wwPDB X-ray Structure Validation Summary Report (i)

Oct 4, 2021 – 02:13 PM EDT

PDB ID	:	7ROY
Title	:	The structure of the Fem1B:FNIP1 complex
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Deposited on	:	2021-08-02
Resolution	:	2.90 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

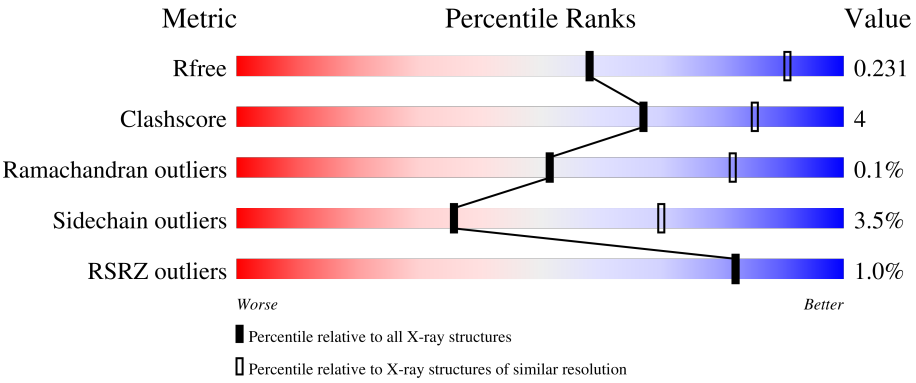
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 <=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	381	83% 15% ••
1	B	381	87% 10% ••
1	C	381	% 89% 10% ••
1	D	381	3% 87% 11% •
2	G	31	3% 39% 10% 52%

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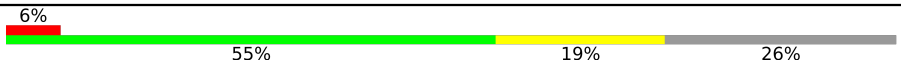
Mol	Chain	Length	Quality of chain
2	H	31	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 12189 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 fem-1 homolog B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	377	Total	C	N	O	S	0	0	0
			2951	1855	535	546	15			
1	B	375	Total	C	N	O	S	0	1	0
			2950	1855	537	543	15			
1	C	379	Total	C	N	O	S	0	1	0
			2975	1869	542	549	15			
1	D	374	Total	C	N	O	S	0	0	0
			2930	1844	531	540	15			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	SER	-	expression tag	UNP Q9Z2G0
A	-2	GLY	-	expression tag	UNP Q9Z2G0
A	-1	SER	-	expression tag	UNP Q9Z2G0
A	0	SER	-	expression tag	UNP Q9Z2G0
B	-3	SER	-	expression tag	UNP Q9Z2G0
B	-2	GLY	-	expression tag	UNP Q9Z2G0
B	-1	SER	-	expression tag	UNP Q9Z2G0
B	0	SER	-	expression tag	UNP Q9Z2G0
C	-3	SER	-	expression tag	UNP Q9Z2G0
C	-2	GLY	-	expression tag	UNP Q9Z2G0
C	-1	SER	-	expression tag	UNP Q9Z2G0
C	0	SER	-	expression tag	UNP Q9Z2G0
D	-3	SER	-	expression tag	UNP Q9Z2G0
D	-2	GLY	-	expression tag	UNP Q9Z2G0
D	-1	SER	-	expression tag	UNP Q9Z2G0
D	0	SER	-	expression tag	UNP Q9Z2G0

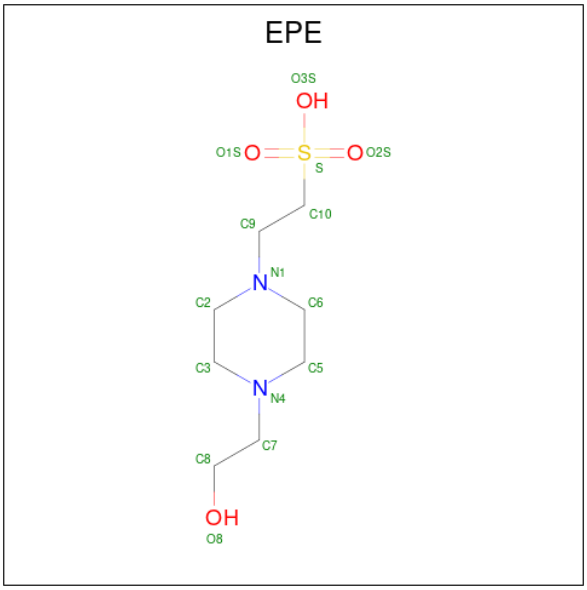
- Molecule 2 is a protein called Folliculin-interacting protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	15	Total	C	N	O	S	0	0	0
			117	70	23	21	3			
2	H	23	Total	C	N	O	S	0	0	0
			181	112	32	34	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	561	GLY	-	expression tag	UNP Q68FD7
H	561	GLY	-	expression tag	UNP Q68FD7

