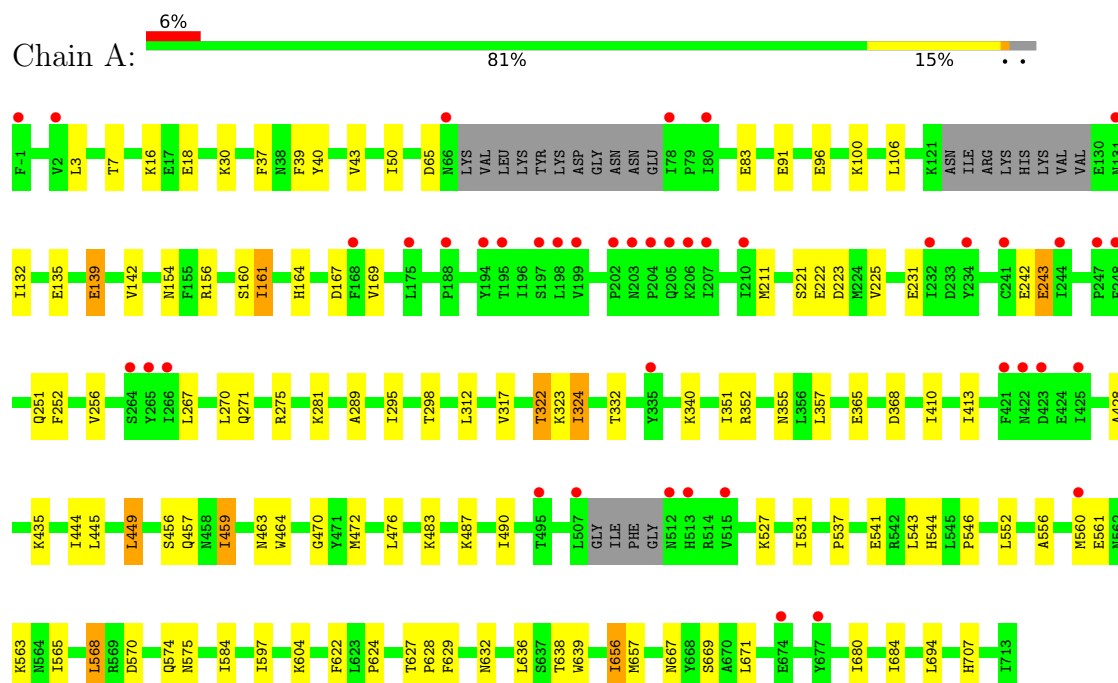
- Molecule 4 is water.

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

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: ARGONAUTE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.48Å 104.93Å 115.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.12 – 2.29 49.12 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.9 (49.12-2.29) 98.8 (49.12-2.29)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.14 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.210 , 0.236 0.223 , 0.254	Depositor DCC
R_{free} test set	1791 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	68.7	Xtriage
Anisotropy	0.275	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 69.9	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	0.95	EDS
Total number of atoms	5570	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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: MG, TRS

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	0/5697	1.28	19/7732 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	622	PHE	CA-CB-CG	6.30	120.10	113.80
1	A	222	GLU	CA-C-N	6.00	128.60	120.38
1	A	222	GLU	C-N-CA	6.00	128.60	120.38
1	A	470	GLY	CA-C-N	5.96	128.19	120.44
1	A	470	GLY	C-N-CA	5.96	128.19	120.44
1	A	16	LYS	CA-C-N	5.75	129.44	120.82
1	A	16	LYS	C-N-CA	5.75	129.44	120.82
1	A	221	SER	N-CA-C	-5.67	102.90	110.55
1	A	231	GLU	CA-C-N	5.54	128.00	120.63
1	A	231	GLU	C-N-CA	5.54	128.00	120.63
1	A	252	PHE	CA-CB-CG	5.47	119.27	113.80
1	A	531	ILE	N-CA-C	-5.34	99.00	106.53
1	A	7	THR	CB-CA-C	5.23	118.37	109.80
1	A	242	GLU	N-CA-C	5.12	116.55	111.07
1	A	570	ASP	N-CA-C	-5.12	102.49	109.71
1	A	271	GLN	CA-C-N	5.11	127.38	120.38
1	A	271	GLN	C-N-CA	5.11	127.38	120.38
1	A	243	GLU	N-CA-C	5.07	117.93	111.69
1	A	37	PHE	N-CA-C	5.02	116.75	111.28

