Full wwPDB X-ray Structure Validation Report (i)

Mar 10, 2025 – 12:10 AM EDT

PDB ID	:	8UY3
Title	:	Fem1B with FNIP1 and Tom20 fragment
Authors	:	Gee, C.L.; Manford, A.G.; McMinimy, R.; Rape, M.
Deposited on	:	2023-11-12
Resolution	:	3.20 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 (i) 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 (1)) were used in the production of this report:

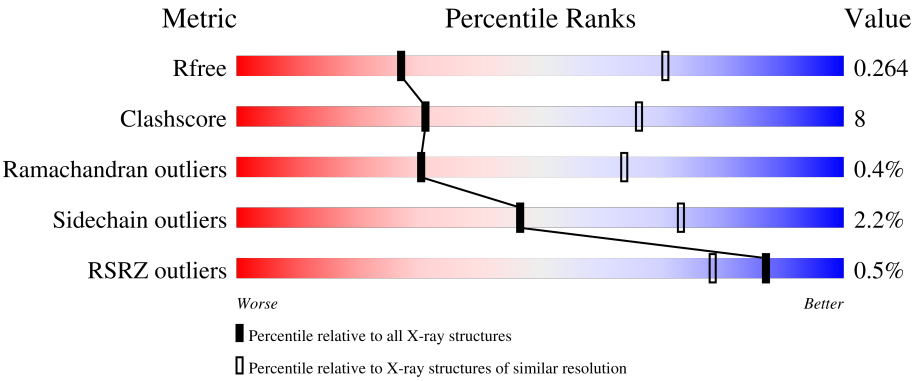
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.41.4

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 3.20 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	1370 (3.20-3.20)
Clashscore	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)
RSRZ outliers	164620	1371 (3.20-3.20)

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	86% 13%
1	B	381	81% 18%
1	C	381	82% 15%
1	D	381	2% 71% 25%
2	E	31	45% 6% 45%

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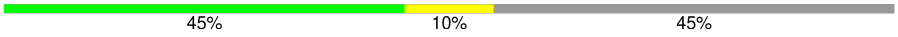
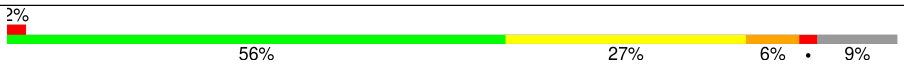
Mol	Chain	Length	Quality of chain
2	F	31	
2	H	31	
2	I	31	
3	J	66	
3	K	66	
3	M	66	

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 13741 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
			2949	1855	535	544	15			
1	C	377	Total	C	N	O	S	0	1	0
			2958	1860	536	547	15			
1	B	376	Total	C	N	O	S	0	0	0
			2944	1852	534	543	15			
1	D	374	Total	C	N	O	S	0	0	0
			2931	1845	533	539	14			

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
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
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
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	E	17	Total	C	N	O	S	0	0	0
			129	78	25	23	3			
2	F	17	Total	C	N	O	S	0	0	0
			129	78	25	23	3			
2	H	12	Total	C	N	O	S	0	0	0
			92	55	17	17	3			
2	I	11	Total	C	N	O	S	0	0	0
			85	51	16	15	3			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1	GLY	-	expression tag	UNP Q68FD7
F	1	GLY	-	expression tag	UNP Q68FD7
H	1	GLY	-	expression tag	UNP Q68FD7
I	1	GLY	-	expression tag	UNP Q68FD7

- Molecule 3 is a protein called Mitochondrial import receptor subunit TOM20 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	J	66	Total	C	N	O	S	0	0	0
			517	334	82	99	2			
3	K	63	Total	C	N	O	S	0	0	0
			495	322	79	92	2			
3	M	60	Total	C	N	O	S	0	0	0
			474	309	75	88	2			

- 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	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	E	1	Total	Zn	0	0
			1	1		
4	F	1	Total	Zn	0	0
			1	1		

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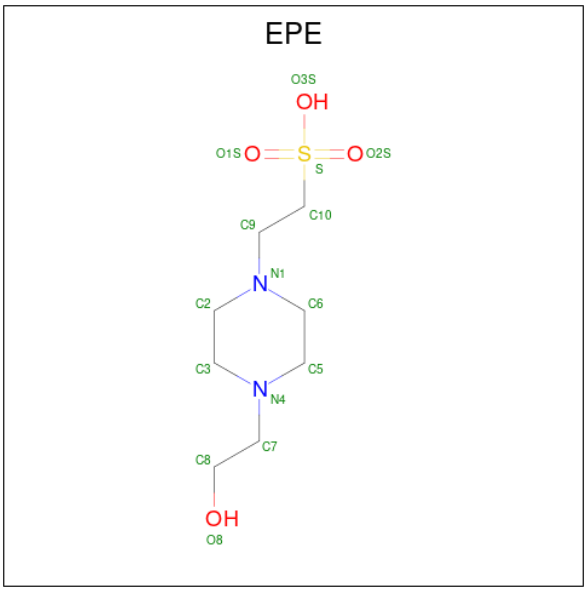
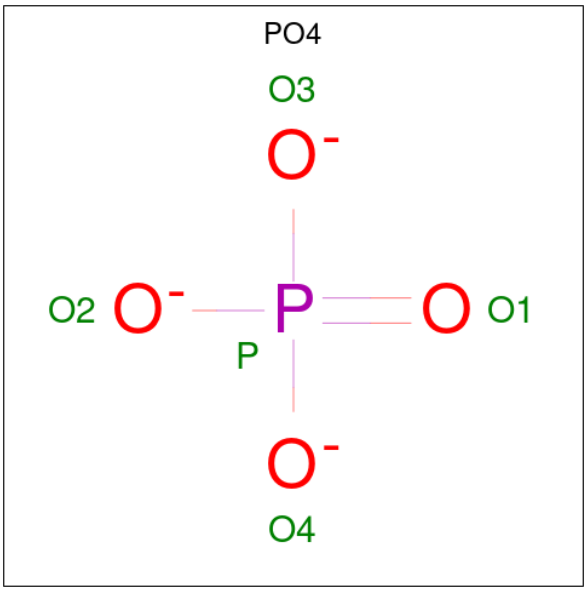
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total Zn 1 1	0	0
4	I	1	Total Zn 1 1	0	0

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



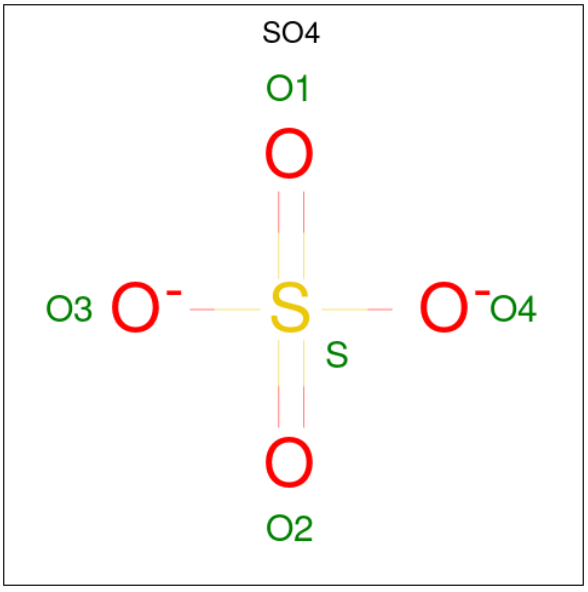
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O S 15 8 2 4 1	0	0

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O P 5 4 1	0	0

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



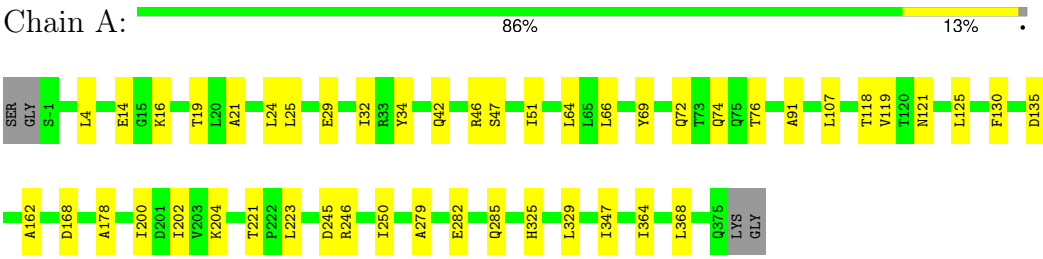
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	C	1	Total O S 5 4 1	0	0
7	B	1	Total O S 5 4 1	0	0

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.