- Molecule 3 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
3	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Zn 1 1	0	0
4	B	2	Total Zn 2 2	0	0
4	C	1	Total Zn 1 1	0	0
4	D	2	Total Zn 2 2	0	0
4	G	1	Total Zn 1 1	0	0
4	H	1	Total Zn 1 1	0	0

- Molecule 5 is water.

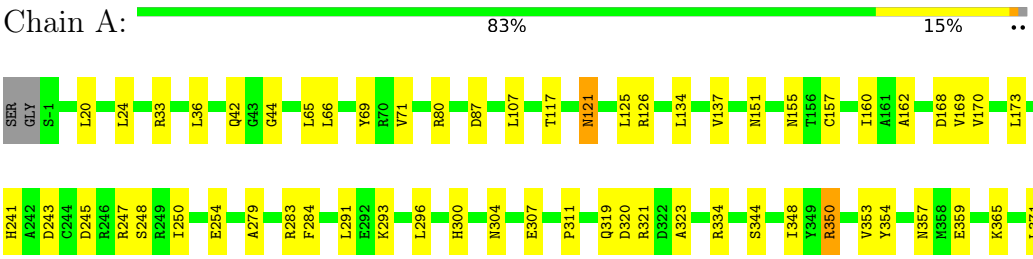
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	3	Total O 3 3	0	0
5	B	7	Total O 7 7	0	0
5	C	5	Total O 5 5	0	0
5	D	2	Total O 2 2	0	0

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.

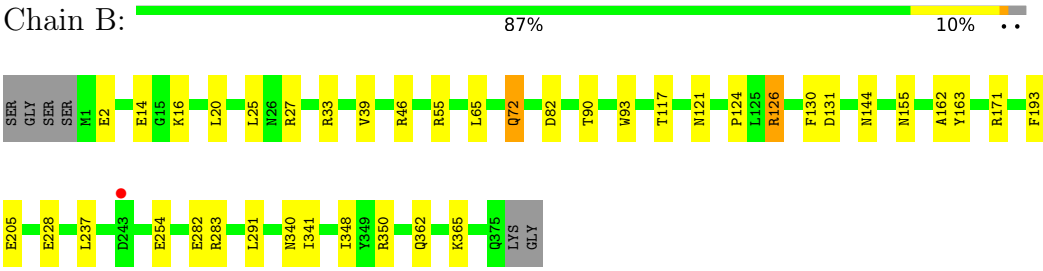
• Molecule 1: Protein fem-1 homolog B

Chain A:



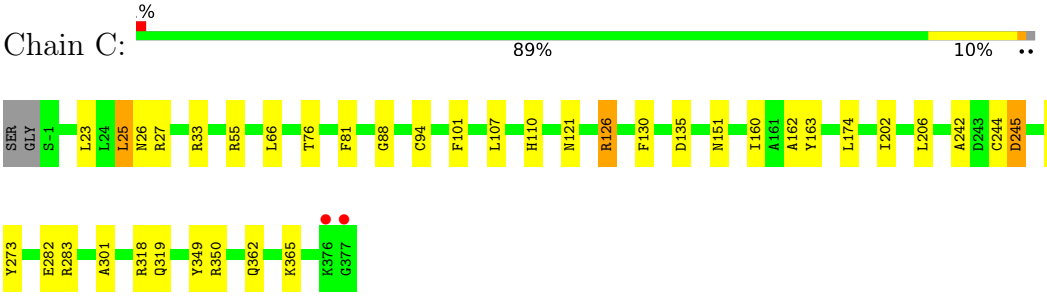
• Molecule 1: Protein fem-1 homolog B

Chain B:



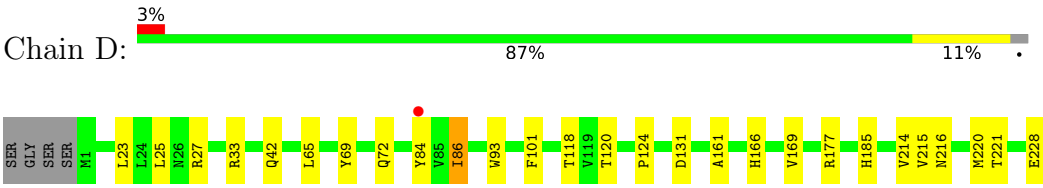
• Molecule 1: Protein fem-1 homolog B

Chain C:

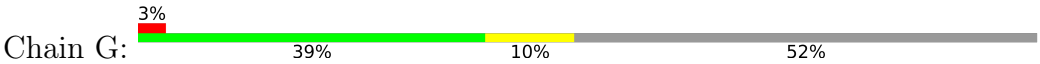


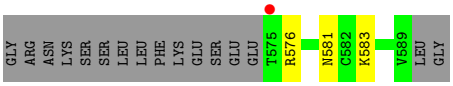
• Molecule 1: Protein fem-1 homolog B

Chain D:

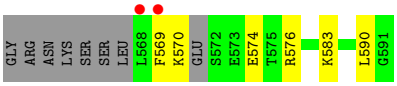


• Molecule 2: Folliculin-interacting protein 1





• Molecule 2: Folliculin-interacting protein 1



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α, β, γ	164.47Å 164.47Å 465.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.33 – 2.90 49.33 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.33-2.90) 100.0 (49.33-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.32	Depositor
$< I/\sigma(I) >$ [1]	1.23 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.206 , 0.230 0.206 , 0.231	Depositor DCC
R_{free} test set	3560 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	75.4	Xtriage
Anisotropy	0.292	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 33.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12189	wwPDB-VP
Average B, all atoms (Å^2)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: EPE, 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	0/3005	0.39	0/4072
1	B	0.23	0/3004	0.38	0/4070
1	C	0.23	0/3029	0.39	0/4102
1	D	0.23	0/2984	0.39	0/4044
2	G	0.22	0/120	0.40	0/163
2	H	0.24	0/184	0.42	0/246
All	All	0.23	0/12326	0.39	0/16697

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	2951	0	2939	30	0
1	B	2950	0	2941	21	0
1	C	2975	0	2967	21	0
1	D	2930	0	2921	19	0
2	G	117	0	107	2	0
2	H	181	0	170	6	0
3	A	15	0	17	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	15	0	17	2	0
3	C	15	0	17	3	0
3	D	15	0	17	1	0
4	A	1	0	0	0	0
4	B	2	0	0	0	0
4	C	1	0	0	0	0
4	D	2	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	3	0	0	0	0
5	B	7	0	0	0	0
5	C	5	0	0	0	0
5	D	2	0	0	0	0
All	All	12189	0	12113	95	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.

The worst 5 of 95 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:B:25:LEU:O	1:D:27:ARG:NH2	2.22	0.72
1:C:81:PHE:HD2	3:C:401:EPE:H82	1.58	0.67
1:C:126:ARG:NH1	3:C:401:EPE:O1S	2.31	0.64
1:A:196:GLU:HG3	2:G:583:LYS:HD2	1.80	0.62
1:C:130:PHE:HD1	1:C:160:ILE:HD11	1.64	0.61

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	375/381 (98%)	359 (96%)	16 (4%)	0	100 100
1	B	374/381 (98%)	360 (96%)	13 (4%)	1 (0%)	41 71
1	C	378/381 (99%)	363 (96%)	15 (4%)	0	100 100
1	D	372/381 (98%)	358 (96%)	14 (4%)	0	100 100
2	G	13/31 (42%)	12 (92%)	1 (8%)	0	100 100
2	H	19/31 (61%)	17 (90%)	1 (5%)	1 (5%)	2 6
All	All	1531/1586 (96%)	1469 (96%)	60 (4%)	2 (0%)	51 82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	574	GLU
1	B	82	ASP

