



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 9, 2026 – 03:19 AM JST

PDB ID : 9X2R / pdb_00009x2r
Title : Crystal structure of Medicago truncatula NSP1-NSP2 heterodimer
Authors : Wan, L.H.; Hu, Y.X.
Deposited on : 2025-10-07
Resolution : 2.41 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	:	4-5-2 with Phenix2.0
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

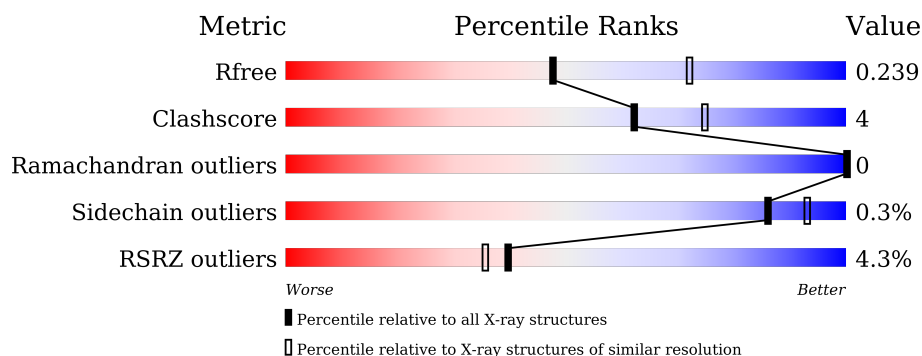
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	554	2% 60% 6% 34%
2	B	508	4% 64% 6% 30%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5915 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 Protein NODULATION SIGNALING PATHWAY 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	367	Total	C	N	O	S	0	0	0
			2919	1835	523	547	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	489	SER	CYS	conflict	UNP Q4VYC8

- Molecule 2 is a protein called Protein NODULATION SIGNALING PATHWAY 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	356	Total	C	N	O	S	0	1	0
			2779	1759	508	502	10			

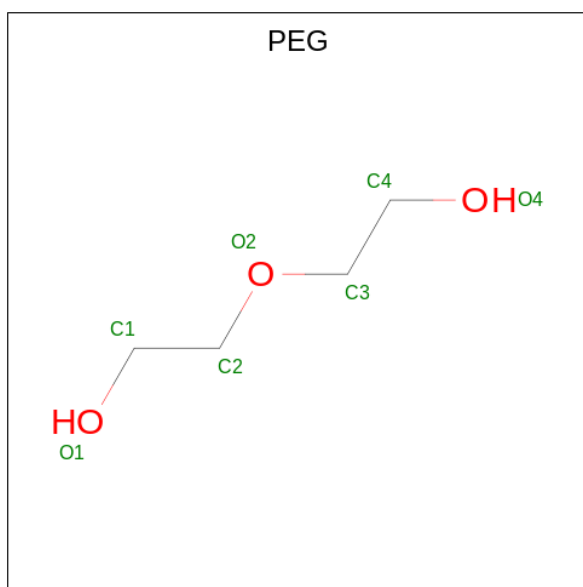
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	136	GLY	ASP	conflict	UNP Q5NE24
B	459	SER	CYS	conflict	UNP Q5NE24

