



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2025 – 01:13 pm BST

PDB ID : 7AK7 / pdb_00007ak7
Title : Structure of Salmonella TacT2 toxin bound to TacA2 antitoxin
Authors : Grabe, G.J.; Morgan, R.M.L.; Hare, S.A.; Helaine, S.
Deposited on : 2020-09-30
Resolution : 2.14 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

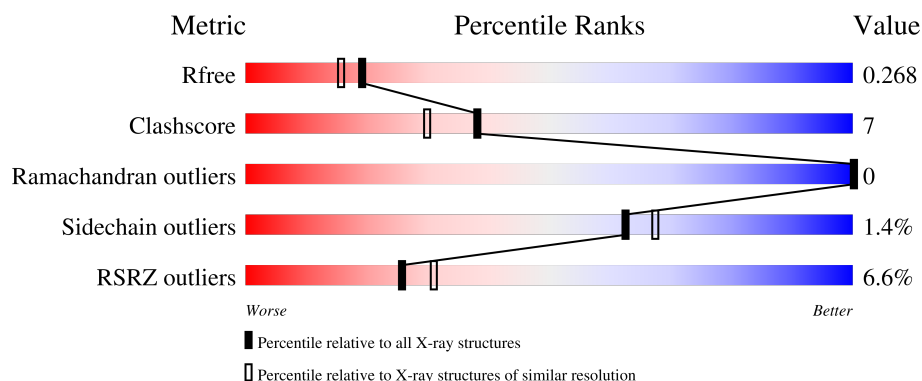
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3336 (2.16-2.12)
Clashscore	180529	3585 (2.16-2.12)
Ramachandran outliers	177936	3554 (2.16-2.12)
Sidechain outliers	177891	3553 (2.16-2.12)
RSRZ outliers	164620	3337 (2.16-2.12)

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	166	<div> <div>2%</div> <div>83%</div> <div>10%</div> <div>7%</div> </div>
1	B	166	<div> <div>5%</div> <div>81%</div> <div>11%</div> <div>7%</div> </div>
2	C	99	<div> <div>8%</div> <div>72%</div> <div>15%</div> <div>12%</div> </div>
2	D	99	<div> <div>7%</div> <div>73%</div> <div>13%</div> <div>13%</div> </div>
2	E	99	<div> <div>8%</div> <div>61%</div> <div>11%</div> <div>28%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	99	<div><div></div><div>6%</div><div>57%</div><div>17%</div><div>26%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5253 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 Acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total	C	N	O	S	0	1	0
			1160	729	202	218	11			
1	B	154	Total	C	N	O	S	0	0	0
			1155	726	202	215	12			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP A0A0D6HSU7
A	-1	GLY	-	expression tag	UNP A0A0D6HSU7
A	0	SER	-	expression tag	UNP A0A0D6HSU7
A	29	LYS	GLU	engineered mutation	UNP A0A0D6HSU7
A	137	PHE	TYR	engineered mutation	UNP A0A0D6HSU7
B	-2	MET	-	initiating methionine	UNP A0A0D6HSU7
B	-1	GLY	-	expression tag	UNP A0A0D6HSU7
B	0	SER	-	expression tag	UNP A0A0D6HSU7
B	29	LYS	GLU	engineered mutation	UNP A0A0D6HSU7
B	137	PHE	TYR	engineered mutation	UNP A0A0D6HSU7

