



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 23, 2022 – 12:05 PM EST

PDB ID : 7JYE  
Title : Human Liver Receptor Homolog-1 in Complex with 9ChoP and a Fragment of Tif2  
Authors : D'Agostino, E.H.; Mays, S.G.; Ortlund, E.A.  
Deposited on : 2020-08-30  
Resolution : 2.55 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](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 : 2.26  
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) : 2.26

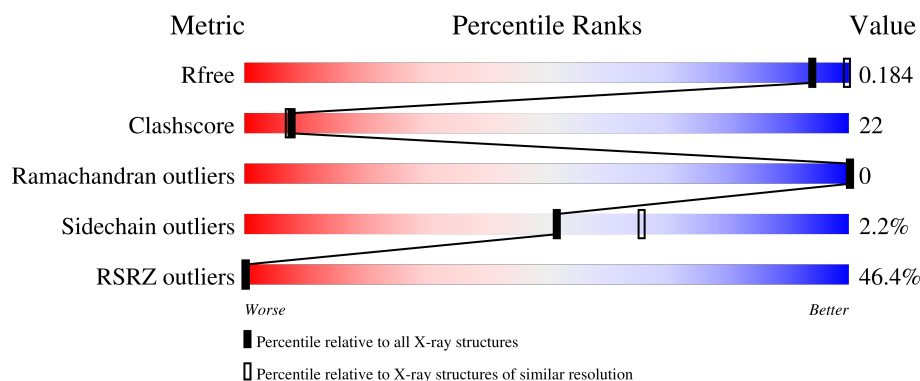
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.55 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	1279 (2.58-2.54)
Clashscore	141614	1327 (2.58-2.54)
Ramachandran outliers	138981	1312 (2.58-2.54)
Sidechain outliers	138945	1312 (2.58-2.54)
RSRZ outliers	127900	1269 (2.58-2.54)

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	246	<div> <div>46%</div> <div>51% 46% ..</div> </div>
2	C	12	<div> <div>42%</div> <div>50% 33% 17%</div> </div>

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	VQY	A	601	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2174 atoms, of which 52 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
1	A	242	Total	C	N	O	S	0	1	0
			1976	1265	334	364	13			

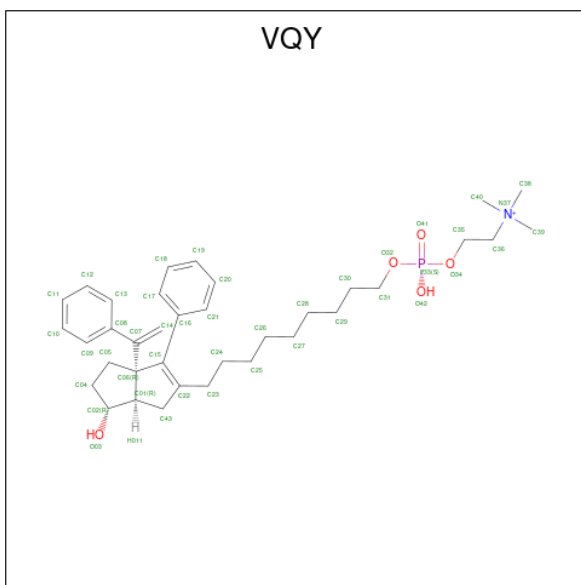
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	296	SER	-	expression tag	UNP O00482
A	297	ASN	-	expression tag	UNP O00482
A	298	ALA	-	expression tag	UNP O00482

- 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
			85	56	15	14			

- Molecule 3 is 9-[(3 {a} {R},6 {R},6 {a} {R})-6-oxidanyl-3-phenyl-3 {a}-(1-phenylethyl)-4,5,6,6 {a}-tetrahydro-1 {H}-pentalen-2-yl]nonyl 2-(trimethyl- $l^4$ -azanyl)ethyl hydrogen phosphate (three-letter code: VQY) (formula: C<sub>36</sub>H<sub>53</sub>NO<sub>5</sub>P) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	H	N	O	P	0	0
			95	36	52	1	5	1		

