



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 03:36 AM JST

PDB ID : 6KP1
Title : Crystal structure of two domain M1 zinc metallopeptidase E323A mutant bound to L-methionine amino acid
Authors : Agrawal, R.; Kumar, A.; Kumar, A.; Makde, R.D.
Deposited on : 2019-08-13
Resolution : 2.19 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

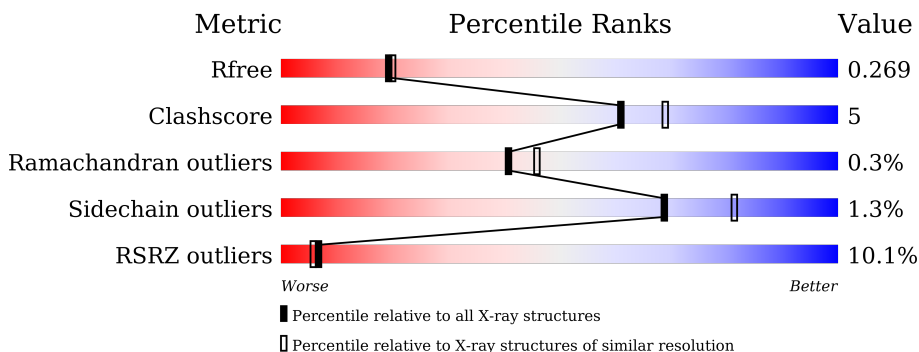
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 $\leq 5\%$. 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	474	 7% 81% 11% 8%
1	B	474	 12% 80% 12% 9%

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 7006 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 Zinc metalloprotease, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	434	3297	2095	582	616	4	0	0	0
1	B	433	3289	2092	579	614	4	0	1	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP Q9RVZ5
A	0	ALA	-	expression tag	UNP Q9RVZ5
A	1	SER	-	expression tag	UNP Q9RVZ5
A	2	TRP	-	expression tag	UNP Q9RVZ5
A	3	SER	-	expression tag	UNP Q9RVZ5
A	4	HIS	-	expression tag	UNP Q9RVZ5
A	5	PRO	-	expression tag	UNP Q9RVZ5
A	6	GLN	-	expression tag	UNP Q9RVZ5
A	7	PHE	-	expression tag	UNP Q9RVZ5
A	8	GLU	-	expression tag	UNP Q9RVZ5
A	9	LYS	-	expression tag	UNP Q9RVZ5
A	10	GLY	-	expression tag	UNP Q9RVZ5
A	11	SER	-	expression tag	UNP Q9RVZ5
A	12	SER	-	expression tag	UNP Q9RVZ5
A	13	HIS	-	expression tag	UNP Q9RVZ5
A	14	HIS	-	expression tag	UNP Q9RVZ5
A	15	HIS	-	expression tag	UNP Q9RVZ5
A	16	HIS	-	expression tag	UNP Q9RVZ5
A	17	HIS	-	expression tag	UNP Q9RVZ5
A	18	HIS	-	expression tag	UNP Q9RVZ5
A	19	SER	-	expression tag	UNP Q9RVZ5
A	20	SER	-	expression tag	UNP Q9RVZ5
A	21	GLY	-	expression tag	UNP Q9RVZ5
A	22	SER	-	expression tag	UNP Q9RVZ5
A	23	GLY	-	expression tag	UNP Q9RVZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	expression tag	UNP Q9RVZ5
A	25	GLY	-	expression tag	UNP Q9RVZ5
A	26	GLY	-	expression tag	UNP Q9RVZ5
A	27	GLY	-	expression tag	UNP Q9RVZ5
A	28	GLU	-	expression tag	UNP Q9RVZ5
A	29	ASN	-	expression tag	UNP Q9RVZ5
A	30	LEU	-	expression tag	UNP Q9RVZ5
A	31	TYR	-	expression tag	UNP Q9RVZ5
A	32	PHE	-	expression tag	UNP Q9RVZ5
A	33	GLN	-	expression tag	UNP Q9RVZ5
A	34	GLY	-	expression tag	UNP Q9RVZ5
A	35	SER	-	expression tag	UNP Q9RVZ5
A	323	ALA	GLU	engineered mutation	UNP Q9RVZ5
B	-1	MET	-	initiating methionine	UNP Q9RVZ5
B	0	ALA	-	expression tag	UNP Q9RVZ5
B	1	SER	-	expression tag	UNP Q9RVZ5
B	2	TRP	-	expression tag	UNP Q9RVZ5
B	3	SER	-	expression tag	UNP Q9RVZ5
B	4	HIS	-	expression tag	UNP Q9RVZ5
B	5	PRO	-	expression tag	UNP Q9RVZ5
B	6	GLN	-	expression tag	UNP Q9RVZ5
B	7	PHE	-	expression tag	UNP Q9RVZ5
B	8	GLU	-	expression tag	UNP Q9RVZ5
B	9	LYS	-	expression tag	UNP Q9RVZ5
B	10	GLY	-	expression tag	UNP Q9RVZ5
B	11	SER	-	expression tag	UNP Q9RVZ5
B	12	SER	-	expression tag	UNP Q9RVZ5
B	13	HIS	-	expression tag	UNP Q9RVZ5
B	14	HIS	-	expression tag	UNP Q9RVZ5
B	15	HIS	-	expression tag	UNP Q9RVZ5
B	16	HIS	-	expression tag	UNP Q9RVZ5
B	17	HIS	-	expression tag	UNP Q9RVZ5
B	18	HIS	-	expression tag	UNP Q9RVZ5
B	19	SER	-	expression tag	UNP Q9RVZ5
B	20	SER	-	expression tag	UNP Q9RVZ5
B	21	GLY	-	expression tag	UNP Q9RVZ5
B	22	SER	-	expression tag	UNP Q9RVZ5
B	23	GLY	-	expression tag	UNP Q9RVZ5
B	24	GLY	-	expression tag	UNP Q9RVZ5
B	25	GLY	-	expression tag	UNP Q9RVZ5
B	26	GLY	-	expression tag	UNP Q9RVZ5
B	27	GLY	-	expression tag	UNP Q9RVZ5

