



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:32 AM GMT

PDB ID : 2XHC
Title : Crystal Structure of Thermotoga maritima N-utilization Substance G (NusG)
Authors : Stegmann, C.M.; Wahl, M.C.
Deposited on : 2010-06-14
Resolution : 2.45 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

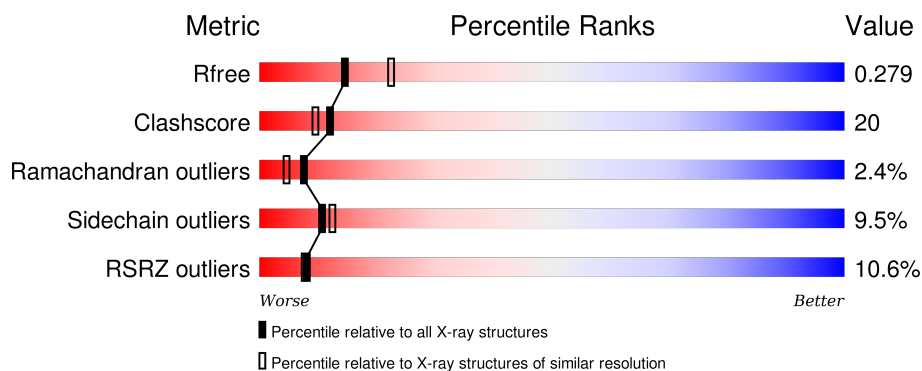
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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}	91344	4776 (2.50-2.42)
Clashscore	102246	1030 (2.48-2.44)
Ramachandran outliers	100387	1024 (2.48-2.44)
Sidechain outliers	100360	1024 (2.48-2.44)
RSRZ outliers	91569	4787 (2.50-2.42)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	352	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2763 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 TRANSCRIPTION ANTITERMINATION PROTEIN NUSG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	341	Total	C	N	O	S	0	0	0
			2736	1756	465	506	9			

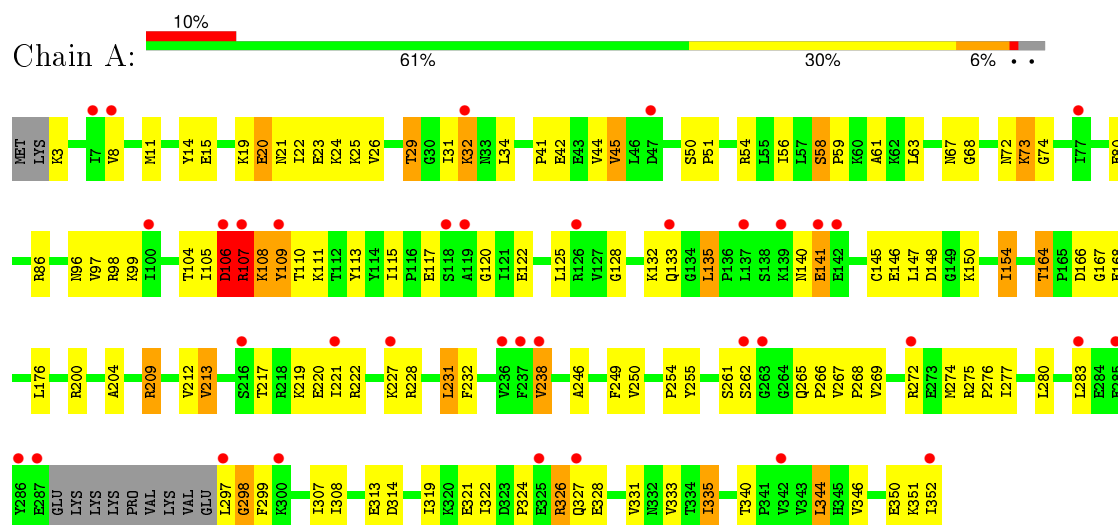
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	27	Total	O	0	0
			27	27		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: TRANSCRIPTION ANTITERMINATION PROTEIN NUSG



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	59.75Å 59.75Å 310.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.71 – 2.45 19.62 – 2.39	Depositor EDS
% Data completeness (in resolution range)	95.4 (32.71-2.45) 99.5 (19.62-2.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.38Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.217 , 0.277 0.212 , 0.279	Depositor DCC
R_{free} test set	1115 reflections (5.16%)	DCC
Wilson B-factor (Å ²)	61.3	Xtriage
Anisotropy	0.548	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 23231 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2763	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.36	0/2782	0.54	0/3744

There are no bond length outliers.

