



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 15, 2026 – 10:08 am BST

PDB ID : 29ZH / pdb_000029zh
Title : Crystal structure of human NIF3L1 - half open hexamer
Authors : Wator-Wilk, E.; Wilk, P.; Zak, K.M.; Grudnik, P.
Deposited on : 2026-04-15
Resolution : 3.50 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
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

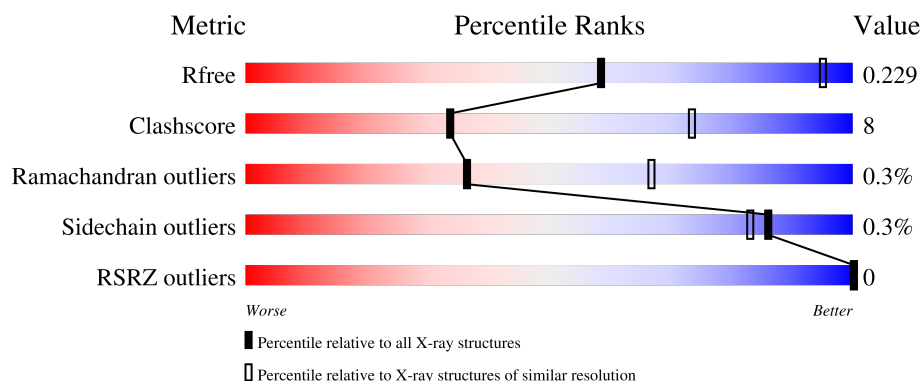
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	366	
1	B	366	
1	C	366	
1	D	366	
1	E	366	

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Mol	Chain	Length	Quality of chain
1	F	366	53% 13% 33%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13977 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 NIF3-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2725	1709	480	523	13			
1	B	248	Total	C	N	O	S	0	1	0
			1930	1215	341	364	10			
1	C	349	Total	C	N	O	S	0	0	0
			2725	1709	480	523	13			
1	D	251	Total	C	N	O	S	0	1	0
			1949	1224	344	370	11			
1	E	349	Total	C	N	O	S	0	0	0
			2725	1709	480	523	13			
1	F	244	Total	C	N	O	S	0	3	0
			1914	1209	336	358	11			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MET	-	initiating methionine	UNP Q9GZT8
A	13	GLY	-	expression tag	UNP Q9GZT8
A	14	HIS	-	expression tag	UNP Q9GZT8
A	15	HIS	-	expression tag	UNP Q9GZT8
A	16	HIS	-	expression tag	UNP Q9GZT8
A	17	HIS	-	expression tag	UNP Q9GZT8
A	18	HIS	-	expression tag	UNP Q9GZT8
A	19	HIS	-	expression tag	UNP Q9GZT8
A	20	GLY	-	expression tag	UNP Q9GZT8
A	21	SER	-	expression tag	UNP Q9GZT8
A	22	GLU	-	expression tag	UNP Q9GZT8
A	23	ASN	-	expression tag	UNP Q9GZT8
A	24	LEU	-	expression tag	UNP Q9GZT8
A	25	TYR	-	expression tag	UNP Q9GZT8
A	26	PHE	-	expression tag	UNP Q9GZT8
A	27	GLN	-	expression tag	UNP Q9GZT8
A	28	GLY	-	expression tag	UNP Q9GZT8

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Chain	Residue	Modelled	Actual	Comment	Reference
A	29	SER	-	expression tag	UNP Q9GZT8
B	12	MET	-	initiating methionine	UNP Q9GZT8
B	13	GLY	-	expression tag	UNP Q9GZT8
B	14	HIS	-	expression tag	UNP Q9GZT8
B	15	HIS	-	expression tag	UNP Q9GZT8
B	16	HIS	-	expression tag	UNP Q9GZT8
B	17	HIS	-	expression tag	UNP Q9GZT8
B	18	HIS	-	expression tag	UNP Q9GZT8
B	19	HIS	-	expression tag	UNP Q9GZT8
B	20	GLY	-	expression tag	UNP Q9GZT8
B	21	SER	-	expression tag	UNP Q9GZT8
B	22	GLU	-	expression tag	UNP Q9GZT8
B	23	ASN	-	expression tag	UNP Q9GZT8
B	24	LEU	-	expression tag	UNP Q9GZT8
B	25	TYR	-	expression tag	UNP Q9GZT8
B	26	PHE	-	expression tag	UNP Q9GZT8
B	27	GLN	-	expression tag	UNP Q9GZT8
B	28	GLY	-	expression tag	UNP Q9GZT8
B	29	SER	-	expression tag	UNP Q9GZT8
C	12	MET	-	initiating methionine	UNP Q9GZT8
C	13	GLY	-	expression tag	UNP Q9GZT8
C	14	HIS	-	expression tag	UNP Q9GZT8
C	15	HIS	-	expression tag	UNP Q9GZT8
C	16	HIS	-	expression tag	UNP Q9GZT8
C	17	HIS	-	expression tag	UNP Q9GZT8
C	18	HIS	-	expression tag	UNP Q9GZT8
C	19	HIS	-	expression tag	UNP Q9GZT8
C	20	GLY	-	expression tag	UNP Q9GZT8
C	21	SER	-	expression tag	UNP Q9GZT8
C	22	GLU	-	expression tag	UNP Q9GZT8
C	23	ASN	-	expression tag	UNP Q9GZT8
C	24	LEU	-	expression tag	UNP Q9GZT8
C	25	TYR	-	expression tag	UNP Q9GZT8
C	26	PHE	-	expression tag	UNP Q9GZT8
C	27	GLN	-	expression tag	UNP Q9GZT8
C	28	GLY	-	expression tag	UNP Q9GZT8
C	29	SER	-	expression tag	UNP Q9GZT8
D	12	MET	-	initiating methionine	UNP Q9GZT8
D	13	GLY	-	expression tag	UNP Q9GZT8
D	14	HIS	-	expression tag	UNP Q9GZT8
D	15	HIS	-	expression tag	UNP Q9GZT8
D	16	HIS	-	expression tag	UNP Q9GZT8