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	307/309 (99%)	294 (96%)	13 (4%)	30 63
1	B	306/309 (99%)	297 (97%)	9 (3%)	42 76
1	C	309/309 (100%)	300 (97%)	9 (3%)	42 76
1	D	304/309 (98%)	291 (96%)	13 (4%)	29 62
2	G	15/29 (52%)	15 (100%)	0	100 100
2	H	22/29 (76%)	22 (100%)	0	100 100
All	All	1263/1294 (98%)	1219 (96%)	44 (4%)	36 70

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	319	GLN
1	D	120	THR
1	C	350	ARG

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Mol	Chain	Res	Type
1	D	84	TYR
1	D	185	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	C	144	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 monosaccharides in this entry.

5.6 Ligand geometry

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	EPE	D	401	-	15,15,15	0.82	1 (6%)	18,20,20	1.75	6 (33%)
3	EPE	A	401	-	15,15,15	0.78	1 (6%)	18,20,20	1.86	4 (22%)
3	EPE	C	401	-	15,15,15	0.76	1 (6%)	18,20,20	1.81	4 (22%)
3	EPE	B	401	-	15,15,15	0.78	1 (6%)	18,20,20	1.92	5 (27%)

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	EPE	D	401	-	-	4/9/19/19	0/1/1/1
3	EPE	A	401	-	-	3/9/19/19	0/1/1/1
3	EPE	C	401	-	-	6/9/19/19	0/1/1/1
3	EPE	B	401	-	-	4/9/19/19	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	401	EPE	C10-S	2.79	1.81	1.77
3	C	401	EPE	C10-S	2.60	1.81	1.77
3	A	401	EPE	C10-S	2.58	1.81	1.77
3	B	401	EPE	C10-S	2.50	1.81	1.77

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	401	EPE	C5-N4-C3	4.77	119.58	108.83
3	D	401	EPE	C5-N4-C3	4.54	119.04	108.83
3	A	401	EPE	C5-N4-C3	4.36	118.65	108.83
3	B	401	EPE	C5-N4-C3	4.02	117.88	108.83
3	A	401	EPE	C7-N4-C3	3.53	120.27	111.23

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	401	EPE	C8-C7-N4-C5
3	B	401	EPE	C10-C9-N1-C2
3	B	401	EPE	C8-C7-N4-C5
3	C	401	EPE	C10-C9-N1-C2
3	C	401	EPE	C10-C9-N1-C6

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	EPE	1	0
3	C	401	EPE	3	0
3	B	401	EPE	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	377/381 (98%)	-0.19	0 100 100	54, 72, 105, 130	0
1	B	375/381 (98%)	-0.10	1 (0%) 94 94	46, 59, 94, 116	0
1	C	379/381 (99%)	-0.16	2 (0%) 91 91	43, 56, 89, 122	0
1	D	374/381 (98%)	0.15	10 (2%) 54 50	53, 88, 133, 163	0
2	G	15/31 (48%)	0.23	1 (6%) 17 13	81, 86, 128, 135	0
2	H	23/31 (74%)	0.52	2 (8%) 10 7	58, 83, 150, 163	0
All	All	1543/1586 (97%)	-0.06	16 (1%) 82 82	43, 67, 116, 163	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	569	PHE	4.6
1	D	84	TYR	4.1
1	D	284	PHE	3.7
1	D	338	ALA	3.6
1	D	339	ASP	3.1

