



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 29, 2022 – 04:08 PM JST

PDB ID : 7VPR  
Title : Crystal structure of the ligand-binding domain of *C. glabrata* Upc2 in complex with ergosterol  
Authors : Tan, L.; Im, Y.J.  
Deposited on : 2021-10-17  
Resolution : 2.59 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.

The types of validation reports are described at <http://www.wwpdb.org/validation/2017/FAQs#types>.

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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	:	2.30
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)	:	2.30

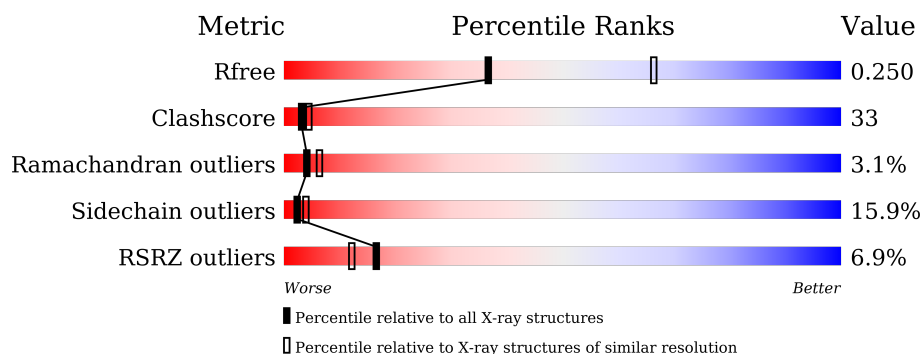
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	308	<div> <div>5%</div> <div>56% 29% 7% 9%</div> </div>
1	B	308	<div> <div>9%</div> <div>47% 34% 9% • 9%</div> </div>
1	C	308	<div> <div>5%</div> <div>48% 34% 8% • 8%</div> </div>
1	D	308	<div> <div>6%</div> <div>40% 29% 11% • 18%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9014 atoms, of which 176 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 Sterol uptake control protein 2 (Upc2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2215	1437	352	413	13			
1	B	280	Total	C	N	O	S	0	0	0
			2208	1431	351	413	13			
1	C	282	Total	C	N	O	S	0	0	0
			2223	1441	353	416	13			
1	D	253	Total	C	N	O	S	0	0	0
			2012	1313	322	366	11			

There are 24 discrepancies between the modelled and reference sequences:

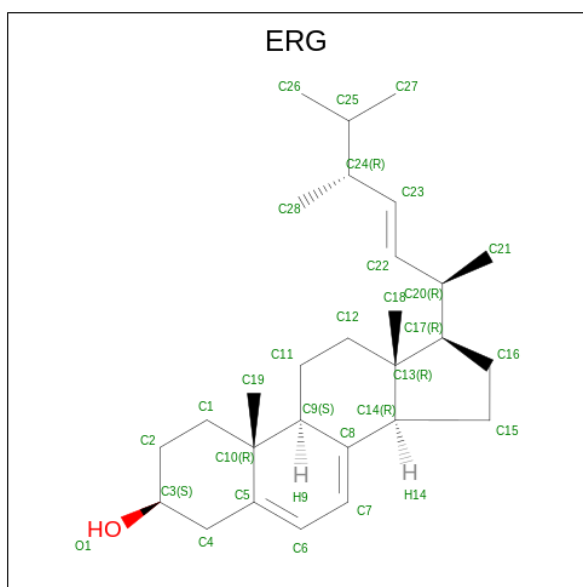
Chain	Residue	Modelled	Actual	Comment	Reference
A	615	GLY	-	expression tag	UNP Q6FX18
A	616	SER	-	expression tag	UNP Q6FX18
A	617	ALA	-	expression tag	UNP Q6FX18
A	618	MET	-	expression tag	UNP Q6FX18
A	619	GLY	-	expression tag	UNP Q6FX18
A	620	SER	-	expression tag	UNP Q6FX18
B	615	GLY	-	expression tag	UNP Q6FX18
B	616	SER	-	expression tag	UNP Q6FX18
B	617	ALA	-	expression tag	UNP Q6FX18
B	618	MET	-	expression tag	UNP Q6FX18
B	619	GLY	-	expression tag	UNP Q6FX18
B	620	SER	-	expression tag	UNP Q6FX18
C	615	GLY	-	expression tag	UNP Q6FX18
C	616	SER	-	expression tag	UNP Q6FX18
C	617	ALA	-	expression tag	UNP Q6FX18
C	618	MET	-	expression tag	UNP Q6FX18
C	619	GLY	-	expression tag	UNP Q6FX18
C	620	SER	-	expression tag	UNP Q6FX18
D	615	GLY	-	expression tag	UNP Q6FX18
D	616	SER	-	expression tag	UNP Q6FX18
D	617	ALA	-	expression tag	UNP Q6FX18

