WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 9, 2023 – 01:53 PM EDT

PDB ID	:	7UJM
Title	:	Estrogen Receptor Alpha Ligand Binding Domain in Complex with a Methylated Lasofoxifene Derivative That Increases Receptor Resonance Time in the Nucleus of Breast Cancer Cells
Authors	:	Hosfield, D.J.; Greene, G.L.; Fanning, S.W.
Deposited on	:	2022-03-31
Resolution	:	1.80 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	:	2.35.1
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)	:	2.35.1

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 1.80 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		0.233
Clashscore		7
Ramachandran outliers		0
Sidechain outliers		0.5%
RSRZ outliers		1.2%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
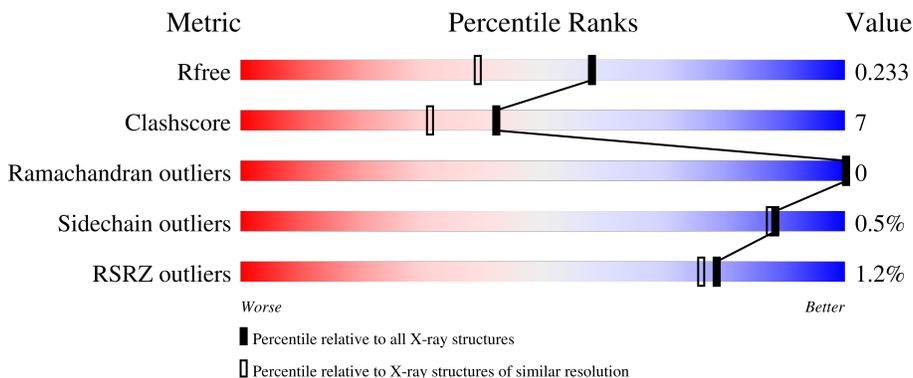
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	262	79% 10% 11%
1	B	262	.% 79% 11% 9%
1	C	262	2% 81% 11% 8%
1	D	262	.% 82% 9% 9%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 8414 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 Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	238	Total	C	N	O	S	0	6	0
			1910	1226	328	340	16			
1	A	233	Total	C	N	O	S	0	2	0
			1852	1192	311	333	16			
1	C	242	Total	C	N	O	S	0	8	0
			1939	1245	327	351	16			
1	D	238	Total	C	N	O	S	0	6	0
			1901	1220	318	347	16			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	293	HIS	-	expression tag	UNP P03372
B	294	HIS	-	expression tag	UNP P03372
B	295	HIS	-	expression tag	UNP P03372
B	296	HIS	-	expression tag	UNP P03372
B	297	HIS	-	expression tag	UNP P03372
B	298	HIS	-	expression tag	UNP P03372
B	299	GLU	-	expression tag	UNP P03372
B	300	ASN	-	expression tag	UNP P03372
B	301	LEU	-	expression tag	UNP P03372
B	302	TYR	-	expression tag	UNP P03372
B	303	GLN	-	expression tag	UNP P03372
B	304	PHE	-	expression tag	UNP P03372
B	305	SER	-	expression tag	UNP P03372
B	306	MET	-	expression tag	UNP P03372
B	381	SER	CYS	engineered mutation	UNP P03372
B	417	SER	CYS	engineered mutation	UNP P03372
B	530	SER	CYS	engineered mutation	UNP P03372
B	536	SER	LEU	conflict	UNP P03372
A	293	HIS	-	expression tag	UNP P03372
A	294	HIS	-	expression tag	UNP P03372
A	295	HIS	-	expression tag	UNP P03372

