



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 11, 2024 – 08:03 AM EDT

PDB ID : 9CGN
Title : Pikromycin Thioesterase with heptaketide adduct
Authors : Smith, J.L.; Choudhary, V.
Deposited on : 2024-06-30
Resolution : 2.80 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.002 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.38.3

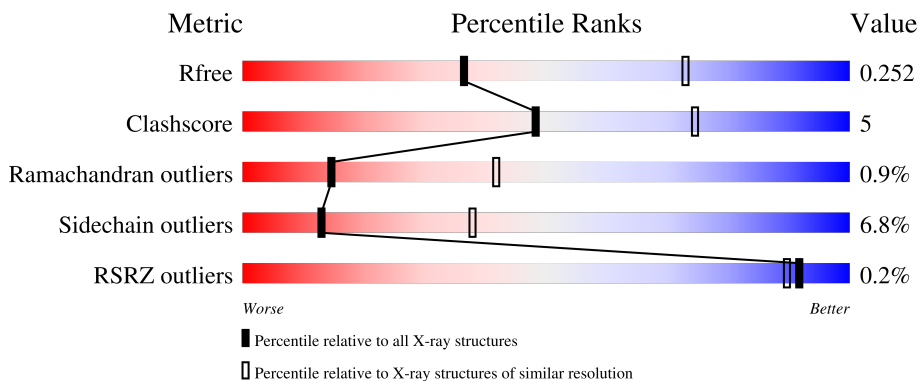
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3657 (2.80-2.80)
Clashscore	180529	4123 (2.80-2.80)
Ramachandran outliers	177936	4071 (2.80-2.80)
Sidechain outliers	177891	4073 (2.80-2.80)
RSRZ outliers	164620	3659 (2.80-2.80)

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	283	 83% 13% ..
1	B	283	 80% 17% ..

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4290 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.

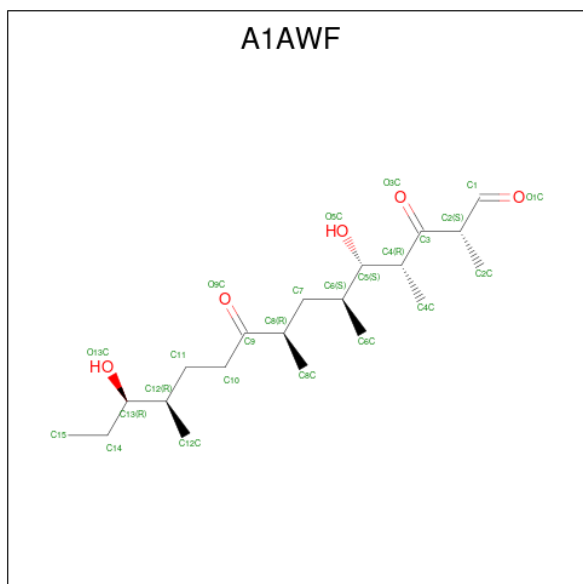
- Molecule 1 is a protein called Narbonolide/10-deoxymethynolide synthase PikA4, module 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	277	Total 2095	C 1324	N 375	O 389	S 7	0	0	0
1	B	277	Total 2095	C 1324	N 375	O 389	S 7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1196	DPP	SER	engineered mutation	UNP Q9ZGI2
B	1196	DPP	SER	engineered mutation	UNP Q9ZGI2

- Molecule 2 is (2S,4R,5S,6S,8R,12R,13R)-5,13-dihydroxy-2,4,6,8,12-pentamethyl-3,9-dioxopentadecanal (three-letter code: A1AWF) (formula: C₂₀H₃₆O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			25	20	5		
2	B	1	Total	C	O	0	0
			25	20	5		