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Chain	Residue	Modelled	Actual	Comment	Reference
D	618	MET	-	expression tag	UNP Q6FX18
D	619	GLY	-	expression tag	UNP Q6FX18
D	620	SER	-	expression tag	UNP Q6FX18

- Molecule 2 is ERGOSTEROL (three-letter code: ERG) (formula:  $C_{28}H_{44}O$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			73	28	44	1		
2	B	1	Total	C	H	O	0	0
			73	28	44	1		
2	C	1	Total	C	H	O	0	0
			73	28	44	1		
2	D	1	Total	C	H	O	0	0
			73	28	44	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	16	Total	O	0	0
			16	16		
3	B	22	Total	O	0	0
			22	22		
3	C	14	Total	O	0	0
			14	14		

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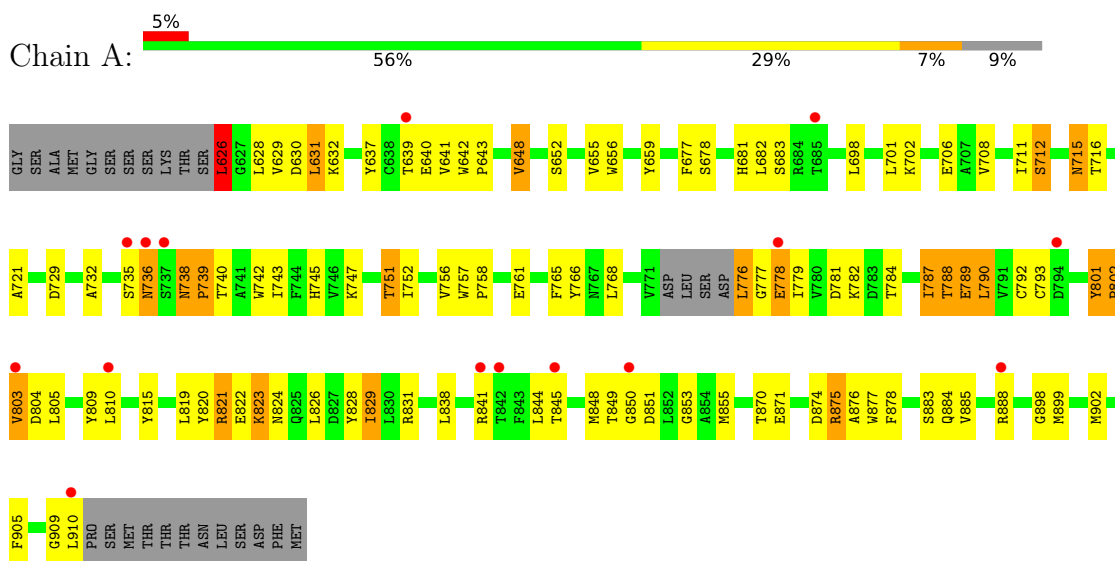
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	12	Total	O	0	0
			12	12		

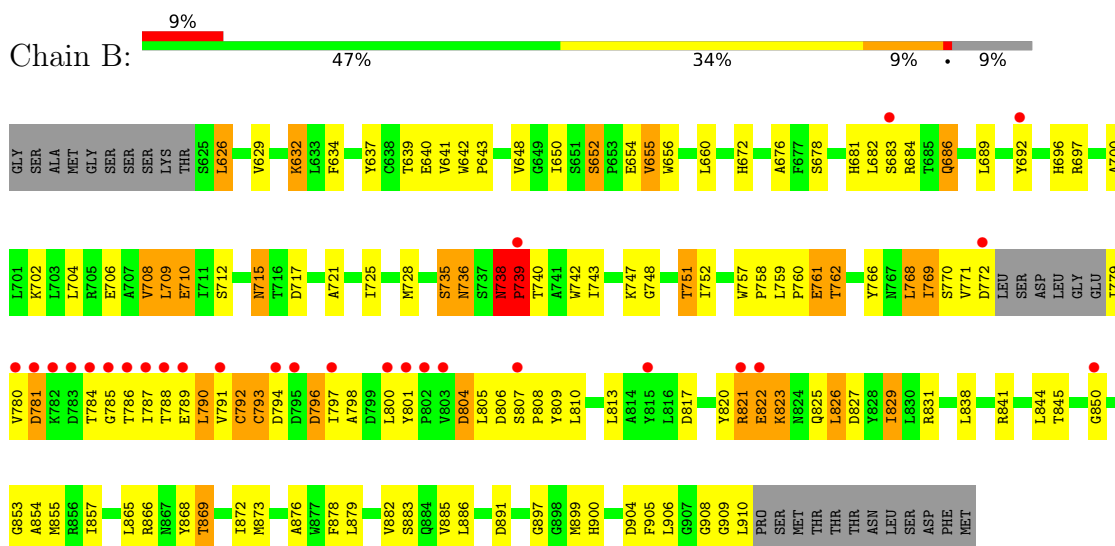
### 3 Residue-property plots [i](#)