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Chain	Residue	Modelled	Actual	Comment	Reference
D	17	HIS	-	expression tag	UNP Q9GZT8
D	18	HIS	-	expression tag	UNP Q9GZT8
D	19	HIS	-	expression tag	UNP Q9GZT8
D	20	GLY	-	expression tag	UNP Q9GZT8
D	21	SER	-	expression tag	UNP Q9GZT8
D	22	GLU	-	expression tag	UNP Q9GZT8
D	23	ASN	-	expression tag	UNP Q9GZT8
D	24	LEU	-	expression tag	UNP Q9GZT8
D	25	TYR	-	expression tag	UNP Q9GZT8
D	26	PHE	-	expression tag	UNP Q9GZT8
D	27	GLN	-	expression tag	UNP Q9GZT8
D	28	GLY	-	expression tag	UNP Q9GZT8
D	29	SER	-	expression tag	UNP Q9GZT8
E	12	MET	-	initiating methionine	UNP Q9GZT8
E	13	GLY	-	expression tag	UNP Q9GZT8
E	14	HIS	-	expression tag	UNP Q9GZT8
E	15	HIS	-	expression tag	UNP Q9GZT8
E	16	HIS	-	expression tag	UNP Q9GZT8
E	17	HIS	-	expression tag	UNP Q9GZT8
E	18	HIS	-	expression tag	UNP Q9GZT8
E	19	HIS	-	expression tag	UNP Q9GZT8
E	20	GLY	-	expression tag	UNP Q9GZT8
E	21	SER	-	expression tag	UNP Q9GZT8
E	22	GLU	-	expression tag	UNP Q9GZT8
E	23	ASN	-	expression tag	UNP Q9GZT8
E	24	LEU	-	expression tag	UNP Q9GZT8
E	25	TYR	-	expression tag	UNP Q9GZT8
E	26	PHE	-	expression tag	UNP Q9GZT8
E	27	GLN	-	expression tag	UNP Q9GZT8
E	28	GLY	-	expression tag	UNP Q9GZT8
E	29	SER	-	expression tag	UNP Q9GZT8
F	12	MET	-	initiating methionine	UNP Q9GZT8
F	13	GLY	-	expression tag	UNP Q9GZT8
F	14	HIS	-	expression tag	UNP Q9GZT8
F	15	HIS	-	expression tag	UNP Q9GZT8
F	16	HIS	-	expression tag	UNP Q9GZT8
F	17	HIS	-	expression tag	UNP Q9GZT8
F	18	HIS	-	expression tag	UNP Q9GZT8
F	19	HIS	-	expression tag	UNP Q9GZT8
F	20	GLY	-	expression tag	UNP Q9GZT8
F	21	SER	-	expression tag	UNP Q9GZT8
F	22	GLU	-	expression tag	UNP Q9GZT8

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Chain	Residue	Modelled	Actual	Comment	Reference
F	23	ASN	-	expression tag	UNP Q9GZT8
F	24	LEU	-	expression tag	UNP Q9GZT8
F	25	TYR	-	expression tag	UNP Q9GZT8
F	26	PHE	-	expression tag	UNP Q9GZT8
F	27	GLN	-	expression tag	UNP Q9GZT8
F	28	GLY	-	expression tag	UNP Q9GZT8
F	29	SER	-	expression tag	UNP Q9GZT8

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0

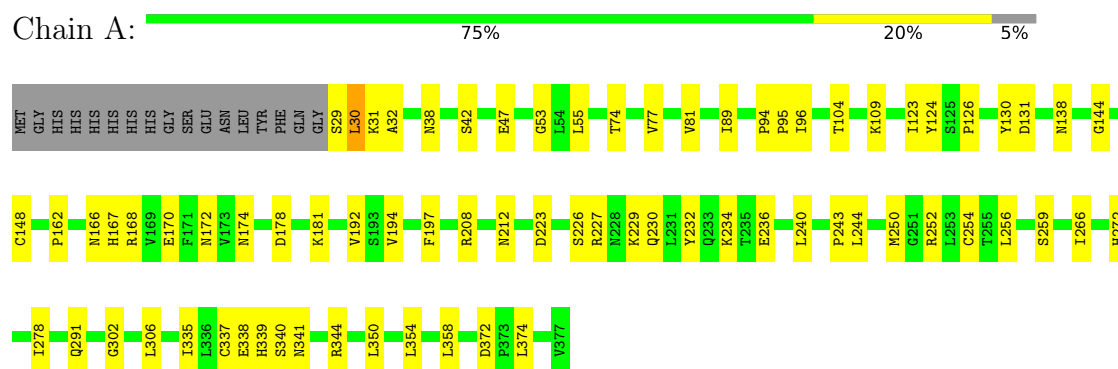
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O 1 1	0	0
3	B	1	Total O 1 1	0	0
3	D	1	Total O 1 1	0	0

