



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:26 PM UTC

PDB ID : 7XYZ / pdb_00007xyz
Title : TRIM E3 ubiquitin ligase
Authors : Park, S.H.; Song, H.K.
Deposited on : 2022-06-02
Resolution : 4.62 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	:	9.0.010 (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

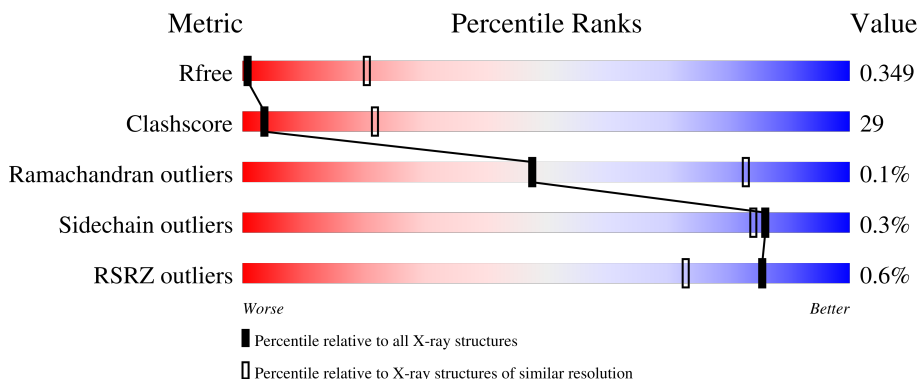
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.62 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	1009 (5.32-3.92)
Clashscore	190562	1025 (5.30-3.94)
Ramachandran outliers	187476	1070 (5.32-3.90)
Sidechain outliers	187428	1052 (5.32-3.90)
RSRZ outliers	180081	1004 (5.32-3.92)

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	466	48% 49% .
1	B	466	% 48% 50% .
1	C	466	52% 45% .
1	D	466	47% 51% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 14236 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 Tripartite motif-containing protein 72.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	0	0	0
			3545	2229	638	656	22			
1	B	456	Total	C	N	O	S	0	0	0
			3569	2244	644	659	22			
1	C	452	Total	C	N	O	S	0	0	0
			3537	2225	637	653	22			
1	D	456	Total	C	N	O	S	0	0	0
			3569	2244	644	659	22			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	GLY	-	expression tag	UNP Q1XH17
A	6	SER	-	expression tag	UNP Q1XH17
A	55	SER	CYS	engineered mutation	UNP Q1XH17
A	144	SER	CYS	engineered mutation	UNP Q1XH17
A	242	SER	CYS	engineered mutation	UNP Q1XH17
A	279	HIS	LYS	engineered mutation	UNP Q1XH17
A	283	HIS	ALA	engineered mutation	UNP Q1XH17
B	5	GLY	-	expression tag	UNP Q1XH17
B	6	SER	-	expression tag	UNP Q1XH17
B	55	SER	CYS	engineered mutation	UNP Q1XH17
B	144	SER	CYS	engineered mutation	UNP Q1XH17
B	242	SER	CYS	engineered mutation	UNP Q1XH17
B	279	HIS	LYS	engineered mutation	UNP Q1XH17
B	283	HIS	ALA	engineered mutation	UNP Q1XH17
C	5	GLY	-	expression tag	UNP Q1XH17
C	6	SER	-	expression tag	UNP Q1XH17
C	55	SER	CYS	engineered mutation	UNP Q1XH17
C	144	SER	CYS	engineered mutation	UNP Q1XH17
C	242	SER	CYS	engineered mutation	UNP Q1XH17
C	279	HIS	LYS	engineered mutation	UNP Q1XH17
C	283	HIS	ALA	engineered mutation	UNP Q1XH17

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	5	GLY	-	expression tag	UNP Q1XH17
D	6	SER	-	expression tag	UNP Q1XH17
D	55	SER	CYS	engineered mutation	UNP Q1XH17
D	144	SER	CYS	engineered mutation	UNP Q1XH17
D	242	SER	CYS	engineered mutation	UNP Q1XH17
D	279	HIS	LYS	engineered mutation	UNP Q1XH17
D	283	HIS	ALA	engineered mutation	UNP Q1XH17

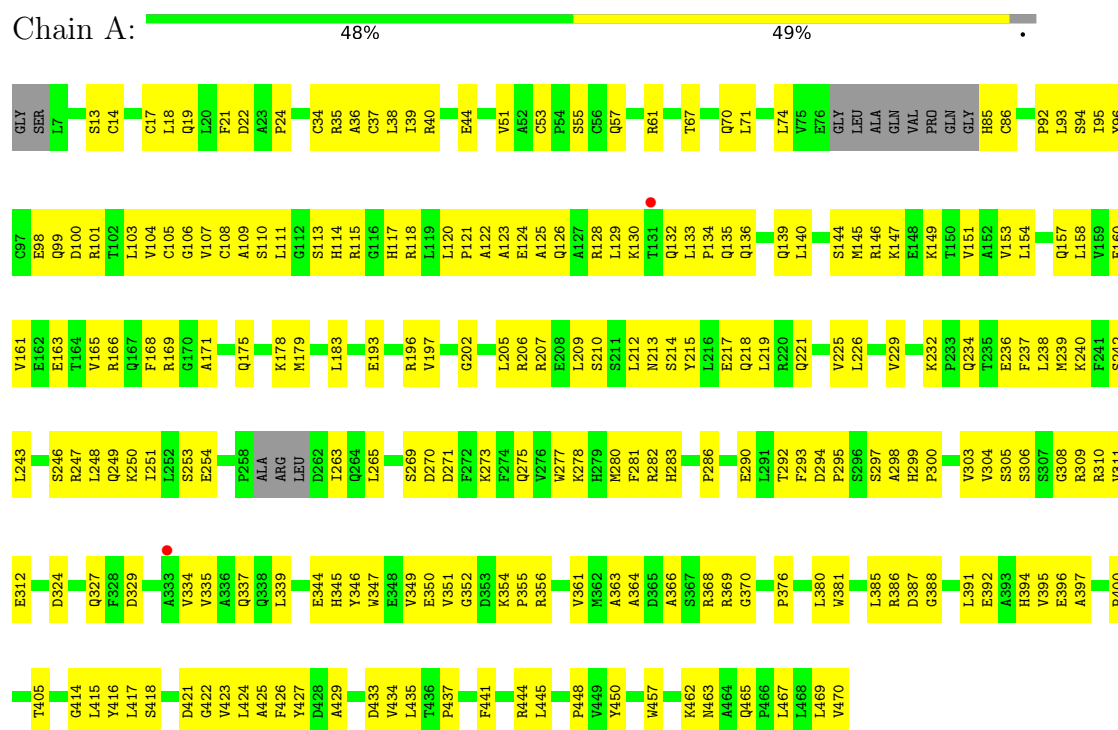
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Zn 4 4	0	0
2	B	4	Total Zn 4 4	0	0
2	C	4	Total Zn 4 4	0	0
2	D	4	Total Zn 4 4	0	0