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: Sterol uptake control protein 2 (Up2)

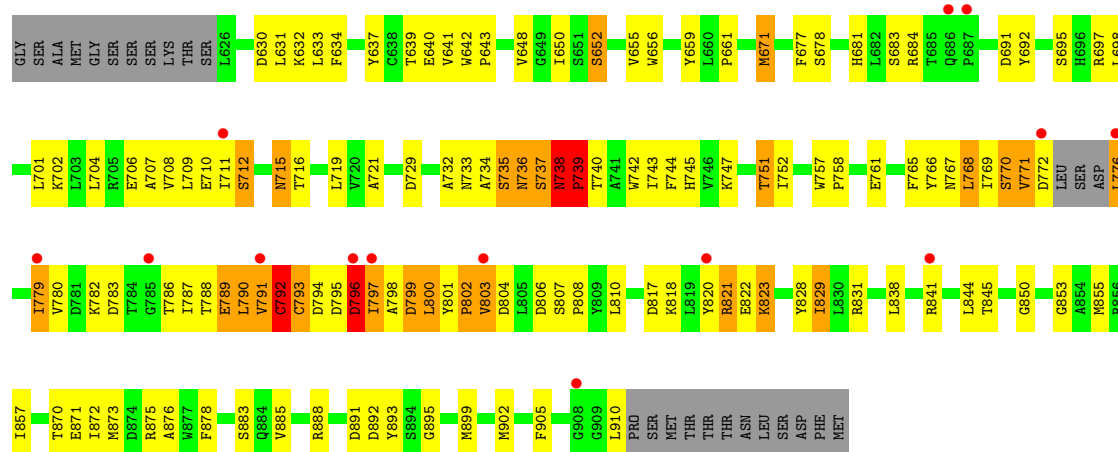


- Molecule 1: Sterol uptake control protein 2 (Up2)

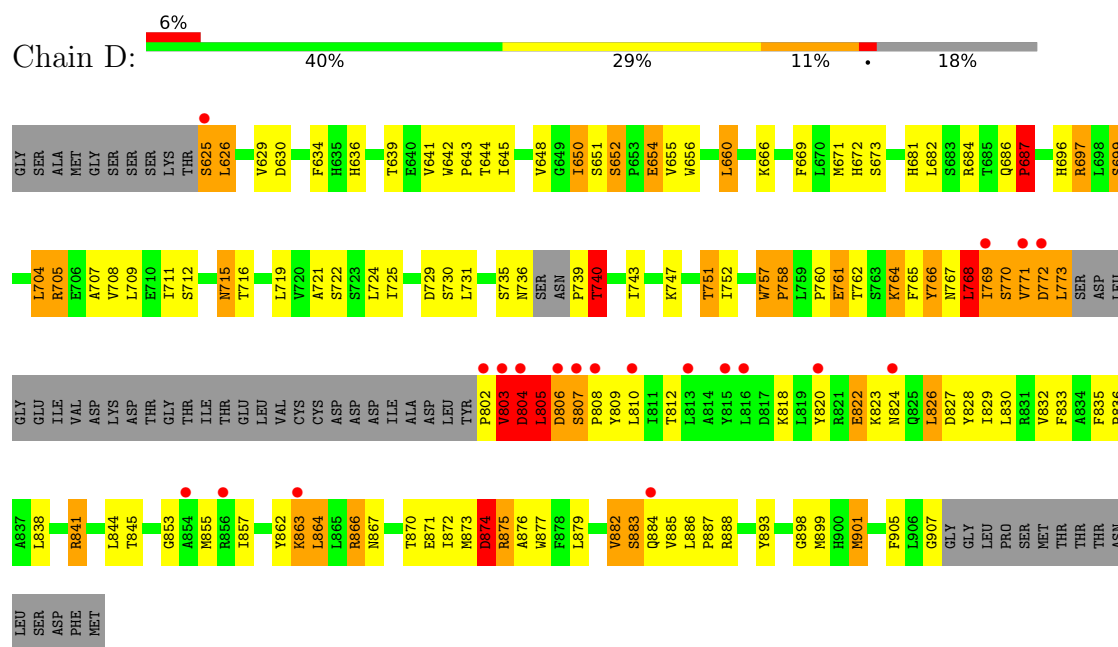


- Molecule 1: Sterol uptake control protein 2 (Up2)