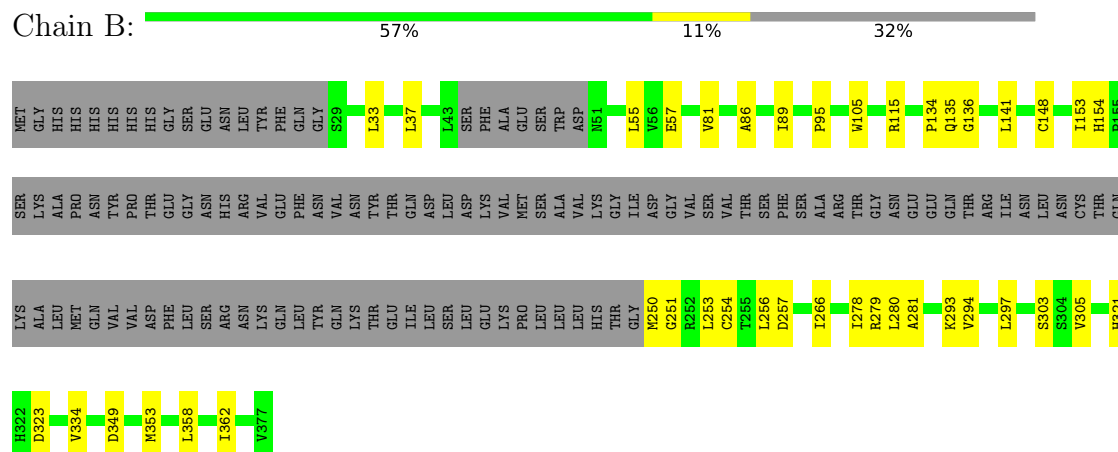
3 Residue-property plots

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.