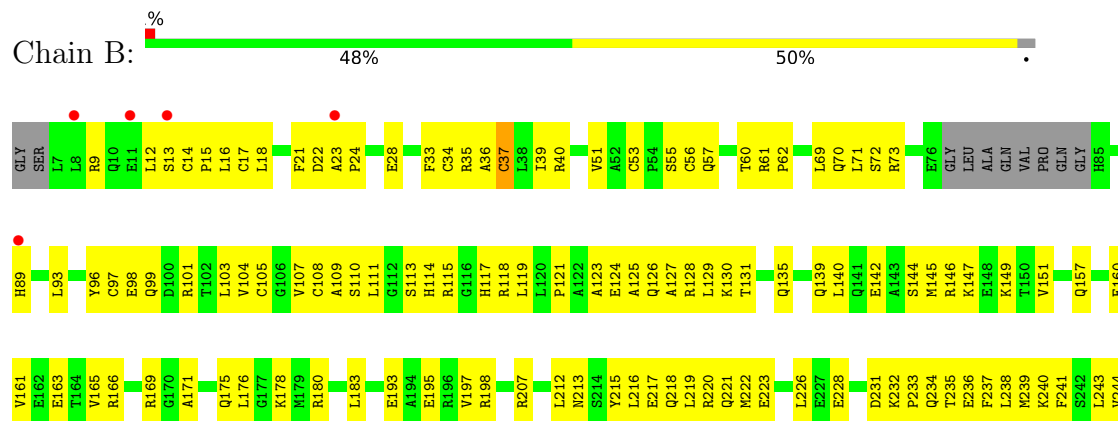
3 Residue-property plots

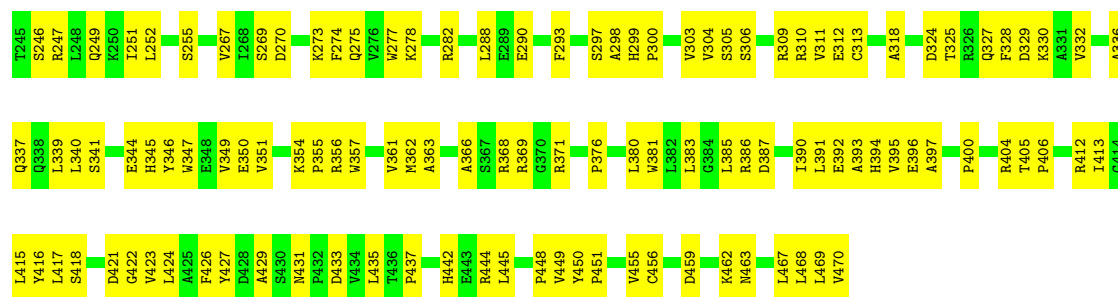
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Tripartite motif-containing protein 72



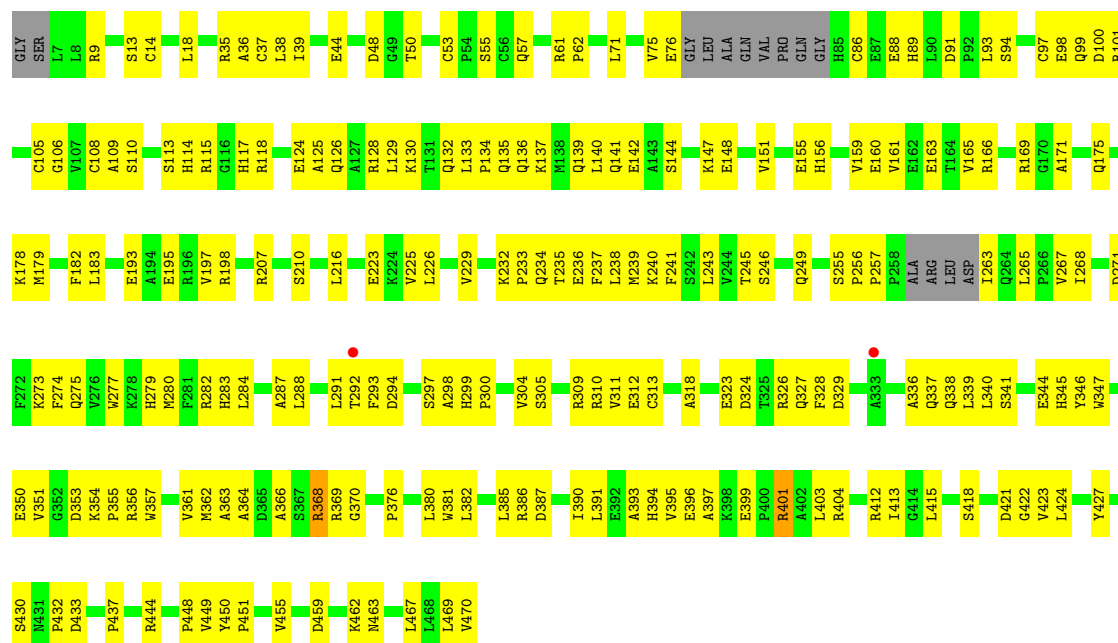
• Molecule 1: Tripartite motif-containing protein 72





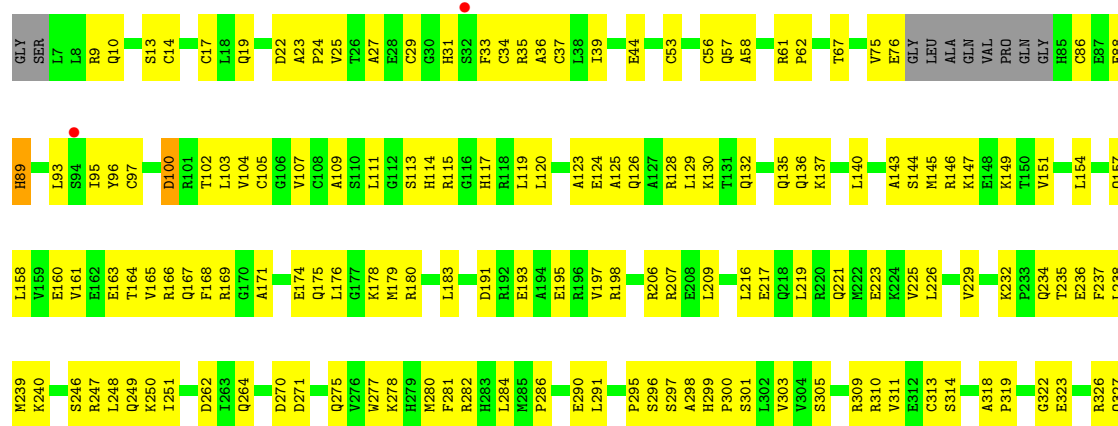
• Molecule 1: Tripartite motif-containing protein 72

Chain C: 52% 45%



• Molecule 1: Tripartite motif-containing protein 72

Chain D: 47% 51%



F328	D329	K330	A331	V332	L333	V334		Q338	L339	L340		E344	H345	Y346	W347	E348	V349	E350	V351	G352	D353	K354	P355	R356	W357		V361	M362	A363		A366	S367	R368	R369	G370	R371	L372	H373	A374	V375	P376		L380	W381	L382		L385		E392	A393	H394	V395	E396	A397		P400		T405	
A411	R412	I413	G414	L415	Y416	L417	S418		D421	G422	V423	L424	A425	F426	Y427	D428	A429	S430	N431	P432	D433	V434	L435	T436	P437	I438	F439	S440	F441	H442	E443	R444		G447	P448	V449	Y450	P451	I452		G456	W457	H458	D459	K460	G461	K462	N463	A464	Q465		L468	L469	V470					

4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	174.38Å 174.38Å 224.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.79 – 4.62 35.79 – 4.62	Depositor EDS
% Data completeness (in resolution range)	88.7 (35.79-4.62) 88.7 (35.79-4.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 4.62Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.312 , 0.348 0.312 , 0.349	Depositor DCC
R_{free} test set	1991 reflections (4.73%)	wwPDB-VP
Wilson B-factor (Å ²)	172.0	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.12 , 309.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.218 for -h,-k,l 0.278 for h,-h-k,-l 0.216 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	14236	wwPDB-VP
Average B, all atoms (Å ²)	332.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.90% 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

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	0.23	0/3619	0.52	0/4901
1	B	0.24	0/3644	0.54	0/4936
1	C	0.24	0/3611	0.54	0/4890
1	D	0.24	0/3644	0.54	0/4936
All	All	0.24	0/14518	0.53	0/19663

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
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	122	ALA	Peptide
1	C	368	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	3545	0	3537	224	1
1	B	3569	0	3567	230	1
1	C	3537	0	3533	213	0
1	D	3569	0	3567	228	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
2	C	4	0	0	0	0
2	D	4	0	0	0	0
All	All	14236	0	14204	835	1

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 29.