• Molecule 1: Sterol uptake control protein 2 (Upc2)



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.42Å 105.63Å 98.87Å 90.00° 93.28° 90.00°	Depositor
Resolution (Å)	27.60 – 2.59 38.20 – 2.59	Depositor EDS
% Data completeness (in resolution range)	98.0 (27.60-2.59) 94.0 (38.20-2.59)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	-0.26 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, $R_{free}$	0.231 , 0.250 0.230 , 0.250	Depositor DCC
$R_{free}$ test set	1723 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.8	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 44.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	9014	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% 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

### 5.1 Standard geometry

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

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	0.89	3/2267 (0.1%)	0.89	2/3089 (0.1%)
1	B	1.07	2/2260 (0.1%)	0.96	8/3080 (0.3%)
1	C	0.77	0/2275	0.83	4/3100 (0.1%)
1	D	1.09	1/2062 (0.0%)	0.88	2/2806 (0.1%)
All	All	0.96	6/8864 (0.1%)	0.89	16/12075 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	802	PRO	N-CA	12.57	1.68	1.47
1	B	739	PRO	N-CA	12.56	1.68	1.47
1	B	738	ASN	C-N	5.56	1.44	1.34
1	A	801	TYR	C-N	5.43	1.44	1.34
1	D	757	TRP	CB-CG	-5.27	1.40	1.50

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	739	PRO	N-CA-CB	-9.69	91.68	103.30
1	B	739	PRO	CA-N-CD	-8.90	99.04	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	802	PRO	CA-N-CD	-7.99	100.31	111.50
1	B	804	ASP	CB-CA-C	-6.66	97.08	110.40
1	C	792	CYS	CA-C-N	-6.06	103.87	117.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	776	LEU	Mainchain
1	B	738	ASN	Peptide

## 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	2215	0	2209	127	0
1	B	2208	0	2198	150	1
1	C	2223	0	2212	151	3
1	D	2012	0	2018	160	2
2	A	29	44	44	4	0
2	B	29	44	44	2	0
2	C	29	44	44	3	0
2	D	29	44	44	9	0
3	A	16	0	0	7	0
3	B	22	0	0	7	0
3	C	14	0	0	0	0
3	D	12	0	0	1	0
All	All	8838	176	8813	587	3

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 33.

The worst 5 of 587 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:779:ILE:HD11	1:A:790:LEU:CD1	1.33	1.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:738:ASN:ND2	1:A:739:PRO:HD3	1.32	1.37
1:D:771:VAL:HG21	1:D:818:LYS:CE	1.53	1.37
1:A:802:PRO:N	1:A:802:PRO:CA	1.68	1.36
1:B:739:PRO:N	1:B:739:PRO:CA	1.68	1.35

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:895:GLY:O	1:D:705:ARG:NH1[2_554]	1.89	0.31
1:C:702:LYS:NZ	1:D:893:TYR:O[2_554]	1.95	0.25
1:B:629:VAL:CG1	1:C:783:ASP:O[1_556]	1.97	0.23

## 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	277/308 (90%)	261 (94%)	14 (5%)	2 (1%)	22	43
1	B	276/308 (90%)	252 (91%)	19 (7%)	5 (2%)	8	16
1	C	278/308 (90%)	240 (86%)	25 (9%)	13 (5%)	2	2
1	D	247/308 (80%)	221 (90%)	13 (5%)	13 (5%)	2	2
All	All	1078/1232 (88%)	974 (90%)	71 (7%)	33 (3%)	4	6

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	777	GLY
1	B	736	ASN
1	B	738	ASN
1	B	794	ASP
1	C	735	SER

### 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	244/268 (91%)	210 (86%)	34 (14%)	3	6
1	B	244/268 (91%)	207 (85%)	37 (15%)	3	4
1	C	245/268 (91%)	210 (86%)	35 (14%)	3	5
1	D	221/268 (82%)	175 (79%)	46 (21%)	1	2
All	All	954/1072 (89%)	802 (84%)	152 (16%)	2	4

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	697	ARG
1	D	874	ASP
1	D	715	ASN
1	D	803	VAL
1	D	899	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	736	ASN
1	D	884	GLN
1	B	715	ASN
1	B	767	ASN
1	C	715	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

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	ERG	B	1001	-	31,32,32	1.93	7 (22%)	47,50,50	1.48	9 (19%)
2	ERG	C	1001	-	31,32,32	1.92	7 (22%)	47,50,50	1.49	9 (19%)
2	ERG	A	1001	-	31,32,32	1.93	7 (22%)	47,50,50	1.49	9 (19%)
2	ERG	D	1001	-	31,32,32	1.94	7 (22%)	47,50,50	1.49	9 (19%)

