



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 30, 2025 – 04:09 PM JST

PDB ID : 9WV4 / pdb_00009wv4
Title : Crystal structure of human ZMYND8 MYND domain
Authors : Srivastava, D.K.; Roy, S.
Deposited on : 2025-09-19
Resolution : 2.29 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
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
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) : 2.46

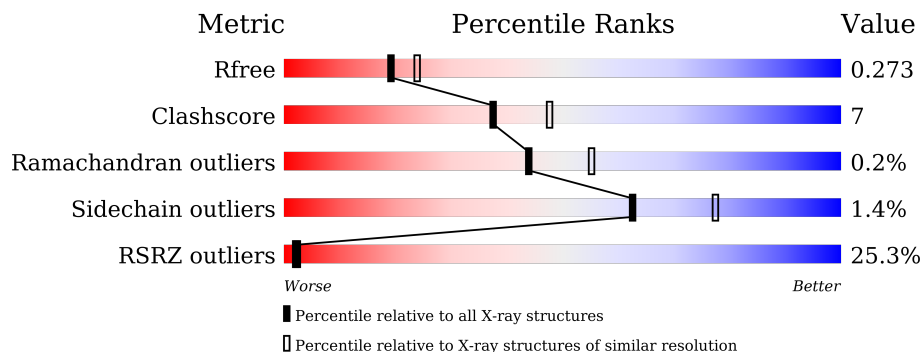
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	126	<div> <div>28%</div> <div> <div></div> <div>74%</div> <div>16%</div> <div>10%</div> </div> </div>
1	B	126	<div> <div>24%</div> <div> <div></div> <div>73%</div> <div>16%</div> <div>10%</div> </div> </div>
1	C	126	<div> <div>17%</div> <div> <div></div> <div>75%</div> <div>13%</div> <div>12%</div> </div> </div>
1	D	126	<div> <div>21%</div> <div> <div></div> <div>72%</div> <div>18%</div> <div>10%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4107 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 MYND-type zinc finger-containing chromatin reader ZMYND8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	113	Total	C	N	O	S	0	0	0
			946	587	169	179	11			
1	C	111	Total	C	N	O	S	0	0	0
			935	581	167	176	11			
1	A	113	Total	C	N	O	S	0	0	0
			947	588	169	179	11			
1	D	114	Total	C	N	O	S	0	0	0
			955	592	171	181	11			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

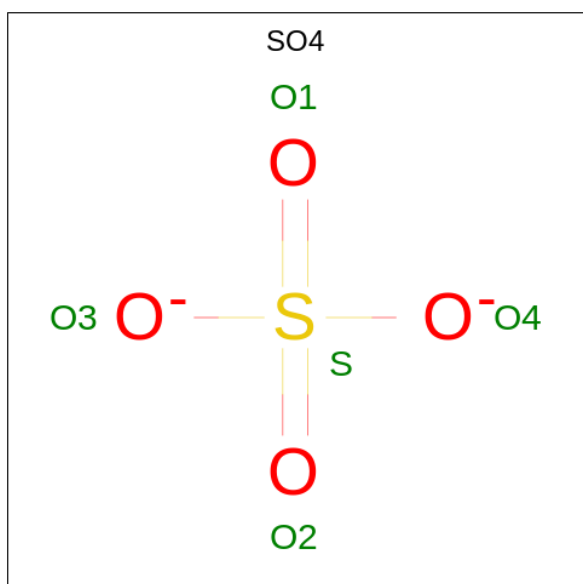
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



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

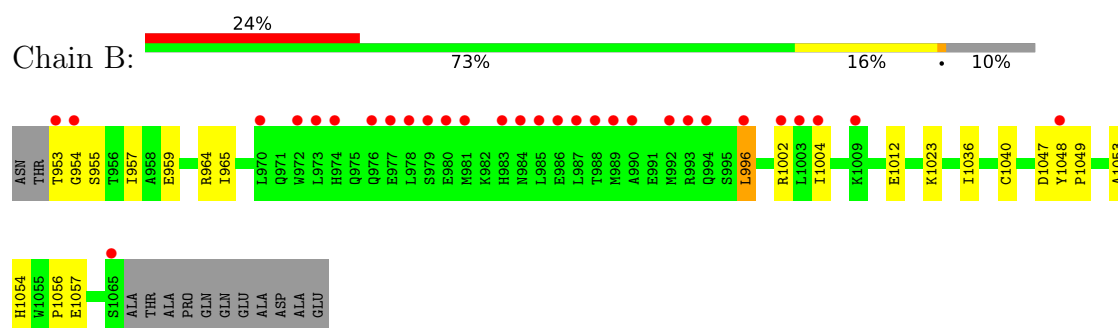
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	79	Total	O	0	0
			79	79		
5	C	84	Total	O	0	0
			84	84		
5	A	64	Total	O	0	0
			64	64		
5	D	63	Total	O	0	0
			63	63		

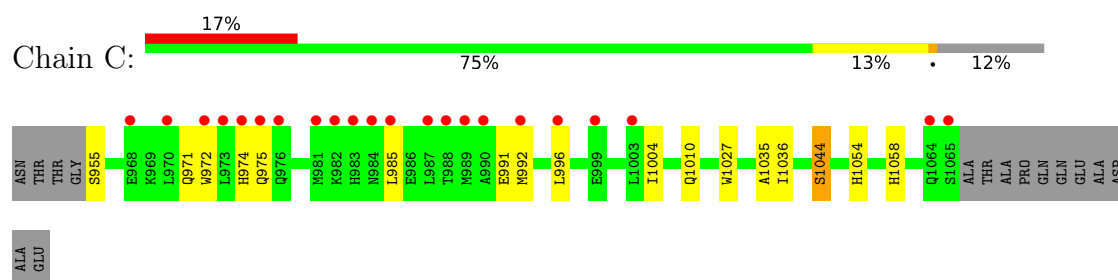
3 Residue-property plots [i](#)

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.

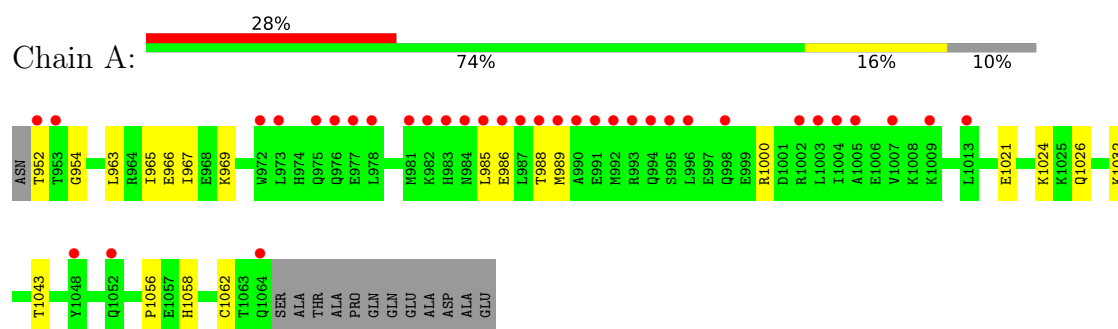
- Molecule 1: MYND-type zinc finger-containing chromatin reader ZMYND8



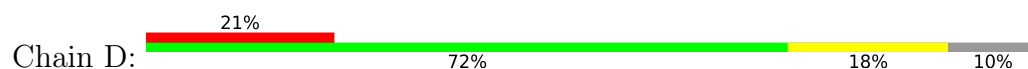
- Molecule 1: MYND-type zinc finger-containing chromatin reader ZMYND8

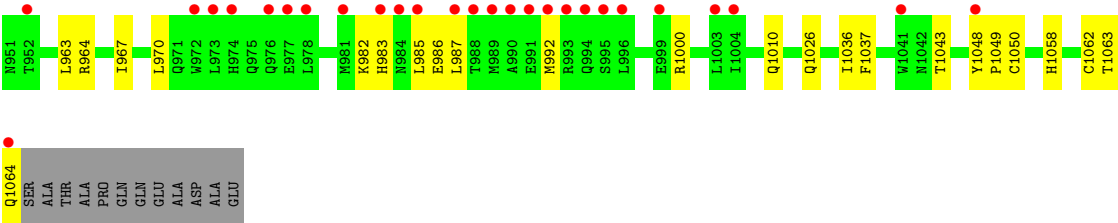


- Molecule 1: MYND-type zinc finger-containing chromatin reader ZMYND8



- Molecule 1: MYND-type zinc finger-containing chromatin reader ZMYND8





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.70Å 71.19Å 230.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.67 – 2.29 38.67 – 2.29	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.67-2.29) 99.6 (38.67-2.29)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.47 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, R_{free}	0.242 , 0.274 0.243 , 0.273	Depositor DCC
R_{free} test set	2401 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4107	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% 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: ZN, PEG, 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	0.41	0/964	0.54	0/1294
1	B	0.39	0/963	0.52	0/1292
1	C	0.40	0/952	0.51	0/1277
1	D	0.38	0/972	0.55	0/1305
All	All	0.39	0/3851	0.53	0/5168

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	947	0	924	15	0
1	B	946	0	922	17	0
1	C	935	0	912	15	0
1	D	955	0	930	19	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	B	14	0	20	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	7	0	10	0	0
4	C	5	0	0	0	0
5	A	64	0	0	1	0
5	B	79	0	0	1	0
5	C	84	0	0	0	0
5	D	63	0	0	2	0
All	All	4107	0	3718	52	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 7.

