



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 03:43 PM UTC

PDB ID : 8WFU / pdb_00008wfu
Title : Crystal structure of beta-glucosidase from Thermoanaerobacterium saccharolyticum (Data 2)
Authors : Nam, K.H.
Deposited on : 2023-09-20
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

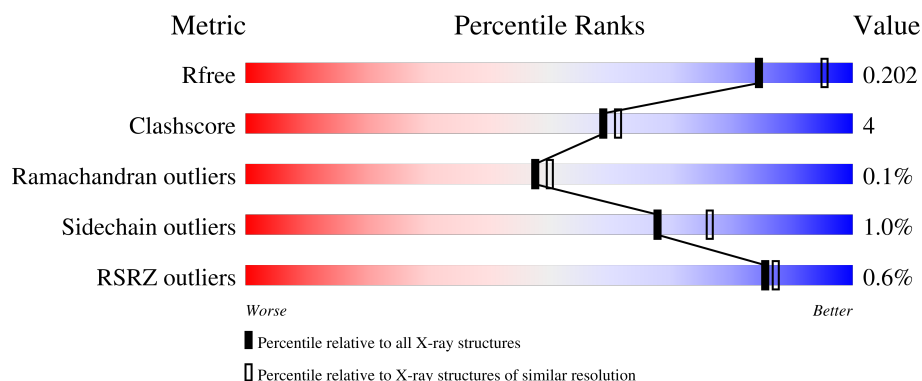
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	444	88% 12%
1	B	444	91% 9%
1	C	444	2% 88% 11%
1	D	444	0% 89% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16073 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.

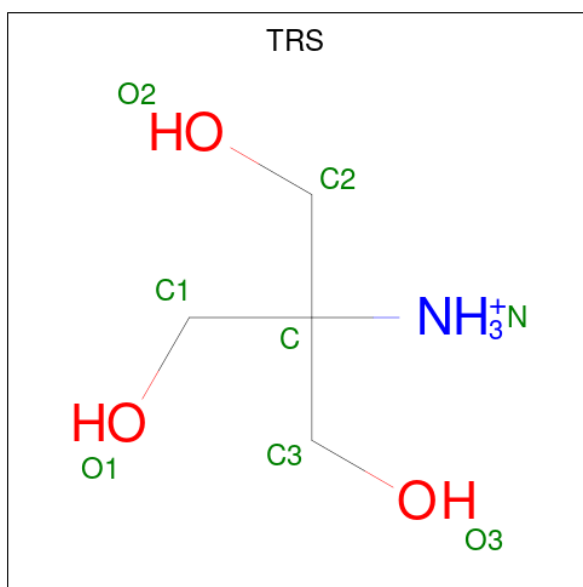
- Molecule 1 is a protein called Beta-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	1	0
			3671	2370	602	687	12			
1	B	443	Total	C	N	O	S	0	5	0
			3695	2386	606	691	12			
1	C	443	Total	C	N	O	S	0	1	0
			3665	2368	601	685	11			
1	D	441	Total	C	N	O	S	0	1	0
			3653	2360	599	683	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	LYS	LEU	conflict	UNP I3VXG7
B	2	LYS	LEU	conflict	UNP I3VXG7
C	2	LYS	LEU	conflict	UNP I3VXG7
D	2	LYS	LEU	conflict	UNP I3VXG7

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



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

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Na	0	0
			3	3		
3	B	3	Total	Na	0	0
			3	3		
3	C	2	Total	Na	0	0
			2	2		
3	D	2	Total	Na	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	352	Total	O	0	0
			352	352		

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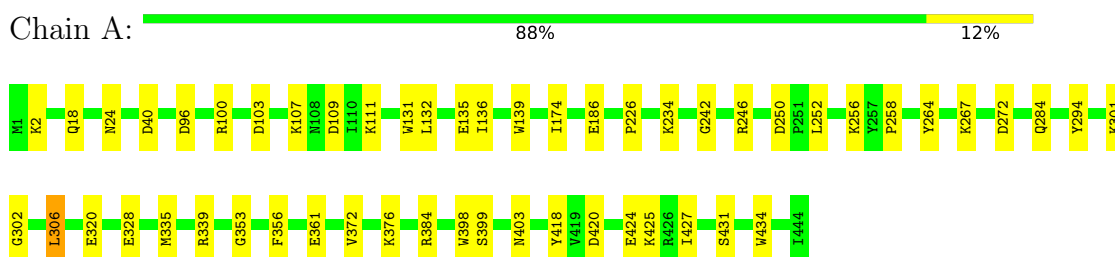
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	351	Total 351	O 351	0	0
4	C	325	Total 325	O 325	0	0
4	D	319	Total 319	O 319	0	0