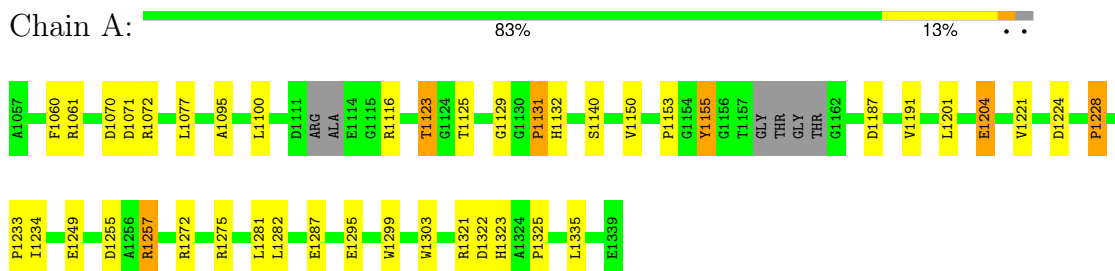
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	36	Total	O	0	0
			36	36		
3	B	14	Total	O	0	0
			14	14		

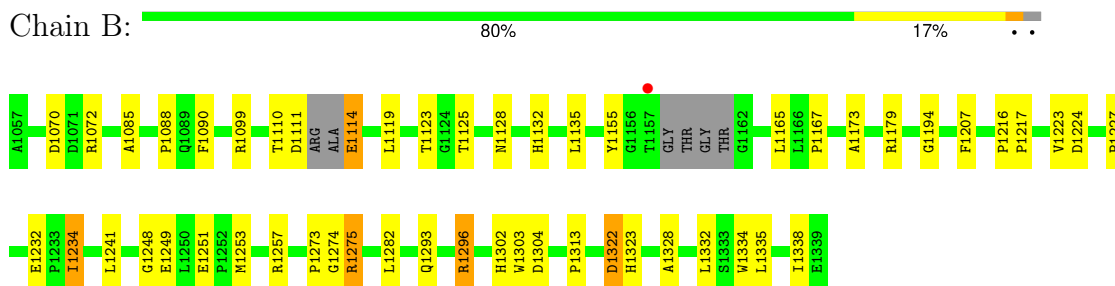
3 Residue-property plots [i](#)

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: Narbonolide/10-deoxymethynolide synthase PikA4, module 6



- Molecule 1: Narbonolide/10-deoxymethynolide synthase PikA4, module 6



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.04Å 105.18Å 114.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.77 – 2.80 40.77 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.77-2.80) 99.9 (40.77-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.81Å)	Xtrriage
Refinement program	PHENIX (1.21_5207: ???)	Depositor
R, R_{free}	0.174 , 0.252 0.173 , 0.252	Depositor DCC
R_{free} test set	16899 reflections (5.51%)	wwPDB-VP
Wilson B-factor (Å ²)	69.4	Xtrriage
Anisotropy	0.227	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4290	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% 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: A1AWF, DPP

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	0.54	0/2143	0.72	1/2919 (0.0%)
1	B	0.51	0/2143	0.68	0/2919
All	All	0.52	0/4286	0.70	1/5838 (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	1228	PRO	C-N-CA	-5.87	109.97	122.30