All (52) 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:952:THR:HG22	1:A:954:GLY:H	1.41	0.86
1:C:991:GLU:HG3	1:A:989:MET:HE1	1.74	0.69
1:A:1026:GLN:HE22	1:D:1026:GLN:HE22	1.40	0.68
1:C:992:MET:HG3	1:D:992:MET:HB2	1.75	0.68
1:B:996:LEU:HD21	1:C:996:LEU:HD12	1.79	0.65
1:A:966:GLU:HA	1:A:969:LYS:HE2	1.81	0.63
1:A:1000:ARG:HG3	1:D:1000:ARG:HG3	1.83	0.61
1:A:963:LEU:HD11	1:D:964:ARG:HB2	1.83	0.60
1:D:1048:TYR:CD1	1:D:1049:PRO:HD3	2.36	0.60
1:B:1004:ILE:HG22	1:C:1004:ILE:HD11	1.85	0.58
1:C:1035:ALA:HB1	1:C:1044:SER:HB3	1.89	0.55
1:C:1035:ALA:CB	1:C:1044:SER:HB3	2.37	0.54
1:C:1010:GLN:HG3	1:D:1010:GLN:OE1	2.09	0.53
1:D:1058:HIS:NE2	1:D:1062:CYS:HB2	2.25	0.51
1:B:954:GLY:H	1:B:957:ILE:HG22	1.75	0.51
1:A:985:LEU:HA	1:A:988:THR:HG22	1.93	0.51
1:D:1043:THR:HG21	1:D:1058:HIS:CE1	2.46	0.51
1:A:965:ILE:O	1:A:969:LYS:HG3	2.12	0.50
1:C:972:TRP:CD1	1:C:975:GLN:HE21	2.30	0.49
1:A:967:ILE:HD11	1:D:967:ILE:HG21	1.93	0.48
1:B:1053:ALA:O	1:B:1056:PRO:HD2	2.14	0.48
1:D:1063:THR:O	1:D:1064:GLN:HB2	2.14	0.48
1:A:1043:THR:HG21	1:A:1058:HIS:CE1	2.50	0.47
1:A:1056:PRO:HG2	5:A:1213:HOH:O	2.13	0.47
1:C:974:HIS:C	1:C:974:HIS:CD2	2.93	0.46
1:B:1023:LYS:HE2	1:C:1027:TRP:CD2	2.51	0.46
1:C:972:TRP:HD1	1:C:975:GLN:HE21	1.63	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:986:GLU:HA	1:A:989:MET:HG2	1.98	0.45
1:B:1054:HIS:HD2	3:B:1104:PEG:H22	1.81	0.45
1:D:987:LEU:HD12	1:D:987:LEU:HA	1.77	0.44
1:A:1058:HIS:CD2	1:A:1062:CYS:HB2	2.53	0.44
1:D:983:HIS:HB2	5:D:1229:HOH:O	2.16	0.44
1:B:965:ILE:HD13	1:B:965:ILE:HA	1.86	0.44
1:B:1002:ARG:HE	1:B:1002:ARG:HB3	1.55	0.44
1:B:1057:GLU:HG3	3:B:1103:PEG:O4	2.18	0.44
1:D:1036:ILE:HG13	1:D:1037:PHE:CD2	2.53	0.43
1:A:1021:GLU:HA	1:A:1024:LYS:HE2	2.00	0.43
1:C:985:LEU:HA	1:D:985:LEU:HD12	2.00	0.43
1:C:1035:ALA:O	1:C:1036:ILE:HD13	2.18	0.43
1:B:1057:GLU:HA	3:B:1103:PEG:H31	2.01	0.43
1:D:982:LYS:O	1:D:986:GLU:HG3	2.18	0.43
1:D:1058:HIS:CD2	1:D:1062:CYS:HB2	2.53	0.43
1:B:964:ARG:HB2	1:D:963:LEU:HD21	2.00	0.42
1:B:1048:TYR:CG	1:B:1049:PRO:HD3	2.54	0.42
1:B:955:SER:O	1:B:959:GLU:HG3	2.20	0.42
1:C:971:GLN:NE2	1:D:970:LEU:HD21	2.34	0.41
1:B:957:ILE:HD11	5:D:1248:HOH:O	2.20	0.41
1:B:1047:ASP:HB3	1:B:1049:PRO:HD2	2.02	0.41
1:B:964:ARG:HE	1:D:963:LEU:HD21	1.87	0.40
1:B:1040:CYS:HB2	5:B:1210:HOH:O	2.21	0.40
1:A:1032:LYS:HD3	1:A:1032:LYS:HA	1.58	0.40
1:C:1054:HIS:CE1	1:C:1058:HIS:HB2	2.57	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	111/126 (88%)	108 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	111/126 (88%)	107 (96%)	3 (3%)	1 (1%)	14	17
1	C	109/126 (86%)	106 (97%)	3 (3%)	0	100	100
1	D	112/126 (89%)	109 (97%)	3 (3%)	0	100	100
All	All	443/504 (88%)	430 (97%)	12 (3%)	1 (0%)	44	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1036	ILE

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	105/114 (92%)	105 (100%)	0	100	100
1	B	105/114 (92%)	102 (97%)	3 (3%)	37	54
1	C	104/114 (91%)	102 (98%)	2 (2%)	52	69
1	D	106/114 (93%)	105 (99%)	1 (1%)	75	87
All	All	420/456 (92%)	414 (99%)	6 (1%)	62	77

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	953	THR
1	B	996	LEU
1	B	1012	GLU
1	C	955	SER
1	C	1044	SER
1	D	1050	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	976	GLN
1	B	998	GLN
1	B	1026	GLN
1	C	975	GLN
1	C	1026	GLN
1	C	1030	ASN
1	A	1016	GLN
1	A	1051	GLN
1	D	971	GLN
1	D	1026	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 12 ligands modelled in this entry, 8 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	$\# Z > 2$
3	PEG	D	1101	-	6,6,6	0.30	0	5,5,5	0.45	0
3	PEG	B	1103	-	6,6,6	0.25	0	5,5,5	0.35	0
4	SO4	C	1101	-	4,4,4	0.79	0	6,6,6	0.33	0
3	PEG	B	1104	-	6,6,6	0.28	0	5,5,5	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
3	PEG	D	1101	-	-	4/4/4/4	-
3	PEG	B	1103	-	-	2/4/4/4	-
3	PEG	B	1104	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	1101	PEG	O2-C3-C4-O4
3	B	1104	PEG	O1-C1-C2-O2
3	B	1104	PEG	O2-C3-C4-O4
3	B	1104	PEG	C4-C3-O2-C2
3	B	1103	PEG	O1-C1-C2-O2
3	B	1103	PEG	C1-C2-O2-C3
3	B	1104	PEG	C1-C2-O2-C3
3	D	1101	PEG	C1-C2-O2-C3
3	D	1101	PEG	O1-C1-C2-O2
3	D	1101	PEG	C4-C3-O2-C2

