



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 8V9A / pdb_00008v9a
Title : GII.NA1 Loreto 1257 norovirus protruding domain
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Deposited on : 2023-12-07
Resolution : 1.67 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

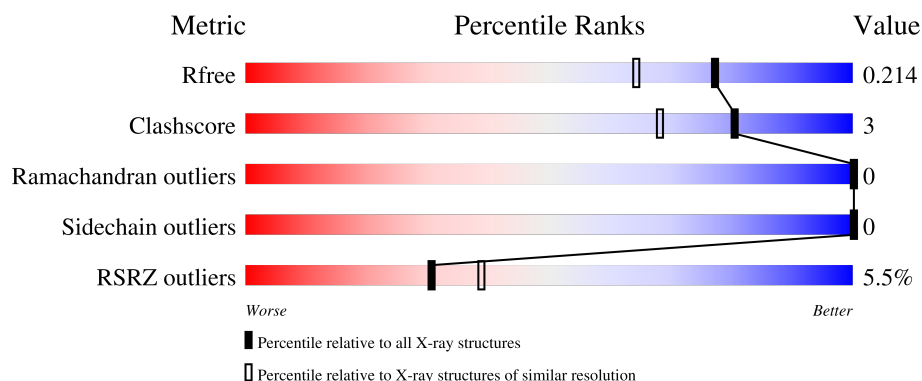
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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	1054 (1.68-1.68)
Clashscore	190562	1078 (1.68-1.68)
Ramachandran outliers	187476	1068 (1.68-1.68)
Sidechain outliers	187428	1067 (1.68-1.68)
RSRZ outliers	180081	1055 (1.68-1.68)

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	542	
1	B	542	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10084 atoms, of which 4748 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 Capsid protein VP1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	309	Total	C	H	N	O	S	0	0	0
			4719	1530	2317	405	458	9			
1	B	309	Total	C	H	N	O	S	0	0	0
			4719	1530	2317	405	458	9			

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		
2	B	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	227	Total	O	0	0
			227	227		
3	B	229	Total	O	0	0
			229	229		

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.

[illegible]

Chain B:

Category	Percentage
Green	3%
Green	54%
Grey	43%

Met
Lys
Met
Ala
Ser
Asn
Asp
Ala
Pro
Ser
Asn
Asp
Gly
Ala
Ala
Gly
Leu
Val
Pro
Glu
Gly
Ile
Asn
Asn
Glu
Thr
Met
Ala
Leu
Glu
Pro
Val
Gly
Ala
Ile
Ala
Pro
Leu
Thr
Gly
Gln
Thr
Asn
Phe
Ile
Asp
Pro
Trp
Ile
Arg
Gly
Asn
Tyr
Val
Gln
Pro
Ala
Tle

Asn
Gly
Leu
Phe
Thr
Val
Ser
Pro
Arg
Asn
Ser
Glu
Pro
Gly
Glu
Ile
Leu
Leu
Asn
Leu
Glu
Pro
Gly
Ile
Pro
His
Ala
Leu
His
Ser
Arg
Met
Tyr
Asn
Gly
Tyr
Ala
Gly
Ala
Gly
Ile
Asn
Met
Gly
Ala
Asn
Phe
Thr
Gly
Lys
Tle

Phe
Ala
Ala
Val
Pro
Pro
His
Phe
Pro
Pro
Val
Val
Glu
Asn
Ile
Ser
Pro
Pro
Gln
Ile
Thr
Met
Phe
Thr
Leu
Ile
Val
Val
Arg
Asn
Asn
Phe
Phe
His
Tyr
Asn
Gln
Asp
Arg
Asp
Ser
Arg
Met
Arg
Leu
Val
Ala

Met
Leu
Tyr
Thr
Pro
Leu
Arg
Ser
Asn
Gly
Ser
Thr
Asp
Asp
Val
Phe
Thr
Val
Val
Cys
Arg
Val
Val
Leu
Thr
Lys
Pro
Ser
Ser
Ala
Asp
Phe
Glu
Phe
Phe
Tyr
Leu
Val
Pro
Pro
Thr
Val
Glu
Ser
Arg
Gln

W380
E381
T382
T383
Q387
L397
M419
F437
L443
K444
P457
V481
N482
P483
E484
T485
G486
R487
V488
P513
A514
N515
M533
Gly
Thr
Gly
Asn
Arg
Arg
Thr
Val
Asn
Asn
Gln

T225
T235
E256
T257
H301
D320
R344
P347
T350

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.70Å 71.16Å 78.39Å 90.00° 110.04° 90.00°	Depositor
Resolution (Å)	45.38 – 1.67 45.38 – 1.67	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.38-1.67) 99.8 (45.38-1.67)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.98 (at 1.66Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.185 , 0.213 0.185 , 0.214	Depositor DCC
R_{free} test set	3764 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10084	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.64% 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: EDO

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	0.46	0/2474	0.59	0/3389
1	B	0.47	0/2474	0.60	0/3389
All	All	0.46	0/4948	0.60	0/6778

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	2402	2317	2322	14	0
1	B	2402	2317	2322	12	0
2	A	32	48	48	1	0
2	B	44	66	66	0	0
3	A	227	0	0	3	0
3	B	229	0	0	2	0
All	All	5336	4748	4758	25	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 3.

