



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 03:42 AM UTC

PDB ID : 4ONI / pdb\_00004oni  
Title : Structure of Human Orphan Receptor LRH1 bound to two bacterial phospholipids  
Authors : Gorman, M.A.; Parker, M.W.; Kusumo, S.  
Deposited on : 2014-01-28  
Resolution : 1.80 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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

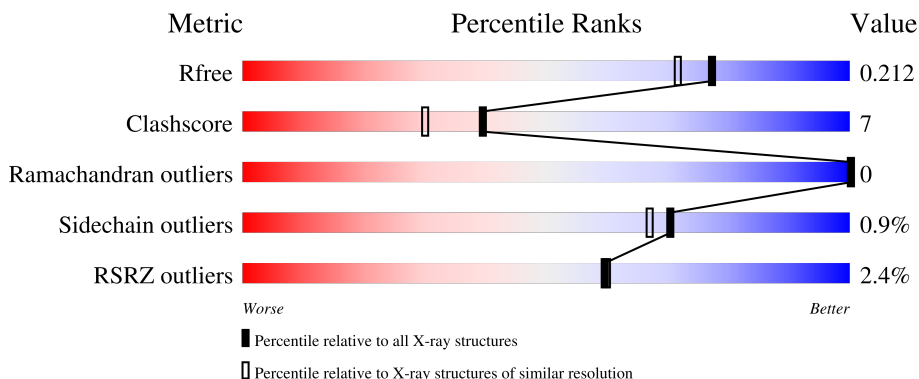
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (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  $\geq 3$ , 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	253	 2% 84% 11% 5%
1	B	253	 % 85% 10% .
2	C	19	 5% 74% 11% 16%
2	D	19	 16% 53% 47%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4780 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 Nuclear receptor subfamily 5 group A member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	241	2052	1317	341	378	16	0	13	0
1	B	242	2062	1317	347	382	16	0	13	0

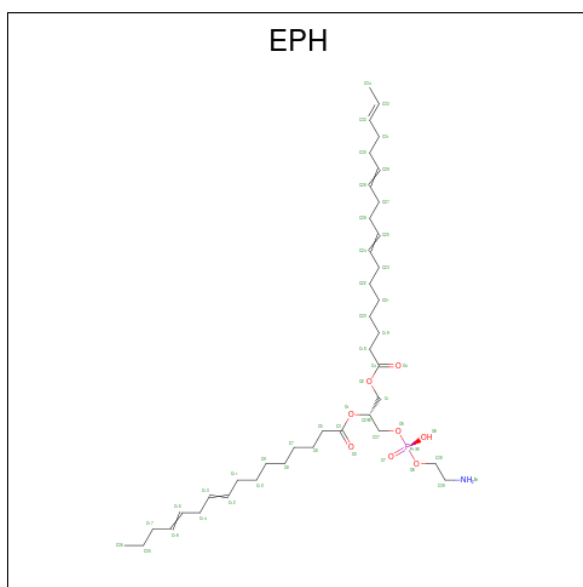
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	289	SER	-	expression tag	UNP O00482
A	290	ASN	-	expression tag	UNP O00482
B	289	SER	-	expression tag	UNP O00482
B	290	ASN	-	expression tag	UNP O00482

- Molecule 2 is a protein called Nuclear receptor subfamily 0 group B member 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	16	110	70	19	21	0	0	0
2	D	10	73	50	10	13	0	0	0

- Molecule 3 is L-ALPHA-PHOSPHATIDYL-BETA-OLEOYL-GAMMA-PALMITOYL-PHOSPHATIDYLETHANOLAMINE (CCD ID: EPH) (formula: C<sub>39</sub>H<sub>68</sub>NO<sub>8</sub>P).



