



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 06:07 am BST

PDB ID : 6R4H
Title : Crystal structure of human GFAT-1 G451E
Authors : Ruegenberg, S.; Horn, M.; Pichlo, C.; Allmeroth, K.; Baumann, U.; Denzel, M.S.
Deposited on : 2019-03-22
Resolution : 2.24 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

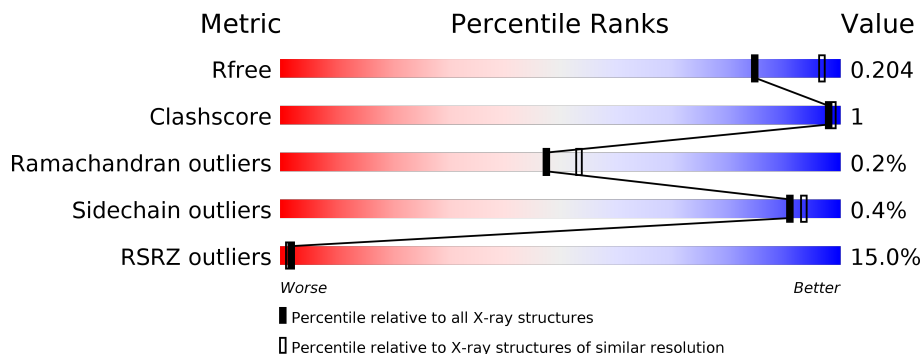
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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}	130704	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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 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	687	 6% 93%
1	B	687	 23% 94%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 21104 atoms, of which 10487 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.

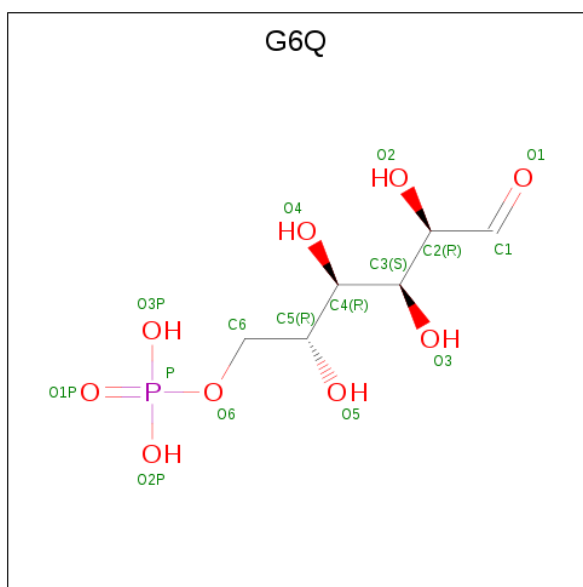
- Molecule 1 is a protein called Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P	S			
1	A	663	10482	3302	5242	913	992	1	32	0	0	0
1	B	657	10418	3282	5214	902	987	1	32	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

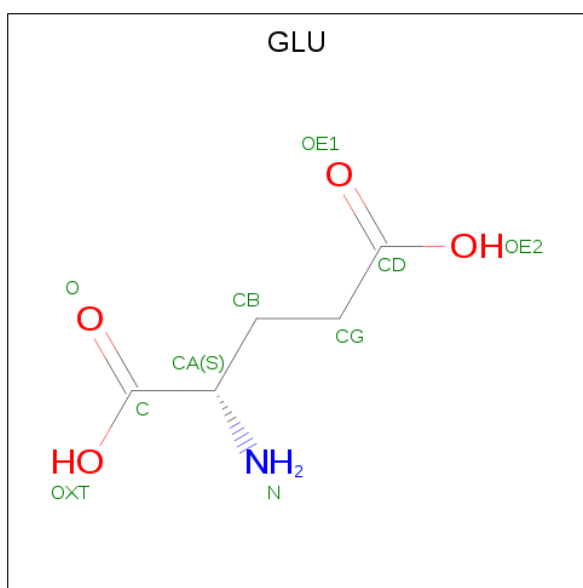
Chain	Residue	Modelled	Actual	Comment	Reference
A	299A	HIS	-	insertion	UNP Q06210
A	299B	HIS	-	insertion	UNP Q06210
A	299C	HIS	-	insertion	UNP Q06210
A	299D	HIS	-	insertion	UNP Q06210
A	299E	HIS	-	insertion	UNP Q06210
A	299F	HIS	-	insertion	UNP Q06210
A	451	GLU	GLY	conflict	UNP Q06210
B	299A	HIS	-	insertion	UNP Q06210
B	299B	HIS	-	insertion	UNP Q06210
B	299C	HIS	-	insertion	UNP Q06210
B	299D	HIS	-	insertion	UNP Q06210
B	299E	HIS	-	insertion	UNP Q06210
B	299F	HIS	-	insertion	UNP Q06210
B	451	GLU	GLY	conflict	UNP Q06210