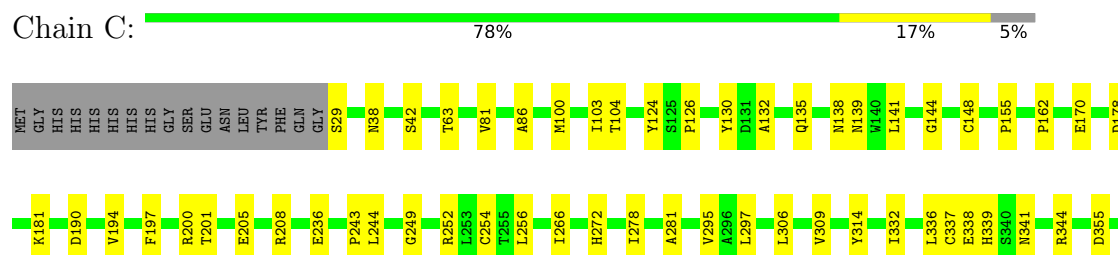
• Molecule 1: NIF3-like protein 1

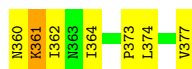


• Molecule 1: NIF3-like protein 1



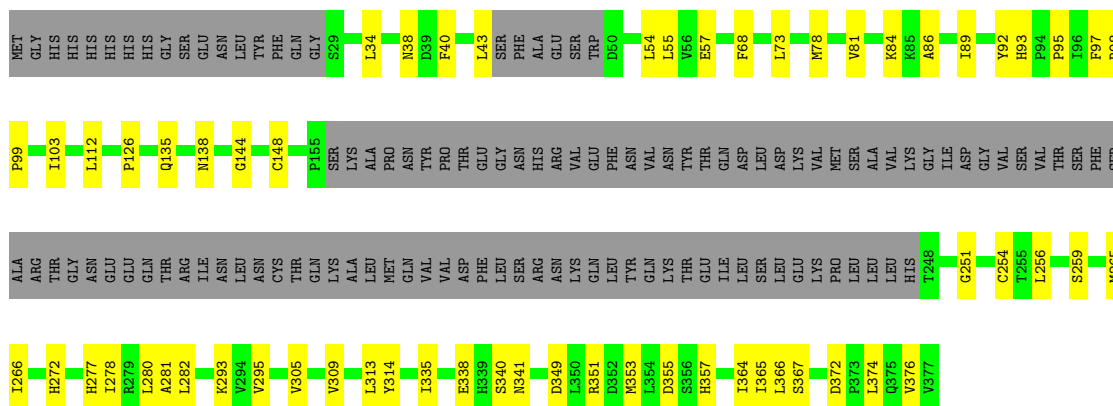
• Molecule 1: NIF3-like protein 1





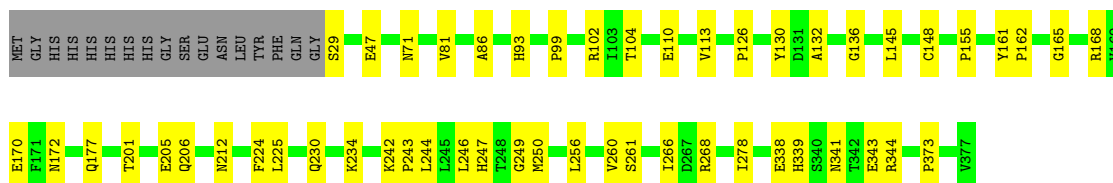
• Molecule 1: NIF3-like protein 1

Chain D: 52% 17% 31%



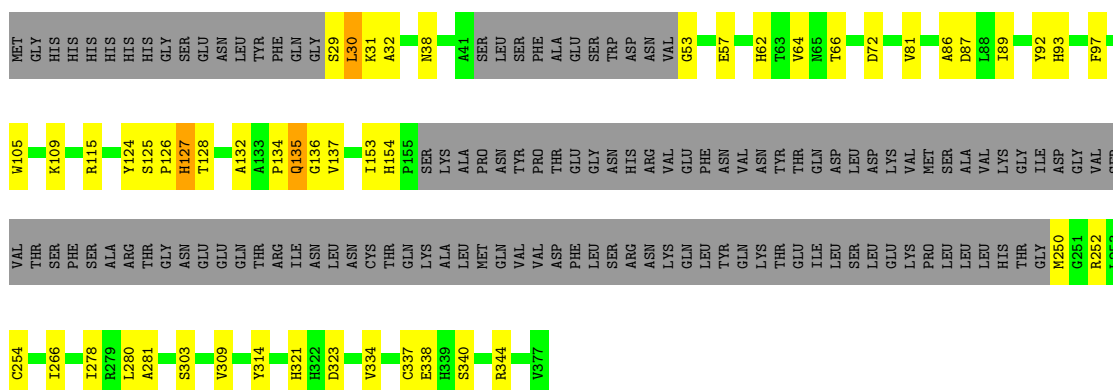
• Molecule 1: NIF3-like protein 1

Chain E: 81% 14% 5%



• Molecule 1: NIF3-like protein 1

Chain F: 53% 13% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	171.60Å 171.60Å 167.53Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.90 – 3.50 42.90 – 3.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (42.90-3.50) 99.9 (42.90-3.50)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 3.48Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.181 , 0.226 0.188 , 0.229	Depositor DCC
R_{free} test set	1796 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	134.0	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 97.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13977	wwPDB-VP
Average B, all atoms (Å ²)	139.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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

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	0.18	0/2773	0.56	1/3763 (0.0%)
1	B	0.11	0/1965	0.31	0/2666
1	C	0.16	0/2773	0.53	1/3763 (0.0%)
1	D	0.15	0/1984	0.39	1/2691 (0.0%)
1	E	0.17	0/2773	0.55	0/3763
1	F	0.13	0/1956	0.35	0/2652
All	All	0.15	0/14224	0.48	3/19298 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	E	0	1
All	All	0	3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	337	CYS	N-CA-C	-6.31	98.45	108.30
1	A	337	CYS	N-CA-C	-5.80	99.25	108.30
1	D	126	PRO	CA-N-CD	-5.52	104.28	112.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	344	ARG	Sidechain
1	C	344	ARG	Sidechain
1	E	344	ARG	Sidechain

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	2725	0	2743	55	0
1	B	1930	0	1962	22	0
1	C	2725	0	2743	44	0
1	D	1949	0	1974	44	0
1	E	2725	0	2741	38	0
1	F	1914	0	1949	33	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
All	All	13977	0	14112	215	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 8.

The worst 5 of 215 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:F:29:SER:O	1:F:31:LYS:N	1.97	0.97
1:C:29:SER:OG	1:C:63:THR:HA	1.81	0.80
1:D:277:HIS:HB2	1:D:376:VAL:HG21	1.65	0.78
1:F:29:SER:O	1:F:30:LEU:C	2.27	0.78
1:A:229:LYS:H	1:A:229:LYS:HD2	1.49	0.76

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	347/366 (95%)	339 (98%)	7 (2%)	1 (0%)	36	67
1	B	243/366 (66%)	230 (95%)	12 (5%)	1 (0%)	30	62
1	C	347/366 (95%)	338 (97%)	8 (2%)	1 (0%)	36	67
1	D	246/366 (67%)	232 (94%)	14 (6%)	0	100	100
1	E	347/366 (95%)	341 (98%)	6 (2%)	0	100	100
1	F	241/366 (66%)	228 (95%)	10 (4%)	3 (1%)	10	41
All	All	1771/2196 (81%)	1708 (96%)	57 (3%)	6 (0%)	36	67

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	30	LEU
1	F	127	HIS
1	A	30	LEU
1	F	135	GLN
1	B	135	GLN

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	309/323 (96%)	309 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	219/323 (68%)	218 (100%)	1 (0%)	81	80
1	C	309/323 (96%)	309 (100%)	0	100	100
1	D	221/323 (68%)	220 (100%)	1 (0%)	81	80
1	E	309/323 (96%)	308 (100%)	1 (0%)	86	83
1	F	217/323 (67%)	216 (100%)	1 (0%)	81	80
All	All	1584/1938 (82%)	1580 (100%)	4 (0%)	86	83

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	254	CYS
1	D	254	CYS
1	E	29	SER
1	F	254	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	38	ASN
1	D	291	GLN
1	D	154	HIS
1	D	341	ASN
1	B	291	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

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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

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 [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	349/366 (95%)	-0.60	0 100 100	100, 138, 170, 229	0
1	B	248/366 (67%)	-0.59	0 100 100	92, 140, 206, 276	1 (0%)
1	C	349/366 (95%)	-0.64	0 100 100	108, 139, 189, 241	0
1	D	251/366 (68%)	-0.54	0 100 100	84, 127, 193, 251	1 (0%)
1	E	349/366 (95%)	-0.65	0 100 100	93, 131, 173, 212	0
1	F	244/366 (66%)	-0.64	0 100 100	81, 127, 188, 285	3 (1%)
All	All	1790/2196 (81%)	-0.61	0 100 100	81, 135, 183, 285	5 (0%)

There are no RSRZ outliers to report.