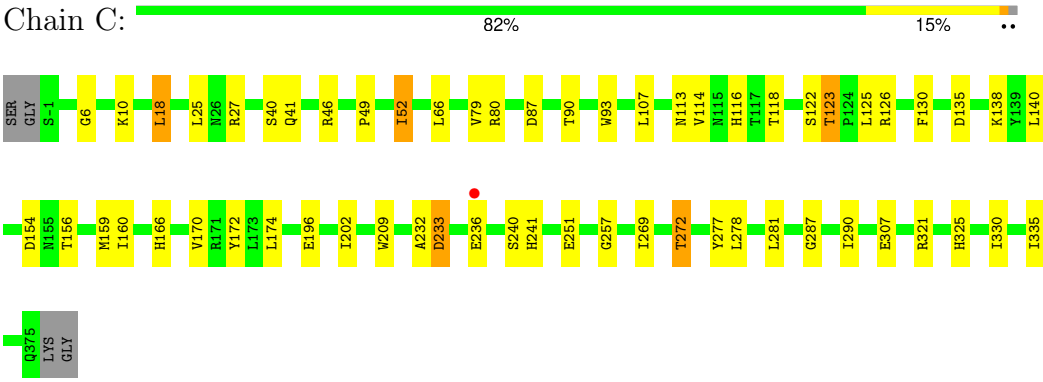
• Molecule 1: Protein fem-1 homolog B

Chain A:



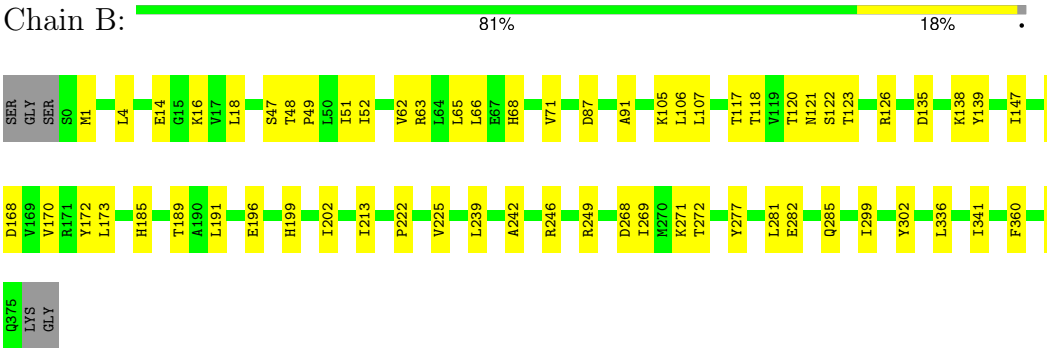
• Molecule 1: Protein fem-1 homolog B

Chain C:



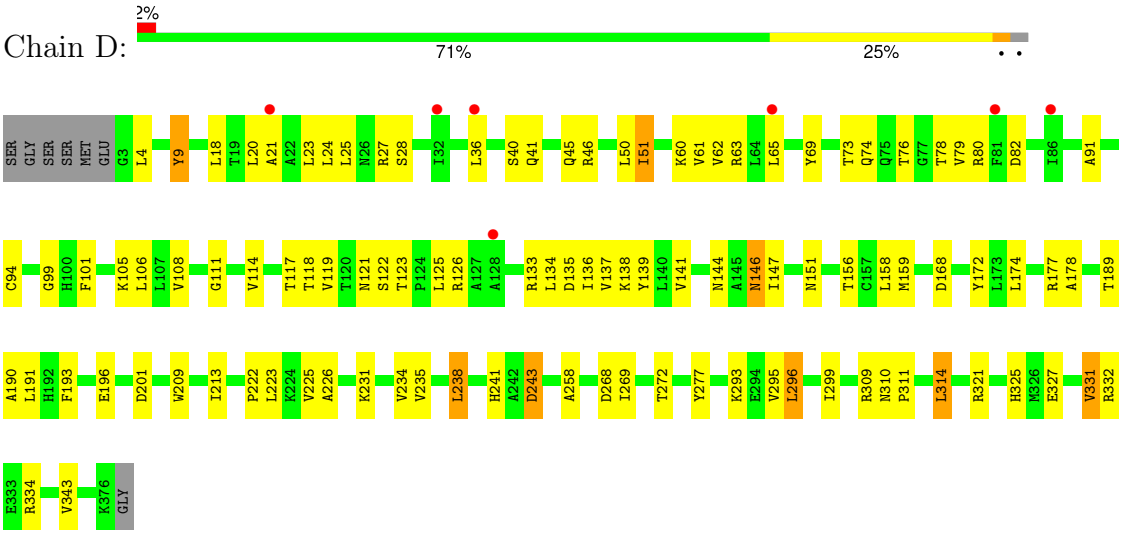
• Molecule 1: Protein fem-1 homolog B

Chain B:



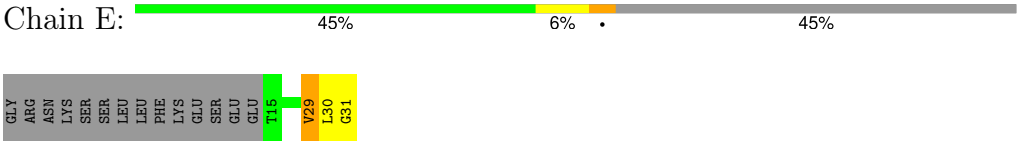
• Molecule 1: Protein fem-1 homolog B

Chain D:



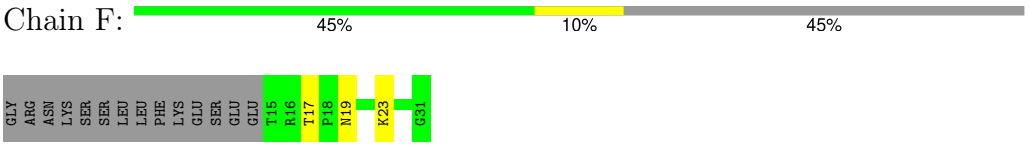
• Molecule 2: Folliculin-interacting protein 1

Chain E:



• Molecule 2: Folliculin-interacting protein 1

Chain F:

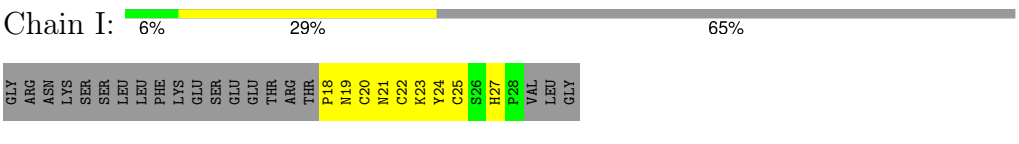


• Molecule 2: Folliculin-interacting protein 1

Chain H:

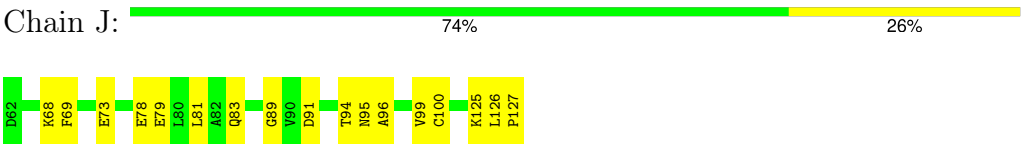
• Molecule 2: Folliculin-interacting protein 1

Chain I:



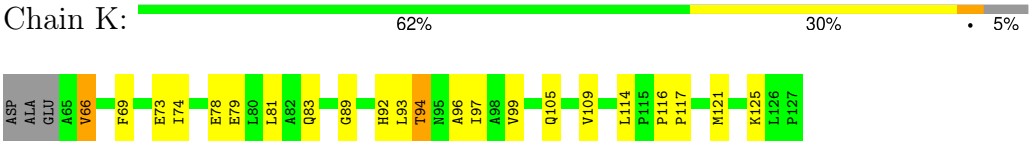
• Molecule 3: Mitochondrial import receptor subunit TOM20 homolog

Chain J:



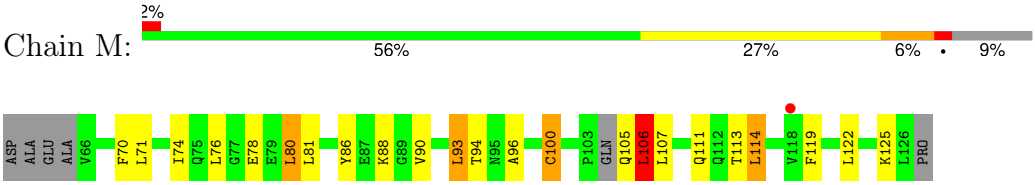
• Molecule 3: Mitochondrial import receptor subunit TOM20 homolog

Chain K:



• Molecule 3: Mitochondrial import receptor subunit TOM20 homolog

Chain M:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α, β, γ	183.72Å 183.72Å 183.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.93 – 3.20 45.93 – 3.20	Depositor EDS
% Data completeness (in resolution range)	91.5 (45.93-3.20) 91.4 (45.93-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.38	Depositor
$< I/\sigma(I) >$ [1]	1.11 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.239 , 0.264 0.239 , 0.264	Depositor DCC
R_{free} test set	1733 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	98.1	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 56.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.056 for l,-k,h	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	13741	wwPDB-VP
Average B, all atoms (Å^2)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.16% 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: SO4, ZN, EPE, PO4

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	0.24	0/3003	0.47	0/4070
1	B	0.25	0/2998	0.47	0/4063
1	C	0.24	0/3012	0.46	0/4082
1	D	0.26	0/2985	0.48	0/4045
2	E	0.23	0/132	0.51	0/179
2	F	0.22	0/132	0.47	0/179
2	H	0.26	0/95	0.41	0/129
2	I	0.24	0/88	0.40	0/118
3	J	0.28	0/526	0.49	0/715
3	K	0.26	0/504	0.44	0/685
3	M	0.27	0/481	0.48	0/651
All	All	0.25	0/13956	0.47	0/18916

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	2949	0	2931	33	0
1	B	2944	0	2931	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2958	0	2938	40	0
1	D	2931	0	2924	69	0
2	E	129	0	121	1	0
2	F	129	0	121	2	0
2	H	92	0	78	1	0
2	I	85	0	72	10	0
3	J	517	0	523	11	0
3	K	495	0	508	15	0
3	M	474	0	487	17	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
5	A	15	0	17	1	0
6	A	5	0	0	0	0
7	B	5	0	0	0	0
7	C	5	0	0	0	0
All	All	13741	0	13651	222	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.

