



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 22, 2024 – 05:59 AM EDT

PDB ID : 4J02  
Title : Crystal structure of hcv ns5b polymerase in complex with [(1R)-5,8-DICHLORO-1-PROPYL-1,3,4,9-TETRAHYDROPYRANO[3,4-B]INDOL-1-YL]ACETIC ACID  
Authors : Coulombe, R.  
Deposited on : 2013-01-30  
Resolution : 2.00 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.

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	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

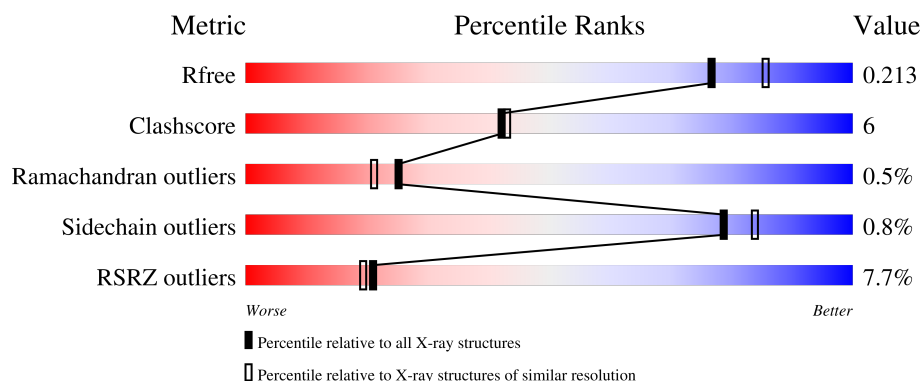
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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	576	
1	B	576	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9514 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.

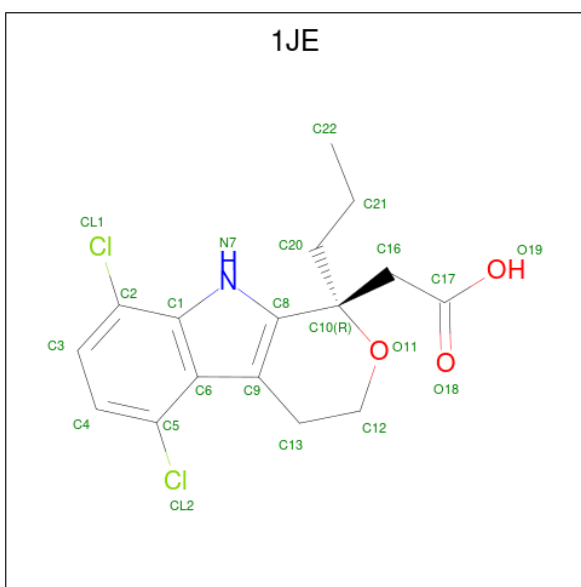
- Molecule 1 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	0	0
			4358	2745	770	811	32			
1	B	558	Total	C	N	O	S	0	0	0
			4346	2737	768	809	32			

There are 12 discrepancies between the modelled and reference sequences:

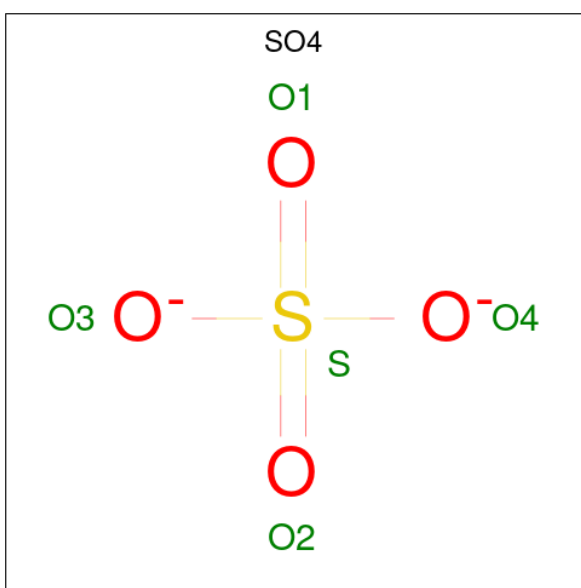
Chain	Residue	Modelled	Actual	Comment	Reference
A	571	HIS	-	expression tag	UNP O92972
A	572	HIS	-	expression tag	UNP O92972
A	573	HIS	-	expression tag	UNP O92972
A	574	HIS	-	expression tag	UNP O92972
A	575	HIS	-	expression tag	UNP O92972
A	576	HIS	-	expression tag	UNP O92972
B	571	HIS	-	expression tag	UNP O92972
B	572	HIS	-	expression tag	UNP O92972
B	573	HIS	-	expression tag	UNP O92972
B	574	HIS	-	expression tag	UNP O92972
B	575	HIS	-	expression tag	UNP O92972
B	576	HIS	-	expression tag	UNP O92972

