Full wwPDB X-ray Structure Validation Report (i)

Oct 9, 2023 – 01:39 PM EDT

PDB ID	:	7UJF
Title	:	Estrogen Receptor Alpha Ligand Binding Domain in Complex with a Methylated Lasofoxifene Derivative with Selective Estrogen Receptor Degrader Properties
Authors	:	Hosfield, D.J.; Greene, G.L.; Fanning, S.W.
Deposited on	:	2022-03-30
Resolution	:	1.70 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 (i) 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 (i)) were used in the production of this report:

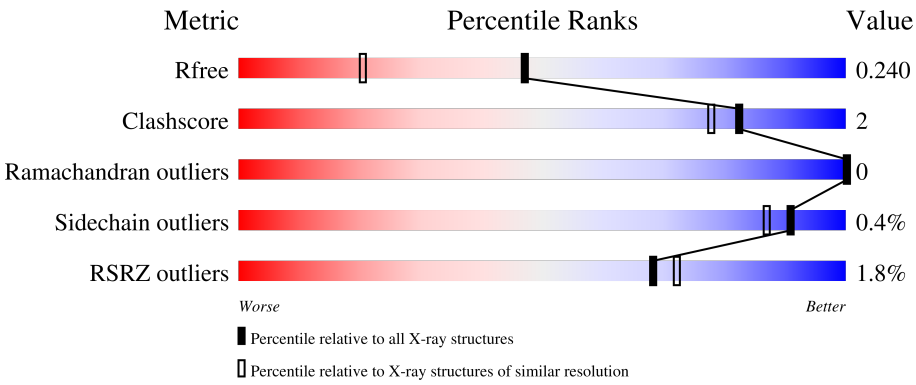
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 <=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	263	.% 83% 5% 12%
1	B	263	.% 83% 6% 11%
1	C	263	2% 84% 7% 10%
1	D	263	2% 83% 5% 11%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8486 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
			Total	C	N	O	S			
1	B	235	1898	1213	324	345	16	0	7	0
1	A	232	1871	1202	312	341	16	0	7	0
1	C	238	1903	1215	325	347	16	0	7	0
1	D	233	1857	1193	311	337	16	0	4	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	292	HIS	-	expression tag	UNP P03372
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	GLU	-	expression tag	UNP P03372
B	299	ASN	-	expression tag	UNP P03372
B	300	TYR	-	expression tag	UNP P03372
B	301	LEU	-	expression tag	UNP P03372
B	302	PHE	-	expression tag	UNP P03372
B	303	GLN	-	expression tag	UNP P03372
B	304	SER	-	expression tag	UNP P03372
B	305	MET	-	expression tag	UNP P03372
B	306	SER	-	expression tag	UNP P03372
B	381	SER	CYS	conflict	UNP P03372
B	417	SER	CYS	conflict	UNP P03372
B	530	SER	CYS	conflict	UNP P03372
B	536	SER	LEU	conflict	UNP P03372
A	292	HIS	-	expression tag	UNP P03372
A	293	HIS	-	expression tag	UNP P03372

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Chain	Residue	Modelled	Actual	Comment	Reference
A	294	HIS	-	expression tag	UNP P03372
A	295	HIS	-	expression tag	UNP P03372
A	296	HIS	-	expression tag	UNP P03372
A	297	HIS	-	expression tag	UNP P03372
A	298	GLU	-	expression tag	UNP P03372
A	299	ASN	-	expression tag	UNP P03372
A	300	TYR	-	expression tag	UNP P03372
A	301	LEU	-	expression tag	UNP P03372
A	302	PHE	-	expression tag	UNP P03372
A	303	GLN	-	expression tag	UNP P03372
A	304	SER	-	expression tag	UNP P03372
A	305	MET	-	expression tag	UNP P03372
A	306	SER	-	expression tag	UNP P03372
A	381	SER	CYS	conflict	UNP P03372
A	417	SER	CYS	conflict	UNP P03372
A	530	SER	CYS	conflict	UNP P03372
A	536	SER	LEU	conflict	UNP P03372
C	292	HIS	-	expression tag	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	GLU	-	expression tag	UNP P03372
C	299	ASN	-	expression tag	UNP P03372
C	300	TYR	-	expression tag	UNP P03372
C	301	LEU	-	expression tag	UNP P03372
C	302	PHE	-	expression tag	UNP P03372
C	303	GLN	-	expression tag	UNP P03372
C	304	SER	-	expression tag	UNP P03372
C	305	MET	-	expression tag	UNP P03372
C	306	SER	-	expression tag	UNP P03372
C	381	SER	CYS	conflict	UNP P03372
C	417	SER	CYS	conflict	UNP P03372
C	530	SER	CYS	conflict	UNP P03372
C	536	SER	LEU	conflict	UNP P03372
D	292	HIS	-	expression tag	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

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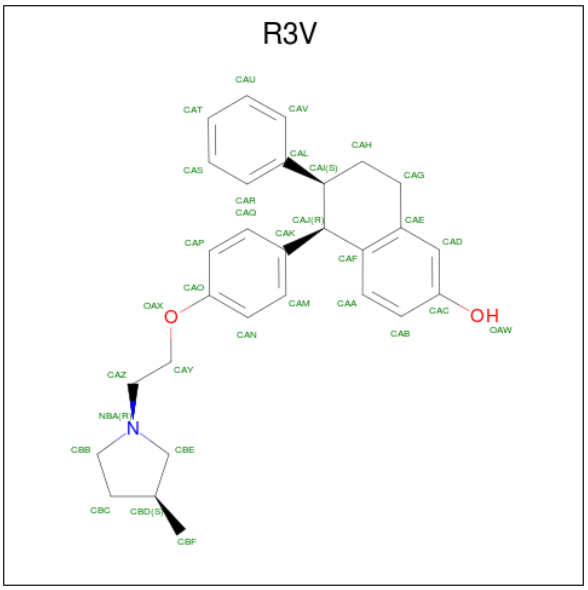
Chain	Residue	Modelled	Actual	Comment	Reference
D	298	GLU	-	expression tag	UNP P03372
D	299	ASN	-	expression tag	UNP P03372
D	300	TYR	-	expression tag	UNP P03372
D	301	LEU	-	expression tag	UNP P03372
D	302	PHE	-	expression tag	UNP P03372
D	303	GLN	-	expression tag	UNP P03372
D	304	SER	-	expression tag	UNP P03372
D	305	MET	-	expression tag	UNP P03372
D	306	SER	-	expression tag	UNP P03372
D	381	SER	CYS	conflict	UNP P03372
D	417	SER	CYS	conflict	UNP P03372
D	530	SER	CYS	conflict	UNP P03372
D	536	SER	LEU	conflict	UNP P03372