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Chain	Residue	Modelled	Actual	Comment	Reference
B	28	GLU	-	expression tag	UNP Q9RVZ5
B	29	ASN	-	expression tag	UNP Q9RVZ5
B	30	LEU	-	expression tag	UNP Q9RVZ5
B	31	TYR	-	expression tag	UNP Q9RVZ5
B	32	PHE	-	expression tag	UNP Q9RVZ5
B	33	GLN	-	expression tag	UNP Q9RVZ5
B	34	GLY	-	expression tag	UNP Q9RVZ5
B	35	SER	-	expression tag	UNP Q9RVZ5
B	323	ALA	GLU	engineered mutation	UNP Q9RVZ5

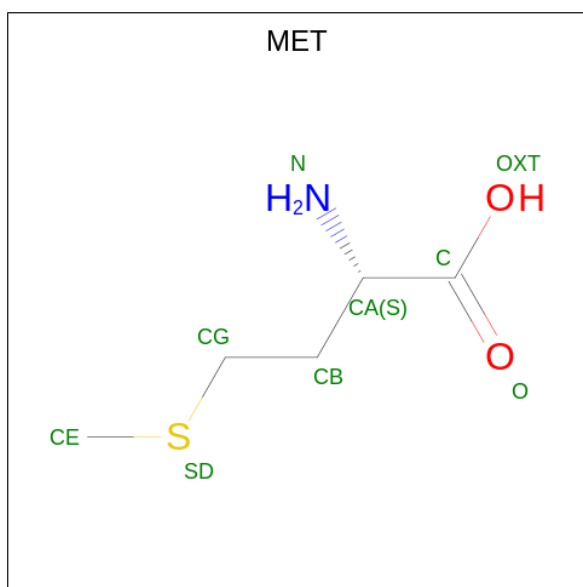
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 4 is METHIONINE (three-letter code: MET) (formula: C₅H₁₁NO₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
4	A	1	9	5	1	2	1	0	0
4	B	1	9	5	1	2	1	0	0

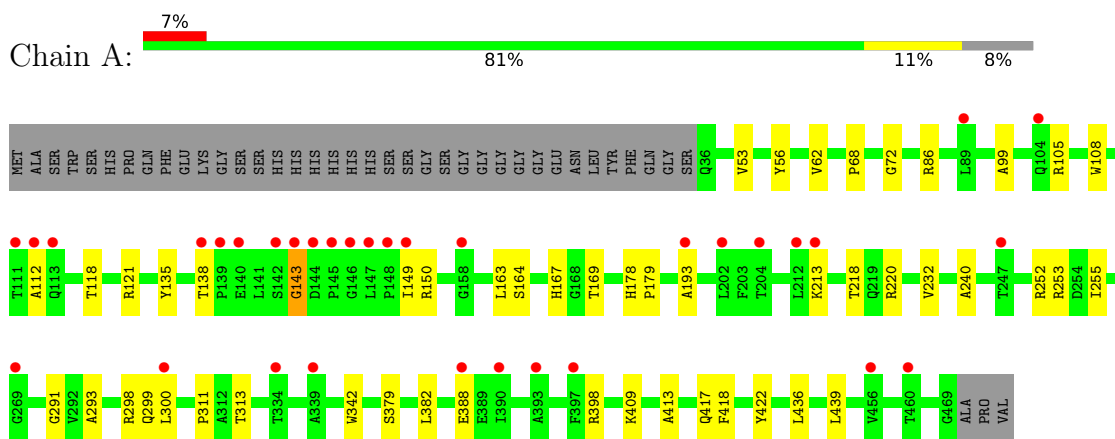
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	212	212	212	0	0
5	B	185	186	186	0	1

