WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Dec 17, 2023 – 12:23 PM EST

PDB ID	:	4W93
Title	:	Human pancreatic alpha-amylase in complex with montbretin A
Authors	:	Williams, L.K.; Caner, S.; Brayer, G.D.
Deposited on	:	2014-08-27
Resolution	:	1.35 Å(reported)

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
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)	:	2.36

1　Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
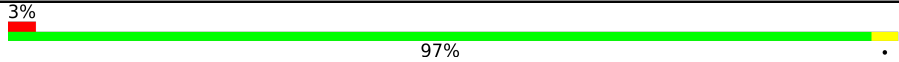*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.35 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.

Percentile relative to all X-ray structures
Percentile relative to X-ray structures of similar resolution
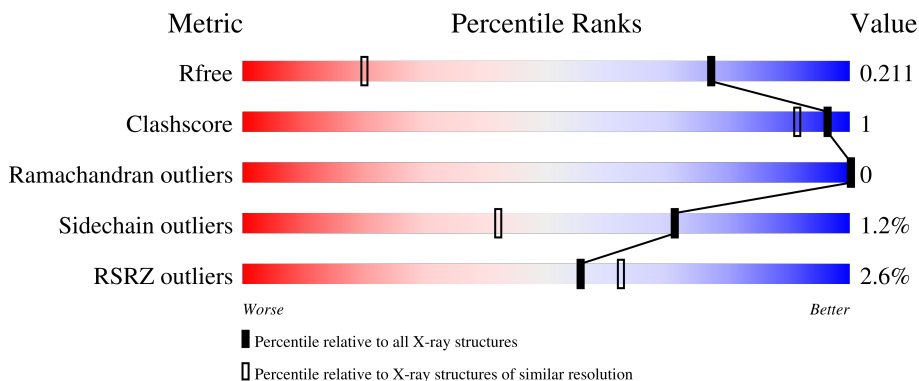
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1509 (1.38-1.34)
Clashscore	141614	1551 (1.38-1.34)
Ramachandran outliers	138981	1530 (1.38-1.34)
Sidechain outliers	138945	1530 (1.38-1.34)
RSRZ outliers	127900	1487 (1.38-1.34)

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	496	3% / 97% ·

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4501 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 Pancreatic alpha-amylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	496	Total 3945	C 2497	N 696	O 732	S 20	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ca 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is Montbretin A (three-letter code: 3L9) (formula: $C_{53}H_{64}O_{33}$).
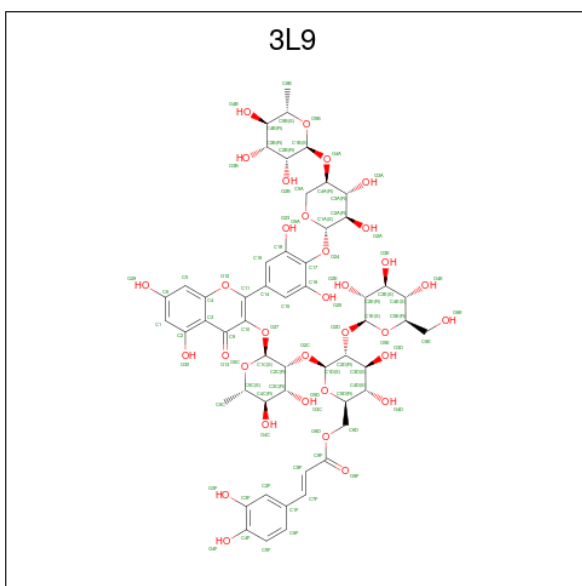
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total C O 86 53 33			0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	468	Total O 468 468		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: Pancreatic alpha-amylase
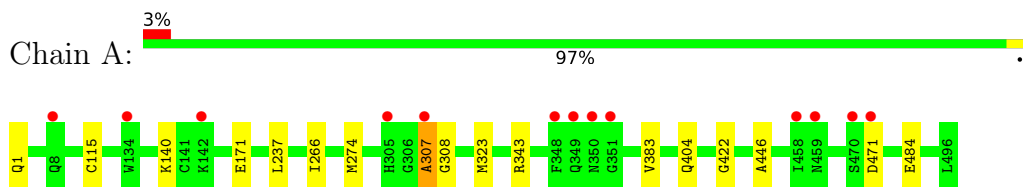
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	52.37Å 74.10Å 135.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.05 – 1.35 37.05 – 1.35	Depositor EDS
% Data completeness (in resolution range)	99.0 (37.05-1.35) 99.0 (37.05-1.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1.13 (at 1.35Å)	Xtriage
Refinement program	PHENIX 1.9_1683	Depositor
R, R_{free}	0.198 , 0.211 0.198 , 0.211	Depositor DCC
R_{free} test set	5752 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	14.8	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 41.2	EDS
L-test for twinning[2]	$< |L| > = 0.40, < L^2 > = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4501	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: CL, PCA, 3L9, CA