- Molecule 2 is (5R,6S)-5-(4-{2-[(3S)-3-methylpyrrolidin-1-yl]ethoxy}phenyl)-6-phenyl-5,6,7,8-tetrahydronaphthalen-2-ol (three-letter code: R3V) (formula: $C_{29}H_{33}NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	B	1	32	29	1	2	0	0
2	A	1	32	29	1	2	0	0
2	C	1	32	29	1	2	0	0
2	D	1	32	29	1	2	0	0

- Molecule 3 is water.

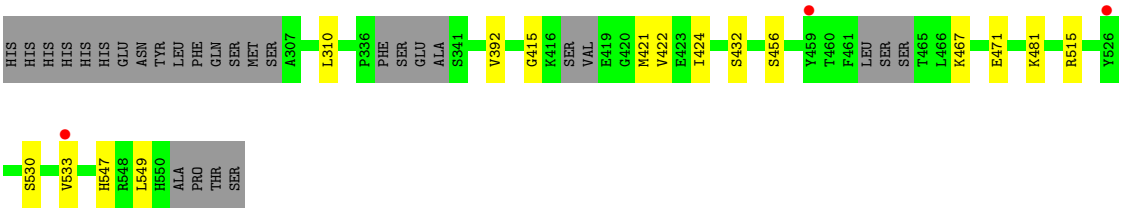
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	214	214	214	0	0
			Total	O		
3	A	203	203	203	0	0
			Total	O		
3	C	205	205	205	0	0
			Total	O		
3	D	207	207	207	0	0

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 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.

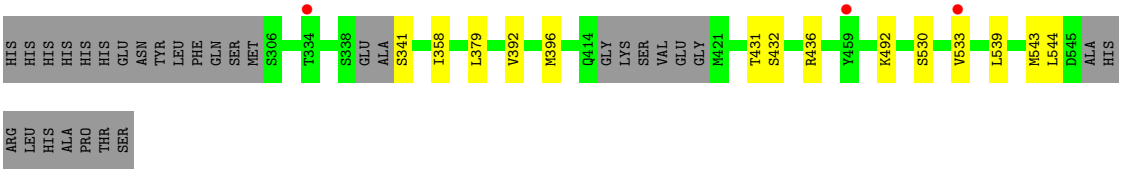
• Molecule 1: Estrogen receptor

Chain B:



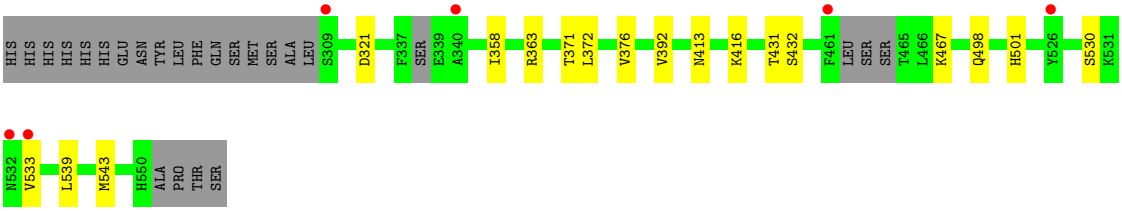
• Molecule 1: Estrogen receptor

Chain A:



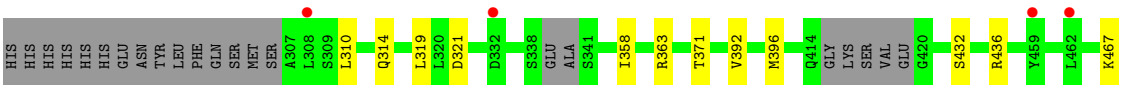
• Molecule 1: Estrogen receptor

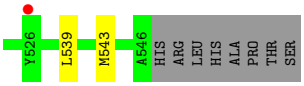
Chain C:



• Molecule 1: Estrogen receptor

Chain D:




Y526
L539
M543
A546
HIS
ARG
LEU
HIS
ALA
PRO
THR
SER

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	58.66Å 58.66Å 276.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.68 – 1.70 47.68 – 1.70	Depositor EDS
% Data completeness (in resolution range)	81.6 (47.68-1.70) 81.6 (47.68-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.195 , 0.239 0.198 , 0.240	Depositor DCC
R_{free} test set	4761 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	14.8	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 29.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.52$, $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	0.467 for -h,-k,l 0.478 for h,-h-k,-l 0.470 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8486	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: R3V

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	0.50	0/1908	0.59	0/2582
1	B	0.45	0/1931	0.55	0/2608
1	C	0.43	0/1940	0.53	0/2623
1	D	0.48	0/1894	0.57	0/2561
All	All	0.47	0/7673	0.56	0/10374

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	1871	0	1885	10	0
1	B	1898	0	1918	9	0
1	C	1903	0	1912	11	0
1	D	1857	0	1880	8	0
2	A	32	0	0	0	0
2	B	32	0	0	0	0
2	C	32	0	0	0	0
2	D	32	0	0	0	0
3	A	203	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	214	0	0	0	0
3	C	205	0	0	0	0
3	D	207	0	0	0	0
All	All	8486	0	7595	38	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 2.