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	ERG	B	1001	-	-	0/13/71/71	0/4/4/4
2	ERG	C	1001	-	-	0/13/71/71	0/4/4/4
2	ERG	A	1001	-	-	0/13/71/71	0/4/4/4
2	ERG	D	1001	-	-	0/13/71/71	0/4/4/4

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1001	ERG	C23-C22	5.95	1.50	1.32
2	C	1001	ERG	C23-C22	5.95	1.50	1.32
2	A	1001	ERG	C23-C22	5.94	1.50	1.32
2	B	1001	ERG	C23-C22	5.94	1.50	1.32
2	A	1001	ERG	C10-C5	-5.36	1.42	1.52

The worst 5 of 36 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1001	ERG	C19-C10-C5	-3.39	102.86	108.34
2	D	1001	ERG	C19-C10-C5	-3.38	102.88	108.34
2	B	1001	ERG	C19-C10-C5	-3.36	102.91	108.34
2	A	1001	ERG	C19-C10-C5	-3.36	102.91	108.34
2	A	1001	ERG	C4-C5-C10	3.13	120.57	116.42

There are no chirality outliers.

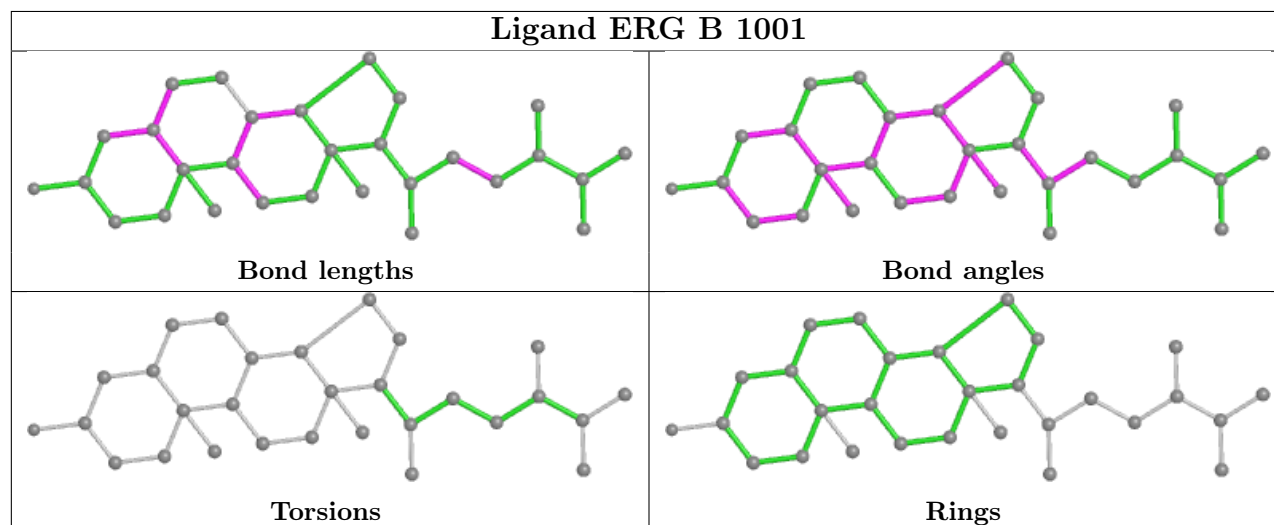
There are no torsion outliers.

