



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 3, 2024 – 03:45 PM EST

PDB ID : 1LOX
Title : RABBIT RETICULOCYTE 15-LIPOXYGENASE
Authors : Gillmor, S.A.; Villasenor, A.; Fletterick, R.J.; Sigal, E.; Browner, M.F.
Deposited on : 1997-10-06
Resolution : 2.40 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 : 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

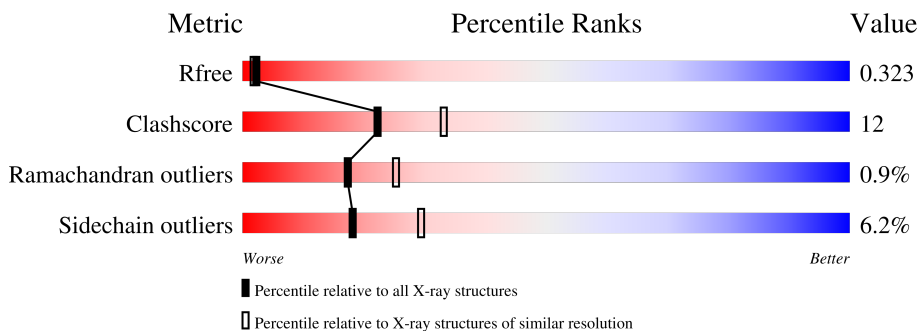
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	662	 72% 23% ..

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			19	17	2		

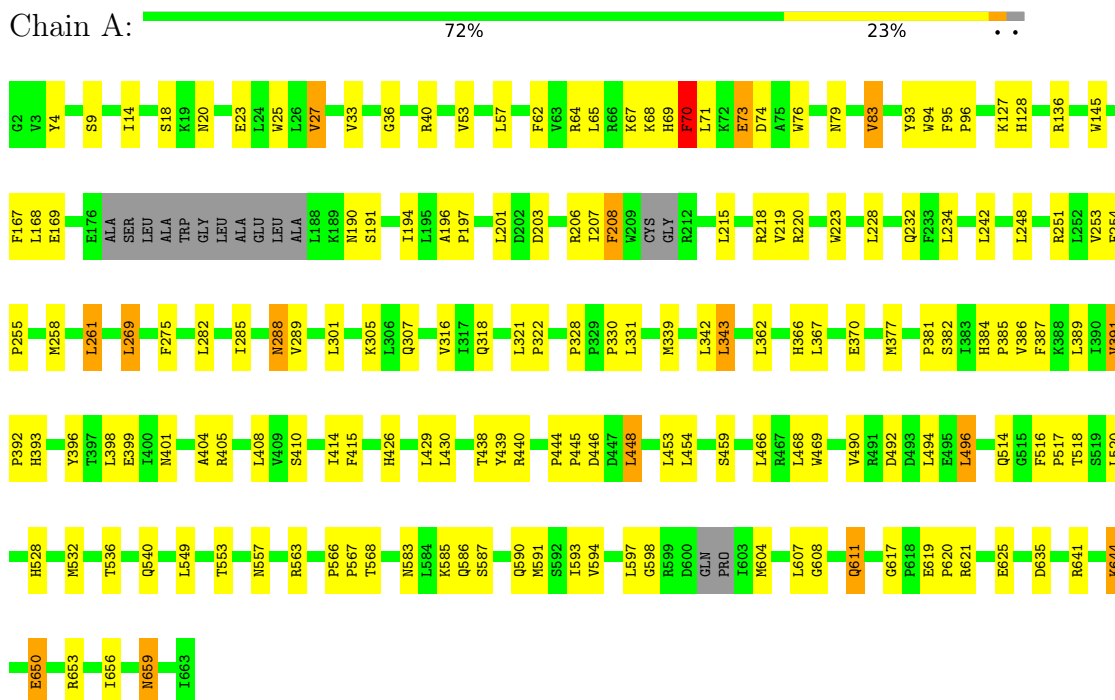
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	94	Total	O	0	0
			94	94		

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. 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. 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: 15-LIPOXYGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	198.90Å 198.90Å 136.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	16.00 – 2.40 24.21 – 2.41	Depositor EDS
% Data completeness (in resolution range)	98.0 (16.00-2.40) 97.8 (24.21-2.41)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.41Å)	Xtrriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.198 , 0.247 0.300 , 0.323	Depositor DCC
R_{free} test set	1967 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	39.7	Xtrriage
Anisotropy	0.009	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5223	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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: FE2, RS7

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	0.38	0/5236	0.60	0/7111

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	5109	0	5021	119	0
2	A	1	0	0	0	0
3	A	19	0	19	6	0
4	A	94	0	0	3	0
All	All	5223	0	5040	119	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 12.