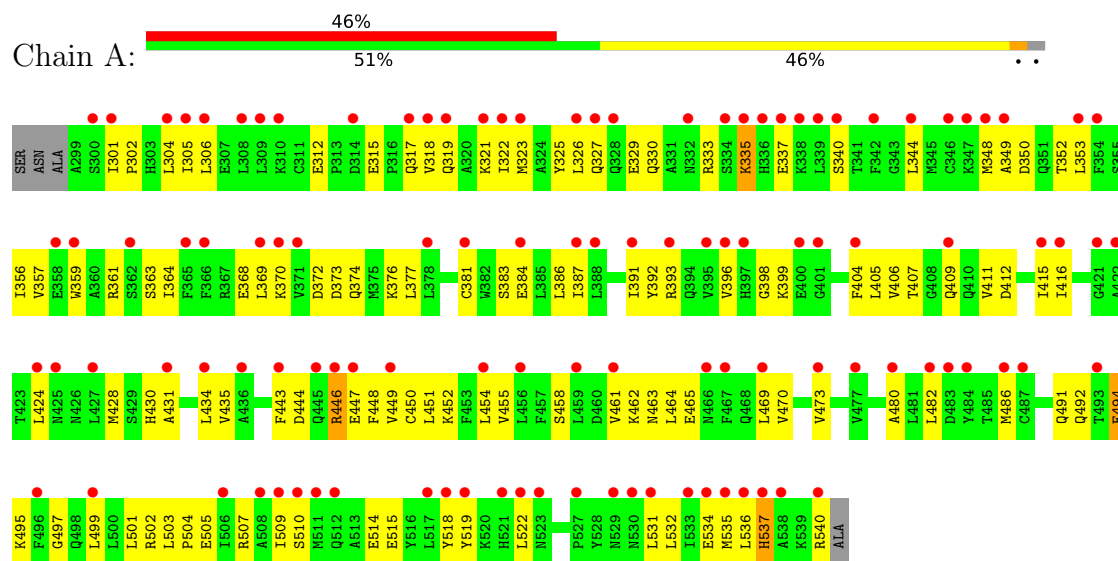
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	17	Total O 17 17	0	0
4	C	1	Total O 1 1	0	0

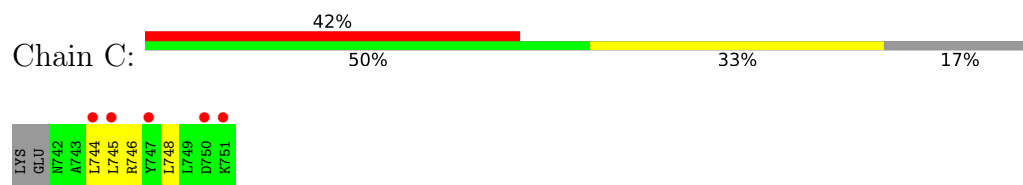
### 3 Residue-property plots [i](#)

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: Nuclear receptor subfamily 5 group A member 2



- Molecule 2: Nuclear receptor coactivator 2



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.24Å 89.24Å 106.54Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	35.51 – 2.55 35.51 – 2.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (35.51-2.55) 100.0 (35.51-2.55)	Depositor EDS
$R_{merge}$	0.27	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	107.23 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.12-2829-000	Depositor
R, $R_{free}$	0.159 , 0.187 0.161 , 0.184	Depositor DCC
$R_{free}$ test set	818 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	55.2	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 42.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.36$ , $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	0.428 for -h,-k,l	Xtriage
Reported twinning fraction	0.480 for -h,-k,l	Depositor
Outliers	0 of 16427 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	2174	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.05% 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: VQY

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	0.24	0/2012	0.35	0/2716
2	C	0.23	0/85	0.29	0/113
All	All	0.24	0/2097	0.34	0/2829

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1976	0	1988	89	0
2	C	85	0	93	3	0
3	A	43	52	0	0	0
4	A	17	0	0	0	0
4	C	1	0	0	1	0
All	All	2122	52	2081	91	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 22.