- Molecule 2 is GLUCOSE-6-PHOSPHATE (three-letter code: G6Q) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			29	6	13	9	1		
2	B	1	Total	C	H	O	P	0	0
			29	6	13	9	1		

- Molecule 3 is GLUTAMIC ACID (three-letter code: GLU) (formula: $C_5H_9NO_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	0	0
			15	5	5	1	4		

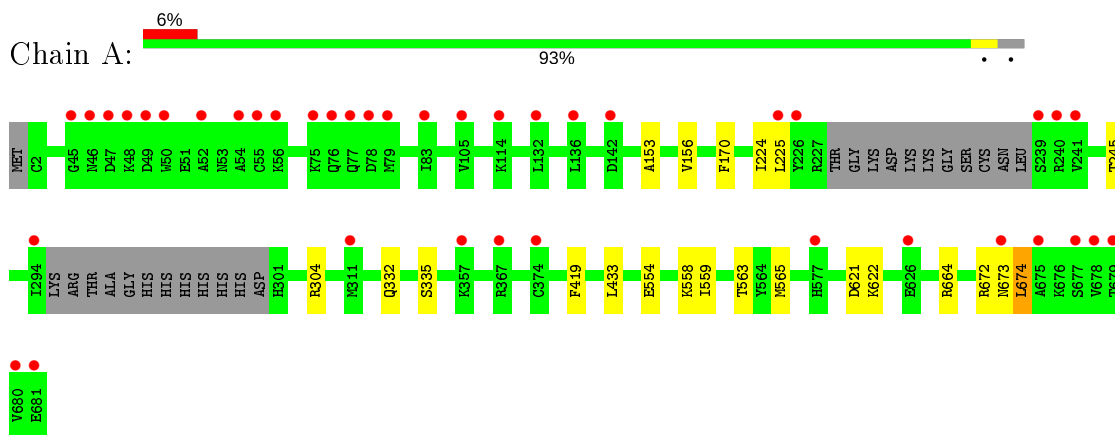
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	83	Total 83	O 83	0	0
4	B	48	Total 48	O 48	0	0

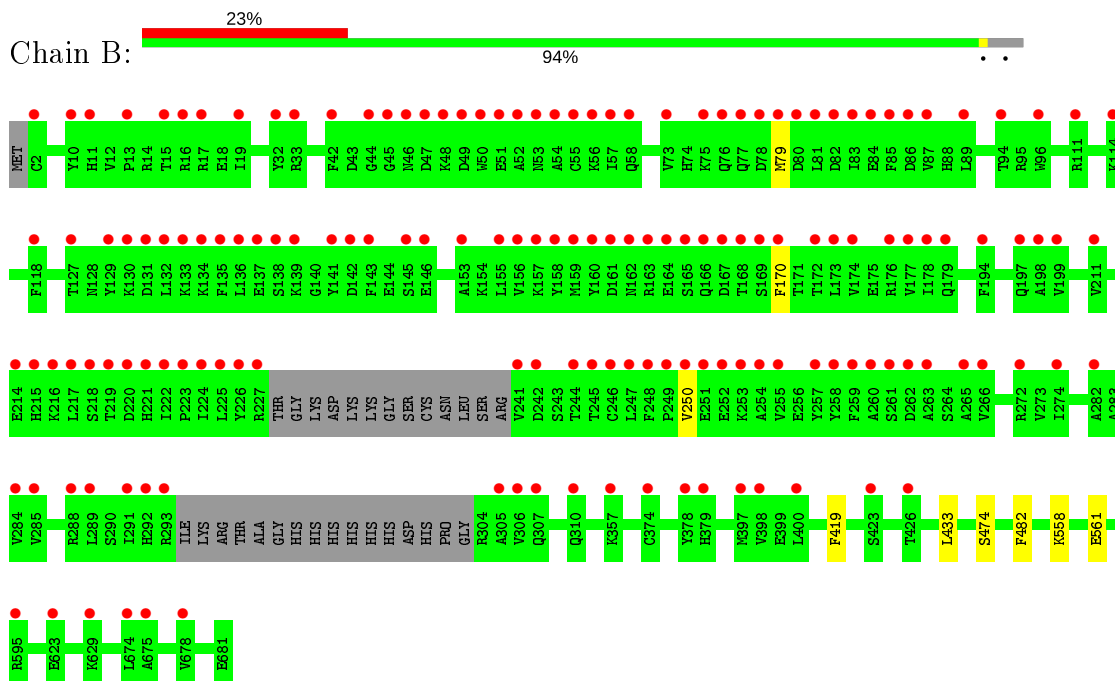
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1



