Full wwPDB X-ray Structure Validation Report (i)

Oct 24, 2026 – 10:04 am BST

PDB ID	:	9TPB / pdb_00009tpb
Title	:	Canilysin from Capnocytophaga canimorsus (Strain 5)
Authors	:	Rodriguez-Banqueri, A.; Goulas, T.; Eckhard, U.; Gomis-Ruth, F.X.
Deposited on	:	2025-12-17
Resolution	:	2.50 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 (i)) were used in the production of this report:

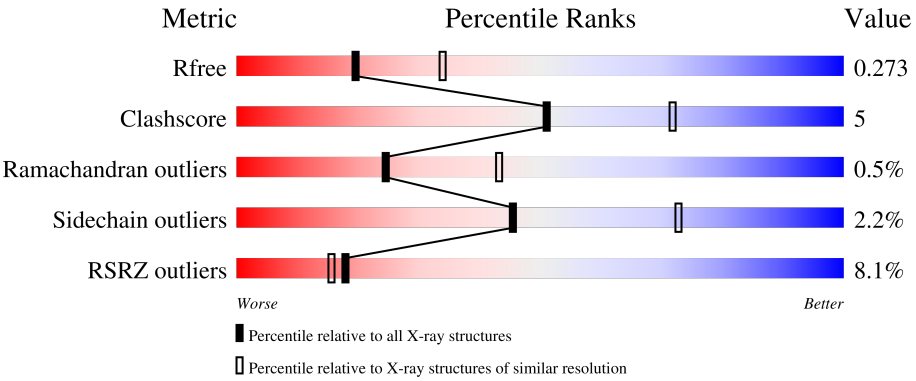
MolProbity	:	4-5-2 with Phenix2.2
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.2
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

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 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 <=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	356	6% 74% 11% · 15%
1	B	356	8% 70% 15% 15%

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 5234 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 Metallopeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	304	Total	C	N	O	S	0	0	0
			2467	1602	399	459	7			
1	B	304	Total	C	N	O	S	0	0	0
			2467	1602	399	459	7			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	MET	-	initiating methionine	UNP F9YTK6
A	11	GLY	-	expression tag	UNP F9YTK6
A	12	SER	-	expression tag	UNP F9YTK6
A	13	SER	-	expression tag	UNP F9YTK6
A	14	HIS	-	expression tag	UNP F9YTK6
A	15	HIS	-	expression tag	UNP F9YTK6
A	16	HIS	-	expression tag	UNP F9YTK6
A	17	HIS	-	expression tag	UNP F9YTK6
A	18	HIS	-	expression tag	UNP F9YTK6
A	19	HIS	-	expression tag	UNP F9YTK6
A	20	SER	-	expression tag	UNP F9YTK6
A	21	SER	-	expression tag	UNP F9YTK6
A	22	GLY	-	expression tag	UNP F9YTK6
A	23	GLU	-	expression tag	UNP F9YTK6
A	24	ASN	-	expression tag	UNP F9YTK6
A	25	LEU	-	expression tag	UNP F9YTK6
A	26	TYR	-	expression tag	UNP F9YTK6
A	27	PHE	-	expression tag	UNP F9YTK6
A	28	GLN	-	expression tag	UNP F9YTK6
A	29	GLY	-	expression tag	UNP F9YTK6
A	30	HIS	-	expression tag	UNP F9YTK6
A	31	MET	-	expression tag	UNP F9YTK6
B	10	MET	-	initiating methionine	UNP F9YTK6
B	11	GLY	-	expression tag	UNP F9YTK6
B	12	SER	-	expression tag	UNP F9YTK6