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	2095	0	2017	16	0
1	B	2095	0	2017	29	0
2	A	25	0	0	0	0
2	B	25	0	0	1	0
3	A	36	0	0	1	0
3	B	14	0	0	3	0
All	All	4290	0	4034	45	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 (45) 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:1232:GLU:OE2	1:B:1296:ARG:NH1	2.00	0.93
1:A:1100:LEU:HD11	1:A:1153:PRO:HG3	1.81	0.62
1:A:1070:ASP:O	1:A:1072:ARG:HG3	2.01	0.61
1:B:1282:LEU:HD13	1:B:1303:TRP:HB2	1.83	0.59
1:B:1234:ILE:HD12	1:B:1241:LEU:HD11	1.84	0.59
1:B:1119:LEU:HD21	1:B:1335:LEU:HD11	1.86	0.57
1:B:1322:ASP:HB2	1:B:1323:HIS:CD2	2.39	0.57
1:B:1227:PRO:HG2	3:B:1501:HOH:O	2.04	0.56
1:B:1207:PHE:CE1	1:B:1274:GLY:HA3	2.40	0.56
1:B:1275:ARG:NH2	1:B:1304:ASP:OD2	2.40	0.54
1:B:1207:PHE:CZ	1:B:1274:GLY:HA3	2.44	0.53
1:B:1302:HIS:HD2	3:B:1501:HOH:O	1.92	0.53
1:A:1282:LEU:HD13	1:A:1303:TRP:HB2	1.91	0.52
1:A:1060:PHE:HB2	1:A:1255:ASP:CG	2.30	0.52
1:A:1322:ASP:HB2	1:A:1323:HIS:CD2	2.46	0.51
1:B:1155:TYR:O	1:B:1257:ARG:NH2	2.45	0.51
1:B:1334:TRP:O	1:B:1338:ILE:HG23	2.11	0.51
1:B:1128:ASN:ND2	1:B:1248:GLY:O	2.44	0.50
1:B:1088:PRO:HB2	1:B:1165:LEU:HD23	1.96	0.48
1:B:1241:LEU:HD22	2:B:1401:A1AWF:C12C	2.43	0.48
1:A:1204:GLU:HG3	1:A:1272:ARG:HH11	1.79	0.48
1:B:1234:ILE:HD13	1:B:1234:ILE:HA	1.61	0.47
1:A:1233:PRO:HG3	1:A:1299:TRP:HA	1.95	0.47
1:A:1201:LEU:HA	1:A:1201:LEU:HD23	1.69	0.47
1:B:1070:ASP:O	1:B:1072:ARG:HG3	2.15	0.47
1:B:1111:ASP:OD2	1:B:1114:GLU:HB3	2.15	0.46
1:B:1194:GLY:O	1:B:1223:VAL:HG23	2.16	0.46
1:B:1249:GLU:OE2	1:B:1253:MET:HG3	2.15	0.46
1:A:1131:PRO:HD2	1:A:1132:HIS:ND1	2.30	0.46
1:B:1328:ALA:O	1:B:1332:LEU:HG	2.16	0.45
1:A:1123:THR:OG1	1:A:1150:VAL:O	2.34	0.45
1:B:1132:HIS:HA	1:B:1135:LEU:HG	1.99	0.45
1:B:1090:PHE:HB3	1:B:1165:LEU:HD13	1.98	0.44
1:A:1155:TYR:O	1:A:1257:ARG:NH2	2.52	0.43
1:B:1179:ARG:NH1	3:B:1502:HOH:O	2.48	0.43
1:B:1167:PRO:HB3	1:B:1173:ALA:HB2	2.01	0.42
1:B:1216:PRO:HA	1:B:1217:PRO:HD2	1.94	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1191:VAL:HG21	1:A:1335:LEU:HD21	2.02	0.42
3:A:1536:HOH:O	1:B:1085:ALA:HB1	2.20	0.41
1:A:1061:ARG:NH2	1:A:1249:GLU:OE1	2.48	0.41
1:A:1221:VAL:HG13	1:A:1281:LEU:HD23	2.03	0.41
1:B:1249:GLU:OE2	1:B:1253:MET:HE2	2.20	0.41
1:B:1313:PRO:HB2	1:B:1323:HIS:ND1	2.35	0.41
1:A:1129:GLY:HA2	1:A:1132:HIS:CE1	2.56	0.40
1:A:1204:GLU:HG3	1:A:1272:ARG:NH1	2.36	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	270/283 (95%)	254 (94%)	13 (5%)	3 (1%)	12	37
1	B	270/283 (95%)	254 (94%)	14 (5%)	2 (1%)	19	48
All	All	540/566 (95%)	508 (94%)	27 (5%)	5 (1%)	14	42

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1273	PRO
1	A	1131	PRO
1	B	1110	THR
1	A	1095	ALA
1	A	1071	ASP

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	206/209 (99%)	189 (92%)	17 (8%)	9	28
1	B	206/209 (99%)	195 (95%)	11 (5%)	19	49
All	All	412/418 (99%)	384 (93%)	28 (7%)	13	38

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1077	LEU
1	A	1116	ARG
1	A	1123	THR
1	A	1125	THR
1	A	1140	SER
1	A	1155	TYR
1	A	1187	ASP
1	A	1204	GLU
1	A	1224	ASP
1	A	1228	PRO
1	A	1234	ILE
1	A	1257	ARG
1	A	1275	ARG
1	A	1287	GLU
1	A	1295	GLU
1	A	1321	ARG
1	A	1325	PRO
1	B	1099	ARG
1	B	1114	GLU
1	B	1123	THR
1	B	1125	THR
1	B	1224	ASP
1	B	1234	ILE
1	B	1251	GLU
1	B	1275	ARG
1	B	1293	GLN
1	B	1296	ARG

