



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 15, 2025 – 02:08 PM EDT

PDB ID : 9C6T / pdb_00009c6t
Title : Structure of the Human ISM1 TSR-AMOP domains
Authors : Stayrook, S.; Li, T.; Klein, D.E.
Deposited on : 2024-06-08
Resolution : 3.41 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

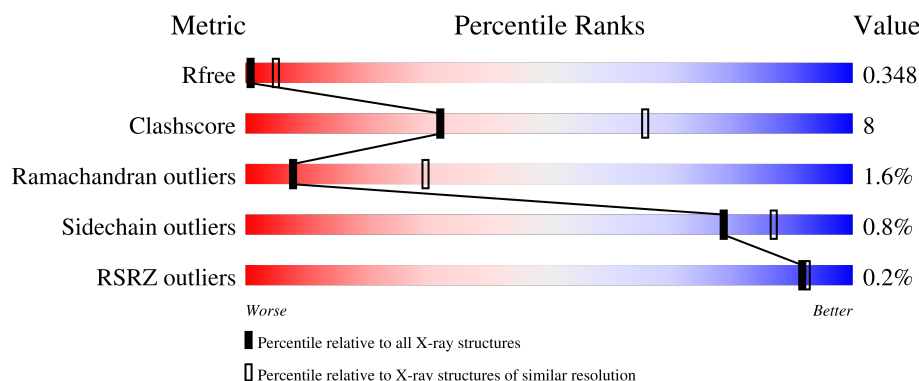
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.41 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}	164625	1112 (3.48-3.36)
Clashscore	180529	1144 (3.48-3.36)
Ramachandran outliers	177936	1146 (3.48-3.36)
Sidechain outliers	177891	1146 (3.48-3.36)
RSRZ outliers	164620	1112 (3.48-3.36)

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	247	 79% 12% 9%
1	B	247	 69% 21% 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MAN	B	601	X	-	-	-

2 Entry composition [i](#)

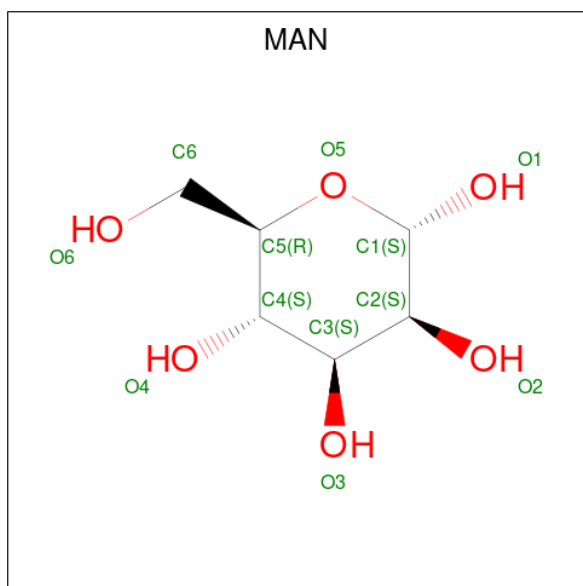
There are 2 unique types of molecules in this entry. The entry contains 3621 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Isthmin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	226	Total	C	N	O	S	0	0	0
			1808	1121	314	354	19			
1	B	222	Total	C	N	O	S	0	0	0
			1769	1097	310	343	19			

- Molecule 2 is alpha-D-mannopyranose (CCD ID: MAN) (formula: C₆H₁₂O₆).

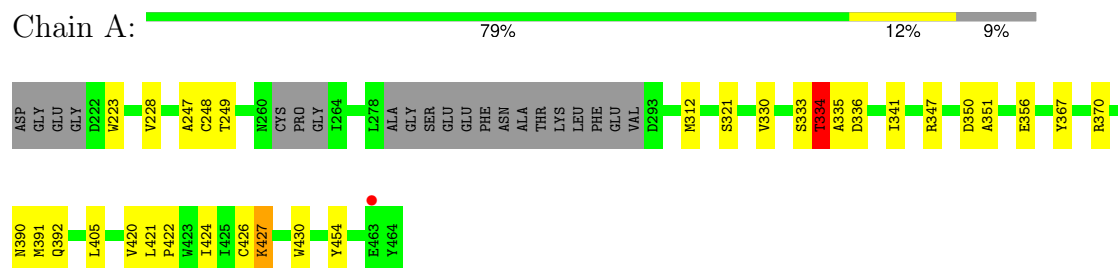


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			11	6	5		
2	A	1	Total	C	O	0	0
			11	6	5		
2	B	1	Total	C	O	0	0
			11	6	5		
2	B	1	Total	C	O	0	0
			11	6	5		

