WORLDWIDE PDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Jan 2, 2024 – 02:33 pm GMT

PDB ID	:	5IV3
Title	:	Crystal structure of human soluble adenylyl cyclase in complex with alpha,beta-methyleneadenosine-5'-triphosphate and the allosteric inhibitor LRE1
Authors	:	Kleinboelting, S.; Steegborn, C.
Deposited on	:	2016-03-18
Resolution	:	1.86 Å(reported)

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

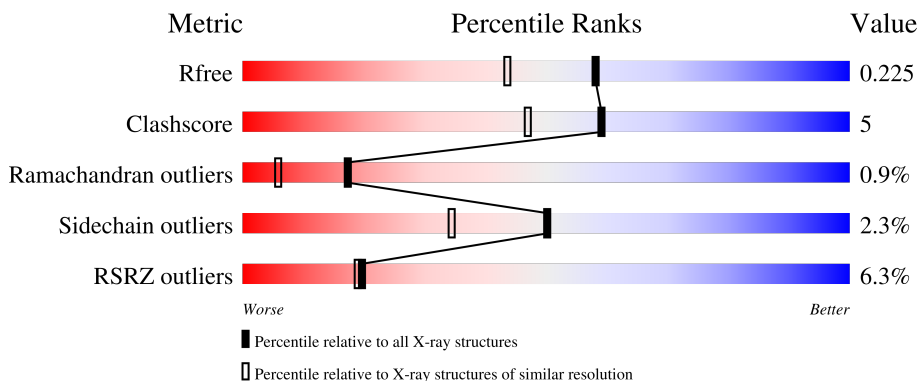|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 1.86 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	Percentile Ranks	Value
Rfree		0.225
Clashscore		5
Ramachandran outliers		0.9%
Sidechain outliers		2.3%
RSRZ outliers		6.3%

Worse *Better*

▌ 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	2469 (1.86-1.86)
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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	475	6% / 85% / 11% / · ·

2 Entry composition ⓘ

There are 10 unique types of molecules in this entry. The entry contains 4005 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 Adenylate cyclase type 10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total 3650	C 2370	N 590	O 656	S 34	0	8	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	470	HIS	-	expression tag	UNP Q96PN6
A	471	HIS	-	expression tag	UNP Q96PN6
A	472	HIS	-	expression tag	UNP Q96PN6
A	473	HIS	-	expression tag	UNP Q96PN6
A	474	HIS	-	expression tag	UNP Q96PN6
A	475	HIS	-	expression tag	UNP Q96PN6

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).
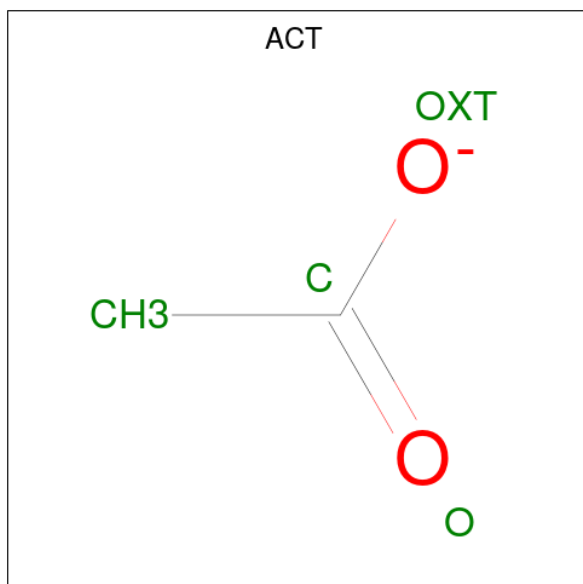
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 4	C 2	O 2	0	0
2	A	1	Total 4	C 2	O 2	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

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

- Molecule 4 is 6-chloro-N 4 -cyclopropyl-N 4 -[(thiophen-2-yl)methyl]pyrimidine-2,4-diamine (three-letter code: LRI) (formula: $C_{12}H_{13}ClN_4S$).
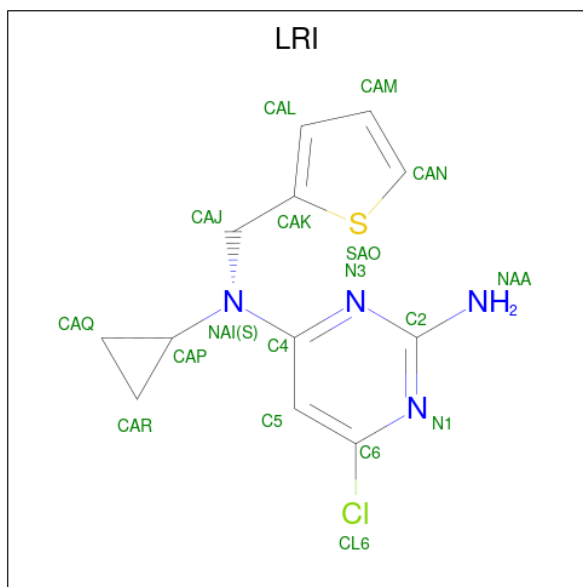
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	S		
4	A	1	18	12	1	4	1	0	0