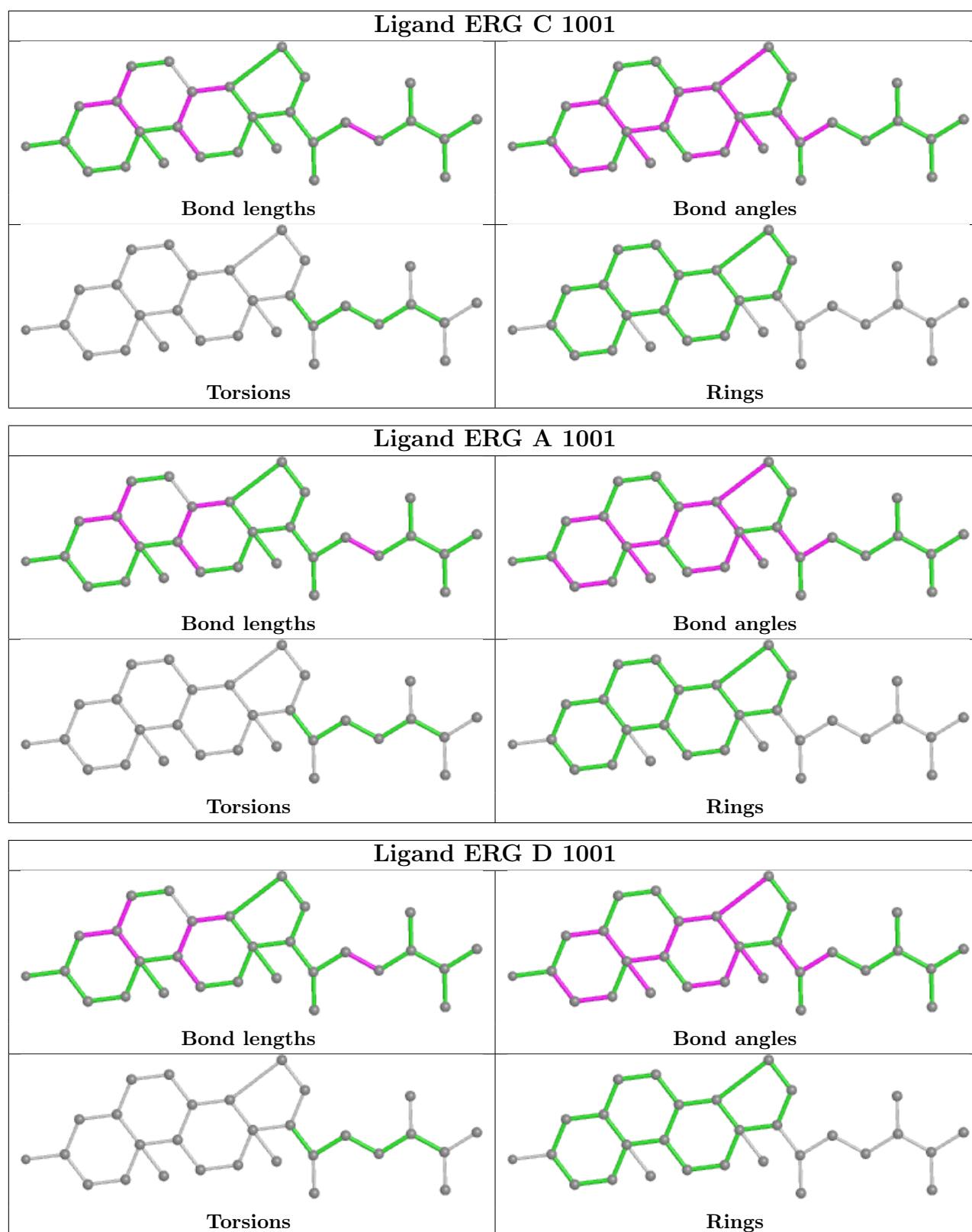
There are no ring outliers.

4 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1001	ERG	2	0
2	C	1001	ERG	3	0
2	A	1001	ERG	4	0
2	D	1001	ERG	9	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 ⓘ

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	281/308 (91%)	0.53	15 (5%) 26 20	30, 47, 79, 95	0
1	B	280/308 (90%)	0.49	27 (9%) 8 5	29, 44, 86, 100	0
1	C	282/308 (91%)	0.40	14 (4%) 28 23	30, 47, 76, 95	0
1	D	253/308 (82%)	0.47	20 (7%) 12 9	34, 55, 84, 105	0
All	All	1096/1232 (88%)	0.47	76 (6%) 16 12	29, 49, 83, 105	0

The worst 5 of 76 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	785	GLY	5.4
1	A	910	LEU	5.1
1	D	810	LEU	4.8
1	A	735	SER	4.8
1	B	786	THR	4.5