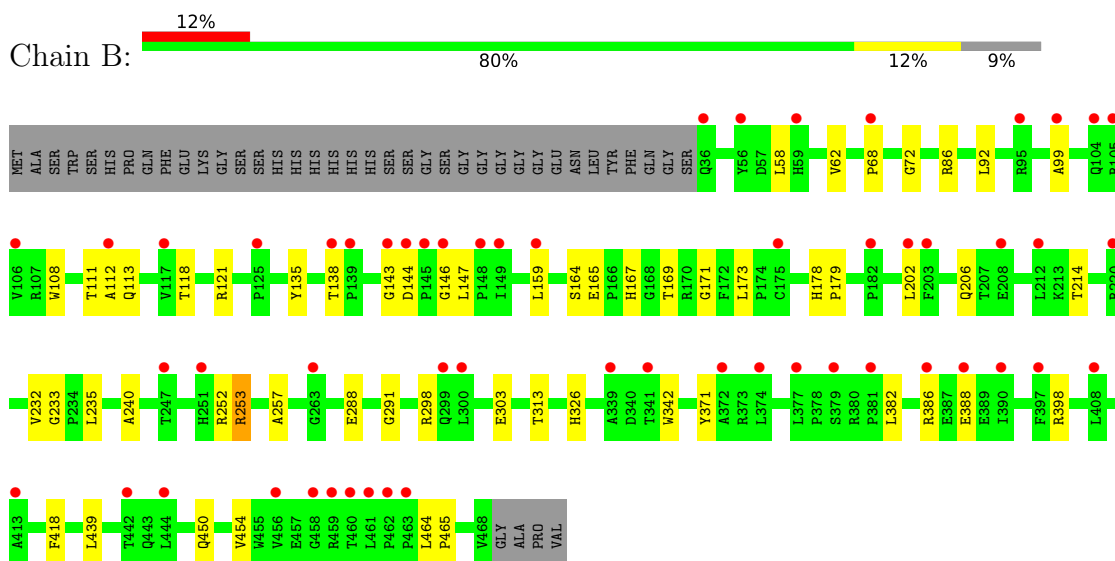
3 Residue-property plots [i](#)

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: Zinc metalloprotease, putative



- Molecule 1: Zinc metalloprotease, putative



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.81Å 57.50Å 69.44Å 89.92° 82.48° 67.83°	Depositor
Resolution (Å)	21.45 – 2.19 47.50 – 2.19	Depositor EDS
% Data completeness (in resolution range)	97.3 (21.45-2.19) 97.3 (47.50-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.20Å)	Xtrriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.218 , 0.270 0.218 , 0.269	Depositor DCC
R_{free} test set	1775 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	19.9	Xtrriage
Anisotropy	0.704	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7006	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.66% 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, NA

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	0.26	0/3385	0.47	0/4642
1	B	0.25	0/3379	0.47	0/4633
All	All	0.26	0/6764	0.47	0/9275

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3297	0	3231	29	0
1	B	3289	0	3219	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	9	0	8	1	0
4	B	9	0	8	1	0
5	A	212	0	0	0	0
5	B	186	0	0	1	0
All	All	7006	0	6466	59	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 5.