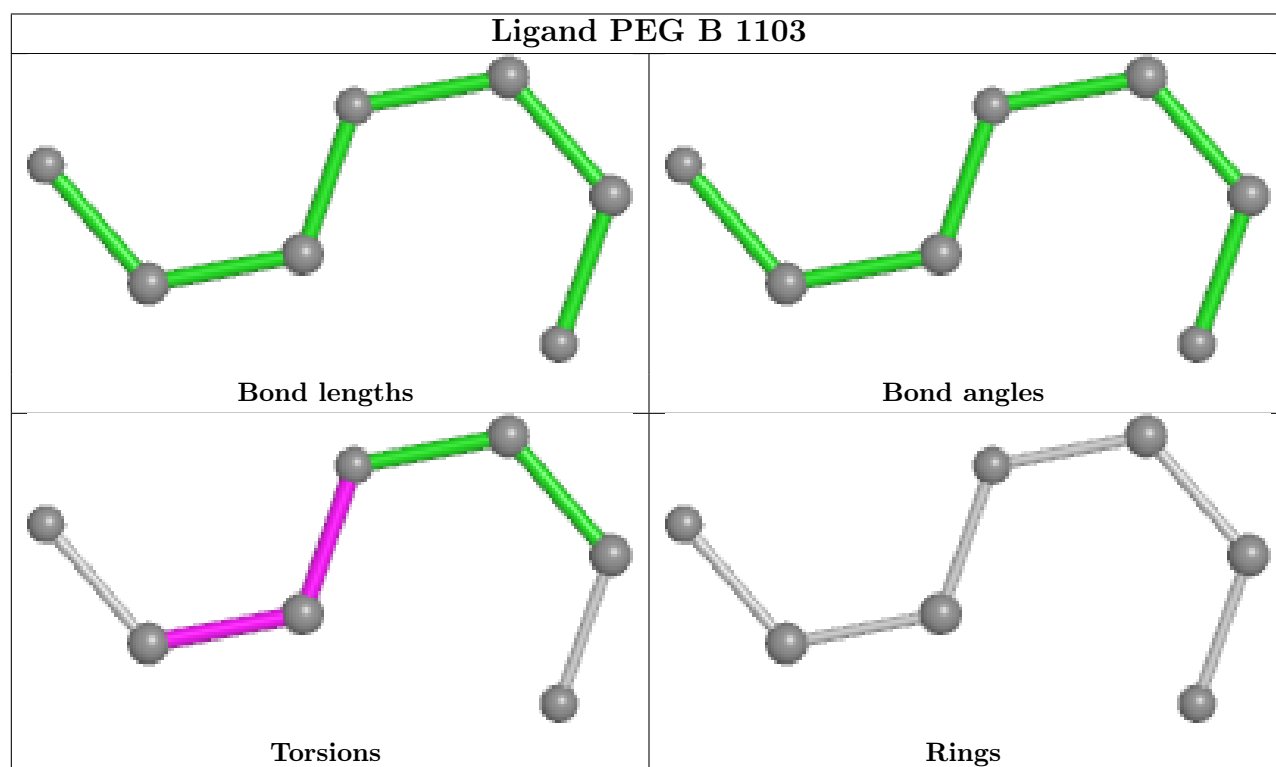
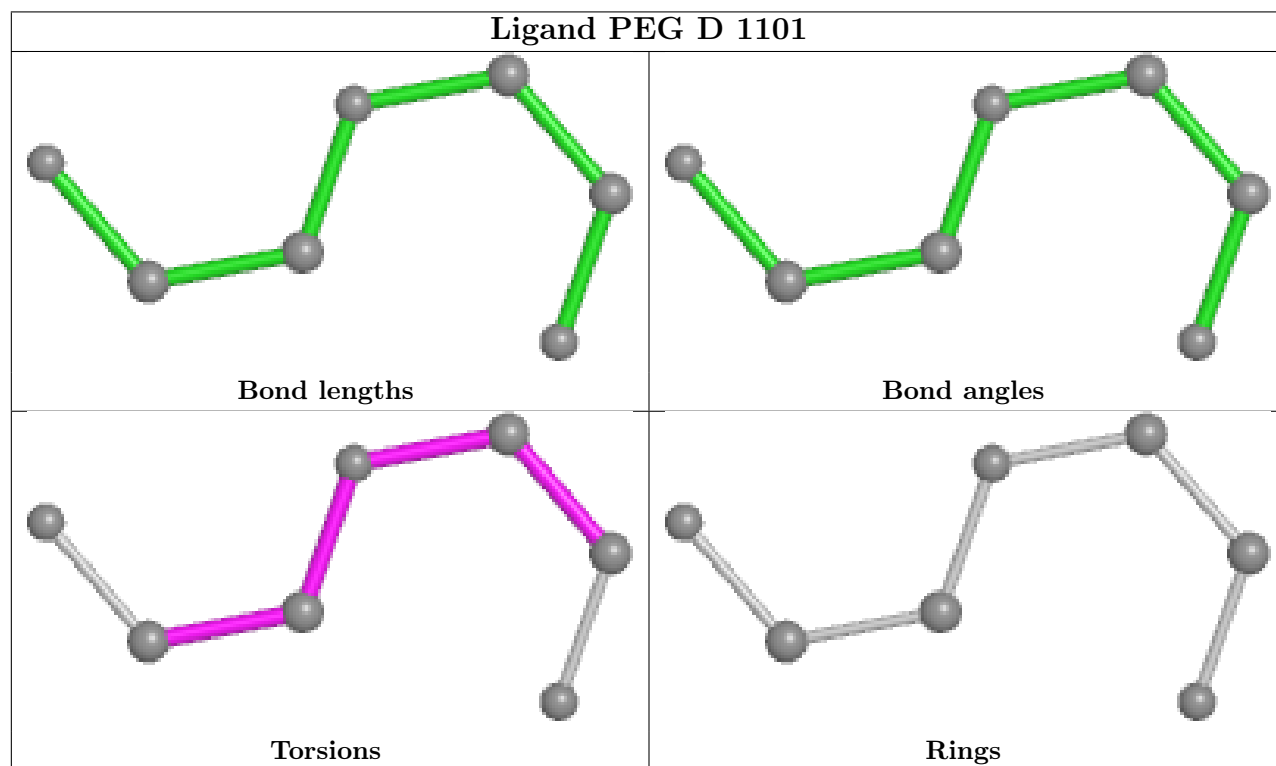
There are no ring outliers.

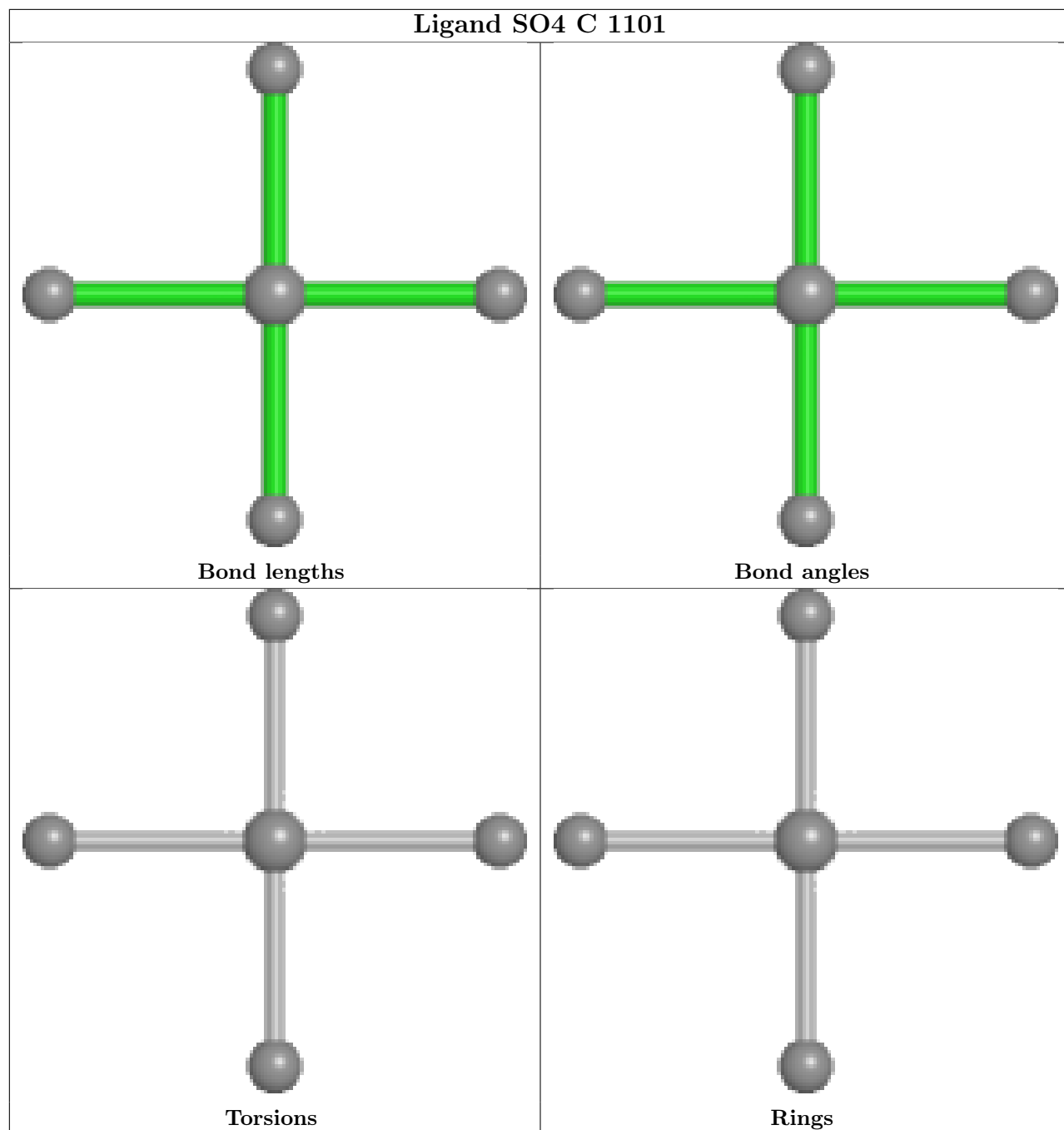
2 monomers are involved in 3 short contacts:

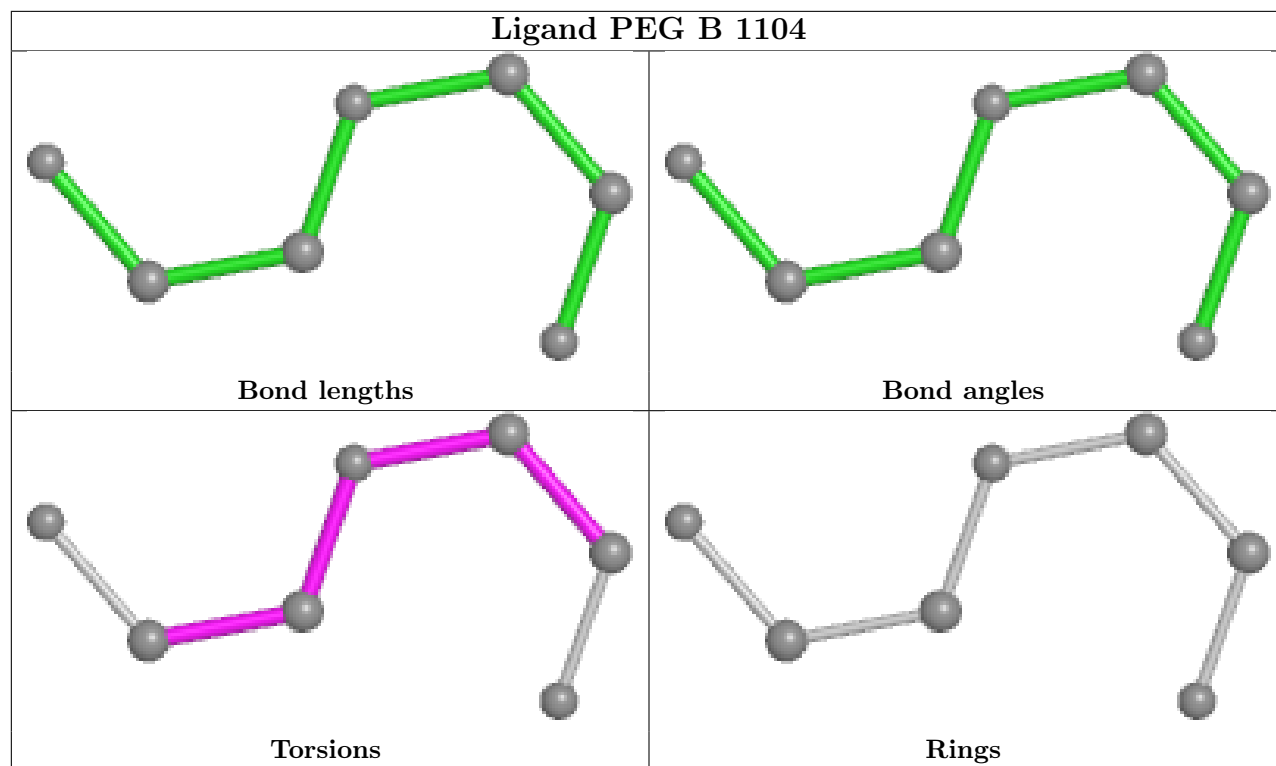
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1103	PEG	2	0
3	B	1104	PEG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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	113/126 (89%)	1.55	35 (30%) 1 1	30, 54, 167, 201	0
1	B	113/126 (89%)	1.28	30 (26%) 2 2	28, 49, 152, 188	0
1	C	111/126 (88%)	1.07	22 (19%) 3 4	29, 45, 99, 123	0
1	D	114/126 (90%)	1.17	27 (23%) 2 3	28, 53, 100, 123	0
All	All	451/504 (89%)	1.27	114 (25%) 2 2	28, 51, 152, 201	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	985	LEU	7.4
1	A	990	ALA	7.2
1	C	1065	SER	7.1
1	A	996	LEU	6.0
1	B	990	ALA	5.6
1	A	987	LEU	5.6
1	A	989	MET	5.6
1	B	987	LEU	5.4
1	B	996	LEU	5.3
1	A	993	ARG	5.1
1	B	1004	ILE	4.9
1	B	989	MET	4.9
1	A	992	MET	4.7
1	A	952	THR	4.5
1	B	973	LEU	4.4
1	B	983	HIS	4.3
1	B	980	GLU	4.3
1	A	982	LYS	4.3
1	C	987	LEU	4.2
1	B	985	LEU	4.1
1	B	988	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	953	THR	3.9
1	B	1065	SER	3.8
1	D	981	MET	3.8
1	D	988	THR	3.8
1	D	1048	TYR	3.7
1	D	984	ASN	3.6
1	D	987	LEU	3.6
1	A	1004	ILE	3.5
1	C	996	LEU	3.5
1	A	986	GLU	3.5
1	A	983	HIS	3.4
1	B	981	MET	3.4
1	D	985	LEU	3.4
1	A	975	GLN	3.3
1	C	992	MET	3.3
1	A	1052	GLN	3.3
1	D	983	HIS	3.3
1	C	976	GLN	3.2
1	A	1013	LEU	3.2
1	A	1048	TYR	3.2
1	C	985	LEU	3.2
1	A	1002	ARG	3.1
1	D	1064	GLN	3.1
1	A	988	THR	3.0
1	C	1003	LEU	3.0
1	C	999	GLU	3.0
1	C	981	MET	2.9
1	D	974	HIS	2.9
1	D	990	ALA	2.9
1	C	982	LYS	2.9
1	A	1007	VAL	2.9
1	A	1009	LYS	2.9
1	A	973	LEU	2.9
1	D	996	LEU	2.9
1	A	995	SER	2.9
1	C	975	GLN	2.8
1	B	1048	TYR	2.8
1	B	992	MET	2.8
1	D	972	TRP	2.8
1	B	1002	ARG	2.7
1	C	973	LEU	2.7
1	A	984	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	977	GLU	2.7
1	D	1004	ILE	2.7
1	B	977	GLU	2.6
1	C	988	THR	2.6
1	D	976	GLN	2.6
1	B	984	ASN	2.5
1	C	1064	GLN	2.5
1	B	979	SER	2.5
1	A	953	THR	2.5
1	B	974	HIS	2.5
1	A	994	GLN	2.5
1	D	993	ARG	2.5
1	C	974	HIS	2.5
1	A	981	MET	2.5
1	C	990	ALA	2.5
1	A	972	TRP	2.4
1	B	978	LEU	2.4
1	D	973	LEU	2.4
1	B	993	ARG	2.4
1	B	976	GLN	2.4
1	A	1003	LEU	2.4
1	A	976	GLN	2.3
1	C	968	GLU	2.3
1	B	1003	LEU	2.3
1	D	977	GLU	2.3
1	A	1005	ALA	2.3
1	C	983	HIS	2.3
1	C	972	TRP	2.2
1	A	991	GLU	2.2
1	A	978	LEU	2.2
1	A	1064	GLN	2.2
1	C	989	MET	2.2
1	D	989	MET	2.2
1	D	978	LEU	2.2
1	D	952	THR	2.2
1	A	998	GLN	2.2
1	D	992	MET	2.2
1	D	995	SER	2.1
1	B	1009	LYS	2.1
1	D	999	GLU	2.1
1	C	970	LEU	2.1
1	B	986	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	954	GLY	2.1
1	B	970	LEU	2.1
1	C	984	ASN	2.1
1	D	1003	LEU	2.1
1	D	991	GLU	2.0
1	B	994	GLN	2.0
1	B	972	TRP	2.0
1	D	1041	TRP	2.0
1	D	994	GLN	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.

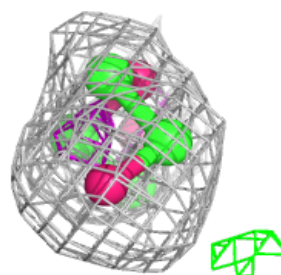
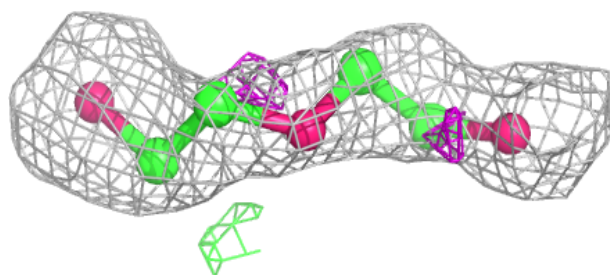
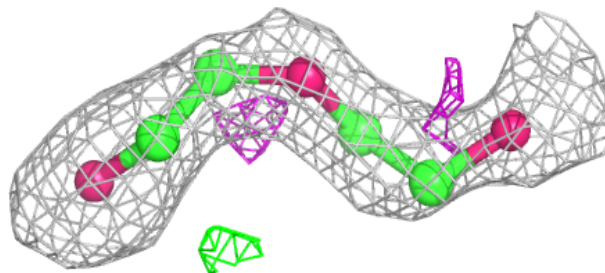
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PEG	D	1101	7/7	0.78	0.21	56,60,66,66	0
3	PEG	B	1104	7/7	0.84	0.17	51,55,55,56	0
3	PEG	B	1103	7/7	0.91	0.16	64,65,70,71	0
4	SO4	C	1101	5/5	0.92	0.15	61,62,67,73	0
2	ZN	D	1103	1/1	0.99	0.03	46,46,46,46	0
2	ZN	C	1102	1/1	0.99	0.04	37,37,37,37	0
2	ZN	C	1103	1/1	0.99	0.03	35,35,35,35	0
2	ZN	A	1101	1/1	0.99	0.03	36,36,36,36	0
2	ZN	A	1102	1/1	0.99	0.02	41,41,41,41	0
2	ZN	D	1102	1/1	1.00	0.01	39,39,39,39	0
2	ZN	B	1101	1/1	1.00	0.09	38,38,38,38	0
2	ZN	B	1102	1/1	1.00	0.05	35,35,35,35	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.