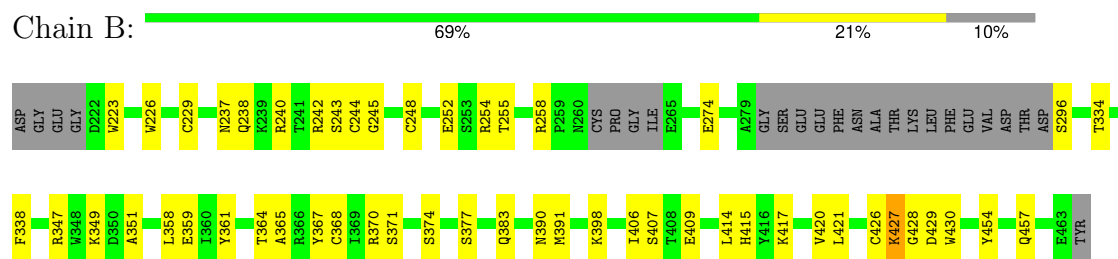
3 Residue-property plots

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: Isthmin-1



• Molecule 1: Isthmin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	114.25Å 114.25Å 168.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.47 – 3.41 49.47 – 3.41	Depositor EDS
% Data completeness (in resolution range)	96.2 (49.47-3.41) 96.3 (49.47-3.41)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 3.40Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.332 , 0.366 0.334 , 0.348	Depositor DCC
R_{free} test set	844 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 78.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.107 for -h,-k,l	Xtriage
F_o, F_c correlation	0.79	EDS
Total number of atoms	3621	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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: MAN

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	0.28	0/1848	0.59	1/2495 (0.0%)
1	B	0.29	0/1808	0.55	0/2441
All	All	0.28	0/3656	0.57	1/4936 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	334	THR	N-CA-C	10.11	138.31	111.00

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	1808	0	1719	21	0
1	B	1769	0	1689	38	0
2	A	22	0	20	0	0
2	B	22	0	20	4	0
All	All	3621	0	3448	56	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 8.

All (56) 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:B:406:ILE:HG13	1:B:414:LEU:HD22	1.70	0.74
1:B:334:THR:OG1	1:B:347:ARG:NH2	2.12	0.72
1:B:237:ASN:HA	1:B:255:THR:HA	1.81	0.62
1:A:248:CYS:SG	1:A:249:THR:N	2.72	0.62
1:A:351:ALA:HB2	1:A:370:ARG:HG3	1.81	0.62
1:A:247:ALA:HB1	1:B:255:THR:HG22	1.82	0.62
1:B:245:GLY:N	1:B:248:CYS:SG	2.73	0.61
1:B:240:ARG:HG2	1:B:252:GLU:HB3	1.84	0.59
1:B:370:ARG:HH22	1:B:415:HIS:CE1	2.19	0.59
1:A:356:GLU:OE1	1:A:370:ARG:NH2	2.36	0.58
1:A:421:LEU:HA	1:A:424:ILE:HD12	1.86	0.57
1:A:347:ARG:HB3	1:A:347:ARG:HH11	1.70	0.56
1:A:347:ARG:HB3	1:A:347:ARG:NH1	2.21	0.56
1:B:417:LYS:HA	1:B:421:LEU:HB2	1.87	0.55
1:B:226:TRP:HB2	2:B:602:MAN:O2	2.06	0.55
1:B:364:THR:HG23	1:B:398:LYS:HE3	1.90	0.54
1:B:370:ARG:HH21	1:B:407:SER:HA	1.72	0.54
1:A:330:VAL:HG22	1:A:335:ALA:HB3	1.90	0.54
1:B:223:TRP:HB2	2:B:601:MAN:C6	2.39	0.53
1:A:390:ASN:O	1:A:392:GLN:NE2	2.38	0.53
1:B:359:GLU:OE1	1:B:359:GLU:N	2.39	0.52
1:A:312:MET:HG2	1:A:405:LEU:HD21	1.91	0.52
1:B:226:TRP:HB3	1:B:238:GLN:OE1	2.09	0.52
1:B:374:SER:N	1:B:377:SER:OG	2.44	0.51
1:B:371:SER:HB2	1:B:383:GLN:H	1.76	0.50
1:B:371:SER:HB2	1:B:383:GLN:N	2.27	0.50
1:A:430:TRP:CH2	1:A:454:TYR:HE1	2.31	0.49
1:A:321:SER:HB3	1:A:341:ILE:HD12	1.93	0.49
1:B:229:CYS:HB3	1:B:258:ARG:NH2	2.28	0.49
1:B:226:TRP:CH2	1:B:240:ARG:HD2	2.47	0.48
1:B:427:LYS:O	1:B:429:ASP:N	2.47	0.48
1:A:330:VAL:HG12	1:A:350:ASP:HB2	1.95	0.47
1:B:223:TRP:CE3	1:B:242:ARG:HD3	2.49	0.47
1:B:430:TRP:CH2	1:B:454:TYR:HE1	2.33	0.47
1:A:420:VAL:HG12	1:A:424:ILE:HD11	1.96	0.47
1:B:223:TRP:HB2	2:B:601:MAN:O5	2.15	0.47
1:B:361:TYR:HE2	1:B:420:VAL:HG13	1.80	0.47
1:B:223:TRP:CZ3	1:B:242:ARG:HB2	2.50	0.46
1:B:358:LEU:HD21	1:B:365:ALA:O	2.16	0.46
1:B:367:TYR:HE2	1:B:391:MET:HG2	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:426:CYS:O	1:B:427:LYS:C	2.55	0.45
1:B:238:GLN:N	1:B:254:ARG:O	2.45	0.44
1:B:334:THR:HG1	1:B:347:ARG:HH22	1.54	0.44
1:B:274:GLU:N	1:B:274:GLU:OE1	2.51	0.44
1:B:398:LYS:HE2	1:B:457:GLN:HG3	2.00	0.43
1:A:426:CYS:O	1:A:427:LYS:C	2.57	0.43
1:B:351:ALA:O	1:B:368:CYS:HB2	2.19	0.43
1:B:364:THR:CG2	1:B:398:LYS:HE3	2.49	0.42
1:A:336:ASP:OD1	1:A:347:ARG:HG2	2.19	0.42
1:A:367:TYR:HE2	1:A:391:MET:HG2	1.84	0.42
1:A:421:LEU:HB3	1:A:422:PRO:HD3	2.01	0.42
1:A:367:TYR:HE1	1:B:338:PHE:CE2	2.38	0.42
1:A:356:GLU:CD	1:A:370:ARG:HH21	2.21	0.42
1:B:349:LYS:NZ	1:B:409:GLU:HG3	2.35	0.41
1:B:223:TRP:HB2	2:B:601:MAN:H61	2.03	0.41
1:A:228:VAL:HB	1:B:390:ASN:HA	2.03	0.41