- Molecule 5 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (three-letter code: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).
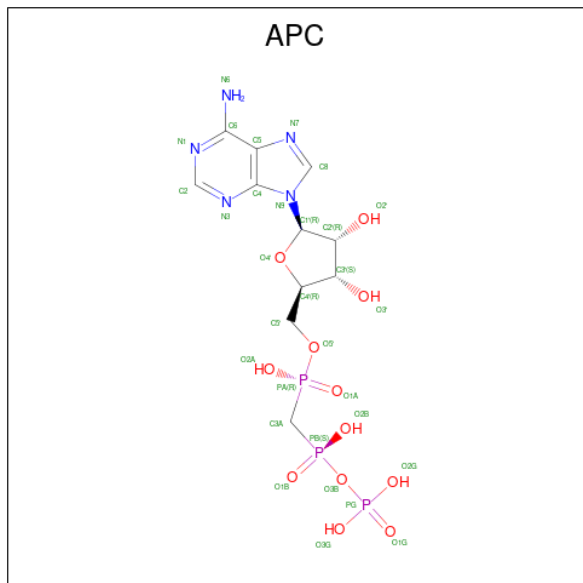
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
5	A	1	31	11	5	12	3	0	0

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).
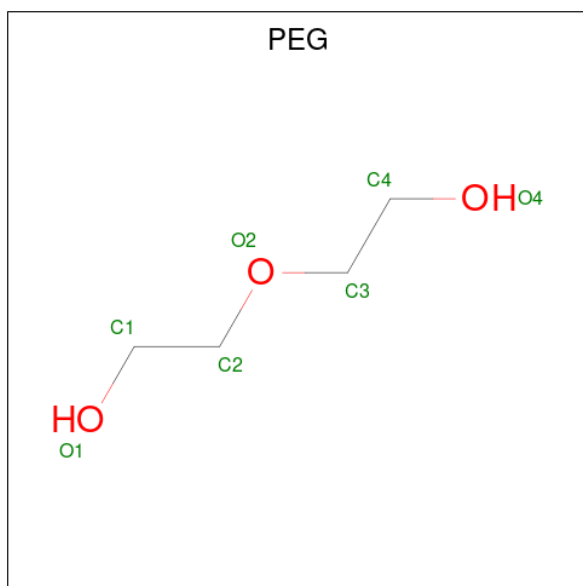
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	A	1	7	4	3	0	0

- Molecule 8 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).
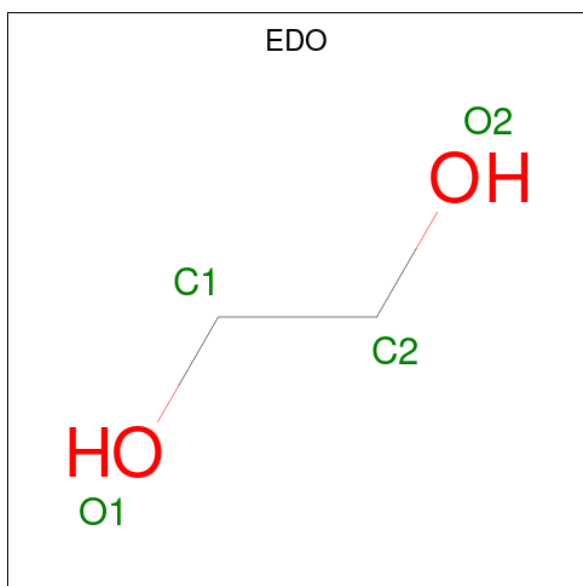
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total 4	C 2	O 2	0	0