- Molecule 2 is [(1R)-5,8-dichloro-1-propyl-1,3,4,9-tetrahydropyrano[3,4-b]indol-1-yl]acetic acid (three-letter code: 1JE) (formula: C<sub>16</sub>H<sub>17</sub>Cl<sub>2</sub>NO<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			22	16	2	1	3		
2	B	1	Total	C	Cl	N	O	0	0
			22	16	2	1	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O S	0	0
			5	4 1		
3	B	1	Total	O S	0	0
			5	4 1		

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Na 1	0	0
4	B	1	Total 1	Na 1	0	0

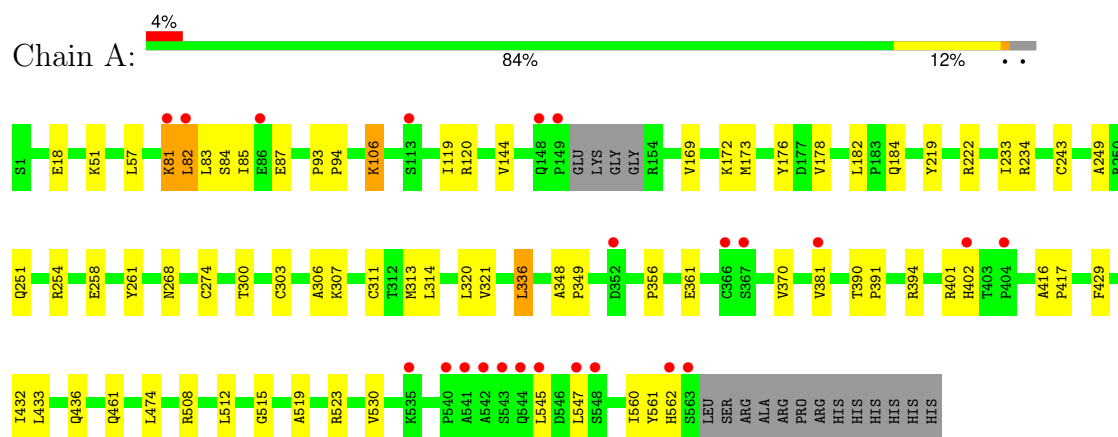
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	423	Total 423	O 423	0	0
5	B	331	Total 331	O 331	0	0

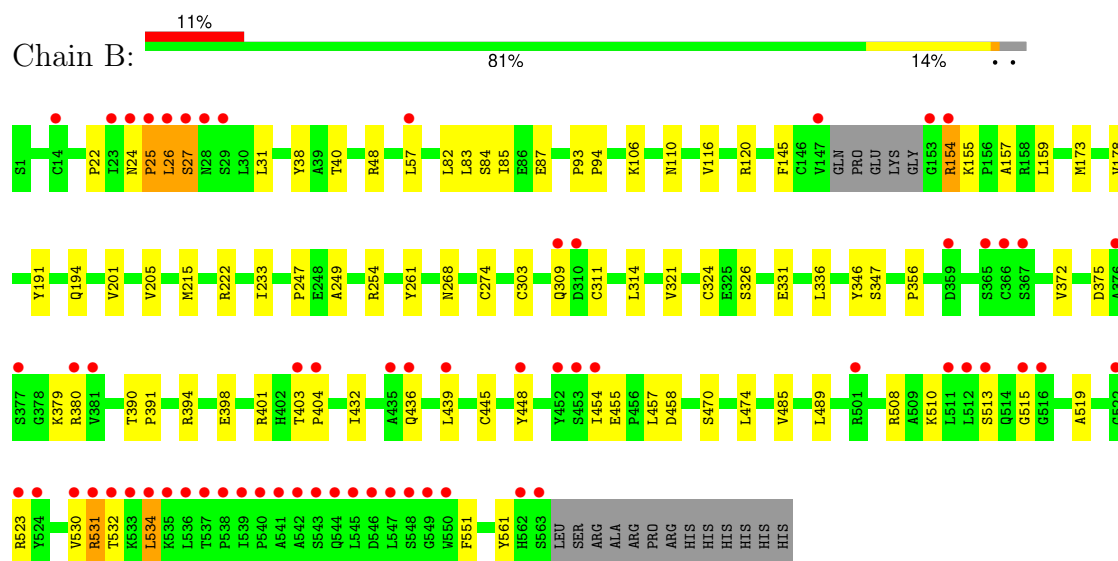
### 3 Residue-property plots [i](#)

