



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:20 AM UTC

PDB ID : 5AVI / pdb_00005avi
Title : Crystal structure of LXRA α in complex with tert-butyl benzoate analog, compound 4
Authors : Matsui, Y.; Hanzawa, H.; Tamaki, K.
Deposited on : 2015-06-16
Resolution : 2.70 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

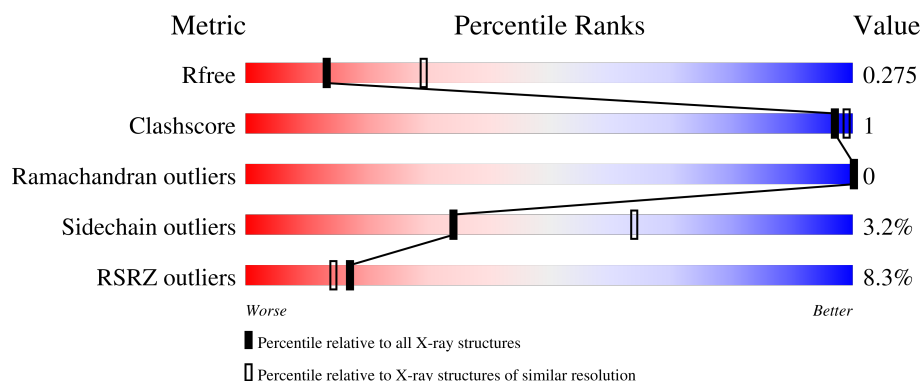
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	5% 75% 5% 19%
1	C	283	10% 73% 6% 20%
2	B	25	60% 40%
2	D	25	60% 40%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4097 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 Oxysterols receptor LXR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	228	Total	C	N	O	S	0	0	0
			1860	1192	325	337	6			
1	C	226	Total	C	N	O	S	0	0	0
			1843	1181	321	335	6			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	MET	-	initiating methionine	UNP Q13133
A	166	LYS	-	expression tag	UNP Q13133
A	167	HIS	-	expression tag	UNP Q13133
A	168	GLN	-	expression tag	UNP Q13133
A	169	HIS	-	expression tag	UNP Q13133
A	170	GLN	-	expression tag	UNP Q13133
A	171	HIS	-	expression tag	UNP Q13133
A	172	GLN	-	expression tag	UNP Q13133
A	173	HIS	-	expression tag	UNP Q13133
A	174	GLN	-	expression tag	UNP Q13133
A	175	HIS	-	expression tag	UNP Q13133
A	176	GLN	-	expression tag	UNP Q13133
A	177	HIS	-	expression tag	UNP Q13133
A	178	GLN	-	expression tag	UNP Q13133
A	179	GLN	-	expression tag	UNP Q13133
A	180	PRO	-	expression tag	UNP Q13133
A	181	LEU	-	expression tag	UNP Q13133
C	165	MET	-	initiating methionine	UNP Q13133
C	166	LYS	-	expression tag	UNP Q13133
C	167	HIS	-	expression tag	UNP Q13133
C	168	GLN	-	expression tag	UNP Q13133
C	169	HIS	-	expression tag	UNP Q13133
C	170	GLN	-	expression tag	UNP Q13133
C	171	HIS	-	expression tag	UNP Q13133
C	172	GLN	-	expression tag	UNP Q13133