- Molecule 1: Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	154.07Å 154.07Å 162.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.98 – 2.24 48.98 – 2.24	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.98-2.24) 96.5 (48.98-2.24)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.24Å)	Xtrriage
Refinement program	PHENIX (dev_2499: ???)	Depositor
R, R_{free}	0.186 , 0.203 0.188 , 0.204	Depositor DCC
R_{free} test set	1976 reflections (2.11%)	wwPDB-VP
Wilson B-factor (Å ²)	42.7	Xtrriage
Anisotropy	0.080	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21104	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: G6Q, SEP

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	0.26	0/5318	0.45	0/7178
1	B	0.25	0/5281	0.44	0/7127
All	All	0.25	0/10599	0.45	0/14305

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	5240	5242	5242	11	0
1	B	5204	5214	5214	3	0
2	A	16	13	11	1	0
2	B	16	13	11	0	0
3	A	10	5	5	0	0
4	A	83	0	0	0	0
4	B	48	0	0	1	0
All	All	10617	10487	10483	14	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 1.

All (14) 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:558:LYS:NZ	2:A:701:G6Q:O1	2.21	0.73
1:A:673:ASN:OD1	1:A:674:LEU:N	2.26	0.68
1:A:621:ASP:OD1	1:A:622:LYS:N	2.29	0.66
1:B:419:PHE:CZ	1:B:433:LEU:HA	2.48	0.48
1:A:224:ILE:HD11	1:A:304:ARG:CZ	2.43	0.48
1:A:332:GLN:HA	1:A:335:SER:OG	2.15	0.47
1:A:419:PHE:CZ	1:A:433:LEU:HA	2.50	0.45
1:A:565:MET:HB3	1:A:664:ARG:HH12	1.84	0.43
1:A:554:GLU:OE2	1:A:558:LYS:HE3	2.19	0.42
1:A:225:LEU:HD21	1:A:245:THR:HG23	2.02	0.42
1:B:561:GLU:OE2	4:B:801:HOH:O	2.21	0.42
1:B:474:SER:O	1:B:558:LYS:CE	2.68	0.41
1:A:559:ILE:O	1:A:563:THR:HB	2.21	0.40
1:A:153:ALA:O	1:A:156:VAL:HG12	2.22	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	656/687 (96%)	643 (98%)	12 (2%)	1 (0%)	47 53
1	B	650/687 (95%)	635 (98%)	14 (2%)	1 (0%)	47 53
All	All	1306/1374 (95%)	1278 (98%)	26 (2%)	2 (0%)	47 53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	250	VAL
1	A	674	LEU

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	576/601 (96%)	574 (100%)	2 (0%)	92	95
1	B	574/601 (96%)	571 (100%)	3 (0%)	88	92
All	All	1150/1202 (96%)	1145 (100%)	5 (0%)	91	93

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	170	PHE
1	A	672	ARG
1	B	79	MET
1	B	170	PHE
1	B	482	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues 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
1	SEP	B	243	1	8,9,10	1.55	1 (12%)	8,12,14	1.37	2 (25%)
1	SEP	A	243	1	8,9,10	1.57	1 (12%)	8,12,14	1.76	2 (25%)