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: Genome polypeptide



#### • Molecule 1: Genome polypeptide



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.76Å 108.34Å 133.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.00 40.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.00) 99.6 (40.00-2.00)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.20 (at 2.00Å)	Xtriage
Refinement program	CNS, CNX 2002	Depositor
R, $R_{free}$	0.195 , 0.220 0.188 , 0.213	Depositor DCC
$R_{free}$ test set	10375 reflections (10.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.7	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 40.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	9514	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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: 1JE, NA, SO4

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	0.27	0/4453	0.58	1/6044 (0.0%)
1	B	0.27	0/4440	0.57	0/6025
All	All	0.27	0/8893	0.57	1/12069 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	81	LYS	N-CA-C	5.19	125.00	111.00

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	4358	0	4371	46	0
1	B	4346	0	4359	64	0
2	A	22	0	16	0	0
2	B	22	0	16	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	423	0	0	1	0
5	B	331	0	0	1	0
All	All	9514	0	8762	108	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 6.

All (108) 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:24:ASN:HB2	1:B:25:PRO:HD2	1.45	0.98
1:B:531:ARG:HH11	1:B:532:THR:H	1.27	0.81
1:A:303:CYS:HG	1:A:311:CYS:HG	1.23	0.77
1:B:314:LEU:HB3	1:B:321:VAL:CG1	2.16	0.76
1:B:85:ILE:HD13	1:B:116:VAL:HG13	1.68	0.74
1:A:314:LEU:HB3	1:A:321:VAL:CG1	2.17	0.74
1:A:81:LYS:O	1:A:82:LEU:HB3	1.91	0.71
1:B:394:ARG:O	1:B:398:GLU:HG3	1.91	0.70
1:A:82:LEU:HD13	1:A:249:ALA:HB2	1.76	0.68
1:B:515:GLY:HA2	1:B:519:ALA:HB2	1.76	0.67
1:A:508:ARG:CZ	1:A:530:VAL:HG11	2.26	0.65
1:B:106:LYS:NZ	1:B:110:ASN:HD21	1.98	0.62
1:B:38:TYR:CE2	1:B:154:ARG:HG3	2.35	0.61
1:B:26:LEU:O	1:B:27:SER:HB3	2.02	0.59
1:B:303:CYS:HG	1:B:311:CYS:HG	1.51	0.59
1:B:24:ASN:HB2	1:B:25:PRO:CD	2.28	0.58
1:B:48:ARG:HG2	1:B:159:LEU:HG	1.84	0.58
1:B:116:VAL:HG12	1:B:120:ARG:NH1	2.19	0.58
1:A:512:LEU:HD21	1:A:523:ARG:HG2	1.87	0.57
1:B:375:ASP:OD1	1:B:379:LYS:HB3	2.04	0.57
1:B:26:LEU:O	1:B:27:SER:CB	2.53	0.56
1:B:455:GLU:HB2	1:B:458:ASP:OD2	2.06	0.56
1:A:381:VAL:HG11	1:A:474:LEU:CD2	2.36	0.56
1:B:106:LYS:HZ3	1:B:110:ASN:HD21	1.54	0.55
1:B:523:ARG:HH11	1:B:534:LEU:HD23	1.72	0.55
1:A:81:LYS:O	1:A:82:LEU:CB	2.53	0.54
1:B:31:LEU:HD12	1:B:31:LEU:O	2.08	0.54
1:B:178:VAL:HG23	5:B:1064:HOH:O	2.06	0.54
1:B:390:THR:HB	1:B:391:PRO:HD3	1.90	0.54
1:B:22:PRO:HG3	1:B:401:ARG:CZ	2.38	0.53
1:B:372:VAL:HG21	1:B:380:ARG:HG2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:336:LEU:HD23	1:B:356:PRO:HD3	1.91	0.53
1:B:531:ARG:NH1	1:B:532:THR:H	1.99	0.53
1:A:233:ILE:HD13	1:A:261:TYR:O	2.08	0.53
1:B:508:ARG:HH21	1:B:534:LEU:HD13	1.74	0.53
1:A:57:LEU:C	1:A:57:LEU:HD23	2.29	0.52
1:A:314:LEU:HB3	1:A:321:VAL:HG12	1.91	0.52