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	0.37	0/4052	0.58	0/5506

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	307	ALA	Peptide

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	3945	0	3718	8	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
4	A	86	0	53	0	0
5	A	468	0	0	2	0
All	All	4501	0	3771	8	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 1.

All (8) 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:446:ALA:HB2	1:A:471:ASP:HA	1.82	0.62
1:A:140:LYS:NZ	5:A:942:HOH:O	2.18	0.61
1:A:237:LEU:HD11	1:A:307:ALA:HB1	1.87	0.56
1:A:343:ARG:HG3	1:A:383:VAL:HG22	1.94	0.50
1:A:404:GLN:OE1	1:A:422:GLY:HA3	2.18	0.43
1:A:307:ALA:HA	1:A:308:GLY:HA2	1.58	0.42
1:A:140:LYS:HB2	1:A:140:LYS:HE3	1.50	0.42
1:A:274:MET:HG3	5:A:813:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	494/496 (100%)	486 (98%)	8 (2%)	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	418/418 (100%)	413 (99%)	5 (1%)	71	42

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	CYS
1	A	171	GLU
1	A	266	ILE
1	A	323	MET
1	A	484	GLU

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

5.3.3　RNA ⓘ

There are no RNA molecules in this entry.

5.4　Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	PCA	A	1	1	7,8,9	1.79	1 (14%)	9,10,12	2.38	5 (55%)

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	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CD-N	4.46	1.46	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1	PCA	CB-CA-C	-3.82	107.44	112.70
1	A	1	PCA	OE-CD-CG	-3.27	121.06	126.76
1	A	1	PCA	CA-N-CD	-2.77	104.08	113.58
1	A	1	PCA	CG-CD-N	2.51	114.89	108.39
1	A	1	PCA	CB-CG-CD	-2.30	100.69	104.40

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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
4	3L9	A	503	-	94,94,94	2.37	34 (36%)	138,141,141	2.30	38 (27%)

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
4	3L9	A	503	-	-	7/36/133/133	0/9/9/9

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	3L9	O5B-C1B	-7.38	1.23	1.41
4	A	503	3L9	O24-C17	-6.94	1.24	1.38
4	A	503	3L9	O2B-C2B	-5.39	1.30	1.43
4	A	503	3L9	C10-C11	5.19	1.48	1.37
4	A	503	3L9	O4A-C4A	-5.05	1.36	1.44
4	A	503	3L9	O4E-C4E	-5.05	1.31	1.43
4	A	503	3L9	C3-C2	-4.80	1.33	1.41
4	A	503	3L9	O4B-C4B	-4.50	1.32	1.43
4	A	503	3L9	O3C-C3C	-4.35	1.32	1.43
4	A	503	3L9	C5F-C4F	-4.14	1.32	1.39
4	A	503	3L9	O2D-C1E	-3.72	1.31	1.41
4	A	503	3L9	O12-C4	-3.71	1.32	1.38
4	A	503	3L9	O25-C16	-3.42	1.29	1.36
4	A	503	3L9	O29-C6	-3.30	1.29	1.37
4	A	503	3L9	O2A-C2A	-3.29	1.35	1.43
4	A	503	3L9	O2C-C1D	-3.16	1.32	1.41
4	A	503	3L9	C3D-C2D	2.91	1.60	1.52
4	A	503	3L9	O23-C18	-2.65	1.31	1.36
4	A	503	3L9	O5C-C1C	-2.56	1.35	1.41
4	A	503	3L9	O24-C1A	-2.49	1.37	1.41
4	A	503	3L9	O2E-C2E	-2.48	1.37	1.43
4	A	503	3L9	O9F-C9F	-2.43	1.16	1.21
4	A	503	3L9	O3A-C3A	-2.40	1.37	1.43
4	A	503	3L9	C15-C16	2.36	1.42	1.38
4	A	503	3L9	O2D-C2D	-2.33	1.37	1.43
4	A	503	3L9	O2C-C2C	-2.32	1.37	1.43
4	A	503	3L9	O5C-C5C	-2.27	1.39	1.44
4	A	503	3L9	O3B-C3B	-2.20	1.37	1.43
4	A	503	3L9	O13-C9	2.18	1.27	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	3L9	O4F-C4F	-2.17	1.32	1.36
4	A	503	3L9	C8F-C9F	2.15	1.53	1.48
4	A	503	3L9	C3E-C4E	2.11	1.57	1.52
4	A	503	3L9	C8F-C7F	2.09	1.38	1.33
4	A	503	3L9	C1-C2	-2.07	1.36	1.38