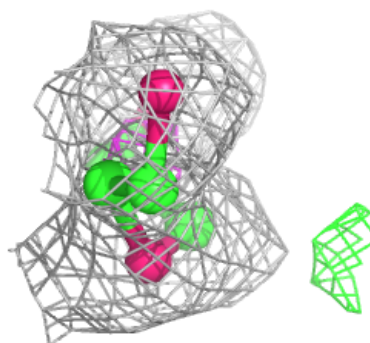
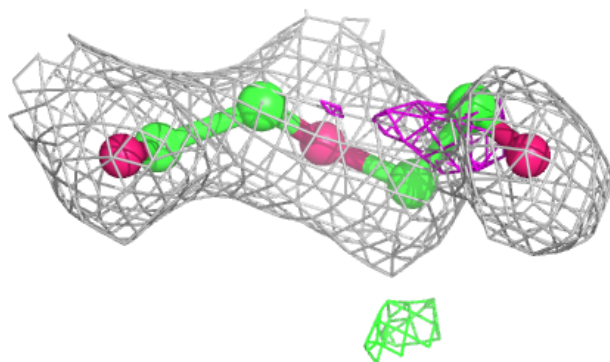
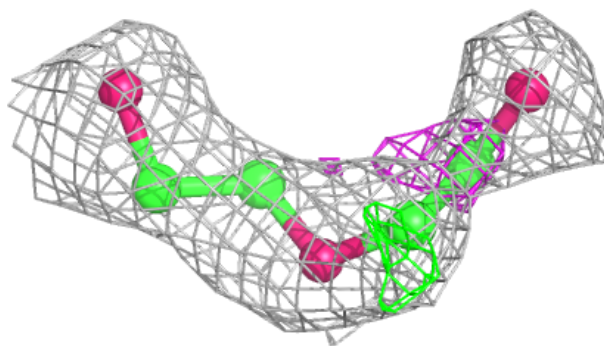
Electron density around PEG D 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

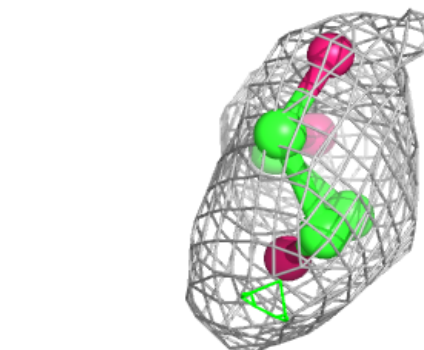
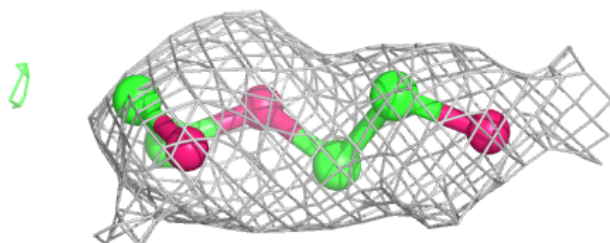
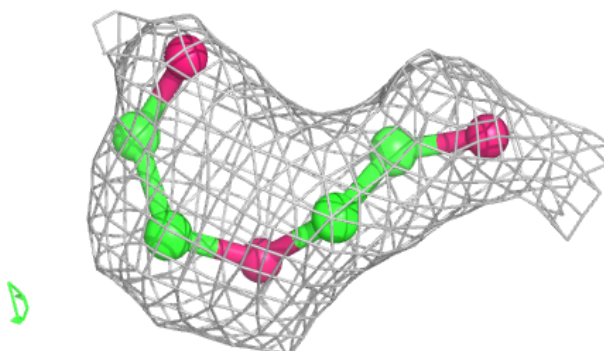


Electron density around PEG B 1104:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

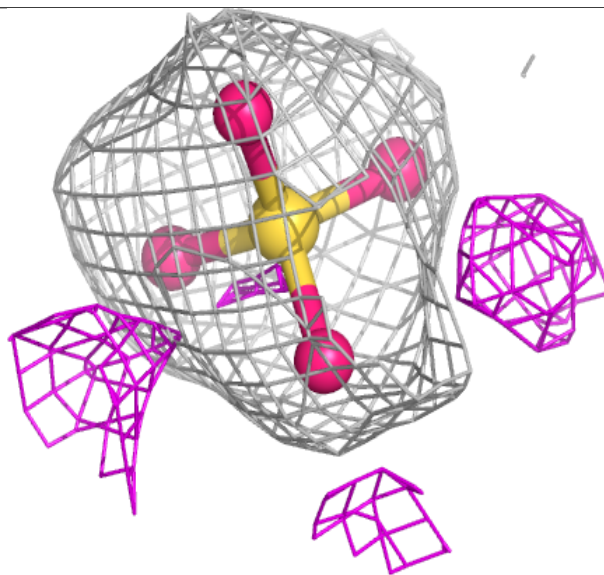
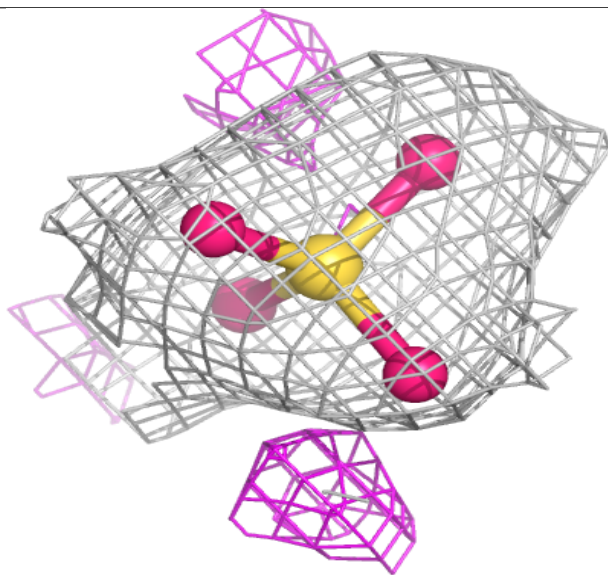
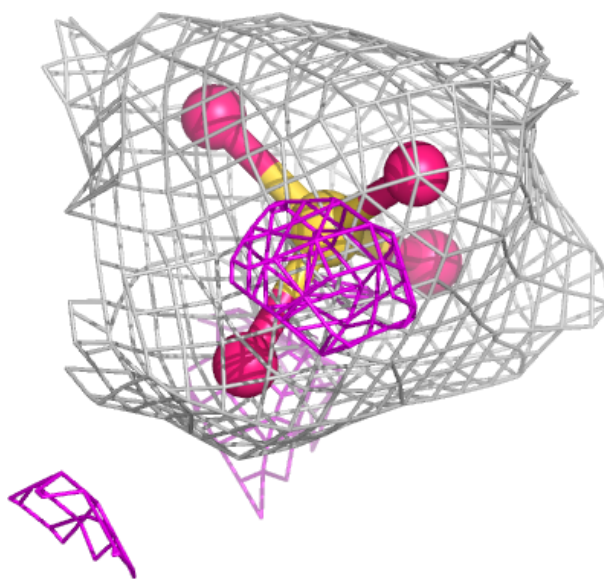
**Electron density around PEG B 1103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