1:B:233:ILE:HD13	1:B:261:TYR:O	2.09	0.52
1:B:331:GLU:OE1	1:B:331:GLU:N	2.38	0.52
1:A:336:LEU:HD12	1:A:356:PRO:HD3	1.91	0.52
1:A:144:VAL:HB	1:A:394:ARG:HG2	1.92	0.51
1:B:314:LEU:HB3	1:B:321:VAL:HG12	1.90	0.51
1:A:429:PHE:O	1:A:433:LEU:HG	2.10	0.51
1:B:309:GLN:O	1:B:324:CYS:HB2	2.11	0.51
1:B:84:SER:OG	1:B:87:GLU:HG3	2.11	0.51
1:A:390:THR:HB	1:A:391:PRO:HD3	1.93	0.50
1:B:85:ILE:CD1	1:B:116:VAL:HG13	2.39	0.50
1:B:508:ARG:CZ	1:B:530:VAL:HG11	2.42	0.50
1:A:83:LEU:HB2	1:A:173:MET:HA	1.94	0.49
1:A:547:LEU:HD12	1:A:547:LEU:N	2.27	0.49
1:B:485:VAL:O	1:B:489:LEU:HG	2.13	0.48
1:A:306:ALA:O	1:A:307:LYS:HB2	2.14	0.47
1:B:448:TYR:CE2	1:B:551:PHE:HD1	2.32	0.47
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.54	0.47
1:B:191:TYR:O	1:B:194:GLN:HG2	2.13	0.47
1:A:300:THR:HA	1:A:313:MET:HE3	1.96	0.47
1:A:51:LYS:HG3	1:A:222:ARG:NH2	2.30	0.46
1:A:508:ARG:NH1	1:A:530:VAL:HG11	2.30	0.46
1:B:445:CYS:SG	1:B:454:ILE:HD12	2.56	0.46
1:A:461:GLN:HB2	1:A:545:LEU:HD11	1.96	0.46
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.98	0.45
1:B:40:THR:HB	1:B:157:ALA:HB2	1.98	0.45
1:B:48:ARG:CG	1:B:159:LEU:HG	2.47	0.45
1:A:18:GLU:HG3	1:A:401:ARG:NH1	2.31	0.45
1:A:314:LEU:HB3	1:A:321:VAL:HG13	1.96	0.45
1:B:83:LEU:HB2	1:B:173:MET:HA	1.98	0.45
1:B:346:TYR:O	1:B:347:SER:HB3	2.16	0.45
1:B:470:SER:O	1:B:474:LEU:HG	2.17	0.45
1:A:106:LYS:NZ	1:A:106:LYS:HB2	2.32	0.45
1:B:93:PRO:HA	1:B:94:PRO:HD3	1.90	0.45
1:B:22:PRO:HB2	1:B:24:ASN:ND2	2.33	0.44
1:A:515:GLY:HA2	1:A:519:ALA:HB2	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:268:ASN:HB3	1:B:274:CYS:SG	2.58	0.44
1:A:119:ILE:HD13	1:A:169:VAL:HG11	1.99	0.44
1:B:24:ASN:CB	1:B:25:PRO:HD2	2.31	0.44
1:B:201:VAL:O	1:B:205:VAL:HG23	2.18	0.44
1:B:432:ILE:HG23	1:B:436:GLN:NE2	2.33	0.44
1:B:82:LEU:HD13	1:B:249:ALA:HB2	2.00	0.43
1:A:234:ARG:HD3	1:B:247:PRO:HG3	2.00	0.43
1:B:93:PRO:HG3	1:B:561:TYR:HB2	2.01	0.43
1:B:515:GLY:CA	1:B:519:ALA:HB2	2.48	0.43
1:A:178:VAL:HG23	5:A:837:HOH:O	2.19	0.43
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.99	0.43
1:B:145:PHE:CE2	1:B:155:LYS:HD2	2.52	0.43
1:B:403:THR:HA	1:B:404:PRO:HD3	1.89	0.43
1:B:531:ARG:H	1:B:531:ARG:HG3	1.30	0.43
1:A:432:ILE:O	1:A:436:GLN:HG3	2.20	0.42
1:A:381:VAL:HG11	1:A:474:LEU:HD21	1.99	0.42
1:A:251:GLN:NE2	1:B:254:ARG:HG2	2.34	0.42
1:A:254:ARG:HH12	1:A:258:GLU:HG3	1.85	0.42
1:B:439:LEU:O	1:B:457:LEU:HG	2.20	0.42
1:B:314:LEU:HB3	1:B:321:VAL:HG13	1.98	0.42
1:B:25:PRO:O	1:B:26:LEU:C	2.57	0.42
1:A:93:PRO:HA	1:A:94:PRO:HD3	1.93	0.41
1:A:182:LEU:HD12	1:A:243:CYS:SG	2.60	0.41
1:A:361:GLU:HG2	1:A:370:VAL:O	2.20	0.41
1:A:416:ALA:N	1:A:417:PRO:CD	2.84	0.41
1:A:176:TYR:OH	1:A:562:HIS:HE1	2.04	0.41
1:B:25:PRO:HG2	1:B:26:LEU:H	1.85	0.41
1:B:215:MET:HB2	1:B:326:SER:HB2	2.03	0.41
1:A:93:PRO:HG3	1:A:561:TYR:HB2	2.02	0.40
1:A:303:CYS:HG	1:A:311:CYS:CB	2.34	0.40
1:B:510:LYS:O	1:B:513:SER:HB3	2.21	0.40
1:A:84:SER:OG	1:A:87:GLU:HG3	2.21	0.40
1:A:85:ILE:HD12	1:A:120:ARG:CZ	2.51	0.40
1:A:348:ALA:N	1:A:349:PRO:CD	2.83	0.40
1:B:22:PRO:CB	1:B:24:ASN:ND2	2.84	0.40
1:B:523:ARG:NH1	1:B:534:LEU:HD23	2.35	0.40