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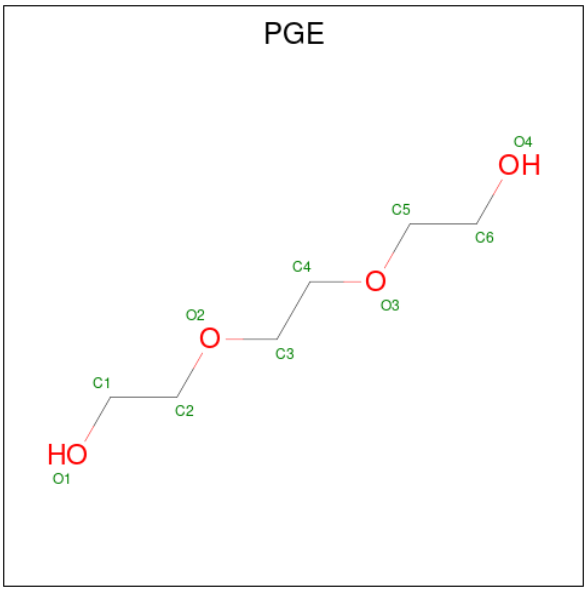
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Chain	Residue	Modelled	Actual	Comment	Reference
B	13	SER	-	expression tag	UNP F9YTK6
B	14	HIS	-	expression tag	UNP F9YTK6
B	15	HIS	-	expression tag	UNP F9YTK6
B	16	HIS	-	expression tag	UNP F9YTK6
B	17	HIS	-	expression tag	UNP F9YTK6
B	18	HIS	-	expression tag	UNP F9YTK6
B	19	HIS	-	expression tag	UNP F9YTK6
B	20	SER	-	expression tag	UNP F9YTK6
B	21	SER	-	expression tag	UNP F9YTK6
B	22	GLY	-	expression tag	UNP F9YTK6
B	23	GLU	-	expression tag	UNP F9YTK6
B	24	ASN	-	expression tag	UNP F9YTK6
B	25	LEU	-	expression tag	UNP F9YTK6
B	26	TYR	-	expression tag	UNP F9YTK6
B	27	PHE	-	expression tag	UNP F9YTK6
B	28	GLN	-	expression tag	UNP F9YTK6
B	29	GLY	-	expression tag	UNP F9YTK6
B	30	HIS	-	expression tag	UNP F9YTK6
B	31	MET	-	expression tag	UNP F9YTK6

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

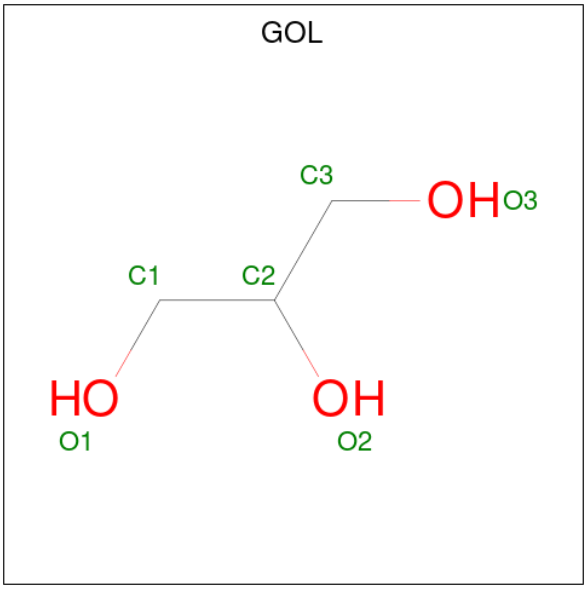
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

- Molecule 3 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



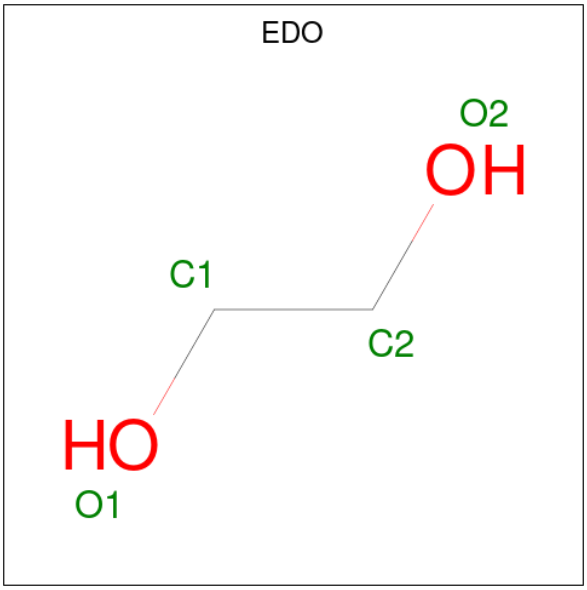
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 6 3 3	0	0
4	B	1	Total C O 6 3 3	0	0

