



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 17, 2023 – 01:40 PM EDT

PDB ID : 8SW1
Title : Puromycin-sensitive aminopeptidase with bound peptide
Authors : Rodgers, D.W.; Madabushi, S.
Deposited on : 2023-05-17
Resolution : 3.65 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
Xtriage (Phenix) : 1.13
EDS : 2.34
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) : 2.34

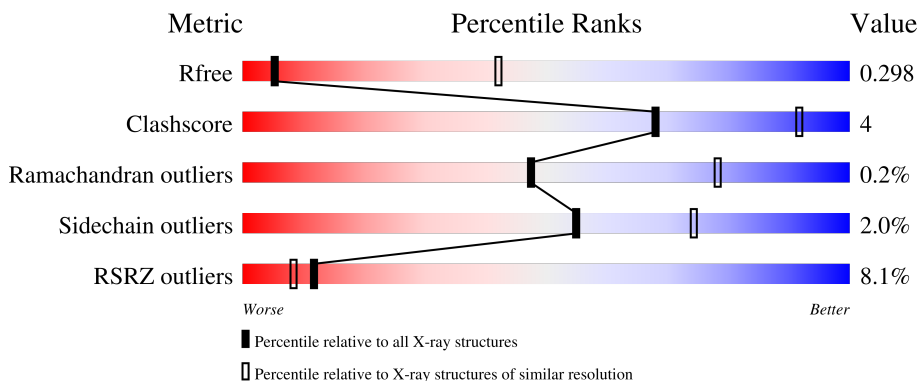
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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	1557 (3.82-3.50)
Clashscore	141614	1037 (3.80-3.52)
Ramachandran outliers	138981	1004 (3.80-3.52)
Sidechain outliers	138945	1002 (3.80-3.52)
RSRZ outliers	127900	1441 (3.82-3.50)

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	902	 8% (red), 84% (green), 12% (yellow), 0% (orange), 0% (red)
2	B	19	 26% (green), 5% (yellow), 68% (grey)

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6887 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 Puromycin-sensitive aminopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	864	6856	4388	1144	1293	31	0	0	0

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	MET	-	initiating methionine	UNP P55786
A	19	SER	-	expression tag	UNP P55786
A	20	TYR	-	expression tag	UNP P55786
A	21	TYR	-	expression tag	UNP P55786
A	22	HIS	-	expression tag	UNP P55786
A	23	HIS	-	expression tag	UNP P55786
A	24	HIS	-	expression tag	UNP P55786
A	25	HIS	-	expression tag	UNP P55786
A	26	HIS	-	expression tag	UNP P55786
A	27	HIS	-	expression tag	UNP P55786
A	28	ASP	-	expression tag	UNP P55786
A	29	TYR	-	expression tag	UNP P55786
A	30	ASP	-	expression tag	UNP P55786
A	31	ILE	-	expression tag	UNP P55786
A	32	PRO	-	expression tag	UNP P55786
A	33	THR	-	expression tag	UNP P55786
A	34	THR	-	expression tag	UNP P55786
A	35	GLU	-	expression tag	UNP P55786
A	36	ASN	-	expression tag	UNP P55786
A	37	LEU	-	expression tag	UNP P55786
A	38	TYR	-	expression tag	UNP P55786
A	39	PHE	-	expression tag	UNP P55786
A	40	GLN	-	expression tag	UNP P55786
A	41	GLY	-	expression tag	UNP P55786
A	42	ALA	-	expression tag	UNP P55786
A	43	MET	-	expression tag	UNP P55786
A	44	GLY	-	expression tag	UNP P55786

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Chain	Residue	Modelled	Actual	Comment	Reference
A	45	SER	-	expression tag	UNP P55786

- Molecule 2 is a protein called Polyglutamine peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	6	30	18	6	6	0	0	0