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Chain	Residue	Modelled	Actual	Comment	Reference
A	296	HIS	-	expression tag	UNP P03372
A	297	HIS	-	expression tag	UNP P03372
A	298	HIS	-	expression tag	UNP P03372
A	299	GLU	-	expression tag	UNP P03372
A	300	ASN	-	expression tag	UNP P03372
A	301	LEU	-	expression tag	UNP P03372
A	302	TYR	-	expression tag	UNP P03372
A	303	GLN	-	expression tag	UNP P03372
A	304	PHE	-	expression tag	UNP P03372
A	305	SER	-	expression tag	UNP P03372
A	306	MET	-	expression tag	UNP P03372
A	381	SER	CYS	engineered mutation	UNP P03372
A	417	SER	CYS	engineered mutation	UNP P03372
A	530	SER	CYS	engineered mutation	UNP P03372
A	536	SER	LEU	conflict	UNP P03372
C	293	HIS	-	expression tag	UNP P03372
C	294	HIS	-	expression tag	UNP P03372
C	295	HIS	-	expression tag	UNP P03372
C	296	HIS	-	expression tag	UNP P03372
C	297	HIS	-	expression tag	UNP P03372
C	298	HIS	-	expression tag	UNP P03372
C	299	GLU	-	expression tag	UNP P03372
C	300	ASN	-	expression tag	UNP P03372
C	301	LEU	-	expression tag	UNP P03372
C	302	TYR	-	expression tag	UNP P03372
C	303	GLN	-	expression tag	UNP P03372
C	304	PHE	-	expression tag	UNP P03372
C	305	SER	-	expression tag	UNP P03372
C	306	MET	-	expression tag	UNP P03372
C	381	SER	CYS	engineered mutation	UNP P03372
C	417	SER	CYS	engineered mutation	UNP P03372
C	530	SER	CYS	engineered mutation	UNP P03372
C	536	SER	LEU	conflict	UNP P03372
D	293	HIS	-	expression tag	UNP P03372
D	294	HIS	-	expression tag	UNP P03372
D	295	HIS	-	expression tag	UNP P03372
D	296	HIS	-	expression tag	UNP P03372
D	297	HIS	-	expression tag	UNP P03372
D	298	HIS	-	expression tag	UNP P03372
D	299	GLU	-	expression tag	UNP P03372
D	300	ASN	-	expression tag	UNP P03372
D	301	LEU	-	expression tag	UNP P03372

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Chain	Residue	Modelled	Actual	Comment	Reference
D	302	TYR	-	expression tag	UNP P03372
D	303	GLN	-	expression tag	UNP P03372
D	304	PHE	-	expression tag	UNP P03372
D	305	SER	-	expression tag	UNP P03372
D	306	MET	-	expression tag	UNP P03372
D	381	SER	CYS	engineered mutation	UNP P03372
D	417	SER	CYS	engineered mutation	UNP P03372
D	530	SER	CYS	engineered mutation	UNP P03372
D	536	SER	LEU	conflict	UNP P03372

- Molecule 2 is (5R,6S)-5-(4-{2-[(2R)-2-methylpyrrolidin-1-yl]ethoxy}phenyl)-6-phenyl-5,6 ,7,8-tetrahydronaphthalen-2-ol (three-letter code: RL4) (formula: $C_{29}H_{33}NO_2$) (labeled as "Ligand of Interest" by depositor).
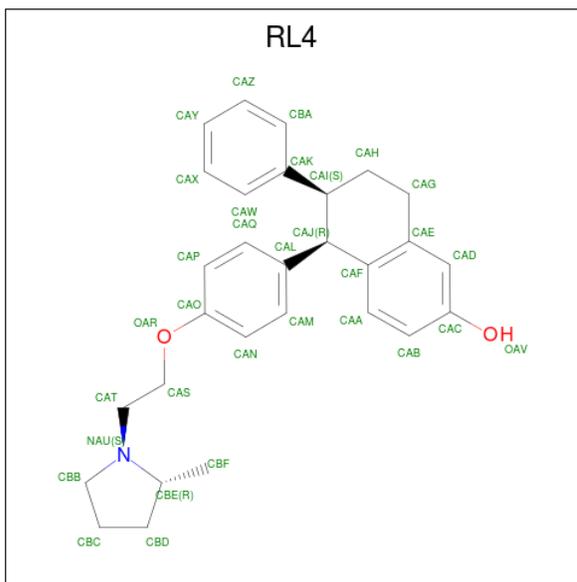
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			32	29	1	2		
2	A	1	Total	C	N	O	0	0
			32	29	1	2		
2	C	1	Total	C	N	O	0	0
			32	29	1	2		
2	D	1	Total	C	N	O	0	0
			32	29	1	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	176	Total 176	O 176	0	0
3	A	169	Total 169	O 169	0	0
3	C	173	Total 173	O 173	0	0
3	D	166	Total 166	O 166	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: Estrogen receptor