All (222) 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:118:THR:HG22	1:B:122:SER:H	1.50	0.77
1:B:47:SER:HA	1:B:51:ILE:HD11	1.70	0.74
1:B:336:LEU:HB3	1:B:341:ILE:HD11	1.69	0.74
1:A:221:THR:HG22	1:A:223:LEU:H	1.53	0.73
3:M:105:GLN:O	3:M:107:LEU:N	2.20	0.71
1:B:18:LEU:HB3	3:K:74:ILE:HD11	1.72	0.71
1:B:246:ARG:NH2	1:B:282:GLU:O	2.26	0.69
1:D:50:LEU:HD13	1:D:65:LEU:HD11	1.78	0.66
1:A:47:SER:HA	1:A:51:ILE:HD11	1.77	0.66
1:D:156:THR:H	1:D:159:MET:HE2	1.60	0.66
3:M:94:THR:HG21	3:M:125:LYS:HG3	1.78	0.65
1:D:327:GLU:O	1:D:331:VAL:HG22	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:223:LEU:HA	1:D:238:LEU:HD23	1.79	0.64
1:A:19:THR:HG23	3:J:78:GLU:HG3	1.79	0.64
3:M:114:LEU:HD13	3:M:119:PHE:HB2	1.80	0.63
1:D:24:LEU:O	1:D:69:TYR:OH	2.10	0.62
1:D:46:ARG:H	1:D:78:THR:HB	1.65	0.62
1:B:246:ARG:HH22	1:B:285:GLN:HG2	1.65	0.61
1:C:196:GLU:HG3	2:F:23:LYS:HE3	1.83	0.61
1:A:282:GLU:HA	1:A:285:GLN:HG3	1.83	0.61
1:D:99:GLY:O	1:D:133:ARG:NH1	2.33	0.61
1:C:118:THR:HG22	1:C:122:SER:H	1.66	0.60
1:C:130:PHE:HD2	1:C:160:ILE:HD11	1.66	0.60
1:C:257:GLY:O	1:C:272:THR:OG1	2.13	0.59
1:D:190:ALA:HA	1:D:193:PHE:HD2	1.67	0.59
1:A:14:GLU:OE1	1:A:16:LYS:NZ	2.36	0.59
3:J:91:ASP:OD1	3:J:125:LYS:NZ	2.35	0.59
1:B:18:LEU:HD12	3:K:78:GLU:HG2	1.84	0.58
3:K:94:THR:HA	3:K:97:ILE:HG12	1.85	0.58
3:M:71:LEU:HD12	3:M:74:ILE:HD11	1.85	0.58
1:B:199:HIS:HB3	1:B:202:ILE:HD13	1.84	0.58
1:C:18:LEU:HD12	1:C:18:LEU:H	1.69	0.58
1:D:174:LEU:HD23	1:D:209:TRP:HB2	1.86	0.58
1:C:269:ILE:O	1:C:272:THR:HG22	2.04	0.57
3:J:94:THR:HG21	3:J:125:LYS:HB3	1.85	0.57
1:D:60:LYS:HD3	3:M:113:THR:HG23	1.86	0.57
1:D:159:MET:HG2	1:D:190:ALA:HB2	1.86	0.57
3:M:80:LEU:HD22	3:M:88:LYS:HB2	1.85	0.57
1:D:135:ASP:N	1:D:135:ASP:OD1	2.38	0.57
1:D:117:THR:HG23	1:D:121:ASN:HA	1.87	0.57
2:I:25:CYS:HB3	2:I:27:HIS:CD2	2.40	0.57
1:D:213:ILE:HG13	1:D:222:PRO:HD2	1.85	0.57
1:B:51:ILE:HG22	1:B:91:ALA:HB2	1.86	0.57
1:D:146:ASN:H	1:D:146:ASN:HD22	1.52	0.56
1:A:329:LEU:HD23	1:A:347:ILE:HG12	1.86	0.56
1:D:225:VAL:HG22	2:I:24:TYR:HE2	1.70	0.56
1:C:156:THR:H	1:C:159:MET:HE3	1.71	0.56
1:C:41:GLN:HG2	1:C:46:ARG:HG2	1.88	0.56
1:D:201:ASP:OD1	1:D:201:ASP:N	2.38	0.56
1:A:76:THR:HG21	1:C:278:LEU:HD21	1.88	0.55
3:K:81:LEU:HD11	3:K:93:LEU:HD11	1.89	0.55
1:B:239:LEU:HD22	1:B:249:ARG:HG3	1.89	0.55
1:A:121:ASN:HB3	1:A:151:ASN:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:PHE:O	1:B:364:ILE:HG12	2.06	0.55
1:B:196:GLU:HG3	2:H:23:LYS:HD2	1.89	0.54
3:K:73:GLU:HB2	3:K:96:ALA:HB2	1.89	0.54
1:A:72:GLN:NE2	1:A:74:GLN:OE1	2.36	0.54
1:B:147:ILE:HD12	1:B:173:LEU:HD22	1.88	0.54
1:C:87:ASP:O	1:C:118:THR:OG1	2.25	0.54
1:D:241:HIS:ND1	1:D:243:ASP:HB2	2.22	0.53
1:D:40:SER:O	1:D:46:ARG:HA	2.08	0.53
1:D:151:ASN:ND2	2:I:19:ASN:OD1	2.42	0.53
1:D:21:ALA:HA	1:D:24:LEU:HB2	1.90	0.53
1:D:118:THR:HG22	1:D:119:VAL:H	1.73	0.53
1:C:66:LEU:HD21	1:C:107:LEU:HD23	1.90	0.53
1:C:135:ASP:OD1	1:C:135:ASP:N	2.40	0.53
1:D:101:PHE:HD1	1:D:136:ILE:HG13	1.74	0.53
1:D:24:LEU:HB3	1:D:69:TYR:CZ	2.44	0.52
1:D:121:ASN:HB3	1:D:151:ASN:HA	1.92	0.52
1:C:40:SER:O	1:C:46:ARG:HA	2.10	0.52
1:A:24:LEU:O	1:A:69:TYR:OH	2.24	0.52
1:A:162:ALA:HA	1:A:202:ILE:HD13	1.92	0.52
1:A:66:LEU:HD11	1:A:107:LEU:HD23	1.92	0.51
1:B:66:LEU:HD21	1:B:107:LEU:HD23	1.92	0.51
3:M:70:PHE:HE1	3:M:96:ALA:HB1	1.75	0.51
1:A:42:GLN:NE2	1:B:168:ASP:OD2	2.42	0.51
3:K:69:PHE:O	3:K:73:GLU:HG2	2.11	0.51
1:B:62:VAL:HG23	1:B:106:LEU:HD23	1.93	0.51
1:B:63:ARG:HB2	1:B:106:LEU:HD21	1.91	0.50
1:B:123:THR:HG23	1:B:126:ARG:H	1.76	0.50
1:D:62:VAL:HG13	1:D:106:LEU:HD23	1.92	0.50
1:D:45:GLN:OE1	1:D:80:ARG:NH1	2.45	0.50
2:I:25:CYS:HB3	2:I:27:HIS:HD2	1.76	0.50
2:F:17:THR:HG22	2:F:19:ASN:H	1.77	0.50
3:J:79:GLU:O	3:J:83:GLN:HG2	2.12	0.50
1:A:245:ASP:OD1	1:A:245:ASP:N	2.44	0.50
1:D:27:ARG:HG3	1:D:28:SER:H	1.76	0.50
1:D:147:ILE:HD11	1:D:178:ALA:HB2	1.93	0.50
1:B:268:ASP:O	1:B:272:THR:HG23	2.12	0.49
1:C:251:GLU:HG3	1:C:335:ILE:HD12	1.95	0.49
2:I:20:CYS:HB3	2:I:27:HIS:CD2	2.47	0.49
1:B:213:ILE:HD13	1:B:242:ALA:HB1	1.95	0.49
1:A:21:ALA:HB2	1:A:64:LEU:HD11	1.94	0.49
1:D:146:ASN:HD22	1:D:146:ASN:N	2.06	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:18:LEU:HD21	3:M:78:GLU:HB2	1.94	0.49
1:A:250:ILE:HG23	1:A:279:ALA:HB1	1.95	0.49
1:B:135:ASP:N	1:B:135:ASP:OD1	2.44	0.49
3:M:111:GLN:HG2	3:M:119:PHE:CE2	2.48	0.49
1:C:232:ALA:O	1:C:236[A]:GLU:HG2	2.12	0.49
1:D:321:ARG:HG2	1:D:325:HIS:CE1	2.48	0.49
1:D:258:ALA:HB1	1:D:332:ARG:HG3	1.95	0.48
1:D:296:LEU:HD11	1:D:334:ARG:HB2	1.93	0.48
1:B:117:THR:HB	1:B:121:ASN:HA	1.95	0.48
1:B:191:LEU:HD23	1:B:222:PRO:HG2	1.95	0.48
1:D:277:TYR:HD1	1:D:314:LEU:HD12	1.77	0.48
1:B:105:LYS:HA	1:B:139:TYR:CE2	2.48	0.48
1:B:269:ILE:O	1:B:272:THR:OG1	2.22	0.48
1:C:321:ARG:HG2	1:C:325:HIS:CE1	2.48	0.48
1:D:20:LEU:HD22	1:D:61:VAL:HG13	1.96	0.48
1:B:68:HIS:NE2	3:K:109:VAL:HG22	2.28	0.48
1:D:51:ILE:HG12	1:D:91:ALA:HB2	1.96	0.48
3:K:105:GLN:O	3:K:109:VAL:HG23	2.13	0.48
1:B:1:MET:HA	1:B:4:LEU:HD23	1.95	0.48
1:A:46:ARG:NH2	1:C:236[B]:GLU:OE1	2.41	0.48
1:C:125:LEU:HD21	1:C:147:ILE:HG22	1.96	0.47
1:A:135:ASP:OD1	1:A:135:ASP:N	2.46	0.47
1:C:123:THR:HG23	1:C:126:ARG:H	1.79	0.47