All (38) 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:B:547:HIS:CD2	1:B:549:LEU:HD12	2.24	0.71
1:B:547:HIS:HD2	1:B:549:LEU:HD12	1.55	0.71
1:B:310:LEU:O	1:B:481:LYS:NZ	2.26	0.62
1:D:321:ASP:OD2	1:D:363:ARG:NH2	2.31	0.62
1:A:530[A]:SER:HB2	1:A:533:VAL:HG13	1.87	0.56
1:C:321:ASP:OD2	1:C:363:ARG:NH2	2.40	0.54
1:B:415:GLY:O	1:B:421:MET:HB3	2.09	0.53
1:A:530[B]:SER:HB3	1:A:533:VAL:HG13	1.90	0.52
1:C:413:ASN:O	1:C:416:LYS:HE2	2.10	0.52
1:C:371:THR:HG21	1:C:467:LYS:HE2	1.91	0.52
1:B:392:VAL:HG13	1:B:432:SER:HA	1.94	0.49
1:D:396:MET:O	1:D:436:ARG:HD3	2.14	0.47
1:B:456:SER:HA	1:B:515:ARG:NH2	2.29	0.47
1:D:539:LEU:O	1:D:543:MET:HG3	2.14	0.47
1:D:310:LEU:HD22	1:D:314:GLN:HB3	1.97	0.47
1:B:530[B]:SER:HB2	1:B:533:VAL:HG23	1.95	0.47
1:A:396:MET:O	1:A:436:ARG:HD3	2.15	0.46
1:C:392:VAL:HG11	1:C:431:THR:HG22	1.97	0.46
1:C:498:GLN:HA	1:C:501:HIS:CE1	2.51	0.46
1:C:530[B]:SER:HB2	1:C:533:VAL:CG1	2.47	0.45
1:A:358:ILE:HG12	1:A:543:MET:HE2	1.98	0.45
1:A:492:LYS:HA	1:A:492:LYS:HD2	1.74	0.45
1:D:358:ILE:HG12	1:D:543:MET:HE2	1.97	0.45
1:B:392:VAL:HG13	1:B:432:SER:CA	2.46	0.44
1:A:392:VAL:HG13	1:A:432:SER:HA	2.00	0.44
1:C:392:VAL:HG13	1:C:432:SER:HA	1.99	0.43
1:A:539:LEU:O	1:A:543:MET:HG3	2.19	0.43
1:D:392:VAL:HG13	1:D:432:SER:HA	2.00	0.43
1:C:358:ILE:HG12	1:C:543:MET:HE2	2.00	0.42
1:D:371:THR:HG21	1:D:467:LYS:HE2	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:372[B]:LEU:O	1:C:376:VAL:HG23	2.19	0.42
1:A:379:LEU:HD12	1:A:544:LEU:HD11	2.01	0.42
1:A:530[A]:SER:HB2	1:A:533:VAL:CG1	2.50	0.41
1:C:539:LEU:O	1:C:543:MET:HG3	2.21	0.41
1:A:392:VAL:HG11	1:A:431:THR:HG22	2.03	0.41
1:B:467:LYS:O	1:B:471:GLU:HG2	2.21	0.41
1:D:319:LEU:HD23	1:D:319:LEU:HA	1.89	0.40
1:C:392:VAL:HG13	1:C:432:SER:CA	2.51	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	233/263 (89%)	231 (99%)	2 (1%)	0	100	100
1	B	233/263 (89%)	232 (100%)	1 (0%)	0	100	100
1	C	238/263 (90%)	234 (98%)	4 (2%)	0	100	100
1	D	231/263 (88%)	229 (99%)	2 (1%)	0	100	100
All	All	935/1052 (89%)	926 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	209/238 (88%)	208 (100%)	1 (0%)	88	83
1	B	212/238 (89%)	210 (99%)	2 (1%)	78	70
1	C	211/238 (89%)	211 (100%)	0	100	100
1	D	207/238 (87%)	207 (100%)	0	100	100
All	All	839/952 (88%)	836 (100%)	3 (0%)	91	87

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	422	VAL
1	B	424	ILE
1	A	341	SER

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

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)

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	R3V	D	601	-	36,36,36	3.56	11 (30%)	46,50,50	2.54	13 (28%)
2	R3V	C	601	-	36,36,36	3.63	11 (30%)	46,50,50	2.47	10 (21%)
2	R3V	A	601	-	36,36,36	3.73	11 (30%)	46,50,50	2.29	11 (23%)
2	R3V	B	601	-	36,36,36	3.54	11 (30%)	46,50,50	2.23	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	R3V	D	601	-	-	2/14/36/36	0/5/5/5
2	R3V	C	601	-	-	3/14/36/36	0/5/5/5
2	R3V	A	601	-	-	3/14/36/36	0/5/5/5
2	R3V	B	601	-	-	3/14/36/36	0/5/5/5

