



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2021 – 05:33 PM EDT

PDB ID : 2G5O  
Title : Human estrogen receptor alpha ligand-binding domain in complex with 2-(but-1-enyl)-17beta-estradiol and a glucocorticoid receptor interacting protein 1 NR BOX II Peptide  
Authors : Rajan, S.S.; Hsieh, R.W.; Sharma, S.K.; Greene, G.L.  
Deposited on : 2006-02-23  
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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 : 2.23.2  
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) : 2.23.2

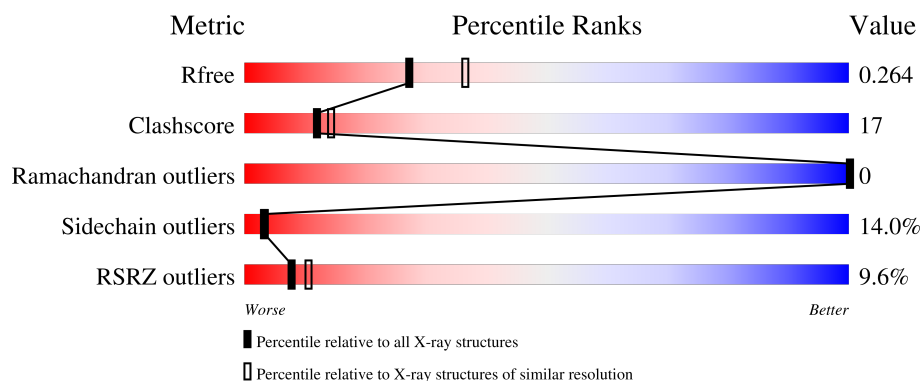
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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  $\geq 3$ , 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	257	
1	B	257	
2	C	13	
2	D	13	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	DRQ	A	201	-	-	X	-
3	DRQ	B	555	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4099 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	A	238	Total	C	N	O	S	0	1	0
			1918	1225	328	343	22			
1	B	239	Total	C	N	O	S	0	2	0
			1933	1235	331	343	24			

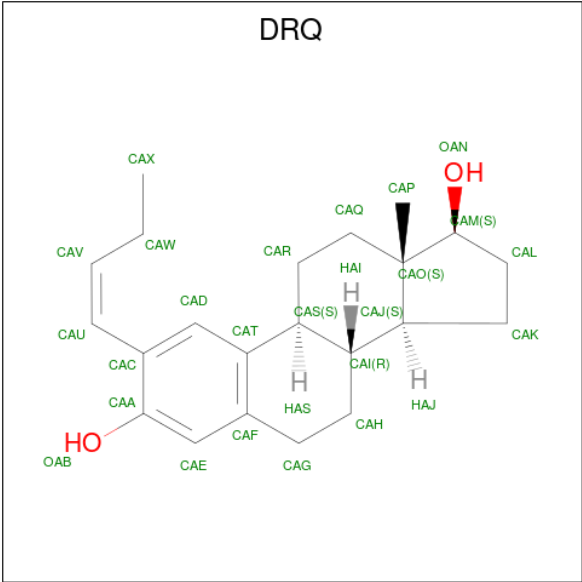
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	381	CME	CYS	modified residue	UNP P03372
A	417	CME	CYS	modified residue	UNP P03372
A	530	CME	CYS	modified residue	UNP P03372
A	537	SER	TYR	engineered mutation	UNP P03372
B	381	CME	CYS	modified residue	UNP P03372
B	417	CME	CYS	modified residue	UNP P03372
B	530	CME	CYS	modified residue	UNP P03372
B	537	SER	TYR	engineered mutation	UNP P03372

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			89	57	19	13			
2	D	9	Total	C	N	O	0	0	0
			79	51	16	12			

- Molecule 3 is (9ALPHA,13BETA,17BETA)-2-[(1Z)-BUT-1-EN-1-YL]ESTRA-1,3,5(10)-TR IENE-3,17-DIOL (three-letter code: DRQ) (formula: C<sub>22</sub>H<sub>30</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			24	22	2		
3	B	1	Total	C	O	0	0
			24	22	2		