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
1	SEP	B	243	1	-	0/5/8/10	-
1	SEP	A	243	1	-	1/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	SEP	P-O1P	3.41	1.61	1.50
1	B	243	SEP	P-O1P	3.37	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	243	SEP	OG-CB-CA	3.31	111.36	108.14
1	A	243	SEP	P-OG-CB	-3.23	109.40	118.30
1	B	243	SEP	P-OG-CB	-2.51	111.39	118.30
1	B	243	SEP	OG-CB-CA	2.25	110.33	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	243	SEP	N-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry i

3 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	G6Q	B	701	-	14,15,15	0.56	0	20,21,21	0.70	0
2	G6Q	A	701	-	14,15,15	0.74	1 (7%)	20,21,21	1.55	3 (15%)

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	G6Q	B	701	-	-	4/18/20/20	-
2	G6Q	A	701	-	-	8/18/20/20	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	G6Q	C3-C2	2.49	1.57	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	G6Q	O2-C2-C3	4.75	120.74	109.46
2	A	701	G6Q	C4-C3-C2	2.75	118.34	113.54
2	A	701	G6Q	O2-C2-C1	-2.15	105.00	110.08

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	701	G6Q	C1-C2-C3-C4

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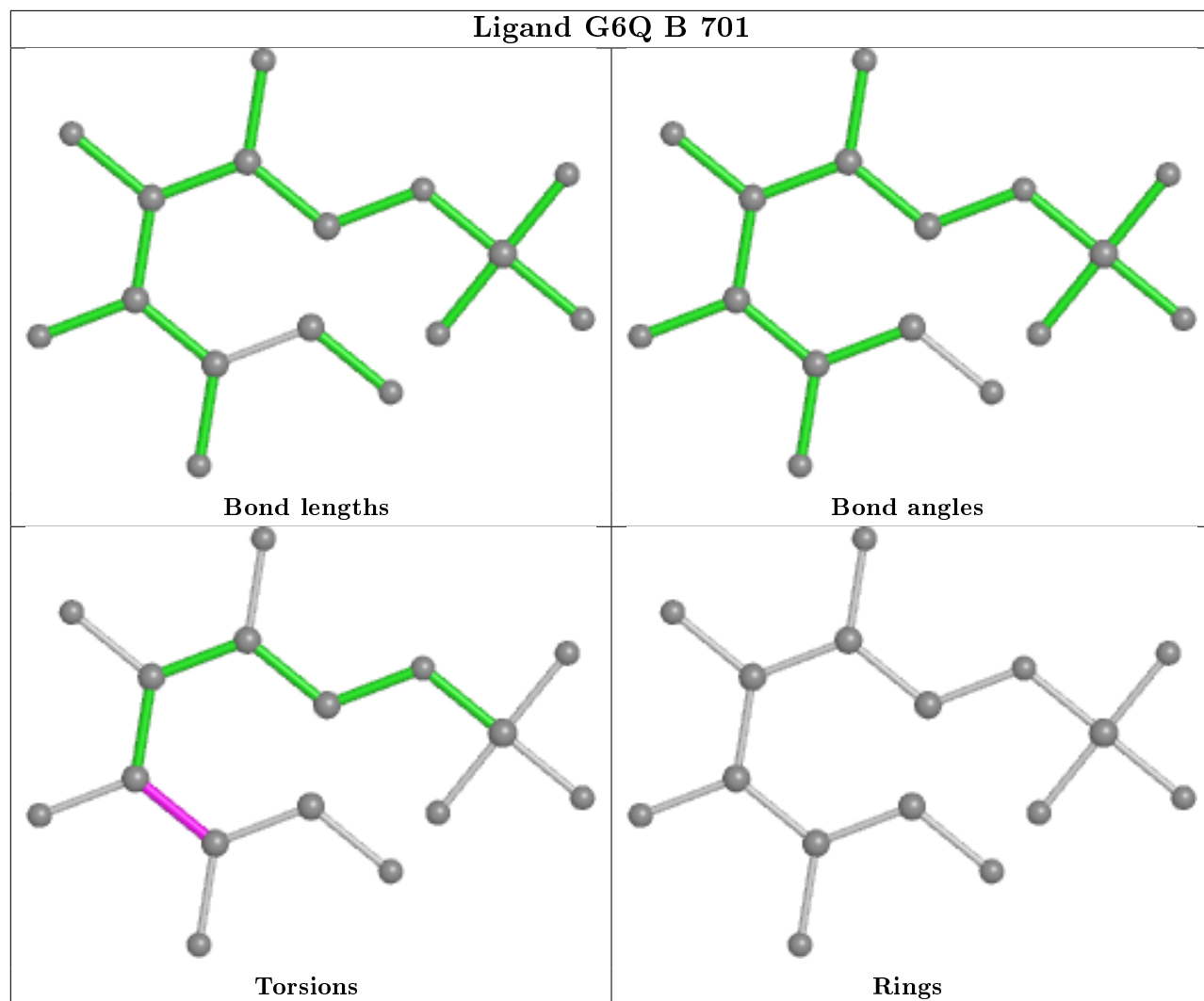
Mol	Chain	Res	Type	Atoms
2	B	701	G6Q	O2-C2-C3-C4
2	B	701	G6Q	O2-C2-C3-O3
2	A	701	G6Q	C4-C5-C6-O6
2	A	701	G6Q	O5-C5-C6-O6
2	A	701	G6Q	O3-C3-C4-O4
2	A	701	G6Q	C2-C3-C4-C5
2	B	701	G6Q	C1-C2-C3-O3
2	A	701	G6Q	O2-C2-C3-O3
2	A	701	G6Q	O3-C3-C4-C5
2	A	701	G6Q	C1-C2-C3-O3
2	A	701	G6Q	C2-C3-C4-O4