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	220/247 (89%)	194 (88%)	23 (10%)	3 (1%)	9	32
1	B	216/247 (87%)	182 (84%)	30 (14%)	4 (2%)	6	26
All	All	436/494 (88%)	376 (86%)	53 (12%)	7 (2%)	8	29

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	427	LYS
1	A	333	SER

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Mol	Chain	Res	Type
1	A	334	THR
1	B	243	SER
1	B	244	CYS
1	B	427	LYS
1	B	428	GLY

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	202/217 (93%)	200 (99%)	2 (1%)	73	83
1	B	197/217 (91%)	196 (100%)	1 (0%)	86	92
All	All	399/434 (92%)	396 (99%)	3 (1%)	79	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	TRP
1	A	334	THR
1	B	296	SER

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

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	MAN	A	501	1	11,11,12	1.29	1 (9%)	15,15,17	1.30	2 (13%)
2	MAN	A	502	1	11,11,12	1.21	2 (18%)	15,15,17	1.66	4 (26%)
2	MAN	B	601	1	11,11,12	1.30	1 (9%)	15,15,17	1.31	2 (13%)
2	MAN	B	602	1	11,11,12	1.07	1 (9%)	15,15,17	1.56	2 (13%)

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	MAN	A	501	1	-	2/2/19/22	0/1/1/1
2	MAN	A	502	1	-	1/2/19/22	0/1/1/1
2	MAN	B	601	1	1/1/4/5	2/2/19/22	0/1/1/1
2	MAN	B	602	1	-	0/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	MAN	C2-C3	2.51	1.56	1.52
2	A	501	MAN	C2-C3	2.51	1.56	1.52
2	B	602	MAN	O5-C5	2.23	1.47	1.43
2	A	502	MAN	C2-C3	2.13	1.55	1.52
2	A	502	MAN	C1-C2	2.05	1.57	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	602	MAN	C1-O5-C5	4.75	118.55	112.19
2	A	502	MAN	C1-O5-C5	4.08	117.66	112.19
2	A	502	MAN	C1-C2-C3	2.91	113.88	109.64
2	B	601	MAN	C1-O5-C5	2.89	116.06	112.19
2	A	501	MAN	C1-O5-C5	2.85	116.00	112.19
2	B	602	MAN	O2-C2-C3	-2.63	104.70	110.15
2	B	601	MAN	C1-C2-C3	2.48	113.26	109.64
2	A	501	MAN	C1-C2-C3	2.47	113.23	109.64
2	A	502	MAN	O2-C2-C3	-2.26	105.48	110.15
2	A	502	MAN	C2-C3-C4	2.10	114.55	110.86

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	601	MAN	C1

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	MAN	C4-C5-C6-O6
2	B	601	MAN	C4-C5-C6-O6
2	A	501	MAN	O5-C5-C6-O6
2	B	601	MAN	O5-C5-C6-O6
2	A	502	MAN	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	MAN	3	0
2	B	602	MAN	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 [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	226/247 (91%)	-0.94	1 (0%) 89 87	21, 64, 116, 211	0
1	B	222/247 (89%)	-0.98	0 100 100	39, 66, 113, 158	0
All	All	448/494 (90%)	-0.96	1 (0%) 92 92	21, 66, 118, 211	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	463	GLU	2.1

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 monosaccharides 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	MAN	A	501	11/12	0.97	0.10	105,121,148,152	0
2	MAN	A	502	11/12	0.98	0.13	106,121,127,130	0
2	MAN	B	601	11/12	0.98	0.09	105,121,148,152	0
2	MAN	B	602	11/12	0.98	0.10	75,96,111,119	0

6.5 Other polymers [i](#)

There are no such residues in this entry.