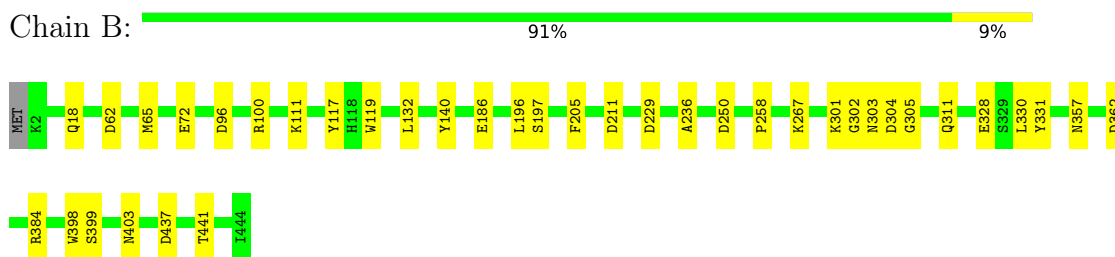
3 Residue-property plots [i](#)

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.

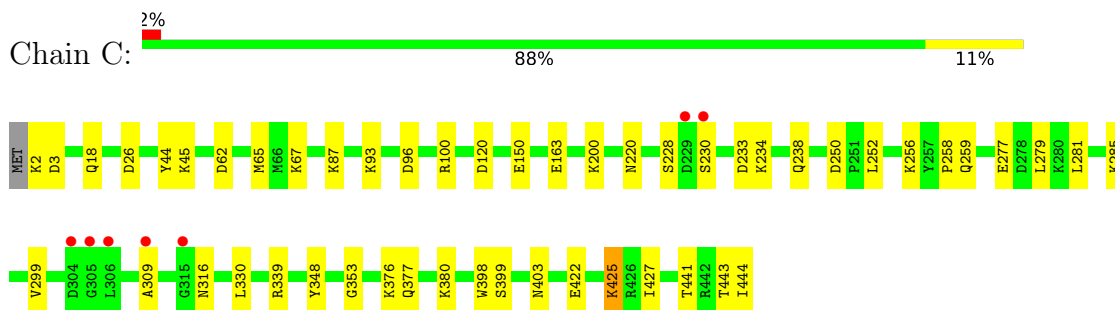
- Molecule 1: Beta-glucosidase



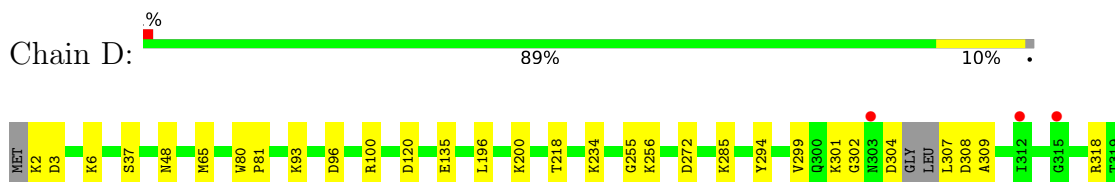
- Molecule 1: Beta-glucosidase



- Molecule 1: Beta-glucosidase



- Molecule 1: Beta-glucosidase



E320	
L330	
A355	
V359	
W398	
S399	
R413	
I416	
V417	
Y418	
I427	
D430	
S431	
A432	
L433	
W434	
Y435	
I439	
T443	
I444	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	63.21Å 72.74Å 97.39Å 92.48° 91.43° 95.22°	Depositor
Resolution (Å)	49.81 – 2.10 49.81 – 2.10	Depositor EDS
% Data completeness (in resolution range)	89.9 (49.81-2.10) 89.9 (49.81-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.160 , 0.202 0.160 , 0.202	Depositor DCC
R_{free} test set	2011 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.653	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.003 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16073	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 65.75 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.7399e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: NA, 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	0.21	0/3774	0.40	0/5102
1	B	0.20	0/3798	0.39	0/5135
1	C	0.20	0/3768	0.40	0/5095
1	D	0.21	0/3755	0.40	0/5076
All	All	0.20	0/15095	0.40	0/20408

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	3671	0	3508	35	0
1	B	3695	0	3529	24	0
1	C	3665	0	3502	37	0
1	D	3653	0	3487	31	0
2	A	8	0	12	1	0
2	B	8	0	12	0	0
2	C	8	0	12	0	0
2	D	8	0	12	1	0
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	3	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	352	0	0	11	7
4	B	351	0	0	8	3
4	C	325	0	0	13	5
4	D	319	0	0	9	9
All	All	16073	0	14074	127	12

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.