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	267	Total 267	O 267	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: Adenylate cyclase type 10
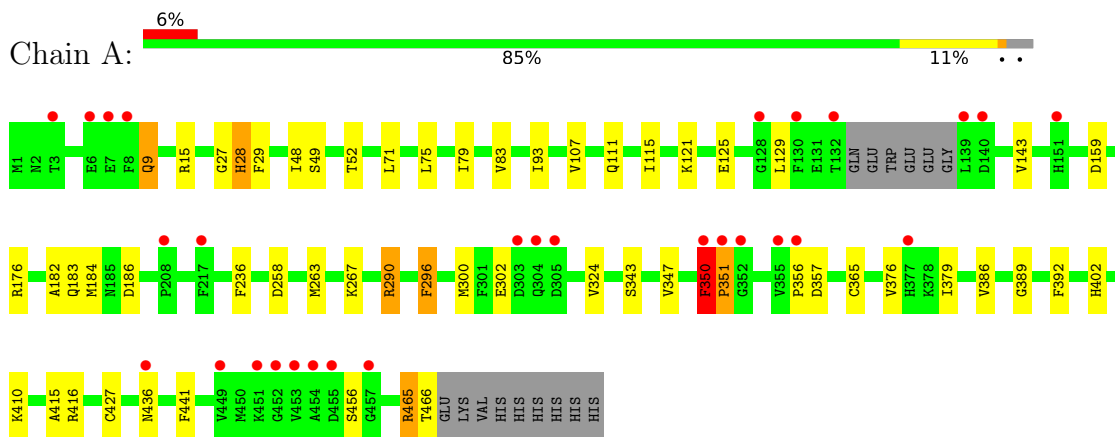
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	100.03Å　　100.03Å　　98.66Å 90.00°　　90.00°　　120.00°	Depositor
Resolution (Å)	44.61　–　1.86 44.61　–　1.86	Depositor EDS
% Data completeness (in resolution range)	99.9 (44.61-1.86) 99.9 (44.61-1.86)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.38 (at 1.87Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.176　,　0.223 0.184　,　0.225	Depositor DCC
R_{free} test set	2101 reflections (4.49%)	wwPDB-VP
Wilson B-factor (Å^2)	26.8	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 45.9	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.058 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	4005	wwPDB-VP
Average B, all atoms (Å^2)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: ACT, APC, CA, LRI, CME, EDO, PEG, CL, 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	0.92	1/3752 (0.0%)	0.95	7/5086 (0.1%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	343	SER	CB-OG	-5.79	1.34	1.42

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	159	ASP	CB-CG-OD2	-6.48	112.47	118.30
1	A	159	ASP	CB-CG-OD1	6.33	123.99	118.30
1	A	350	PHE	CB-CG-CD1	6.14	125.10	120.80
1	A	290	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	A	15	ARG	NE-CZ-NH2	-5.21	117.69	120.30
1	A	176	ARG	NE-CZ-NH2	5.21	122.91	120.30
1	A	258	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	436	ASN	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	3650	0	3601	35	0
2	A	8	0	6	0	0
3	A	18	0	24	2	0
4	A	18	0	0	0	0
5	A	31	0	14	0	0
6	A	1	0	0	0	0
7	A	7	0	10	0	0
8	A	4	0	6	0	0
9	A	1	0	0	0	0
10	A	267	0	0	6	0
All	All	4005	0	3661	35	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 (35) 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:107:VAL:HG11	1:A:115:ILE:HG13	1.81	0.63
1:A:324:VAL:HG12	1:A:365:CYS:SG	2.41	0.61
1:A:83:VAL:HG13	1:A:93:ILE:HD13	1.90	0.53
1:A:75:LEU:HD11	1:A:79:ILE:HD11	1.90	0.53
1:A:9:GLN:HB2	10:A:809:HOH:O	2.08	0.52
1:A:71[A]:LEU:HD23	1:A:392:PHE:CD1	2.44	0.52
1:A:350:PHE:CG	1:A:351:PRO:HD2	2.44	0.51
1:A:52[A]:THR:HG22	10:A:646:HOH:O	2.10	0.51
1:A:376:VAL:HB	1:A:379:ILE:HD12	1.92	0.50
1:A:111:GLN:HG3	1:A:236:PHE:CG	2.46	0.50
1:A:296:PHE:CE2	1:A:415:ALA:HB2	2.49	0.48
1:A:290:ARG:NE	1:A:350:PHE:HA	2.30	0.47
1:A:29:PHE:CZ	3:A:505:GOL:H11	2.50	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:VAL:HG11	1:A:350:PHE:CD2	2.49	0.47
1:A:416:ARG:NH1	10:A:612:HOH:O	2.48	0.47
1:A:267:LYS:NZ	10:A:611:HOH:O	2.48	0.46
1:A:182:ALA:HB1	1:A:186:ASP:HB2	1.97	0.46
1:A:389:GLY:HA3	1:A:410:LYS:HG3	1.97	0.46
1:A:48:ILE:CD1	1:A:143:VAL:HG22	2.46	0.45
1:A:48:ILE:HD12	1:A:143:VAL:HG22	1.98	0.45
1:A:75:LEU:HD11	1:A:79:ILE:CD1	2.45	0.45
1:A:441:PHE:CE2	1:A:465:ARG:HG3	2.50	0.45
1:A:350:PHE:CD1	1:A:351:PRO:HD2	2.52	0.45
1:A:9:GLN:OE1	1:A:9:GLN:N	2.48	0.44
1:A:121:LYS:O	1:A:125:GLU:HG3	2.18	0.44
1:A:28[B]:HIS:CD2	10:A:609:HOH:O	2.70	0.43
1:A:300:MET:HE2	10:A:647:HOH:O	2.19	0.42
1:A:357:ASP:HA	3:A:504:GOL:O2	2.20	0.42
1:A:386:VAL:O	1:A:427:CYS:HA	2.20	0.41
1:A:9:GLN:N	1:A:9:GLN:CD	2.74	0.41
1:A:183:GLN:O	1:A:184:MET:C	2.57	0.41
1:A:263[B]:MET:HE3	1:A:263[B]:MET:HB3	1.84	0.41