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Mol	Chain	Res	Type
1	B	1322	ASP

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	1323	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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
1	DPP	A	1196	1,2	4,5,6	0.79	0	1,5,7	0.65	0
1	DPP	B	1196	1,2	4,5,6	0.76	0	1,5,7	1.02	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
1	DPP	A	1196	1,2	-	0/2/4/6	-
1	DPP	B	1196	1,2	-	0/2/4/6	-

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.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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
2	A1AWF	B	1401	1	23,24,24	2.11	5 (21%)	29,32,32	2.19	13 (44%)
2	A1AWF	A	1401	1	23,24,24	1.98	5 (21%)	29,32,32	2.60	12 (41%)

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
2	A1AWF	B	1401	1	-	7/37/37/37	-
2	A1AWF	A	1401	1	-	8/37/37/37	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1401	A1AWF	C11-C10	-6.49	1.33	1.52
2	B	1401	A1AWF	C11-C10	-5.86	1.35	1.52
2	B	1401	A1AWF	C12-C13	4.12	1.60	1.53
2	B	1401	A1AWF	C2-C3	3.87	1.57	1.53
2	B	1401	A1AWF	C10-C9	3.46	1.55	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1401	A1AWF	C2-C3	3.44	1.56	1.53
2	A	1401	A1AWF	C10-C9	3.11	1.55	1.51
2	A	1401	A1AWF	C12-C13	2.72	1.58	1.53
2	B	1401	A1AWF	C4-C3	2.52	1.56	1.52
2	A	1401	A1AWF	C4-C3	2.09	1.56	1.52

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1401	A1AWF	C12C-C12-C13	8.42	122.55	111.61
2	A	1401	A1AWF	C10-C11-C12	5.10	123.98	114.46
2	B	1401	A1AWF	C12C-C12-C13	4.91	118.00	111.61
2	A	1401	A1AWF	C4-C3-C2	4.57	123.94	117.09
2	B	1401	A1AWF	C4-C5-C6	-4.07	108.10	114.66
2	B	1401	A1AWF	C4-C3-C2	3.95	123.02	117.09
2	B	1401	A1AWF	C10-C9-C8	3.29	123.88	117.08
2	A	1401	A1AWF	C4-C5-C6	-3.14	109.60	114.66
2	B	1401	A1AWF	C4C-C4-C3	3.05	113.43	108.09
2	B	1401	A1AWF	O13C-C13-C12	2.99	115.38	109.05
2	A	1401	A1AWF	O3C-C3-C4	-2.96	116.52	120.64
2	B	1401	A1AWF	O3C-C3-C4	-2.85	116.67	120.64
2	A	1401	A1AWF	O13C-C13-C12	2.80	114.98	109.05
2	B	1401	A1AWF	C6C-C6-C7	2.72	114.80	110.68
2	A	1401	A1AWF	C11-C10-C9	-2.70	109.07	114.55
2	A	1401	A1AWF	C8C-C8-C9	-2.49	103.76	109.58
2	B	1401	A1AWF	C10-C11-C12	2.40	118.95	114.46
2	A	1401	A1AWF	C6C-C6-C7	2.39	114.29	110.68
2	A	1401	A1AWF	C2C-C2-C3	2.31	112.81	109.58
2	B	1401	A1AWF	C7-C8-C9	2.30	115.68	110.96
2	B	1401	A1AWF	O9C-C9-C8	-2.12	116.28	120.78
2	A	1401	A1AWF	C4C-C4-C5	-2.12	108.68	112.42
2	B	1401	A1AWF	C8C-C8-C9	-2.09	104.69	109.58
2	A	1401	A1AWF	C4C-C4-C3	2.03	111.64	108.09
2	B	1401	A1AWF	C12C-C12-C11	-2.01	107.22	110.34

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1401	A1AWF	C11-C12-C13-C14
2	A	1401	A1AWF	C11-C12-C13-O13C
2	A	1401	A1AWF	C12C-C12-C13-C14