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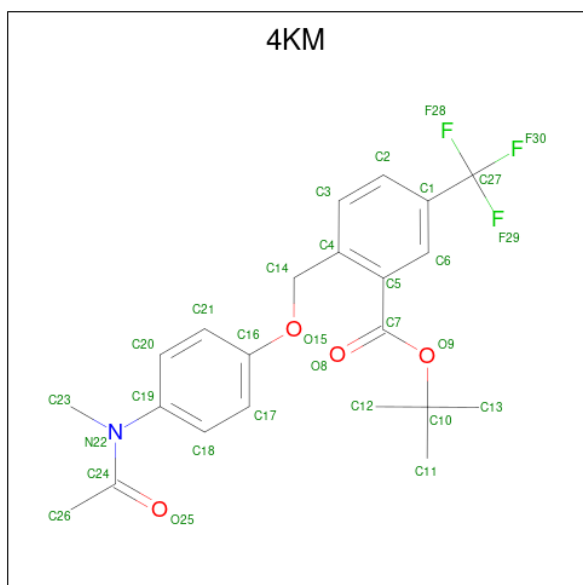
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Chain	Residue	Modelled	Actual	Comment	Reference
C	173	HIS	-	expression tag	UNP Q13133
C	174	GLN	-	expression tag	UNP Q13133
C	175	HIS	-	expression tag	UNP Q13133
C	176	GLN	-	expression tag	UNP Q13133
C	177	HIS	-	expression tag	UNP Q13133
C	178	GLN	-	expression tag	UNP Q13133
C	179	GLN	-	expression tag	UNP Q13133
C	180	PRO	-	expression tag	UNP Q13133
C	181	LEU	-	expression tag	UNP Q13133

- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	15	Total	C	N	O	0	0	0
			131	82	27	22			
2	D	15	Total	C	N	O	0	0	0
			131	82	27	22			

- Molecule 3 is tert-butyl 2-[[4-[ethanoyl(methyl)amino]phenoxy]methyl]-5-(trifluoromethyl)benzoate (CCD ID: 4KM) (formula: C₂₂H₂₄F₃NO₄).

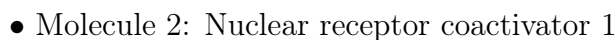
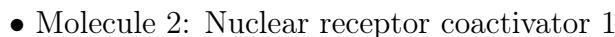


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0
			30	22	3	1	4	0
3	C	1	Total	C	F	N	O	0
			30	22	3	1	4	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total 32	O 32	0	0
4	B	4	Total 4	O 4	0	0
4	C	31	Total 31	O 31	0	0
4	D	5	Total 5	O 5	0	0

- Molecule 1: Oxysterols receptor LXR-alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 21 2	Depositor
Cell constants a, b, c, α , β , γ	124.36Å 124.36Å 91.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 20.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (20.00-2.70) 99.4 (20.00-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.06 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.244 , 0.274 0.244 , 0.275	Depositor DCC
R_{free} test set	2009 reflections (9.89%)	wwPDB-VP
Wilson B-factor (Å ²)	33.2	Xtriage
Anisotropy	0.115	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 15.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4097	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 51.57 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5031e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 4KM

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	0.61	0/1901	1.24	7/2571 (0.3%)
1	C	0.60	0/1882	1.21	7/2545 (0.3%)
2	B	0.52	0/132	1.02	0/175
2	D	0.49	0/132	0.91	0/175
All	All	0.60	0/4047	1.21	14/5466 (0.3%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	436	PRO	CA-C-N	8.35	130.28	119.84
1	A	436	PRO	C-N-CA	8.35	130.28	119.84
1	A	404	PHE	CA-C-N	-6.97	112.61	119.64
1	A	404	PHE	C-N-CA	-6.97	112.61	119.64
1	C	404	PHE	CA-C-N	-5.96	113.54	119.56
1	C	404	PHE	C-N-CA	-5.96	113.54	119.56
1	A	336	ILE	N-CA-C	5.84	115.96	110.30
1	A	436	PRO	O-C-N	5.65	123.81	121.15
1	C	436	PRO	CA-C-N	5.58	125.94	119.47
1	C	436	PRO	C-N-CA	5.58	125.94	119.47
1	C	337	ASN	CA-C-N	-5.31	114.34	119.87
1	C	337	ASN	C-N-CA	-5.31	114.34	119.87
1	C	336	ILE	N-CA-C	5.06	115.28	110.42
1	A	432	ASP	N-CA-C	5.02	118.99	112.86

There are no chirality outliers.

There are no planarity outliers.