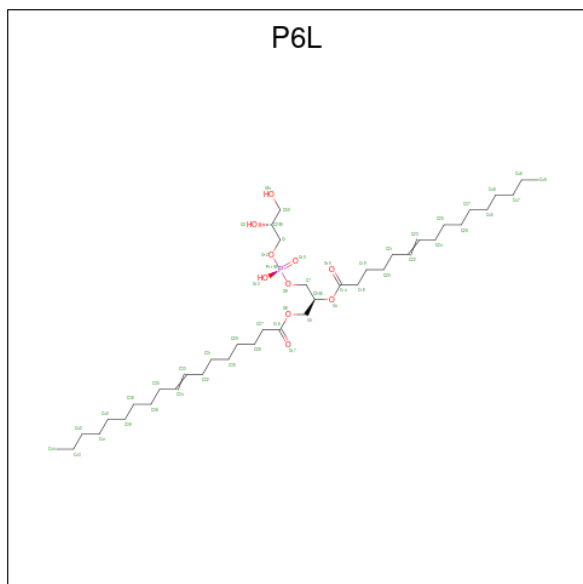
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	49	39	1	8	1	0	0

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



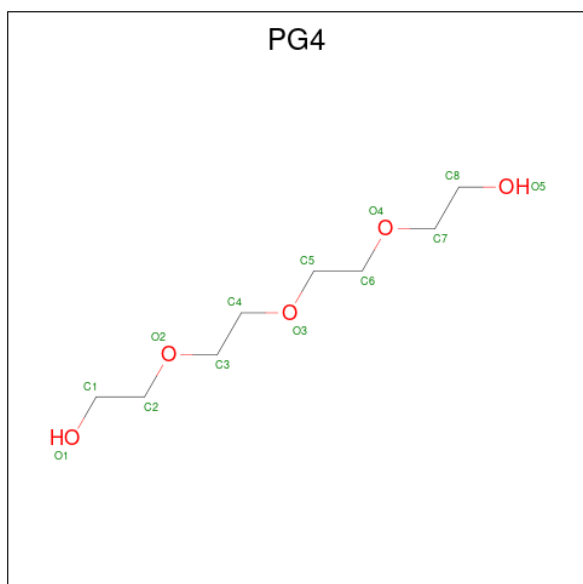
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	3	3	0	0
4	A	1	6	3	3	0	0
4	A	1	6	3	3	0	0

- Molecule 5 is (2S)-3-[[[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY]-2-[(6E)-HEXADEC-6-ENOYL]OXY]PROPYL (8E)-OCTADEC-8-ENOATE (CCD ID: P6L) (formula: C<sub>40</sub>H<sub>75</sub>O<sub>10</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	P		
5	B	1	51	40	10	1	0	0

- Molecule 6 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: C<sub>8</sub>H<sub>18</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	B	1	13	8	5	0	0

- Molecule 7 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
7	A	187	Total 187	O 187	0	0
7	C	15	Total 15	O 15	0	0
7	B	149	Total 149	O 149	0	0
7	D	1	Total 1	O 1	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.87Å 59.86Å 73.94Å 90.00° 93.86° 90.00°	Depositor
Resolution (Å)	43.67 – 1.80 43.67 – 1.80	Depositor EDS
% Data completeness (in resolution range)	94.8 (43.67-1.80) 94.8 (43.67-1.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.89 (at 1.79Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.156 , 0.202 0.166 , 0.212	Depositor DCC
$R_{free}$ test set	2487 reflections (3.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.6	Xtrriage
Anisotropy	0.145	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 38.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4780	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.56% 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: GOL, PG4, P6L, EPH

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	1.23	3/2091 (0.1%)	1.11	2/2823 (0.1%)
1	B	1.17	1/2105 (0.0%)	1.04	2/2840 (0.1%)
2	C	1.31	0/111	1.17	1/150 (0.7%)
2	D	0.80	0/74	0.89	0/100
All	All	1.20	4/4381 (0.1%)	1.07	5/5913 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	462	LYS	C-O	6.83	1.32	1.23
1	A	378	LEU	N-CA	-5.46	1.39	1.46
1	A	303	HIS	N-CA	-5.40	1.39	1.46
1	B	360	ALA	N-CA	-5.39	1.40	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	314	ASP	N-CA-C	-5.63	99.95	108.67
1	B	484	TYR	N-CA-C	5.43	116.90	111.09
1	A	356	ILE	N-CA-C	5.14	115.36	110.42
2	C	19	ALA	N-CA-C	5.06	116.79	111.28
1	B	380	ASN	N-CA-C	5.03	116.84	111.36