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

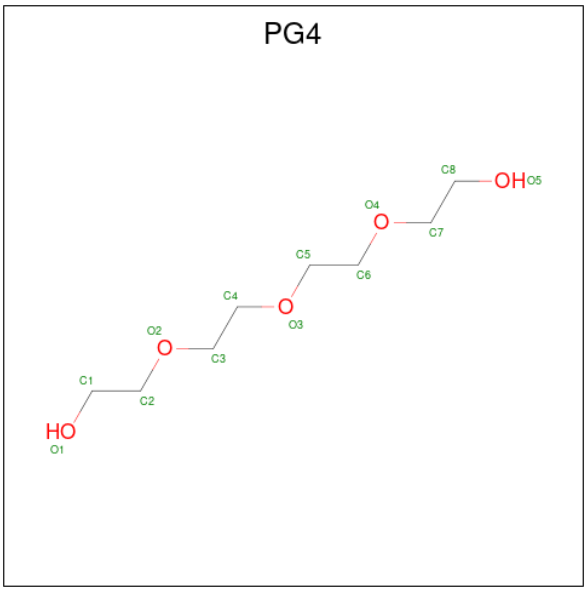


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total Ca 1 1	0	0

- Molecule 7 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C O 13 8 5	0	0

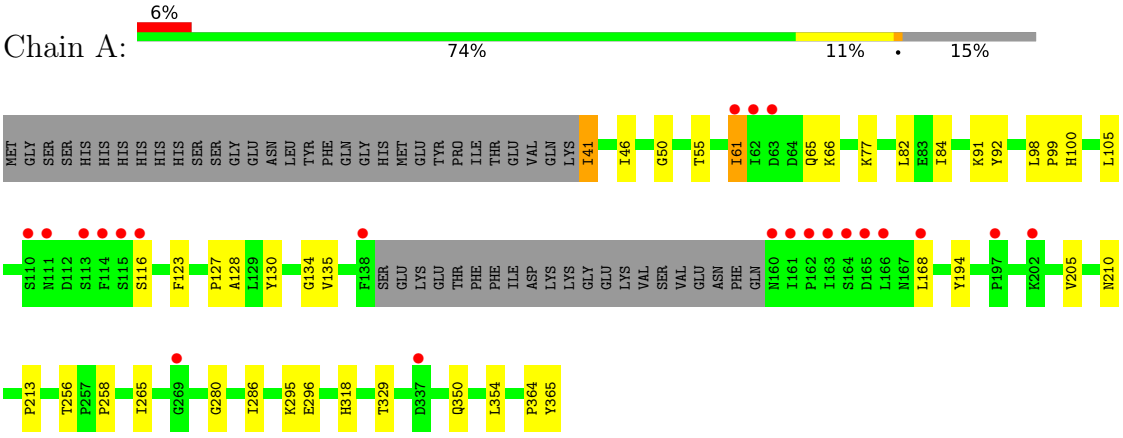
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	120	Total O 120 120	0	0
8	B	104	Total O 104 104	0	0

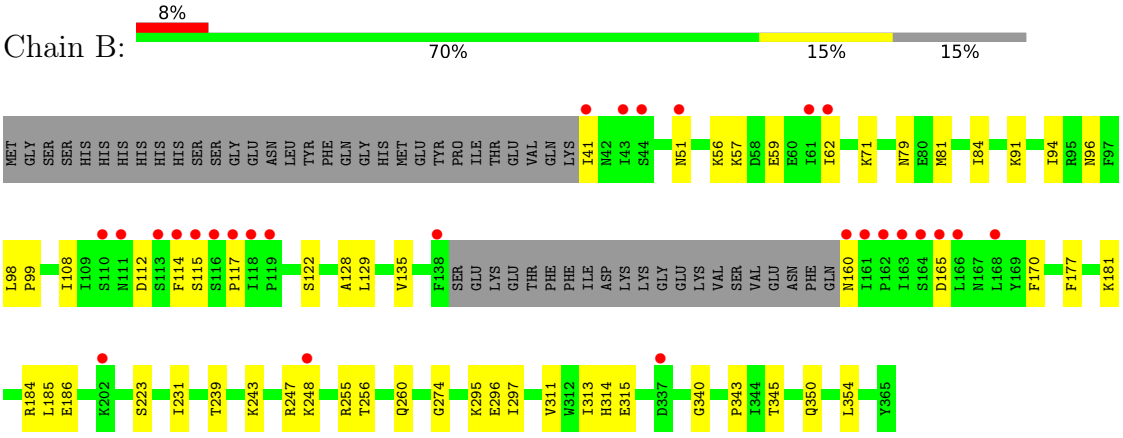
3 Residue-property plots (i)