The worst 5 of 835 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:C:280:MET:HE1	1:C:284:LEU:CD1	1.61	1.29
1:C:179:MET:CA	1:C:284:LEU:HD11	1.68	1.22
1:D:114:HIS:ND1	1:D:117:HIS:ND1	1.89	1.20
1:C:280:MET:HE1	1:C:284:LEU:HD12	1.12	1.09
1:C:179:MET:HA	1:C:284:LEU:CD1	1.86	1.05

All (1) 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)
1:A:305:SER:OG	1:B:300:PRO:O[3_654]	2.13	0.07

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	447/466 (96%)	383 (86%)	64 (14%)	0	100	100
1	B	452/466 (97%)	388 (86%)	64 (14%)	0	100	100
1	C	446/466 (96%)	381 (85%)	64 (14%)	1 (0%)	43	77
1	D	452/466 (97%)	378 (84%)	74 (16%)	0	100	100
All	All	1797/1864 (96%)	1530 (85%)	266 (15%)	1 (0%)	48	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	256	PRO

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	386/394 (98%)	386 (100%)	0	100	100
1	B	388/394 (98%)	387 (100%)	1 (0%)	86	84
1	C	385/394 (98%)	383 (100%)	2 (0%)	81	81
1	D	388/394 (98%)	386 (100%)	2 (0%)	81	81
All	All	1547/1576 (98%)	1542 (100%)	5 (0%)	86	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	37	CYS
1	C	292	THR
1	C	401	ARG
1	D	89	HIS
1	D	100	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	132	GLN
1	D	31	HIS
1	C	338	GLN
1	D	57	GLN
1	B	89	HIS

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 16 ligands modelled in this entry, 16 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 [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	453/466 (97%)	-0.30	2 (0%) 88 77	142, 332, 513, 619	0
1	B	456/466 (97%)	-0.26	5 (1%) 78 63	95, 343, 537, 656	0
1	C	452/466 (96%)	-0.35	2 (0%) 88 77	67, 318, 508, 585	0
1	D	456/466 (97%)	-0.32	2 (0%) 88 77	73, 319, 506, 616	0
All	All	1817/1864 (97%)	-0.31	11 (0%) 85 73	67, 330, 513, 656	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	94	SER	4.8
1	B	11	GLU	3.3
1	C	333	ALA	2.8
1	A	131	THR	2.7
1	A	333	ALA	2.6

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](#)

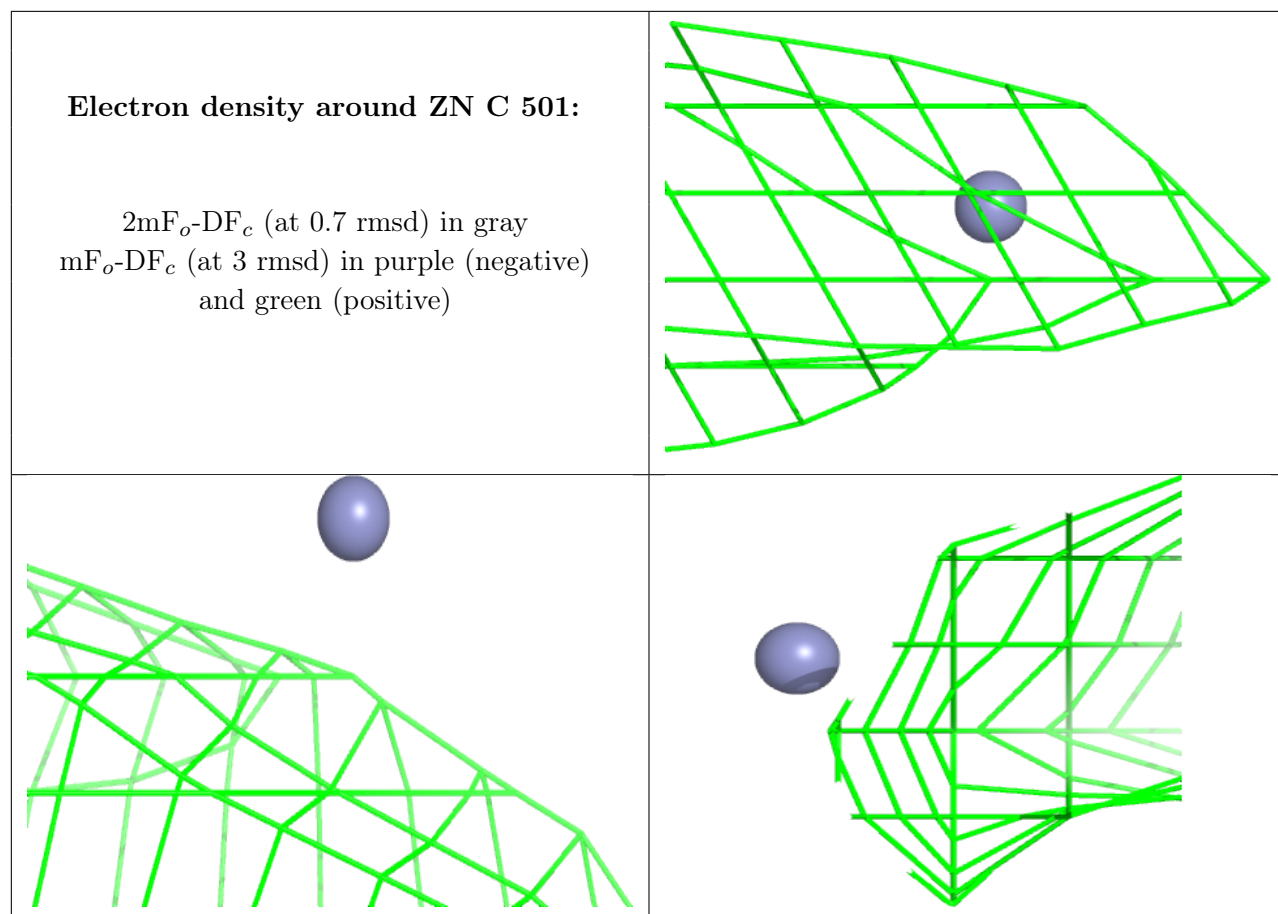
There are no oligosaccharides in this entry.

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.

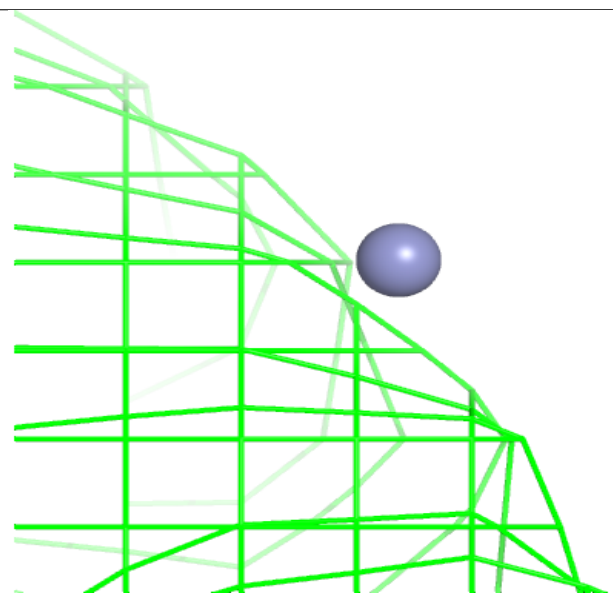
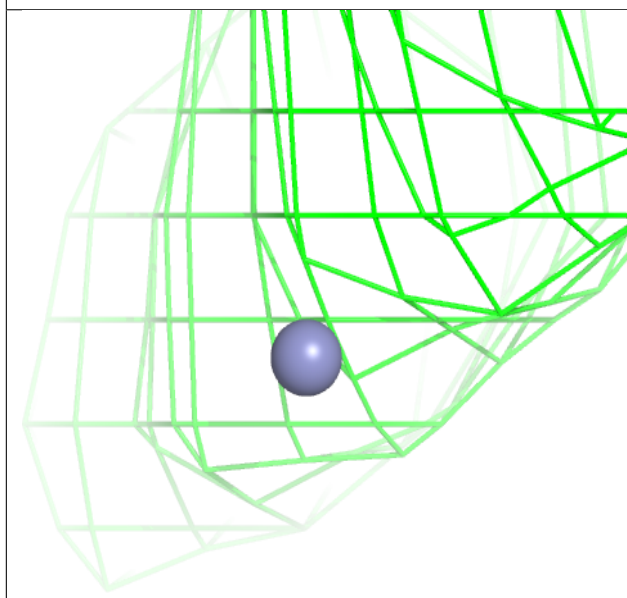
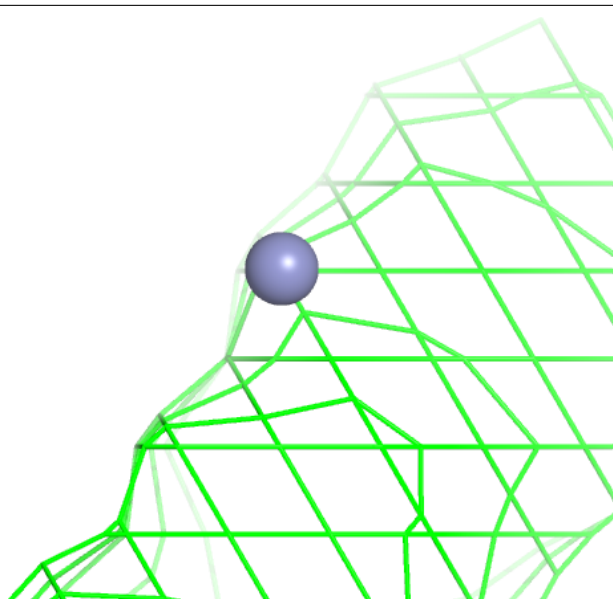
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ZN	C	501	1/1	0.87	0.11	566,566,566,566	0
2	ZN	D	503	1/1	0.92	0.07	568,568,568,568	0
2	ZN	C	503	1/1	0.93	0.07	581,581,581,581	0
2	ZN	C	502	1/1	0.94	0.06	522,522,522,522	0
2	ZN	B	501	1/1	0.94	0.07	606,606,606,606	0
2	ZN	C	504	1/1	0.94	0.07	552,552,552,552	0
2	ZN	A	501	1/1	0.94	0.09	551,551,551,551	0
2	ZN	B	504	1/1	0.95	0.05	595,595,595,595	0
2	ZN	A	504	1/1	0.95	0.07	544,544,544,544	0
2	ZN	D	501	1/1	0.95	0.05	584,584,584,584	0
2	ZN	A	502	1/1	0.95	0.06	511,511,511,511	0
2	ZN	D	502	1/1	0.96	0.05	568,568,568,568	0
2	ZN	B	502	1/1	0.97	0.06	580,580,580,580	0
2	ZN	B	503	1/1	0.97	0.09	707,707,707,707	0
2	ZN	D	504	1/1	0.97	0.07	563,563,563,563	0
2	ZN	A	503	1/1	0.99	0.05	533,533,533,533	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.