All (119) 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:362:LEU:HB2	3:A:841:RS7:H132	1.49	0.92
1:A:404:ALA:HB2	3:A:841:RS7:H173	1.65	0.79
1:A:343:LEU:HD13	1:A:567:PRO:HG2	1.66	0.77
1:A:232:GLN:HE22	1:A:557:ASN:HD21	1.32	0.77
1:A:25:TRP:HB2	1:A:64:ARG:HB2	1.66	0.75
1:A:391:VAL:HG23	1:A:392:PRO:HD3	1.70	0.74
1:A:387:PHE:O	1:A:391:VAL:HG22	1.90	0.70
1:A:608:GLY:H	1:A:659:ASN:ND2	1.90	0.70
1:A:33:VAL:HG13	1:A:57:LEU:HD21	1.74	0.68
1:A:253:VAL:HG23	1:A:328:PRO:HB3	1.75	0.68
1:A:255:PRO:HD2	1:A:258:MET:HG3	1.77	0.65
1:A:414:ILE:CG2	1:A:593:ILE:HD12	2.27	0.65
1:A:27:VAL:HG13	1:A:62:PHE:HB2	1.78	0.65
1:A:220:ARG:HG2	1:A:220:ARG:HH11	1.63	0.63
1:A:583:ASN:H	1:A:586:GLN:NE2	1.97	0.62
1:A:532:MET:O	1:A:536:THR:HG23	2.02	0.59
1:A:203:ASP:O	1:A:206:ARG:HG2	2.02	0.59
1:A:644:LYS:HE3	1:A:644:LYS:HA	1.83	0.59
1:A:362:LEU:CB	3:A:841:RS7:H132	2.30	0.58
1:A:414:ILE:HG21	1:A:593:ILE:HD12	1.85	0.58
1:A:611:GLN:HE21	1:A:611:GLN:HA	1.68	0.58
1:A:305:LYS:HE3	1:A:307:GLN:HE21	1.70	0.57
1:A:362:LEU:HB2	3:A:841:RS7:C13	2.30	0.56
1:A:27:VAL:CG1	1:A:62:PHE:HB2	2.35	0.56
1:A:288:ASN:ND2	1:A:289:VAL:H	2.03	0.56
1:A:384:HIS:CD2	1:A:385:PRO:HD2	2.41	0.55
1:A:583:ASN:H	1:A:586:GLN:HE21	1.54	0.55
1:A:384:HIS:HD2	1:A:386:VAL:H	1.55	0.55
1:A:223:TRP:HA	1:A:228:LEU:HD23	1.89	0.54
1:A:553:THR:O	1:A:591:MET:SD	2.66	0.54
1:A:563:ARG:HD3	1:A:586:GLN:HE22	1.74	0.53
1:A:253:VAL:CG2	1:A:328:PRO:HB3	2.39	0.53
1:A:381:PRO:HD2	1:A:384:HIS:HB2	1.91	0.53
1:A:536:THR:HG22	4:A:898:HOH:O	2.09	0.53
1:A:23:GLU:HA	1:A:36:GLY:O	2.09	0.52
1:A:282:LEU:HA	1:A:285:ILE:HD12	1.91	0.52
1:A:414:ILE:HG22	1:A:593:ILE:HD12	1.92	0.52
1:A:650:GLU:O	1:A:656:ILE:HD11	2.09	0.52
1:A:94:TRP:CD1	1:A:96:PRO:HG3	2.45	0.52
1:A:196:ALA:HB1	1:A:206:ARG:HH12	1.75	0.52
1:A:343:LEU:HD13	1:A:567:PRO:CG	2.38	0.52
1:A:20:ASN:HB3	1:A:68:LYS:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:LYS:HG3	1:A:128:HIS:N	2.25	0.51
1:A:619:GLU:HB2	1:A:620:PRO:HD3	1.93	0.51
1:A:288:ASN:HD22	1:A:289:VAL:H	1.59	0.51
1:A:440:ARG:NH1	1:A:446:ASP:HB3	2.26	0.51
1:A:496:LEU:CD1	1:A:520:LEU:HD12	2.40	0.51
1:A:597:LEU:HB3	3:A:841:RS7:C1	2.40	0.50
1:A:33:VAL:HG21	1:A:53:VAL:HG11	1.93	0.50
1:A:20:ASN:ND2	1:A:73:GLU:O	2.45	0.50
1:A:14:ILE:HD12	1:A:169:GLU:HG3	1.93	0.50
1:A:444:PRO:HD2	1:A:469:TRP:CE3	2.46	0.50
1:A:23:GLU:O	1:A:65:LEU:HA	2.12	0.49
1:A:219:VAL:O	1:A:223:TRP:HB3	2.13	0.49
1:A:9:SER:HB3	1:A:79:ASN:HB2	1.95	0.49
1:A:196:ALA:HB1	1:A:206:ARG:NH1	2.28	0.49
1:A:70:PHE:HD1	1:A:71:LEU:H	1.61	0.49
1:A:167:PHE:CE1	1:A:399:GLU:HG2	2.47	0.48
1:A:440:ARG:HG3	4:A:880:HOH:O	2.13	0.48
1:A:496:LEU:HD11	1:A:520:LEU:HD12	1.95	0.48