### 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](#)

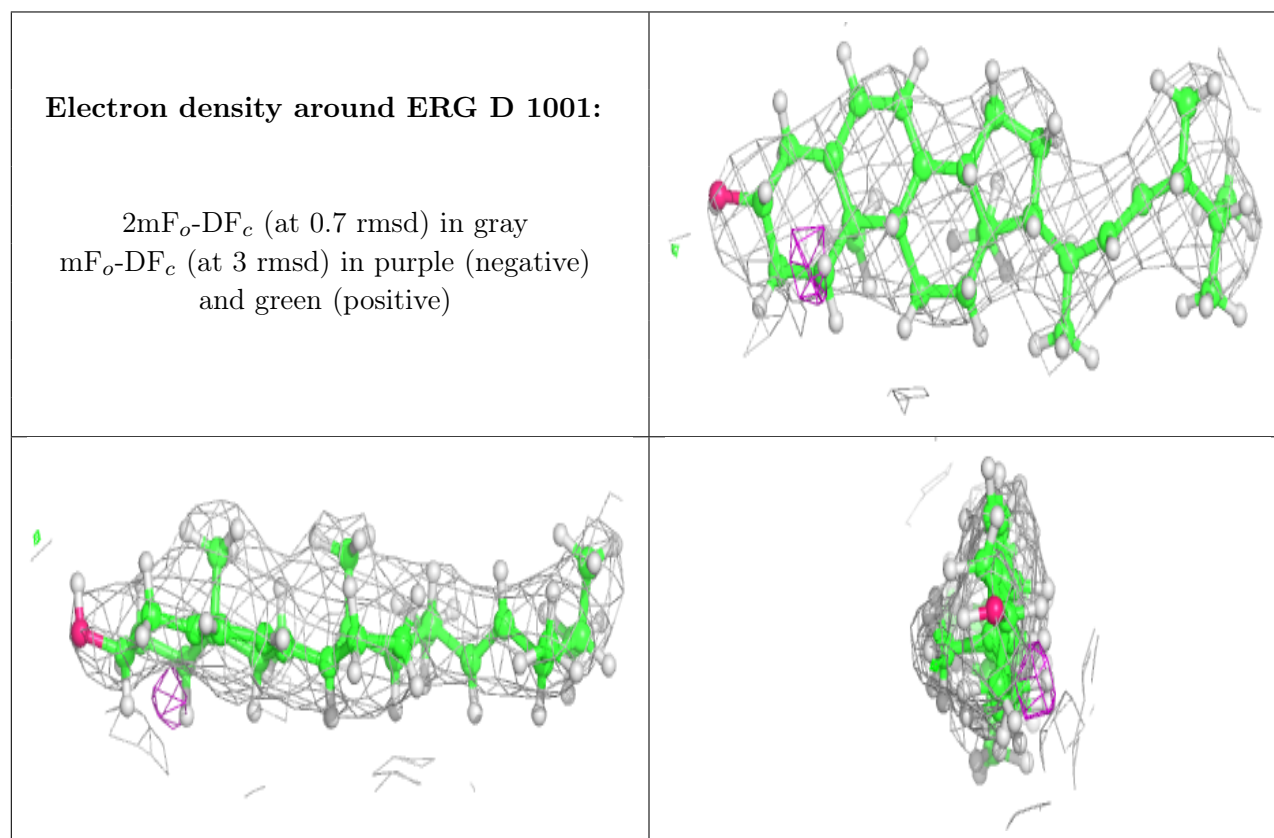
There are no monosaccharides in this entry.

### 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, 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.

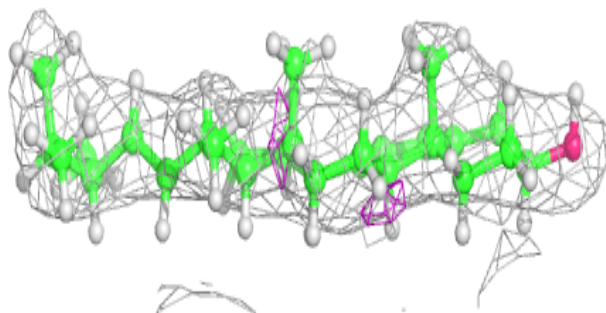
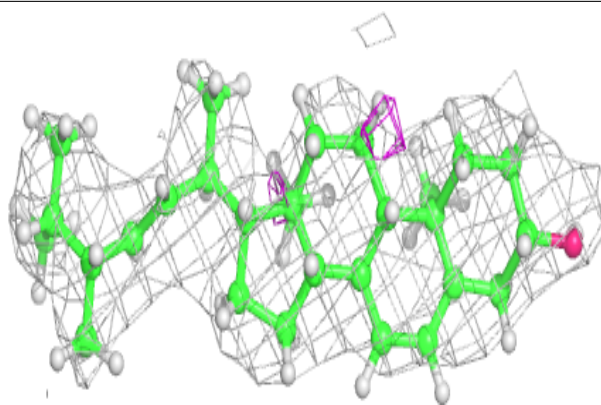
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ERG	D	1001	29/29	0.86	0.21	35,55,68,75	0
2	ERG	B	1001	29/29	0.90	0.17	26,40,47,54	0
2	ERG	C	1001	29/29	0.92	0.15	33,45,54,57	0
2	ERG	A	1001	29/29	0.92	0.17	24,41,49,52	0

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.