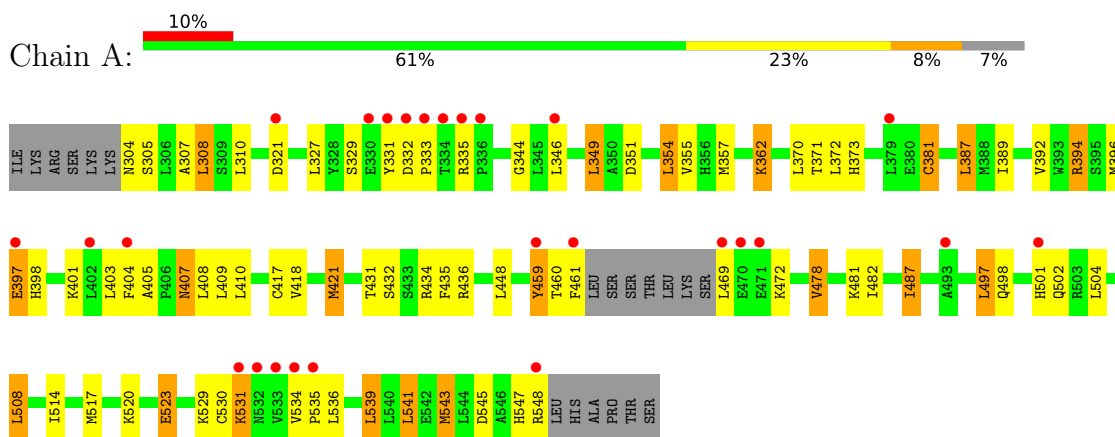
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	19	Total	O	0	0
			19	19		
4	B	13	Total	O	0	0
			13	13		

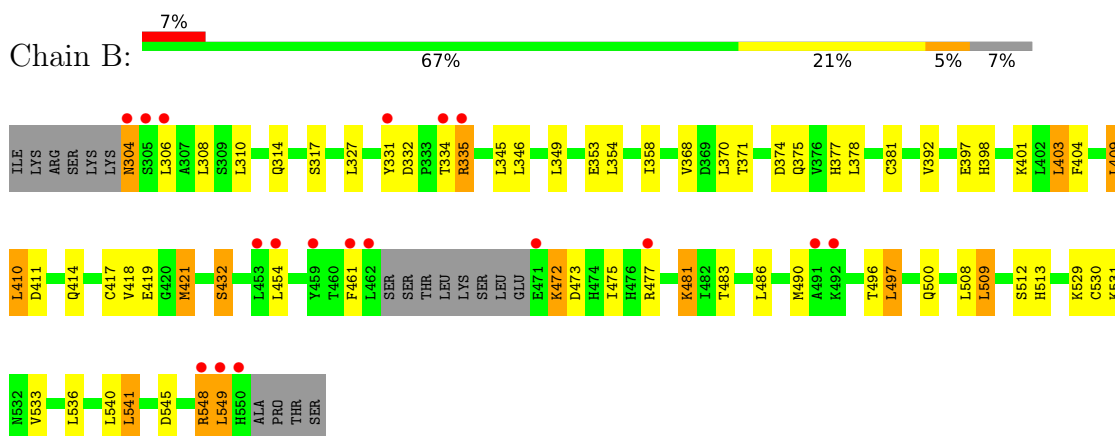
### 3 Residue-property plots [i](#)

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.

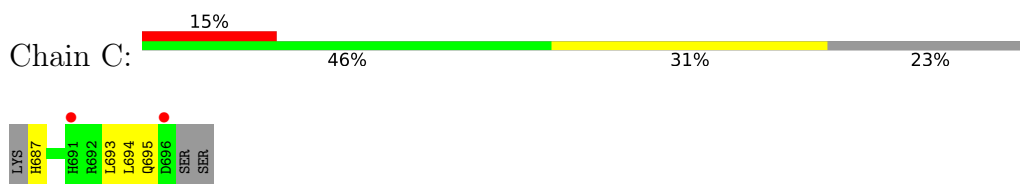
- Molecule 1: Estrogen receptor



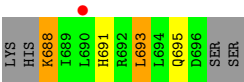
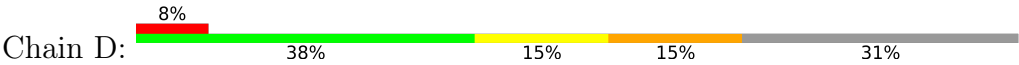
- Molecule 1: Estrogen receptor