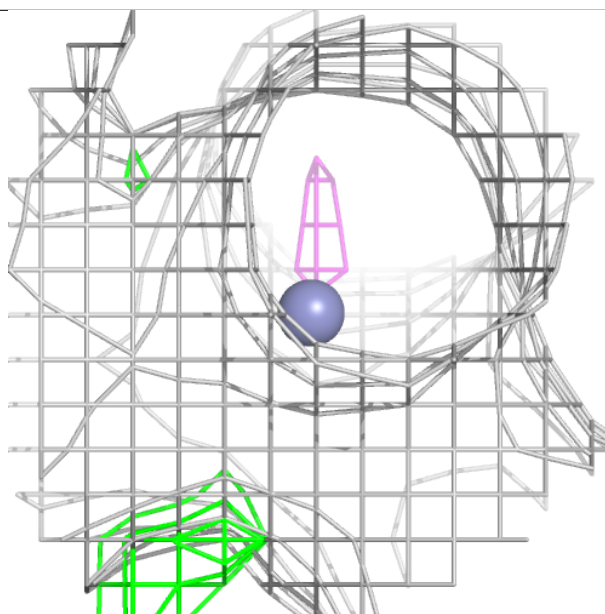
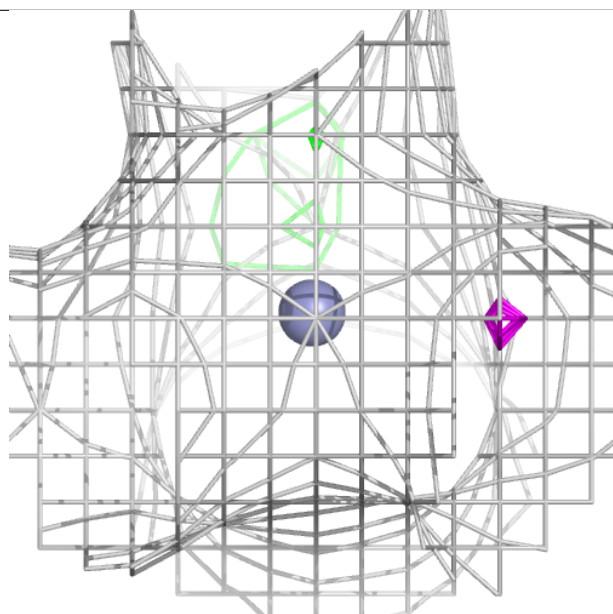
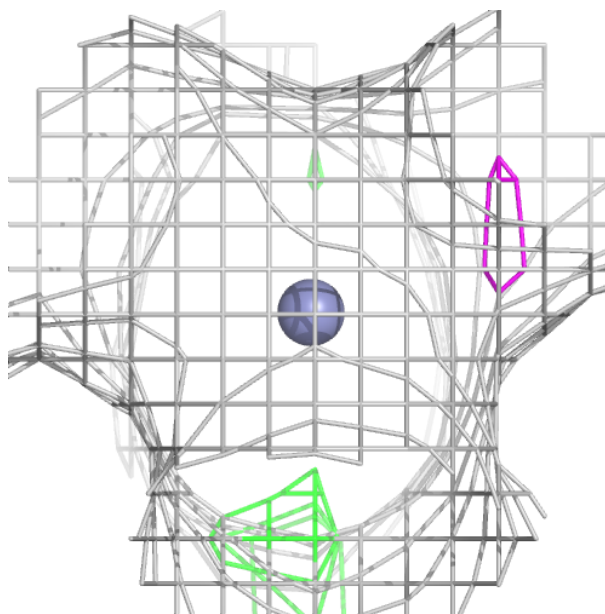
Electron density around SO4 C 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



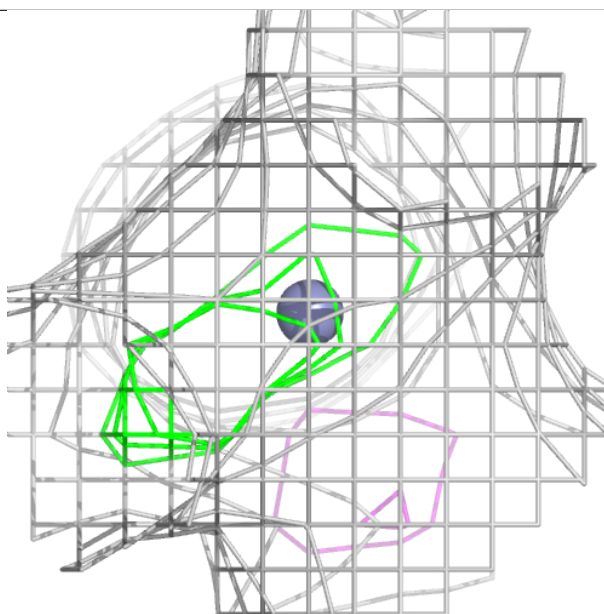
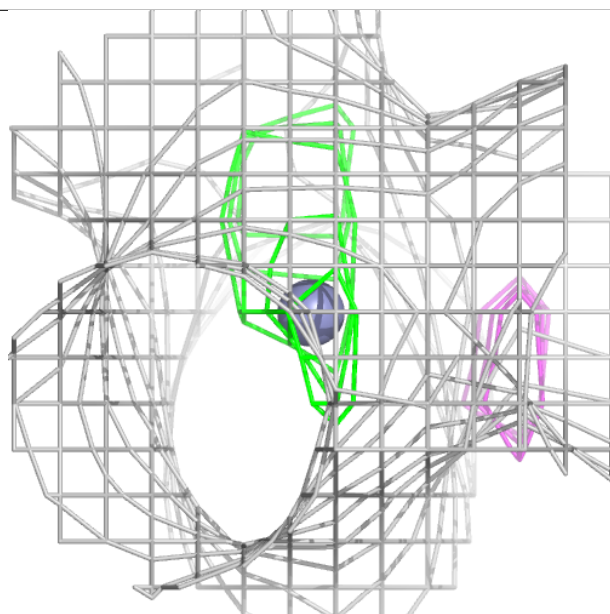
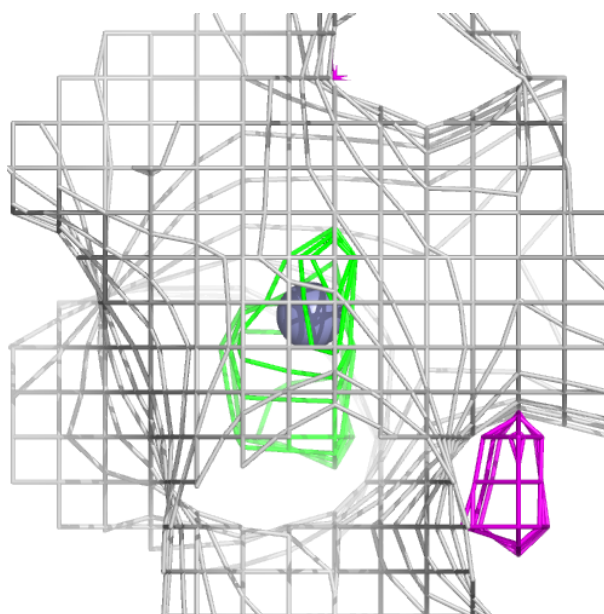
Electron density around ZN D 1103:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



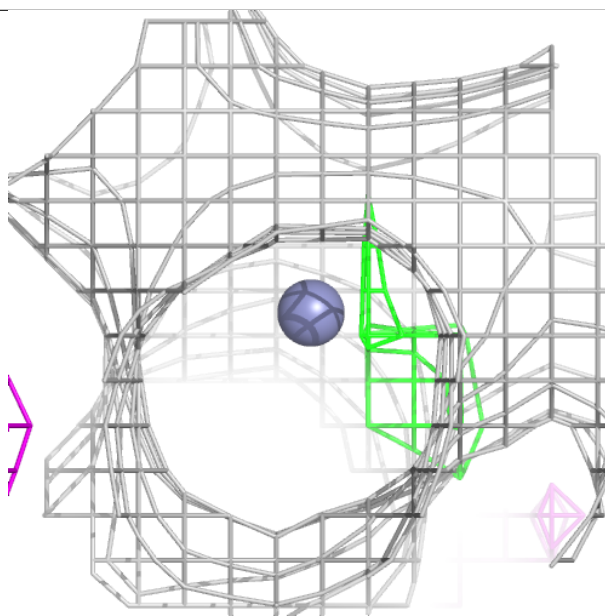
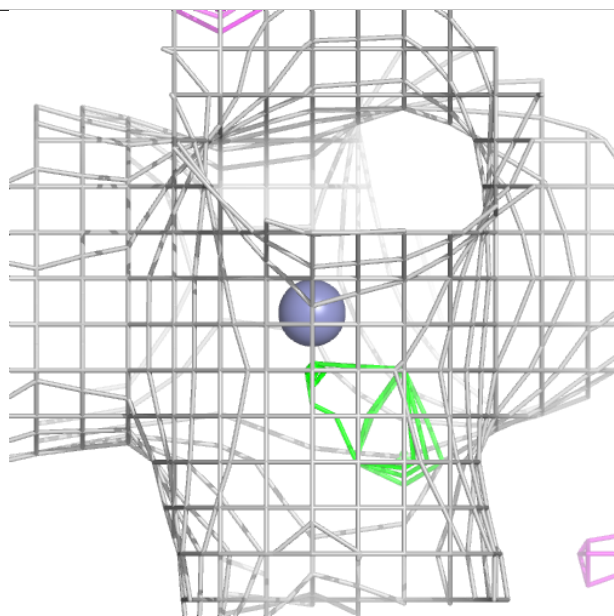
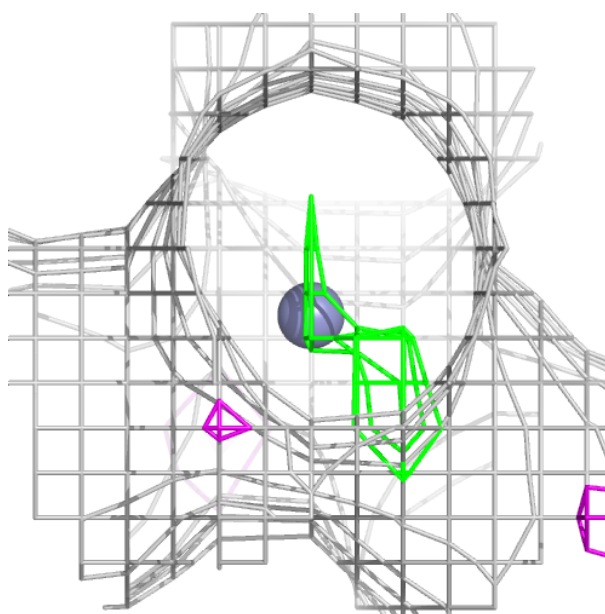
Electron density around ZN C 1102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