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	1860	0	1865	3	0
1	C	1843	0	1850	4	0
2	B	131	0	139	0	0
2	D	131	0	139	0	0
3	A	30	0	24	0	0
3	C	30	0	24	0	0
4	A	32	0	0	0	0
4	B	4	0	0	0	0
4	C	31	0	0	0	0
4	D	5	0	0	0	0
All	All	4097	0	4041	7	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 (7) 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:C:236:THR:O	1:C:256:HIS:ND1	2.38	0.54
1:A:341:GLU:OE2	1:A:344:ARG:NH1	2.46	0.48
1:A:427:ALA:HA	1:A:430:LEU:HD12	1.97	0.46
1:A:336:ILE:HA	1:A:339:ILE:HD12	2.00	0.43
1:C:336:ILE:HA	1:C:339:ILE:HD12	2.02	0.41
1:C:273:LYS:HG2	1:C:279:LEU:HD21	2.03	0.41
1:C:307:ASN:HA	1:C:308:PRO:HD2	1.92	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	222/283 (78%)	218 (98%)	4 (2%)	0	100	100
1	C	220/283 (78%)	216 (98%)	4 (2%)	0	100	100
2	B	13/25 (52%)	12 (92%)	1 (8%)	0	100	100
2	D	13/25 (52%)	12 (92%)	1 (8%)	0	100	100
All	All	468/616 (76%)	458 (98%)	10 (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	206/257 (80%)	199 (97%)	7 (3%)	32	62
1	C	204/257 (79%)	197 (97%)	7 (3%)	32	62
2	B	15/24 (62%)	15 (100%)	0	100	100
2	D	15/24 (62%)	15 (100%)	0	100	100
All	All	440/562 (78%)	426 (97%)	14 (3%)	34	64

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	216	LYS
1	A	257	PHE
1	A	316	LEU
1	A	333	VAL
1	A	334	GLU
1	A	435	LEU
1	A	445	VAL
1	C	209	GLU
1	C	234	ARG
1	C	292	THR

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Mol	Chain	Res	Type
1	C	313	ILE
1	C	317	LYS
1	C	333	VAL
1	C	435	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	GLN
1	A	252	GLN
1	A	280	GLN
1	A	350	GLN
1	A	397	HIS
1	A	421	HIS
2	B	695	GLN
1	C	252	GLN
1	C	280	GLN
1	C	322	ASN
1	C	352	ASN
1	C	375	GLN
1	C	377	GLN
1	C	397	HIS
2	D	695	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](#)

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$
3	4KM	C	501	-	30,31,31	0.81	1 (3%)	43,46,46	1.89	11 (25%)
3	4KM	A	501	-	30,31,31	0.85	1 (3%)	43,46,46	1.93	10 (23%)

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	4KM	C	501	-	-	5/28/28/28	0/2/2/2
3	4KM	A	501	-	-	5/28/28/28	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	4KM	O9-C10	-2.38	1.44	1.48
3	C	501	4KM	O9-C10	-2.01	1.44	1.48

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	4KM	C4-C5-C7	4.97	131.72	122.32
3	C	501	4KM	C19-N22-C24	4.89	131.85	123.55
3	A	501	4KM	C6-C5-C7	-4.87	108.78	118.41
3	A	501	4KM	C19-N22-C24	4.67	131.49	123.55
3	C	501	4KM	C4-C5-C7	4.31	130.47	122.32
3	C	501	4KM	C14-C4-C5	4.30	128.34	122.06
3	C	501	4KM	C6-C5-C7	-4.18	110.14	118.41
3	A	501	4KM	C14-C4-C5	4.04	127.96	122.06
3	A	501	4KM	C14-O15-C16	-3.49	109.30	117.62
3	C	501	4KM	O9-C10-C11	3.25	120.03	107.21
3	A	501	4KM	O9-C10-C11	3.04	119.19	107.21
3	C	501	4KM	C14-O15-C16	-2.89	110.74	117.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	4KM	C23-N22-C19	-2.89	112.19	117.01
3	A	501	4KM	C14-C4-C3	-2.67	113.74	119.51
3	C	501	4KM	C14-C4-C3	-2.62	113.86	119.51
3	C	501	4KM	O9-C7-O8	2.55	128.68	124.72
3	A	501	4KM	O9-C7-O8	2.50	128.61	124.72
3	A	501	4KM	C23-N22-C19	-2.49	112.85	117.01
3	C	501	4KM	O9-C7-C5	2.33	114.68	111.33
3	C	501	4KM	C13-C10-C12	-2.26	105.49	111.13
3	A	501	4KM	O9-C7-C5	2.11	114.37	111.33

There are no chirality outliers.