There are no bond angle outliers.

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	2736	0	2846	111	0
2	A	27	0	0	2	0
All	All	2763	0	2846	111	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 20.

All (111) 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:25:LYS:O	1:A:29:THR:HB	1.81	0.81
1:A:68:GLY:O	1:A:209:ARG:HD2	1.80	0.81
1:A:105:ILE:H	1:A:105:ILE:HD12	1.51	0.74
1:A:269:VAL:CG1	1:A:274:MET:HG2	2.16	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ASP:O	1:A:107:ARG:HD3	1.87	0.74
1:A:232:PHE:HE2	1:A:335:ILE:HD13	1.53	0.72
1:A:107:ARG:HG2	1:A:108:LYS:N	2.04	0.72
1:A:331:VAL:HG13	1:A:344:LEU:HD21	1.70	0.72
1:A:20:GLU:HG2	1:A:21:ASN:N	2.04	0.71
1:A:275:ARG:CG	1:A:276:PRO:HD3	2.21	0.70
1:A:307:ILE:HG22	1:A:313:GLU:HA	1.72	0.70
1:A:20:GLU:O	1:A:24:LYS:HG3	1.93	0.69
1:A:44:VAL:HG23	1:A:209:ARG:HH12	1.59	0.68
1:A:113:TYR:OH	1:A:146:GLU:HG2	1.93	0.67
1:A:164:THR:HG23	1:A:166:ASP:H	1.59	0.66
1:A:98:ARG:HH11	1:A:154:ILE:HD11	1.61	0.66
1:A:115:ILE:HD12	1:A:115:ILE:N	2.11	0.66
1:A:213:VAL:HG22	1:A:220:GLU:HB2	1.81	0.63
1:A:44:VAL:HG12	1:A:228:ARG:HG3	1.81	0.63
1:A:108:LYS:HE3	1:A:109:TYR:CD2	2.34	0.62
1:A:29:THR:CG2	1:A:31:ILE:H	2.13	0.61
1:A:327:GLN:HB3	1:A:346:VAL:HG12	1.81	0.61
1:A:105:ILE:HD12	1:A:105:ILE:N	2.15	0.61
1:A:335:ILE:HD12	1:A:335:ILE:H	1.66	0.60
1:A:269:VAL:HG11	1:A:274:MET:HG2	1.83	0.60
1:A:63:LEU:HD22	1:A:221:ILE:HD11	1.84	0.60
1:A:299:PHE:HE1	1:A:346:VAL:HG23	1.67	0.59
1:A:108:LYS:HG3	1:A:109:TYR:N	2.16	0.59
1:A:32:LYS:HD3	1:A:32:LYS:H	1.68	0.59
1:A:275:ARG:HG3	1:A:276:PRO:HD3	1.84	0.59
1:A:58:SER:HB3	1:A:80:GLU:OE2	2.03	0.59
1:A:322:ILE:HG22	1:A:324:PRO:HD3	1.85	0.59
1:A:269:VAL:HB	1:A:274:MET:HG2	1.85	0.58
1:A:108:LYS:HG3	1:A:109:TYR:H	1.69	0.57
1:A:275:ARG:HG2	1:A:276:PRO:HD3	1.85	0.57
1:A:299:PHE:HE2	1:A:351:LYS:HB3	1.69	0.57
1:A:122:GLU:HB3	1:A:125:LEU:HD13	1.87	0.56
1:A:335:ILE:HD11	1:A:340:THR:HB	1.87	0.56
1:A:80:GLU:HG2	1:A:200:ARG:NH1	2.20	0.56
1:A:73:LYS:O	1:A:204:ALA:O	2.24	0.56
1:A:29:THR:HG23	1:A:31:ILE:H	1.71	0.55
1:A:299:PHE:CE1	1:A:346:VAL:HG23	2.42	0.55
1:A:44:VAL:HG23	1:A:209:ARG:NH1	2.21	0.55
1:A:105:ILE:H	1:A:105:ILE:CD1	2.19	0.55
1:A:105:ILE:C	1:A:107:ARG:H	2.08	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:PHE:CE2	1:A:351:LYS:HB3	2.42	0.55
1:A:269:VAL:CB	1:A:274:MET:HG2	2.37	0.55
1:A:96:ASN:HB3	1:A:117:GLU:HG3	1.88	0.54
1:A:15:GLU:H	1:A:15:GLU:CD	2.09	0.54
1:A:107:ARG:CG	1:A:108:LYS:N	2.71	0.54
1:A:326:ARG:CZ	1:A:326:ARG:HB2	2.38	0.52
1:A:254:PRO:O	1:A:255:TYR:HB2	2.08	0.52