All (91) 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:534:GLU:HA	1:A:537:HIS:HB3	1.66	0.77
1:A:391:ILE:HG23	1:A:435:VAL:HG22	1.68	0.76
1:A:348:MET:HE1	1:A:405:LEU:HD13	1.68	0.76
1:A:458:SER:HB3	1:A:461:VAL:HG23	1.69	0.75
1:A:318:VAL:HA	1:A:321:LYS:HD2	1.70	0.74
1:A:497:GLY:O	1:A:501:LEU:HD13	1.92	0.69
1:A:335:LYS:HE2	1:A:335:LYS:N	2.08	0.68
1:A:333:ARG:HB3	1:A:337:GLU:HB2	1.77	0.67
1:A:317:GLN:O	1:A:321:LYS:HG3	1.94	0.67
1:A:411:VAL:HG21	1:A:416:ILE:HG13	1.76	0.66
1:A:319:GLN:HG2	1:A:406:VAL:O	1.96	0.66
1:A:323:MET:SD	1:A:409:GLN:NE2	2.54	0.66
1:A:326:LEU:HD11	1:A:348:MET:HG2	1.78	0.65
1:A:531:LEU:HD12	1:A:532:LEU:N	2.12	0.65
1:A:350:ASP:HA	1:A:353:LEU:HD12	1.79	0.65
1:A:377:LEU:HD23	1:A:461:VAL:HG21	1.78	0.64
1:A:507:ARG:O	1:A:510:SER:OG	2.14	0.64
1:A:330:GLN:OE1	1:A:333:ARG:NH2	2.24	0.62
1:A:325:TYR:O	1:A:329:GLU:HG2	2.00	0.62
1:A:302:PRO:HD2	1:A:305:ILE:HD12	1.82	0.61
1:A:357:VAL:O	1:A:361:ARG:HG3	1.99	0.61
1:A:333:ARG:HD2	1:A:337:GLU:HB3	1.84	0.60
1:A:495:LYS:O	1:A:499:LEU:HG	2.01	0.59
1:A:398:GLY:HA2	1:A:404:PHE:CD1	2.38	0.58
1:A:448:PHE:CZ	1:A:452:LYS:HD2	2.39	0.58
1:A:515:GLU:OE2	1:A:540:ARG:NE	2.37	0.57
1:A:534:GLU:OE1	2:C:744:LEU:HB3	2.05	0.56
1:A:373:ASP:OD2	1:A:465:GLU:HB3	2.06	0.55
1:A:503:LEU:HB2	1:A:504:PRO:HD3	1.89	0.55
1:A:335:LYS:HE2	1:A:335:LYS:H	1.71	0.55
1:A:398:GLY:O	1:A:399:LYS:HD3	2.06	0.55
1:A:318:VAL:HA	1:A:321:LYS:CD	2.36	0.54
1:A:443:PHE:CZ	1:A:448:PHE:HA	2.43	0.54
1:A:370:LYS:O	1:A:374:GLN:HG3	2.07	0.54
1:A:301:ILE:HG22	1:A:306:LEU:HG	1.91	0.53
1:A:370:LYS:HE2	1:A:465:GLU:CB	2.38	0.53
1:A:491:GLN:HG3	1:A:492:GLN:OE1	2.07	0.53
1:A:514:GLU:HG3	1:A:536:LEU:HD21	1.90	0.53
1:A:315:GLU:HA	1:A:318:VAL:HG12	1.89	0.53
1:A:501:LEU:HB3	1:A:502:ARG:NH1	2.24	0.52
1:A:462:LYS:O	1:A:463:ASN:HB2	2.07	0.52
1:A:531:LEU:O	1:A:535:MET:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:GLU:OE2	1:A:449:VAL:HG12	2.09	0.52
1:A:364:ILE:O	1:A:368:GLU:HG3	2.09	0.52
1:A:377:LEU:CD2	1:A:461:VAL:HG21	2.39	0.52
1:A:518:TYR:HB2	1:A:536:LEU:HD22	1.92	0.52
1:A:369:LEU:O	1:A:374:GLN:NE2	2.36	0.51
1:A:482:LEU:HD12	1:A:486:MET:HG3	1.92	0.51
1:A:304:LEU:HD23	1:A:480:ALA:HB2	1.92	0.50