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	2052	0	2068	23	0
1	B	2062	0	2064	32	0
2	C	110	0	115	1	0
2	D	73	0	80	0	0
3	A	49	0	67	3	0
4	A	18	0	24	0	0
5	B	51	0	74	11	0
6	B	13	0	18	0	0
7	A	187	0	0	9	1
7	B	149	0	0	11	1
7	C	15	0	0	0	0
7	D	1	0	0	0	0
All	All	4780	0	4510	60	1

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 60 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:511[A]:MET:HE3	7:B:845:HOH:O	1.40	1.19
1:A:311:CYS:SG	7:A:884:HOH:O	2.21	0.97
1:B:511[A]:MET:HA	1:B:511[A]:MET:HE2	1.53	0.88
1:A:311:CYS:HB2	7:A:883:HOH:O	1.86	0.75
1:B:424:LEU:HD21	5:B:601:P6L:H181	1.68	0.75

All (1) 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)
7:A:832:HOH:O	7:B:742:HOH:O[2_546]	2.00	0.20

## 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	252/253 (100%)	247 (98%)	5 (2%)	0	100	100
1	B	253/253 (100%)	249 (98%)	4 (2%)	0	100	100
2	C	14/19 (74%)	14 (100%)	0	0	100	100
2	D	8/19 (42%)	8 (100%)	0	0	100	100
All	All	527/544 (97%)	518 (98%)	9 (2%)	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	230/228 (101%)	228 (99%)	2 (1%)	70	67
1	B	231/228 (101%)	229 (99%)	2 (1%)	70	67
2	C	11/14 (79%)	11 (100%)	0	100	100
2	D	8/14 (57%)	8 (100%)	0	100	100
All	All	480/484 (99%)	476 (99%)	4 (1%)	70	70

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

Mol	Chain	Res	Type
1	A	419	GLN
1	A	502	ARG

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Mol	Chain	Res	Type
1	B	502	ARG
1	B	533	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	523	ASN
1	A	537	HIS
1	B	466	ASN
1	A	463	ASN
1	A	476	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

6 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	$\# Z  > 2$
5	P6L	B	601	-	50,50,50	1.10	3 (6%)	53,56,56	1.73	9 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	GOL	A	604	-	5,5,5	0.33	0	5,5,5	0.73	0
3	EPH	A	601	-	48,48,48	1.02	2 (4%)	51,53,53	1.10	3 (5%)
4	GOL	A	603	-	5,5,5	0.38	0	5,5,5	0.48	0
4	GOL	A	602	-	5,5,5	0.37	0	5,5,5	0.62	0
6	PG4	B	602	-	12,12,12	0.69	0	11,11,11	0.56	0

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
5	P6L	B	601	-	-	23/55/55/55	-
4	GOL	A	604	-	-	2/4/4/4	-
3	EPH	A	601	-	-	23/52/52/52	-
4	GOL	A	603	-	-	0/4/4/4	-
4	GOL	A	602	-	-	2/4/4/4	-
6	PG4	B	602	-	-	4/10/10/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	601	P6L	O4-C14	4.32	1.46	1.34
3	A	601	EPH	O1-C3	4.19	1.46	1.34
3	A	601	EPH	O2-C4	4.06	1.45	1.33
5	B	601	P6L	O8-C16	3.81	1.44	1.33
5	B	601	P6L	O4-C5	-3.29	1.38	1.46