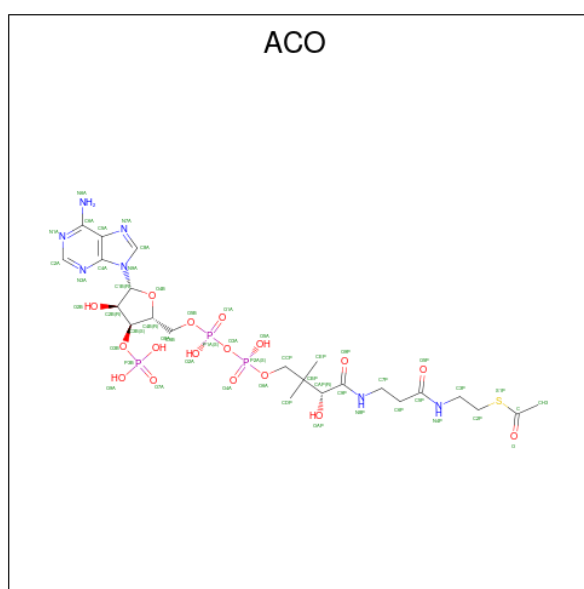
- Molecule 2 is a protein called CopG family transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	87	Total	C	N	O	S	0	0	0
			697	433	131	130	3			
2	D	86	Total	C	N	O	S	0	0	0
			675	420	125	128	2			
2	E	71	Total	C	N	O	S	0	0	0
			566	351	107	107	1			
2	F	73	Total	C	N	O	S	0	0	0
			576	357	109	109	1			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	expression tag	UNP A0A0D6HUM3
C	0	SER	-	expression tag	UNP A0A0D6HUM3
D	-1	GLY	-	expression tag	UNP A0A0D6HUM3
D	0	SER	-	expression tag	UNP A0A0D6HUM3
E	-1	GLY	-	expression tag	UNP A0A0D6HUM3
E	0	SER	-	expression tag	UNP A0A0D6HUM3
F	-1	GLY	-	expression tag	UNP A0A0D6HUM3
F	0	SER	-	expression tag	UNP A0A0D6HUM3

- Molecule 3 is ACETYL COENZYME *A (CCD ID: ACO) (formula: C₂₃H₃₈N₇O₁₇P₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		
3	B	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		

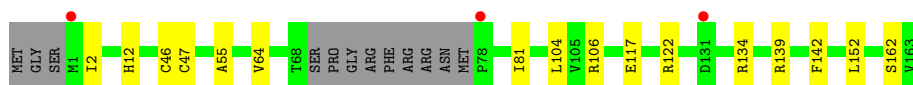
- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Cl	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	73	Total 73	O 73	0	0
5	B	77	Total 77	O 77	0	0
5	C	60	Total 60	O 60	0	0
5	D	43	Total 43	O 43	0	0
5	E	34	Total 34	O 34	0	0
5	F	34	Total 34	O 34	0	0

- Molecule 1: Acetyltransferase



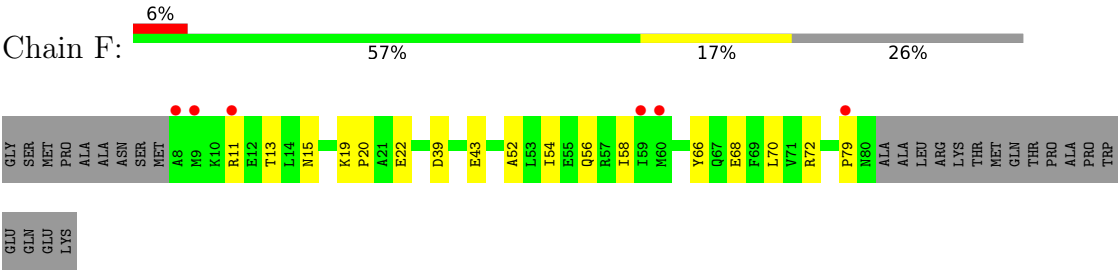
- | Metabolite | Log ₂ FC | P-value |
|------------|---------------------|---------|
| MET | | |
| GLY | | |
| SER | | |
| R11 | | |
| I2 | | |
| H12 | | |
| C46 | | |
| C47 | | |
| A55 | | |
| N67 | | |
| THR | | |
| SER | | |
| PRO | | |
| GLY | | |
| ARG | | |
| PHE | | |
| ARG | | |
| ARG | | |
| ASN | | |
| F78 | | |
| D79 | | |
| V83 | | |
| L104 | | |
| V105 | | |
| R106 | | |
| L110 | | |
| E117 | | |
| T118 | | |
| L125 | | |
| D131 | | |
| Q138 | | |
| F142 | | |
| P146 | | |
| M151 | | |
| L152 | | |
| D158 | | |
| V163 | | |

- [illegible]

- [illegible]