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

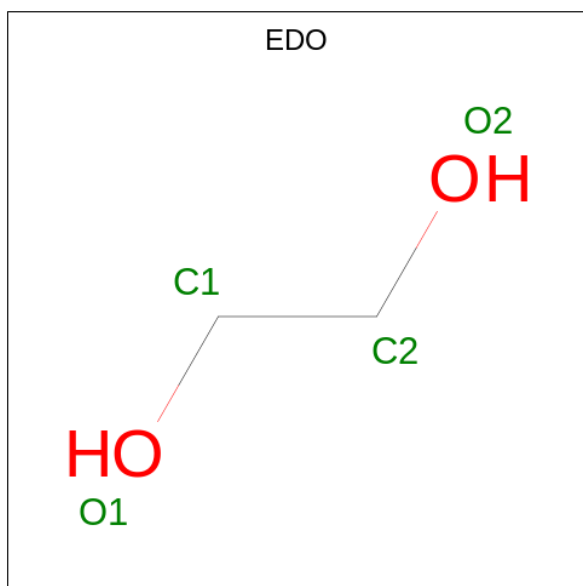
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	110	Total 110	O 110	0	0
6	B	95	Total 95	O 95	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	191.64Å 46.39Å 127.12Å 90.00° 122.03° 90.00°	Depositor
Resolution (Å)	30.89 – 2.41 30.89 – 2.41	Depositor EDS
% Data completeness (in resolution range)	97.8 (30.89-2.41) 98.0 (30.89-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.196 , 0.242 0.196 , 0.239	Depositor DCC
R_{free} test set	1829 reflections (4.27%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.715	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5915	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: ZN, PEG, 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	0.10	0/2985	0.27	0/4038
2	B	0.15	0/2836	0.31	0/3828
All	All	0.13	0/5821	0.29	0/7866

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

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	2919	0	2836	25	0
2	B	2779	0	2785	25	0
3	A	1	0	0	0	0
4	A	7	0	10	1	0
5	B	4	0	6	2	0
6	A	110	0	0	2	0
6	B	95	0	0	1	0
All	All	5915	0	5637	47	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 4.