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	ZN	C	400	1/1	0.91	0.07	165,165,165,165	0

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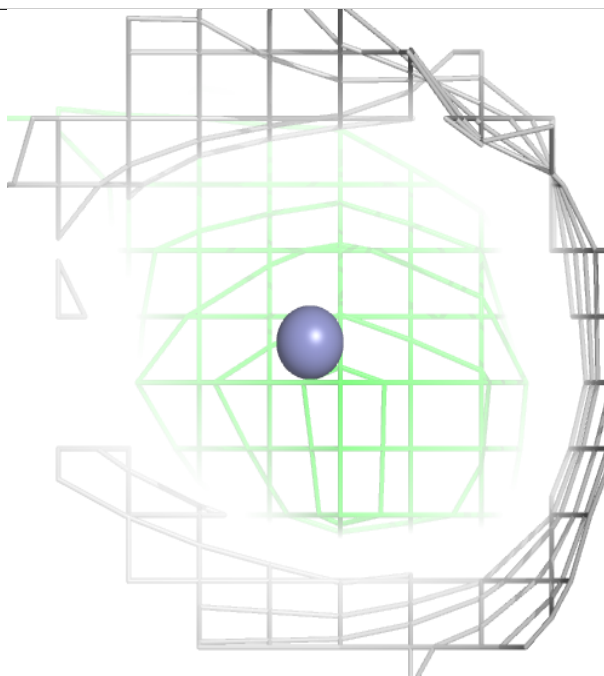
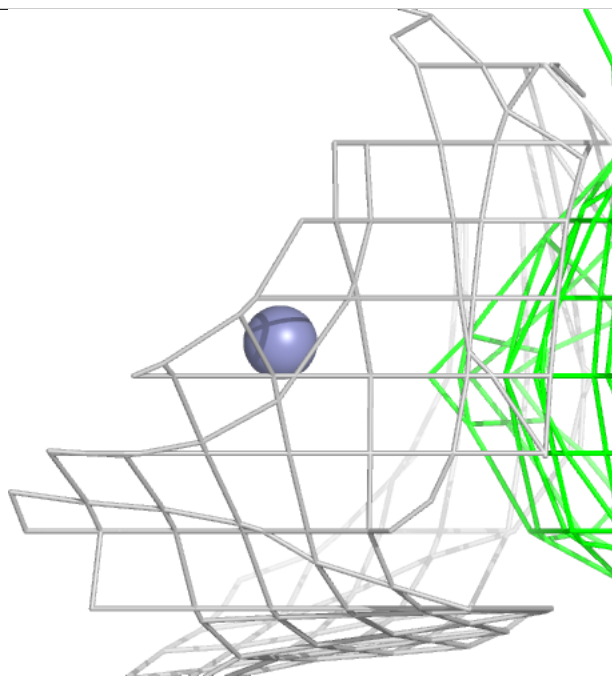
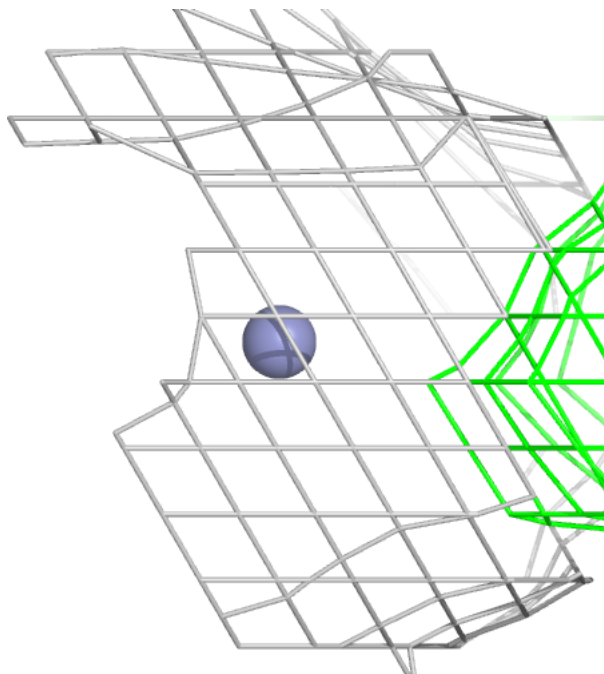
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	E	400	1/1	0.95	0.12	183,183,183,183	0
2	ZN	F	400	1/1	0.96	0.04	120,120,120,120	0
2	ZN	A	400	1/1	0.97	0.04	132,132,132,132	0
2	ZN	B	400	1/1	0.98	0.08	159,159,159,159	0
2	ZN	D	400	1/1	0.99	0.05	115,115,115,115	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.