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	463/475 (98%)	447 (96%)	11 (2%)	5 (1%)	14	4

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	356	PRO
1	A	28[A]	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	28[B]	HIS
1	A	129	LEU
1	A	351	PRO

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	396/418 (95%)	387 (98%)	9 (2%)	50	34

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	49	SER
1	A	296	PHE
1	A	302	GLU
1	A	350	PHE
1	A	402	HIS
1	A	456	SER
1	A	465	ARG
1	A	466	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	ASN
1	A	127	HIS
1	A	223	ASN

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	CME	A	253	1	8,9,10	0.71	0	5,9,11	0.77	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	CME	A	253	1	-	1/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	253	CME	CZ-CE-SD-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	GOL	A	505	-	5,5,5	0.86	0	5,5,5	1.68	1 (20%)
4	LRI	A	506	-	19,20,20	1.43	2 (10%)	20,28,28	3.88	11 (55%)
3	GOL	A	504	-	5,5,5	0.77	0	5,5,5	1.07	0
5	APC	A	507	6	27,33,33	1.68	6 (22%)	31,52,52	2.28	9 (29%)
2	ACT	A	502	-	3,3,3	0.80	0	3,3,3	0.97	0
8	EDO	A	510	-	3,3,3	0.75	0	2,2,2	0.49	0
7	PEG	A	509	-	6,6,6	0.56	0	5,5,5	0.81	0
3	GOL	A	503	-	5,5,5	0.69	0	5,5,5	0.68	0
2	ACT	A	501	-	3,3,3	1.05	0	3,3,3	1.34	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	GOL	A	505	-	-	1/4/4/4	-
4	LRI	A	506	-	-	0/11/14/14	0/3/3/3
3	GOL	A	504	-	-	3/4/4/4	-
5	APC	A	507	6	-	1/15/38/38	0/3/3/3
8	EDO	A	510	-	-	0/1/1/1	-
7	PEG	A	509	-	-	4/4/4/4	-
3	GOL	A	503	-	-	1/4/4/4	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	507	APC	PB-O3B	4.14	1.63	1.58
5	A	507	APC	PA-O1A	4.01	1.61	1.51
5	A	507	APC	PB-O2B	-3.57	1.48	1.56
4	A	506	LRI	CAQ-CAP	3.37	1.56	1.48
4	A	506	LRI	C2-N3	-3.07	1.29	1.35
5	A	507	APC	O4'-C1'	2.55	1.44	1.41