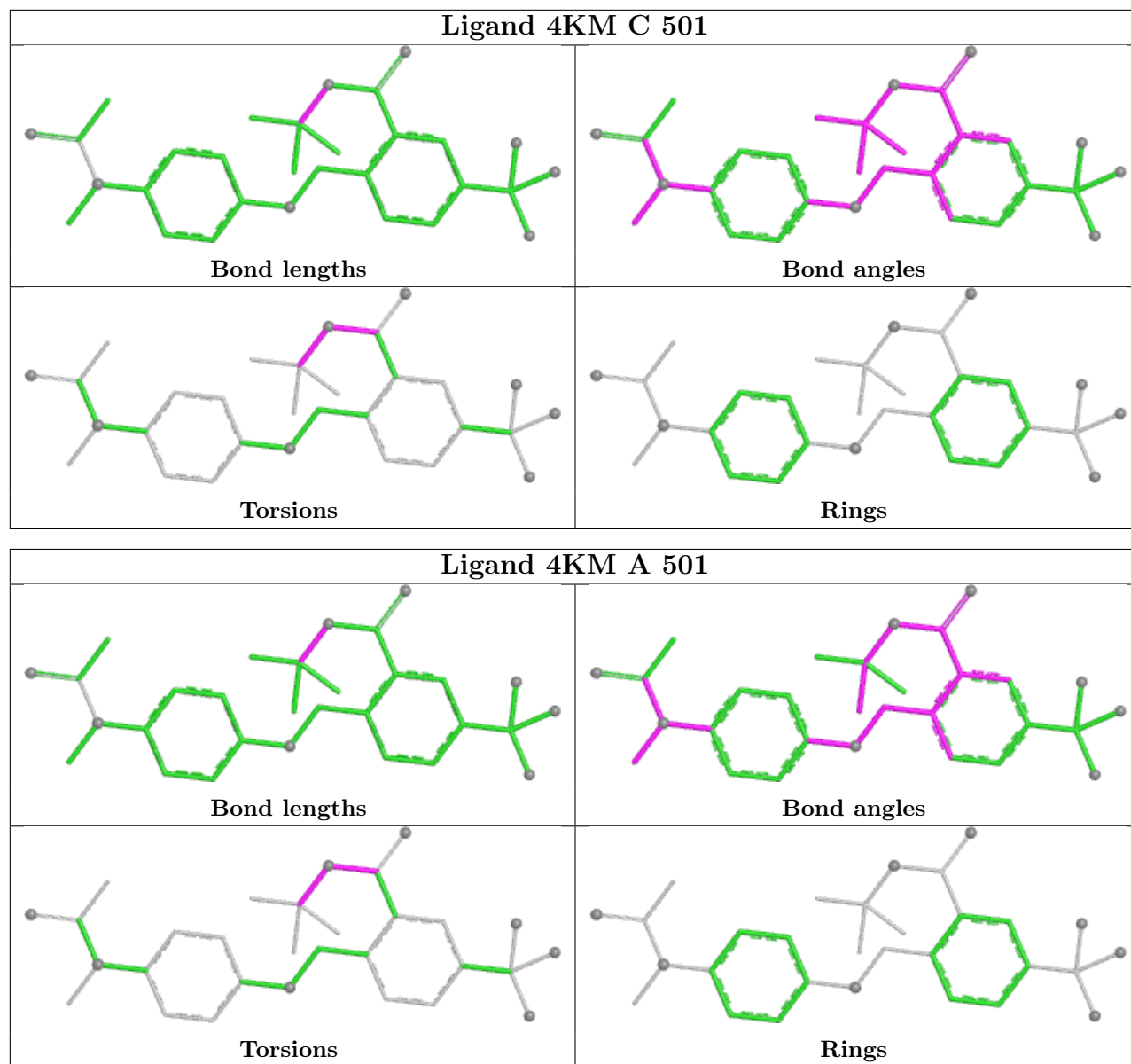
All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	4KM	C5-C7-O9-C10
3	A	501	4KM	O8-C7-O9-C10
3	C	501	4KM	C5-C7-O9-C10
3	C	501	4KM	O8-C7-O9-C10
3	A	501	4KM	C13-C10-O9-C7
3	C	501	4KM	C13-C10-O9-C7
3	C	501	4KM	C11-C10-O9-C7
3	A	501	4KM	C11-C10-O9-C7
3	A	501	4KM	C12-C10-O9-C7
3	C	501	4KM	C12-C10-O9-C7