1:A:248:LEU:HD13	1:A:269:LEU:HD12	1.95	0.48
1:A:261:LEU:HD21	1:A:316:VAL:HG22	1.95	0.48
1:A:384:HIS:CD2	1:A:386:VAL:H	2.32	0.48
1:A:261:LEU:HD11	1:A:316:VAL:HG21	1.95	0.48
1:A:191:SER:O	1:A:194:ILE:HB	2.13	0.48
1:A:40:ARG:NH2	1:A:70:PHE:HE2	2.12	0.47
1:A:285:ILE:HD13	1:A:429:LEU:HB2	1.95	0.47
1:A:607:LEU:HD12	1:A:659:ASN:HD22	1.80	0.47
1:A:136:ARG:HD2	1:A:377:MET:O	2.16	0.46
1:A:593:ILE:HG23	1:A:594:VAL:N	2.30	0.46
1:A:145:TRP:CG	1:A:405:ARG:HD2	2.50	0.46
1:A:536:THR:HA	1:A:540:GLN:HB3	1.97	0.46
1:A:590:GLN:O	1:A:593:ILE:HG22	2.16	0.46
1:A:494:LEU:H	1:A:494:LEU:HD22	1.79	0.46
1:A:136:ARG:HB3	1:A:377:MET:O	2.16	0.46
1:A:439:TYR:OH	1:A:528:HIS:HD2	1.99	0.46
1:A:251:ARG:HE	1:A:318:GLN:NE2	2.14	0.45
1:A:587:SER:O	1:A:591:MET:HE2	2.17	0.45
1:A:18:SER:HB2	1:A:76:TRP:HB2	1.99	0.45
1:A:251:ARG:HE	1:A:318:GLN:HE22	1.65	0.45
1:A:370:GLU:HG3	1:A:398:LEU:CD2	2.46	0.45
1:A:208:PHE:HE2	1:A:591:MET:HG3	1.81	0.44
1:A:220:ARG:HG2	1:A:220:ARG:NH1	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:516:PHE:HA	1:A:517:PRO:HD3	1.83	0.44
1:A:330:PRO:HG2	1:A:568:THR:O	2.17	0.44
1:A:607:LEU:HA	1:A:659:ASN:HD22	1.82	0.44
1:A:566:PRO:HA	1:A:567:PRO:HD3	1.84	0.44
1:A:366:HIS:HD1	1:A:401:ASN:HD21	1.65	0.43
1:A:251:ARG:O	1:A:322:PRO:HG2	2.18	0.43
1:A:387:PHE:CZ	1:A:391:VAL:HG11	2.53	0.43
1:A:382:SER:HA	1:A:387:PHE:CD1	2.54	0.43
1:A:254:PHE:HA	1:A:255:PRO:HD3	1.89	0.42
1:A:258:MET:HE2	1:A:331:LEU:HD12	2.00	0.42
1:A:611:GLN:HE21	1:A:611:GLN:CA	2.32	0.42
1:A:448:LEU:HD12	1:A:453:LEU:HB2	2.01	0.42
1:A:444:PRO:HB2	1:A:445:PRO:HD3	2.01	0.42
1:A:232:GLN:HE22	1:A:557:ASN:ND2	2.08	0.42
1:A:597:LEU:HD22	3:A:841:RS7:C3	2.50	0.42
1:A:261:LEU:HD21	1:A:316:VAL:CG2	2.49	0.42
1:A:384:HIS:HD2	1:A:386:VAL:N	2.16	0.42
1:A:621:ARG:O	1:A:625:GLU:HG2	2.19	0.42
1:A:4:TYR:HB3	1:A:83:VAL:HG23	2.02	0.42
1:A:536:THR:HA	1:A:540:GLN:CB	2.50	0.41
1:A:93:TYR:HB3	1:A:95:PHE:CE2	2.55	0.41
1:A:635:ASP:OD1	1:A:653:ARG:HB3	2.21	0.41
1:A:67:LYS:HE2	1:A:67:LYS:HB3	1.92	0.41
1:A:339:MET:O	1:A:343:LEU:HB2	2.20	0.41
1:A:585:LYS:HB3	1:A:585:LYS:NZ	2.35	0.41
1:A:20:ASN:OD1	1:A:69:HIS:HA	2.21	0.41
1:A:393:HIS:HA	1:A:659:ASN:O	2.21	0.41
1:A:438:THR:HA	1:A:514:GLN:HB3	2.01	0.41
1:A:196:ALA:HA	1:A:197:PRO:HD3	1.89	0.41
1:A:454:LEU:HD23	1:A:454:LEU:HA	1.80	0.41
1:A:215:LEU:O	1:A:218:ARG:HB3	2.21	0.41
1:A:234:LEU:HD22	1:A:459:SER:HB2	2.03	0.40
1:A:492:ASP:O	1:A:494:LEU:HD22	2.21	0.40
1:A:242:LEU:HD11	1:A:275:PHE:HB3	2.04	0.40
1:A:396:TYR:HA	4:A:875:HOH:O	2.22	0.40
1:A:405:ARG:O	1:A:410:SER:HB3	2.21	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	639/662 (96%)	607 (95%)	26 (4%)	6 (1%)	17 25