The worst 5 of 127 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:205:PHE:O	4:B:601:HOH:O	1.88	0.92
1:D:6:LYS:H	1:D:6:LYS:HE2	1.34	0.91
1:C:150:GLU:OE2	4:C:601:HOH:O	1.98	0.79
1:B:72:GLU:OE2	4:B:602:HOH:O	2.01	0.79
1:D:200:LYS:NZ	4:D:601:HOH:O	1.93	0.76

The worst 5 of 12 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:922:HOH:O	4:D:844:HOH:O[1_565]	1.75	0.45
4:A:926:HOH:O	4:D:873:HOH:O[1_565]	1.98	0.22
4:A:859:HOH:O	4:D:894:HOH:O[1_565]	2.01	0.19
4:A:901:HOH:O	4:D:853:HOH:O[1_565]	2.05	0.15
4:A:654:HOH:O	4:D:793:HOH:O[1_565]	2.07	0.13

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	443/444 (100%)	427 (96%)	15 (3%)	1 (0%)	43	44
1	B	446/444 (100%)	430 (96%)	16 (4%)	0	100	100
1	C	442/444 (100%)	427 (97%)	15 (3%)	0	100	100
1	D	438/444 (99%)	422 (96%)	16 (4%)	0	100	100
All	All	1769/1776 (100%)	1706 (96%)	62 (4%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	306	LEU

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	386/385 (100%)	386 (100%)	0	100	100
1	B	389/385 (101%)	384 (99%)	5 (1%)	61	69
1	C	385/385 (100%)	380 (99%)	5 (1%)	61	69
1	D	384/385 (100%)	376 (98%)	8 (2%)	47	54
All	All	1544/1540 (100%)	1526 (99%)	18 (1%)	68	72

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	307	LEU
1	D	359	VAL
1	D	330[B]	LEU
1	C	330[B]	LEU
1	D	304	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	209	ASN
1	B	303	ASN
1	D	303	ASN
1	C	408	HIS
1	D	39	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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](#)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 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	$\# Z > 2$
2	TRS	A	501	-	7,7,7	0.35	0	9,9,9	0.37	0
2	TRS	C	501	-	7,7,7	0.31	0	9,9,9	0.49	0
2	TRS	D	501	-	7,7,7	0.26	0	9,9,9	0.35	0
2	TRS	B	501	-	7,7,7	0.32	0	9,9,9	0.44	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	TRS	A	501	-	-	2/9/9/9	-
2	TRS	C	501	-	-	3/9/9/9	-
2	TRS	D	501	-	-	2/9/9/9	-
2	TRS	B	501	-	-	2/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	501	TRS	N-C-C3-O3
2	C	501	TRS	C2-C-C3-O3
2	A	501	TRS	C2-C-C3-O3
2	C	501	TRS	C1-C-C3-O3
2	D	501	TRS	C2-C-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	TRS	1	0
2	D	501	TRS	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	444/444 (100%)	-0.45	0 100 100	9, 22, 37, 55	1 (0%)
1	B	443/444 (99%)	-0.49	0 100 100	8, 20, 36, 53	5 (1%)
1	C	443/444 (99%)	-0.35	7 (1%) 70 73	8, 22, 44, 82	1 (0%)
1	D	441/444 (99%)	-0.32	3 (0%) 84 86	8, 23, 46, 64	1 (0%)
All	All	1771/1776 (99%)	-0.40	10 (0%) 85 87	8, 22, 41, 82	8 (0%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	315	GLY	3.1
1	D	312	ILE	2.8
1	C	305	GLY	2.8
1	C	306	LEU	2.5
1	C	309	ALA	2.4

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
2	TRS	D	501	8/8	0.93	0.09	23,26,29,29	0
3	NA	A	504	1/1	0.93	0.08	28,28,28,28	0
3	NA	B	503	1/1	0.93	0.11	34,34,34,34	0
2	TRS	C	501	8/8	0.94	0.07	18,21,24,26	0
2	TRS	B	501	8/8	0.94	0.07	16,20,23,25	0
2	TRS	A	501	8/8	0.95	0.07	17,20,24,26	0
3	NA	A	503	1/1	0.95	0.07	26,26,26,26	0
3	NA	C	503	1/1	0.96	0.09	24,24,24,24	0
3	NA	D	502	1/1	0.98	0.06	22,22,22,22	0
3	NA	D	503	1/1	0.98	0.04	26,26,26,26	0
3	NA	C	502	1/1	0.99	0.07	19,19,19,19	0
3	NA	B	502	1/1	0.99	0.06	17,17,17,17	0
3	NA	A	502	1/1	0.99	0.08	21,21,21,21	0
3	NA	B	504	1/1	0.99	0.06	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.