



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:49 PM UTC

PDB ID : 8K05 / pdb_00008k05
Title : Pseudouridine 5'-monophosphate glycosylase from Arabidopsis thaliana – sulfate bound holoenzyme
Authors : Lee, J.Y.; Kim, S.H.; Rhee, S.K.
Deposited on : 2023-07-07
Resolution : 1.45 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

<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

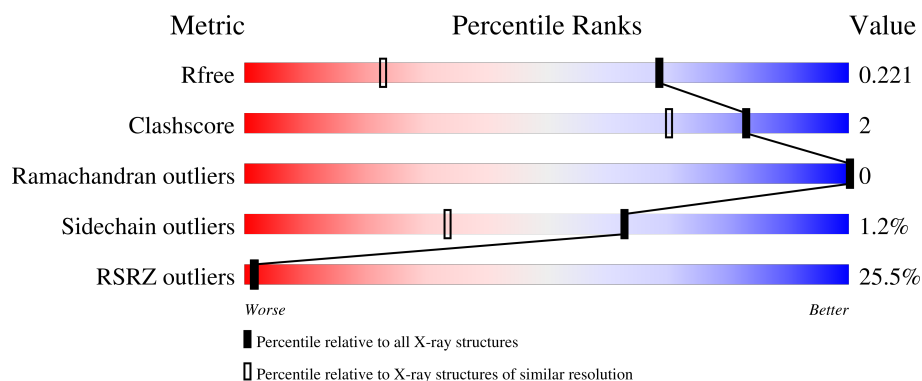
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.45 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}	180053	1756 (1.46-1.46)
Clashscore	190562	1795 (1.46-1.46)
Ramachandran outliers	187476	1776 (1.46-1.46)
Sidechain outliers	187428	1776 (1.46-1.46)
RSRZ outliers	180081	1756 (1.46-1.46)

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	340	23% 85% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2571 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 Pseudouridine-5'-phosphate glycosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	0	0	0
			2260	1413	399	440	8			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	331	LEU	-	expression tag	UNP Q84K35
A	332	GLU	-	expression tag	UNP Q84K35
A	333	HIS	-	expression tag	UNP Q84K35
A	334	HIS	-	expression tag	UNP Q84K35
A	335	HIS	-	expression tag	UNP Q84K35
A	336	HIS	-	expression tag	UNP Q84K35
A	337	HIS	-	expression tag	UNP Q84K35
A	338	HIS	-	expression tag	UNP Q84K35
A	339	HIS	-	expression tag	UNP Q84K35
A	340	HIS	-	expression tag	UNP Q84K35

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

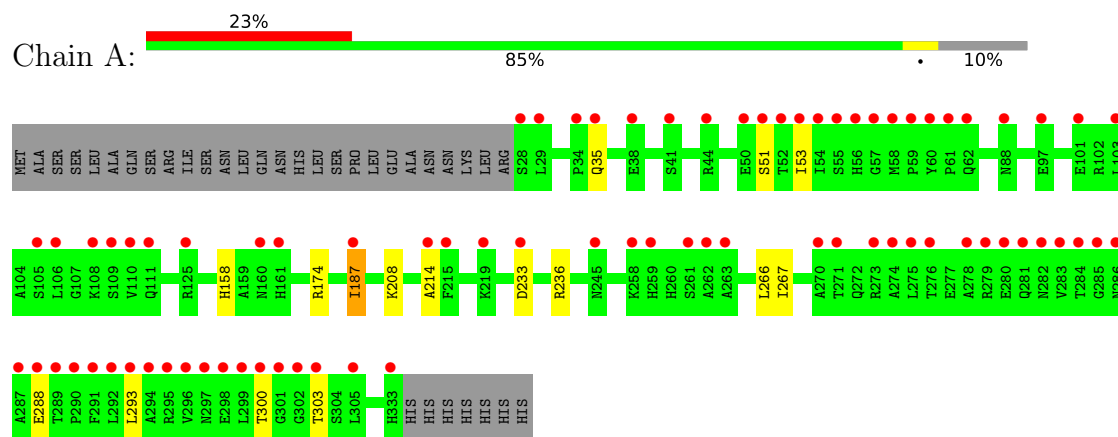
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	300	Total	O	0	0
			300	300		

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: Pseudouridine-5'-phosphate glycosidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	121.13Å 121.13Å 121.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.55 – 1.45 28.55 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.8 (28.55-1.45) 99.8 (28.55-1.45)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.33 (at 1.45Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.206 , 0.217 0.208 , 0.221	Depositor DCC
R_{free} test set	2000 reflections (1.91%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2571	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, SO4

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	0.44	0/2291	0.69	1/3112 (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	214	ALA	N-CA-C	-6.46	101.43	110.35

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2260	0	2307	11	0
2	A	1	0	0	0	0
3	A	10	0	0	0	0
4	A	300	0	0	3	0
All	All	2571	0	2307	11	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 2.