All (59) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:ALA:HA	1:A:213:LYS:HG3	1.67	0.76
1:B:86:ARG:HG2	1:B:118:THR:HA	1.70	0.73
1:B:165:GLU:OE1	4:B:503:MET:N	2.26	0.68
1:A:99:ALA:H	1:A:105:ARG:NH1	1.95	0.64
1:B:58:LEU:HD22	1:B:173:LEU:HD13	1.81	0.62
1:A:149:ILE:HG12	1:A:163:LEU:HD23	1.82	0.62
1:A:413:ALA:O	1:A:417:GLN:HG3	2.01	0.60
1:A:62:VAL:HG11	1:A:232:VAL:HG21	1.86	0.58
1:A:253:ARG:O	1:A:291:GLY:HA3	2.04	0.57
1:A:240:ALA:HB3	1:A:252:ARG:HB3	1.86	0.57
1:B:240:ALA:HB3	1:B:252:ARG:HB3	1.87	0.55
1:A:298:ARG:HG3	1:A:313:THR:HG21	1.88	0.54
1:A:143:GLY:HA2	1:A:150:ARG:HA	1.90	0.53
1:A:99:ALA:H	1:A:105:ARG:HH12	1.57	0.53
1:B:146:GLY:HA3	1:B:388:GLU:HG3	1.91	0.52
1:B:62:VAL:HG11	1:B:232:VAL:HG21	1.90	0.52
1:B:298:ARG:HG3	1:B:313:THR:HG21	1.91	0.51
1:B:99:ALA:HB3	1:B:108:TRP:CD1	2.45	0.51
1:B:143:GLY:HA2	1:B:147:LEU:HD12	1.94	0.50
1:B:382:LEU:HD21	1:B:398:ARG:HG2	1.94	0.50
1:A:382:LEU:HD21	1:A:398:ARG:HG2	1.95	0.49
1:B:450:GLN:O	1:B:454:VAL:HG23	2.13	0.49
1:A:164:SER:HB3	1:A:169:THR:N	2.29	0.48
1:A:68:PRO:HB2	1:A:138:THR:HG23	1.95	0.47
1:B:253:ARG:O	1:B:291:GLY:HA3	2.15	0.46
1:A:218:THR:HG22	1:A:220:ARG:HG2	1.98	0.45
1:A:342:TRP:CD1	1:A:382:LEU:HB3	2.52	0.44
1:B:202:LEU:HD21	1:B:288:GLU:HB2	2.00	0.44
1:B:235:LEU:HA	1:B:257:ALA:HA	1.99	0.44
1:A:99:ALA:HB3	1:A:108:TRP:CD1	2.52	0.44
1:B:303:GLU:HG3	1:B:326:HIS:HB3	2.00	0.44
1:B:464:LEU:HD12	1:B:465:PRO:HD2	1.99	0.44
1:B:388:GLU:H	1:B:388:GLU:CD	2.21	0.43
1:B:342:TRP:CD1	1:B:382:LEU:HB3	2.53	0.43
1:A:72:GLY:HA3	1:A:135:TYR:CZ	2.53	0.43
1:A:342:TRP:CD2	1:A:382:LEU:HD13	2.54	0.43
1:B:68:PRO:HB2	1:B:138:THR:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:GLY:HA3	5:B:716:HOH:O	2.19	0.43
1:A:149:ILE:HD13	1:A:299:GLN:NE2	2.34	0.43
1:A:255:ILE:HB	1:A:293:ALA:HA	2.01	0.42
1:A:299:GLN:HB3	1:A:311:PRO:HG2	1.99	0.42
1:B:111:THR:O	1:B:113:GLN:N	2.52	0.42
1:A:300:LEU:HD22	4:A:503:MET:HE2	2.02	0.42
1:A:418:PHE:CE1	1:A:439:LEU:HG	2.55	0.42
1:B:159:LEU:HD23	1:B:233:GLY:HA3	2.02	0.42
1:B:92:LEU:HD13	1:B:113:GLN:OE1	2.20	0.42
1:B:178:HIS:CG	1:B:179:PRO:HD2	2.55	0.41
1:A:178:HIS:CG	1:A:179:PRO:HD2	2.55	0.41
1:B:371:TYR:HB2	1:B:464:LEU:HD13	2.01	0.41
1:A:53:VAL:HG11	1:A:56:TYR:CZ	2.55	0.41
1:A:86:ARG:HG2	1:A:118:THR:HA	2.03	0.41
1:A:388:GLU:H	1:A:388:GLU:CD	2.24	0.41
1:A:422:TYR:CE1	1:A:436:LEU:HD13	2.55	0.41
1:B:164:SER:HB3	1:B:169:THR:N	2.35	0.41
1:B:418:PHE:HE1	1:B:439:LEU:HG	1.86	0.41
1:B:72:GLY:HA3	1:B:135:TYR:CZ	2.57	0.40
1:B:206:GLN:HA	1:B:214:THR:O	2.21	0.40
1:A:382:LEU:HD23	1:A:382:LEU:HA	1.83	0.40
1:B:342:TRP:CD2	1:B:382:LEU:HD13	2.56	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	432/474 (91%)	416 (96%)	14 (3%)	2 (0%)	29 31
1	B	432/474 (91%)	415 (96%)	16 (4%)	1 (0%)	47 55
All	All	864/948 (91%)	831 (96%)	30 (4%)	3 (0%)	41 46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	112	ALA
1	A	143	GLY
1	A	112	ALA

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	341/381 (90%)	337 (99%)	4 (1%)	71	83
1	B	339/381 (89%)	334 (98%)	5 (2%)	65	78
All	All	680/762 (89%)	671 (99%)	9 (1%)	69	81

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	121	ARG
1	A	167	HIS
1	A	379	SER
1	A	409	LYS
1	B	121	ARG
1	B	144	ASP
1	B	167	HIS
1	B	253	ARG
1	B	386	ARG

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

Mol	Chain	Res	Type
1	A	417	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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
4	MET	B	503	2	7,8,8	0.85	1 (14%)	7,9,9	1.33	2 (28%)
4	MET	A	503	2	7,8,8	0.86	1 (14%)	7,9,9	1.37	2 (28%)

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
4	MET	B	503	2	-	3/8/8/8	-
4	MET	A	503	2	-	5/8/8/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	MET	OXT-C	-2.14	1.23	1.30
4	B	503	MET	OXT-C	-2.10	1.23	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	503	MET	OXT-C-O	-2.84	117.65	124.09
4	B	503	MET	OXT-C-O	-2.71	117.94	124.09
4	B	503	MET	OXT-C-CA	2.23	121.00	113.38
4	A	503	MET	OXT-C-CA	2.22	120.94	113.38

There are no chirality outliers.

All (8) torsion outliers are listed below:

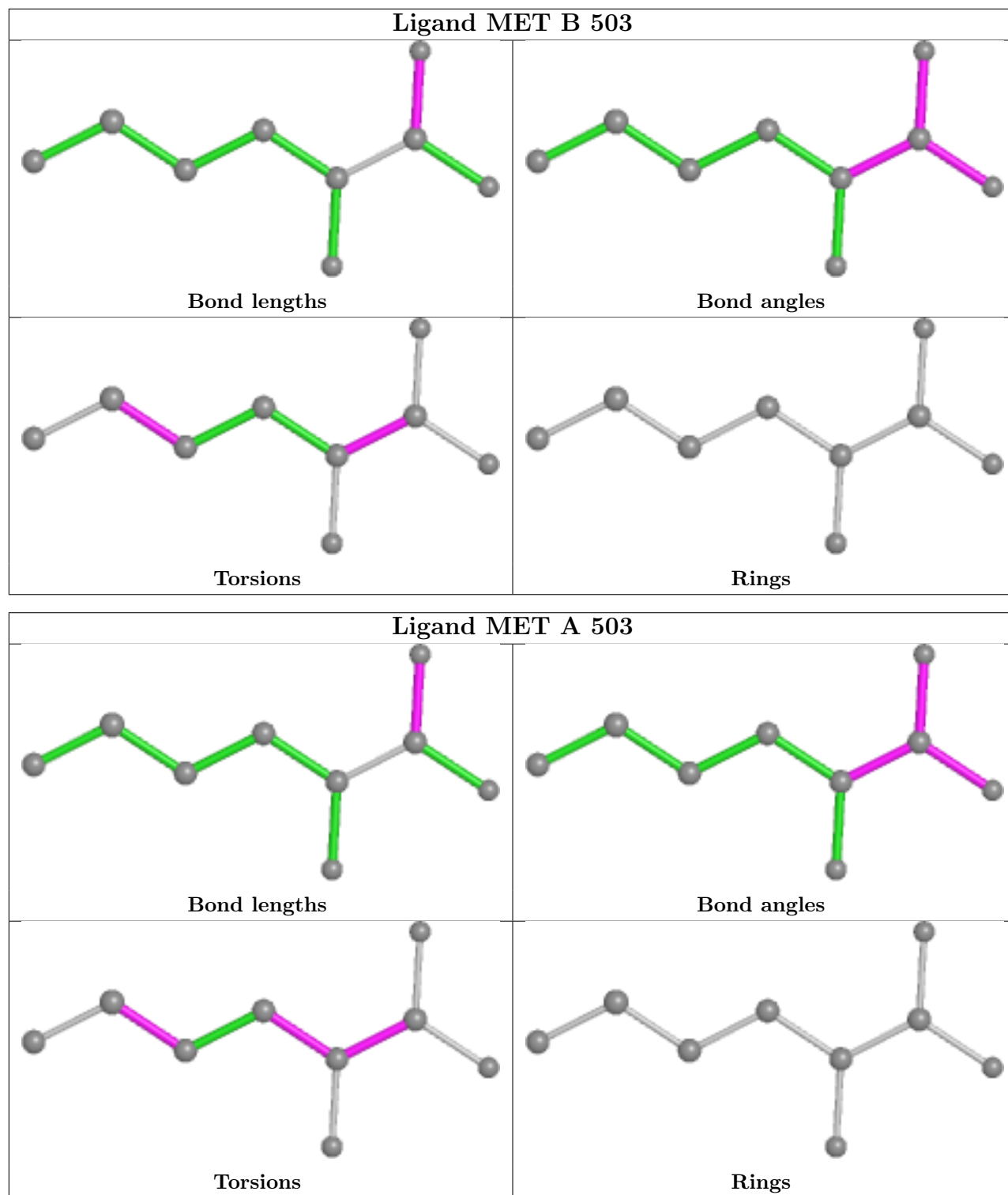
Mol	Chain	Res	Type	Atoms
4	A	503	MET	CB-CG-SD-CE
4	A	503	MET	C-CA-CB-CG
4	A	503	MET	N-CA-CB-CG
4	B	503	MET	OXT-C-CA-CB
4	A	503	MET	O-C-CA-CB
4	A	503	MET	OXT-C-CA-CB
4	B	503	MET	O-C-CA-CB
4	B	503	MET	CB-CG-SD-CE