- Molecule 2: Nuclear receptor coactivator 2



- Molecule 2: Nuclear receptor coactivator 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.07Å 83.35Å 58.83Å 90.00° 109.05° 90.00°	Depositor
Resolution (Å)	19.65 – 2.30 19.65 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.4 (19.65-2.30) 97.4 (19.65-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.63 (at 2.30Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.209 , 0.264 0.209 , 0.264	Depositor DCC
$R_{free}$ test set	1134 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.9	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 57.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4099	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: DRQ, CME

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	0.40	0/1925	0.56	0/2596
1	B	0.40	0/1935	0.54	0/2610
2	C	0.30	0/90	0.46	0/119
2	D	0.39	0/79	0.65	0/104
All	All	0.40	0/4029	0.55	0/5429

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	1918	0	1960	83	0
1	B	1933	0	1981	59	0
2	C	89	0	95	2	0
2	D	79	0	88	8	0
3	A	24	0	30	16	0
3	B	24	0	29	13	0
4	A	19	0	0	2	0
4	B	13	0	0	0	0
All	All	4099	0	4183	142	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 17.

The worst 5 of 142 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:394:ARG:HG2	1:A:394:ARG:HH21	1.03	1.08
1:B:349:LEU:HG	3:B:555:DRQ:HAV	1.42	1.01
1:A:349:LEU:HB3	3:A:201:DRQ:HAV	1.46	0.96
1:B:418:VAL:HB	1:B:421:MET:HG3	1.50	0.91
1:A:394:ARG:HG2	1:A:394:ARG:NH2	1.86	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	232/257 (90%)	228 (98%)	4 (2%)	0	100	100
1	B	233/257 (91%)	229 (98%)	4 (2%)	0	100	100
2	C	8/13 (62%)	8 (100%)	0	0	100	100
2	D	7/13 (54%)	7 (100%)	0	0	100	100
All	All	480/540 (89%)	472 (98%)	8 (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	212/229 (93%)	179 (84%)	33 (16%)	2	2
1	B	213/229 (93%)	188 (88%)	25 (12%)	5	6
2	C	10/13 (77%)	8 (80%)	2 (20%)	1	1
2	D	9/13 (69%)	7 (78%)	2 (22%)	1	1
All	All	444/484 (92%)	382 (86%)	62 (14%)	3	3

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	539	LEU
1	B	545	ASP
1	B	335	ARG
1	B	541	LEU
2	C	693	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	414	GLN
1	B	506	GLN
1	B	547	HIS
1	B	519	ASN
1	A	499	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

7 non-standard protein/DNA/RNA residues 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
1	CME	A	381	1	8,9,10	0.82	0	5,9,11	4.30	2 (40%)
1	CME	B	417	1	8,9,10	0.92	1 (12%)	5,9,11	3.66	2 (40%)
1	CME	A	417	1	8,9,10	0.75	0	5,9,11	4.75	2 (40%)
1	CME	B	530	1	8,9,10	0.82	0	5,9,11	3.36	2 (40%)
1	CME	B	381[B]	-	8,9,10	0.76	0	5,9,11	3.50	2 (40%)
1	CME	B	381[A]	-	8,9,10	0.76	0	5,9,11	3.97	2 (40%)
1	CME	A	530	1	8,9,10	0.82	0	5,9,11	4.00	2 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CME	A	381	1	-	3/5/8/10	-
1	CME	B	417	1	-	3/5/8/10	-
1	CME	A	417	1	-	2/5/8/10	-
1	CME	B	530	1	-	2/5/8/10	-
1	CME	B	381[B]	-	-	2/5/8/10	-
1	CME	B	381[A]	-	-	3/5/8/10	-
1	CME	A	530	1	-	2/5/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	417	CME	CB-SG	-2.05	1.75	1.81

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	417	CME	CB-SG-SD	9.06	127.28	103.82
1	A	530	CME	CB-SG-SD	7.39	122.96	103.82
1	A	381	CME	CB-SG-SD	7.22	122.53	103.82
1	B	381[A]	CME	CB-SG-SD	7.08	122.18	103.82
1	B	381[B]	CME	CB-SG-SD	6.37	120.33	103.82

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	381	CME	SD-CE-CZ-OH
1	A	417	CME	CA-CB-SG-SD
1	A	417	CME	SD-CE-CZ-OH
1	A	530	CME	SD-CE-CZ-OH
1	B	381[A]	CME	CE-SD-SG-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	381	CME	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides 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	DRQ	A	201	-	27,27,27	1.37	4 (14%)	41,41,41	1.74	9 (21%)
3	DRQ	B	555	-	27,27,27	1.32	3 (11%)	41,41,41	1.56	7 (17%)