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	601	P6L	O4-C14-C18	8.61	130.12	111.48
3	A	601	EPH	O1-C3-C5	3.39	118.81	111.48
5	B	601	P6L	C1-C2-C50	-3.31	100.64	111.77
5	B	601	P6L	O4-C14-O15	-3.07	116.54	123.70
5	B	601	P6L	O15-C14-C18	-2.71	113.18	123.78

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

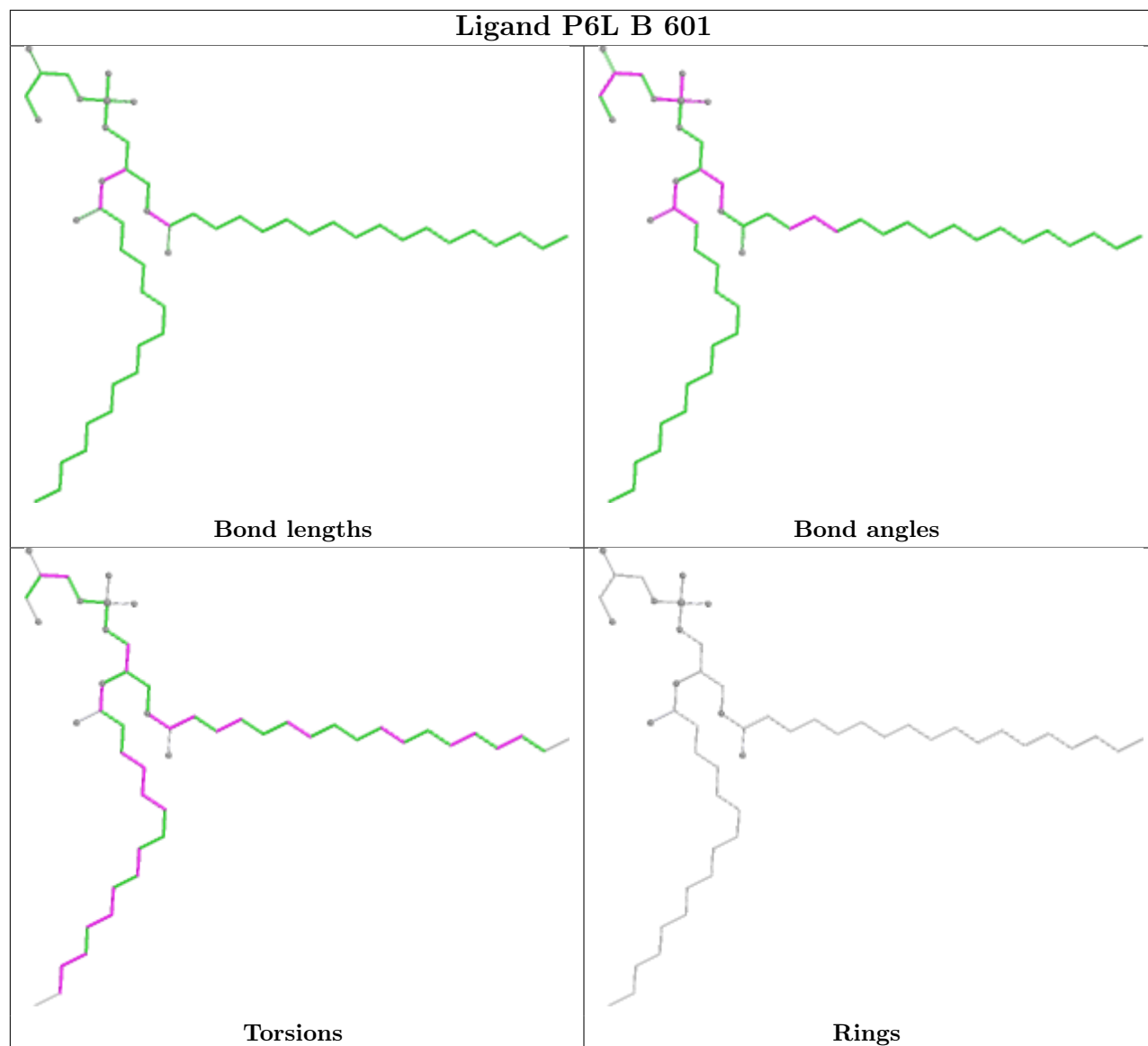
Mol	Chain	Res	Type	Atoms
3	A	601	EPH	C25-C26-C27-C28
3	A	601	EPH	C29-C30-C31-C32
3	A	601	EPH	C16-C17-C35-C36
3	A	601	EPH	C38-O8-P1-O5
3	A	601	EPH	C38-O8-P1-O6