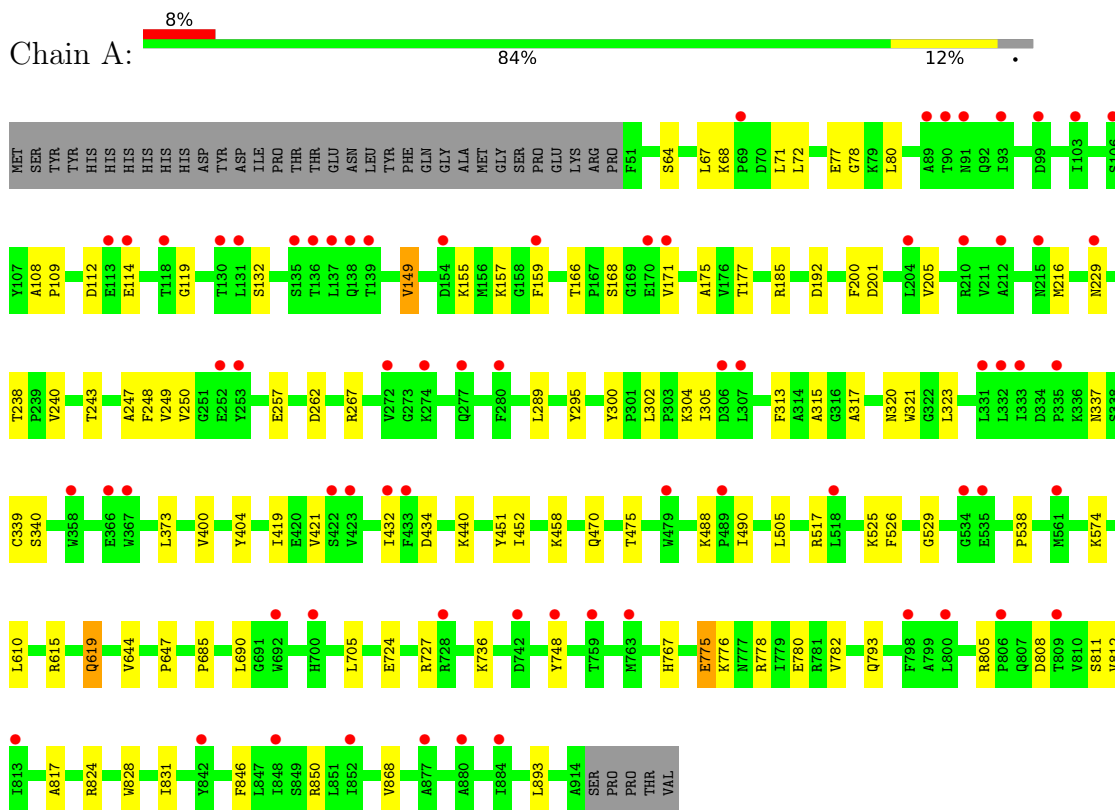
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	1	1	1	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Puromycin-sensitive aminopeptidase



- Molecule 2: Polyglutamine peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	70.75Å 256.56Å 60.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.52 – 3.65 47.52 – 3.59	Depositor EDS
% Data completeness (in resolution range)	98.8 (47.52-3.65) 88.9 (47.52-3.59)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 3.57Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.257 , 0.295 0.259 , 0.298	Depositor DCC
R_{free} test set	12043 reflections (89.99%)	wwPDB-VP
Wilson B-factor (Å ²)	101.7	Xtrriage
Anisotropy	0.415	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 71.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	6887	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.41% 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	0.24	0/7017	0.44	0/9523

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	6856	0	6773	52	0
2	B	30	0	9	2	0
3	A	1	0	0	0	0
All	All	6887	0	6782	52	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.