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	DRQ	A	201	-	-	2/4/44/44	0/4/4/4
3	DRQ	B	555	-	-	3/4/44/44	0/4/4/4

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	555	DRQ	CAC-CAU	-4.87	1.39	1.47
3	A	201	DRQ	CAC-CAU	-4.74	1.39	1.47
3	A	201	DRQ	CAW-CAV	-2.54	1.39	1.51
3	B	555	DRQ	CAW-CAV	-2.48	1.39	1.51
3	A	201	DRQ	CAU-CAV	2.34	1.39	1.31

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	201	DRQ	CAW-CAV-CAU	-5.23	120.15	125.86
3	A	201	DRQ	CAL-CAM-CAO	-5.10	100.48	104.53
3	B	555	DRQ	CAW-CAV-CAU	-4.91	120.50	125.86
3	B	555	DRQ	CAL-CAM-CAO	-4.28	101.13	104.53
3	A	201	DRQ	CAH-CAI-CAS	3.36	112.56	109.28

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	201	DRQ	CAA-CAC-CAU-CAV
3	B	555	DRQ	CAA-CAC-CAU-CAV
3	B	555	DRQ	CAD-CAC-CAU-CAV
3	A	201	DRQ	CAD-CAC-CAU-CAV
3	B	555	DRQ	CAU-CAV-CAW-CAX

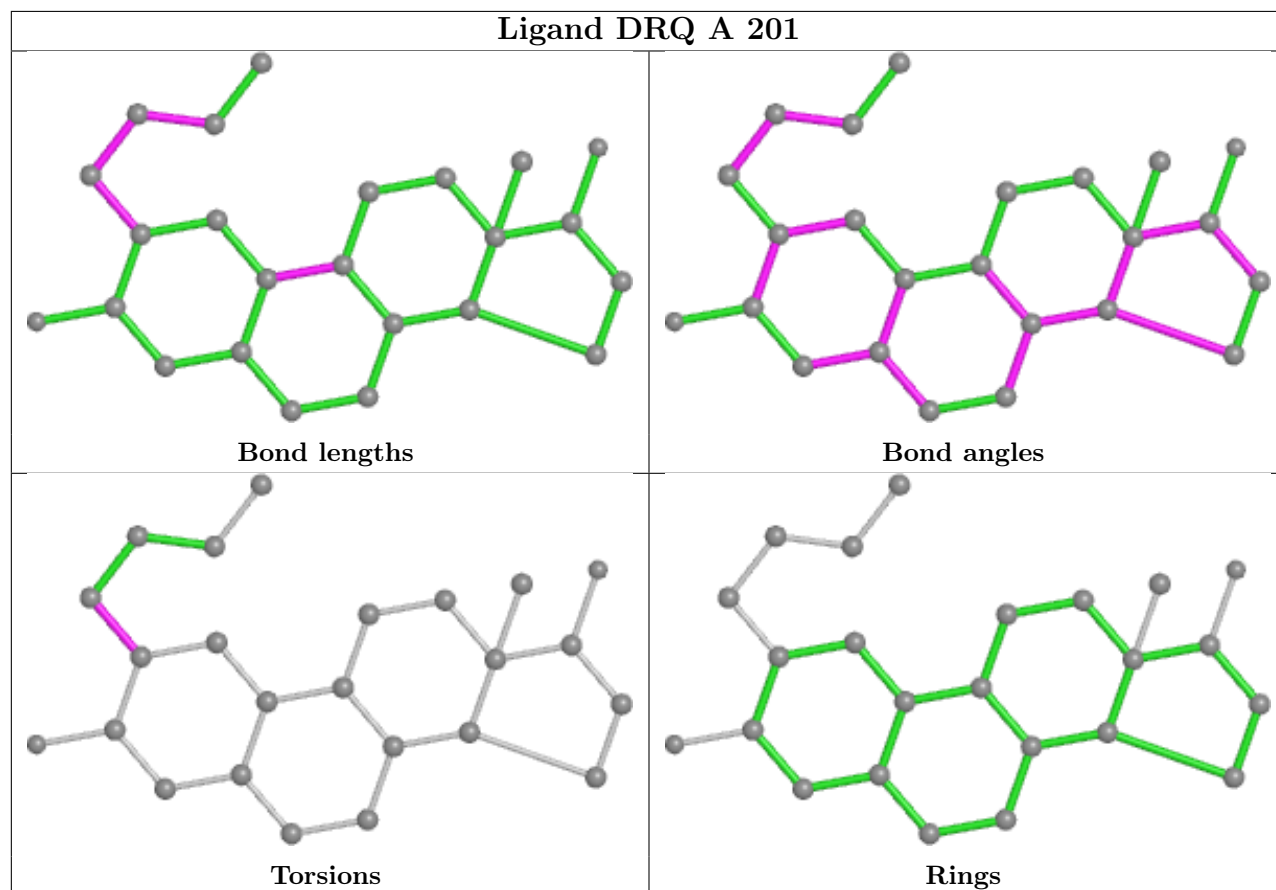
There are no ring outliers.