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 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

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	228/283 (80%)	0.45	13 (5%) 29 26	22, 33, 71, 108	0
1	C	226/283 (79%)	0.60	27 (11%) 9 7	19, 36, 86, 118	0
2	B	15/25 (60%)	0.33	0 100 100	29, 35, 42, 48	0
2	D	15/25 (60%)	0.23	0 100 100	28, 32, 41, 46	0
All	All	484/616 (78%)	0.51	40 (8%) 17 14	19, 35, 78, 118	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	244	PRO	5.7
1	C	319	PHE	4.9
1	A	204	PRO	4.6
1	C	246	SER	4.5
1	C	239	PRO	4.2
1	C	204	PRO	4.0
1	C	248	GLU	3.7
1	A	235	VAL	3.6
1	C	234	ARG	3.6
1	C	430	LEU	3.5
1	C	320	SER	3.3
1	C	238	TRP	3.3
1	A	316	LEU	3.3
1	A	245	HIS	3.2
1	C	316	LEU	3.1
1	C	237	PRO	3.1
1	A	319	PHE	3.0
1	A	249	ALA	2.9
1	C	235	VAL	2.9
1	C	433	LYS	2.9
1	A	446	HIS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	250	ARG	2.8
1	A	239	PRO	2.7
1	C	247	ARG	2.6
1	C	222	GLN	2.6
1	C	327	ALA	2.6
1	C	419	SER	2.5
1	A	317	LYS	2.5
1	C	317	LYS	2.4
1	C	446	HIS	2.4
1	C	255	ALA	2.4
1	C	352	ASN	2.4
1	A	253	ARG	2.2
1	A	433	LYS	2.2
1	C	205	GLN	2.1
1	A	321	TYR	2.1
1	C	432	ASP	2.0
1	C	434	LYS	2.0
1	C	322	ASN	2.0
1	C	251	GLN	2.0

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 [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.

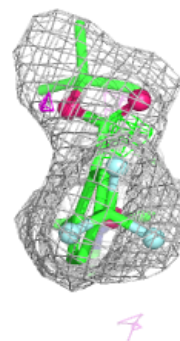
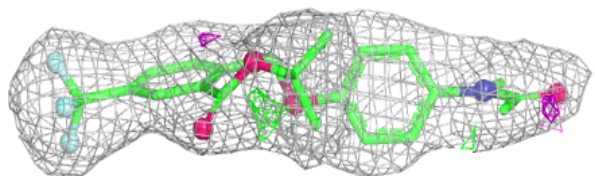
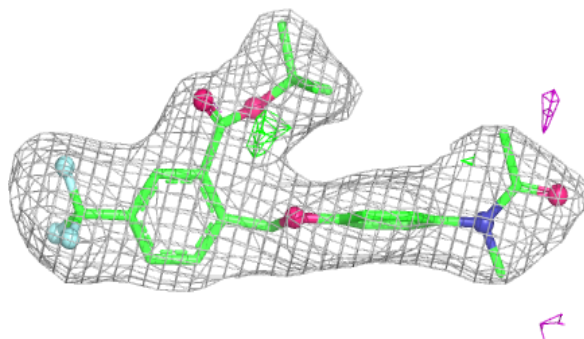
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	4KM	A	501	30/30	0.91	0.11	33,34,36,37	0
3	4KM	C	501	30/30	0.91	0.11	33,34,37,38	0