- GLY
SER
MET
MET
PRO
ALA
ALA
ASN
SER
SER
MET
MET
ALA
MET
K10
R11
E12
T13
R17
R23
R28
R33
I54
E55
Q56
K57
R58
I59
M60
Y66
L70
Q75
P79
N80
ALA
ALA
LEU
ARG
LYS
THR
MET
MET
GLN
THR
PRO
PRO
PRO
TRP
GLU
GLN
GLU

- 
- WORLD WIDE
PDB
PROTEIN DATA BANK



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.49Å 54.45Å 76.90Å 100.57° 97.73° 117.00°	Depositor
Resolution (Å)	46.66 – 2.14 46.66 – 2.14	Depositor EDS
% Data completeness (in resolution range)	97.1 (46.66-2.14) 97.1 (46.66-2.14)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.220 , 0.263 0.224 , 0.268	Depositor DCC
R_{free} test set	1795 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.006 for -h,-k,h+k+l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5253	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.02% 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: ACO, CL

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	1.01	0/1183	1.32	0/1605
1	B	1.02	0/1175	1.31	0/1594
2	C	0.96	0/707	1.36	0/954
2	D	0.98	0/685	1.36	0/928
2	E	0.95	0/572	1.37	0/770
2	F	0.98	0/582	1.39	0/784
All	All	0.99	0/4904	1.34	0/6635

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	1160	0	1176	16	0
1	B	1155	0	1171	15	0
2	C	697	0	711	16	0
2	D	675	0	674	14	0
2	E	566	0	577	10	0
2	F	576	0	584	14	0
3	A	51	0	34	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	51	0	34	1	0
4	C	1	0	0	0	0
5	A	73	0	0	3	0
5	B	77	0	0	3	0
5	C	60	0	0	2	0
5	D	43	0	0	0	0
5	E	34	0	0	2	0
5	F	34	0	0	1	0
All	All	5253	0	4961	67	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 7.

The worst 5 of 67 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)
2:F:22:GLU:OE1	5:F:101:HOH:O	1.84	0.95
2:C:51:GLU:OE2	5:C:201:HOH:O	1.91	0.89
2:C:15:ASN:OD1	2:F:15:ASN:ND2	2.09	0.86
1:B:125:LEU:HD13	1:B:151:MET:CE	2.08	0.82
1:A:117:GLU:OE2	5:A:301:HOH:O	2.00	0.79

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	151/166 (91%)	151 (100%)	0	0	100	100
1	B	150/166 (90%)	150 (100%)	0	0	100	100
2	C	85/99 (86%)	83 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	84/99 (85%)	83 (99%)	1 (1%)	0	100	100
2	E	69/99 (70%)	68 (99%)	1 (1%)	0	100	100
2	F	71/99 (72%)	70 (99%)	1 (1%)	0	100	100
All	All	610/728 (84%)	605 (99%)	5 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	130/139 (94%)	130 (100%)	0	100	100
1	B	129/139 (93%)	128 (99%)	1 (1%)	79	83
2	C	71/79 (90%)	69 (97%)	2 (3%)	38	38
2	D	67/79 (85%)	66 (98%)	1 (2%)	60	65
2	E	57/79 (72%)	55 (96%)	2 (4%)	31	29
2	F	57/79 (72%)	56 (98%)	1 (2%)	54	57
All	All	511/594 (86%)	504 (99%)	7 (1%)	62	67

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	14	LEU
2	E	12	GLU
2	F	13	THR
2	E	13	THR
2	C	51	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	56	GLN
2	F	56	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is 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	$\# Z > 2$
3	ACO	A	201	-	45,53,53	0.60	0	56,79,79	0.95	2 (3%)
3	ACO	B	201	-	45,53,53	0.66	1 (2%)	56,79,79	0.79	1 (1%)

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	ACO	A	201	-	-	12/47/67/67	0/3/3/3
3	ACO	B	201	-	-	16/47/67/67	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	201	ACO	P3B-O3B	2.62	1.64	1.59

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	ACO	P2A-O3A-P1A	-3.36	121.31	132.83
3	B	201	ACO	P2A-O3A-P1A	-2.42	124.51	132.83
3	A	201	ACO	C5A-C6A-N6A	2.11	123.56	120.35