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: Metallopeptidase



• Molecule 1: Metallopeptidase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	123.25Å 94.56Å 83.96Å 90.00° 128.43° 90.00°	Depositor
Resolution (Å)	62.68 – 2.50 62.68 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (62.68-2.50) 99.8 (62.68-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20_4459	Depositor
R, R_{free}	0.212 , 0.273 0.212 , 0.273	Depositor DCC
R_{free} test set	595 reflections (2.27%)	wwPDB-VP
Wilson B-factor (Å^2)	47.9	Xtriage
Anisotropy	0.557	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 51.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5234	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.53% 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: PG4, PGE, CA, ZN, EDO, GOL

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	0.36	0/2529	0.58	0/3421
1	B	0.38	0/2529	0.59	0/3421
All	All	0.37	0/5058	0.58	0/6842

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	2467	0	2437	23	0
1	B	2467	0	2437	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	14	0	0
3	B	20	0	28	0	0
4	A	6	0	8	0	0
4	B	12	0	15	1	0
5	A	12	0	18	1	0
6	B	1	0	0	0	0
7	B	13	0	18	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	120	0	0	2	0
8	B	104	0	0	2	0
All	All	5234	0	4975	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 5.

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:41:ILE:HD11	1:B:311:VAL:HA	1.62	0.81
1:B:296:GLU:HB2	1:B:354:LEU:HD21	1.65	0.78
1:B:112:ASP:HB2	1:B:165:ASP:HA	1.73	0.70
1:B:51:ASN:OD1	1:B:57:LYS:NZ	2.29	0.66
1:A:213:PRO:HG3	1:A:364:PRO:HG3	1.79	0.64
1:A:61:ILE:HA	1:A:66:LYS:HA	1.80	0.62
1:A:50:GLY:O	4:B:406:GOL:O2	2.18	0.61
1:B:112:ASP:N	1:B:165:ASP:O	2.32	0.61
1:B:248:LYS:HE2	7:B:403:PG4:H42	1.83	0.61
1:A:41:ILE:HG23	1:B:314:HIS:CE1	2.36	0.60
1:B:91:LYS:HE3	1:B:135:VAL:HG22	1.84	0.59
1:B:313:ILE:HD13	1:B:345:THR:HB	1.88	0.56
1:B:108:ILE:CG2	1:B:117:PRO:HB2	2.38	0.54
1:A:65:GLN:NE2	8:A:503:HOH:O	2.36	0.53
1:A:91:LYS:HE3	1:A:135:VAL:HG22	1.89	0.53
1:B:297:ILE:H	1:B:350:GLN:HE22	1.58	0.51
1:A:296:GLU:HB2	1:A:354:LEU:HD21	1.91	0.50
1:B:231:ILE:O	1:B:247:ARG:HD3	2.12	0.49