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	507	APC	PA-O2A	-2.12	1.51	1.56
5	A	507	APC	PB-O1B	2.06	1.56	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	506	LRI	C2-N3-C4	9.19	123.24	116.73
4	A	506	LRI	CAM-CAN-SAO	-9.14	105.56	112.98
4	A	506	LRI	C6-N1-C2	6.16	120.83	114.43
5	A	507	APC	C1'-N9-C4	-6.11	115.90	126.64
5	A	507	APC	O3G-PG-O2G	-5.15	87.95	107.64
5	A	507	APC	N3-C2-N1	-4.95	120.94	128.68
4	A	506	LRI	C5-C6-N1	-3.67	121.47	125.50
4	A	506	LRI	CAJ-NAI-CAP	-3.61	114.00	118.20
4	A	506	LRI	N1-C2-N3	-3.56	119.83	125.42
5	A	507	APC	O3G-PG-O3B	3.23	115.47	104.64
5	A	507	APC	O3G-PG-O1G	3.17	123.08	110.68
4	A	506	LRI	CAQ-CAR-CAP	3.03	62.42	59.80
3	A	505	GOL	O2-C2-C1	3.01	122.38	109.12
5	A	507	APC	C5'-C4'-C3'	-2.90	104.30	115.18
4	A	506	LRI	N3-C4-NAI	2.79	119.67	116.57
4	A	506	LRI	C5-C4-N3	-2.67	117.95	123.15
4	A	506	LRI	CAR-CAQ-CAP	-2.56	57.59	59.80
5	A	507	APC	O4'-C1'-C2'	2.46	110.52	106.93
5	A	507	APC	O1B-PB-C3A	-2.45	102.59	109.07
4	A	506	LRI	C6-C5-C4	2.42	116.42	115.14
5	A	507	APC	O3'-C3'-C2'	2.39	119.55	111.82

There are no chirality outliers.
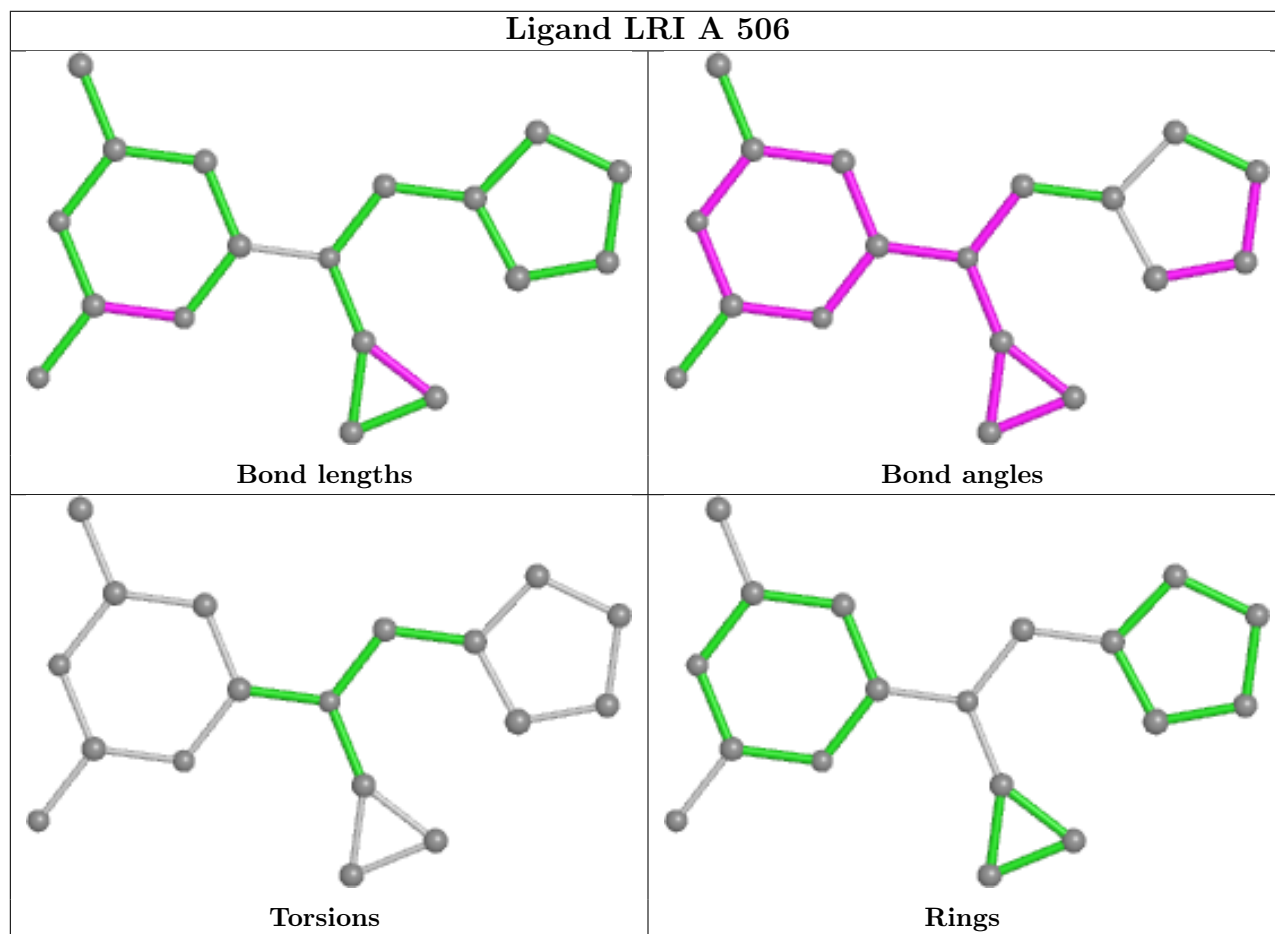
All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	504	GOL	O1-C1-C2-C3
3	A	505	GOL	C1-C2-C3-O3
7	A	509	PEG	O1-C1-C2-O2
3	A	504	GOL	O1-C1-C2-O2
3	A	503	GOL	C1-C2-C3-O3
7	A	509	PEG	C1-C2-O2-C3
5	A	507	APC	PA-C3A-PB-O3B
7	A	509	PEG	C4-C3-O2-C2
3	A	504	GOL	O2-C2-C3-O3
7	A	509	PEG	O2-C3-C4-O4