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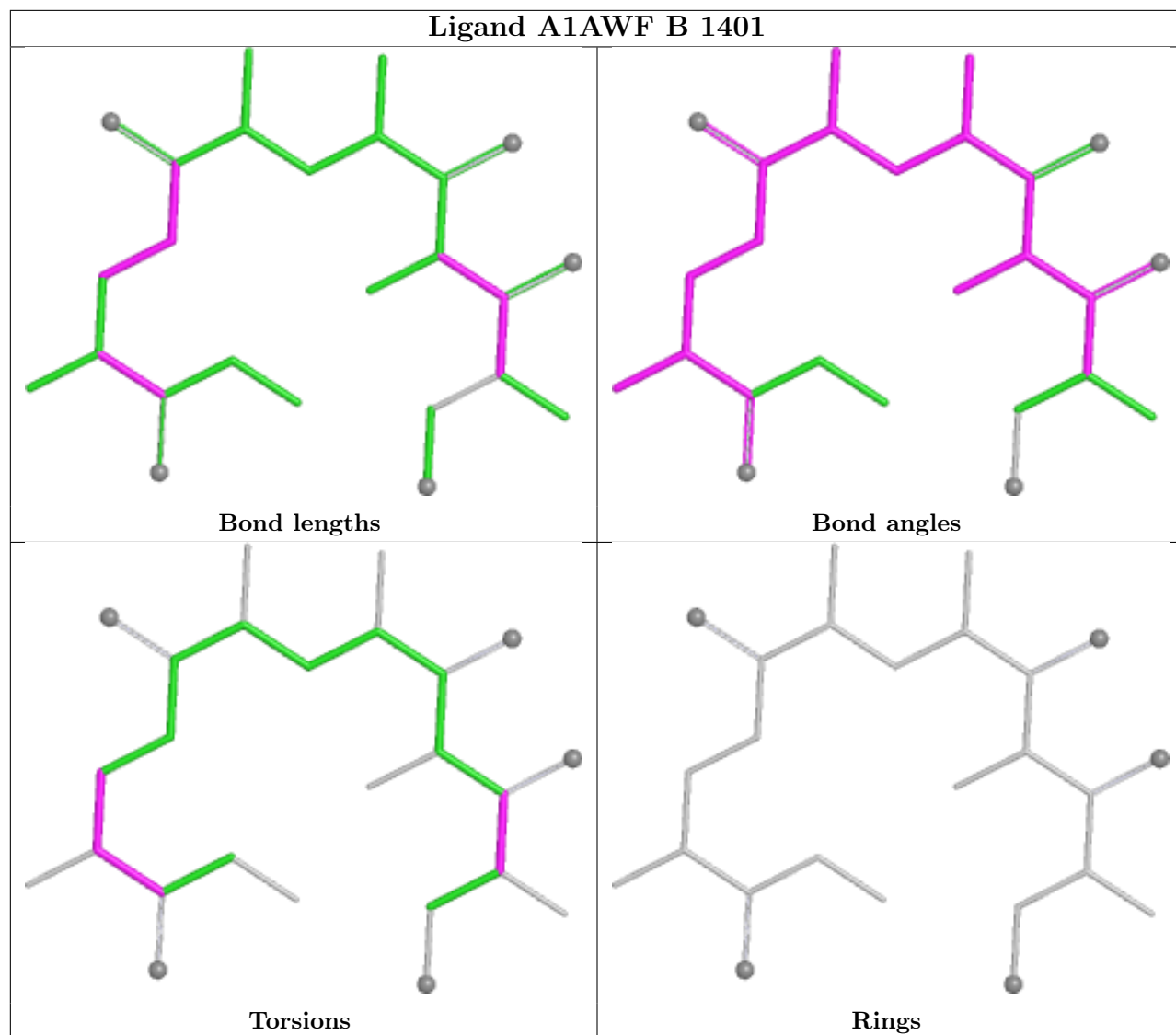
Mol	Chain	Res	Type	Atoms
2	A	1401	A1AWF	C12C-C12-C13-O13C
2	A	1401	A1AWF	C12-C13-C14-C15
2	A	1401	A1AWF	O13C-C13-C14-C15
2	B	1401	A1AWF	C11-C12-C13-O13C
2	B	1401	A1AWF	C12C-C12-C13-C14
2	B	1401	A1AWF	C12C-C12-C13-O13C
2	A	1401	A1AWF	C10-C11-C12-C12C
2	B	1401	A1AWF	C10-C11-C12-C12C
2	A	1401	A1AWF	C1-C2-C3-O3C
2	B	1401	A1AWF	C1-C2-C3-O3C
2	B	1401	A1AWF	C11-C12-C13-C14
2	B	1401	A1AWF	C10-C11-C12-C13