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	R3V	CAA-CAF	10.35	1.53	1.39
2	C	601	R3V	CAA-CAF	9.74	1.52	1.39
2	B	601	R3V	CAA-CAF	9.35	1.51	1.39
2	D	601	R3V	CAA-CAF	9.28	1.51	1.39
2	A	601	R3V	CAQ-CAK	8.34	1.52	1.39
2	D	601	R3V	CAQ-CAK	8.10	1.52	1.39
2	C	601	R3V	CAQ-CAK	8.01	1.52	1.39
2	A	601	R3V	CAB-CAC	8.00	1.54	1.38
2	B	601	R3V	CAM-CAN	7.94	1.53	1.38
2	C	601	R3V	CAM-CAN	7.93	1.53	1.38
2	D	601	R3V	CAM-CAN	7.84	1.53	1.38
2	A	601	R3V	CAM-CAN	7.84	1.53	1.38
2	B	601	R3V	CAB-CAC	7.75	1.53	1.38
2	C	601	R3V	CAB-CAC	7.63	1.53	1.38
2	D	601	R3V	CAB-CAC	7.41	1.53	1.38
2	B	601	R3V	CAD-CAE	7.40	1.52	1.39
2	A	601	R3V	CAD-CAE	7.35	1.52	1.39
2	D	601	R3V	CAD-CAE	7.30	1.52	1.39
2	C	601	R3V	CAD-CAE	7.21	1.51	1.39
2	C	601	R3V	CAP-CAO	7.12	1.52	1.38
2	B	601	R3V	CAQ-CAK	6.90	1.50	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	R3V	CAP-CAO	6.59	1.51	1.38
2	A	601	R3V	CAP-CAO	6.58	1.51	1.38
2	B	601	R3V	CAP-CAO	6.34	1.51	1.38
2	B	601	R3V	CAF-CAJ	-6.32	1.42	1.51
2	A	601	R3V	CAF-CAJ	-6.27	1.43	1.51
2	D	601	R3V	CAF-CAJ	-5.83	1.43	1.51
2	C	601	R3V	CAF-CAJ	-5.74	1.43	1.51
2	C	601	R3V	CAE-CAF	-3.62	1.34	1.40
2	B	601	R3V	CAE-CAF	-3.51	1.34	1.40
2	D	601	R3V	CAE-CAF	-3.36	1.34	1.40
2	A	601	R3V	CAE-CAF	-3.34	1.34	1.40
2	B	601	R3V	CAZ-NBA	-3.31	1.39	1.47
2	A	601	R3V	CAZ-NBA	-3.28	1.39	1.47
2	D	601	R3V	CAZ-NBA	-3.18	1.40	1.47
2	C	601	R3V	CAZ-NBA	-3.06	1.40	1.47
2	C	601	R3V	CAG-CAE	2.65	1.55	1.51
2	D	601	R3V	OAX-CAO	2.49	1.43	1.37
2	B	601	R3V	OAX-CAO	2.47	1.43	1.37
2	C	601	R3V	OAX-CAO	2.46	1.43	1.37
2	A	601	R3V	OAX-CAO	2.28	1.42	1.37
2	B	601	R3V	CAG-CAE	2.19	1.55	1.51
2	D	601	R3V	CAG-CAE	2.14	1.54	1.51
2	A	601	R3V	CAG-CAE	2.05	1.54	1.51

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	601	R3V	CAG-CAE-CAD	-7.80	104.28	119.91
2	D	601	R3V	CAG-CAE-CAD	-7.42	105.04	119.91
2	A	601	R3V	CAG-CAE-CAD	-6.87	106.15	119.91
2	B	601	R3V	CAG-CAE-CAD	-6.86	106.16	119.91
2	D	601	R3V	CAC-CAD-CAE	-6.48	113.63	120.83
2	D	601	R3V	CAH-CAG-CAE	-6.45	100.64	112.87
2	C	601	R3V	CAC-CAD-CAE	-6.34	113.78	120.83
2	C	601	R3V	CAH-CAG-CAE	-6.00	101.49	112.87
2	C	601	R3V	CAG-CAE-CAF	5.56	129.46	121.13
2	A	601	R3V	CAH-CAG-CAE	-5.52	102.39	112.87
2	D	601	R3V	CAK-CAJ-CAF	-5.40	104.71	112.86
2	A	601	R3V	CAK-CAJ-CAF	-5.31	104.84	112.86
2	D	601	R3V	CAD-CAE-CAF	5.23	126.29	119.50
2	C	601	R3V	CAD-CAE-CAF	5.20	126.25	119.50
2	A	601	R3V	CAG-CAE-CAF	5.18	128.88	121.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	R3V	CAC-CAD-CAE	-5.08	115.18	120.83
2	B	601	R3V	CAK-CAJ-CAF	-5.05	105.23	112.86
2	D	601	R3V	CAG-CAE-CAF	5.03	128.66	121.13
2	A	601	R3V	CAC-CAD-CAE	-4.95	115.33	120.83
2	B	601	R3V	CAG-CAE-CAF	4.91	128.47	121.13
2	B	601	R3V	CAH-CAG-CAE	-4.64	104.07	112.87
2	C	601	R3V	CAK-CAJ-CAF	-4.58	105.95	112.86
2	B	601	R3V	CAD-CAE-CAF	4.51	125.36	119.50
2	A	601	R3V	CAD-CAE-CAF	4.21	124.96	119.50
2	D	601	R3V	CAA-CAF-CAJ	-4.13	114.21	124.90
2	A	601	R3V	CAA-CAF-CAJ	-4.00	114.53	124.90
2	C	601	R3V	CAA-CAF-CAJ	-3.82	115.00	124.90
2	B	601	R3V	CAA-CAF-CAJ	-3.66	115.41	124.90
2	D	601	R3V	CAB-CAA-CAF	-3.02	116.03	121.13
2	D	601	R3V	CAE-CAF-CAJ	2.73	125.97	120.80
2	C	601	R3V	CAB-CAA-CAF	-2.69	116.58	121.13
2	A	601	R3V	CAE-CAF-CAJ	2.65	125.81	120.80
2	B	601	R3V	CBC-CBD-CBE	2.51	107.45	102.82
2	D	601	R3V	CBB-NBA-CBE	2.43	106.39	104.02
2	D	601	R3V	CAP-CAQ-CAK	-2.43	118.76	121.20
2	C	601	R3V	CAE-CAF-CAJ	2.39	125.32	120.80
2	D	601	R3V	CAA-CAB-CAC	2.37	122.47	119.88
2	B	601	R3V	CAE-CAF-CAJ	2.34	125.22	120.80
2	B	601	R3V	CAN-CAM-CAK	-2.31	118.87	121.20
2	A	601	R3V	CBC-CBD-CBE	2.28	107.02	102.82
2	A	601	R3V	CAB-CAA-CAF	-2.22	117.38	121.13
2	D	601	R3V	CBC-CBD-CBE	2.21	106.90	102.82
2	B	601	R3V	CAQ-CAK-CAJ	-2.19	116.74	121.04
2	C	601	R3V	CAP-CAQ-CAK	-2.19	119.00	121.20
2	B	601	R3V	CAB-CAA-CAF	-2.11	117.56	121.13
2	A	601	R3V	CAP-CAQ-CAK	-2.07	119.11	121.20