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	5559	0	5331	42	0
2	A	1	0	0	0	0
3	A	8	0	12	0	0
4	A	2	0	0	0	0
All	All	5570	0	5343	42	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.

All (42) 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:164:HIS:CD2	1:A:251:GLN:HA	2.36	0.60
1:A:139:GLU:HG3	1:A:154:ASN:HB3	1.85	0.59
1:A:463:ASN:HB3	1:A:472:MET:HE1	1.85	0.58
1:A:627:THR:HG22	1:A:628:PRO:HD2	1.89	0.55
1:A:322:THR:HG21	1:A:340:LYS:HE2	1.90	0.54
1:A:30:LYS:HB3	1:A:83:GLU:HB2	1.90	0.53
1:A:667:ASN:ND2	1:A:669:SER:H	2.08	0.52
1:A:627:THR:CG2	1:A:628:PRO:HD2	2.40	0.52
1:A:43:VAL:HG21	1:A:50:ILE:HG13	1.92	0.51
1:A:639:TRP:CZ3	1:A:656[A]:ILE:HG12	2.46	0.50
1:A:667:ASN:HD21	1:A:669:SER:HB2	1.76	0.50
1:A:40:TYR:HA	1:A:50:ILE:HD11	1.93	0.49
1:A:312:LEU:HB2	1:A:324:ILE:HG22	1.95	0.49
1:A:568:LEU:HG	1:A:597:ILE:HD12	1.95	0.48
1:A:544:HIS:CD2	1:A:546:PRO:HD2	2.50	0.47
1:A:487:LYS:HG2	1:A:527:LYS:HD2	1.97	0.46
1:A:680:ILE:HD12	1:A:684:ILE:HG23	1.98	0.46
1:A:275:ARG:HB2	1:A:629:PHE:CD1	2.51	0.45
1:A:39:PHE:CE2	1:A:50:ILE:HG12	2.51	0.45
1:A:537:PRO:HG2	1:A:541:GLU:HG3	1.99	0.45
1:A:267:LEU:HA	1:A:270:LEU:HD12	1.99	0.44
1:A:561:GLU:O	1:A:563:LYS:HG2	2.17	0.44
1:A:160:SER:HB3	1:A:256:VAL:HG22	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:GLN:HE21	1:A:483:LYS:HD2	1.82	0.44
1:A:457:GLN:NE2	1:A:483:LYS:HD2	2.32	0.44
1:A:459:ILE:HD12	1:A:464:TRP:HB2	2.00	0.44
1:A:132:ILE:HD11	1:A:161:ILE:HD13	2.00	0.44
1:A:410:ILE:HG21	1:A:444:ILE:HG22	2.00	0.44
1:A:552:LEU:HA	1:A:556:ALA:HB3	2.00	0.44
1:A:211:MET:HG2	1:A:225:VAL:HG11	2.00	0.43
1:A:445:LEU:O	1:A:449:LEU:HB2	2.18	0.43
1:A:164:HIS:CD2	1:A:167:ASP:H	2.36	0.43
1:A:476:LEU:HA	1:A:671:LEU:HD11	2.01	0.43
1:A:428:ALA:HB3	1:A:456:SER:HB3	2.01	0.42
1:A:560:MET:HE3	1:A:565:ILE:HD13	2.02	0.42
1:A:487:LYS:NZ	1:A:707:HIS:O	2.53	0.42
1:A:636:LEU:HD12	1:A:657:MET:HE3	2.01	0.41
1:A:40:TYR:CD1	1:A:40:TYR:C	2.97	0.41
1:A:459:ILE:HD11	1:A:472:MET:SD	2.60	0.41
1:A:604:LYS:HE3	1:A:632:ASN:OD1	2.21	0.40
1:A:289:ALA:HA	1:A:295:ILE:HD11	2.03	0.40
1:A:365:GLU:OE1	1:A:435:LYS:NZ	2.54	0.40