Chain B:

- Molecule 1: Estrogen receptor

Chain A:

- Molecule 1: Estrogen receptor

Chain C:

- Molecule 1: Estrogen receptor

Chain D:

HIS HIS HIS HIS HIS HIS GLU ASN LEU TYR GLN PHE SER MET A307 D332 P333 I358 N359 L372 V376 L379 M396 K416 S417 V418 E419 G420 M421 V422 E423 R436 T465 L469 N519 Y526 S530 V533 L539 M543 L544 ASP ALA HIS

ARG LEU HIS ALA PRO THR SER

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	58.47Å 58.47Å 275.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.33 – 1.80 47.52 – 1.64	Depositor EDS
% Data completeness (in resolution range)	76.8 (44.33-1.80) 61.4 (47.52-1.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.16 (at 1.64Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.190 , 0.233 0.190 , 0.233	Depositor DCC
R_{free} test set	4047 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	14.8	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 32.5	EDS
L-test for twinning[2]	$< |L| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.488 for -h,-k,l 0.488 for h,-h-k,-l 0.488 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8414	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% 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: RL4

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	0.49	0/1886	0.55	0/2549
1	B	0.42	0/1945	0.56	0/2629
1	C	0.43	0/1979	0.57	0/2678
1	D	0.52	0/1940	0.58	0/2627
All	All	0.47	0/7750	0.57	0/10483

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 ⓘ

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	1852	0	1884	21	0
1	B	1910	0	1944	31	0
1	C	1939	0	1958	25	0
1	D	1901	0	1917	30	0
2	A	32	0	0	1	0
2	B	32	0	0	3	0
2	C	32	0	0	1	0
2	D	32	0	0	1	0
3	A	169	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	176	0	0	6	0
3	C	173	0	0	3	0
3	D	166	0	0	1	0
All	All	8414	0	7703	106	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 106 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:496:THR:HG21	3:C:839:HOH:O	1.50	1.11
1:D:418:VAL:CG2	1:D:421:MET:HE2	1.81	1.09
1:C:530:SER:HB2	1:C:533:VAL:HG13	1.43	0.99
1:D:418:VAL:CG2	1:D:421:MET:CE	2.45	0.95
1:D:418:VAL:CB	1:D:421:MET:HE2	2.00	0.89

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	229/262 (87%)	228 (100%)	1 (0%)	0	100	100
1	B	237/262 (90%)	232 (98%)	5 (2%)	0	100	100
1	C	245/262 (94%)	244 (100%)	1 (0%)	0	100	100
1	D	242/262 (92%)	239 (99%)	3 (1%)	0	100	100
All	All	953/1048 (91%)	943 (99%)	10 (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	206/237 (87%)	204 (99%)	2 (1%)	76	71
1	B	213/237 (90%)	213 (100%)	0	100	100
1	C	216/237 (91%)	214 (99%)	2 (1%)	78	75
1	D	211/237 (89%)	211 (100%)	0	100	100
All	All	846/948 (89%)	842 (100%)	4 (0%)	88	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	321	ASP
1	A	396	MET
1	C	432	SER
1	C	464	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	524	HIS
1	A	413	ASN
1	C	359	ASN
1	C	519	ASN
1	D	359	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	$\#|Z| > 2$
2	RL4	A	601	-	35,36,36	3.06	14 (40%)	46,50,50	1.85	12 (26%)
2	RL4	B	601	-	35,36,36	3.14	16 (45%)	46,50,50	1.82	8 (17%)
2	RL4	C	601	-	35,36,36	3.01	16 (45%)	46,50,50	1.74	10 (21%)
2	RL4	D	601	-	35,36,36	3.02	13 (37%)	46,50,50	1.87	12 (26%)