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	MET	1	0
4	A	503	MET	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	434/474 (91%)	0.87	33 (7%) 13 12	11, 20, 33, 60	0
1	B	433/474 (91%)	1.06	55 (12%) 3 3	12, 23, 38, 68	0
All	All	867/948 (91%)	0.96	88 (10%) 7 6	11, 22, 37, 68	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	145	PRO	12.4
1	B	112	ALA	7.9
1	A	145	PRO	6.2
1	A	143	GLY	5.7
1	A	112	ALA	5.6
1	A	144	ASP	5.4
1	B	149	ILE	4.5
1	B	379	SER	4.4
1	B	146	GLY	4.2
1	B	95	ARG	4.2
1	A	146	GLY	4.1
1	B	148	PRO	4.0
1	B	444	LEU	3.9
1	A	139	PRO	3.8
1	A	212	LEU	3.6
1	B	460	THR	3.6
1	B	117	VAL	3.5
1	B	463	PRO	3.5
1	A	202	LEU	3.4
1	B	139	PRO	3.4
1	B	339	ALA	3.3
1	B	104	GLN	3.2
1	B	263	GLY	3.0
1	A	247	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	247	THR	3.0
1	A	111	THR	2.9
1	B	212	LEU	2.9
1	A	113	GLN	2.9
1	B	202	LEU	2.9
1	A	334	THR	2.9
1	B	390	ILE	2.8
1	B	208	GLU	2.8
1	B	461	LEU	2.8
1	B	456	VAL	2.7
1	B	68	PRO	2.7
1	B	374	LEU	2.7
1	B	381	PRO	2.7
1	A	149	ILE	2.6
1	A	140	GLU	2.6
1	A	148	PRO	2.6
1	A	397	PHE	2.6
1	B	144	ASP	2.5
1	B	203	PHE	2.5
1	B	300	LEU	2.5
1	B	143	GLY	2.5
1	B	442	THR	2.5
1	A	456	VAL	2.4
1	B	372	ALA	2.4
1	B	36	GLN	2.4
1	A	158	GLY	2.4
1	B	182	PRO	2.4
1	A	193	ALA	2.4
1	B	159	LEU	2.4
1	B	138	THR	2.3
1	B	462	PRO	2.3
1	B	220	ARG	2.3
1	A	269	GLY	2.3
1	A	393	ALA	2.3
1	A	142	SER	2.3
1	B	413	ALA	2.3
1	B	175	CYS	2.3
1	B	458	GLY	2.3
1	A	339	ALA	2.2
1	B	397	PHE	2.2
1	A	213	LYS	2.2
1	B	388	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	138	THR	2.2
1	A	460	THR	2.2
1	B	341	THR	2.2
1	A	147	LEU	2.1
1	B	106	VAL	2.1
1	B	251	HIS	2.1
1	A	390	ILE	2.1
1	A	388	GLU	2.1
1	B	125	PRO	2.1
1	A	104	GLN	2.1
1	A	204	THR	2.1
1	B	386	ARG	2.1
1	B	377	LEU	2.1
1	B	59	HIS	2.1
1	B	56	TYR	2.1
1	A	300	LEU	2.0
1	B	408	LEU	2.0
1	B	99	ALA	2.0
1	A	89	LEU	2.0
1	B	105	ARG	2.0
1	B	459	ARG	2.0
1	B	299	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [\(i\)](#)

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

6.3 Carbohydrates [\(i\)](#)

There are no 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, 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.

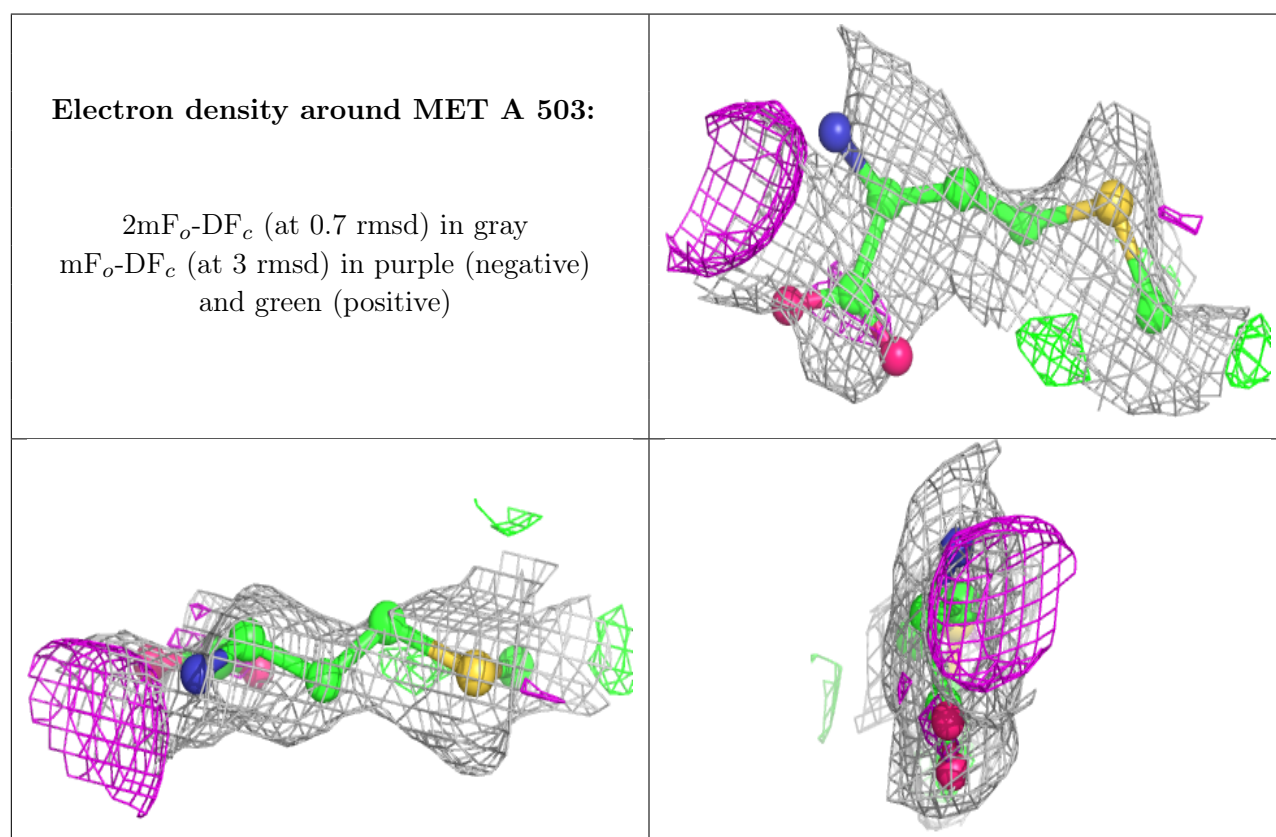
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	MET	A	503	9/9	0.69	0.33	28,34,42,55	0