3:J:73:GLU:HB2	3:J:96:ALA:HB2	1.95	0.47
3:J:81:LEU:HD12	3:J:89:GLY:HA3	1.97	0.47
1:A:168:ASP:OD1	1:A:168:ASP:N	2.45	0.47
1:C:90:THR:HG23	1:C:93:TRP:H	1.79	0.47
1:B:65:LEU:HD12	1:B:71:VAL:HG21	1.97	0.47
1:B:118:THR:HG23	1:B:120:THR:H	1.79	0.47
1:D:269:ILE:O	1:D:272:THR:OG1	2.22	0.47
2:E:29:VAL:O	2:E:31:GLY:N	2.47	0.47
1:A:368:LEU:HD11	1:B:364:ILE:HD11	1.96	0.47
3:J:69:PHE:O	3:J:73:GLU:HG2	2.15	0.47
3:K:66:VAL:HG21	3:K:99:VAL:HG21	1.97	0.47
1:D:196:GLU:CD	2:I:23:LYS:HB2	2.35	0.46
1:D:268:ASP:O	1:D:272:THR:HG23	2.15	0.46
3:K:89:GLY:O	3:K:93:LEU:HG	2.14	0.46
1:C:277:TYR:CE2	1:C:281:LEU:HD11	2.50	0.46
1:D:27:ARG:HD2	1:D:27:ARG:HA	1.67	0.46
3:M:78:GLU:HA	3:M:81:LEU:HD12	1.97	0.46
3:M:93:LEU:HD23	3:M:122:LEU:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:ASP:OD1	1:C:233:ASP:N	2.47	0.46
1:C:287:GLY:HA2	1:C:290:ILE:HD11	1.98	0.46
1:C:156:THR:HG23	1:C:159:MET:H	1.80	0.46
1:D:293:LYS:HD2	1:D:309:ARG:HA	1.97	0.46
1:C:240:SER:HG	1:C:241:HIS:HD1	1.60	0.46
1:B:299:ILE:HG22	1:B:302:TYR:H	1.80	0.46
1:D:63:ARG:HA	1:D:106:LEU:HD21	1.97	0.46
1:D:134:LEU:HD22	1:D:168:ASP:HB3	1.98	0.46
1:B:14:GLU:OE1	1:B:16:LYS:NZ	2.48	0.45
1:A:25:LEU:HD21	3:J:100:CYS:SG	2.57	0.45
1:B:87:ASP:O	1:B:118:THR:OG1	2.34	0.45
3:M:107:LEU:O	3:M:111:GLN:HG3	2.16	0.45
3:M:76:LEU:O	3:M:80:LEU:HD12	2.17	0.45
1:A:246:ARG:O	1:A:250:ILE:HG12	2.16	0.45
1:D:158:LEU:HD12	1:D:178:ALA:HB1	1.99	0.45
1:B:49:PRO:HA	1:B:52:ILE:HG22	2.00	0.44
1:C:79:VAL:HG22	1:C:80:ARG:H	1.83	0.44
1:C:138:LYS:HG2	1:C:172:TYR:CE2	2.53	0.44
1:D:108:VAL:HG11	1:D:139:TYR:CE2	2.52	0.44
1:B:268:ASP:OD2	1:B:271:LYS:NZ	2.47	0.44
1:B:153:TYR:HB3	1:B:185:HIS:CD2	2.53	0.44
1:D:138:LYS:HG2	1:D:172:TYR:CZ	2.53	0.44
3:K:121:MET:O	3:K:125:LYS:HD3	2.18	0.44
1:D:9:TYR:HA	1:D:23:LEU:HD21	2.00	0.43
1:D:122:SER:HB2	1:D:126:ARG:HD3	2.00	0.43
1:D:24:LEU:HD21	1:D:36:LEU:HD21	1.99	0.43
1:C:49:PRO:HA	1:C:52:ILE:HD11	2.00	0.43
1:C:156:THR:HG22	1:C:159:MET:HG3	2.00	0.43
1:D:196:GLU:HG3	2:I:23:LYS:HD2	1.99	0.43
1:C:6:GLY:O	1:C:10:LYS:HG3	2.19	0.43
1:B:138:LYS:HG2	1:B:172:TYR:CZ	2.54	0.43
3:K:114:LEU:HD12	3:K:114:LEU:HA	1.90	0.43
3:M:105:GLN:HB3	3:M:106:LEU:H	1.54	0.43
1:D:310:ASN:HB2	1:D:311:PRO:HD2	2.01	0.43
1:C:150:ALA:HB1	1:C:154:ASP:HA	2.01	0.43
1:D:105:LYS:HG2	1:D:139:TYR:CZ	2.54	0.43
1:D:189:THR:HG22	1:D:191:LEU:H	1.84	0.43
1:A:200:ILE:O	1:A:204:LYS:HG3	2.19	0.43
3:K:79:GLU:O	3:K:83:GLN:HG2	2.19	0.43
1:A:34:TYR:HE1	1:C:241:HIS:CE1	2.37	0.42
1:B:120:THR:HG23	1:B:152:LYS:HE2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:174:LEU:HD13	1:C:209:TRP:CD1	2.55	0.42
1:C:166:HIS:O	1:C:170:VAL:HG23	2.18	0.42
1:B:277:TYR:CE2	1:B:281:LEU:HD11	2.55	0.42
1:D:79:VAL:HG11	1:D:94:CYS:SG	2.59	0.42
3:M:86:TYR:O	3:M:90:VAL:HG13	2.19	0.42
3:M:114:LEU:CD1	3:M:119:PHE:HB2	2.48	0.42
1:B:68:HIS:CD2	3:K:109:VAL:HG22	2.54	0.42
1:B:168:ASP:OD1	1:B:168:ASP:N	2.51	0.42
1:D:234:VAL:O	1:D:238:LEU:HD13	2.20	0.42
1:C:170:VAL:HG21	1:C:202:ILE:HD12	2.02	0.42
1:D:73:THR:HG21	1:D:111:GLY:O	2.20	0.42
1:A:147:ILE:HD12	1:A:178:ALA:HB2	2.02	0.41
1:B:105:LYS:HG2	1:B:139:TYR:CZ	2.55	0.41
1:D:191:LEU:HD23	1:D:222:PRO:HG2	2.02	0.41
1:C:349:TYR:O	1:C:353:VAL:HG13	2.20	0.41
1:D:158:LEU:HD21	1:D:174:LEU:HD11	2.01	0.41
1:D:193:PHE:CD1	2:I:21:ASN:HB2	2.55	0.41
3:M:70:PHE:CE1	3:M:100:CYS:HB3	2.55	0.41
1:C:25:LEU:O	1:C:27:ARG:HG2	2.20	0.41
1:D:296:LEU:HD12	1:D:296:LEU:H	1.85	0.41
2:I:22:CYS:HB3	2:I:25:CYS:SG	2.61	0.41
1:A:118:THR:HG22	1:A:119:VAL:N	2.36	0.41
1:A:364:ILE:HG23	1:B:367:TRP:HE3	1.85	0.41
1:D:125:LEU:HD11	1:D:141:VAL:HG23	2.02	0.41
1:D:332:ARG:HH12	1:D:343:VAL:HG22	1.86	0.41
3:J:126:LEU:HG	3:J:127:PRO:HD3	2.02	0.41
1:A:51:ILE:HG22	1:A:91:ALA:HB2	2.02	0.41
1:C:113:ASN:HB3	1:C:116:HIS:HB2	2.02	0.41
1:D:73:THR:HG23	1:D:74:GLN:HG2	2.01	0.41
1:D:105:LYS:HG2	1:D:139:TYR:CE2	2.56	0.41
1:A:329:LEU:HD21	1:A:347:ILE:HA	2.02	0.41
1:C:114:VAL:HG23	1:C:140:LEU:HD22	2.03	0.41
1:B:167:THR:O	1:B:170:VAL:HG22	2.21	0.41
1:D:134:LEU:HA	1:D:137:VAL:HG12	2.03	0.41
3:J:68:LYS:HD3	3:J:68:LYS:HA	1.81	0.41
1:A:325:HIS:O	1:A:329:LEU:HD12	2.21	0.40
1:C:307:GLU:HB2	1:C:330:ILE:HG21	2.02	0.40
1:D:226:ALA:HB1	1:D:234:VAL:HG23	2.04	0.40
3:K:116:PRO:N	3:K:117:PRO:HD2	2.36	0.40
2:I:18:PRO:HB2	2:I:19:ASN:H	1.64	0.40
1:A:29:GLU:HA	1:A:32:ILE:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:PHE:CD1	5:A:402:EPE:H52	2.56	0.40
1:D:231:LYS:O	1:D:235:VAL:HG23	2.22	0.40
3:J:95:ASN:O	3:J:99:VAL:HG23	2.22	0.40
1:A:125:LEU:HD21	1:A:147:ILE:HG22	2.04	0.40
1:D:146:ASN:ND2	1:D:146:ASN:O	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	375/381 (98%)	357 (95%)	18 (5%)	0	100 100
1	B	374/381 (98%)	354 (95%)	20 (5%)	0	100 100
1	C	376/381 (99%)	357 (95%)	19 (5%)	0	100 100
1	D	372/381 (98%)	343 (92%)	25 (7%)	4 (1%)	12 44
2	E	15/31 (48%)	12 (80%)	1 (7%)	2 (13%)	0 1
2	F	15/31 (48%)	14 (93%)	1 (7%)	0	100 100
2	H	10/31 (32%)	10 (100%)	0	0	100 100
2	I	9/31 (29%)	8 (89%)	1 (11%)	0	100 100
3	J	64/66 (97%)	60 (94%)	4 (6%)	0	100 100
3	K	61/66 (92%)	58 (95%)	3 (5%)	0	100 100
3	M	56/66 (85%)	53 (95%)	2 (4%)	1 (2%)	7 35
All	All	1727/1846 (94%)	1626 (94%)	94 (5%)	7 (0%)	30 64