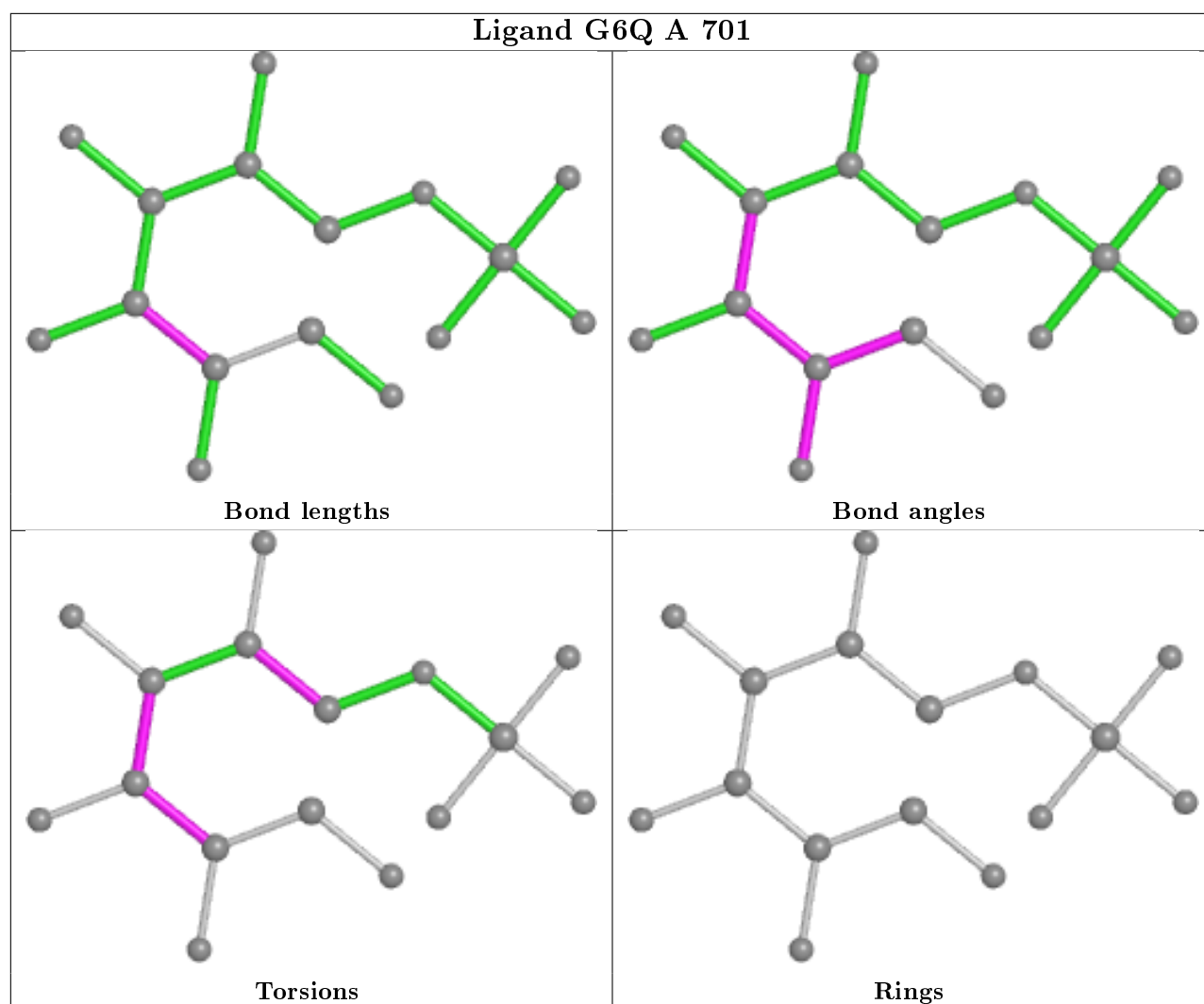
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	G6Q	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	662/687 (96%)	0.28	40 (6%) 21 21	33, 51, 104, 158	0
1	B	656/687 (95%)	1.16	158 (24%) 0 0	35, 67, 157, 226	0
All	All	1318/1374 (95%)	0.72	198 (15%) 2 1	33, 57, 141, 226	0