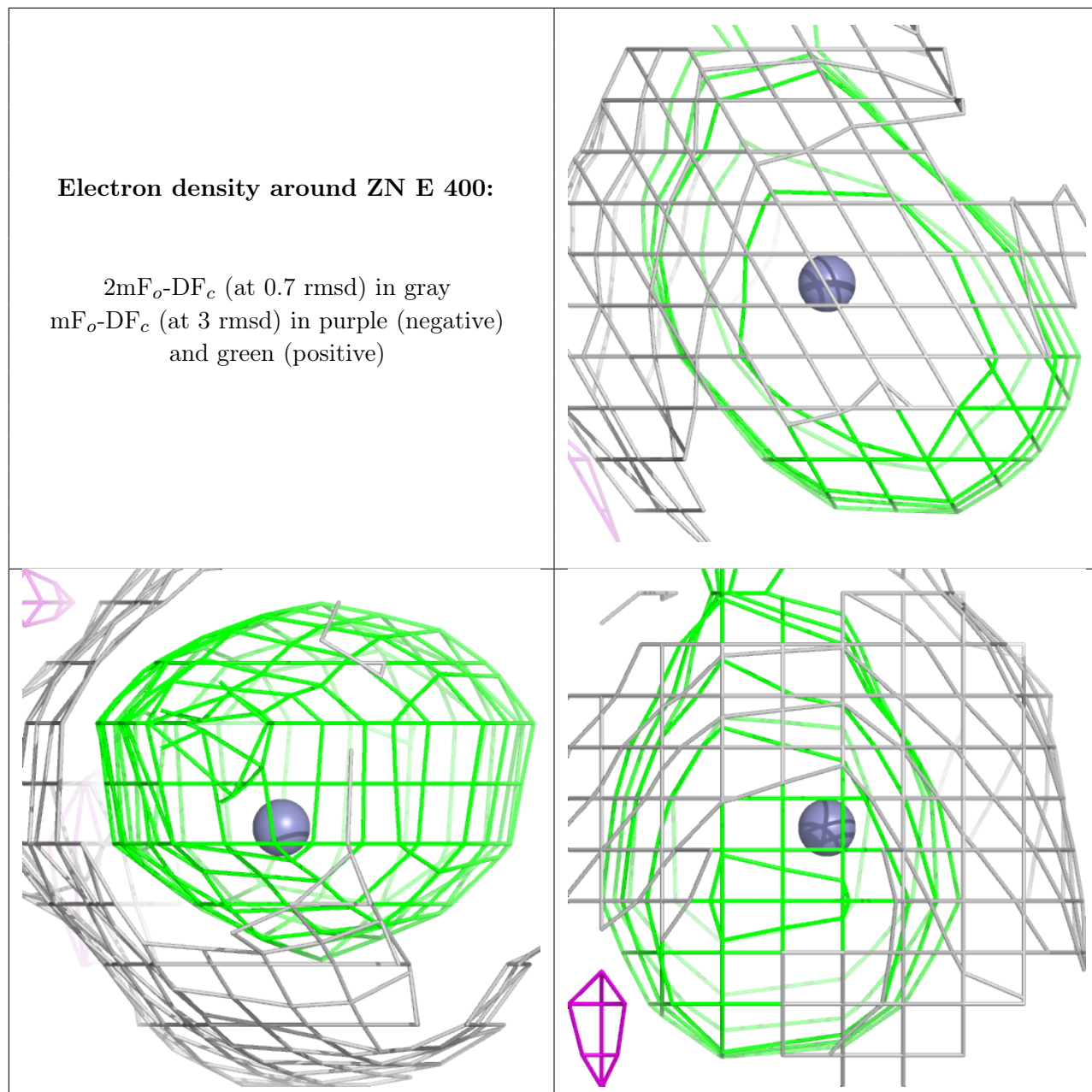
Electron density around ZN C 400:

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



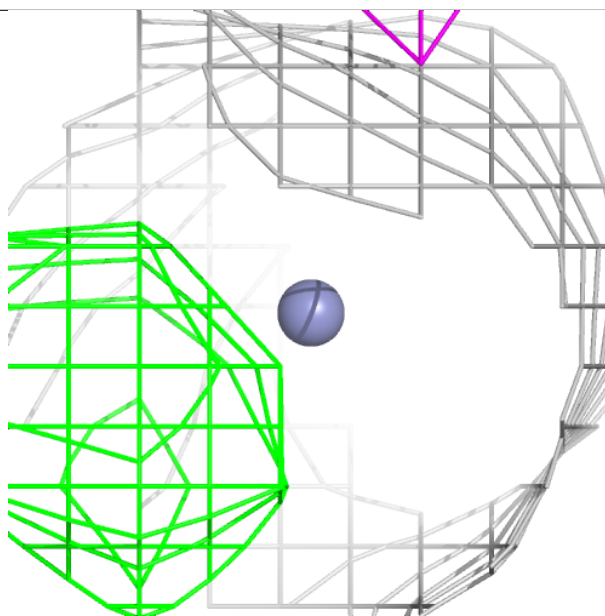
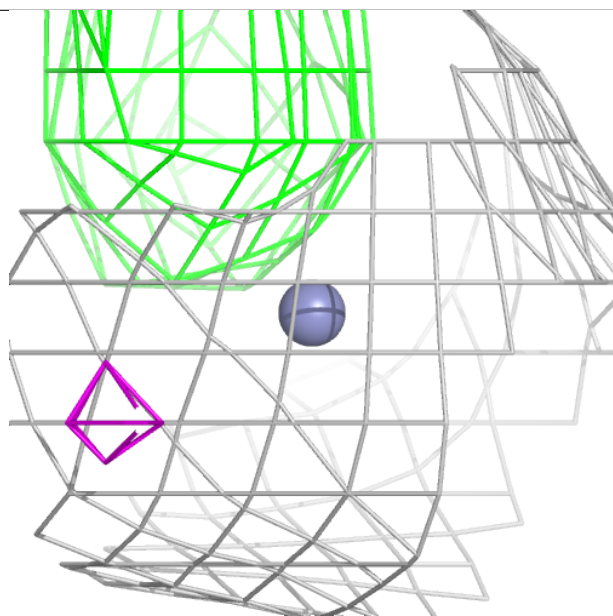
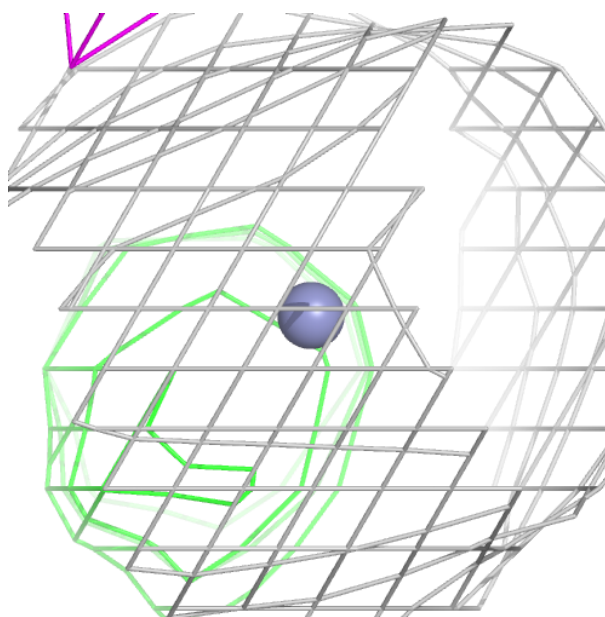
Electron density around ZN E 400:

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



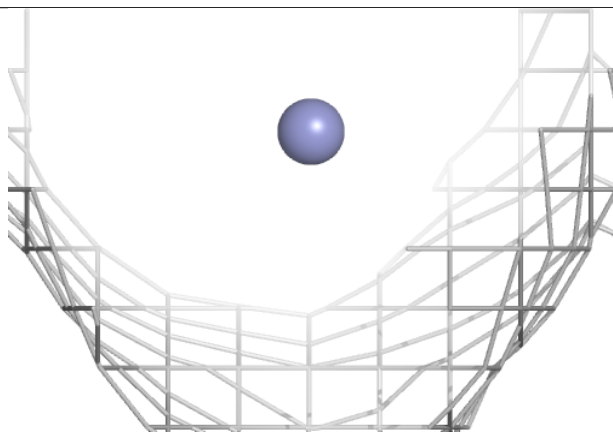
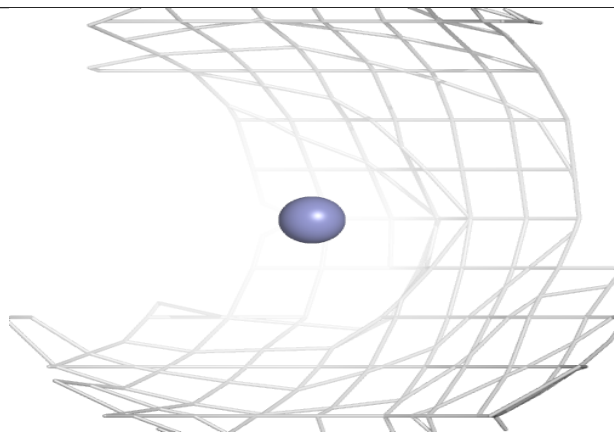
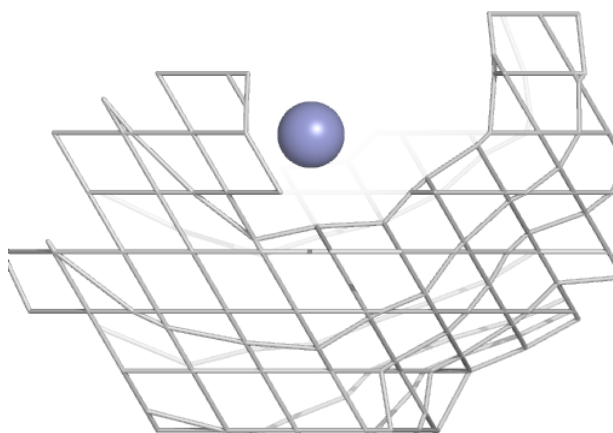
Electron density around ZN F 400:

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



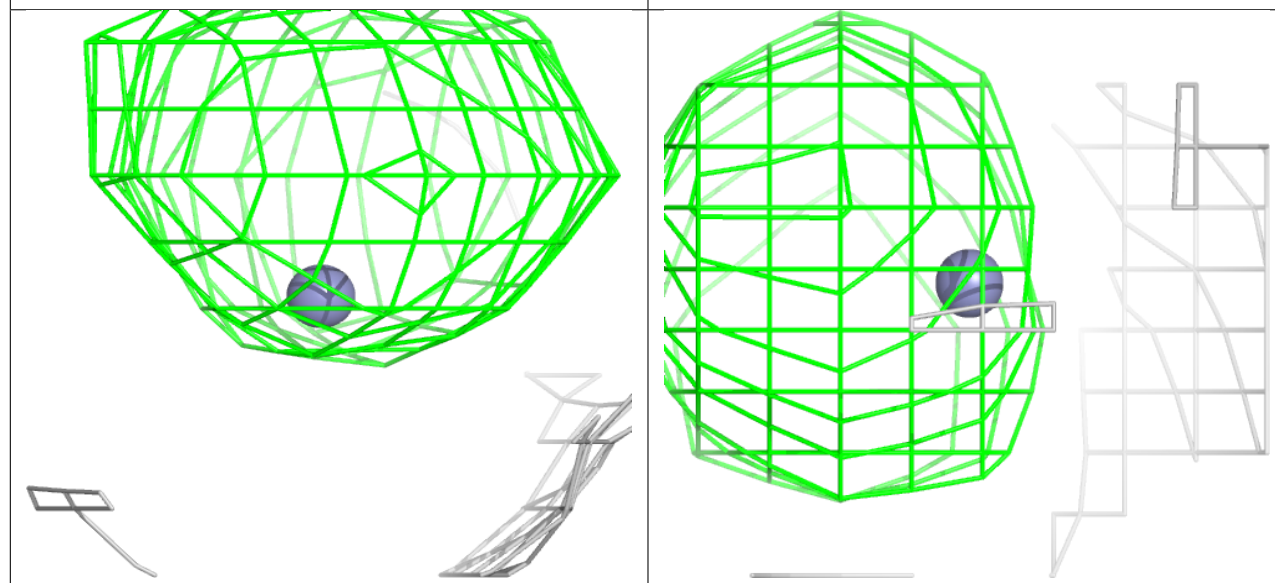
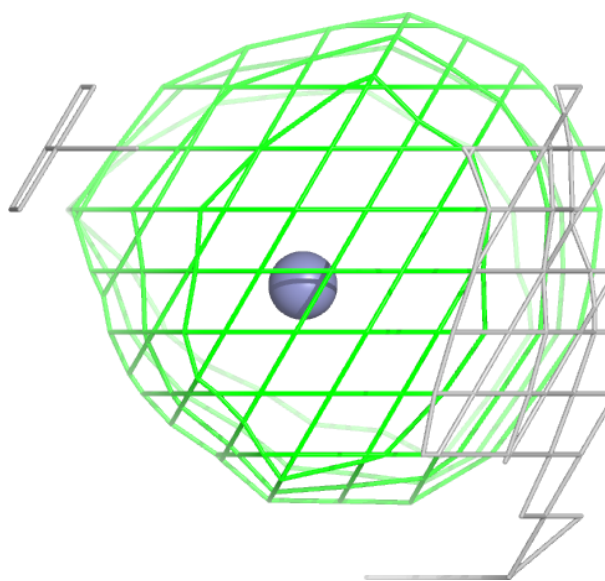
Electron density around ZN A 400:

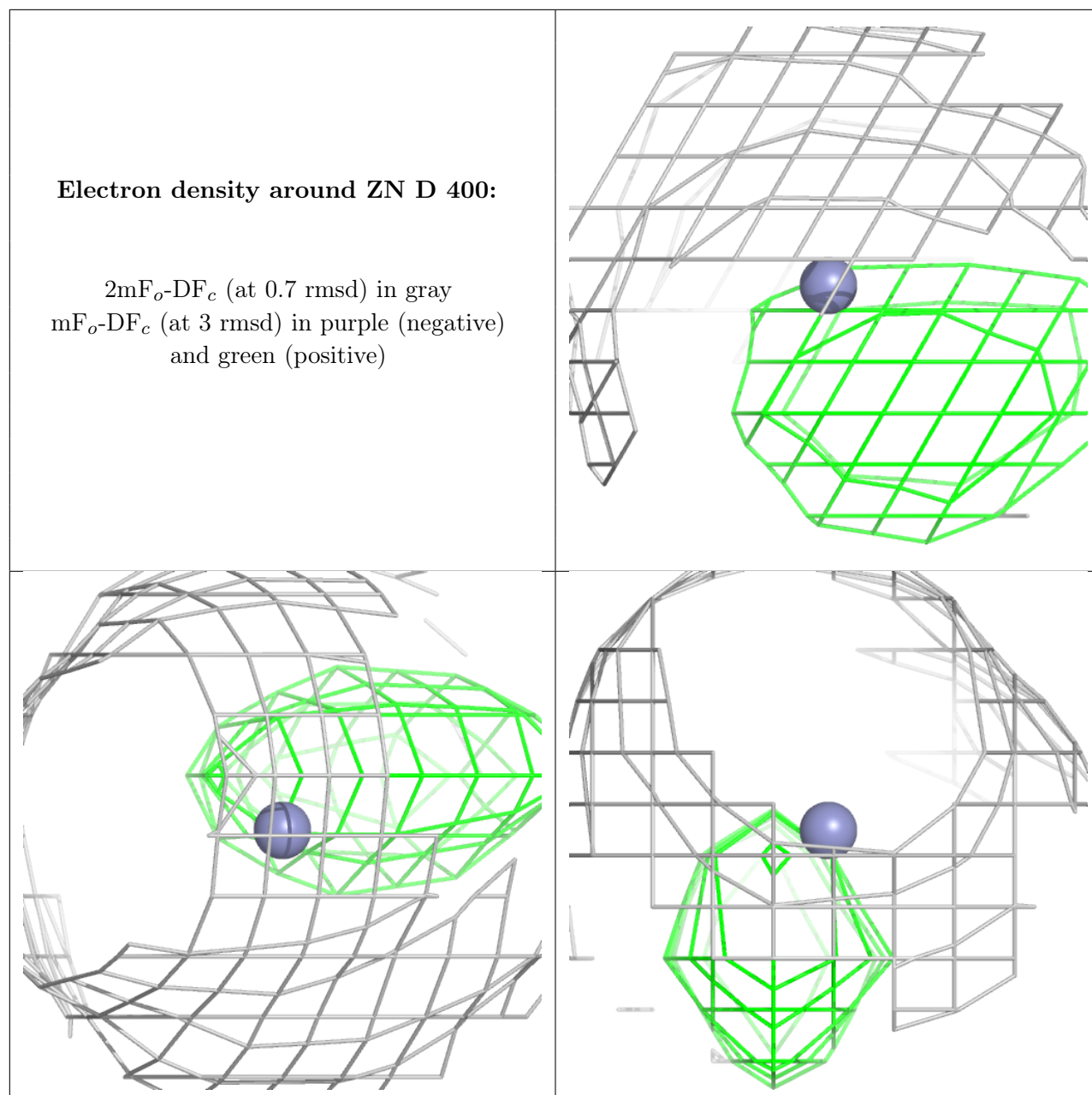
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN B 400:

$2mF_o-DF_c$ (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.