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	ASP
1	A	208	PHE
1	A	207	ILE
1	A	70	PHE
1	A	617	GLY
1	A	598	GLY

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	546/576 (95%)	512 (94%)	34 (6%)	18 29

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	VAL
1	A	70	PHE
1	A	73	GLU
1	A	83	VAL
1	A	168	LEU

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Mol	Chain	Res	Type
1	A	190	ASN
1	A	201	LEU
1	A	261	LEU
1	A	269	LEU
1	A	288	ASN
1	A	301	LEU
1	A	321	LEU
1	A	342	LEU
1	A	343	LEU
1	A	367	LEU
1	A	389	LEU
1	A	391	VAL
1	A	408	LEU
1	A	415	PHE
1	A	426	HIS
1	A	430	LEU
1	A	448	LEU
1	A	466	LEU
1	A	468	LEU
1	A	490	VAL
1	A	496	LEU
1	A	518	THR
1	A	549	LEU
1	A	604	MET
1	A	611	GLN
1	A	641	ARG
1	A	644	LYS
1	A	650	GLU
1	A	659	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	126	GLN
1	A	131	GLN
1	A	238	ASN
1	A	284	ASN
1	A	288	ASN
1	A	307	GLN
1	A	318	GLN
1	A	384	HIS
1	A	401	ASN

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Mol	Chain	Res	Type
1	A	426	HIS
1	A	528	HIS
1	A	540	GLN
1	A	557	ASN
1	A	586	GLN
1	A	610	HIS
1	A	611	GLN
1	A	659	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is 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
3	RS7	A	841	-	19,19,19	4.18	5 (26%)	22,22,22	0.87	1 (4%)