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	503	3L9	C11-C10-C9	-8.14	113.41	121.96
4	A	503	3L9	C18-C17-C16	-7.03	114.24	120.03
4	A	503	3L9	C1B-O4A-C4A	6.34	125.14	115.33
4	A	503	3L9	C14-C11-C10	-6.20	120.32	128.59
4	A	503	3L9	O12-C11-C14	5.72	119.26	110.86
4	A	503	3L9	O5D-C5D-C6D	5.35	117.47	106.67
4	A	503	3L9	C14-C19-C18	5.26	124.55	120.09
4	A	503	3L9	C1D-O5D-C5D	5.09	123.69	113.69
4	A	503	3L9	O2C-C2C-C3C	4.89	120.28	107.28
4	A	503	3L9	C19-C14-C15	-4.86	113.78	119.63
4	A	503	3L9	C14-C15-C16	4.70	124.08	120.09
4	A	503	3L9	C15-C14-C11	4.68	127.13	120.64
4	A	503	3L9	O27-C10-C11	-4.66	114.03	119.89
4	A	503	3L9	O2C-C1D-C2D	4.31	117.84	109.10
4	A	503	3L9	C1B-O5B-C5B	4.09	120.70	113.67
4	A	503	3L9	C3-C9-C10	3.99	123.33	115.74
4	A	503	3L9	O12-C11-C10	-3.83	115.58	120.49
4	A	503	3L9	C4-O12-C11	3.73	126.29	120.62
4	A	503	3L9	C6F-C1F-C2F	-3.55	114.28	118.71
4	A	503	3L9	C7F-C8F-C9F	-3.29	112.25	122.26
4	A	503	3L9	C2-C3-C9	3.25	126.23	121.47
4	A	503	3L9	C4-C3-C9	-3.24	115.84	120.03
4	A	503	3L9	O5D-C1D-C2D	2.86	115.19	109.51
4	A	503	3L9	O13-C9-C10	-2.82	115.20	121.52
4	A	503	3L9	C1C-O5C-C5C	2.70	118.32	113.67
4	A	503	3L9	C1F-C2F-C3F	2.70	122.69	120.76
4	A	503	3L9	O12-C4-C5	2.65	119.76	115.79
4	A	503	3L9	O3D-C3D-C2D	-2.62	102.99	109.94
4	A	503	3L9	O27-C1C-C2C	2.45	111.60	107.23
4	A	503	3L9	C1C-C2C-C3C	-2.38	106.28	110.38
4	A	503	3L9	C1E-O2D-C2D	2.23	123.47	117.96
4	A	503	3L9	O5E-C1E-C2E	-2.21	105.67	110.35
4	A	503	3L9	O6D-C6D-C5D	2.17	113.04	108.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	503	3L9	C1-C2-C3	2.12	123.40	120.93
4	A	503	3L9	O2C-C1D-O5D	2.12	116.60	110.67
4	A	503	3L9	O3F-C3F-C4F	2.11	124.08	118.45
4	A	503	3L9	O2E-C2E-C3E	2.10	115.20	110.35
4	A	503	3L9	O30-C2-C3	-2.05	117.30	121.14

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	503	3L9	O12-C11-C14-C19
4	A	503	3L9	O12-C11-C14-C15
4	A	503	3L9	C4E-C5E-C6E-O6E
4	A	503	3L9	C6F-C1F-C7F-C8F
4	A	503	3L9	O5B-C1B-O4A-C4A
4	A	503	3L9	C2F-C1F-C7F-C8F
4	A	503	3L9	C10-C11-C14-C19

There are no ring outliers.

No monomer is involved in short contacts.

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 then 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.