1:B:112:ASP:HB2	1:B:165:ASP:CA	2.42	0.49
1:A:92:TYR:CZ	1:A:134:GLY:HA3	2.48	0.48
1:A:99:PRO:HA	1:A:128:ALA:HB1	1.96	0.48
1:B:71:LYS:NZ	8:B:503:HOH:O	2.45	0.48
1:B:297:ILE:O	1:B:350:GLN:NE2	2.47	0.48
7:B:403:PG4:H52	7:B:403:PG4:H72	1.77	0.47
1:B:94:ILE:HD13	1:B:170:PHE:HZ	1.79	0.47
1:A:46:ILE:HD11	1:A:123:PHE:CE1	2.49	0.47
1:B:96:ASN:O	1:B:129:LEU:HA	2.15	0.46
1:A:365:TYR:O	8:A:501:HOH:O	2.20	0.46
1:A:318:HIS:CE1	1:A:329:THR:HG21	2.51	0.45
1:A:194:TYR:HA	5:A:405:EDO:H12	1.97	0.45
1:B:115:SER:O	1:B:117:PRO:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:GLY:N	1:B:315:GLU:OE1	2.49	0.45
1:A:84:ILE:HD11	1:A:168:LEU:HD23	1.99	0.44
1:B:99:PRO:HA	1:B:128:ALA:HB1	1.99	0.44
1:B:185:LEU:HG	1:B:255:ARG:HA	1.99	0.44
1:A:98:LEU:C	1:A:100:HIS:H	2.26	0.44
1:B:177:PHE:CE2	1:B:181:LYS:HD2	2.53	0.44
1:B:239:THR:HA	1:B:243:LYS:O	2.19	0.43
1:B:184:ARG:NH1	1:B:223:SER:O	2.46	0.43
1:B:79:ASN:ND2	1:B:186:GLU:HG2	2.34	0.43
1:B:81:MET:HB3	1:B:98:LEU:HD12	2.01	0.42
1:A:127:PRO:HG2	1:A:130:TYR:CG	2.55	0.42
1:A:210:ASN:HB3	1:A:286:ILE:O	2.19	0.42
1:B:295:LYS:HA	1:B:295:LYS:HD3	1.83	0.42
1:B:112:ASP:CB	1:B:165:ASP:HA	2.47	0.42
1:B:340:GLY:C	1:B:343:PRO:HD2	2.45	0.42
1:B:260:GLN:NE2	8:B:502:HOH:O	2.43	0.42
1:A:55:THR:O	1:A:205:VAL:HG11	2.20	0.41
1:A:77:LYS:HB3	1:A:77:LYS:HE3	1.86	0.41
1:A:82:LEU:HD21	1:A:105:LEU:HD11	2.03	0.41
1:A:265:ILE:HD12	1:A:280:GLY:O	2.22	0.40
1:A:296:GLU:HG3	1:A:350:GLN:NE2	2.35	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	300/356 (84%)	287 (96%)	11 (4%)	2 (1%)	18	34
1	B	300/356 (84%)	288 (96%)	11 (4%)	1 (0%)	36	55
All	All	600/712 (84%)	575 (96%)	22 (4%)	3 (0%)	24	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	256	THR
1	B	256	THR
1	A	258	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	268/316 (85%)	264 (98%)	4 (2%)	57 80
1	B	268/316 (85%)	260 (97%)	8 (3%)	36 64
All	All	536/632 (85%)	524 (98%)	12 (2%)	45 73

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	ILE
1	A	61	ILE
1	A	116	SER
1	A	295	LYS
1	B	41	ILE
1	B	56	LYS
1	B	59	GLU
1	B	62	ILE
1	B	84	ILE
1	B	114	PHE
1	B	122	SER
1	B	160	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	167	ASN
1	B	100	HIS