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
2	RL4	A	601	-	-	3/14/37/37	0/5/5/5
2	RL4	B	601	-	-	3/14/37/37	0/5/5/5
2	RL4	C	601	-	-	3/14/37/37	0/5/5/5
2	RL4	D	601	-	-	3/14/37/37	0/5/5/5

The worst 5 of 59 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	RL4	CAQ-CAP	7.97	1.53	1.38
2	A	601	RL4	CAQ-CAP	7.47	1.52	1.38
2	C	601	RL4	CAQ-CAP	7.44	1.52	1.38
2	D	601	RL4	CAQ-CAP	6.99	1.51	1.38
2	C	601	RL4	CAE-CAF	-6.51	1.29	1.40

The worst 5 of 42 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	RL4	CAL-CAJ-CAF	-6.00	103.80	112.86
2	B	601	RL4	CAB-CAC-CAD	-5.84	113.78	120.17
2	D	601	RL4	CAB-CAC-CAD	-5.06	114.63	120.17
2	D	601	RL4	CBB-NAU-CBE	-4.92	97.13	104.87
2	B	601	RL4	CAA-CAB-CAC	4.92	125.27	119.88

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	RL4	OAR-CAS-CAT-NAU
2	D	601	RL4	OAR-CAS-CAT-NAU
2	B	601	RL4	CAN-CAO-OAR-CAS
2	C	601	RL4	OAR-CAS-CAT-NAU
2	A	601	RL4	OAR-CAS-CAT-NAU

There are no ring outliers.

4 monomers are involved in 6 short contacts:

| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	RL4	1	0
2	B	601	RL4	3	0
2	C	601	RL4	1	0
2	D	601	RL4	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 RL4 A 601