All (52) 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:525:LYS:HD2	1:A:538:PRO:HG2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:PRO:HG2	1:A:112:ASP:HB2	1.79	0.64
1:A:517:ARG:NH2	1:A:574:LYS:O	2.32	0.63
1:A:805:ARG:NH2	1:A:808:ASP:OD2	2.32	0.62
1:A:177:THR:HG21	1:A:248:PHE:H	1.64	0.61
1:A:373:LEU:HD22	1:A:475:THR:HG23	1.88	0.56
1:A:175:ALA:HB3	1:A:250:VAL:HB	1.88	0.55
1:A:529:GLY:HA2	1:A:893:LEU:HD21	1.87	0.55
1:A:67:LEU:HD13	1:A:78:GLY:HA3	1.89	0.54
1:A:185:ARG:HH21	1:A:192:ASP:HB3	1.71	0.54
1:A:724:GLU:HA	1:A:727:ARG:HE	1.74	0.53
1:A:289:LEU:HD11	1:A:305:ILE:HG21	1.95	0.49
1:A:295:TYR:HA	1:A:458:LYS:HE3	1.95	0.49
1:A:811:SER:OG	1:A:850:ARG:NH2	2.45	0.49
1:A:108:ALA:HB2	1:A:114:GLU:HB3	1.95	0.49
1:A:68:LYS:HG3	1:A:205:VAL:HB	1.94	0.49
1:A:748:TYR:HB3	1:A:782:VAL:HG21	1.95	0.49
1:A:775:GLU:HG2	1:A:778:ARG:HH12	1.78	0.48
1:A:315:ALA:O	2:B:2:UNK:HA	2.13	0.48
1:A:817:ALA:HA	1:A:824:ARG:HA	1.94	0.48
1:A:216:MET:HG2	1:A:238:THR:HG22	1.96	0.48
1:A:610:LEU:O	1:A:615:ARG:NH1	2.47	0.48
1:A:339:CYS:SG	1:A:340:SER:N	2.84	0.48
1:A:775:GLU:OE1	1:A:778:ARG:NH1	2.48	0.47
1:A:452:ILE:HD11	1:A:490:ILE:HD11	1.97	0.46
1:A:240:VAL:HB	1:A:470:GLN:HB3	1.98	0.46
1:A:119:GLY:HA3	1:A:132:SER:HB2	1.97	0.46
1:A:451:TYR:CZ	1:A:488:LYS:HD3	2.51	0.45
1:A:249:VAL:HG12	1:A:323:LEU:HD21	1.99	0.45
1:A:177:THR:HG21	1:A:247:ALA:HA	1.99	0.45
1:A:200:PHE:HZ	1:A:243:THR:HG22	1.81	0.45
1:A:320:ASN:HB2	1:A:323:LEU:O	2.16	0.45
1:A:644:VAL:HB	1:A:685:PRO:HG3	1.99	0.45
1:A:317:ALA:O	2:B:2:UNK:N	2.50	0.44
1:A:690:LEU:HD11	1:A:705:LEU:HG	2.00	0.44
1:A:421:VAL:HB	1:A:432:ILE:HD13	1.99	0.44
1:A:828:TRP:CE3	1:A:831:ILE:HD11	2.54	0.43
1:A:400:VAL:HA	1:A:404:TYR:HB3	2.01	0.43
1:A:780:GLU:HB3	1:A:812:VAL:HG22	2.01	0.43
1:A:77:GLU:HB3	1:A:149:VAL:HG23	2.01	0.42
1:A:71:LEU:HG	1:A:72:LEU:HD22	2.01	0.42
1:A:64:SER:HA	1:A:201:ASP:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:PHE:CE2	1:A:315:ALA:HB3	2.55	0.41
1:A:434:ASP:N	1:A:434:ASP:OD1	2.54	0.41
1:A:767:HIS:O	1:A:776:LYS:NZ	2.54	0.41
1:A:257:GLU:HB3	1:A:267:ARG:HG2	2.03	0.41
1:A:300:TYR:CE2	1:A:302:LEU:HB2	2.56	0.41
1:A:155:LYS:HB2	1:A:157:LYS:HG2	2.02	0.41
1:A:619:GLN:HE21	1:A:619:GLN:HB3	1.59	0.41
1:A:505:LEU:HB2	1:A:526:PHE:HB2	2.03	0.40
1:A:736:LYS:HB2	1:A:736:LYS:HE3	1.90	0.40
1:A:419:ILE:HD11	1:A:440:LYS:HG2	2.02	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	862/902 (96%)	824 (96%)	36 (4%)	2 (0%)	47 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	171	VAL
1	A	647	PRO