Ligand 3L9 A 503

Bond lengths — Bond angles — Torsions — Rings
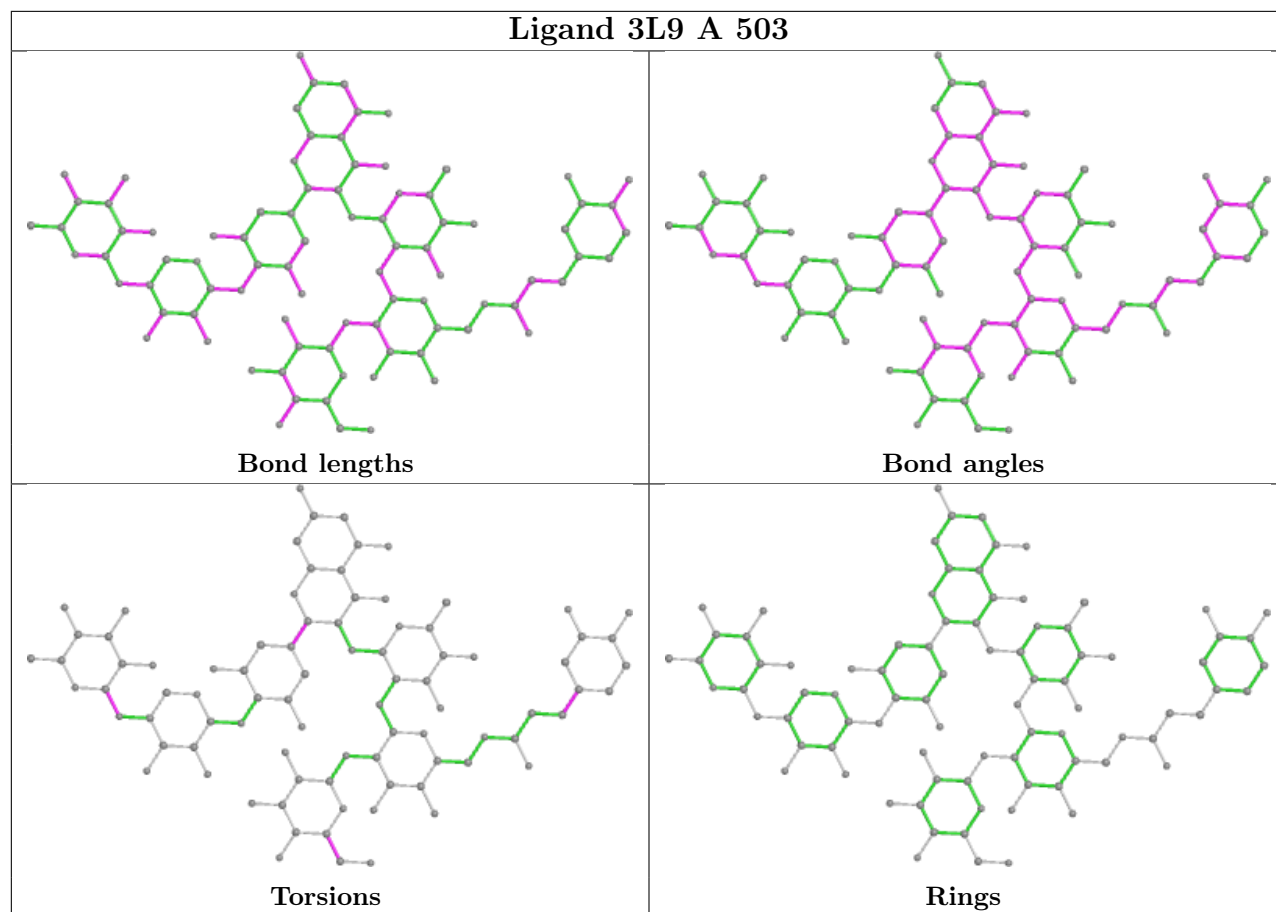
5.7 Other polymers ⓘ

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(Å²)	Q<0.9
1	A	495/496 (99%)	0.02	13 (2%)	56	62	10, 16, 28, 46	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	350	ASN	8.0
1	A	134	TRP	7.5
1	A	459	ASN	6.4
1	A	351	GLY	5.1
1	A	307	ALA	4.5
1	A	305	HIS	3.6
1	A	471	ASP	3.2
1	A	458	ILE	2.9
1	A	348	PHE	2.7
1	A	8	GLN	2.5
1	A	349	GLN	2.4
1	A	142	LYS	2.3
1	A	470	SER	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.