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

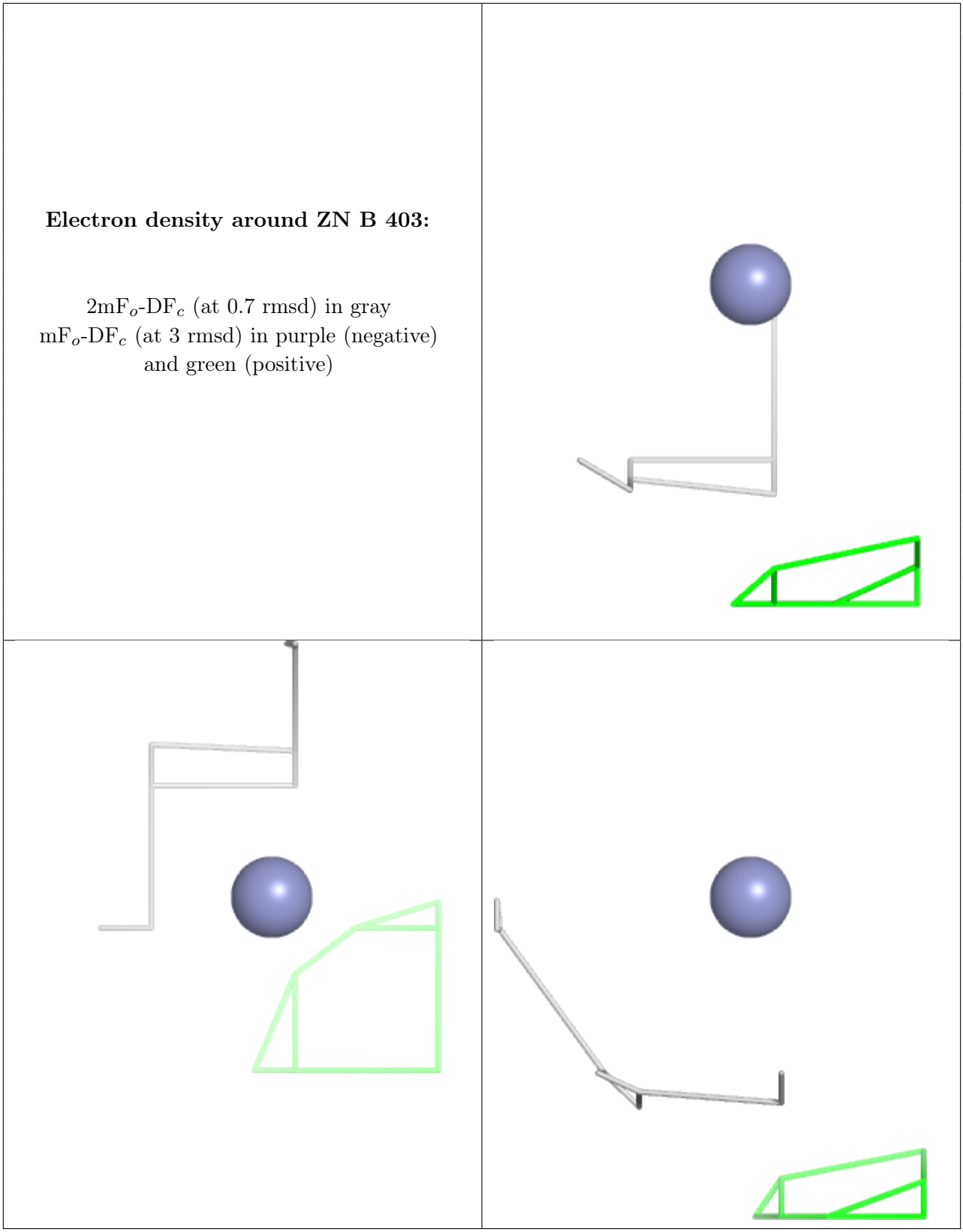
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	ZN	B	403	1/1	0.63	0.09	131,131,131,131	0
4	ZN	B	402	1/1	0.85	0.10	143,143,143,143	1
3	EPE	A	401	15/15	0.85	0.43	89,106,122,125	0
4	ZN	D	402	1/1	0.86	0.17	158,158,158,158	0
4	ZN	D	403	1/1	0.86	0.11	132,132,132,132	0
3	EPE	C	401	15/15	0.90	0.29	75,90,105,137	0
3	EPE	B	401	15/15	0.93	0.23	62,83,104,114	0
3	EPE	D	401	15/15	0.94	0.22	80,101,111,123	0
4	ZN	A	402	1/1	0.99	0.08	80,80,80,80	0
4	ZN	C	402	1/1	0.99	0.12	58,58,58,58	0
4	ZN	G	1001	1/1	1.00	0.10	81,81,81,81	0
4	ZN	H	1001	1/1	1.00	0.12	60,60,60,60	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.