1:A:407:THR:OG1	1:A:409:GLN:HG3	2.11	0.50
1:A:317:GLN:HG3	1:A:321:LYS:HE3	1.94	0.50
1:A:448:PHE:CE2	1:A:452:LYS:HD2	2.46	0.50
1:A:322:ILE:HD12	1:A:406:VAL:HG22	1.94	0.50
1:A:372:ASP:O	1:A:376:LYS:HG3	2.11	0.50
1:A:322:ILE:HD12	1:A:406:VAL:CG2	2.41	0.50
1:A:519:TYR:OH	1:A:540:ARG:NH2	2.45	0.49
2:C:745:LEU:HA	2:C:748:LEU:HD12	1.94	0.49
1:A:359:TRP:CZ2	1:A:452:LYS:HE2	2.47	0.49
1:A:431:ALA:O	1:A:435:VAL:HG23	2.13	0.49
1:A:430:HIS:ND1	1:A:509:ILE:HD11	2.28	0.48
1:A:325:TYR:CD2	1:A:326:LEU:HD23	2.48	0.48
1:A:383:SER:O	1:A:387:ILE:HG12	2.13	0.48
1:A:412:ASP:HB3	1:A:415:ILE:HG12	1.94	0.48
1:A:381:CYS:HB2	1:A:455:VAL:HG12	1.95	0.48
1:A:323:MET:HB2	1:A:407:THR:HB	1.96	0.48
1:A:384:GLU:OE1	1:A:507:ARG:HD3	2.13	0.48
1:A:494:GLU:OE1	1:A:494:GLU:N	2.44	0.48
1:A:317:GLN:HG3	1:A:318:VAL:N	2.31	0.46
1:A:340:SER:O	1:A:344:LEU:HG	2.15	0.46
1:A:352:THR:O	1:A:356:ILE:HG13	2.16	0.46
1:A:392:TYR:O	1:A:396:VAL:HG23	2.16	0.46
1:A:450:CYS:O	1:A:454:LEU:HG	2.16	0.45
1:A:443:PHE:HZ	1:A:448:PHE:HA	1.79	0.45
1:A:424:LEU:O	1:A:428:MET:HG3	2.16	0.45
1:A:518:TYR:CE2	1:A:522:LEU:HD11	2.52	0.45
1:A:451:LEU:O	1:A:455:VAL:HG23	2.17	0.45
1:A:469:LEU:O	1:A:473:VAL:HG23	2.17	0.44
1:A:446:ARG:O	1:A:449:VAL:HG22	2.17	0.44
2:C:746:ARG:NH2	4:C:801:HOH:O	2.50	0.44
1:A:322:ILE:HG22	1:A:407:THR:HG22	2.00	0.44
1:A:370:LYS:HE2	1:A:465:GLU:HB2	2.00	0.44
1:A:323:MET:O	1:A:327:GLN:HG3	2.19	0.43
1:A:518:TYR:O	1:A:522:LEU:HG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:537:HIS:ND1	1:A:537:HIS:O	2.52	0.43
1:A:393:ARG:CZ	1:A:393:ARG:HB2	2.50	0.42
1:A:444:ASP:OD1	1:A:447:GLU:HG3	2.20	0.41
1:A:349:ALA:HB1	1:A:386:LEU:HD21	2.01	0.41
1:A:447:GLU:OE2	1:A:495:LYS:NZ	2.44	0.41
1:A:434:LEU:HD21	1:A:505:GLU:OE1	2.21	0.41
1:A:464:LEU:HD13	1:A:470:VAL:HG21	2.02	0.41
1:A:315:GLU:O	1:A:319:GLN:HG3	2.21	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	241/246 (98%)	236 (98%)	5 (2%)	0	100	100
2	C	8/12 (67%)	7 (88%)	1 (12%)	0	100	100
All	All	249/258 (96%)	243 (98%)	6 (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	219/220 (100%)	214 (98%)	5 (2%)	50	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	9/11 (82%)	9 (100%)	0	100	100
All	All	228/231 (99%)	223 (98%)	5 (2%)	52	66