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	177	ARG

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Mol	Chain	Res	Type
2	E	30	LEU
3	M	106	LEU
1	D	4	LEU
2	E	29	VAL
1	D	82	ASP
1	D	295	VAL

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	305/309 (99%)	304 (100%)	1 (0%)	91 96
1	B	305/309 (99%)	302 (99%)	3 (1%)	73 87
1	C	306/309 (99%)	301 (98%)	5 (2%)	58 79
1	D	304/309 (98%)	289 (95%)	15 (5%)	21 54
2	E	16/29 (55%)	16 (100%)	0	100 100
2	F	16/29 (55%)	16 (100%)	0	100 100
2	H	12/29 (41%)	12 (100%)	0	100 100
2	I	11/29 (38%)	11 (100%)	0	100 100
3	J	57/57 (100%)	57 (100%)	0	100 100
3	K	55/57 (96%)	52 (94%)	3 (6%)	18 51
3	M	53/57 (93%)	48 (91%)	5 (9%)	7 28
All	All	1440/1523 (95%)	1408 (98%)	32 (2%)	47 73

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	C	18	LEU
1	C	52	ILE
1	C	123	THR
1	C	233	ASP

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Mol	Chain	Res	Type
1	C	272	THR
1	B	48	THR
1	B	189	THR
1	B	225	VAL
1	D	9	TYR
1	D	25	LEU
1	D	41	GLN
1	D	51	ILE
1	D	76	THR
1	D	114	VAL
1	D	123	THR
1	D	144	ASN
1	D	146	ASN
1	D	238	LEU
1	D	243	ASP
1	D	296	LEU
1	D	299	ILE
1	D	314	LEU
1	D	331	VAL
3	K	66	VAL
3	K	92	HIS
3	K	94	THR
3	M	80	LEU
3	M	93	LEU
3	M	100	CYS
3	M	106	LEU
3	M	114	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	146	ASN

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	$\#\|Z\| > 2$
5	EPE	A	402	-	15,15,15	0.82	1 (6%)	19,20,20	1.78	3 (15%)
7	SO4	B	402	-	4,4,4	0.23	0	6,6,6	0.09	0
6	PO4	A	403	-	4,4,4	1.01	0	6,6,6	0.43	0
7	SO4	C	402	-	4,4,4	0.24	0	6,6,6	0.06	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
5	EPE	A	402	-	-	4/9/19/19	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	402	EPE	C10-S	2.79	1.81	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	402	EPE	C5-N4-C3	5.59	120.88	108.84
5	A	402	EPE	C7-N4-C5	2.95	119.09	111.24
5	A	402	EPE	C7-N4-C3	2.15	116.96	111.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	402	EPE	C8-C7-N4-C5
5	A	402	EPE	C9-C10-S-O1S
5	A	402	EPE	C9-C10-S-O2S
5	A	402	EPE	C9-C10-S-O3S

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	402	EPE	1	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%)	-0.54	0 100 100	56, 74, 97, 113	0
1	B	376/381 (98%)	-0.41	0 100 100	68, 87, 115, 138	0
1	C	377/381 (98%)	-0.49	1 (0%) 90 84	44, 77, 101, 126	1 (0%)
1	D	374/381 (98%)	0.06	7 (1%) 66 50	68, 109, 149, 166	0
2	E	17/31 (54%)	-0.35	0 100 100	73, 89, 118, 123	0
2	F	17/31 (54%)	-0.26	0 100 100	73, 88, 110, 115	0
2	H	12/31 (38%)	-0.27	0 100 100	96, 102, 109, 112	0
2	I	11/31 (35%)	-0.10	0 100 100	105, 116, 121, 124	0
3	J	66/66 (100%)	-0.25	0 100 100	98, 116, 137, 143	0
3	K	63/66 (95%)	-0.12	0 100 100	123, 145, 160, 164	0
3	M	60/66 (90%)	0.25	1 (1%) 69 53	151, 170, 180, 185	0
All	All	1750/1846 (94%)	-0.31	9 (0%) 87 78	44, 87, 151, 185	1 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	236[A]	GLU	2.9
1	D	65	LEU	2.3
1	D	21	ALA	2.3
3	M	118	VAL	2.3
1	D	81	PHE	2.2
1	D	32	ILE	2.1
1	D	128	ALA	2.1
1	D	86	ILE	2.0
1	D	36	LEU	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 monosaccharides in this entry.

6.4 Ligands (i)

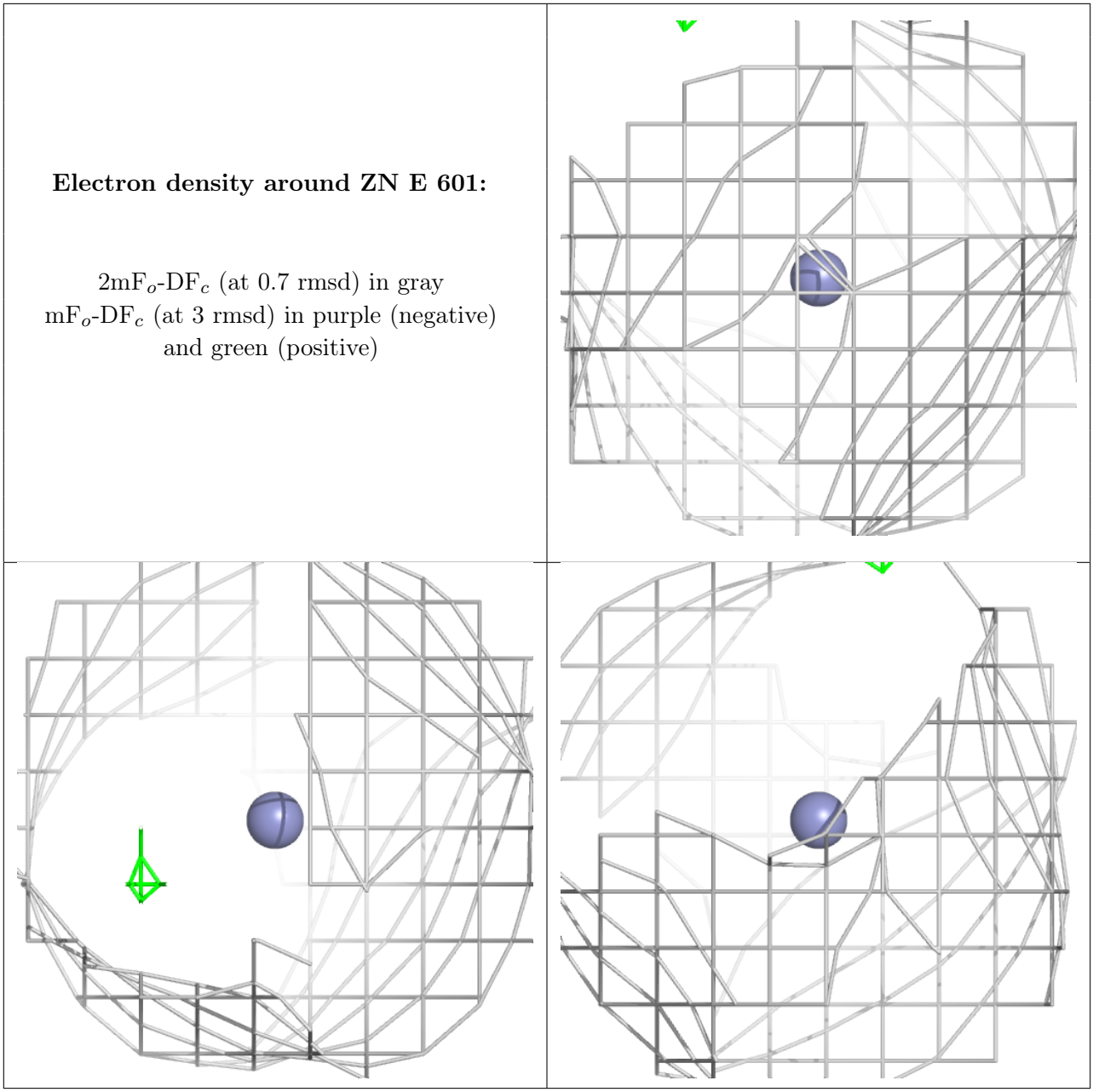
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
5	EPE	A	402	15/15	0.73	0.16	88,96,105,117	0
7	SO4	B	402	5/5	0.83	0.18	105,106,123,127	0
6	PO4	A	403	5/5	0.86	0.10	111,111,114,181	0
7	SO4	C	402	5/5	0.92	0.13	89,92,110,119	0
4	ZN	E	601	1/1	0.97	0.03	62,62,62,62	0
4	ZN	I	601	1/1	0.97	0.04	119,119,119,119	0
4	ZN	H	601	1/1	0.98	0.04	94,94,94,94	0
4	ZN	D	401	1/1	0.98	0.04	119,119,119,119	0
4	ZN	A	401	1/1	0.99	0.03	68,68,68,68	0
4	ZN	B	401	1/1	0.99	0.03	94,94,94,94	0
4	ZN	F	601	1/1	0.99	0.03	68,68,68,68	0
4	ZN	C	401	1/1	1.00	0.01	62,62,62,62	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.