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Mol	Chain	Res	Type
1	B	167	ASN
1	B	260	GLN
1	B	300	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 13 ligands modelled in this entry, 3 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	PGE	B	404	-	9,9,9	0.35	0	8,8,8	0.36	0
4	GOL	B	407	-	5,5,5	0.97	0	5,5,5	1.14	0
5	EDO	A	404	-	3,3,3	0.50	0	2,2,2	0.30	0
5	EDO	A	406	-	3,3,3	0.74	0	2,2,2	0.29	0
7	PG4	B	403	-	12,12,12	0.14	0	11,11,11	0.55	0
4	GOL	B	406	-	5,5,5	1.22	1 (20%)	5,5,5	0.87	0
5	EDO	A	405	-	3,3,3	0.62	0	2,2,2	0.10	0
3	PGE	A	402	-	9,9,9	0.28	0	8,8,8	0.54	0
3	PGE	B	405	-	9,9,9	0.35	0	8,8,8	0.36	0
4	GOL	A	403	-	5,5,5	1.03	0	5,5,5	0.87	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
3	PGE	B	404	-	-	2/7/7/7	-
4	GOL	B	407	-	-	2/4/4/4	-
5	EDO	A	404	-	-	0/1/1/1	-
5	EDO	A	406	-	-	0/1/1/1	-
7	PG4	B	403	-	-	5/10/10/10	-
4	GOL	B	406	-	-	0/4/4/4	-
5	EDO	A	405	-	-	0/1/1/1	-
3	PGE	A	402	-	-	1/7/7/7	-
3	PGE	B	405	-	-	3/7/7/7	-
4	GOL	A	403	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	406	GOL	O2-C2	-2.42	1.36	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	GOL	C1-C2-C3-O3
3	B	405	PGE	C6-C5-O3-C4
7	B	403	PG4	O2-C3-C4-O3
3	A	402	PGE	O3-C5-C6-O4
3	B	404	PGE	O3-C5-C6-O4
3	B	405	PGE	O1-C1-C2-O2
7	B	403	PG4	C5-C6-O4-C7
3	B	405	PGE	C1-C2-O2-C3
4	A	403	GOL	O2-C2-C3-O3
7	B	403	PG4	C1-C2-O2-C3
3	B	404	PGE	C4-C3-O2-C2
7	B	403	PG4	O1-C1-C2-O2
7	B	403	PG4	C3-C4-O3-C5
4	B	407	GOL	C1-C2-C3-O3
4	B	407	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	403	PG4	2	0
4	B	406	GOL	1	0
5	A	405	EDO	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	304/356 (85%)	0.67	22 (7%)	21	19	39, 51, 95, 179	0
1	B	304/356 (85%)	0.64	27 (8%)	15	13	38, 50, 100, 172	0
All	All	608/712 (85%)	0.66	49 (8%)	18	15	38, 50, 96, 179	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	138	PHE	5.6
1	B	161	ILE	5.2
1	B	138	PHE	4.9
1	A	161	ILE	4.8
1	A	114	PHE	4.8
1	B	114	PHE	4.7
1	B	44	SER	4.7
1	B	116	SER	4.6
1	A	111	ASN	4.3
1	B	115	SER	4.0
1	A	163	ILE	3.8
1	A	162	PRO	3.7
1	B	117	PRO	3.6
1	A	115	SER	3.5
1	A	62	ILE	3.4
1	A	337	ASP	3.2
1	B	163	ILE	3.1
1	A	160	ASN	3.0
1	B	160	ASN	3.0
1	B	62	ILE	2.8
1	A	197	PRO	2.8
1	B	111	ASN	2.8
1	B	162	PRO	2.8
1	B	43	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	110	SER	2.7
1	B	118	ILE	2.7
1	B	248	LYS	2.6
1	A	269	GLY	2.6
1	B	41	ILE	2.5
1	B	166	LEU	2.5
1	B	113	SER	2.5
1	B	337	ASP	2.4
1	A	166	LEU	2.4
1	B	51	ASN	2.4
1	B	119	PRO	2.3
1	A	168	LEU	2.3
1	B	61	ILE	2.3
1	A	61	ILE	2.3
1	A	164	SER	2.2
1	B	168	LEU	2.2
1	B	164	SER	2.2
1	A	63	ASP	2.2
1	A	116	SER	2.1
1	B	110	SER	2.1
1	B	165	ASP	2.1
1	B	202	LYS	2.1
1	A	113	SER	2.0
1	A	202	LYS	2.0
1	A	165	ASP	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 oligosaccharides in this entry.