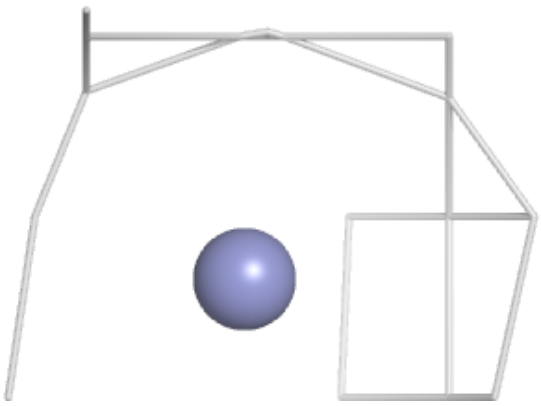
Electron density around ZN B 403:

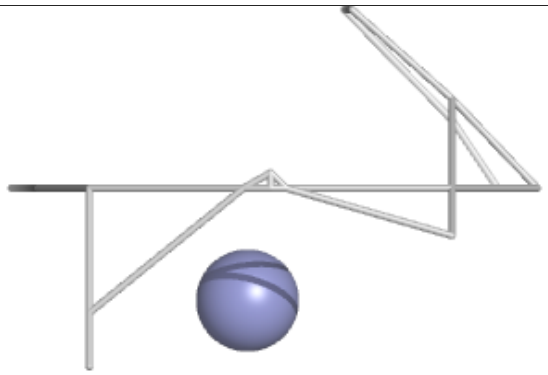
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

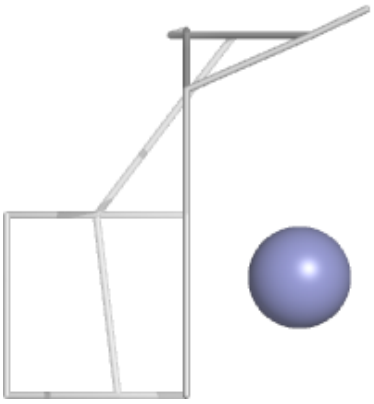


Electron density around ZN B 402:

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

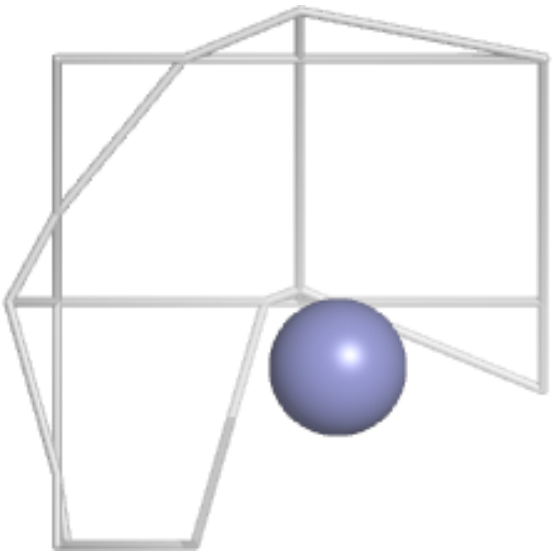


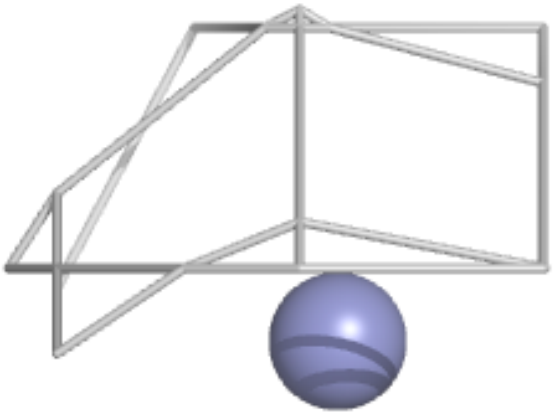


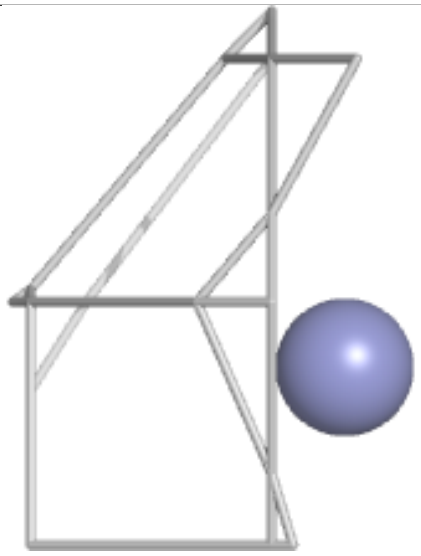


Electron density around ZN D 402:

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

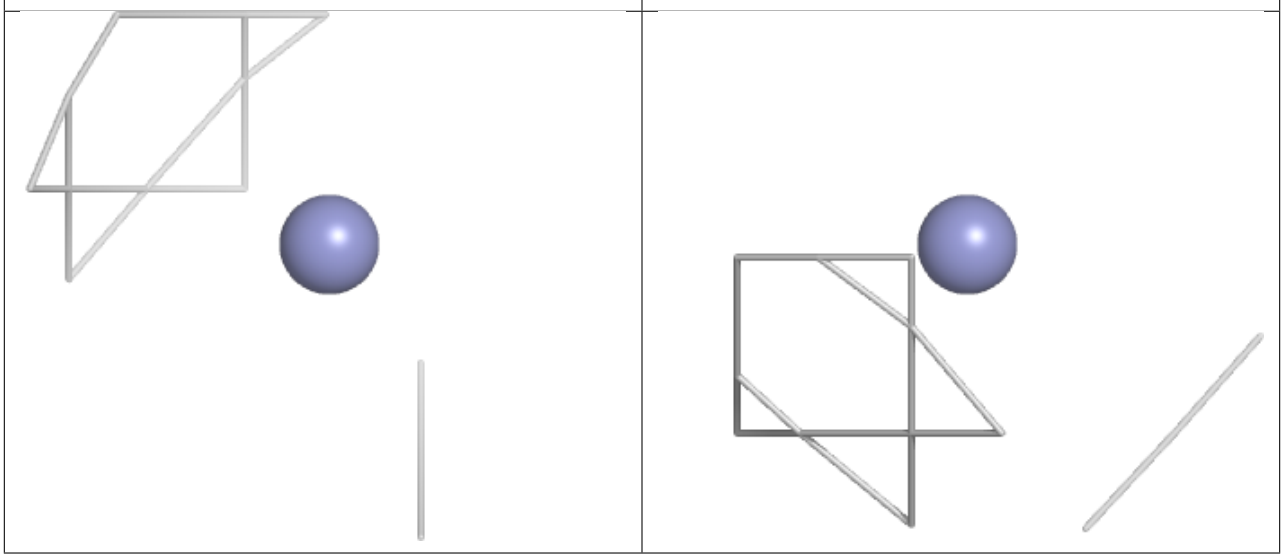






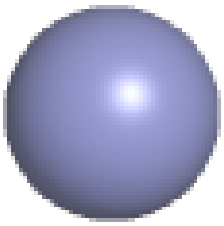
Electron density around ZN D 403:

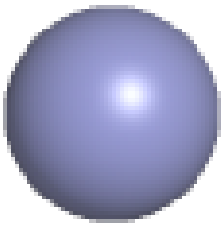
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

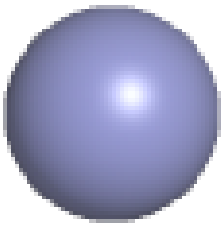


Electron density around ZN A 402:

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

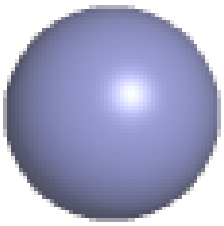


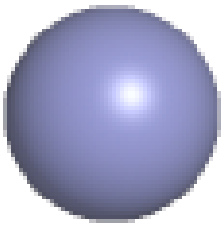


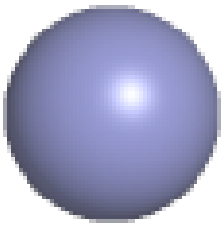


Electron density around ZN C 402:

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

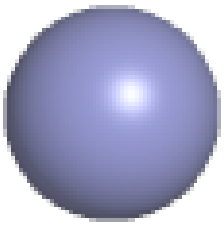


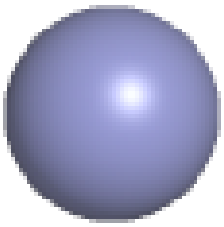


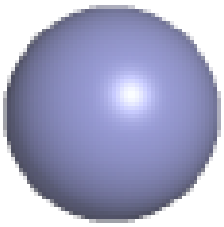


Electron density around ZN G 1001:

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

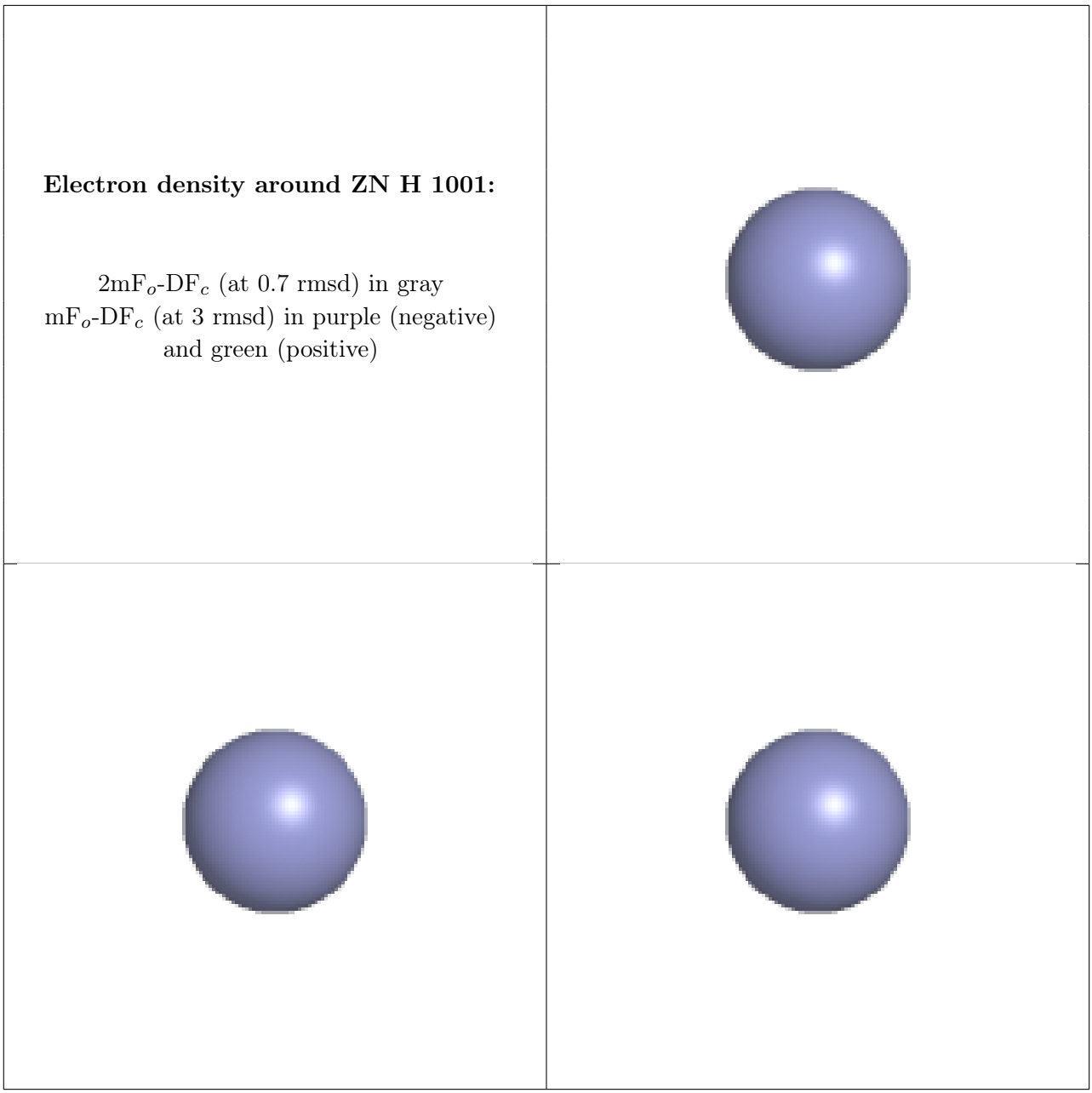






Electron density around ZN H 1001:

$2mF_o$-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 (i)

There are no such residues in this entry.