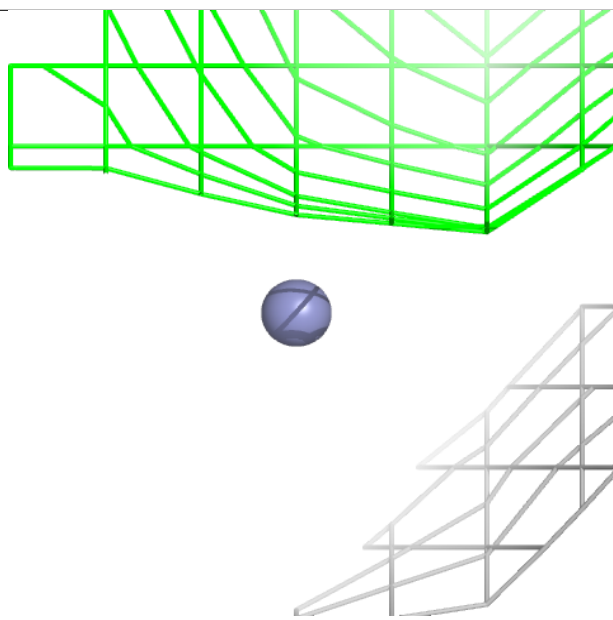
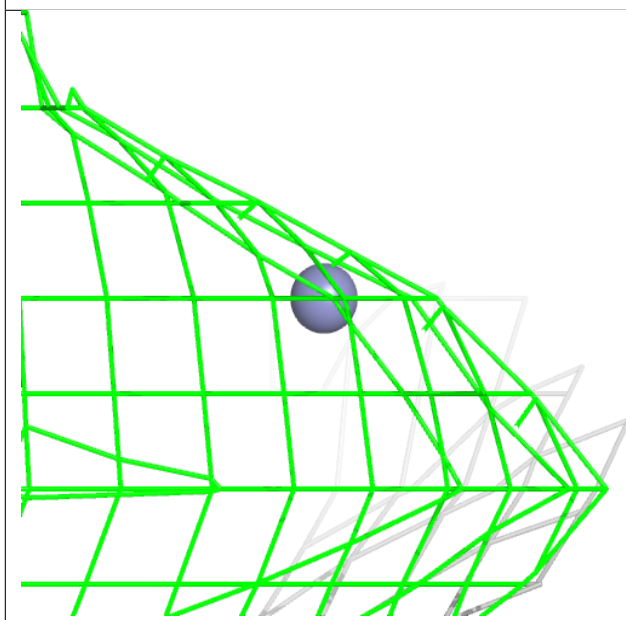
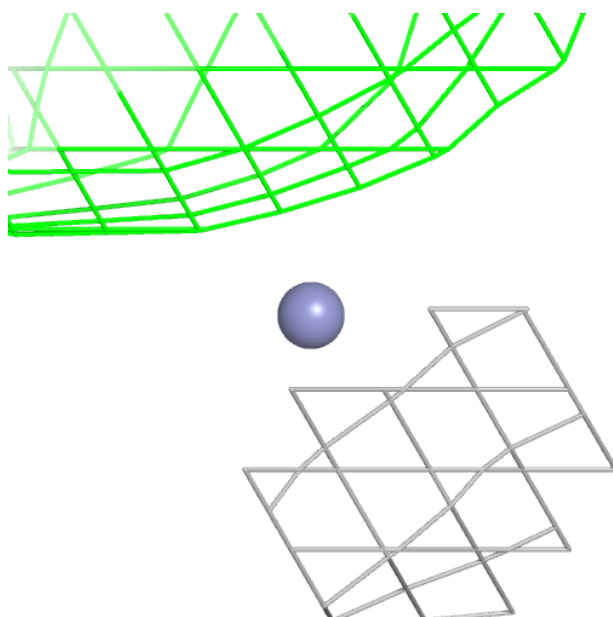
Electron density around ZN D 503:

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



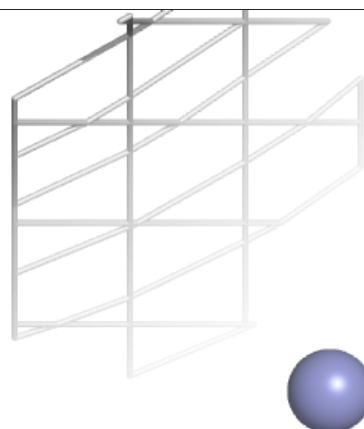
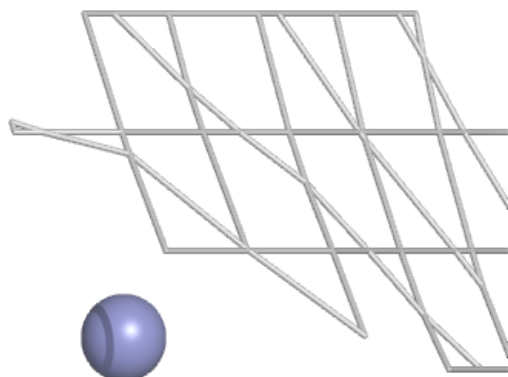
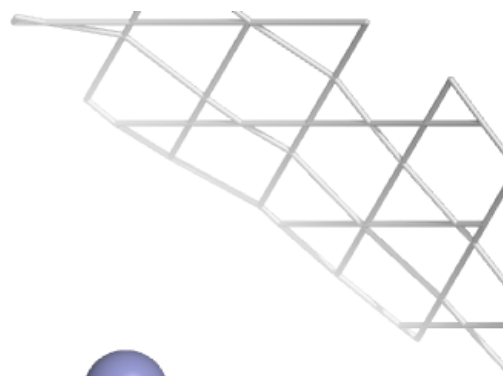
Electron density around ZN C 503:

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



Electron density around ZN C 502:

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

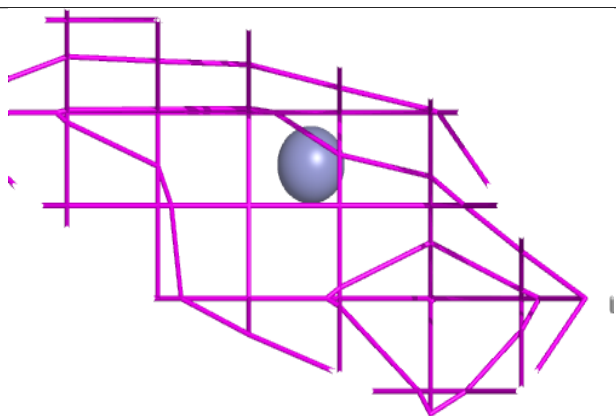
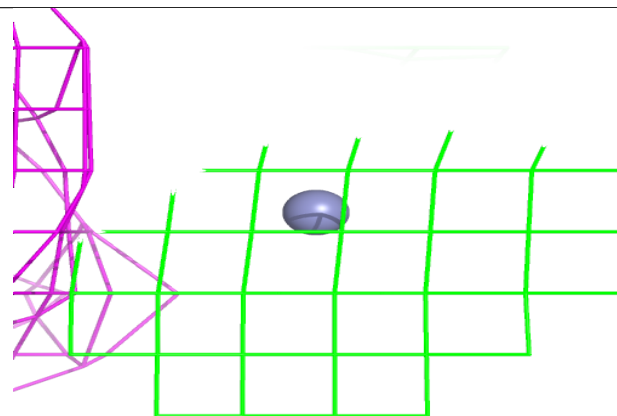
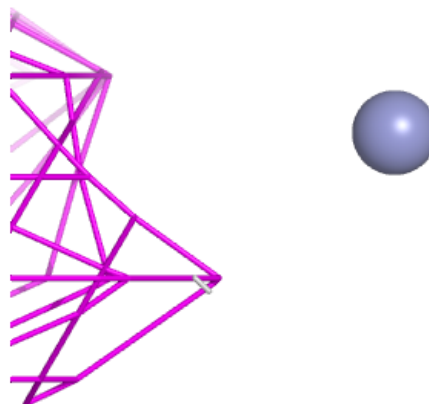
**Electron density around ZN B 501:**

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



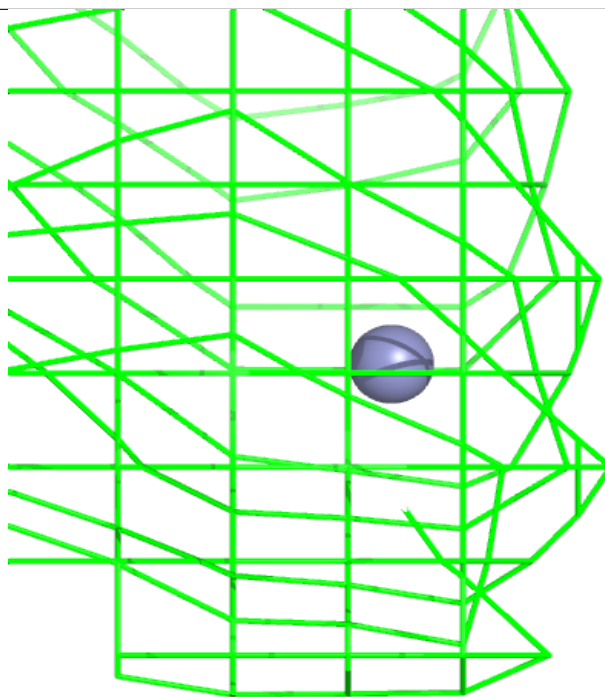
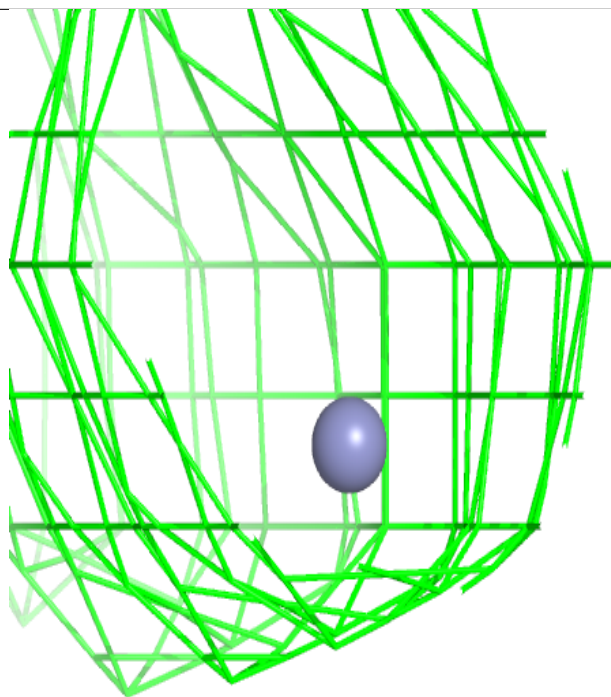
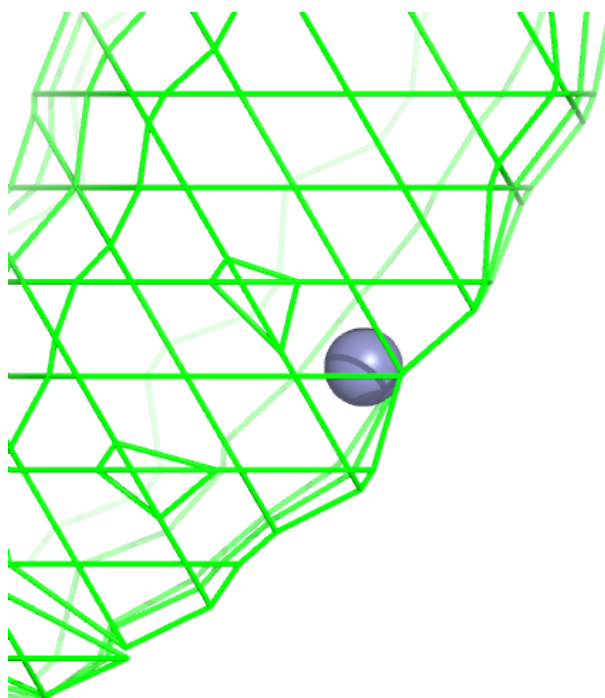
Electron density around ZN C 504:

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



Electron density around ZN A 501:

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

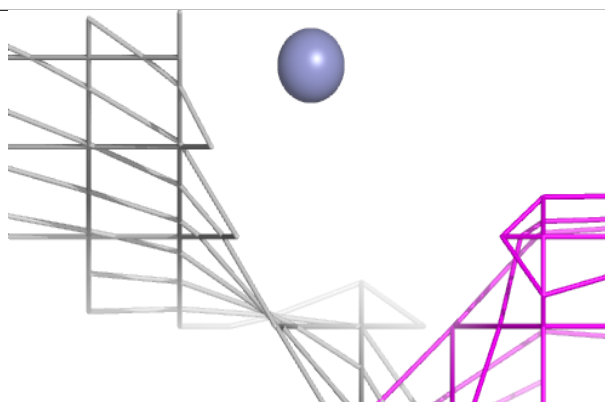
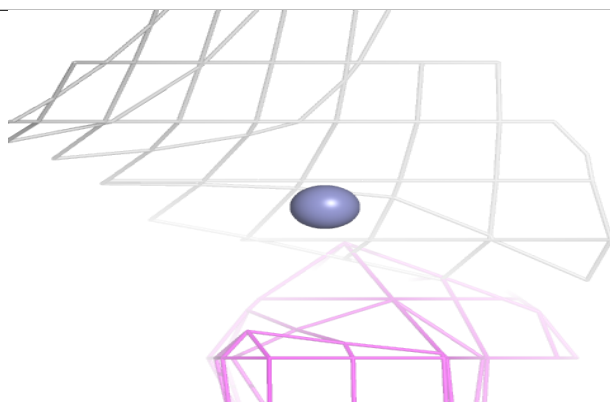
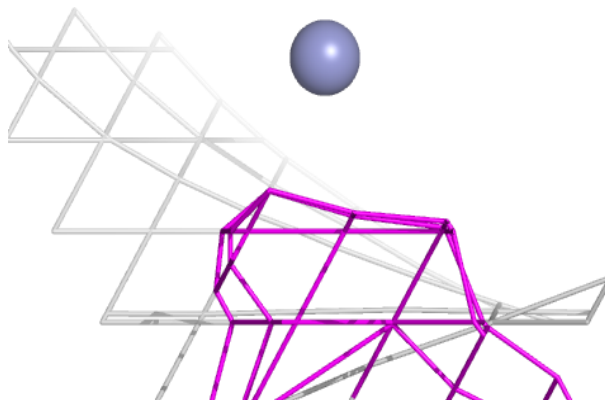