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	RS7	A	841	-	-	0/13/13/13	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	841	RS7	C10-C11	16.68	1.41	1.19
3	A	841	RS7	C4-C3	-4.77	1.39	1.47
3	A	841	RS7	C4-C9	3.51	1.44	1.41
3	A	841	RS7	C2-C3	2.47	1.39	1.33
3	A	841	RS7	O18-C1	-2.01	1.25	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	841	RS7	C4-C3-C2	-2.92	121.13	126.93

There are no chirality outliers.

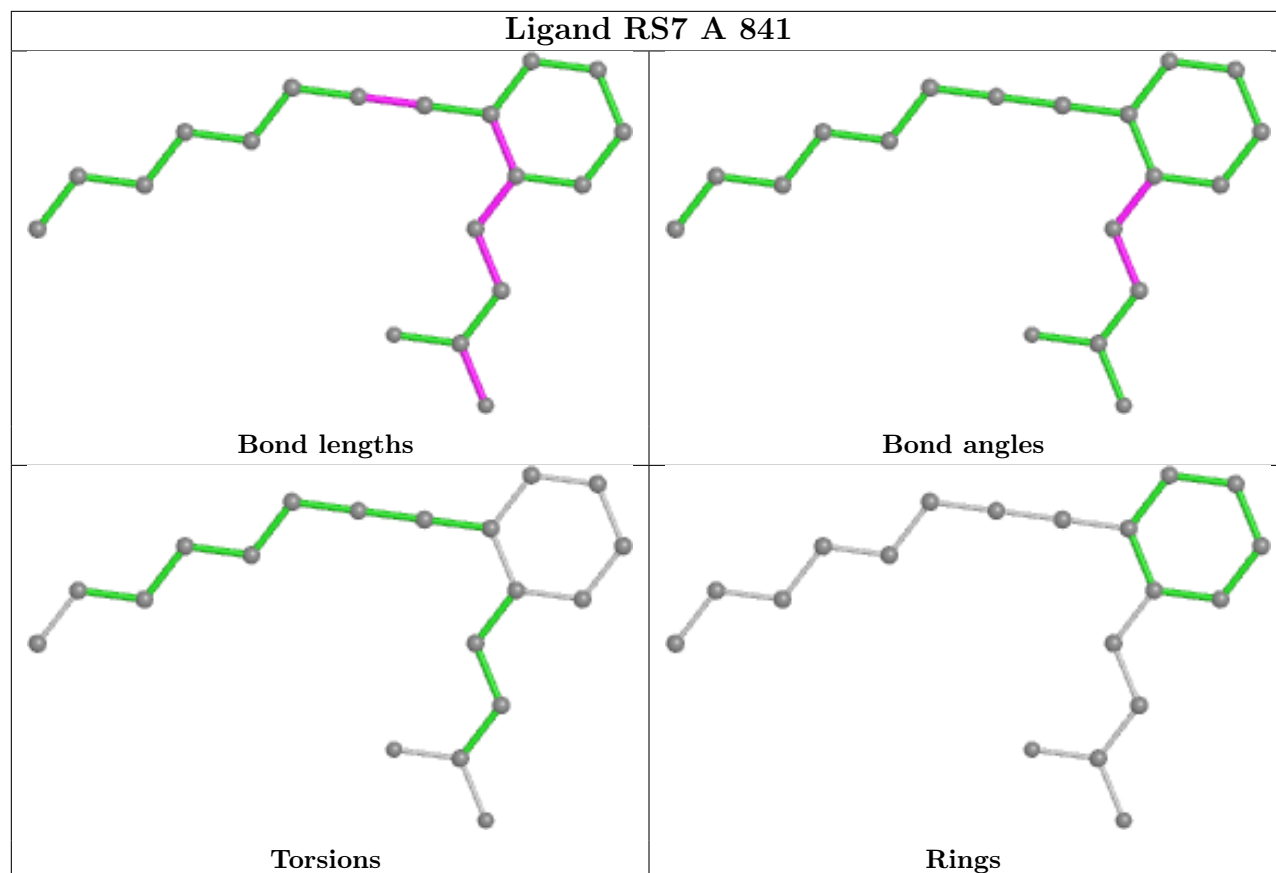
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	841	RS7	6	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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