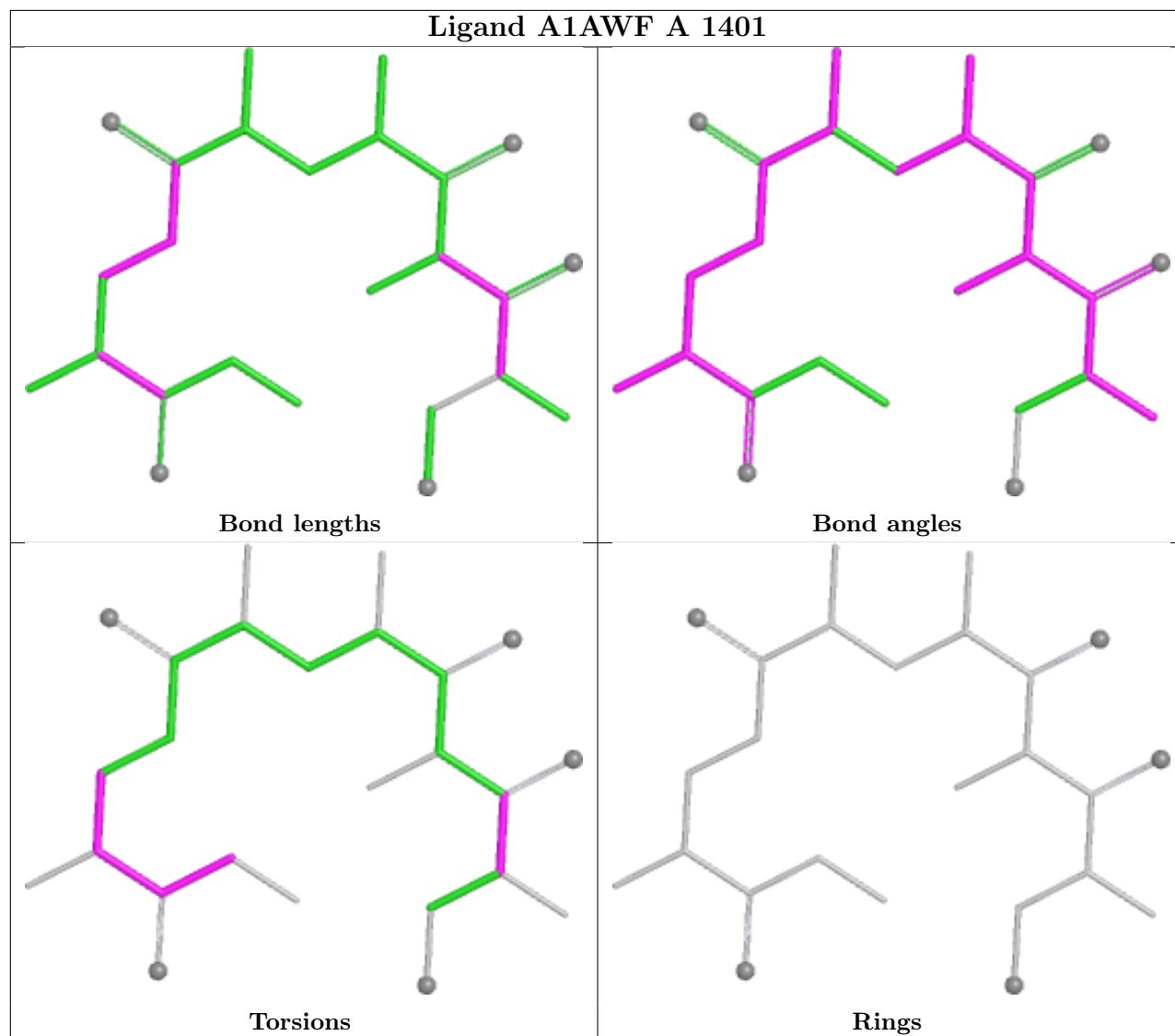
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1401	A1AWF	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 [i](#)

There are no chain breaks in this entry.