1:A:164:THR:HG22	1:A:168:GLU:H	1.75	0.51
1:A:19:LYS:O	1:A:23:GLU:HG3	2.09	0.51
1:A:42:GLU:HB3	1:A:228:ARG:HG2	1.92	0.51
1:A:335:ILE:N	1:A:335:ILE:HD12	2.24	0.51
1:A:164:THR:HG22	1:A:167:GLY:H	1.76	0.51
1:A:122:GLU:HB3	1:A:125:LEU:CD1	2.40	0.51
1:A:11:MET:HB2	1:A:14:TYR:CD2	2.46	0.51
1:A:135:LEU:O	1:A:135:LEU:HD23	2.12	0.50
1:A:232:PHE:CE2	1:A:335:ILE:HD13	2.40	0.49
1:A:61:ALA:HB2	1:A:80:GLU:OE2	2.11	0.49
1:A:41:PRO:HG3	1:A:277:ILE:HG23	1.95	0.49
1:A:22:ILE:O	1:A:26:VAL:HG23	2.12	0.49
1:A:308:ILE:HD13	1:A:350:GLU:HG3	1.94	0.48
1:A:272:ARG:O	1:A:275:ARG:HG2	2.14	0.48
1:A:72:ASN:O	1:A:74:GLY:N	2.47	0.48
1:A:133:GLN:HG3	1:A:148:ASP:OD1	2.14	0.48
1:A:99:LYS:O	1:A:154:ILE:HA	2.14	0.48
1:A:45:VAL:HG22	1:A:227:LYS:HB3	1.95	0.48
1:A:73:LYS:O	1:A:73:LYS:HG2	2.15	0.46
1:A:104:THR:HG22	1:A:148:ASP:O	2.16	0.46
1:A:275:ARG:HG3	1:A:276:PRO:CD	2.45	0.46
1:A:133:GLN:HA	1:A:145:CYS:O	2.16	0.46
1:A:29:THR:HG21	1:A:249:PHE:HE1	1.80	0.46
1:A:132:LYS:O	1:A:135:LEU:HB3	2.15	0.46
1:A:59:PRO:O	1:A:219:LYS:HE3	2.15	0.46
1:A:29:THR:HG23	1:A:31:ILE:HG13	1.99	0.45
1:A:56:ILE:HG13	1:A:220:GLU:HG2	1.98	0.45
1:A:265:GLN:HA	1:A:266:PRO:HD3	1.86	0.45
1:A:351:LYS:O	1:A:352:ILE:HB	2.17	0.44
1:A:44:VAL:O	1:A:44:VAL:HG23	2.17	0.44
1:A:327:GLN:HB3	1:A:346:VAL:CG1	2.45	0.44
1:A:333:VAL:HG12	1:A:340:THR:O	2.18	0.44
1:A:344:LEU:HD23	1:A:344:LEU:N	2.33	0.44
1:A:20:GLU:CG	1:A:21:ASN:N	2.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:ASP:C	1:A:107:ARG:HD3	2.38	0.44
1:A:267:VAL:HG23	1:A:267:VAL:O	2.18	0.43
1:A:3:LYS:HB2	1:A:3:LYS:HE3	1.86	0.43
1:A:86:ARG:NH1	2:A:2007:HOH:O	2.51	0.43
1:A:313:GLU:O	1:A:314:ASP:HB2	2.19	0.43
1:A:231:LEU:CD2	1:A:280:LEU:HD11	2.49	0.43
1:A:297:LEU:O	1:A:298:GLY:C	2.57	0.43
1:A:54:ARG:NH2	1:A:222:ARG:NH2	2.67	0.43
1:A:29:THR:HG22	1:A:31:ILE:H	1.81	0.43
1:A:50:SER:HB2	1:A:51:PRO:HD2	1.99	0.43
1:A:267:VAL:HA	1:A:268:PRO:HD3	1.86	0.43
1:A:108:LYS:CG	1:A:109:TYR:N	2.80	0.42
1:A:105:ILE:C	1:A:107:ARG:N	2.73	0.42
1:A:107:ARG:HG2	1:A:108:LYS:H	1.84	0.42
1:A:297:LEU:HD12	1:A:297:LEU:N	2.35	0.42
1:A:128:GLY:O	1:A:150:LYS:HE3	2.20	0.42
1:A:8:VAL:HG23	1:A:238:VAL:CG1	2.49	0.42
1:A:344:LEU:CD2	1:A:344:LEU:N	2.83	0.41
1:A:324:PRO:C	1:A:326:ARG:N	2.74	0.41
1:A:261:SER:HB2	1:A:266:PRO:HA	2.03	0.41
1:A:34:LEU:HD13	1:A:246:ALA:HA	2.03	0.41
1:A:3:LYS:N	2:A:2001:HOH:O	2.54	0.40
1:A:147:LEU:HA	1:A:147:LEU:HD12	1.93	0.40
1:A:299:PHE:HB3	1:A:319:ILE:CD1	2.51	0.40
1:A:140:ASN:HB2	1:A:141:GLU:H	1.68	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	337/352 (96%)	310 (92%)	19 (6%)	8 (2%)	7 4