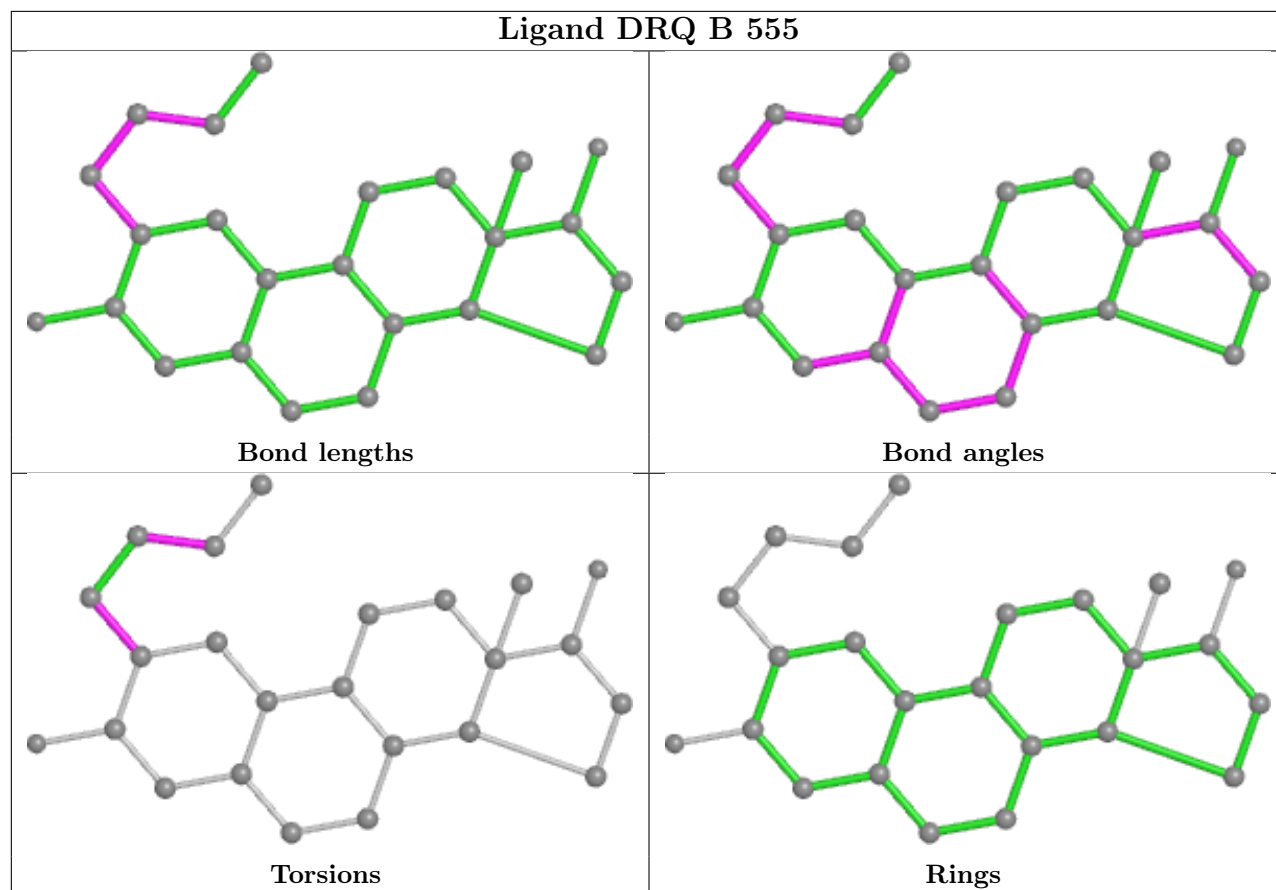
2 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	201	DRQ	16	0
3	B	555	DRQ	13	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	235/257 (91%)	0.67	26 (11%) 5 7	36, 47, 70, 78	0
1	B	236/257 (91%)	0.61	18 (7%) 13 18	36, 47, 70, 74	0
2	C	10/13 (76%)	1.46	2 (20%) 1 1	53, 62, 71, 74	0
2	D	9/13 (69%)	1.08	1 (11%) 5 7	56, 62, 71, 75	0
All	All	490/540 (90%)	0.67	47 (9%) 8 10	36, 47, 71, 78	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	550	HIS	9.5
1	B	471	GLU	6.0
1	A	469	LEU	6.0
1	A	533	VAL	5.7
1	B	306	LEU	5.5