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	276/283 (97%)	-0.54	0 100 100	45, 58, 85, 110	0
1	B	276/283 (97%)	-0.39	1 (0%) 89 85	48, 64, 93, 108	0
All	All	552/566 (97%)	-0.46	1 (0%) 92 89	45, 61, 90, 110	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1157	THR	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	DPP	A	1196	6/7	0.97	0.05	49,51,55,56	0
1	DPP	B	1196	6/7	0.97	0.06	58,63,65,68	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

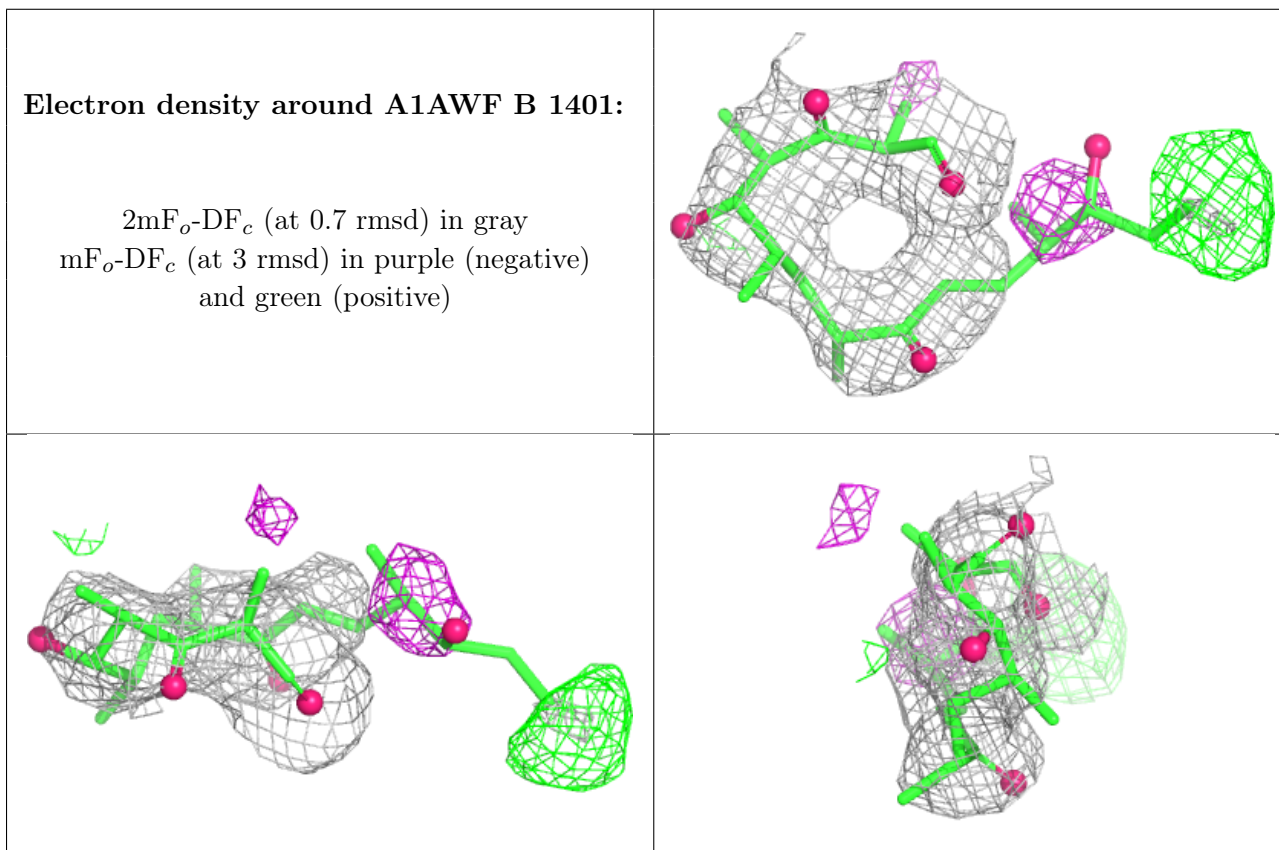
6.4 Ligands [i](#)