All (198) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	54	ALA	12.3
1	B	53	ASN	9.0
1	B	250	VAL	9.0
1	B	47	ASP	7.9
1	B	77	GLN	7.7
1	B	255	VAL	7.6
1	B	55	CYS	7.3
1	B	50	TRP	7.2
1	A	680	VAL	7.2
1	B	52	ALA	7.1
1	B	46	ASN	7.0
1	B	261	SER	6.9
1	B	48	LYS	6.9
1	B	216	LYS	6.9
1	B	226	TYR	6.7
1	B	49	ASP	6.6
1	B	79	MET	6.5
1	B	160	TYR	6.4
1	A	77	GLN	6.3
1	B	215	HIS	6.3
1	B	222	ILE	6.3
1	B	263	ALA	6.0
1	B	249	PRO	5.9
1	B	173	LEU	5.9

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Mol	Chain	Res	Type	RSRZ
1	B	217	LEU	5.9
1	B	225	LEU	5.9
1	B	33	ARG	5.9
1	B	291	ILE	5.7
1	B	44	GLY	5.7
1	B	56	LYS	5.7
1	B	251	GLU	5.6
1	B	168	THR	5.5
1	B	248	PHE	5.4
1	B	118	PHE	5.4
1	B	81	LEU	5.4
1	B	223	PRO	5.4
1	B	51	GLU	5.3
1	B	45	GLY	5.3
1	B	241	VAL	5.2
1	B	253	LYS	5.2
1	A	240	ARG	5.2
1	B	262	ASP	5.2
1	B	247	LEU	5.1
1	B	245	THR	5.1
1	B	132	LEU	5.0
1	B	167	ASP	4.9
1	B	11	HIS	4.9
1	B	198	ALA	4.9
1	A	48	LYS	4.8
1	B	134	LYS	4.8
1	B	224	ILE	4.8
1	B	164	GLU	4.7
1	A	673	ASN	4.6
1	B	218	SER	4.6
1	B	292	HIS	4.5
1	A	681	GLU	4.4
1	A	76	GLN	4.4
1	B	136	LEU	4.3
1	B	135	PHE	4.2
1	B	246	CYS	4.2
1	B	78	ASP	4.1
1	B	254	ALA	4.1
1	B	170	PHE	4.1
1	A	79	MET	4.0
1	A	239	SER	4.0
1	B	221	HIS	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	242	ASP	3.9
1	B	174	VAL	3.8
1	B	142	ASP	3.8
1	B	379	HIS	3.8
1	B	159	MET	3.8
1	B	158	TYR	3.8
1	B	166	GLN	3.8
1	B	162	ASN	3.7
1	B	244	THR	3.7
1	A	45	GLY	3.7
1	B	284	VAL	3.7
1	B	219	THR	3.6
1	B	285	VAL	3.5
1	A	49	ASP	3.5
1	B	146	GLU	3.5
1	B	172	THR	3.5
1	B	75	LYS	3.4
1	B	288	ARG	3.4
1	B	58	GLN	3.4
1	A	54	ALA	3.4
1	B	73	VAL	3.4
1	B	42	PHE	3.4
1	B	161	ASP	3.3
1	B	87	VAL	3.3
1	B	214	GLU	3.3
1	B	141	TYR	3.3
1	B	176	ARG	3.3
1	B	156	VAL	3.2
1	B	153	ALA	3.2
1	B	130	LYS	3.2
1	A	142	ASP	3.2
1	A	75	LYS	3.2
1	B	83	ILE	3.2
1	B	76	GLN	3.2
1	A	132	LEU	3.2
1	B	155	LEU	3.1
1	A	677	SER	3.1