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	601	R3V	CAP-CAO-OAX-CAY
2	B	601	R3V	CAN-CAO-OAX-CAY
2	C	601	R3V	CAN-CAO-OAX-CAY
2	B	601	R3V	CAP-CAO-OAX-CAY
2	A	601	R3V	CAP-CAO-OAX-CAY
2	A	601	R3V	CAN-CAO-OAX-CAY

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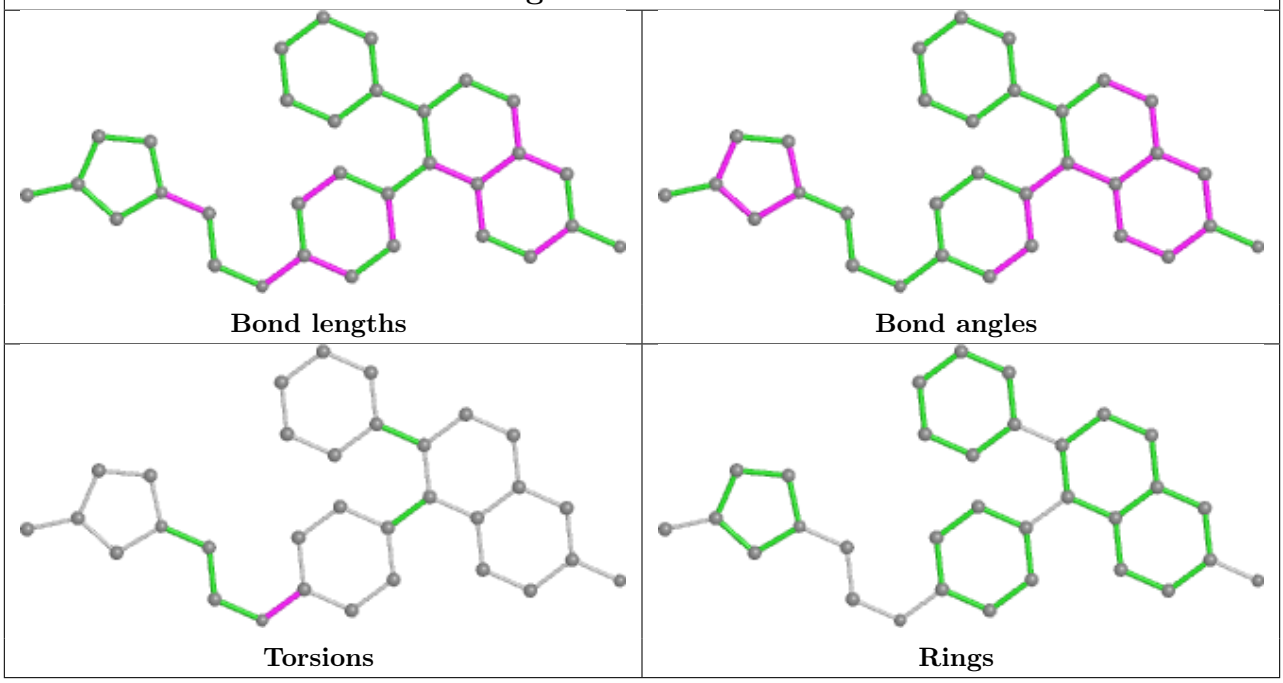
Mol	Chain	Res	Type	Atoms
2	D	601	R3V	CAP-CAO-OAX-CAY
2	D	601	R3V	CAN-CAO-OAX-CAY
2	C	601	R3V	OAX-CAY-CAZ-NBA
2	B	601	R3V	OAX-CAY-CAZ-NBA
2	A	601	R3V	OAX-CAY-CAZ-NBA

There are no ring outliers.