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	742/777 (96%)	727 (98%)	15 (2%)	55 74

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LEU
1	A	149	VAL
1	A	159	PHE
1	A	166	THR
1	A	168	SER
1	A	229	ASN
1	A	262	ASP
1	A	304	LYS
1	A	321	TRP
1	A	337	ASN
1	A	619	GLN
1	A	775	GLU
1	A	793	GLN
1	A	846	PHE
1	A	868	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 1 ligands modelled in this entry, 1 is 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

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	864/902 (95%)	0.49	70 (8%) 12 8	80, 129, 172, 196	0
2	B	0/19	-	-	-	-
All	All	864/921 (93%)	0.49	70 (8%) 12 8	80, 129, 172, 196	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	130	THR	6.5
1	A	848	ILE	6.5
1	A	93	ILE	6.0
1	A	136	THR	5.3
1	A	138	GLN	4.4
1	A	763	MET	4.2
1	A	809	THR	4.2
1	A	114	GLU	4.1
1	A	432	ILE	3.8
1	A	433	PHE	3.8
1	A	884	ILE	3.6
1	A	137	LEU	3.5
1	A	253	TYR	3.5
1	A	748	TYR	3.5
1	A	274	LYS	3.5
1	A	852	ILE	3.5
1	A	272	VAL	3.4
1	A	880	ALA	3.3
1	A	170	GLU	3.3
1	A	423	VAL	3.2
1	A	69	PRO	3.1
1	A	813	ILE	3.1
1	A	535	GLU	3.1
1	A	131	LEU	3.1
1	A	135	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	798	PHE	3.1
1	A	728	ARG	2.9
1	A	358	TRP	2.9
1	A	280	PHE	2.9
1	A	800	LEU	2.9
1	A	90	THR	2.9
1	A	366	GLU	2.9
1	A	118	THR	2.8
1	A	113	GLU	2.8
1	A	229	ASN	2.8
1	A	759	THR	2.8
1	A	333	ILE	2.7
1	A	210	ARG	2.7
1	A	139	THR	2.7
1	A	331	LEU	2.5
1	A	106	SER	2.5
1	A	479	TRP	2.4
1	A	842	TYR	2.4
1	A	277	GLN	2.4
1	A	159	PHE	2.4
1	A	367	TRP	2.3
1	A	332	LEU	2.3
1	A	103	ILE	2.3
1	A	204	LEU	2.3
1	A	215	ASN	2.3
1	A	99	ASP	2.3
1	A	307	LEU	2.3
1	A	877	ALA	2.3
1	A	489	PRO	2.2
1	A	252	GLU	2.2
1	A	212	ALA	2.2
1	A	306	ASP	2.2
1	A	154	ASP	2.2
1	A	806	PRO	2.1
1	A	335	PRO	2.1
1	A	700	HIS	2.1
1	A	561	MET	2.1
1	A	534	GLY	2.1
1	A	89	ALA	2.1
1	A	422	SER	2.1
1	A	518	LEU	2.1
1	A	171	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	742	ASP	2.0
1	A	91	ASN	2.0
1	A	692	TRP	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](#)