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

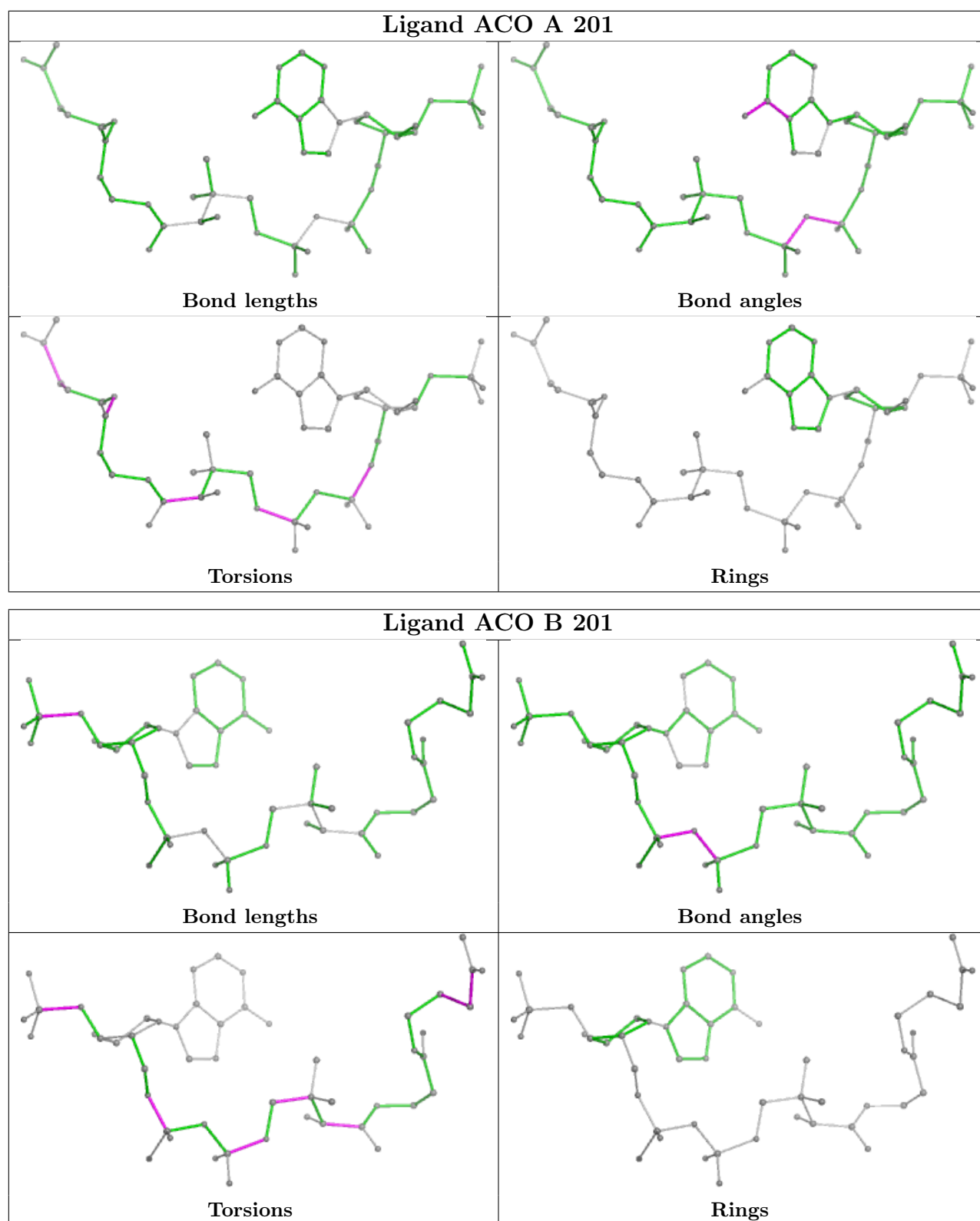
Mol	Chain	Res	Type	Atoms
3	A	201	ACO	C5B-O5B-P1A-O2A
3	A	201	ACO	N8P-C9P-CAP-OAP
3	A	201	ACO	C6P-C5P-N4P-C3P
3	A	201	ACO	O5P-C5P-N4P-C3P
3	A	201	ACO	C3P-C2P-S1P-C