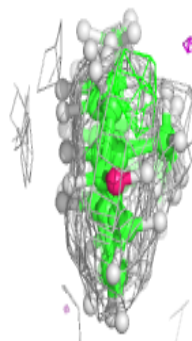
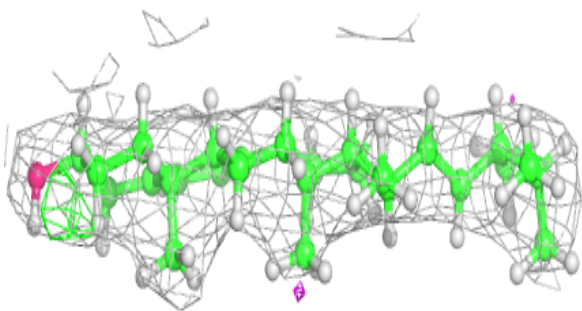
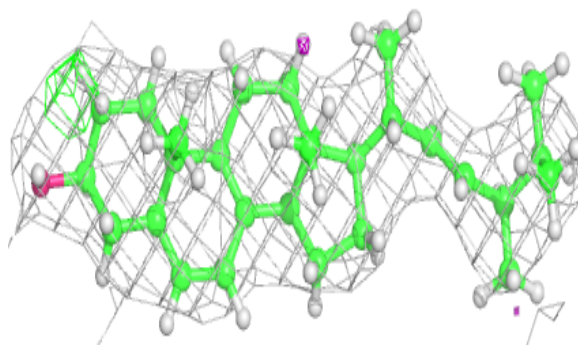


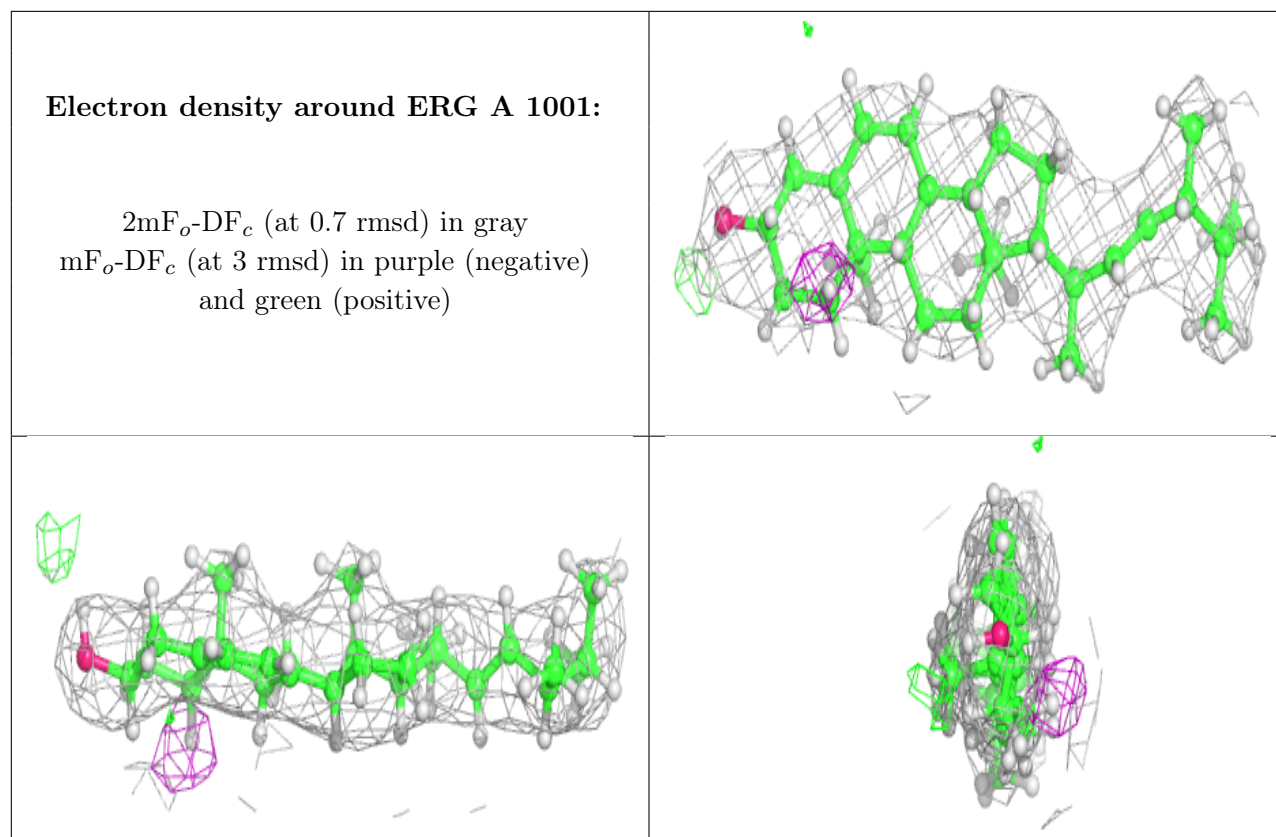
**Electron density around ERG B 1001:**

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

**Electron density around ERG C 1001:**

$2mF_o-DF_c$  (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.