All (25) 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:481:VAL:HG12	1:A:488:VAL:HG22	1.75	0.69
1:B:320:ASP:HA	1:B:419:MET:HE1	1.79	0.64
1:A:320:ASP:HA	1:A:419:MET:HE1	1.83	0.61
1:A:382:THR:HG23	1:A:383:THR:HG23	1.82	0.61
1:B:481:VAL:HG12	1:B:488:VAL:HG22	1.85	0.59
1:B:487:ARG:NH2	3:B:702:HOH:O	2.37	0.58
1:B:301:HIS:CD2	1:B:382:THR:HG22	2.42	0.54
1:B:225:THR:O	1:B:225:THR:HG23	2.07	0.53
1:A:225:THR:O	1:A:225:THR:HG23	2.11	0.49
1:B:482:ASN:OD1	1:B:482:ASN:C	2.55	0.49
1:A:496:ARG:NH2	3:A:707:HOH:O	2.45	0.48
1:B:419:MET:C	1:B:419:MET:SD	2.96	0.48
1:A:419:MET:HE3	3:A:722:HOH:O	2.15	0.46
1:A:397:LEU:HB2	1:A:443:LEU:HD23	1.98	0.45
1:B:387:GLN:NE2	3:B:713:HOH:O	2.48	0.45
1:A:483:PRO:HG3	3:A:708:HOH:O	2.15	0.45
1:A:419:MET:SD	1:A:419:MET:C	3.01	0.44
1:B:397:LEU:HB2	1:B:443:LEU:HD23	2.00	0.44
1:A:482:ASN:OD1	1:A:482:ASN:C	2.62	0.43
1:B:437:PHE:CE1	1:B:457:PRO:HD3	2.53	0.43
1:A:287:LEU:HD13	1:A:375:VAL:HG21	2.02	0.42
1:B:483:PRO:CD	1:B:515:ASN:O	2.69	0.41
1:A:290:ALA:HB2	2:A:607:EDO:H11	2.02	0.41
1:A:356:ALA:HB3	1:B:444:LYS:HA	2.04	0.40
1:A:483:PRO:CD	1:A:515:ASN:O	2.70	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	307/542 (57%)	301 (98%)	6 (2%)	0	100	100
1	B	307/542 (57%)	299 (97%)	8 (3%)	0	100	100
All	All	614/1084 (57%)	600 (98%)	14 (2%)	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	267/462 (58%)	267 (100%)	0	100	100
1	B	267/462 (58%)	267 (100%)	0	100	100
All	All	534/924 (58%)	534 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	304	HIS
1	B	346	ASN
1	B	387	GLN
1	B	407	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 oligosaccharides in this entry.