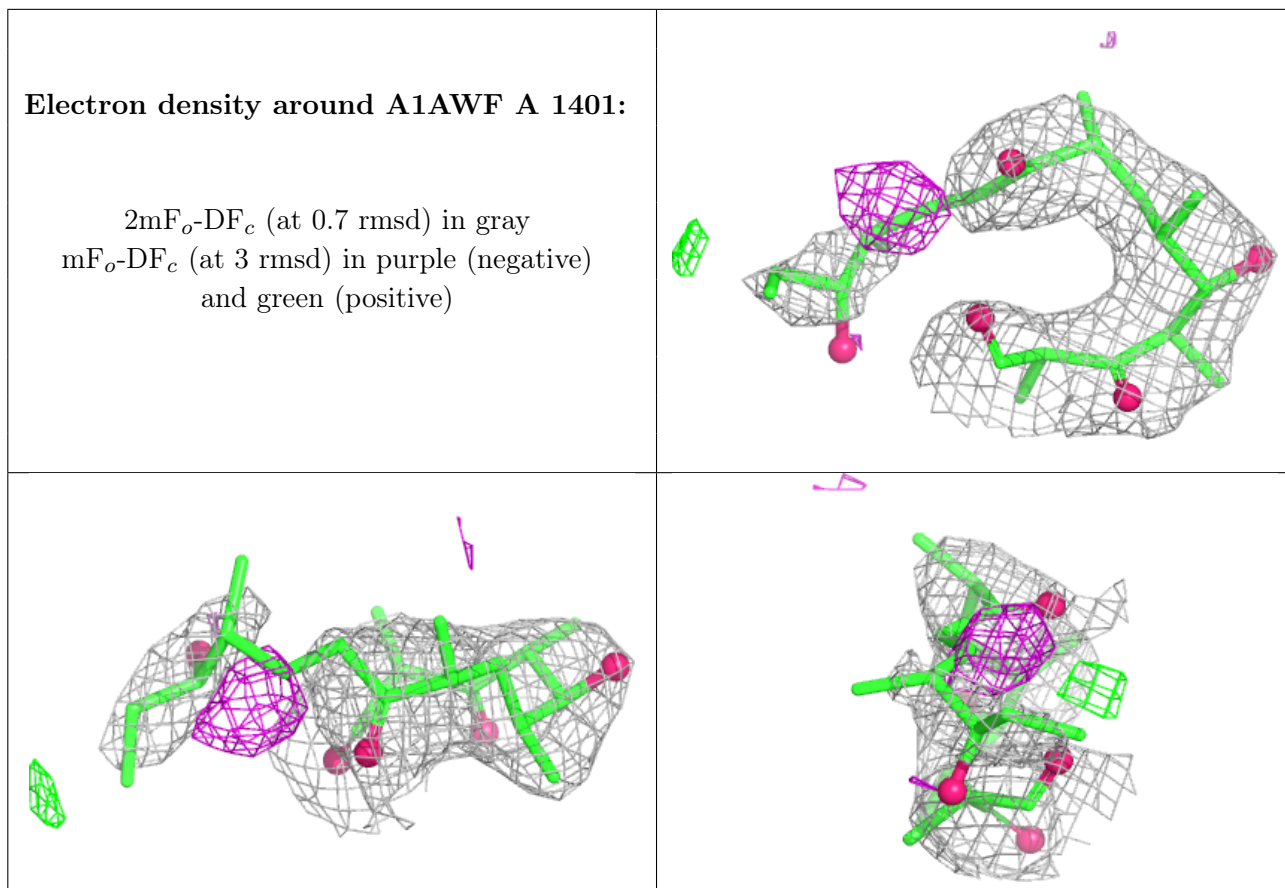
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

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
2	A1AWF	B	1401	25/25	0.85	0.17	67,75,92,96	0
2	A1AWF	A	1401	25/25	0.90	0.14	57,68,76,83	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.