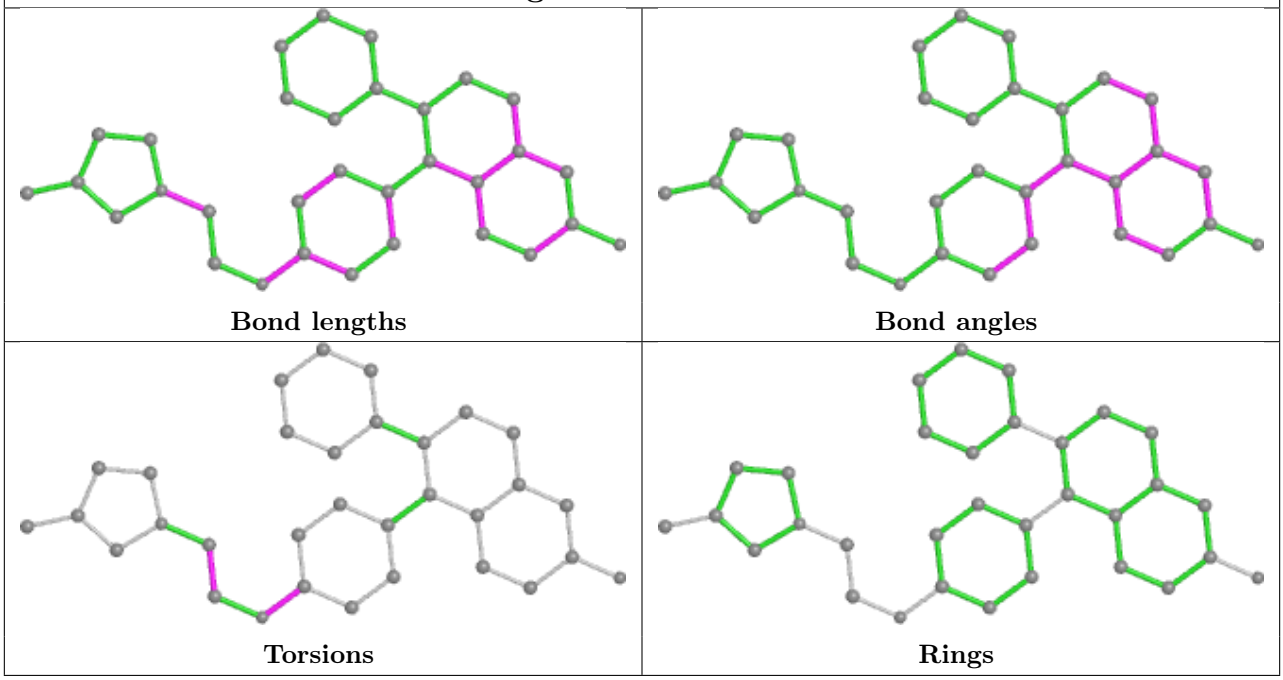
No monomer is involved in short contacts.

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.