5.6 Ligand geometry

19 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	EDO	B	602	-	3,3,3	0.41	0	2,2,2	0.54	0
2	EDO	B	601	-	3,3,3	0.54	0	2,2,2	0.17	0
2	EDO	A	601	-	3,3,3	0.49	0	2,2,2	0.42	0
2	EDO	A	607	-	3,3,3	0.40	0	2,2,2	0.59	0
2	EDO	B	605	-	3,3,3	0.35	0	2,2,2	0.60	0
2	EDO	B	604	-	3,3,3	0.40	0	2,2,2	0.44	0
2	EDO	B	608	-	3,3,3	0.54	0	2,2,2	0.33	0
2	EDO	B	603	-	3,3,3	0.35	0	2,2,2	0.98	0
2	EDO	A	604	-	3,3,3	0.36	0	2,2,2	0.57	0
2	EDO	A	603	-	3,3,3	0.52	0	2,2,2	0.25	0
2	EDO	B	611	-	3,3,3	0.48	0	2,2,2	0.75	0
2	EDO	B	607	-	3,3,3	0.57	0	2,2,2	0.51	0
2	EDO	A	605	-	3,3,3	0.39	0	2,2,2	0.45	0
2	EDO	B	610	-	3,3,3	0.46	0	2,2,2	0.39	0
2	EDO	A	608	-	3,3,3	0.40	0	2,2,2	0.79	0
2	EDO	B	606	-	3,3,3	0.34	0	2,2,2	0.31	0
2	EDO	B	609	-	3,3,3	0.38	0	2,2,2	0.73	0
2	EDO	A	606	-	3,3,3	0.36	0	2,2,2	0.77	0
2	EDO	A	602	-	3,3,3	0.45	0	2,2,2	0.38	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
2	EDO	B	602	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	601	-	-	1/1/1/1	-
2	EDO	A	601	-	-	0/1/1/1	-
2	EDO	A	607	-	-	1/1/1/1	-
2	EDO	B	605	-	-	1/1/1/1	-
2	EDO	B	604	-	-	0/1/1/1	-
2	EDO	B	608	-	-	1/1/1/1	-
2	EDO	B	603	-	-	1/1/1/1	-
2	EDO	A	604	-	-	1/1/1/1	-
2	EDO	A	603	-	-	1/1/1/1	-
2	EDO	B	611	-	-	0/1/1/1	-
2	EDO	B	607	-	-	1/1/1/1	-
2	EDO	A	605	-	-	1/1/1/1	-
2	EDO	B	610	-	-	1/1/1/1	-
2	EDO	A	608	-	-	0/1/1/1	-
2	EDO	B	606	-	-	1/1/1/1	-
2	EDO	B	609	-	-	1/1/1/1	-
2	EDO	A	606	-	-	1/1/1/1	-
2	EDO	A	602	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	610	EDO	O1-C1-C2-O2
2	B	601	EDO	O1-C1-C2-O2
2	B	606	EDO	O1-C1-C2-O2
2	B	608	EDO	O1-C1-C2-O2
2	B	603	EDO	O1-C1-C2-O2
2	A	604	EDO	O1-C1-C2-O2
2	A	605	EDO	O1-C1-C2-O2
2	A	606	EDO	O1-C1-C2-O2
2	A	603	EDO	O1-C1-C2-O2
2	B	602	EDO	O1-C1-C2-O2
2	B	609	EDO	O1-C1-C2-O2
2	A	607	EDO	O1-C1-C2-O2
2	B	605	EDO	O1-C1-C2-O2
2	B	607	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	607	EDO	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

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	309/542 (57%)	0.03	16 (5%) 33 41	12, 20, 44, 62	0
1	B	309/542 (57%)	-0.02	18 (5%) 29 37	13, 20, 41, 57	0
All	All	618/1084 (57%)	0.00	34 (5%) 30 39	12, 20, 43, 62	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	225	THR	5.3
1	A	527	PHE	4.9
1	B	382	THR	4.6
1	A	514	ALA	4.5
1	B	514	ALA	4.0
1	B	383	THR	4.0
1	B	225	THR	3.5
1	B	347	PRO	3.2
1	B	483	PRO	3.0
1	B	486	GLY	3.0
1	A	383	THR	2.9
1	A	347	PRO	2.9
1	A	483	PRO	2.9
1	A	297	ASN	2.8
1	B	256	GLU	2.7
1	B	380	TRP	2.7
1	A	515	ASN	2.6
1	A	382	THR	2.5
1	A	256	GLU	2.5
1	A	258	LEU	2.5
1	A	485	THR	2.5
1	B	350	THR	2.4
1	A	298	ASP	2.4
1	B	257	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	482	ASN	2.3
1	A	257	ASN	2.3
1	B	344	ASN	2.3
1	A	486	GLY	2.3
1	B	487	ARG	2.3
1	B	513	PRO	2.3
1	A	487	ARG	2.3
1	B	485	THR	2.2
1	B	515	ASN	2.2
1	B	235	ILE	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 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(Å ²)	Q<0.9
2	EDO	B	611	4/4	0.71	0.16	33,42,50,56	0
2	EDO	A	607	4/4	0.75	0.18	28,37,44,49	0
2	EDO	B	609	4/4	0.77	0.16	33,41,49,59	0
2	EDO	A	605	4/4	0.77	0.17	30,38,51,53	0
2	EDO	B	607	4/4	0.78	0.17	30,38,46,48	0
2	EDO	B	605	4/4	0.82	0.14	32,45,54,54	0
2	EDO	B	610	4/4	0.83	0.26	27,36,52,62	0
2	EDO	B	603	4/4	0.84	0.15	28,34,35,40	0
2	EDO	A	606	4/4	0.84	0.14	34,44,55,55	0
2	EDO	A	604	4/4	0.85	0.15	27,34,38,46	0
2	EDO	A	608	4/4	0.88	0.11	30,41,49,53	0
2	EDO	B	606	4/4	0.88	0.13	32,44,49,59	0
2	EDO	A	602	4/4	0.89	0.11	33,40,46,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	EDO	A	603	4/4	0.90	0.13	22,26,32,39	0
2	EDO	B	604	4/4	0.92	0.14	22,32,38,39	0
2	EDO	B	602	4/4	0.93	0.10	23,29,41,45	0
2	EDO	B	601	4/4	0.93	0.11	18,27,34,35	0
2	EDO	B	608	4/4	0.93	0.11	23,28,40,40	0
2	EDO	A	601	4/4	0.95	0.08	19,27,32,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.