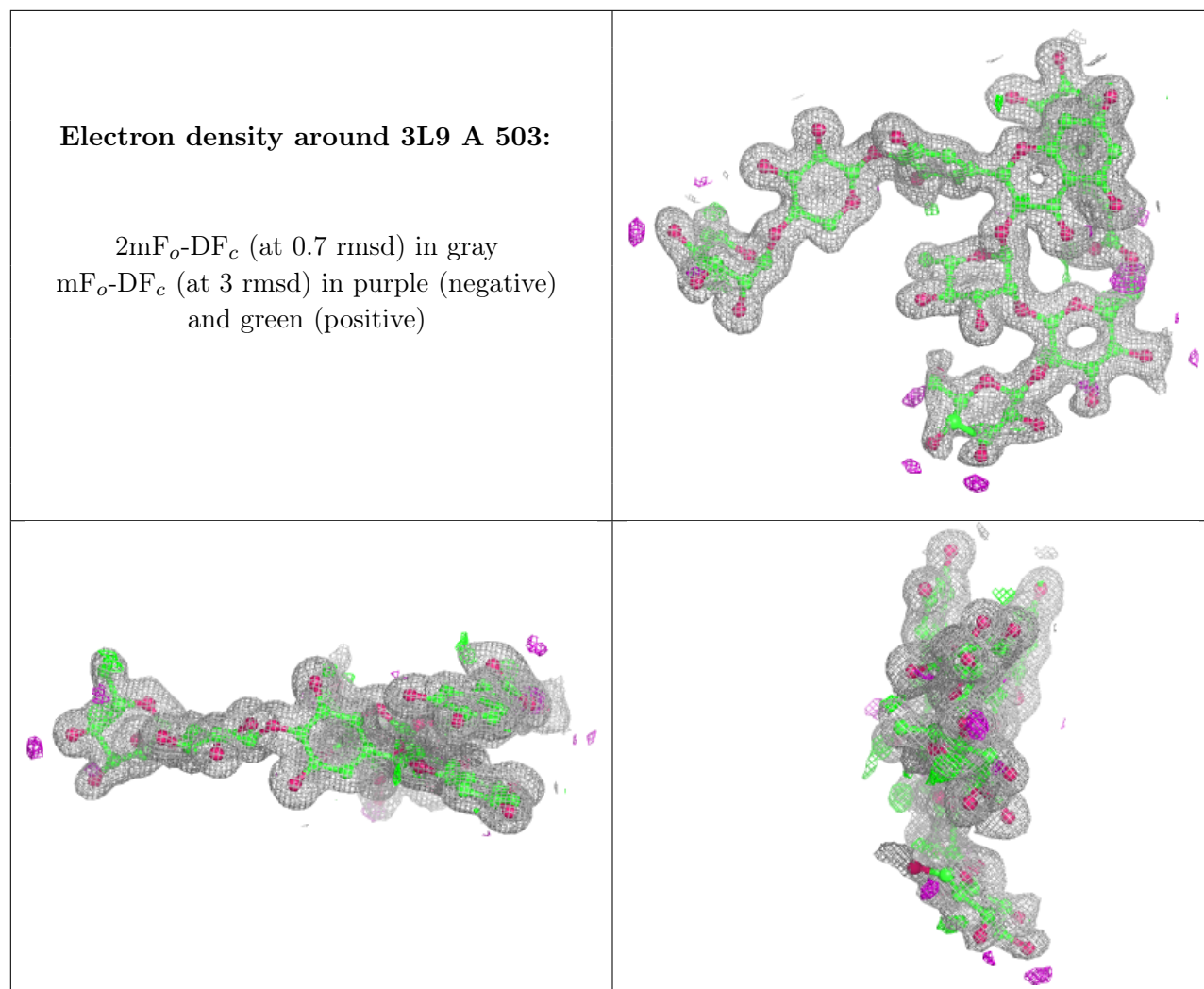| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å²)	Q<0.9
1	PCA	A	1	8/9	0.94	0.07	13,14,16,18	0

6.3 Carbohydrates ⓘ

There are no monosaccharides 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	3L9	A	503	86/86	0.92	0.09	11,18,43,46	0
2	CA	A	501	1/1	0.99	0.06	15,15,15,15	0
3	CL	A	502	1/1	1.00	0.07	10,10,10,10	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 3L9 A 503:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

6.5 Other polymers ⓘ

There are no such residues in this entry.