### 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CME	B	381[A]	10/11	0.77	0.28	39,41,44,44	6
1	CME	B	381[B]	10/11	0.77	0.28	39,44,50,50	6
1	CME	A	381	10/11	0.84	0.22	40,48,62,62	0
1	CME	A	417	10/11	0.86	0.26	55,58,60,60	0
1	CME	A	530	10/11	0.87	0.31	52,53,54,54	5
1	CME	B	417	10/11	0.88	0.18	54,57,60,60	5
1	CME	B	530	10/11	0.91	0.19	50,51,52,52	5

## 6.3 Carbohydrates [i](#)

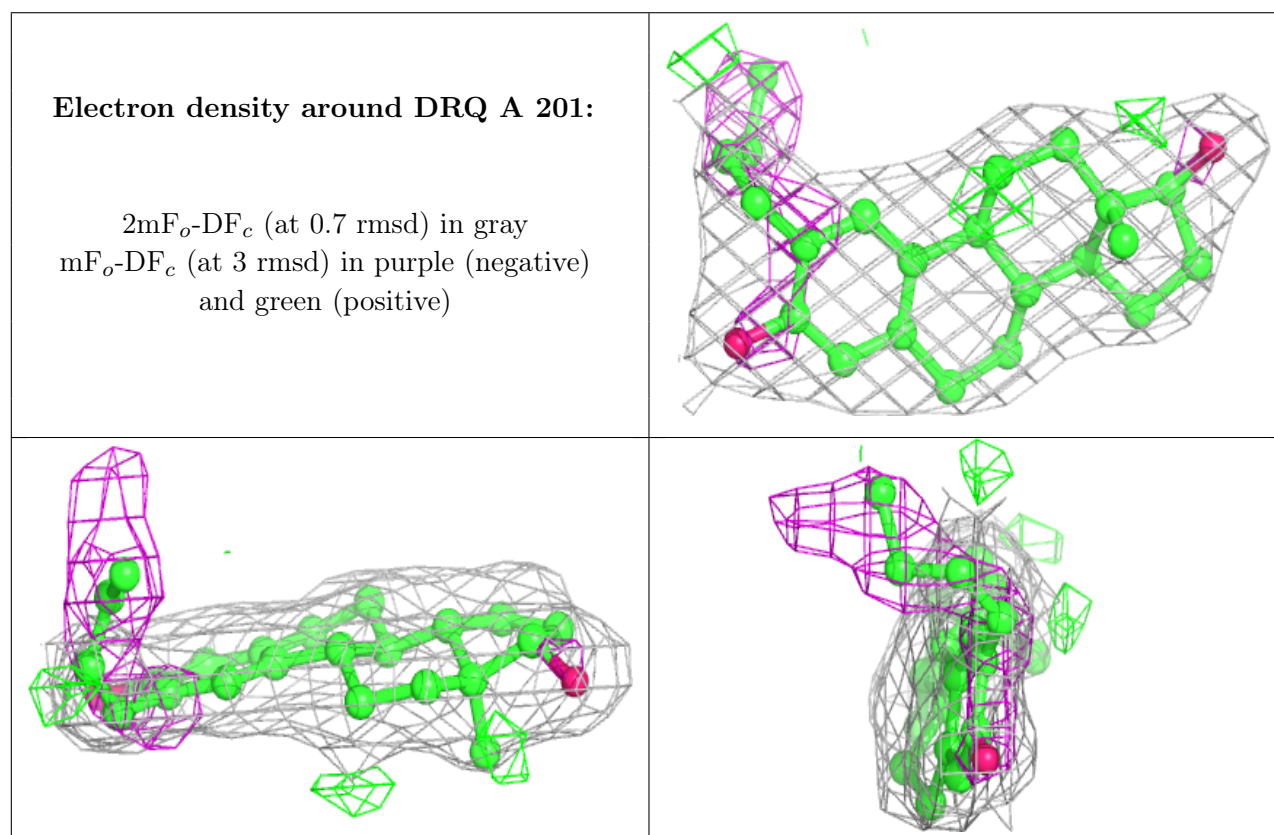
There are no monosaccharides in this entry.