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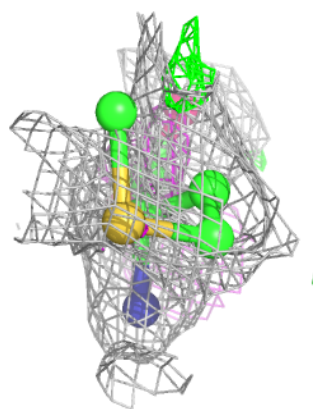
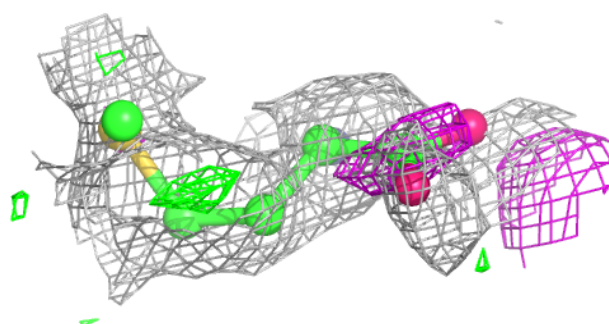
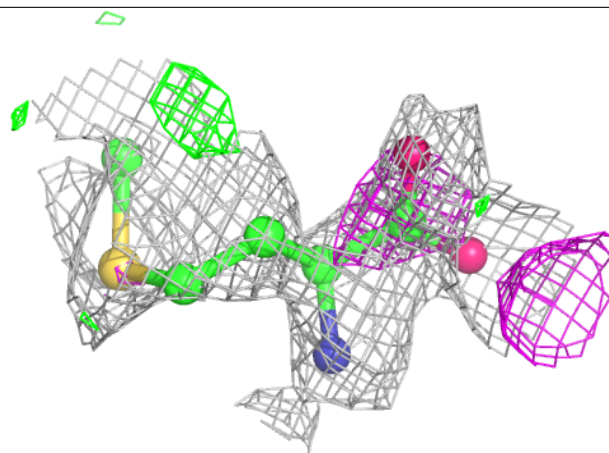
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MET	B	503	9/9	0.76	0.32	28,34,49,58	0
3	NA	B	502	1/1	0.93	0.16	9,9,9,9	0
3	NA	A	502	1/1	0.96	0.16	7,7,7,7	0
2	ZN	A	501	1/1	0.98	0.07	17,17,17,17	0
2	ZN	B	501	1/1	0.99	0.07	19,19,19,19	0

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.



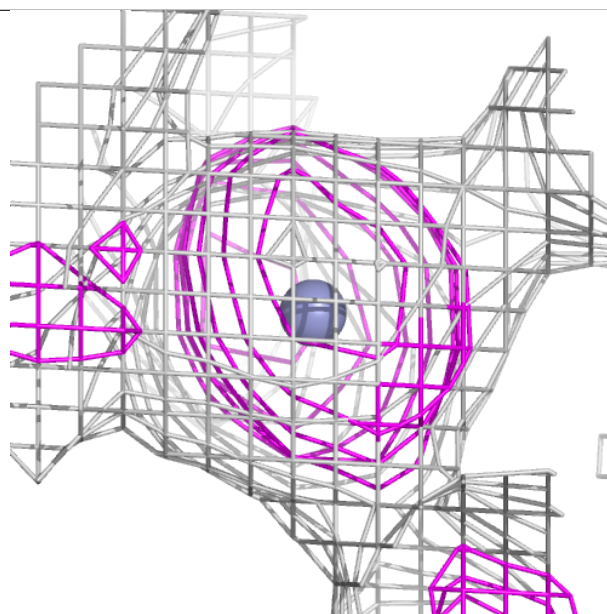
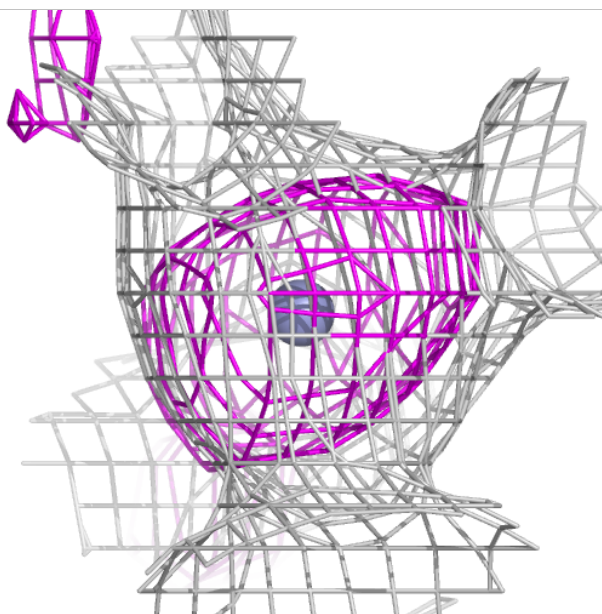
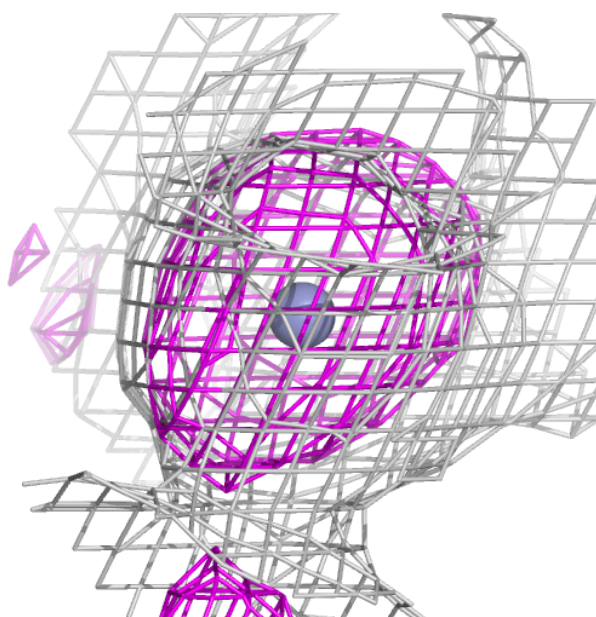
Electron density around MET B 503:

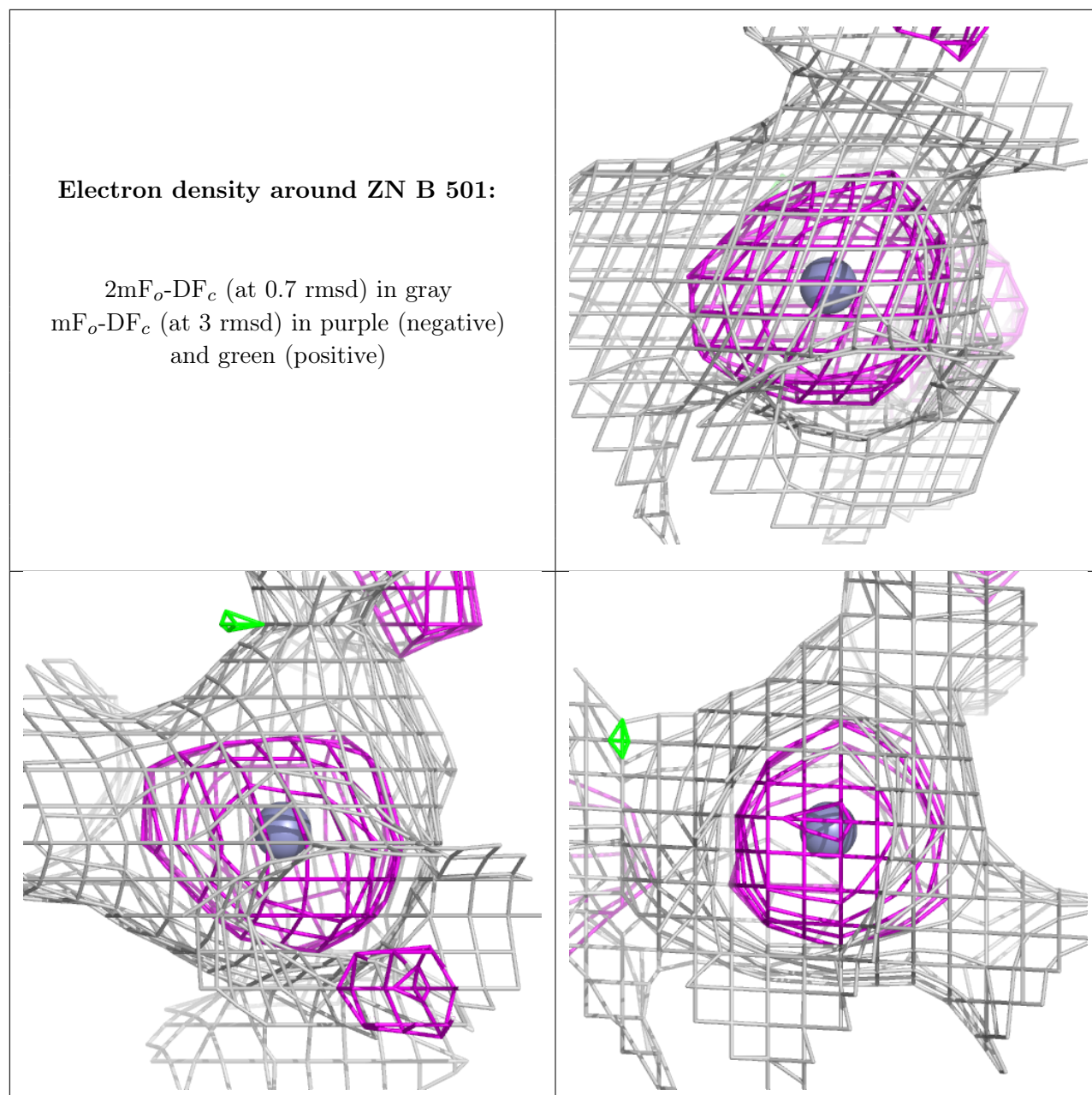
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZN 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.