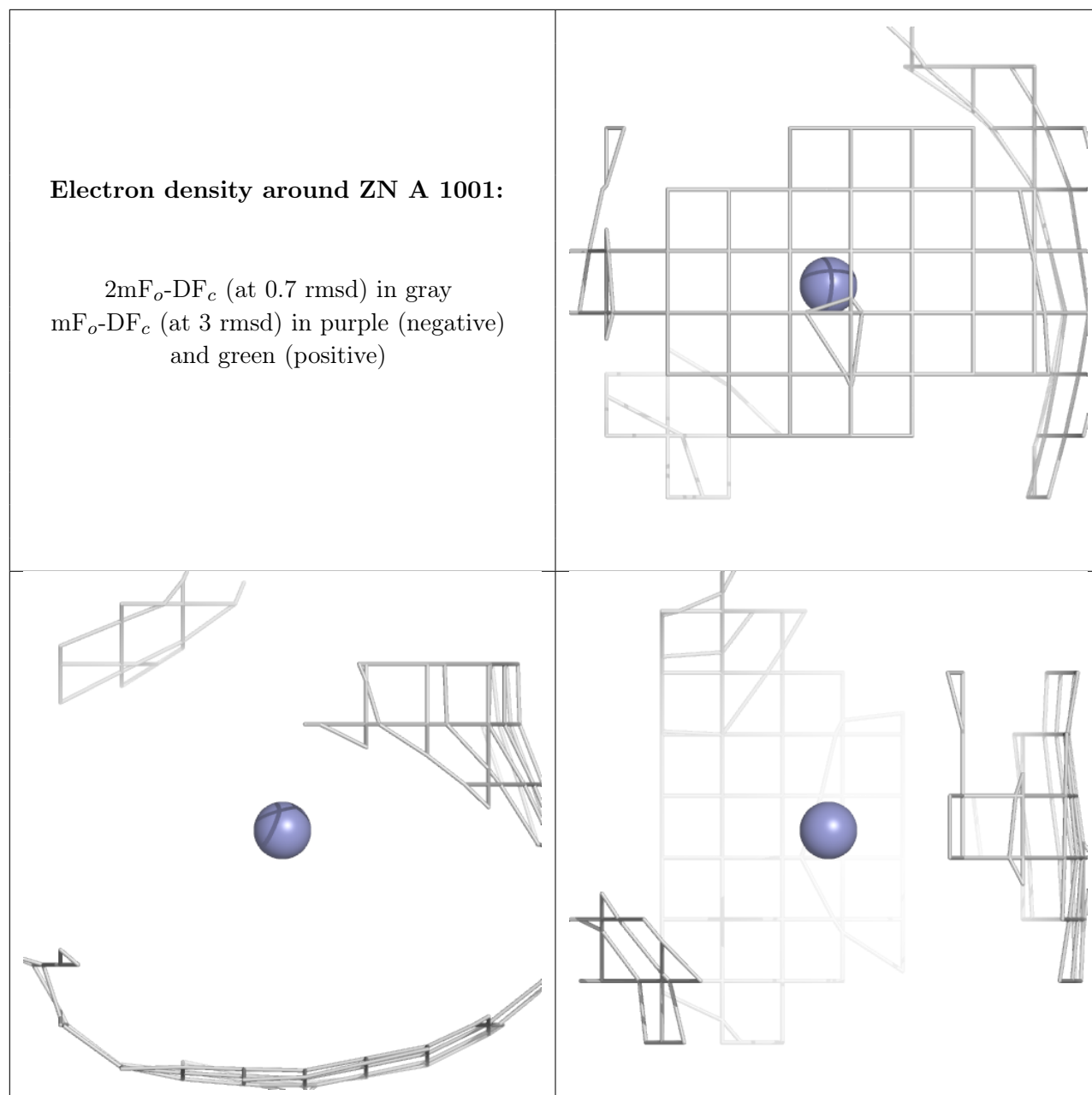
There are no monosaccharides in this entry.

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(\AA^2)	Q<0.9
3	ZN	A	1001	1/1	0.84	0.17	140,140,140,140	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.