



Full wwPDB X-ray Structure Validation Report ⓘ

May 30, 2022 – 12:03 AM JST

PDB ID : 7XV2
Title : TRIM E3 ubiquitin ligase
Deposited on : 2022-05-20
Resolution : 2.75 Å (reported)

This wwPDB validation report is for manuscript review

This is a Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB biocuration pipeline after annotation of the structure.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.28.1
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)	:	2.28.1

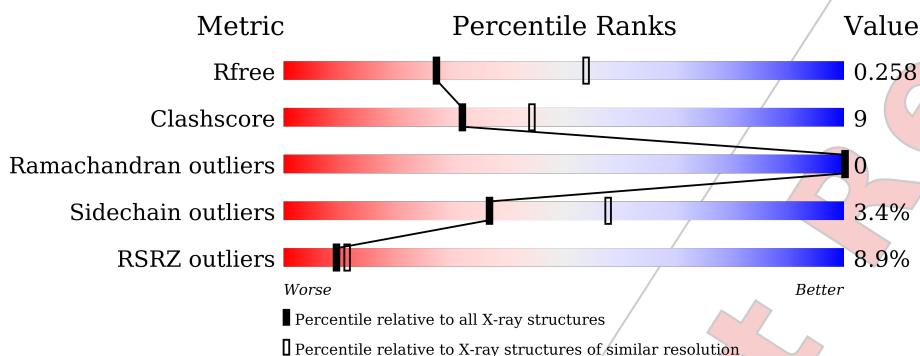
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	394	9% 77% 20% ..

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3024 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	382	Total	C	N	O	S	0	0	0
			3022	1907	544	556	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	GLY	-	expression tag	UNP Q1XH17
A	78	SER	-	expression tag	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

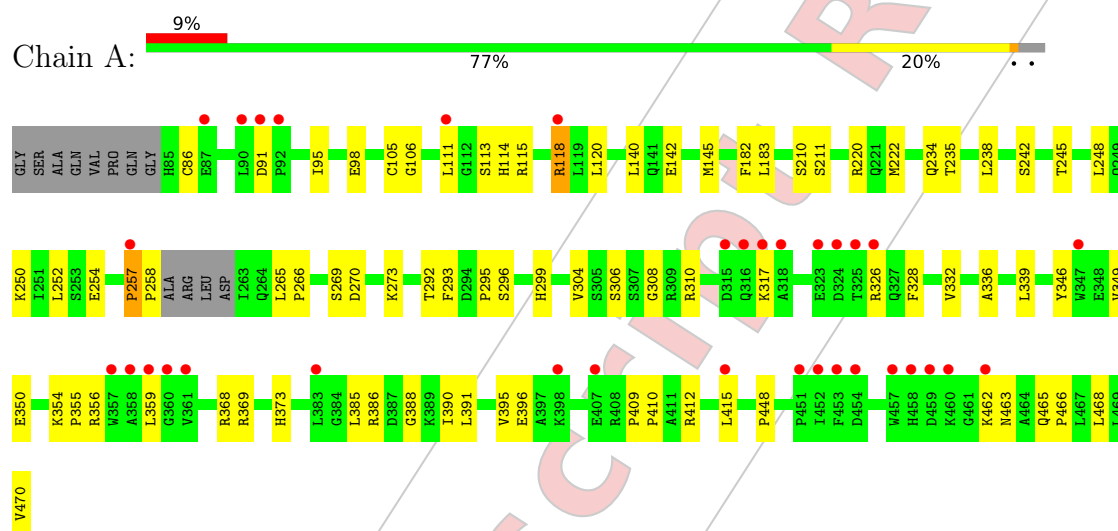
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

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

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: Tripartite motif-containing protein 72



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	73.30Å 110.17Å 95.94Å 90.00° 100.80° 90.00°	Depositor
Resolution (Å)	27.41 – 2.75 27.41 – 2.75	Depositor EDS
% Data completeness (in resolution range)	97.5 (27.41-2.75) 97.5 (27.41-2.75)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.76Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.205 , 0.258 0.205 , 0.258	Depositor DCC
R_{free} test set	1900 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	80.4	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3024	wwPDB-VP
Average B, all atoms (Å ²)	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.37% 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	0.46	0/3088	0.63	1/4177 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	391	LEU	CA-CB-CG	5.76	128.55	115.30

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	3022	0	3021	54	0
2	A	2	0	0	0	0
All	All	3024	0	3021	54	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 9.