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	505	GOL	1	0
3	A	504	GOL	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 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 LRI A 506

Bond lengths

Bond angles

Torsions

Rings

Ligand APC A 507

Bond lengths

Bond angles

Torsions

Rings
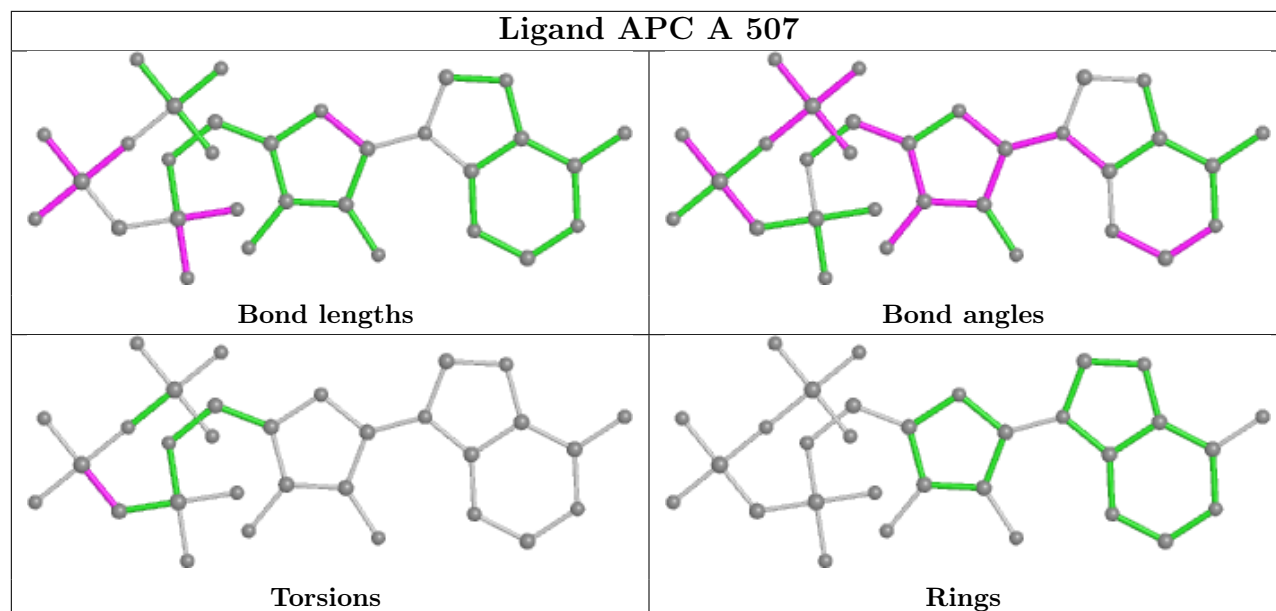
5.7 Other polymers (i)

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, 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	459/475 (96%)	-0.01	29 (6%)	20	19	16, 30, 67, 108	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	356	PRO	6.0
1	A	449	VAL	5.4
1	A	453	VAL	4.8
1	A	352	GLY	4.8
1	A	132	THR	4.4
1	A	139	LEU	4.3
1	A	6	GLU	3.9
1	A	8	PHE	3.6
1	A	130	PHE	3.6
1	A	351	PRO	3.6
1	A	452	GLY	3.5
1	A	355	VAL	3.5
1	A	454	ALA	3.5
1	A	304	GLN	3.3
1	A	350	PHE	3.3
1	A	451	LYS	3.3
1	A	377	HIS	2.7
1	A	208	PRO	2.7
1	A	305	ASP	2.6
1	A	217	PHE	2.6
1	A	7	GLU	2.5
1	A	140	ASP	2.3
1	A	436	ASN	2.3
1	A	3	THR	2.3
1	A	303	ASP	2.3
1	A	457	GLY	2.2
1	A	151	HIS	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	128	GLY	2.1
1	A	455	ASP	2.1

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

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.