All (11) 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:233:ASP:OD1	1:A:236:ARG:NH2	2.22	0.71
1:A:267:ILE:HD11	1:A:303:THR:HG23	1.71	0.71
1:A:174:ARG:NH2	4:A:506:HOH:O	2.36	0.58
1:A:187:ILE:HD13	1:A:293:LEU:HD22	1.85	0.58
1:A:35:GLN:NE2	4:A:504:HOH:O	2.33	0.52
1:A:300:THR:O	1:A:303:THR:HG22	2.12	0.50
1:A:158:HIS:ND1	1:A:288:GLU:OE2	2.41	0.49
1:A:300:THR:HB	1:A:303:THR:CG2	2.44	0.48
1:A:158:HIS:HD1	1:A:288:GLU:CD	2.23	0.46
1:A:266:LEU:HD23	1:A:303:THR:HG21	1.97	0.46
1:A:208:LYS:NZ	4:A:517:HOH:O	2.51	0.43

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	304/340 (89%)	301 (99%)	3 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	244/275 (89%)	241 (99%)	3 (1%)	63 33

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

Mol	Chain	Res	Type
1	A	51	SER
1	A	53	ILE
1	A	187	ILE

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	62	GLN
1	A	77	ASN
1	A	247	GLN
1	A	308	ASN

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 ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
3	SO4	A	403	-	4,4,4	0.23	0	6,6,6	0.22	0
3	SO4	A	402	-	4,4,4	0.25	0	6,6,6	0.08	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	306/340 (90%)	1.32	78 (25%) ⓘ ⓘ	15, 25, 54, 66	0

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	53	ILE	11.9
1	A	283	VAL	7.9
1	A	52	THR	7.6
1	A	287	ALA	7.3
1	A	294	ALA	7.1
1	A	59	PRO	6.7
1	A	291	PHE	6.4
1	A	278	ALA	6.4
1	A	56	HIS	6.1
1	A	54	ILE	6.0
1	A	284	THR	5.8
1	A	289	THR	5.7
1	A	214	ALA	5.4
1	A	282	ASN	5.3
1	A	161	HIS	5.2
1	A	28	SER	5.1
1	A	293	LEU	5.0
1	A	285	GLY	4.9
1	A	292	LEU	4.9
1	A	303	THR	4.8
1	A	296	VAL	4.7
1	A	302	GLY	4.7
1	A	219	LYS	4.6
1	A	290	PRO	4.6
1	A	160	ASN	4.6
1	A	58	MET	4.5
1	A	280	GLU	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	288	GLU	4.3
1	A	301	GLY	4.2
1	A	297	ASN	4.1
1	A	109	SER	4.0
1	A	60	TYR	3.9
1	A	286	ASN	3.9
1	A	298	GLU	3.5
1	A	276	THR	3.5
1	A	108	LYS	3.4
1	A	279	ARG	3.4
1	A	51	SER	3.3
1	A	55	SER	3.3
1	A	258	LYS	3.3
1	A	110	VAL	3.3
1	A	333	HIS	3.2
1	A	281	GLN	3.2
1	A	29	LEU	3.1
1	A	259	HIS	3.1
1	A	34	PRO	3.1
1	A	299	LEU	3.0
1	A	273	ARG	3.0
1	A	105	SER	3.0
1	A	295	ARG	3.0
1	A	275	LEU	3.0
1	A	187	ILE	2.8
1	A	106	LEU	2.8
1	A	300	THR	2.7
1	A	125	ARG	2.7
1	A	38	GLU	2.6
1	A	271	THR	2.6
1	A	103	LEU	2.5
1	A	215	PHE	2.5
1	A	111	GLN	2.5
1	A	62	GLN	2.4
1	A	97	GLU	2.4
1	A	61	PRO	2.4
1	A	305	LEU	2.4
1	A	262	ALA	2.3
1	A	263	ALA	2.2
1	A	88	ASN	2.2
1	A	35	GLN	2.2
1	A	57	GLY	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	50	GLU	2.1
1	A	270	ALA	2.1
1	A	101	GLU	2.1
1	A	233	ASP	2.1
1	A	44	ARG	2.1
1	A	245	ASN	2.1
1	A	274	ALA	2.0
1	A	41	SER	2.0
1	A	261	SER	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