1	A	294	ILE	3.1
1	B	13	PRO	3.1
1	A	56	LYS	3.1
1	B	2	CYS	3.1
1	B	274	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	265	ALA	3.1
1	A	50	TRP	3.1
1	B	259	PHE	3.0
1	A	78	ASP	3.0
1	A	52	ALA	3.0
1	B	199	VAL	3.0
1	B	85	PHE	3.0
1	A	679	THR	2.9
1	A	226	TYR	2.9
1	B	143	PHE	2.8
1	B	257	TYR	2.8
1	B	258	TYR	2.8
1	B	131	ASP	2.7
1	B	211	VAL	2.7
1	B	138	SER	2.7
1	B	84	GLU	2.7
1	A	47	ASP	2.7
1	B	305	ALA	2.7
1	B	96	TRP	2.7
1	A	675	ALA	2.7
1	B	629	LYS	2.7
1	B	194	PHE	2.7
1	B	252	GLU	2.6
1	B	80	ASP	2.6
1	A	83	ILE	2.6
1	B	220	ASP	2.6
1	A	225	LEU	2.6
1	B	289	LEU	2.6
1	B	129	TYR	2.6
1	B	114	LYS	2.6
1	B	133	LYS	2.6
1	B	157	LYS	2.6
1	B	272	ARG	2.5
1	B	165	SER	2.5
1	A	577	HIS	2.5
1	B	89	LEU	2.5
1	B	282	ALA	2.5
1	A	367	ARG	2.5
1	B	169	SER	2.4
1	B	310	GLN	2.4
1	B	145	SER	2.4
1	B	293	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	136	LEU	2.4
1	B	397	MET	2.4
1	B	306	VAL	2.4
1	B	163	ARG	2.4
1	B	32	TYR	2.4
1	B	57	ILE	2.4
1	B	111	ARG	2.3
1	A	626	GLU	2.3
1	B	177	VAL	2.3
1	B	10	TYR	2.3
1	B	17	ARG	2.3
1	B	227	ARG	2.3
1	A	114	LYS	2.3
1	B	15	THR	2.2
1	B	86	ASP	2.2
1	B	94	THR	2.2
1	B	197	GLN	2.2
1	B	137	GLU	2.2
1	B	266	VAL	2.2
1	B	678	VAL	2.2
1	B	82	ASP	2.2
1	A	311	MET	2.2
1	B	16	ARG	2.2
1	B	378	TYR	2.2
1	A	46	ASN	2.2
1	B	595	ARG	2.2
1	A	55	CYS	2.2
1	B	674	LEU	2.2
1	B	623	GLU	2.1
1	B	178	ILE	2.1
1	B	307	GLN	2.1
1	B	398	VAL	2.1
1	B	260	ALA	2.1
1	B	357	LYS	2.1
1	B	423	SER	2.1
1	B	400	LEU	2.1
1	B	426	THR	2.1
1	B	179	GLN	2.0
1	A	105	VAL	2.0
1	A	241	VAL	2.0
1	A	678	VAL	2.0
1	A	357	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	19	ILE	2.0
1	B	127	THR	2.0
1	B	675	ALA	2.0
1	A	374	CYS	2.0
1	B	374	CYS	2.0
1	B	139	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	B	243	10/11	0.46	0.35	164,179,202,212	0
1	SEP	A	243	10/11	0.82	0.23	117,127,147,150	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