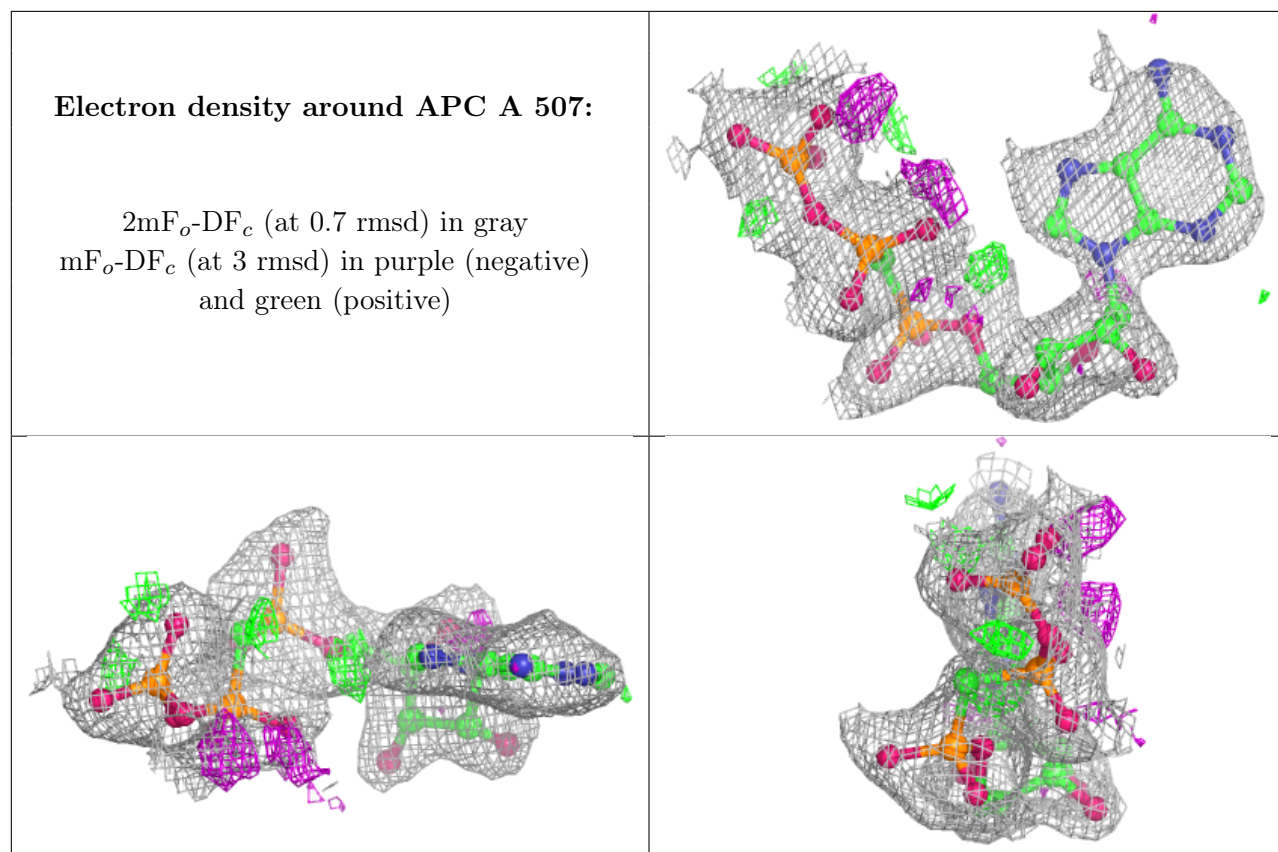| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	CME	A	253	10/11	0.98	0.07	20,25,34,34	0