Bond lengths

Bond angles

Torsions

Rings

Ligand RL4 B 601

Bond lengths

Bond angles

Torsions

Rings

Ligand RL4 C 601

Bond lengths

Bond angles

Torsions

Rings

Ligand RL4 D 601

Bond lengths

Bond angles

Torsions

Rings
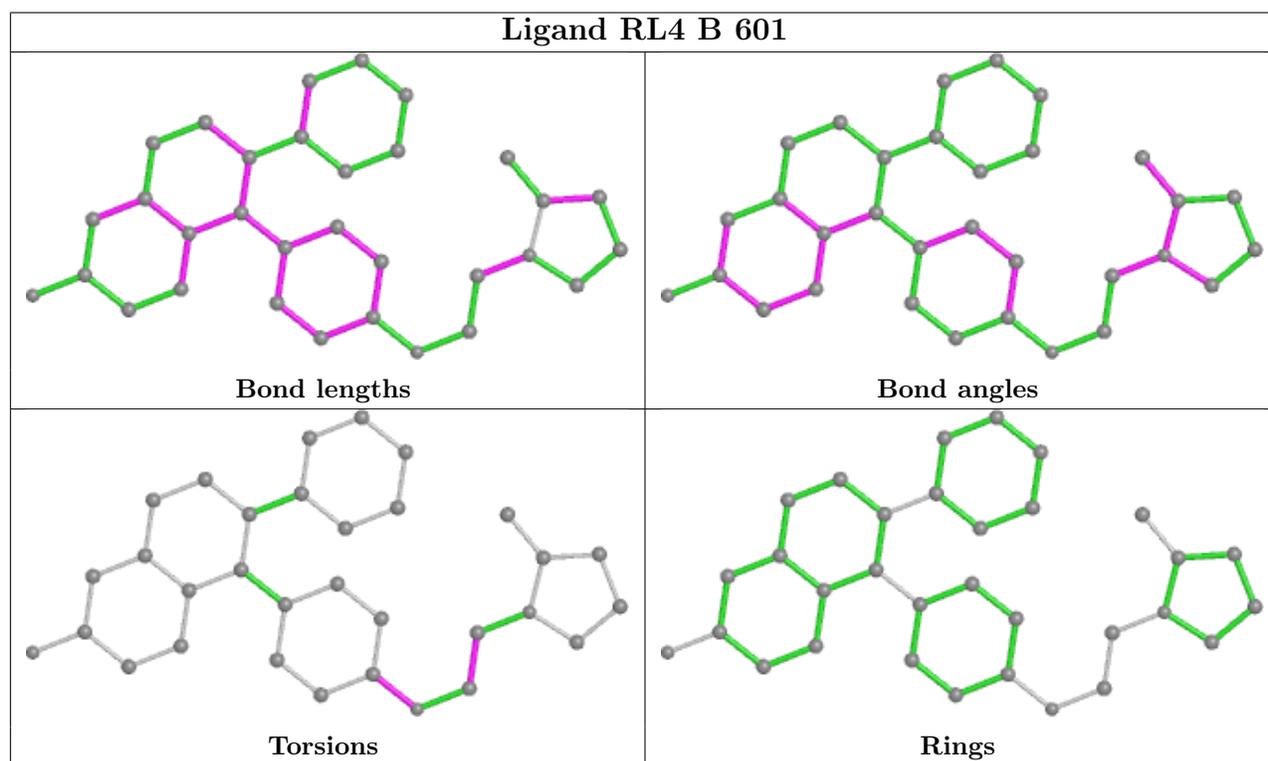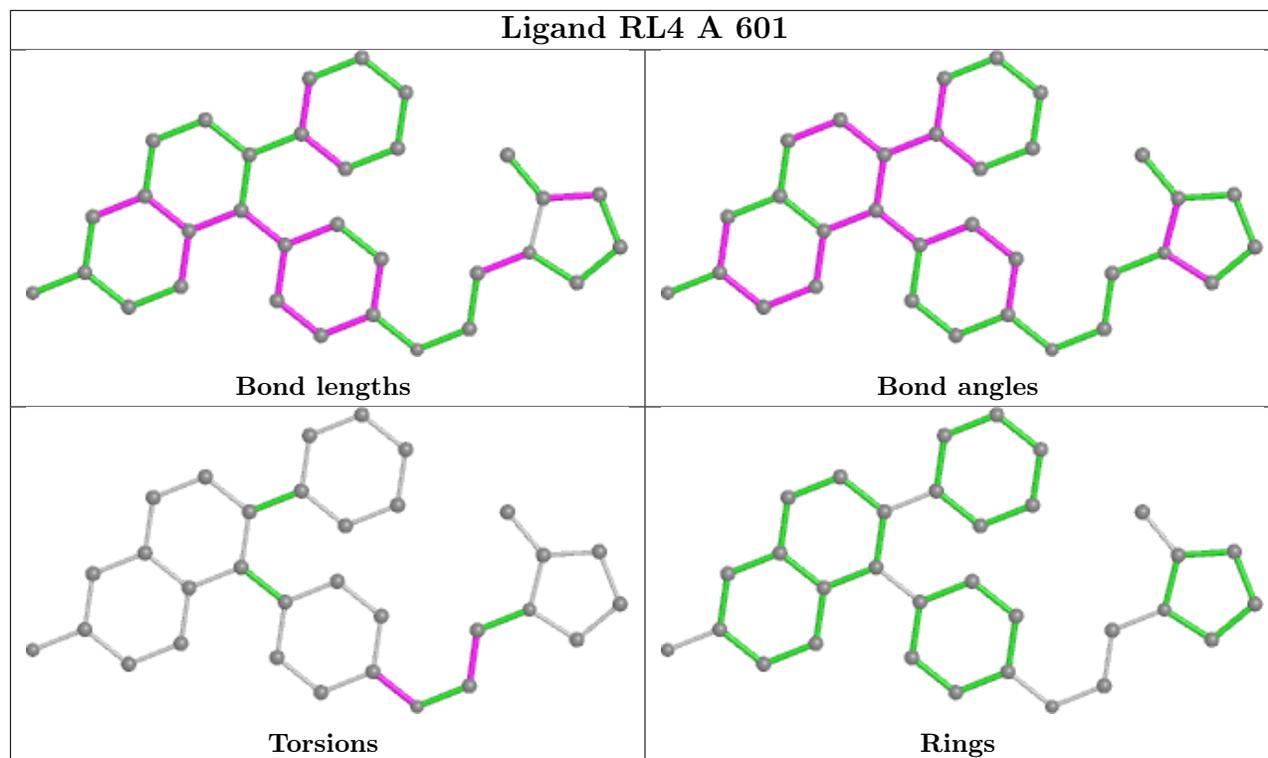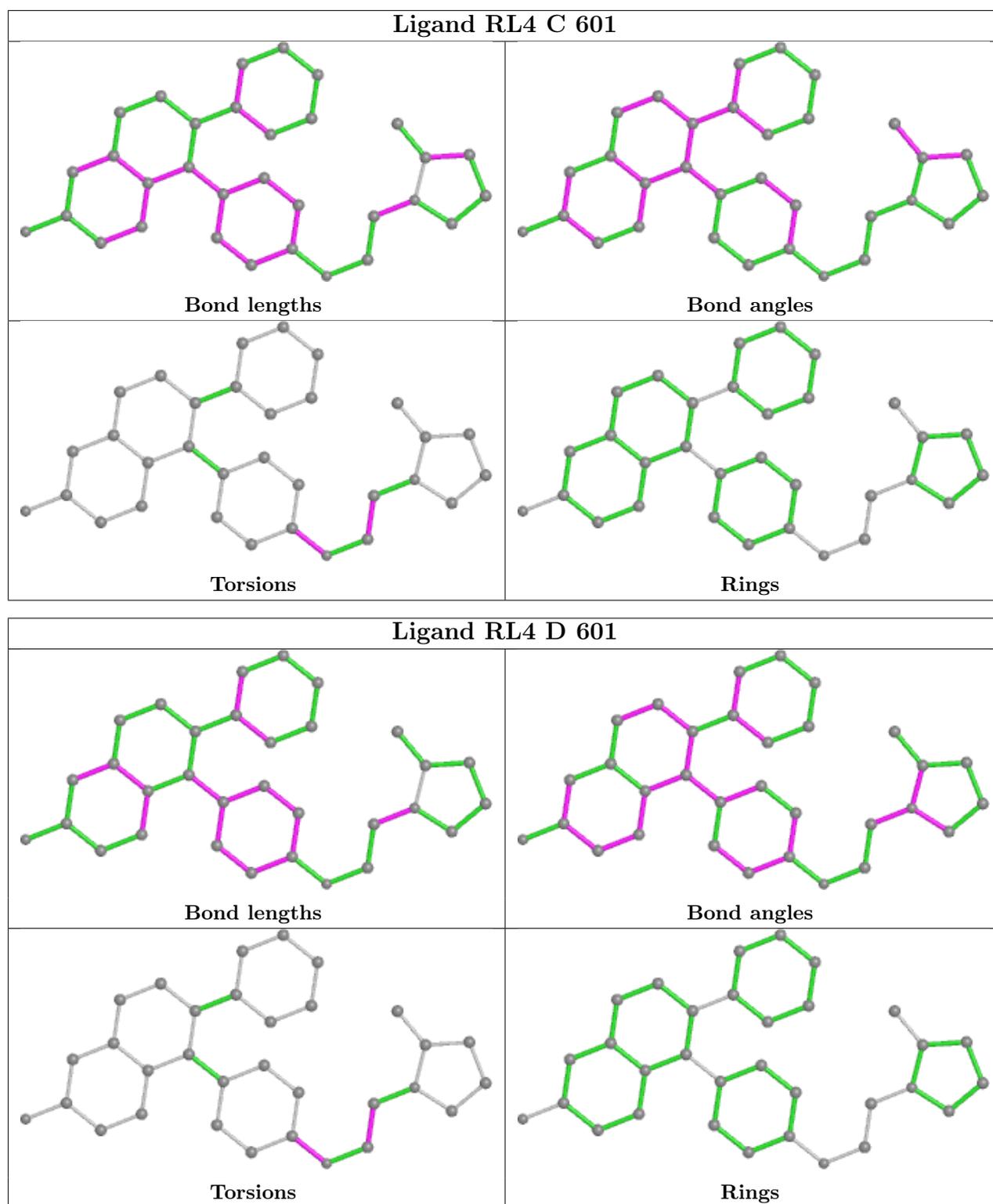
5.7 Other polymers ⓘ