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	335	LYS
1	A	363	SER
1	A	446	ARG
1	A	494	GLU
1	A	537	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	GLN
1	A	442	GLN
1	A	491	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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	VQY	A	601	-	45,46,46	1.93	8 (17%)	48,65,65	0.71	1 (2%)

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	VQY	A	601	-	-	16/35/66/66	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	VQY	C22-C15	7.06	1.43	1.34
3	A	601	VQY	C06-C01	-5.69	1.47	1.56
3	A	601	VQY	C06-C15	3.50	1.59	1.53
3	A	601	VQY	O03-C02	-3.21	1.36	1.43
3	A	601	VQY	C16-C15	2.60	1.53	1.48
3	A	601	VQY	P33-O34	2.60	1.69	1.59
3	A	601	VQY	C23-C22	2.60	1.61	1.51
3	A	601	VQY	P33-O32	2.10	1.67	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	VQY	C23-C22-C43	2.15	125.44	121.55

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	VQY	C01-C06-C07-C14
3	A	601	VQY	C05-C06-C07-C14
3	A	601	VQY	C43-C22-C23-C24
3	A	601	VQY	O34-C35-C36-N37
3	A	601	VQY	C31-O32-P33-O41

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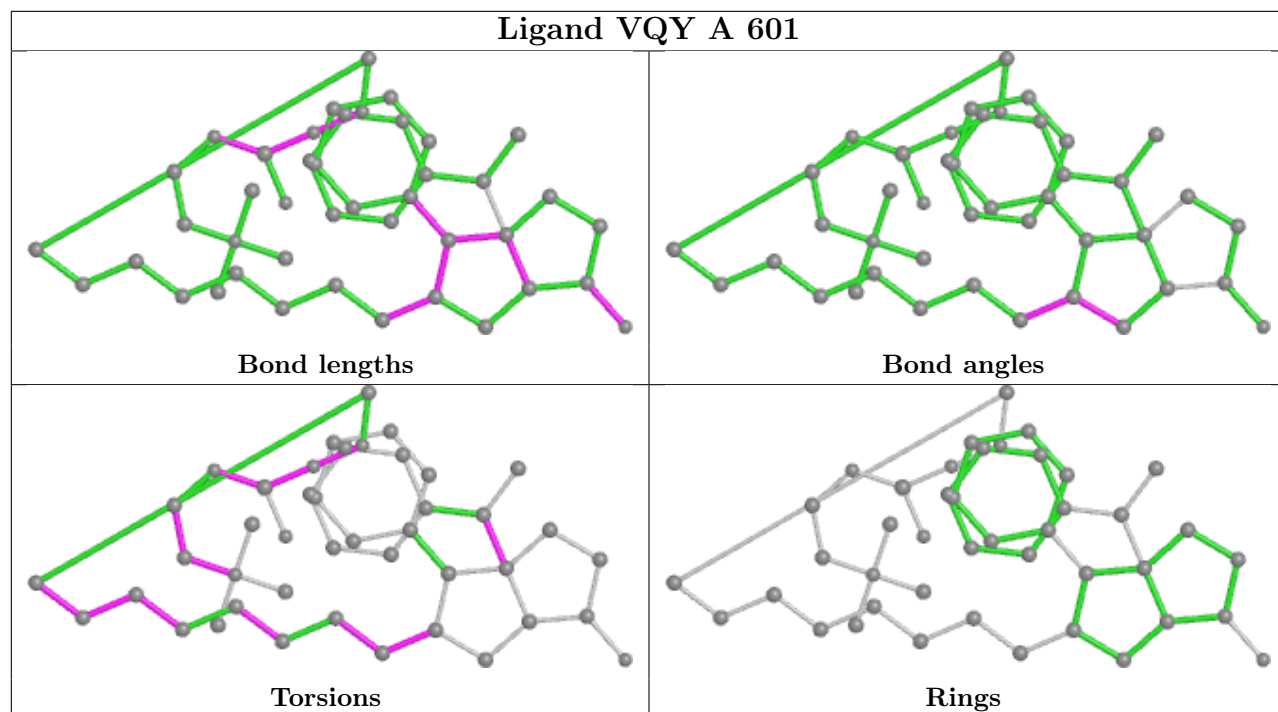
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Mol	Chain	Res	Type	Atoms
3	A	601	VQY	C31-O32-P33-O42
3	A	601	VQY	C35-O34-P33-O32
3	A	601	VQY	C35-O34-P33-O41
3	A	601	VQY	C35-O34-P33-O42
3	A	601	VQY	C22-C23-C24-C25
3	A	601	VQY	C31-O32-P33-O34
3	A	601	VQY	C26-C27-C28-C29
3	A	601	VQY	C24-C25-C26-C27
3	A	601	VQY	C28-C29-C30-C31
3	A	601	VQY	C27-C28-C29-C30
3	A	601	VQY	C35-C36-N37-C39