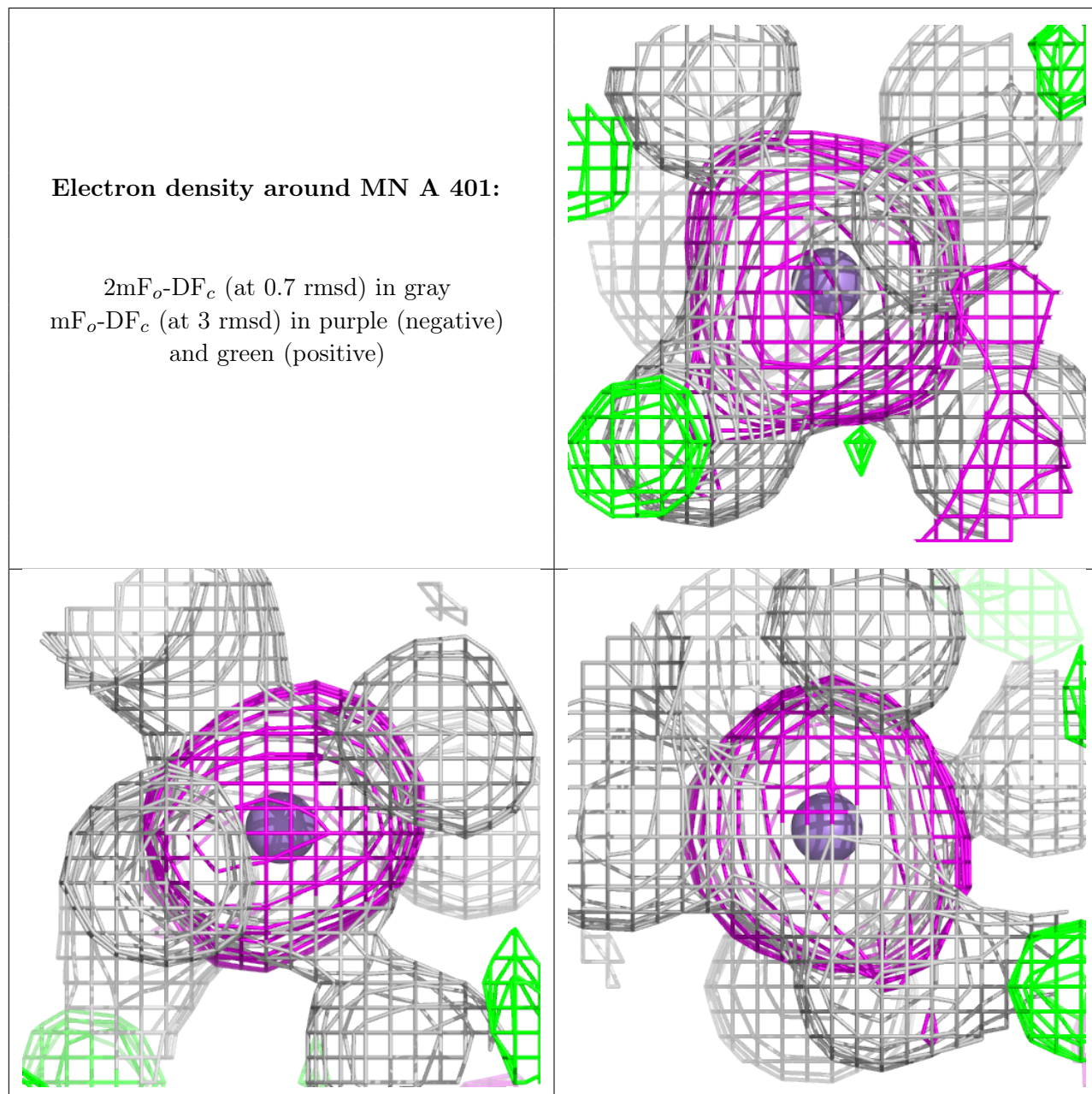
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	SO4	A	402	5/5	0.79	0.12	54,55,66,68	0
3	SO4	A	403	5/5	0.96	0.09	24,26,32,36	0
2	MN	A	401	1/1	0.99	0.22	34,34,34,34	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 MN A 401:

$2mF_o-DF_c$ (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.