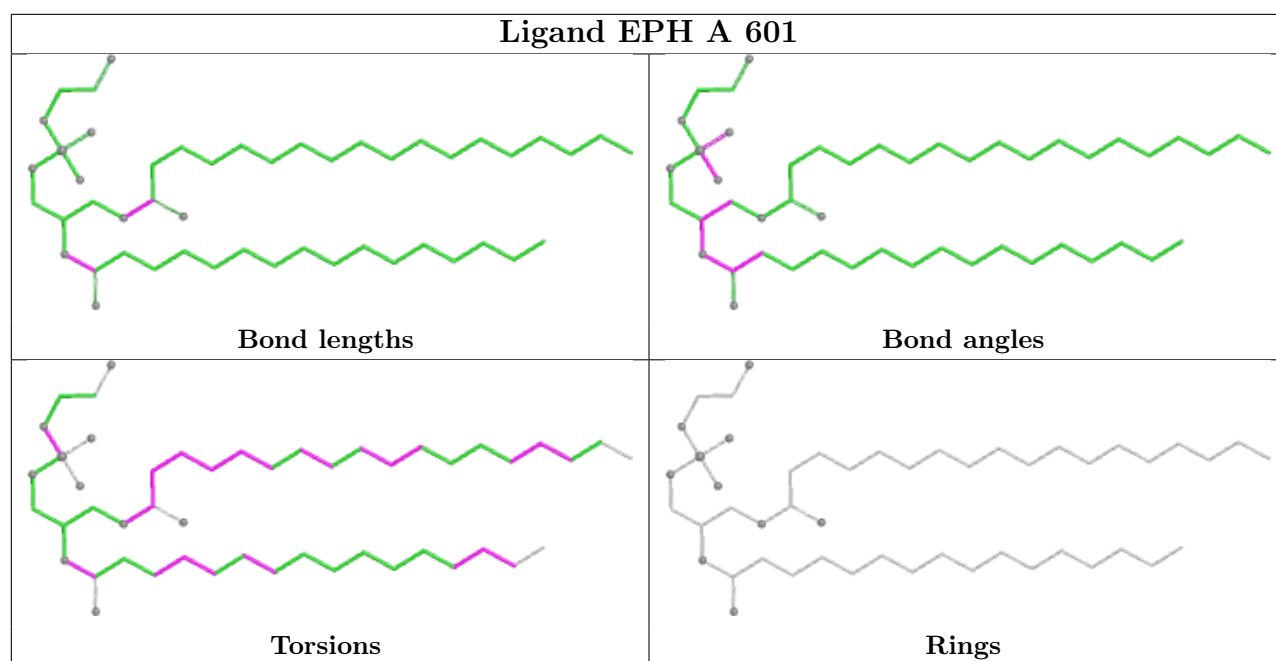
There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	601	P6L	11	0
3	A	601	EPH	3	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	241/253 (95%)	-0.36	5 (2%) 63 64	3, 13, 32, 58	13 (5%)
1	B	242/253 (95%)	-0.21	3 (1%) 76 77	5, 17, 35, 49	13 (5%)
2	C	16/19 (84%)	0.07	1 (6%) 26 24	8, 12, 44, 46	0
2	D	10/19 (52%)	1.77	3 (30%) 1 1	31, 40, 52, 61	0
All	All	509/544 (93%)	-0.23	12 (2%) 59 60	3, 16, 39, 61	26 (5%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	336	HIS	4.2
2	C	15	ALA	4.0
1	B	467	PHE	3.2
1	A	299	ALA	2.4
1	A	539	LYS	2.4