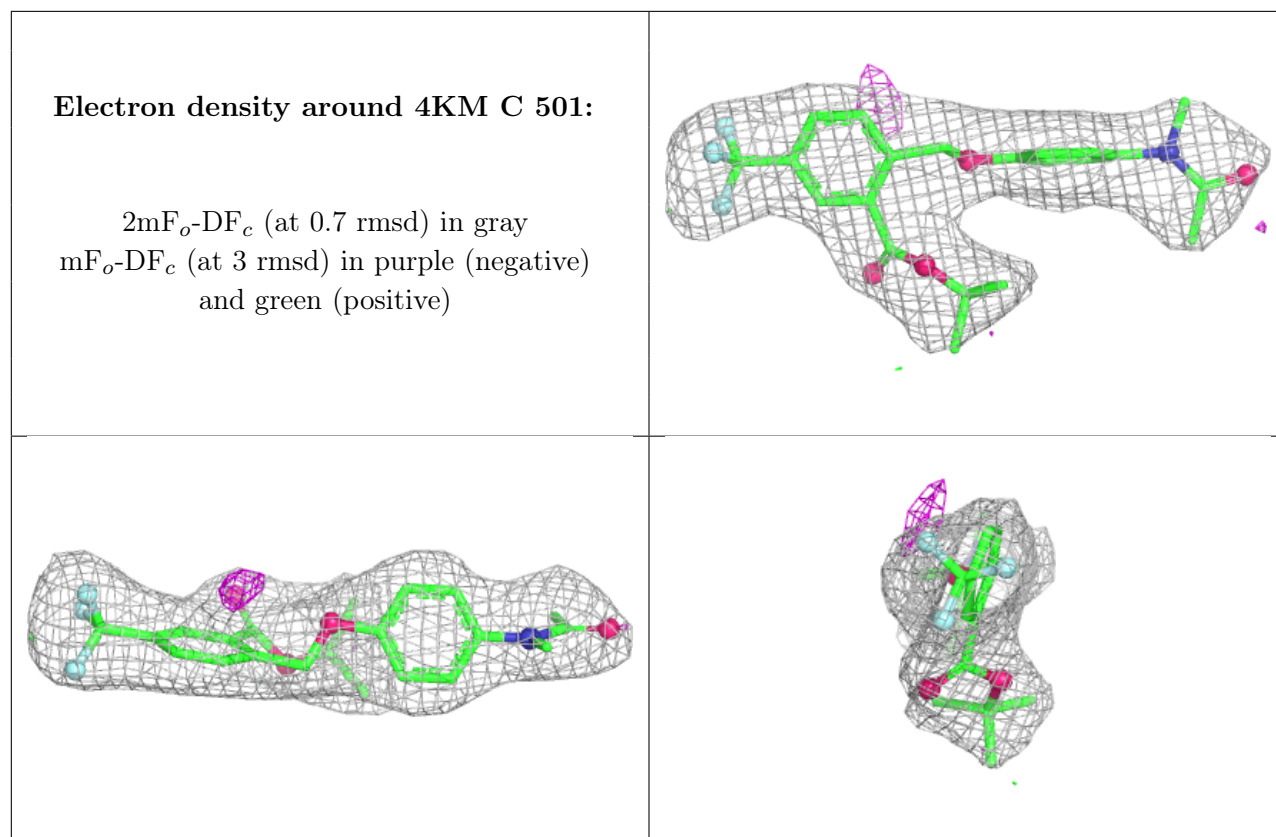
The following is a graphical depiction of the model fit to experimental electron density of all

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 4KM A 501:

$2mF_o-DF_c$ (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.