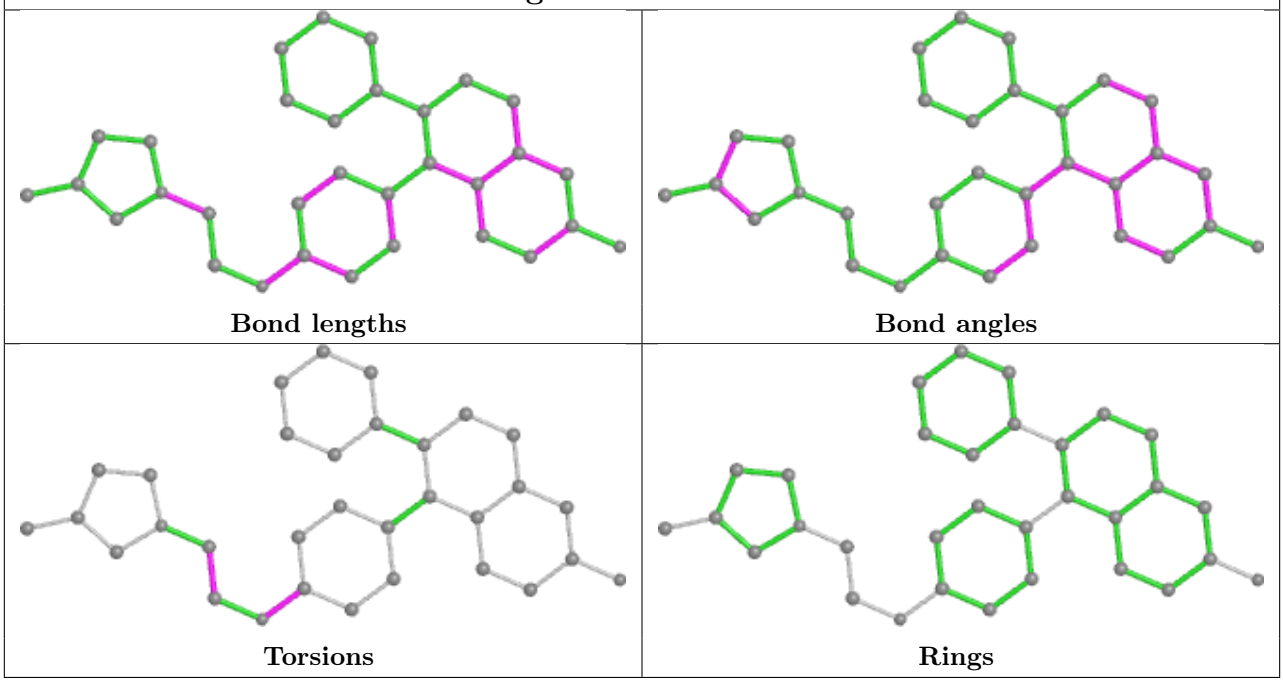
Ligand R3V D 601



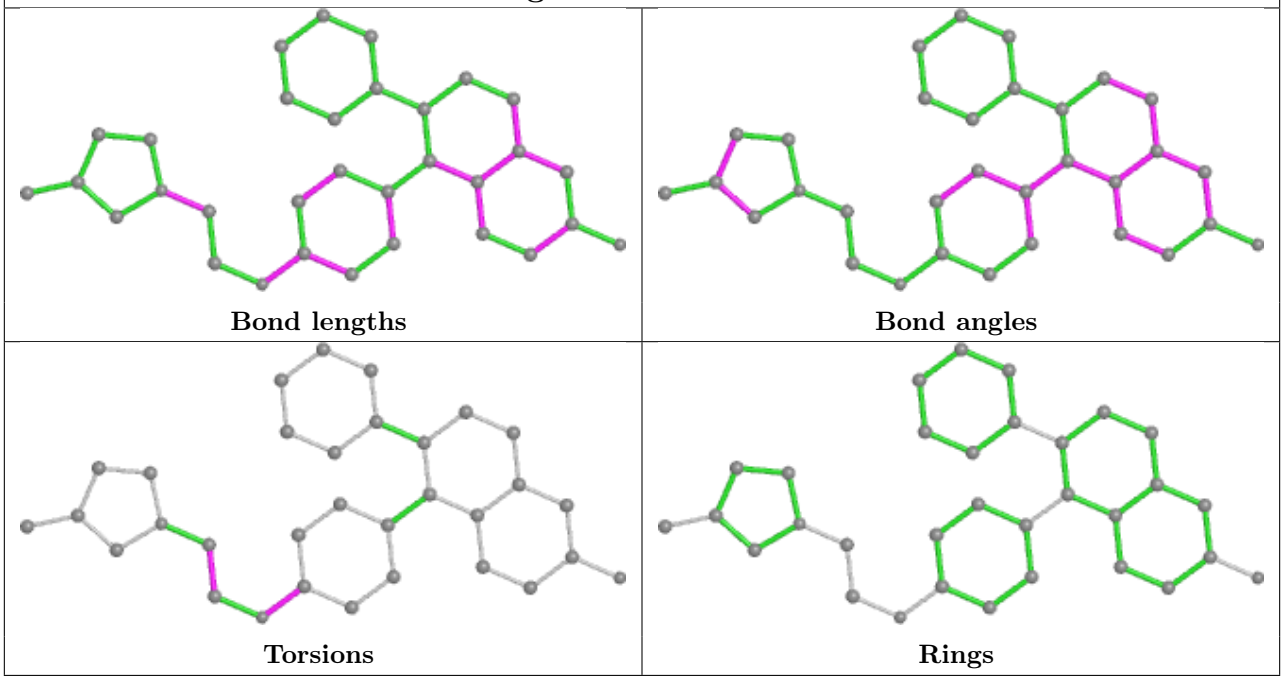
Ligand R3V C 601



Ligand R3V A 601



Ligand R3V B 601



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 (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(Å^2)	Q<0.9
1	A	232/263 (88%)	-0.31	3 (1%)	77	81	6, 21, 51, 65	0
1	B	235/263 (89%)	-0.24	3 (1%)	77	81	6, 20, 49, 61	2 (0%)
1	C	238/263 (90%)	-0.25	6 (2%)	57	61	6, 20, 52, 59	2 (0%)
1	D	233/263 (88%)	-0.27	5 (2%)	63	67	6, 21, 52, 67	1 (0%)
All	All	938/1052 (89%)	-0.27	17 (1%)	68	72	6, 21, 52, 67	5 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	459	TYR	4.5
1	C	309	SER	4.3
1	C	533	VAL	3.8
1	A	334	THR	3.1
1	C	532	ASN	3.1
1	B	526	TYR	3.0
1	D	526	TYR	3.0
1	D	462	LEU	2.9
1	D	459	TYR	2.8
1	C	526	TYR	2.8
1	B	533	VAL	2.7
1	B	459	TYR	2.6
1	C	340	ALA	2.6
1	C	461	PHE	2.5
1	D	308	LEU	2.2
1	A	533	VAL	2.1
1	D	332	ASP	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 monosaccharides in this entry.

6.4 Ligands (i)

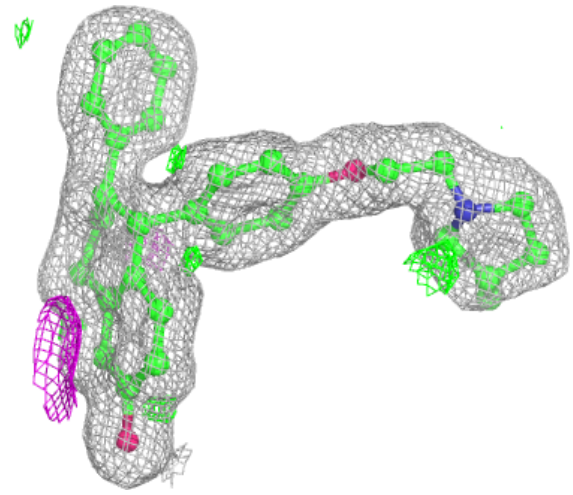
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

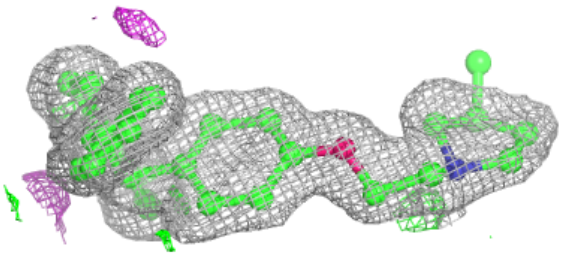
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	R3V	B	601	32/32	0.95	0.10	3,14,29,79	0
2	R3V	A	601	32/32	0.95	0.08	7,15,30,63	0
2	R3V	C	601	32/32	0.95	0.08	7,13,29,72	0
2	R3V	D	601	32/32	0.95	0.09	6,13,31,71	0

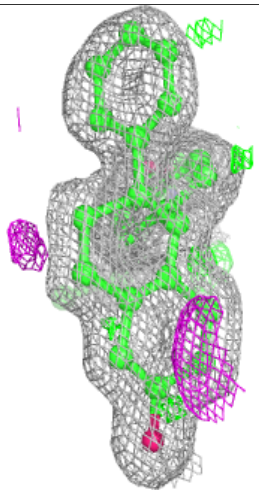
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around R3V 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)