6.4 Ligands (i)

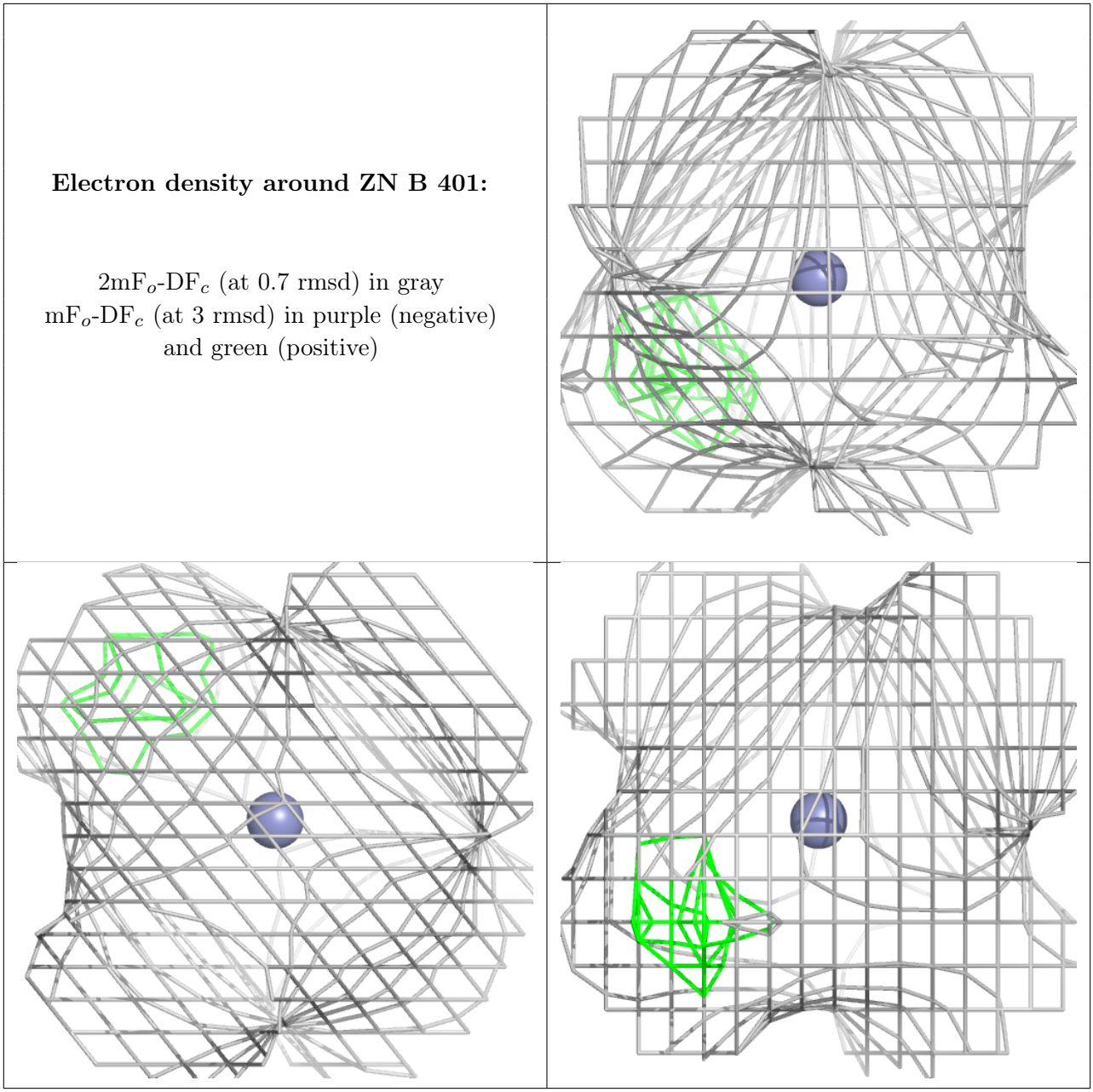
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	EDO	A	406	4/4	0.65	0.20	50,52,61,62	0
5	EDO	A	405	4/4	0.69	0.20	52,53,58,59	0
4	GOL	B	407	6/6	0.77	0.20	61,65,69,69	0
4	GOL	B	406	6/6	0.79	0.14	58,61,64,65	0
3	PGE	B	405	10/10	0.79	0.17	59,70,73,77	0
5	EDO	A	404	4/4	0.80	0.17	65,68,73,74	0
3	PGE	A	402	10/10	0.81	0.19	56,63,67,70	0
4	GOL	A	403	6/6	0.82	0.14	64,71,75,80	0
3	PGE	B	404	10/10	0.88	0.17	62,71,75,79	0
7	PG4	B	403	13/13	0.88	0.14	59,65,70,72	0
6	CA	B	402	1/1	0.94	0.14	87,87,87,87	0
2	ZN	B	401	1/1	0.99	0.03	44,44,44,44	0
2	ZN	A	401	1/1	1.00	0.02	44,44,44,44	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