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

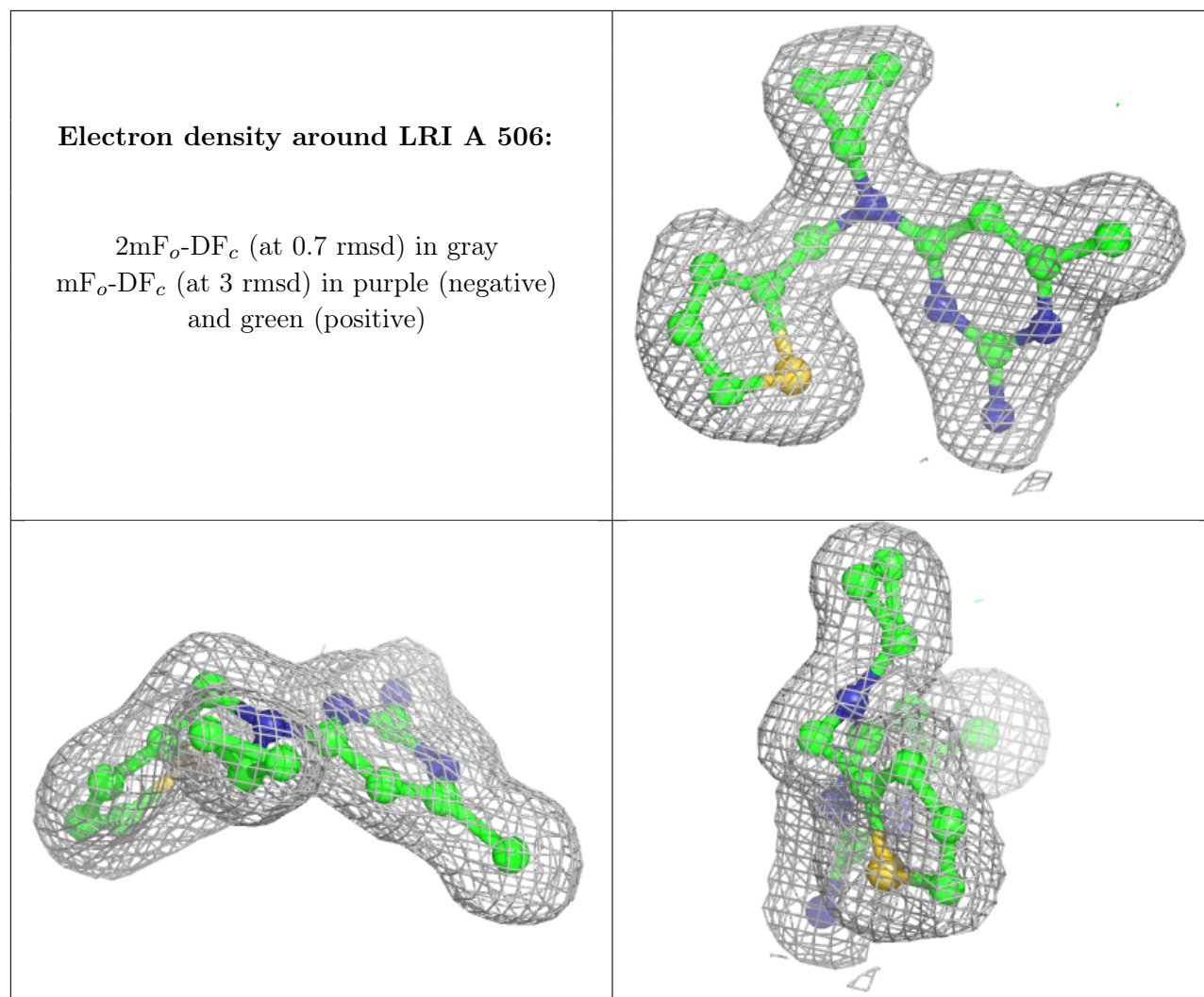## 6.4 Ligands ⓘ

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
3	GOL	A	504	6/6	0.73	0.18	49,58,62,66	0
3	GOL	A	505	6/6	0.82	0.20	43,49,50,50	0
8	EDO	A	510	4/4	0.86	0.11	38,41,51,64	0
2	ACT	A	502	4/4	0.87	0.12	54,56,56,62	0
7	PEG	A	509	7/7	0.89	0.14	33,50,66,67	0
5	APC	A	507	31/31	0.94	0.13	28,52,62,63	0
3	GOL	A	503	6/6	0.96	0.11	30,35,37,37	0
2	ACT	A	501	4/4	0.96	0.11	22,24,24,24	0
9	CL	A	511	1/1	0.96	0.09	42,42,42,42	0
6	CA	A	508	1/1	0.98	0.10	50,50,50,50	0
4	LRI	A	506	18/18	0.98	0.08	19,21,24,27	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 APC A 507:

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

Electron density around LRI A 506:

$2mF_o-DF_c$ (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.