All (47) 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:170:GLN:HE22	2:B:134:ASN:HB2	1.42	0.85
2:B:438:SER:HB3	2:B:441:GLU:HG3	1.64	0.79
2:B:135:ARG:H	2:B:135:ARG:HD3	1.49	0.77
1:A:269:GLN:HG3	4:A:602:PEG:H41	1.76	0.68
1:A:377:THR:HG21	1:A:383:LEU:HD22	1.77	0.67
1:A:304:ARG:NH2	1:A:307:GLY:O	2.29	0.65
1:A:410:ARG:HH21	1:A:550:ASP:HB2	1.62	0.64
1:A:166:ARG:HD3	1:A:446:TRP:CE2	2.32	0.63
1:A:166:ARG:NH2	1:A:539:GLN:OE1	2.32	0.63
1:A:479:ARG:HA	1:A:481:MET:HE3	1.85	0.58
1:A:347:LEU:HG	1:A:359:ILE:HD12	1.87	0.56
1:A:367:LEU:HB2	1:A:394:LEU:HD21	1.88	0.56
1:A:170:GLN:NE2	2:B:134:ASN:HB2	2.16	0.54
2:B:127:ALA:HA	2:B:133:LYS:HB2	1.90	0.54
1:A:170:GLN:HE22	2:B:134:ASN:CB	2.18	0.54
2:B:134:ASN:ND2	6:B:711:HOH:O	2.40	0.53
2:B:234:VAL:CG1	2:B:267:PRO:HG3	2.41	0.51
1:A:263:ALA:HA	1:A:418:ILE:HG12	1.92	0.51
1:A:304:ARG:HG2	1:A:305:PRO:HD2	1.94	0.50
2:B:209:PHE:HE2	2:B:249[A]:GLU:HG3	1.75	0.50
2:B:126:GLU:HG2	2:B:133:LYS:HE2	1.93	0.50
1:A:489:SER:HB2	6:A:797:HOH:O	2.10	0.49
1:A:238:GLU:OE1	1:A:240:ARG:NH2	2.45	0.49
1:A:461:SER:OG	1:A:463:GLU:OE2	2.28	0.48
2:B:337:LEU:O	2:B:369:GLU:HA	2.14	0.48
1:A:424:MET:HE3	1:A:424:MET:HB2	1.79	0.47
2:B:127:ALA:HA	2:B:133:LYS:CB	2.44	0.47
2:B:249[A]:GLU:HG2	2:B:251:VAL:H	1.80	0.47
2:B:357:ALA:O	2:B:362:PRO:HD3	2.15	0.47
1:A:371:ASN:OD1	1:A:373:LYS:N	2.48	0.46
2:B:483:LYS:HB3	2:B:483:LYS:HE3	1.59	0.45
2:B:358:LYS:HD2	2:B:501:CYS:SG	2.56	0.45
1:A:241:PHE:O	1:A:245:SER:OG	2.20	0.45
2:B:170:HIS:O	2:B:174:GLU:HG2	2.16	0.44
2:B:208:ALA:HB2	2:B:410:LEU:HG	1.99	0.44
1:A:349:TYR:OH	6:A:701:HOH:O	2.21	0.44
2:B:458:HIS:NE2	2:B:462:LYS:HE2	2.32	0.43
2:B:483:LYS:CD	5:B:601:EDO:H11	2.49	0.42
1:A:424:MET:HE1	1:A:440:ARG:O	2.19	0.42
1:A:465:LYS:HB3	1:A:465:LYS:HE3	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:484:LEU:HD12	2:B:484:LEU:HA	1.81	0.42
2:B:483:LYS:CG	5:B:601:EDO:H11	2.50	0.41
1:A:424:MET:SD	1:A:444:TYR:HB2	2.60	0.41
2:B:128:LEU:HD23	2:B:128:LEU:HA	1.79	0.41
2:B:371:GLU:OE1	2:B:495:SER:OG	2.33	0.41
2:B:234:VAL:HG13	2:B:267:PRO:HG3	2.01	0.41
1:A:284:LEU:HD12	1:A:284:LEU:HA	1.93	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	359/554 (65%)	357 (99%)	2 (1%)	0	100	100
2	B	349/508 (69%)	346 (99%)	3 (1%)	0	100	100
All	All	708/1062 (67%)	703 (99%)	5 (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	319/485 (66%)	318 (100%)	1 (0%)	86	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	295/431 (68%)	294 (100%)	1 (0%)	86	93
All	All	614/916 (67%)	612 (100%)	2 (0%)	86	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	549	LEU
2	B	469	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	GLN
1	A	195	HIS
1	A	243	GLN
1	A	351	GLN
1	A	422	ASN
1	A	458	ASN
2	B	170	HIS
2	B	263	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	$\# Z > 2$
4	PEG	A	602	-	6,6,6	0.13	0	5,5,5	0.08	0
5	EDO	B	601	-	3,3,3	0.07	0	2,2,2	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
4	PEG	A	602	-	-	1/4/4/4	-
5	EDO	B	601	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	602	PEG	C1-C2-O2-C3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	602	PEG	1	0
5	B	601	EDO	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	367/554 (66%)	0.08	10 (2%) 56 52	33, 52, 83, 103	0
2	B	356/508 (70%)	0.12	21 (5%) 28 24	27, 48, 84, 118	1 (0%)
All	All	723/1062 (68%)	0.10	31 (4%) 40 35	27, 50, 83, 118	1 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	376	ILE	4.3
2	B	235	ALA	3.8
1	A	222	SER	3.7
1	A	241	PHE	3.7
2	B	265	ASN	3.6
2	B	132	THR	3.5
2	B	431	GLY	3.0
2	B	133	LYS	2.9
2	B	503	SER	2.6
1	A	458	ASN	2.6
1	A	342	PHE	2.5
2	B	374	SER	2.5
2	B	266	GLY	2.5
2	B	149	VAL	2.4
2	B	375	VAL	2.4
1	A	162	ASN	2.4
1	A	331	THR	2.4
2	B	130	GLY	2.4
1	A	232	ILE	2.3
2	B	309	HIS	2.3
2	B	437	ARG	2.3
2	B	438	SER	2.2
2	B	134	ASN	2.2
1	A	398	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	129	THR	2.2
2	B	372	VAL	2.1
2	B	262	SER	2.1
2	B	131	SER	2.1
2	B	429	ARG	2.0
1	A	367	LEU	2.0
1	A	465	LYS	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](#)