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	ACO	2	0
3	B	201	ACO	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 ⓘ

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 [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	154/166 (92%)	0.38	3 (1%) 66 70	22, 33, 53, 78	1 (0%)
1	B	154/166 (92%)	0.35	9 (5%) 30 35	22, 33, 53, 86	0
2	C	87/99 (87%)	0.78	8 (9%) 16 20	26, 39, 63, 98	0
2	D	86/99 (86%)	0.71	7 (8%) 19 23	22, 40, 61, 86	0
2	E	71/99 (71%)	0.95	8 (11%) 11 14	25, 44, 72, 82	0
2	F	73/99 (73%)	1.03	6 (8%) 19 23	27, 44, 69, 81	0
All	All	625/728 (85%)	0.61	41 (6%) 26 31	22, 37, 64, 98	1 (0%)

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	9	MET	4.8
2	F	8	ALA	4.7
2	D	60	MET	4.6
2	D	9	MET	4.0
1	A	78	PRO	3.8

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](#)

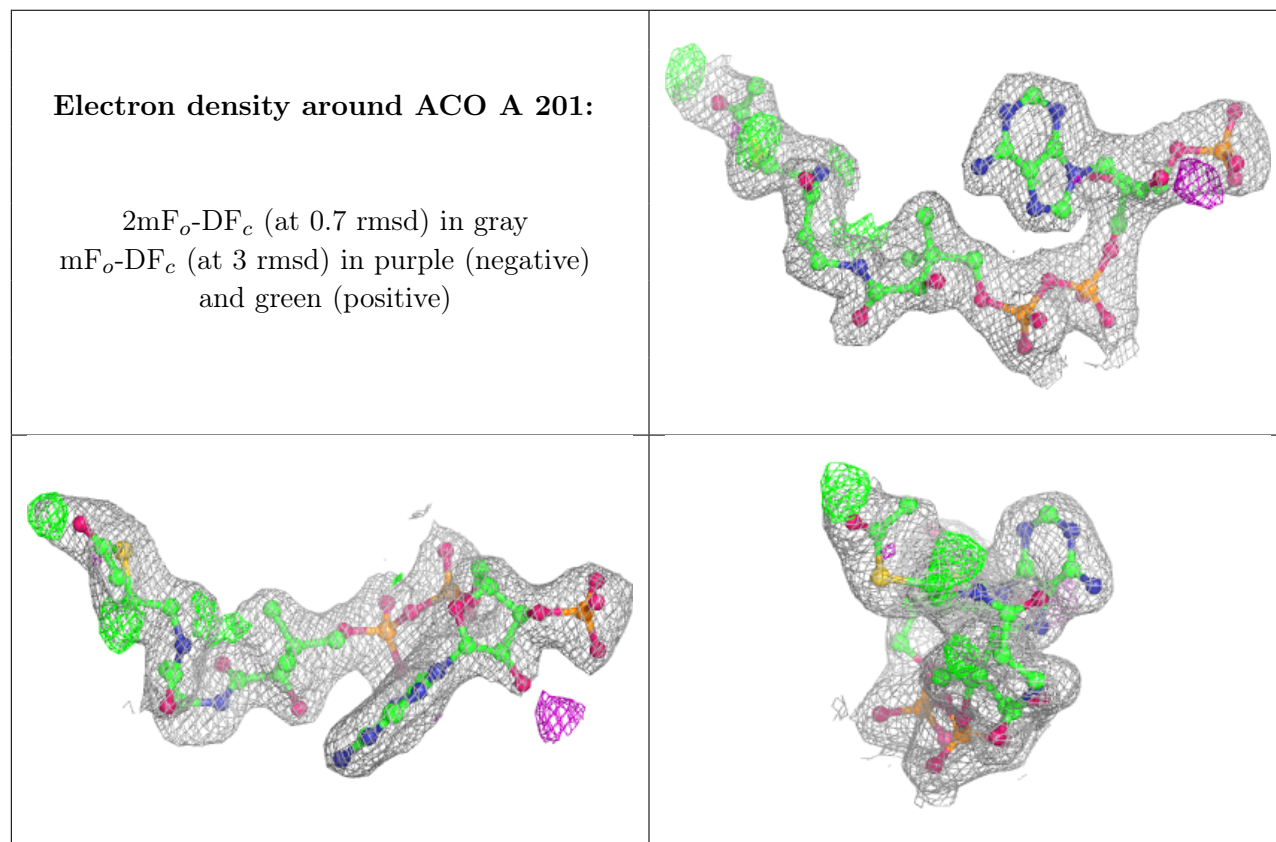
There are no oligosaccharides in this entry.