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	233/262 (88%)	-0.57	1 (0%)	92	90	7, 21, 43, 53	1 (0%)
1	B	238/262 (90%)	-0.52	3 (1%)	77	74	6, 21, 44, 54	1 (0%)
1	C	242/262 (92%)	-0.52	4 (1%)	70	66	6, 21, 45, 52	1 (0%)
1	D	238/262 (90%)	-0.50	3 (1%)	77	74	6, 21, 48, 58	0
All	All	951/1048 (90%)	-0.52	11 (1%)	79	76	6, 21, 45, 58	3 (0%)

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	418	VAL	3.6
1	C	308	LEU	3.1
1	C	462	LEU	3.1
1	D	526	TYR	2.5
1	D	417	SER	2.4

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

There are no non-standard protein/DNA/RNA residues in this entry.

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
2	RL4	B	601	32/32	0.89	0.10	14,16,39,43	0
2	RL4	A	601	32/32	0.92	0.10	14,14,30,35	0
2	RL4	D	601	32/32	0.92	0.10	14,14,31,42	0
2	RL4	C	601	32/32	0.94	0.09	14,14,32,38	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 RL4 B 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)
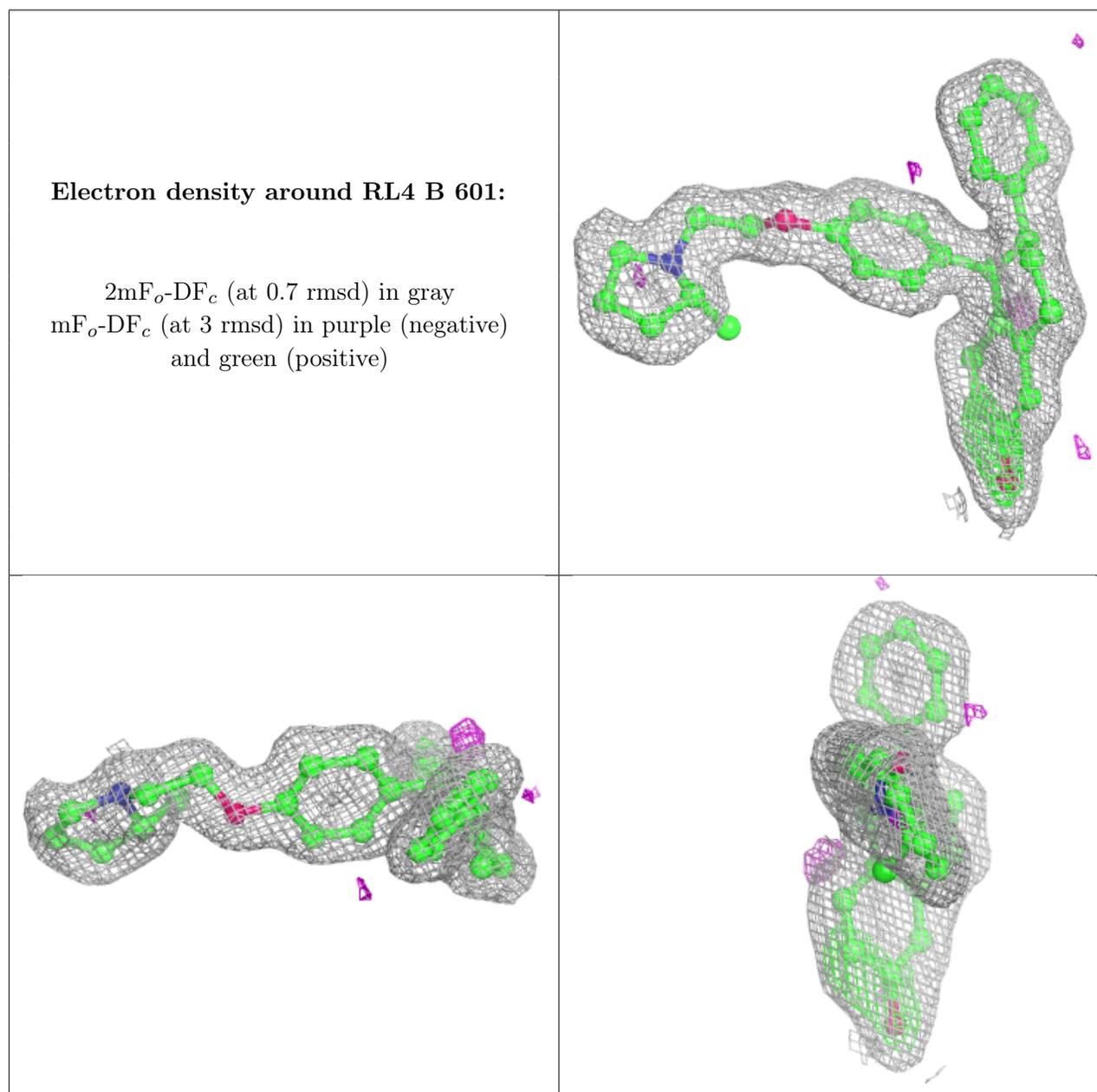
Electron density around RL4 A 601:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
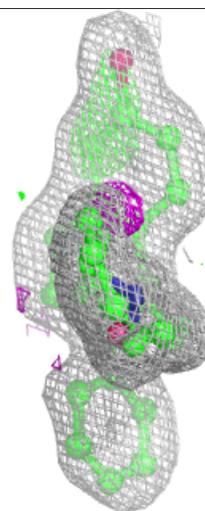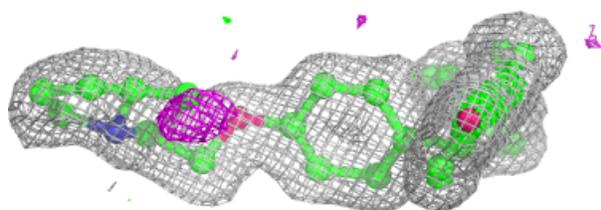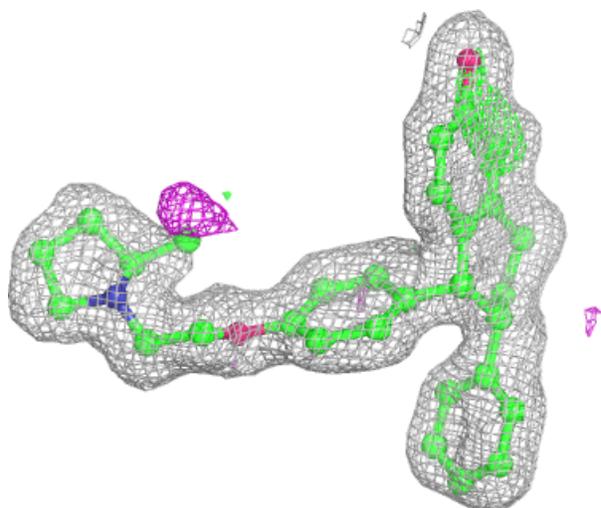
Electron density around RL4 D 601:

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

Electron density around RL4 C 601:

$2mF_o$-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.