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	73	LYS
1	A	107	ARG
1	A	120	GLY
1	A	262	SER
1	A	298	GLY
1	A	326	ARG
1	A	67	ASN
1	A	106	ASP

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	304/315 (96%)	275 (90%)	29 (10%)	11	12

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	GLU
1	A	29	THR
1	A	32	LYS
1	A	45	VAL
1	A	58	SER
1	A	97	VAL
1	A	106	ASP
1	A	107	ARG
1	A	108	LYS
1	A	109	TYR
1	A	110	THR
1	A	111	LYS
1	A	135	LEU
1	A	141	GLU
1	A	154	ILE
1	A	164	THR
1	A	176	LEU

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Mol	Chain	Res	Type
1	A	209	ARG
1	A	212	VAL
1	A	213	VAL
1	A	217	THR
1	A	231	LEU
1	A	238	VAL
1	A	250	VAL
1	A	283	LEU
1	A	321	GLU
1	A	328	GLU
1	A	335	ILE
1	A	344	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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 ⓘ

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	341/352 (96%)	0.46	36 (10%) 8 8	44, 71, 110, 154	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	297	LEU	6.2
1	A	109	TYR	4.8
1	A	106	ASP	4.3
1	A	216	SER	4.3
1	A	285	GLU	4.2
1	A	272	ARG	3.8
1	A	238	VAL	3.8
1	A	325	GLU	3.5
1	A	236	VAL	3.5
1	A	141	GLU	3.4
1	A	139	LYS	3.4
1	A	8	VAL	3.4
1	A	352	ILE	3.0
1	A	262	SER	2.9
1	A	237	PHE	2.7
1	A	286	TYR	2.7
1	A	327	GLN	2.7
1	A	47	ASP	2.6
1	A	100	ILE	2.6
1	A	227	LYS	2.5
1	A	32	LYS	2.5
1	A	119	ALA	2.5
1	A	133	GLN	2.5
1	A	342	VAL	2.4
1	A	283	LEU	2.4
1	A	7	ILE	2.4
1	A	221	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	287	GLU	2.2
1	A	263	GLY	2.2
1	A	118	SER	2.1
1	A	137	LEU	2.1
1	A	77	ILE	2.1
1	A	142	GLU	2.1
1	A	300	LYS	2.1
1	A	107	ARG	2.0
1	A	126	ARG	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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.