Electron density around ZN B 504:

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

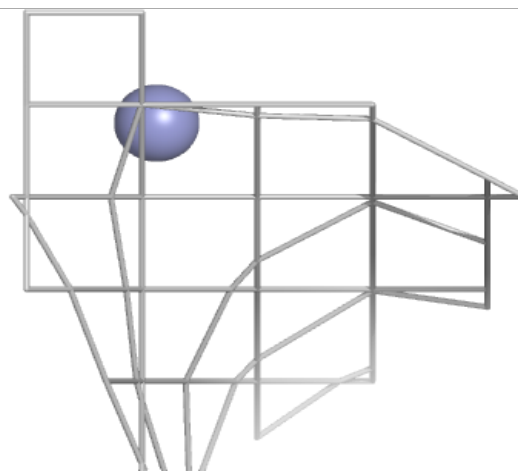
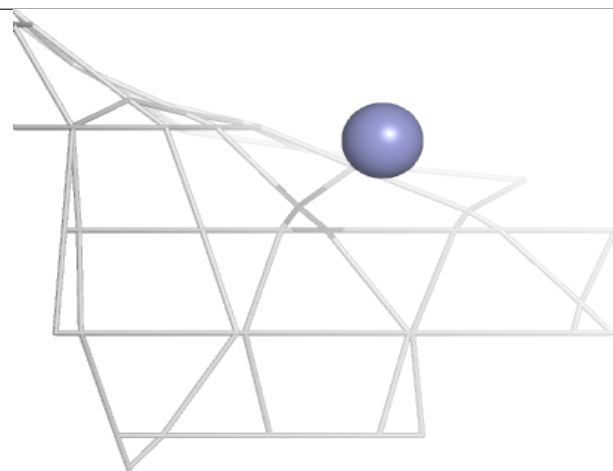
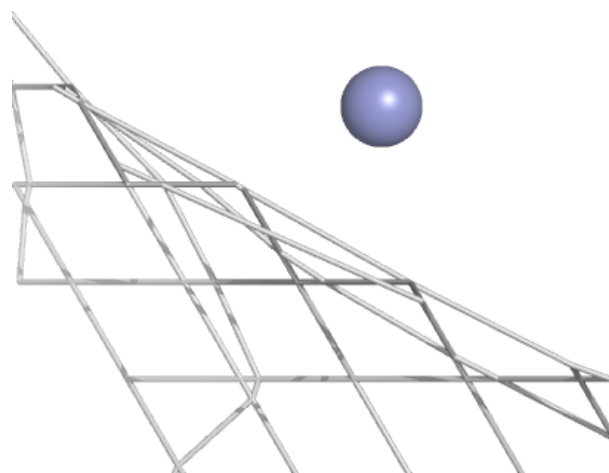
**Electron density around ZN A 504:**

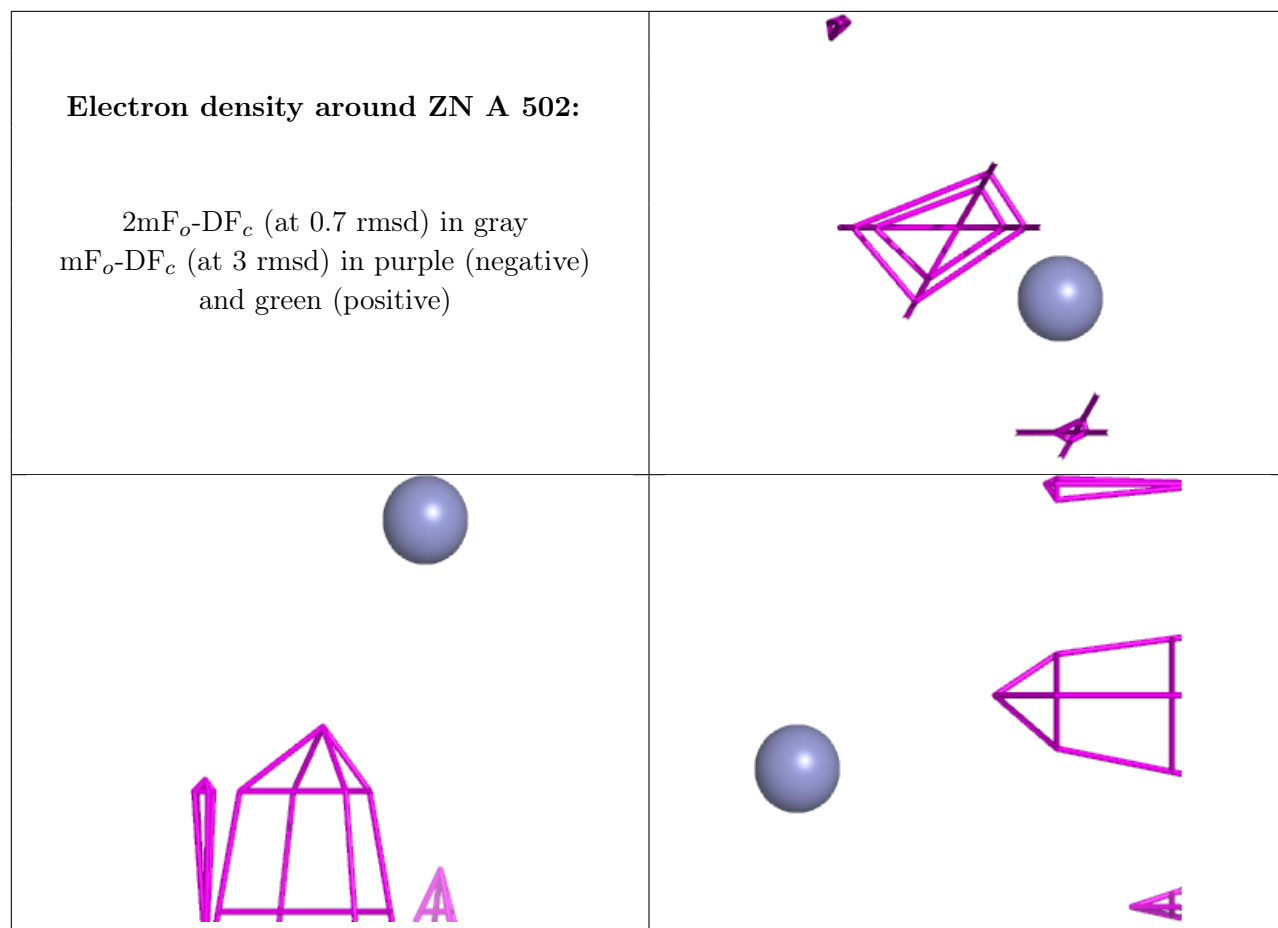
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