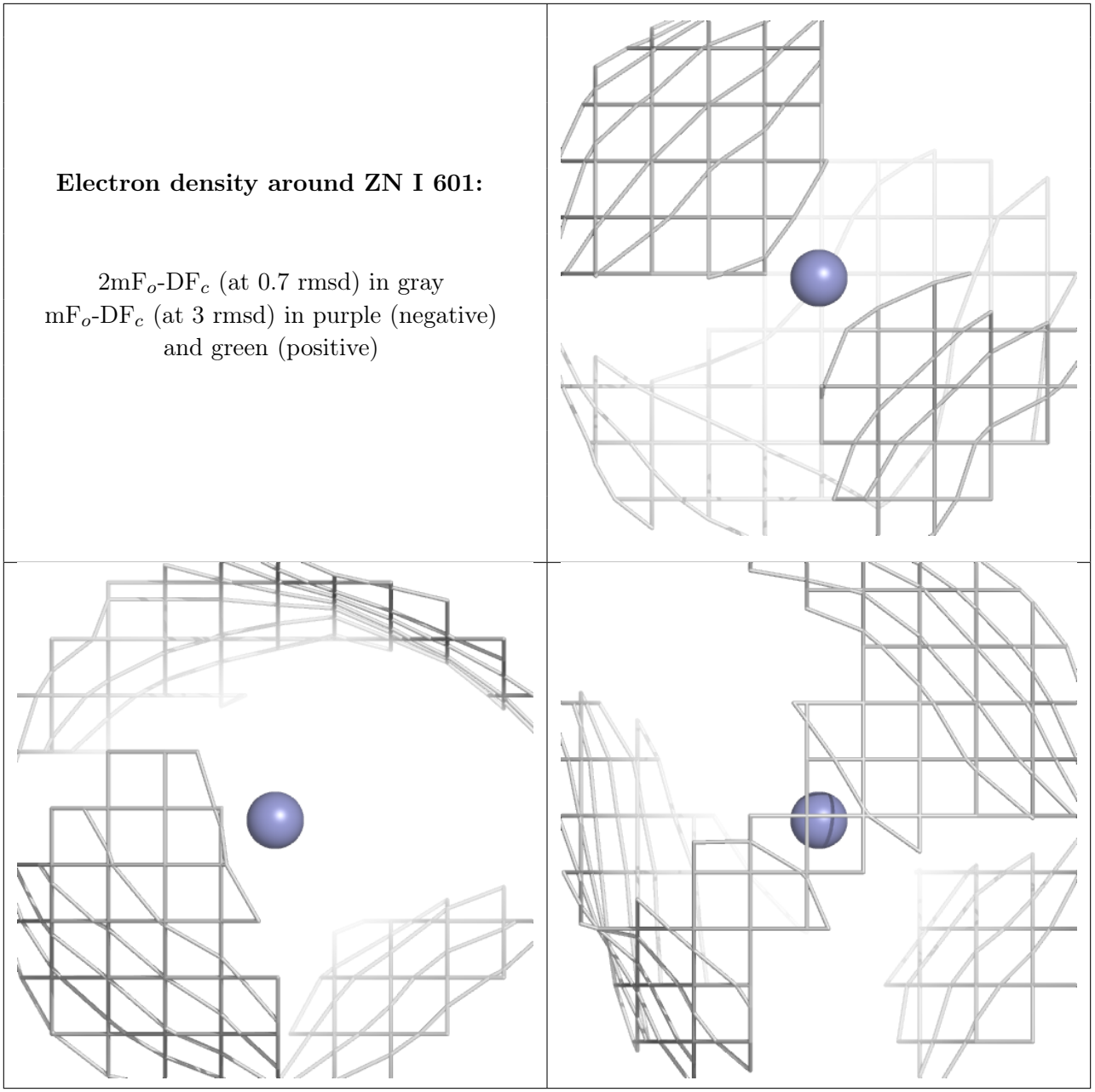
Electron density around ZN E 601:

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



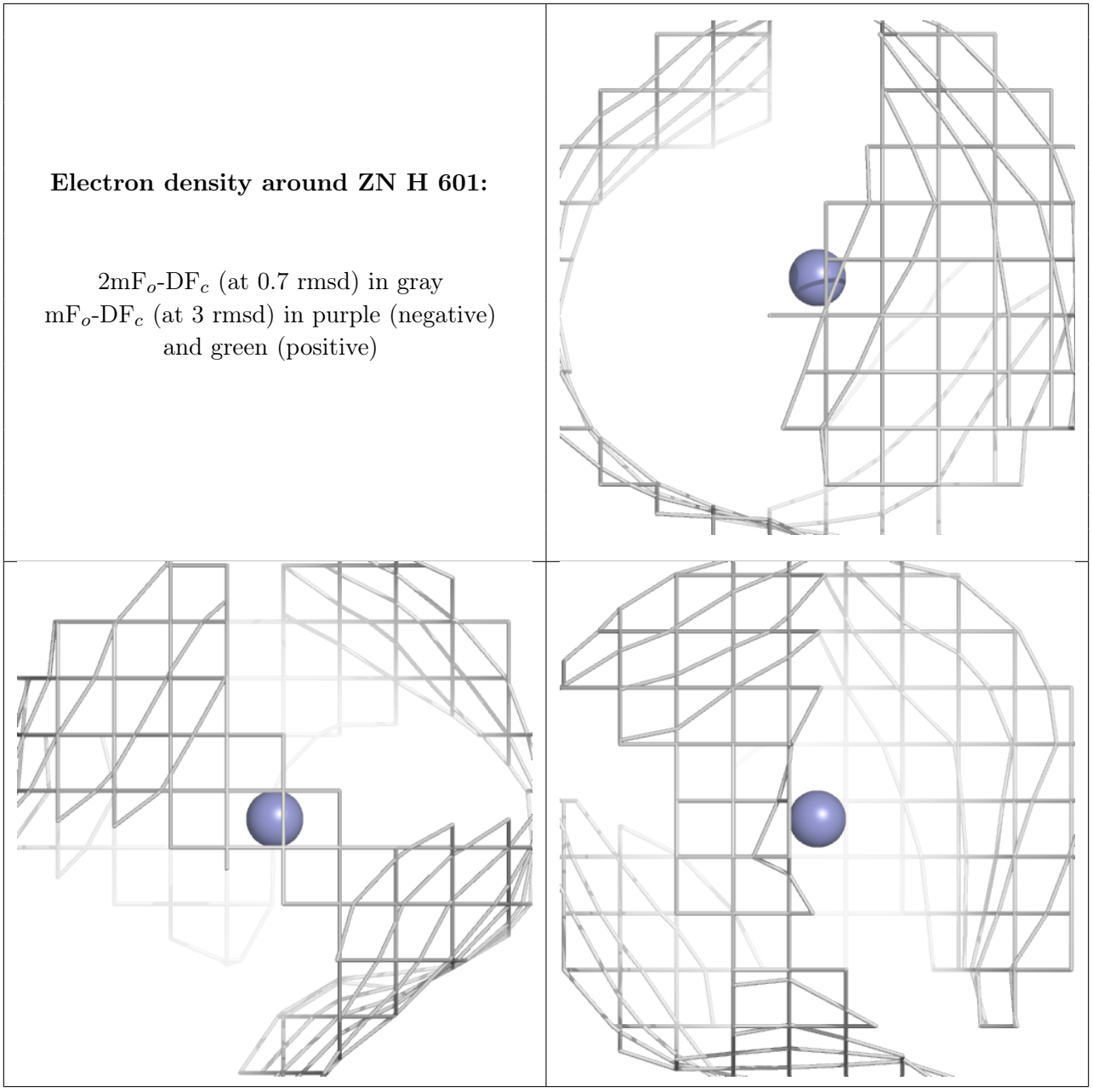
Electron density around ZN I 601:

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



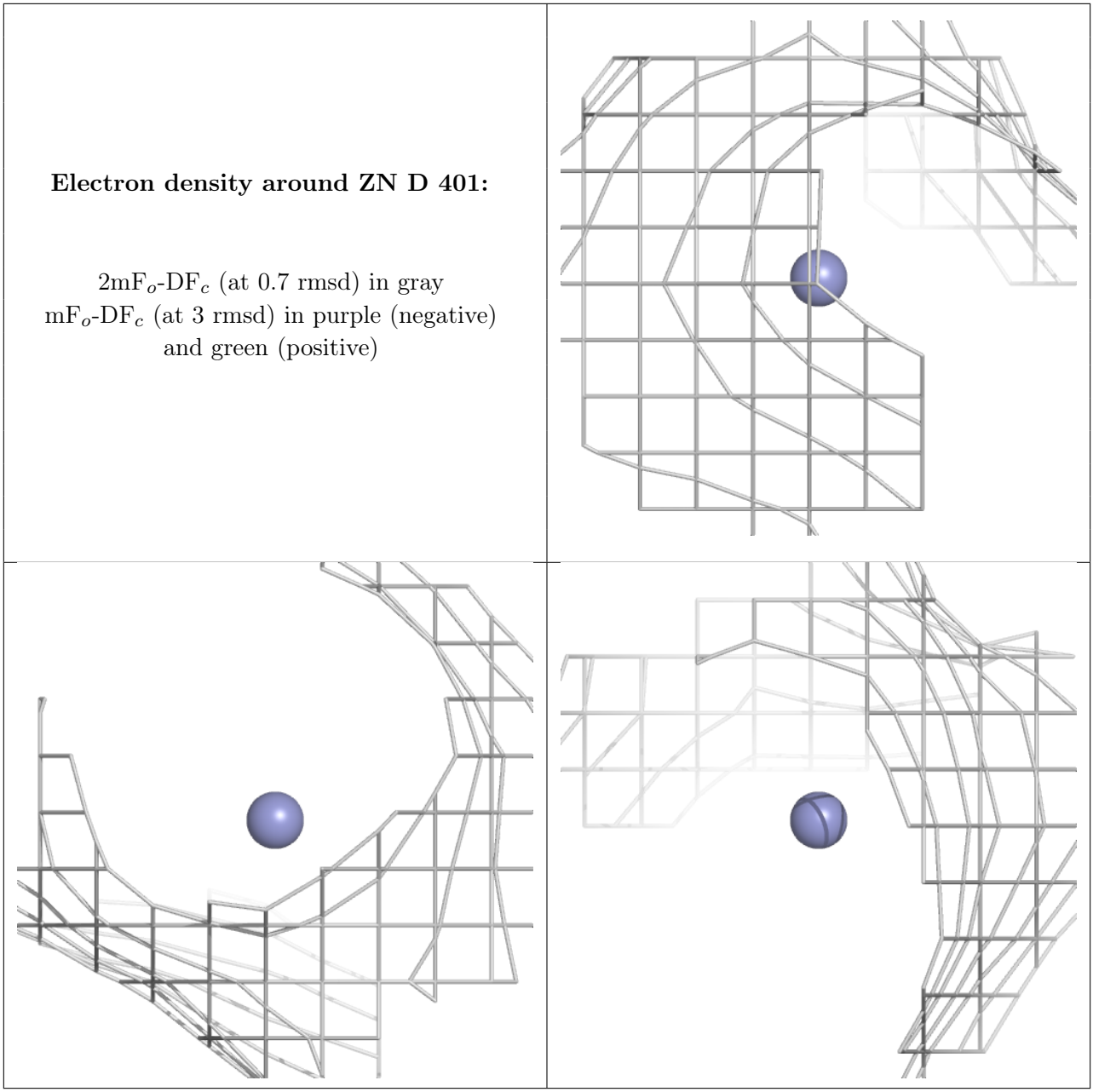
Electron density around ZN H 601:

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



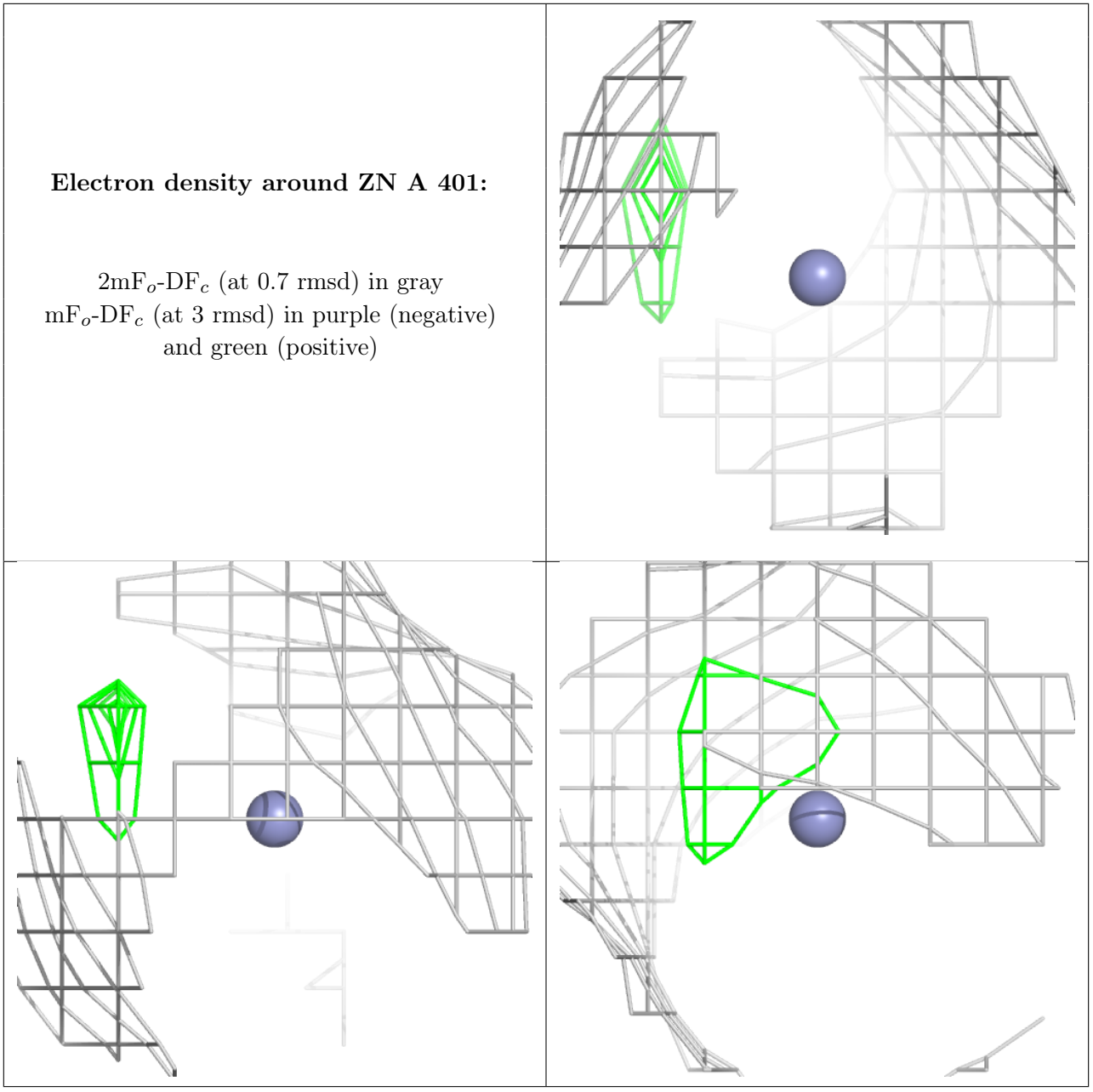
Electron density around ZN D 401:

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



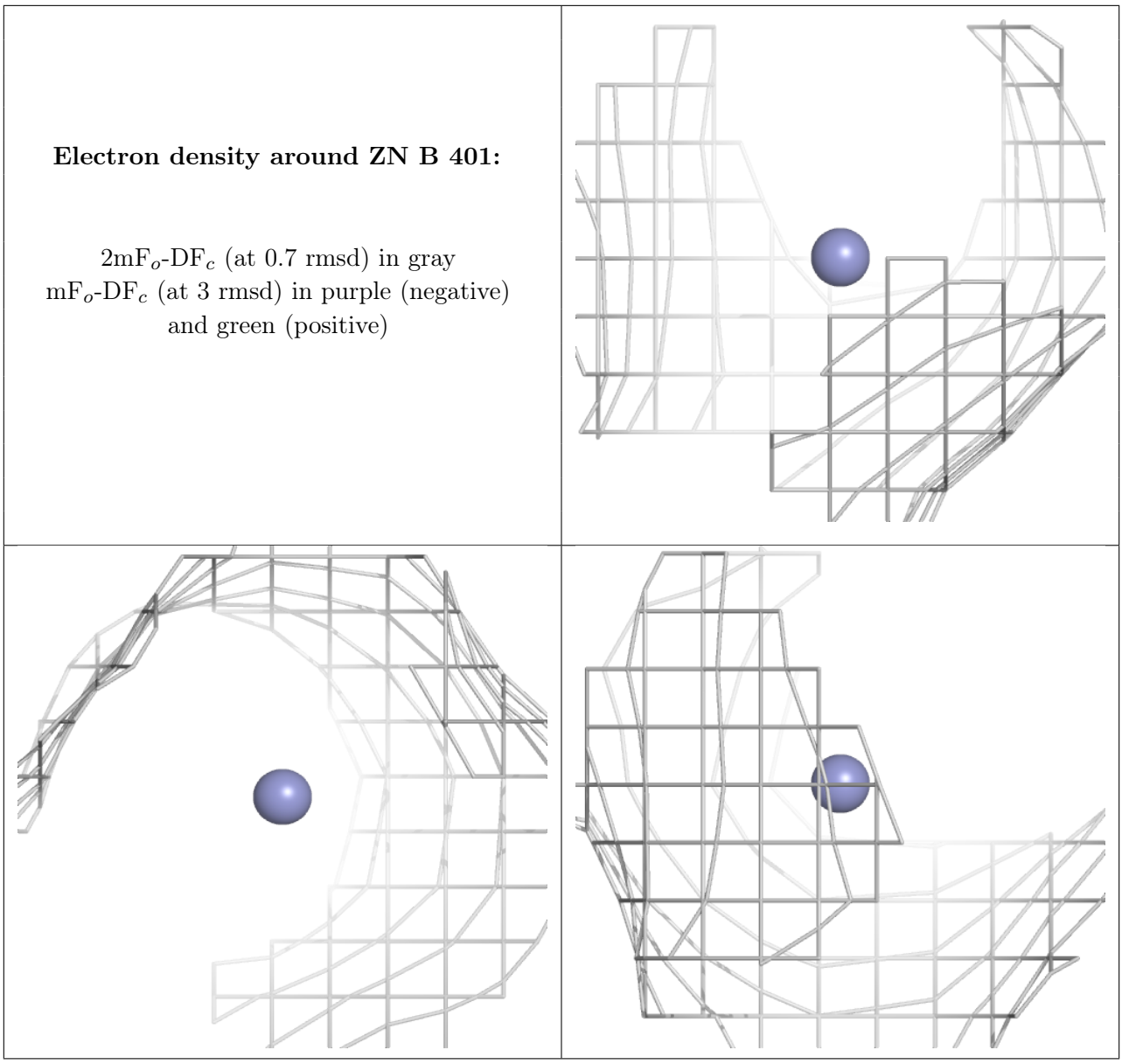
Electron density around ZN A 401:

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



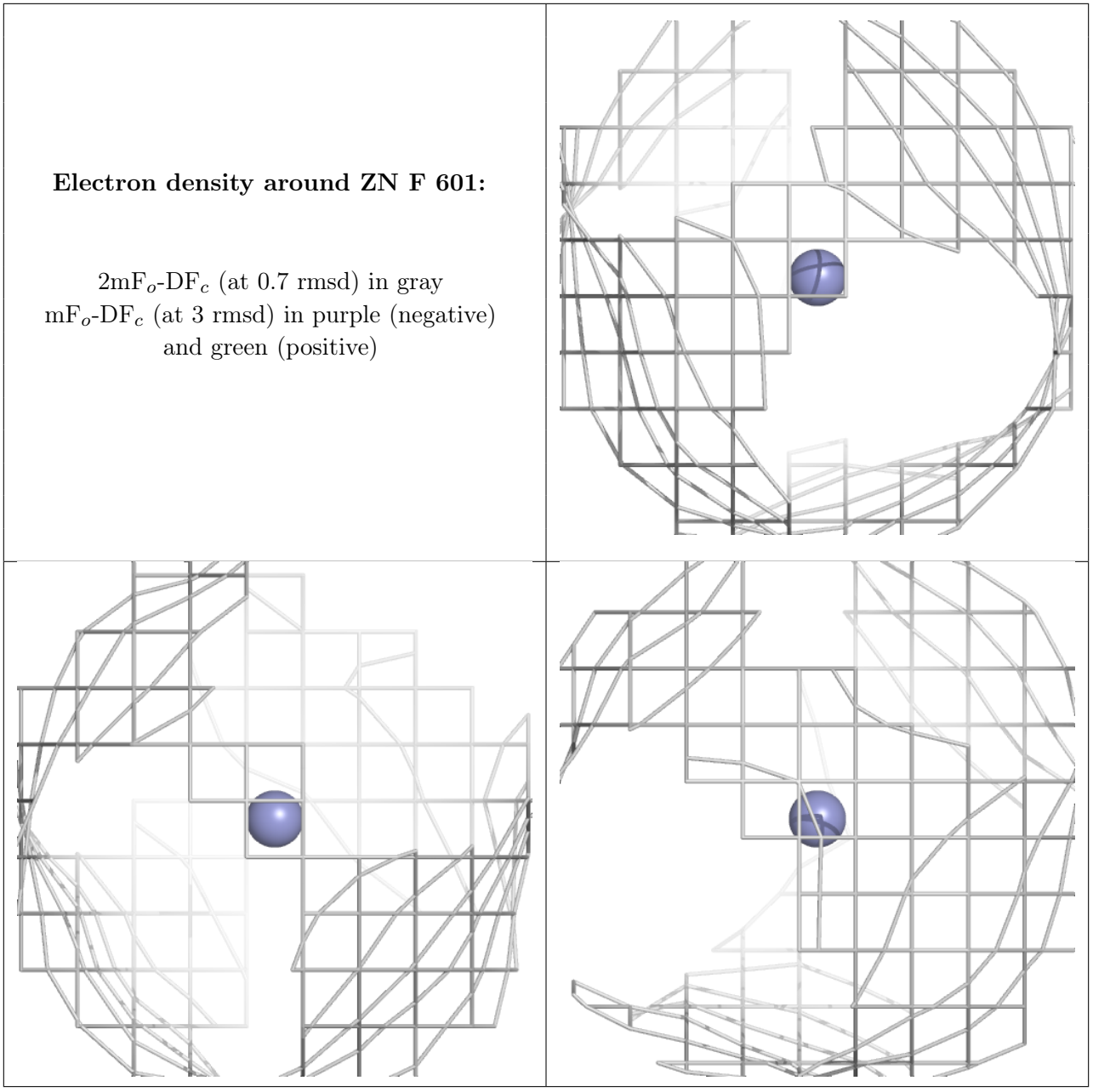
Electron density around ZN B 401:

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



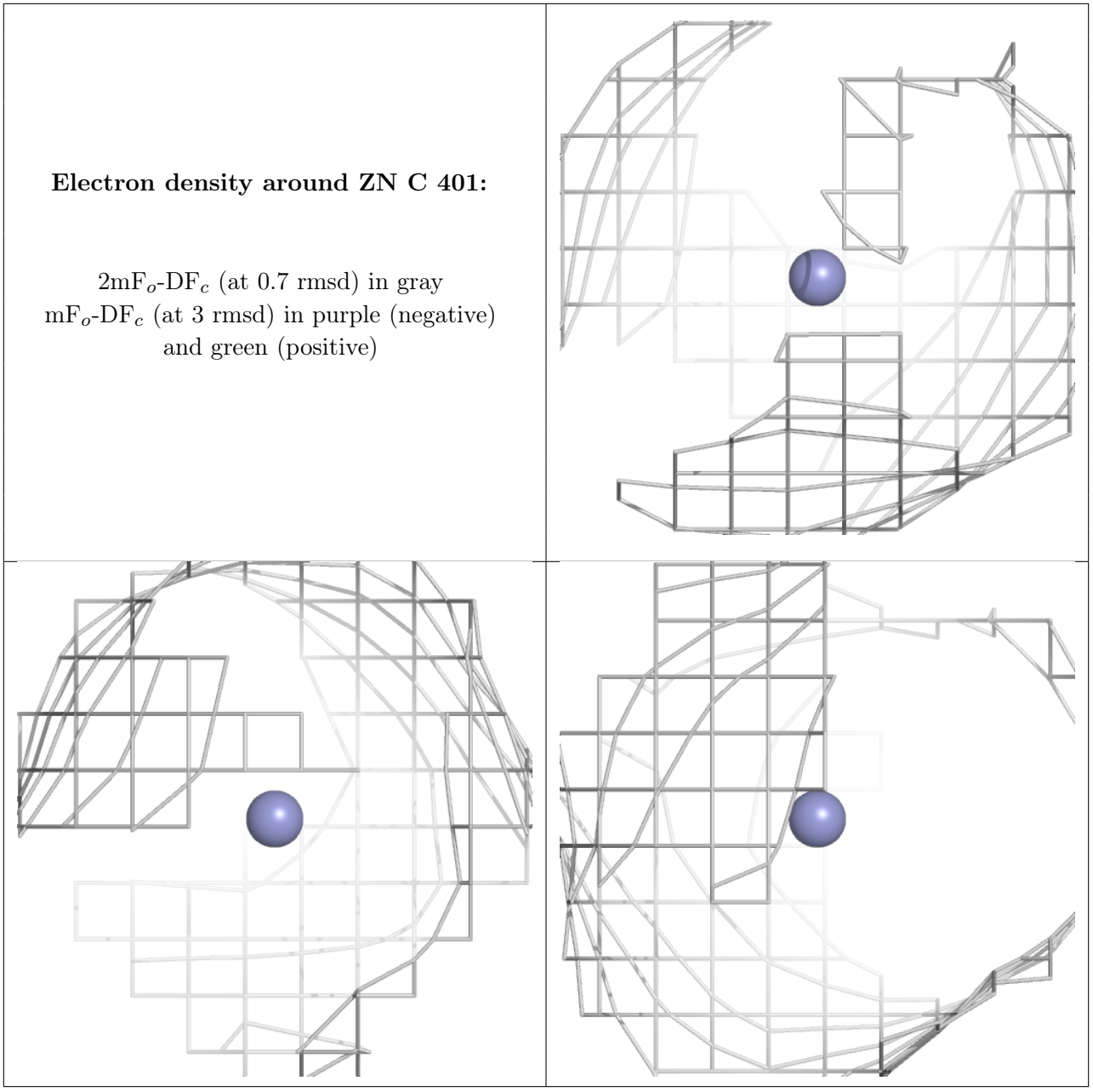
Electron density around ZN F 601:

$2mF_o$-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 401:

$2mF_o$-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.