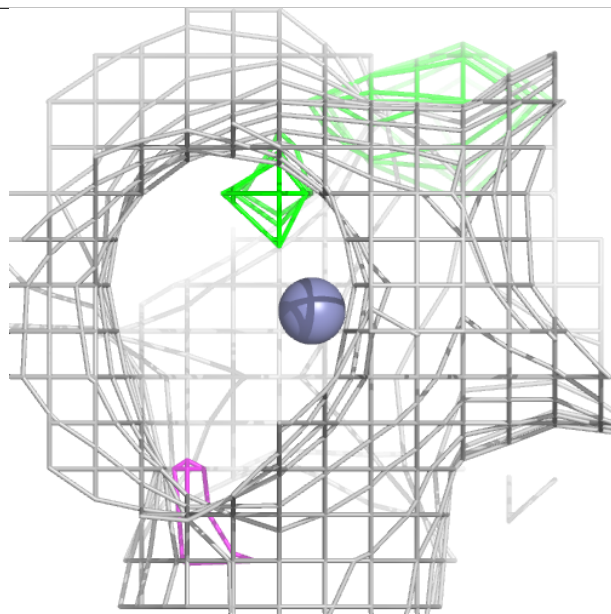
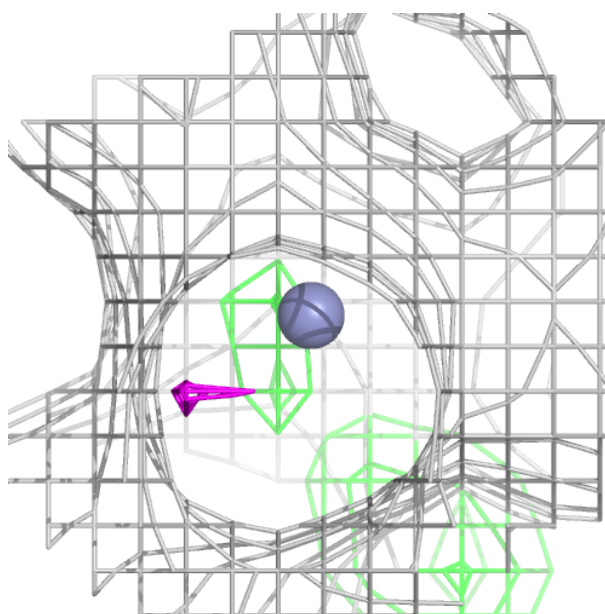
Electron density around ZN C 1103:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



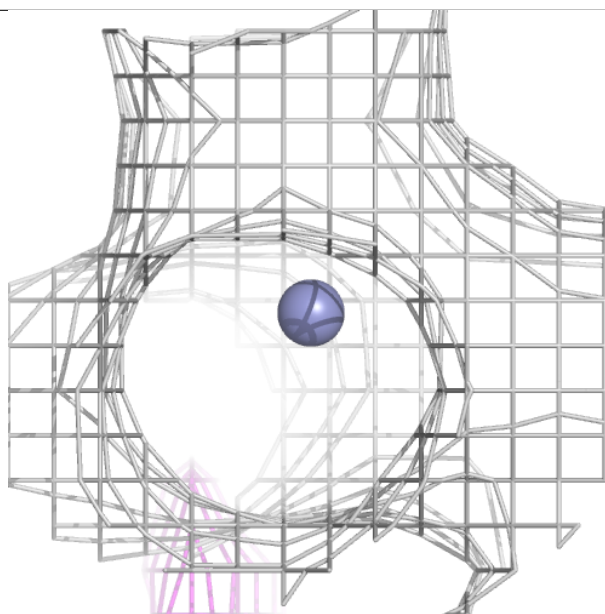
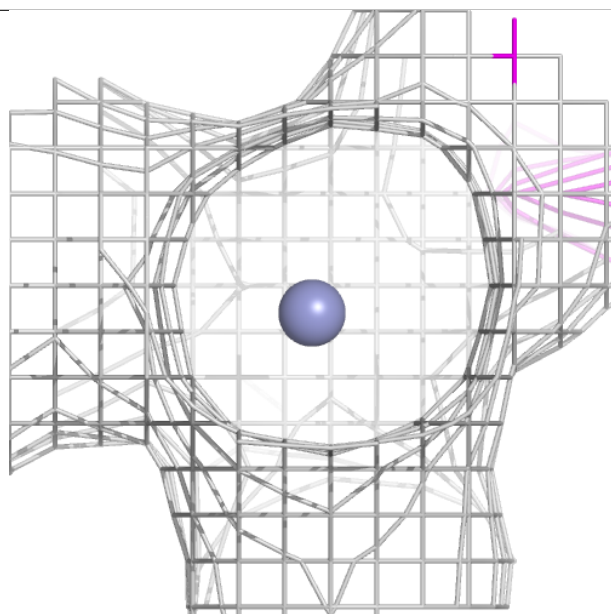
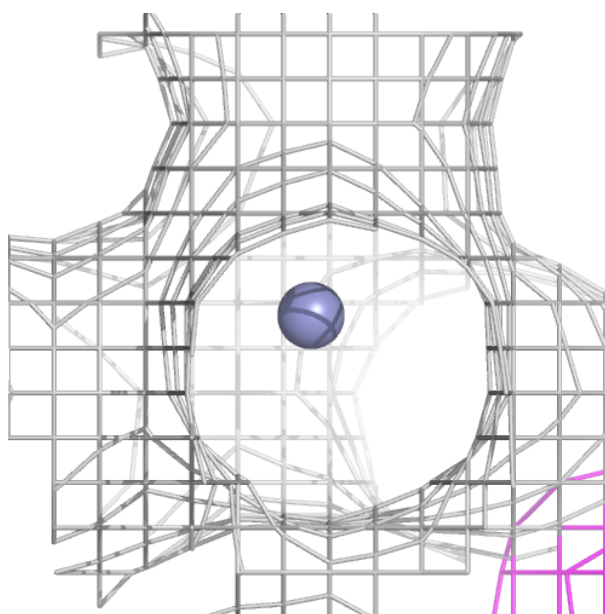
Electron density around ZN A 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



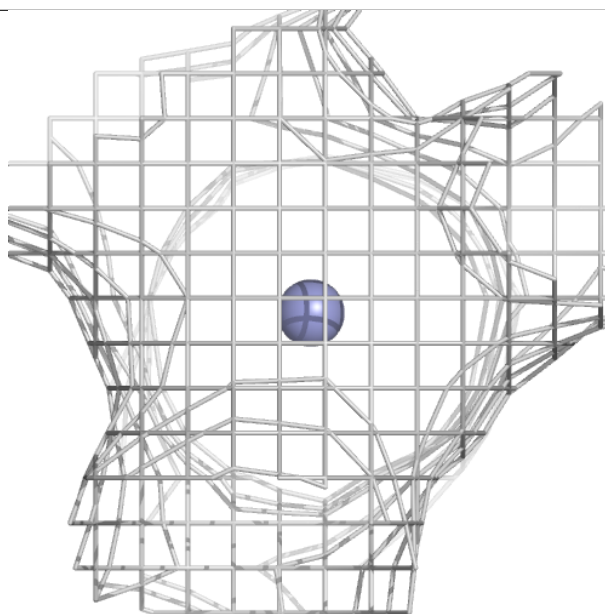
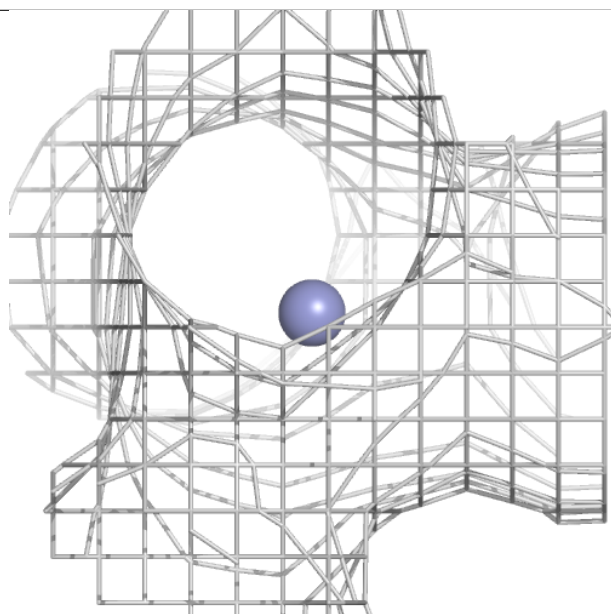
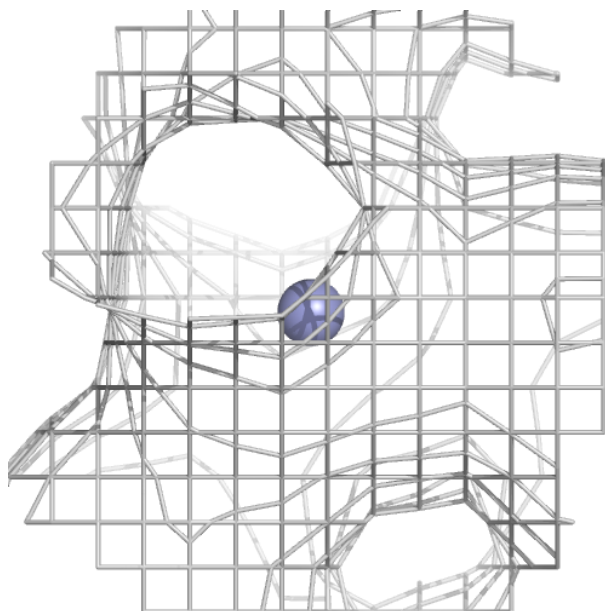
Electron density around ZN A 1102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