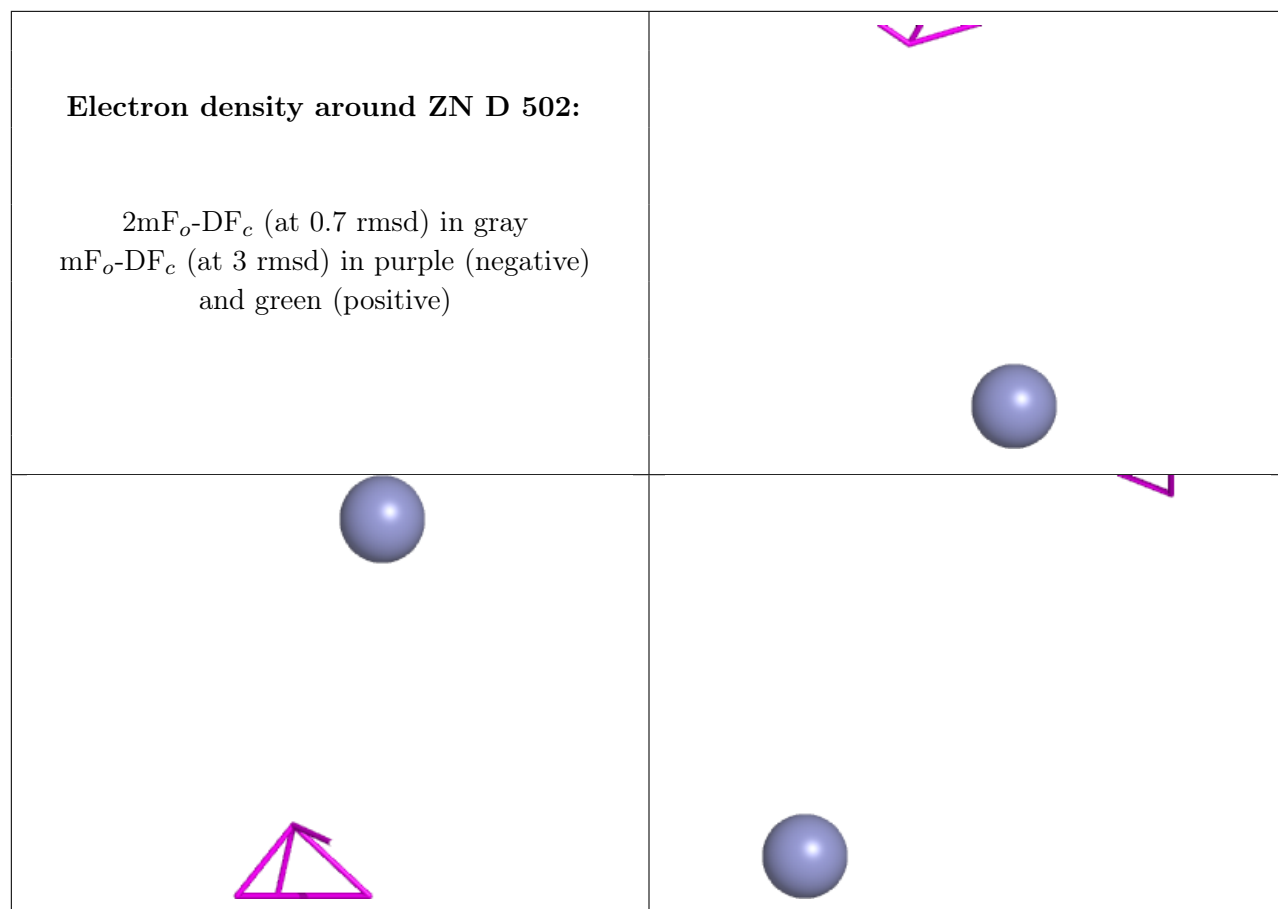


Electron density around ZN D 501:

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

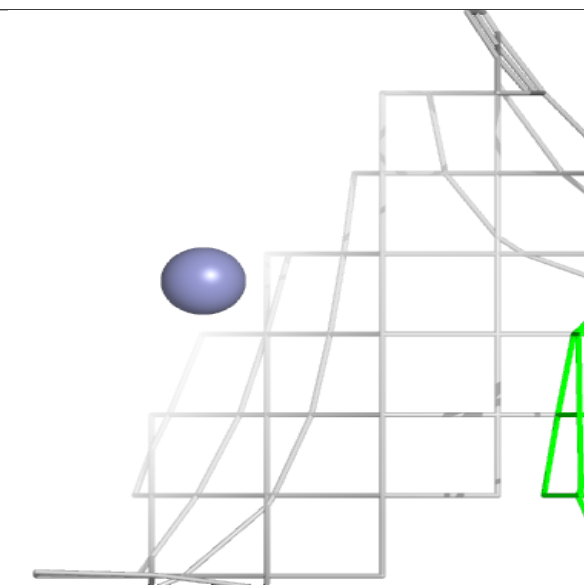
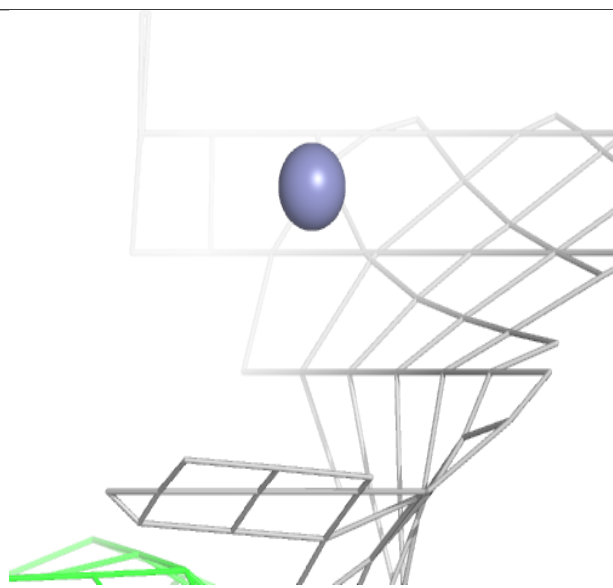
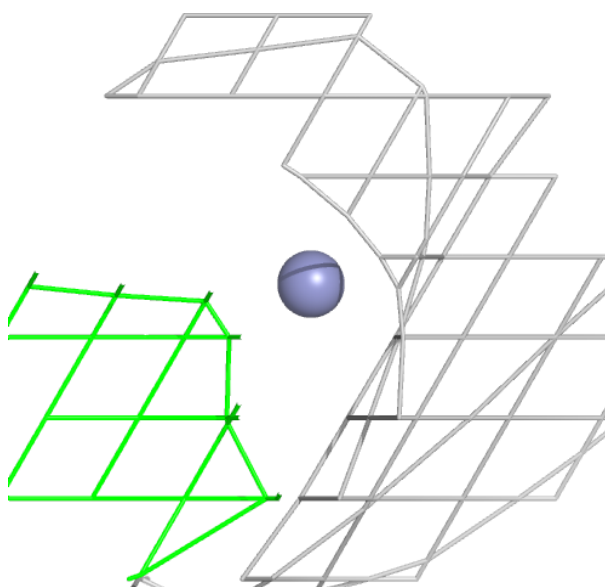






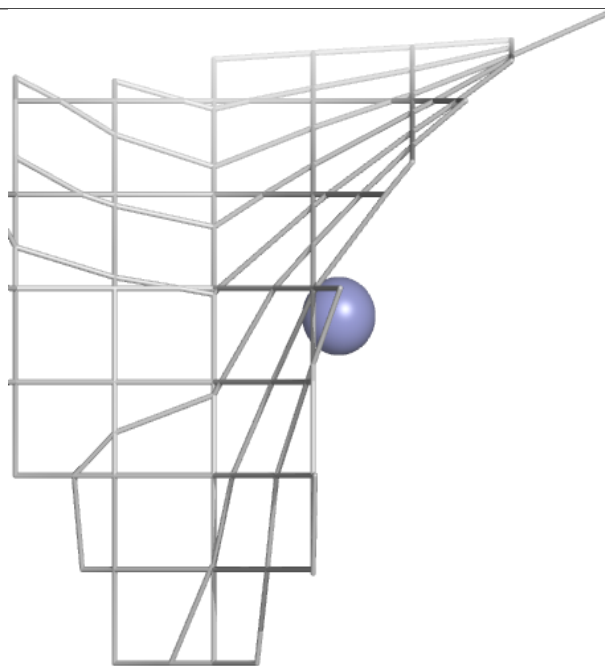
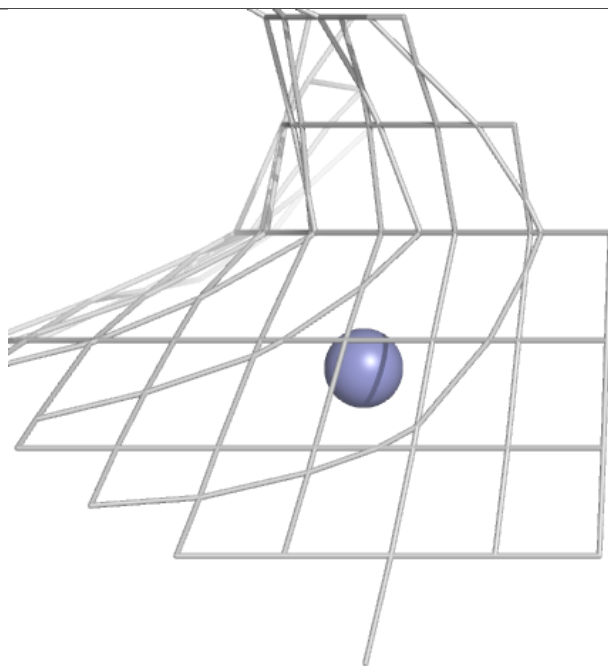
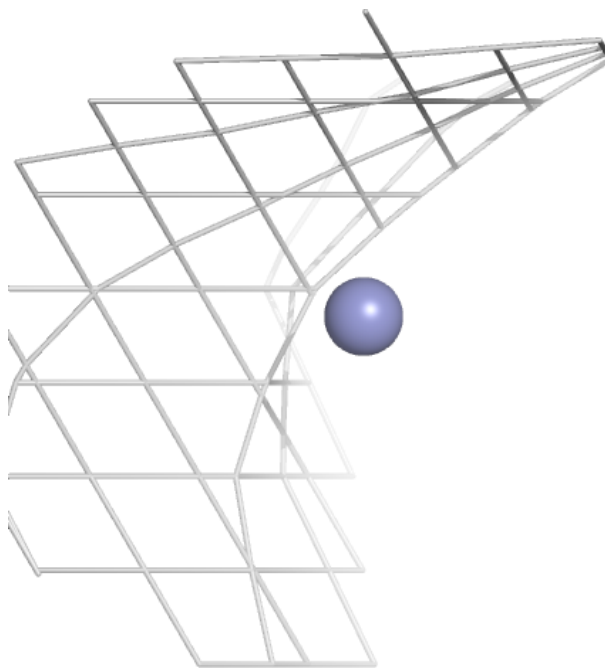
Electron density around ZN B 502:

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



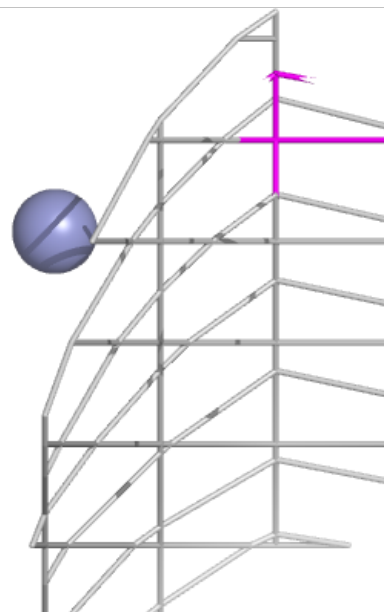
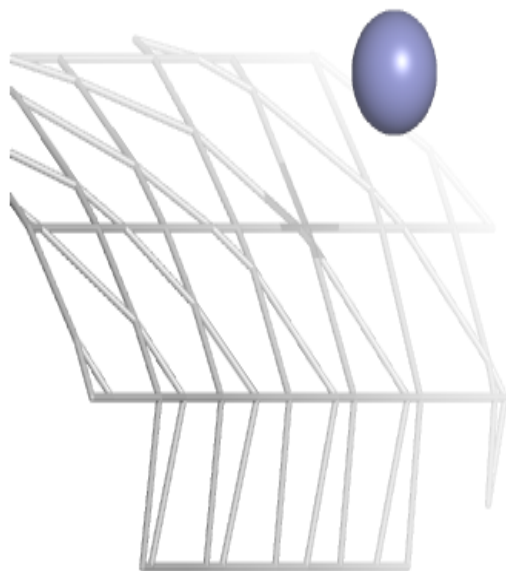
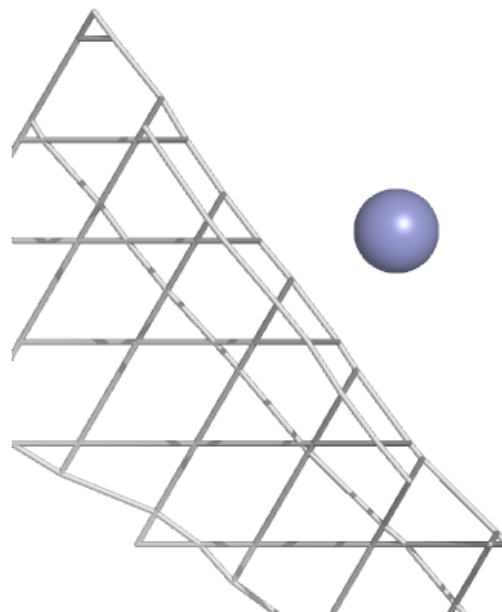
Electron density around ZN B 503:

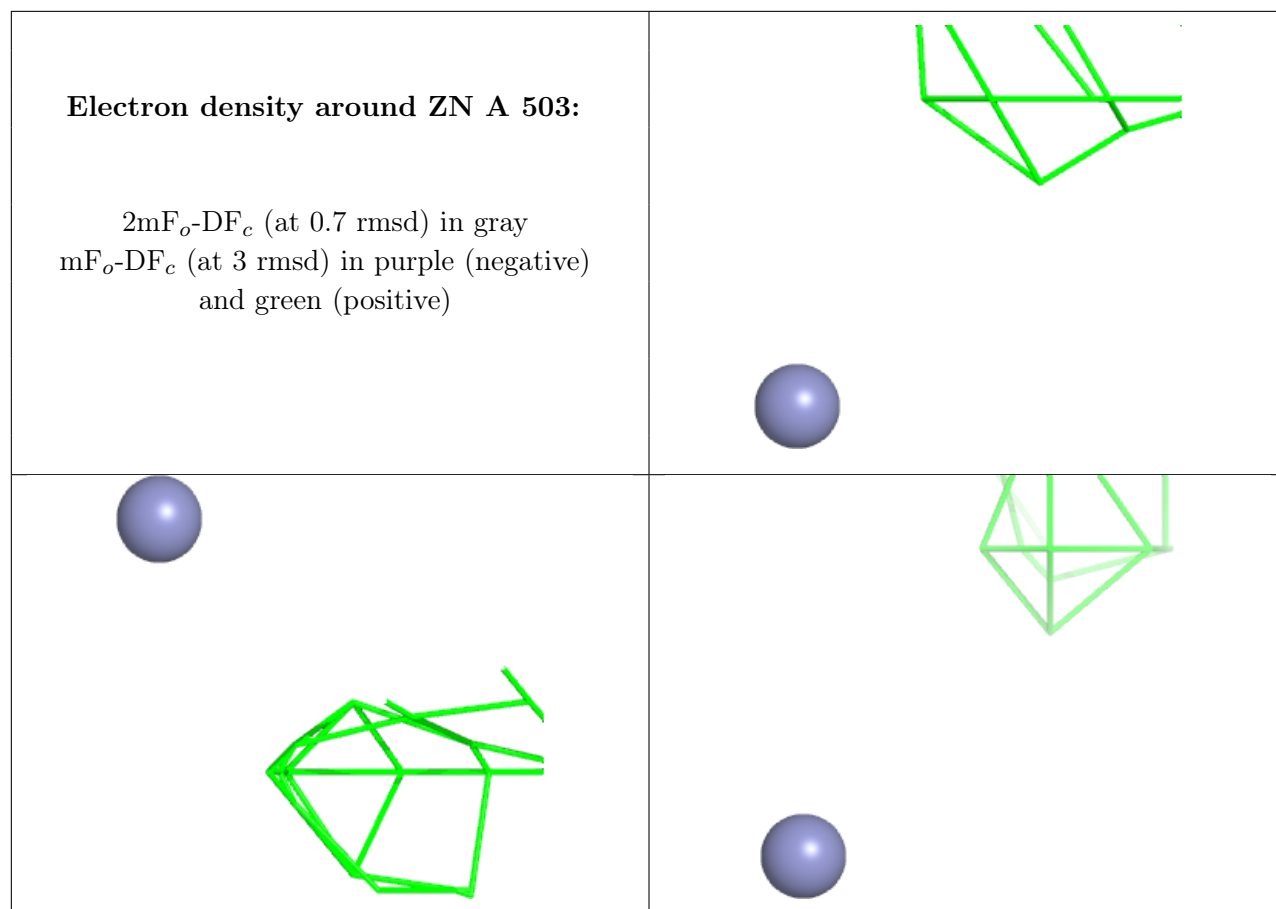
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN D 504:

$2mF_o-DF_c$ (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.