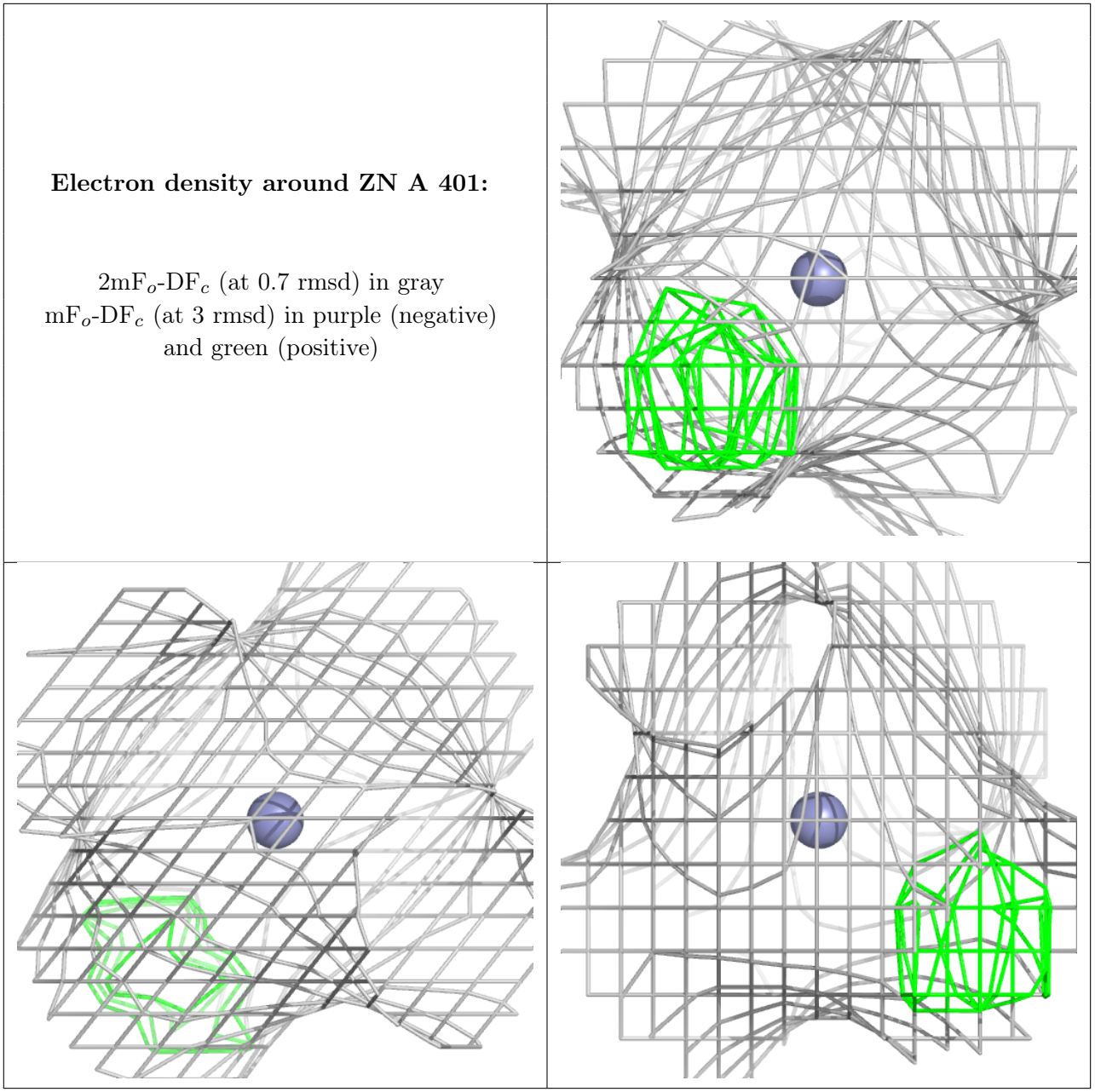
Electron density around ZN B 401:

$2mF_o$-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)



6.5 Other polymers

There are no such residues in this entry.