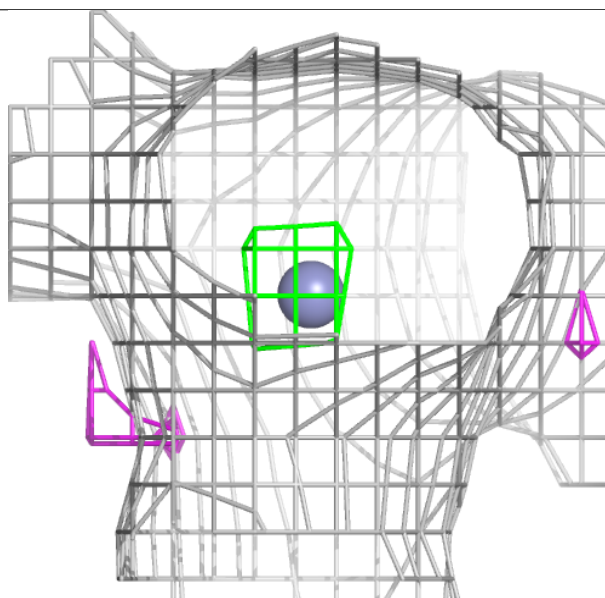
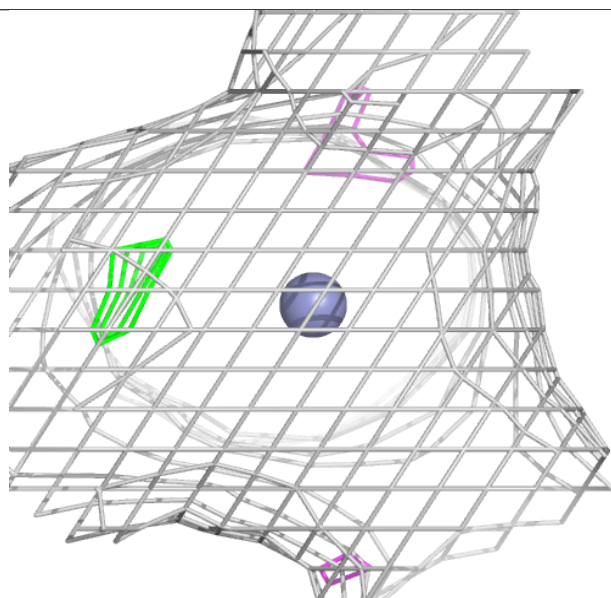
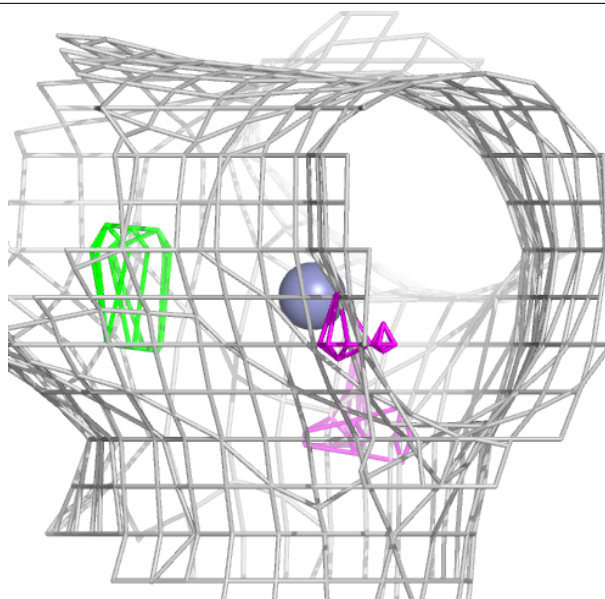
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
5	EDO	B	601	4/4	0.73	0.23	47,52,56,61	0
4	PEG	A	602	7/7	0.82	0.21	48,52,66,69	0
3	ZN	A	601	1/1	0.99	0.03	57,57,57,57	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 ZN A 601:

$2mF_o-DF_c$ (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.