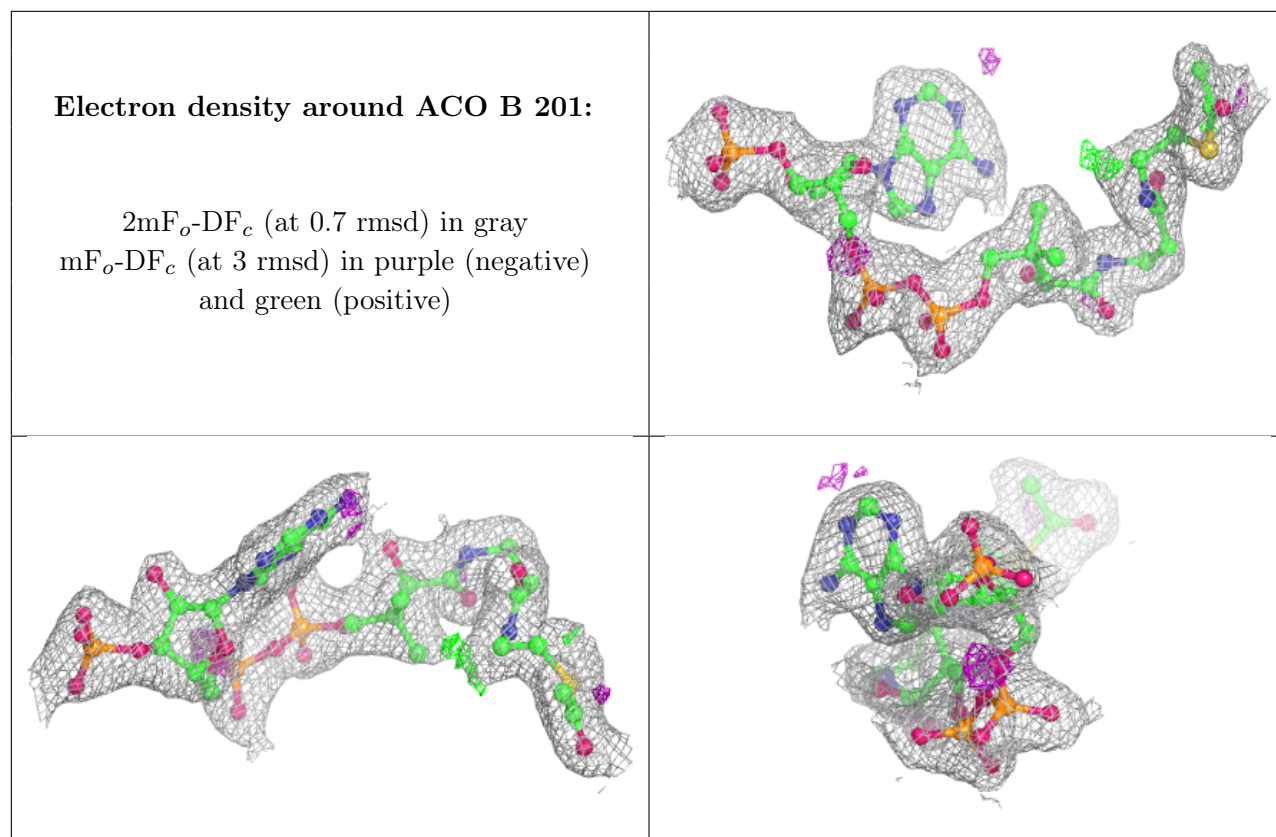
6.4 Ligands ⓘ

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	CL	C	101	1/1	0.85	0.12	65,65,65,65	0
3	ACO	A	201	51/51	0.89	0.11	29,47,58,64	0
3	ACO	B	201	51/51	0.90	0.10	30,41,52,60	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.