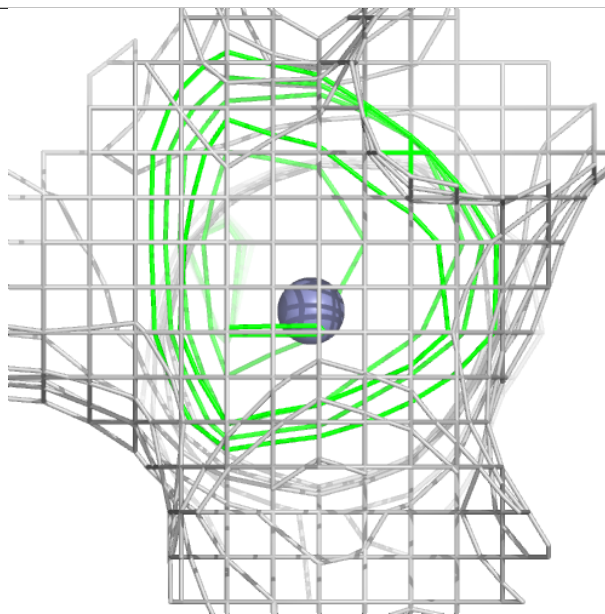
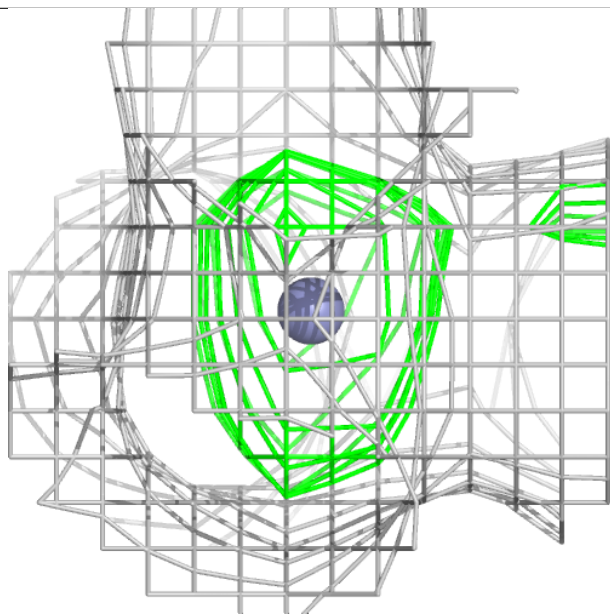
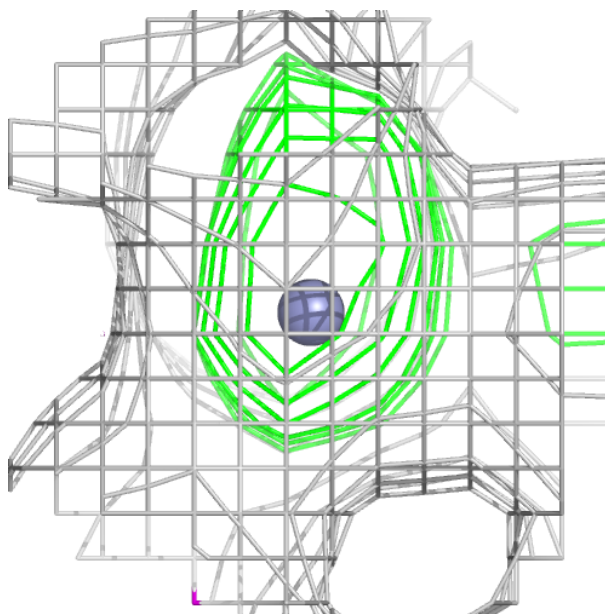
Electron density around ZN D 1102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



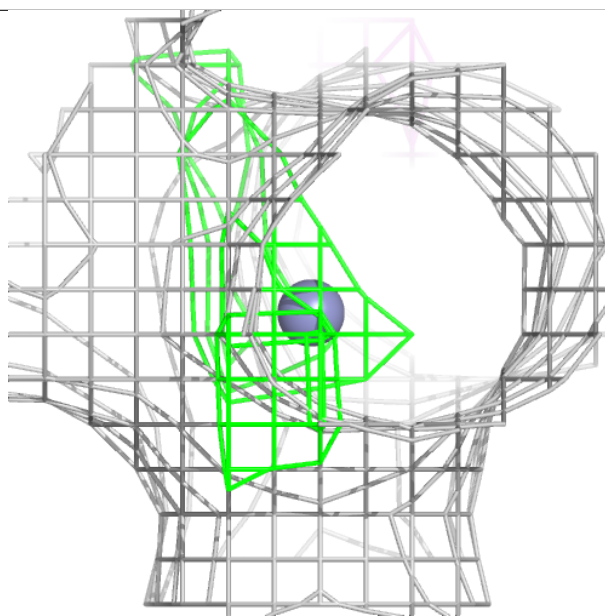
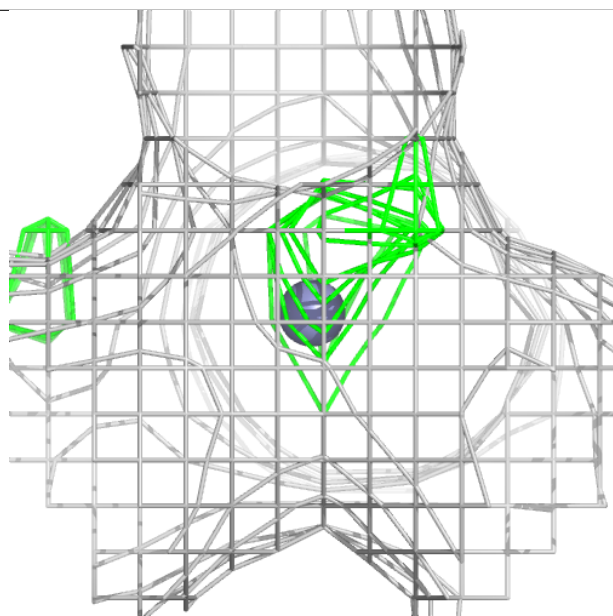
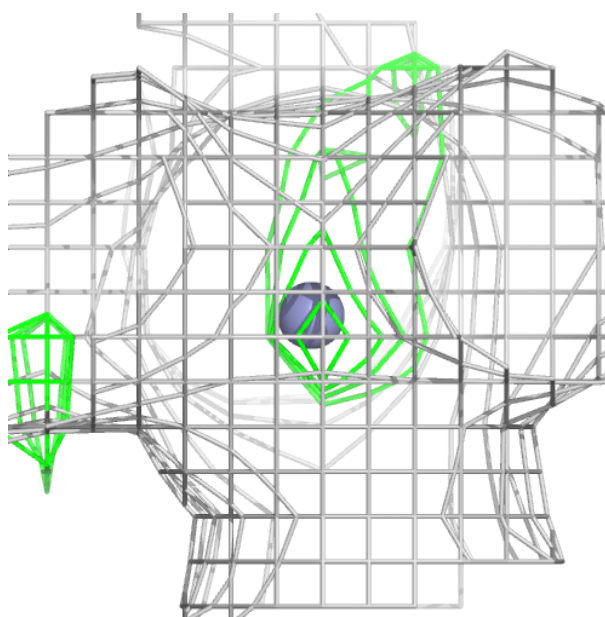
Electron density around ZN B 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN B 1102:

$2mF_o-DF_c$ (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.