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

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

### 6.3 Carbohydrates [i](#)

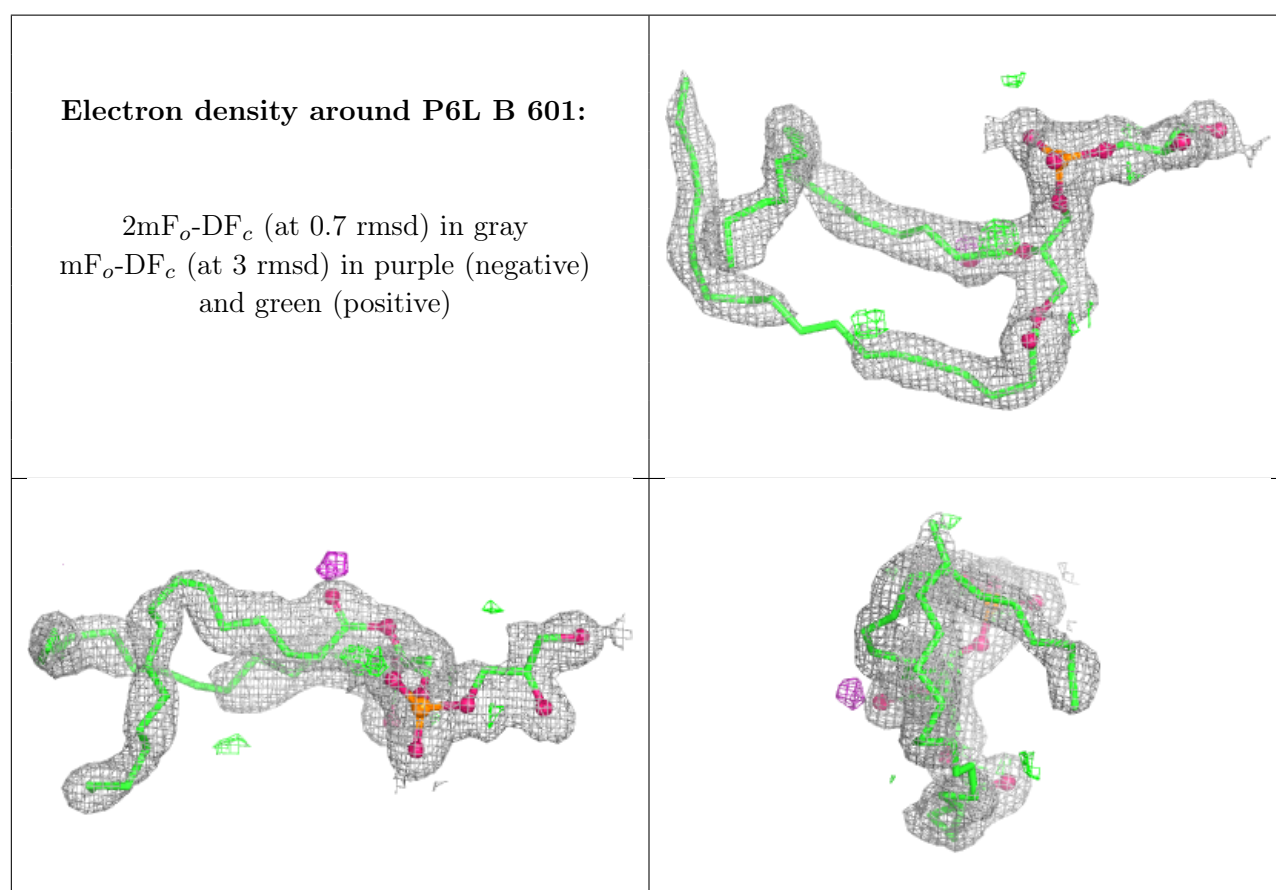
There are no oligosaccharides in this entry.