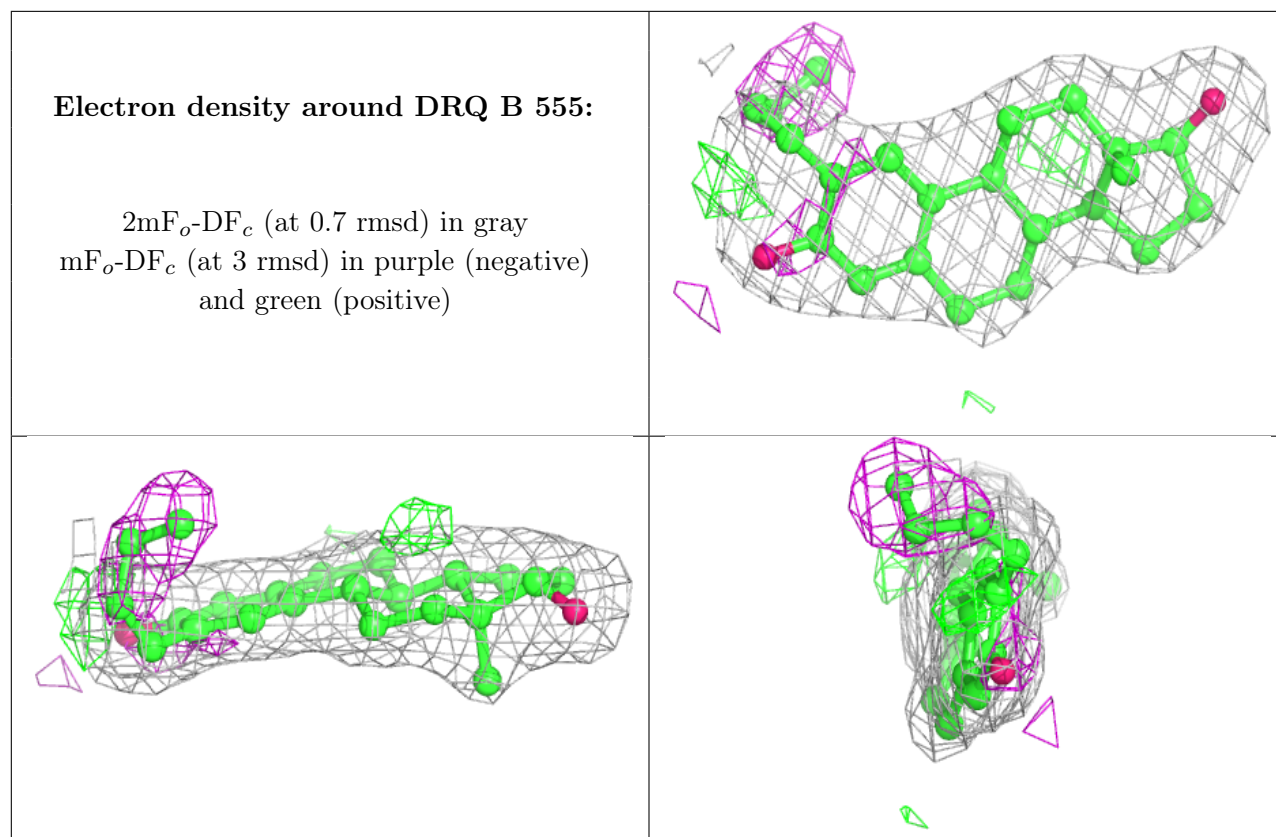
## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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	DRQ	A	201	24/24	0.86	0.18	46,46,51,53	0
3	DRQ	B	555	24/24	0.89	0.16	44,46,51,53	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.





## 6.5 Other polymers [i](#)

There are no such residues in this entry.