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 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

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	242/246 (98%)	2.20	112 (46%)  	34, 56, 105, 158	0
2	C	10/12 (83%)	3.01	5 (50%)  	59, 90, 123, 156	0
All	All	252/258 (97%)	2.23	117 (46%)  	34, 57, 111, 158	0

All (117) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	338	LYS	13.0
1	A	335	LYS	8.7
1	A	323	MET	7.5
1	A	459	LEU	7.4
1	A	336	HIS	7.4
1	A	358	GLU	6.9
2	C	750	ASP	6.8
1	A	322	ILE	6.6
2	C	751	LYS	6.4
1	A	531	LEU	6.3
1	A	365	PHE	6.3
1	A	305	ILE	6.2
1	A	339	LEU	5.8
1	A	340	SER	5.3
1	A	400	GLU	5.3
1	A	337	GLU	4.9
1	A	523	ASN	4.9
1	A	461	VAL	4.9
1	A	469	LEU	4.6
1	A	306	LEU	4.6
1	A	482	LEU	4.5
1	A	342	PHE	4.5
1	A	366	PHE	4.3
1	A	510	SER	4.2

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Mol	Chain	Res	Type	RSRZ
2	C	747	TYR	4.2
1	A	536	LEU	4.1
1	A	328	GLN	4.1
1	A	326	LEU	4.1
1	A	431	ALA	3.9
1	A	300	SER	3.9
1	A	519	TYR	3.9
1	A	310	LYS	3.8
1	A	486	MET	3.6
1	A	473	VAL	3.5
1	A	334	SER	3.5
1	A	369	LEU	3.5
1	A	446	ARG	3.4
1	A	319	GLN	3.4
1	A	359	TRP	3.4
1	A	540	ARG	3.4
1	A	415	ILE	3.3
1	A	521	HIS	3.3
1	A	421	GLY	3.3
1	A	518	TYR	3.3
1	A	404	PHE	3.3
1	A	427	LEU	3.3
1	A	434	LEU	3.3
1	A	530	ASN	3.2
1	A	401	GLY	3.2
1	A	391	ILE	3.2
1	A	353	LEU	3.2
1	A	314	ASP	3.1
1	A	533	ILE	3.1
1	A	304	LEU	3.1
1	A	344	LEU	3.1
1	A	370	LYS	3.1
1	A	511	MET	3.1
1	A	362	SER	3.0
1	A	538	ALA	3.0
1	A	347	LYS	3.0
1	A	387	ILE	3.0
1	A	506	ILE	3.0
1	A	529	ASN	3.0
1	A	499	LEU	2.9
1	A	480	ALA	2.9
1	A	449	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	535	MET	2.9
1	A	393	ARG	2.8
1	A	388	LEU	2.8
2	C	744	LEU	2.8
1	A	378	LEU	2.7
1	A	301	ILE	2.7
1	A	508	ALA	2.7
1	A	467	PHE	2.7
1	A	483	ASP	2.7
1	A	537	HIS	2.6
2	C	745	LEU	2.6
1	A	509	ILE	2.6
1	A	517	LEU	2.6
1	A	534	GLU	2.6
1	A	332	ASN	2.6
1	A	317	GLN	2.6
1	A	484	TYR	2.5
1	A	456	LEU	2.5
1	A	477	VAL	2.5
1	A	425	ASN	2.5
1	A	493	THR	2.5
1	A	384	GLU	2.5
1	A	512	GLN	2.4
1	A	309	LEU	2.4
1	A	496	PHE	2.4
1	A	348	MET	2.4
1	A	443	PHE	2.4
1	A	447	GLU	2.4
1	A	424	LEU	2.4
1	A	396	VAL	2.4
1	A	454	LEU	2.4
1	A	321	LYS	2.3
1	A	422	ALA	2.3
1	A	327	GLN	2.3
1	A	436	ALA	2.3
1	A	466	ASN	2.3
1	A	346	CYS	2.2
1	A	395	VAL	2.2
1	A	445	GLN	2.2
1	A	354	PHE	2.2
1	A	487	CYS	2.2
1	A	318	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	371	VAL	2.2
1	A	416	ILE	2.2
1	A	381	CYS	2.1
1	A	527	PRO	2.1
1	A	349	ALA	2.1
1	A	397	HIS	2.1
1	A	409	GLN	2.0
1	A	308	LEU	2.0
1	A	522	LEU	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](#)