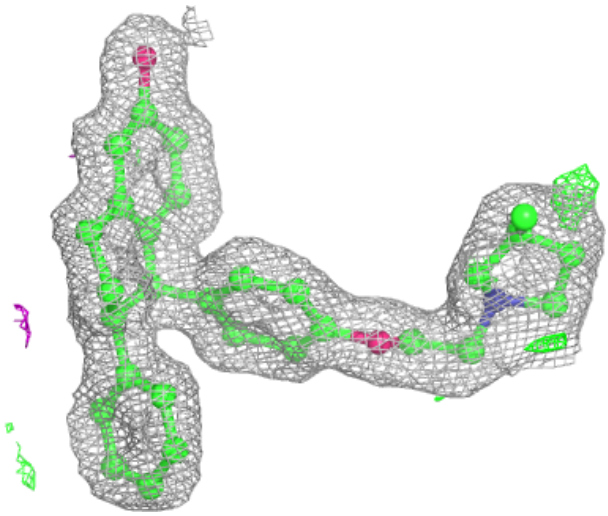


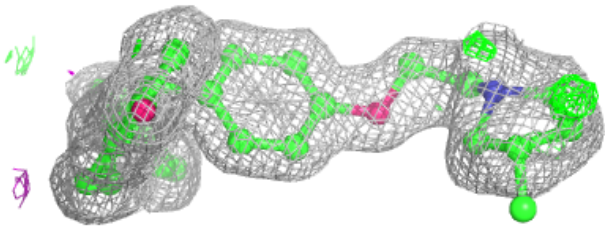




Electron density around R3V A 601:

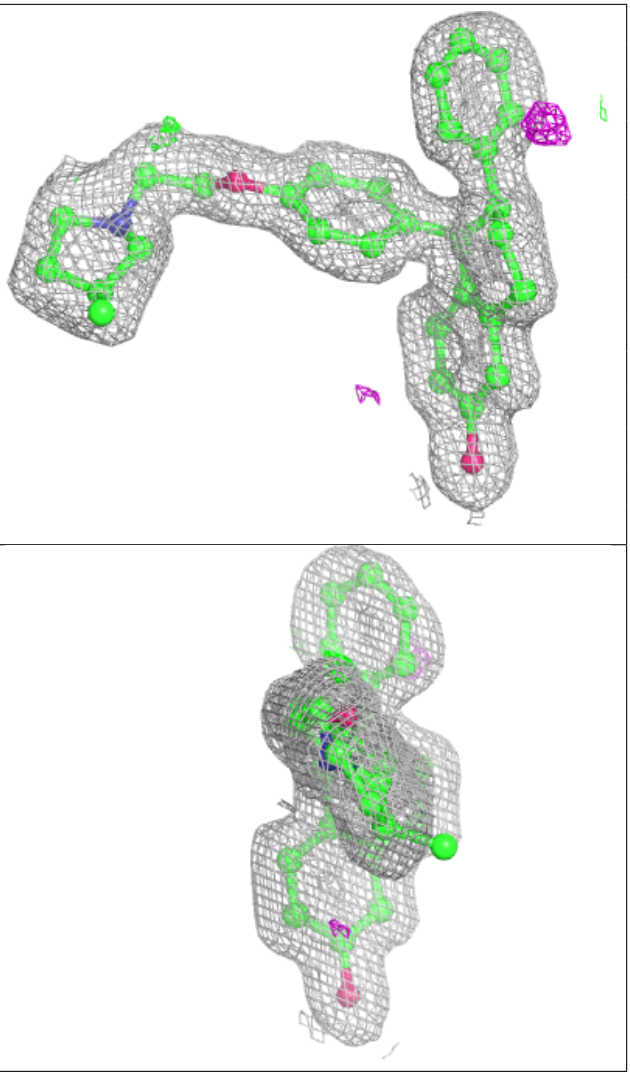
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

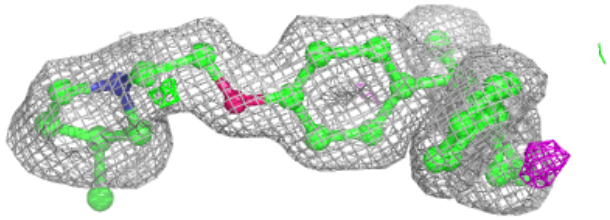




Electron density around R3V C 601:

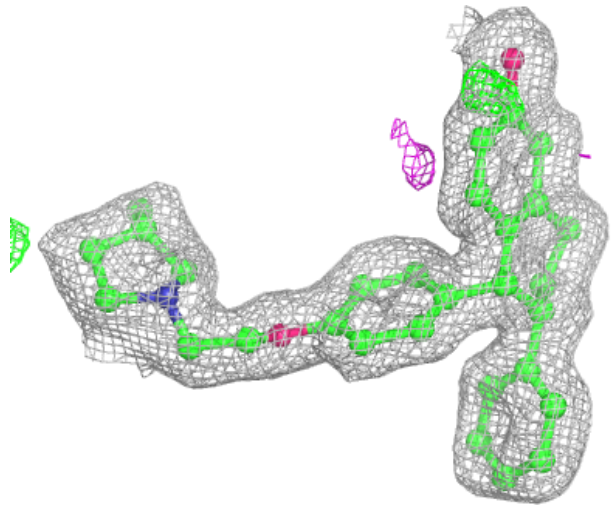
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

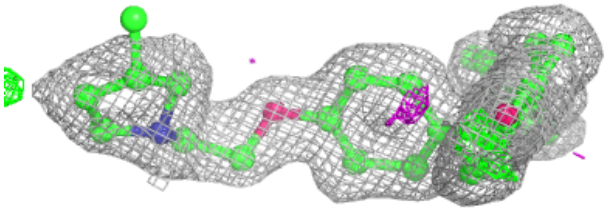


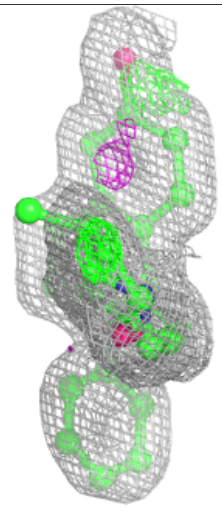


Electron density around R3V D 601:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.