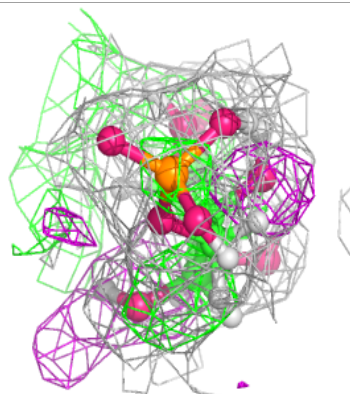
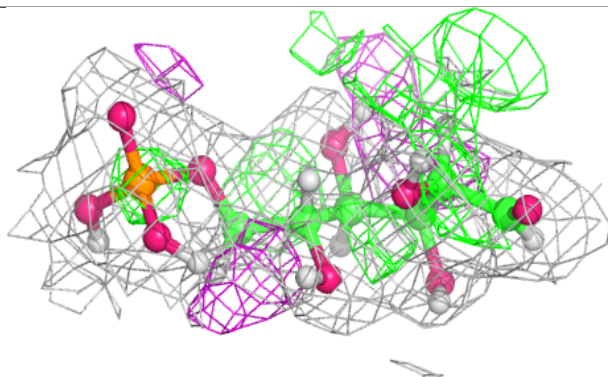
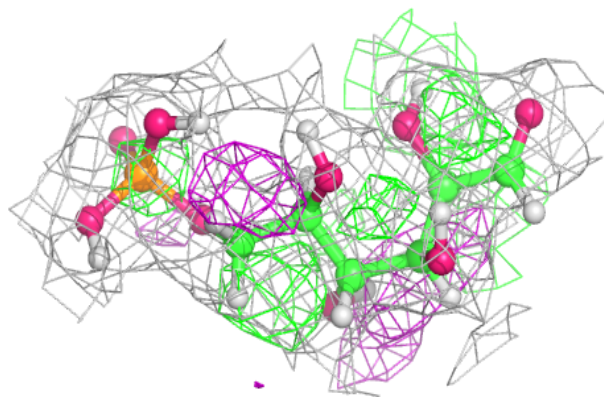
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GLU	A	702	10/10	0.94	0.10	52,61,70,74	0
2	G6Q	A	701	16/16	0.94	0.27	35,45,58,65	0
2	G6Q	B	701	16/16	0.98	0.26	38,48,59,68	0

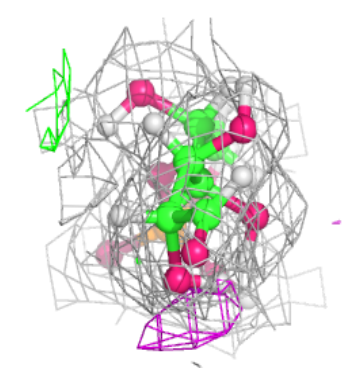
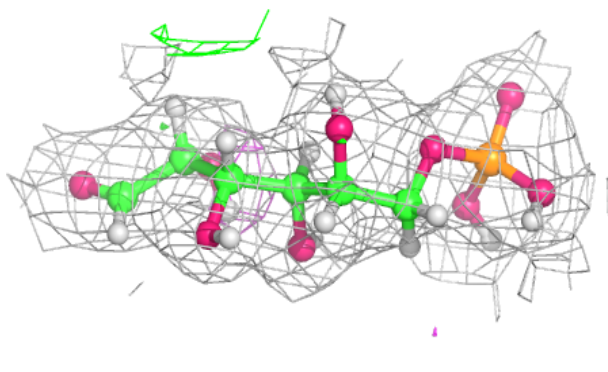
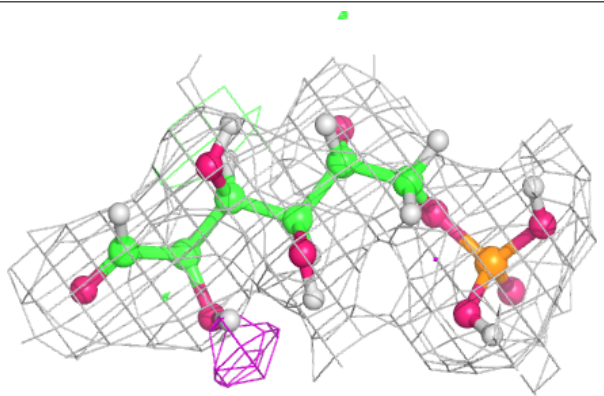
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around G6Q A 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around G6Q B 701:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers

There are no such residues in this entry.