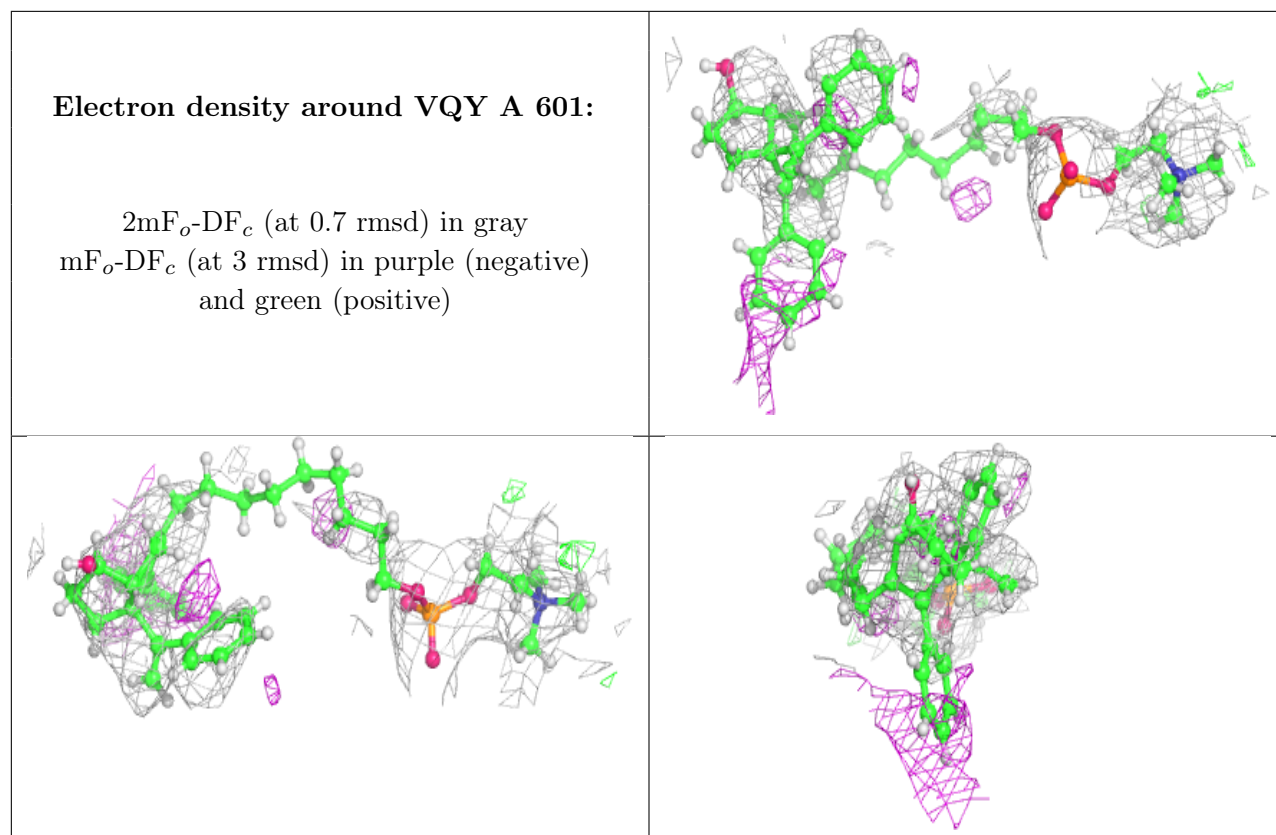
There are no monosaccharides in this entry.

## 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, 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	VQY	A	601	43/43	0.74	0.47	42,72,114,124	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.