All (54) 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:111:LEU:CD1	1:A:115:ARG:HD3	1.98	0.94
1:A:339:LEU:HD11	1:A:448:PRO:HB2	1.56	0.86
1:A:234:GLN:O	1:A:238:LEU:HD22	1.85	0.75
1:A:111:LEU:HD11	1:A:115:ARG:HD3	1.70	0.73
1:A:98:GLU:OE2	1:A:118:ARG:HD2	1.90	0.72
1:A:111:LEU:HD12	1:A:115:ARG:HD3	1.73	0.70
1:A:234:GLN:O	1:A:238:LEU:CD2	2.44	0.66
1:A:295:PRO:HG3	1:A:304:VAL:HG21	1.78	0.64
1:A:98:GLU:HG2	1:A:118:ARG:HB3	1.80	0.63
1:A:86:CYS:SG	1:A:105:CYS:HB3	2.39	0.62
1:A:234:GLN:HG2	1:A:238:LEU:CD2	2.34	0.57
1:A:355:PRO:HA	1:A:388:GLY:HA2	1.86	0.57
1:A:222:MET:CE	1:A:248:LEU:HB2	2.34	0.57
1:A:250:LYS:O	1:A:254:GLU:HG2	2.05	0.56
1:A:355:PRO:HD2	1:A:463:ASN:HD22	1.71	0.55
1:A:293:PHE:N	1:A:308:GLY:O	2.43	0.51
1:A:332:VAL:O	1:A:332:VAL:HG23	2.12	0.51
1:A:354:LYS:NZ	1:A:465:GLN:O	2.40	0.50
1:A:235:THR:HA	1:A:238:LEU:HD23	1.94	0.50
1:A:113:SER:HB2	1:A:114:HIS:CD2	2.46	0.50
1:A:98:GLU:CD	1:A:118:ARG:HD2	2.32	0.49
1:A:292:THR:O	1:A:336:ALA:HA	2.12	0.49
1:A:299:HIS:CD2	1:A:332:VAL:HG12	2.47	0.49
1:A:328:PHE:CE1	1:A:368:ARG:HB3	2.48	0.48
1:A:257:PRO:HG2	1:A:258:PRO:HD3	1.95	0.48
1:A:95:ILE:HD13	1:A:106:GLY:HA2	1.96	0.48
1:A:269:SER:OG	1:A:270:ASP:N	2.46	0.47
1:A:349:VAL:HG11	1:A:359:LEU:HD13	1.95	0.47
1:A:395:VAL:HG22	1:A:396:GLU:H	1.78	0.47
1:A:350:GLU:HB3	1:A:468:LEU:HB2	1.96	0.47
1:A:265:LEU:HD12	1:A:266:PRO:HD2	1.97	0.47
1:A:242:SER:HA	1:A:245:THR:HB	1.96	0.46
1:A:182:PHE:CD1	1:A:183:LEU:HD23	2.50	0.46
1:A:120:LEU:HD23	1:A:120:LEU:HA	1.84	0.45
1:A:462:LYS:N	1:A:462:LYS:HD2	2.31	0.45
1:A:182:PHE:HD1	1:A:183:LEU:HD23	1.82	0.45
1:A:385:LEU:HD12	1:A:390:ILE:O	2.16	0.45
1:A:111:LEU:HD12	1:A:111:LEU:HA	1.79	0.45
1:A:234:GLN:HG2	1:A:238:LEU:HD23	1.97	0.45
1:A:270:ASP:O	1:A:273:LYS:NZ	2.31	0.45
1:A:111:LEU:CD1	1:A:115:ARG:CD	2.83	0.45
1:A:412:ARG:NE	1:A:470:VAL:HG21	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:LEU:HA	1:A:140:LEU:HD12	1.47	0.43
1:A:222:MET:HE1	1:A:248:LEU:HB2	1.98	0.43
1:A:142:GLU:HA	1:A:145:MET:HE2	2.01	0.42
1:A:234:GLN:HG2	1:A:238:LEU:HD21	2.01	0.42
1:A:355:PRO:HD2	1:A:463:ASN:ND2	2.32	0.42
1:A:346:TYR:HA	1:A:415:LEU:O	2.20	0.41
1:A:86:CYS:HB2	1:A:91:ASP:O	2.20	0.41
1:A:252:LEU:HA	1:A:252:LEU:HD23	1.75	0.41
1:A:310:ARG:NH2	1:A:466:PRO:HG3	2.36	0.41
1:A:326:ARG:HA	1:A:368:ARG:HD2	2.01	0.41
1:A:356:ARG:HA	1:A:385:LEU:O	2.21	0.41
1:A:409:PRO:HA	1:A:410:PRO:HD3	1.96	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	378/394 (96%)	357 (94%)	21 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	327/335 (98%)	316 (97%)	11 (3%)	37 58

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	118	ARG
1	A	210	SER
1	A	211	SER
1	A	220	ARG
1	A	257	PRO
1	A	296	SER
1	A	306	SER
1	A	317	LYS
1	A	369	ARG
1	A	373	HIS
1	A	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	463	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 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.