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	A	687/715 (96%)	662 (96%)	23 (3%)	2 (0%)	36 46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	624	PRO
1	A	169	VAL

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	578/664 (87%)	538 (93%)	40 (7%)	14	20

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	18	GLU
1	A	65	ASP
1	A	91	GLU
1	A	96	GLU
1	A	100	LYS
1	A	106	LEU
1	A	135	GLU
1	A	139	GLU
1	A	142[A]	VAL
1	A	142[B]	VAL
1	A	156	ARG
1	A	161	ILE
1	A	223	ASP
1	A	243	GLU
1	A	281	LYS
1	A	298	THR
1	A	317	VAL
1	A	322	THR
1	A	323	LYS
1	A	324	ILE
1	A	332	THR
1	A	351	ILE
1	A	352	ARG
1	A	355	ASN
1	A	357	LEU
1	A	368	ASP
1	A	413	ILE
1	A	449	LEU
1	A	459	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	490	ILE
1	A	543	LEU
1	A	568	LEU
1	A	574	GLN
1	A	575	ASN
1	A	584	ILE
1	A	638	THR
1	A	656[A]	ILE
1	A	656[B]	ILE
1	A	694	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	254	ASN
1	A	353	ASN
1	A	457	GLN
1	A	562	ASN
1	A	589	ASN
1	A	591	ASN
1	A	643	ASN
1	A	667	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	TRS	A	1715	-	7,7,7	0.27	0	9,9,9	0.22	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	TRS	A	1715	-	-	0/9/9/9	-

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 [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	692/715 (96%)	0.53	43 (6%) 26 28	27, 88, 128, 160	4 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	ILE	5.2
1	A	-1	PHE	4.7
1	A	560	MET	3.9
1	A	204	PRO	3.6
1	A	80	ILE	3.5
1	A	199	VAL	3.4
1	A	234	TYR	3.4
1	A	207	ILE	3.3
1	A	188	PRO	3.2
1	A	507	LEU	3.1
1	A	205	GLN	3.0
1	A	512	ASN	3.0
1	A	66	ASN	3.0
1	A	241	CYS	2.9
1	A	515	VAL	2.7
1	A	247	PRO	2.7
1	A	194	TYR	2.7
1	A	197	SER	2.6
1	A	206	LYS	2.6
1	A	203	ASN	2.6
1	A	248	PHE	2.5
1	A	495	THR	2.5
1	A	677	TYR	2.5
1	A	195	THR	2.4
1	A	168	PHE	2.4
1	A	674	GLU	2.4
1	A	2	VAL	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	131	ASN	2.3
1	A	422	ASN	2.3
1	A	202	PRO	2.3
1	A	265	TYR	2.3
1	A	210	ILE	2.3
1	A	264	SER	2.3
1	A	423	ASP	2.2
1	A	232	ILE	2.2
1	A	266	ILE	2.2
1	A	175	LEU	2.1
1	A	198	LEU	2.1
1	A	421	PHE	2.1
1	A	513	HIS	2.1
1	A	335	TYR	2.1
1	A	244	ILE	2.0
1	A	425	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($\text{\AA}^2$)	Q<0.9
3	TRS	A	1715	8/8	0.81	0.12	108,109,110,110	0
2	MG	A	1714	1/1	0.92	0.06	87,87,87,87	0

6.5 Other polymers [i](#)

There are no such residues in this entry.