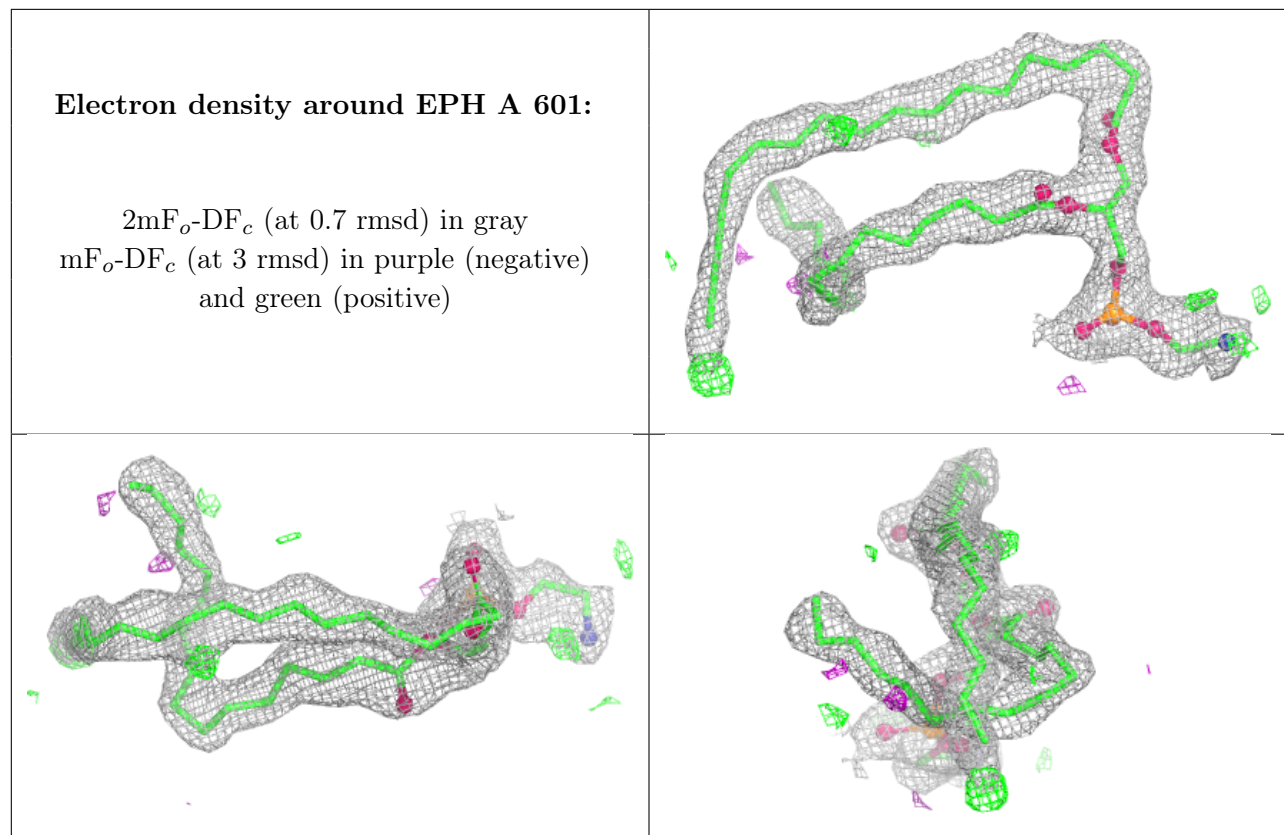
### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
6	PG4	B	602	13/13	0.81	0.14	37,40,42,42	0
4	GOL	A	604	6/6	0.88	0.12	34,41,44,46	0
4	GOL	A	602	6/6	0.89	0.11	35,38,39,41	0
5	P6L	B	601	51/51	0.92	0.13	21,36,48,54	0
3	EPH	A	601	49/49	0.93	0.12	24,37,41,45	0
4	GOL	A	603	6/6	0.94	0.11	22,24,27,27	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.