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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	382/394 (96%)	0.23	34 (8%) 9 11	61, 110, 173, 238	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90	LEU	6.6
1	A	358	ALA	5.1
1	A	360	GLY	5.1
1	A	452	ILE	4.7
1	A	453	PHE	4.5
1	A	317	LYS	4.4
1	A	454	ASP	4.2
1	A	458	HIS	4.0
1	A	359	LEU	3.9
1	A	451	PRO	3.7
1	A	87	GLU	3.5
1	A	91	ASP	3.4
1	A	459	ASP	3.3
1	A	257	PRO	3.3
1	A	457	TRP	3.1
1	A	318	ALA	2.9
1	A	324	ASP	2.9
1	A	118	ARG	2.8
1	A	92	PRO	2.6
1	A	398	LYS	2.6
1	A	407	GLU	2.5
1	A	326	ARG	2.5
1	A	361	VAL	2.5
1	A	316	GLN	2.4
1	A	462	LYS	2.4
1	A	347	TRP	2.3
1	A	111	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	415	LEU	2.3
1	A	323	GLU	2.3
1	A	357	TRP	2.2
1	A	315	ASP	2.2
1	A	460	LYS	2.1
1	A	325	THR	2.1
1	A	383	LEU	2.1

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](#)

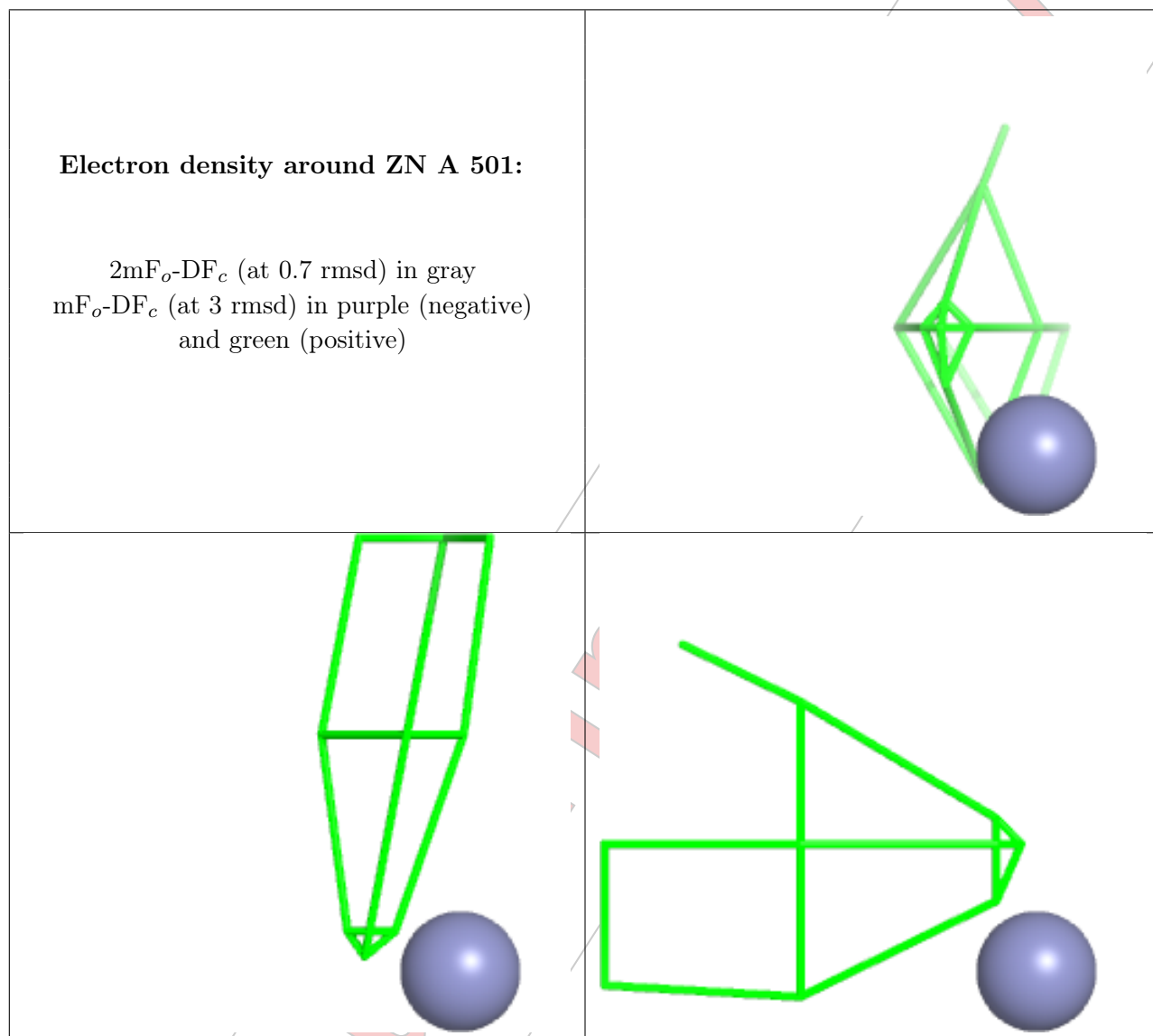
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ZN	A	501	1/1	0.93	0.16	189,189,189,189	0
2	ZN	A	502	1/1	0.97	0.05	106,106,106,106	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 A 501:

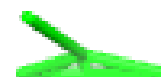
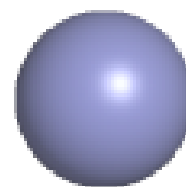
2mF_o-DF_c (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
 and green (positive)



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Electron density around ZN A 502:

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.

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