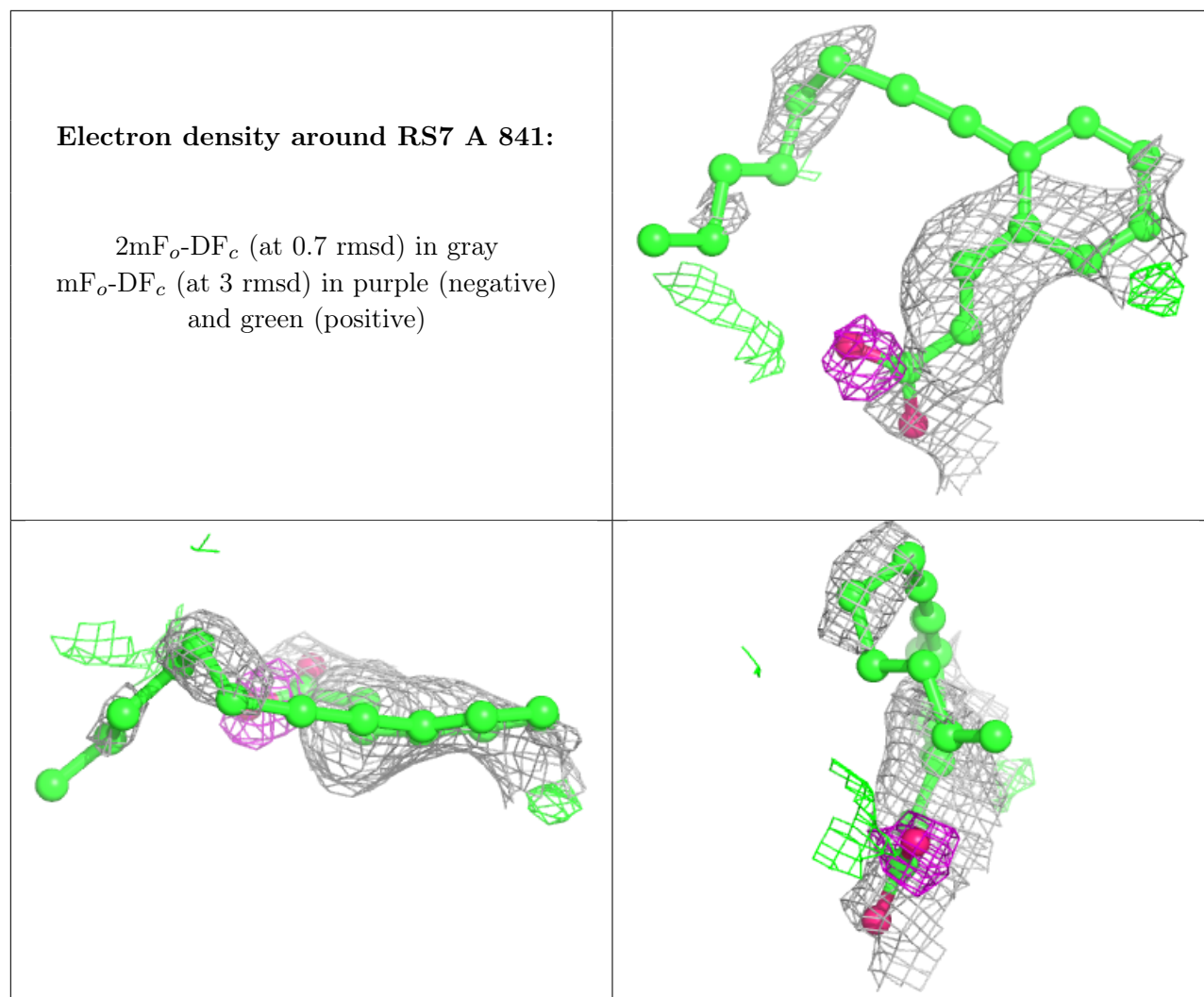
6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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](#)

Unable to reproduce the depositors R factor - this section is therefore empty.