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	555/576 (96%)	543 (98%)	11 (2%)	1 (0%)	44	42
1	B	554/576 (96%)	536 (97%)	14 (2%)	4 (1%)	19	14
All	All	1109/1152 (96%)	1079 (97%)	25 (2%)	5 (0%)	25	21

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	154	ARG
1	B	27	SER
1	B	26	LEU
1	A	82	LEU
1	B	25	PRO

### 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	477/491 (97%)	473 (99%)	4 (1%)	79	84
1	B	475/491 (97%)	471 (99%)	4 (1%)	79	84
All	All	952/982 (97%)	944 (99%)	8 (1%)	79	84

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LYS

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Mol	Chain	Res	Type
1	A	184	GLN
1	A	336	LEU
1	A	402	HIS
1	B	57	LEU
1	B	222	ARG
1	B	531	ARG
1	B	534	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	GLN
1	A	273	ASN
1	A	438	GLN
1	A	502	HIS
1	A	544	GLN
1	A	562	HIS
1	B	110	ASN
1	B	251	GLN
1	B	273	ASN
1	B	309	GLN
1	B	406	ASN
1	B	438	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](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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	1JE	A	601	-	17,24,24	1.96	4 (23%)	18,36,36	1.74	5 (27%)
3	SO4	B	602	-	4,4,4	0.38	0	6,6,6	0.09	0
3	SO4	A	602	-	4,4,4	0.36	0	6,6,6	0.10	0
2	1JE	B	601	-	17,24,24	2.00	5 (29%)	18,36,36	1.75	5 (27%)

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	1JE	A	601	-	-	0/9/22/22	0/3/3/3
2	1JE	B	601	-	-	0/9/22/22	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	1JE	C9-C6	5.06	1.49	1.41
2	B	601	1JE	C9-C6	4.94	1.48	1.41
2	B	601	1JE	C4-C5	3.09	1.43	1.36
2	B	601	1JE	C4-C3	3.04	1.43	1.38
2	A	601	1JE	C4-C5	2.83	1.42	1.36
2	B	601	1JE	C3-C2	2.79	1.42	1.36
2	A	601	1JE	C3-C2	2.61	1.42	1.36
2	A	601	1JE	C4-C3	2.56	1.42	1.38
2	B	601	1JE	O11-C12	2.04	1.47	1.44

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	1JE	C9-C6-C1	-3.76	104.67	110.65
2	A	601	1JE	C9-C6-C1	-3.71	104.76	110.65
2	B	601	1JE	C3-C2-C1	-3.17	118.79	121.08
2	A	601	1JE	C3-C2-C1	-3.07	118.86	121.08

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	1JE	C1-C2-CL1	2.74	121.42	118.97
2	B	601	1JE	C4-C5-C6	-2.48	118.91	122.36
2	A	601	1JE	C4-C5-C6	-2.35	119.10	122.36
2	B	601	1JE	C1-C2-CL1	2.31	121.04	118.97
2	B	601	1JE	C12-O11-C10	2.23	117.71	114.60
2	A	601	1JE	C12-O11-C10	2.12	117.56	114.60

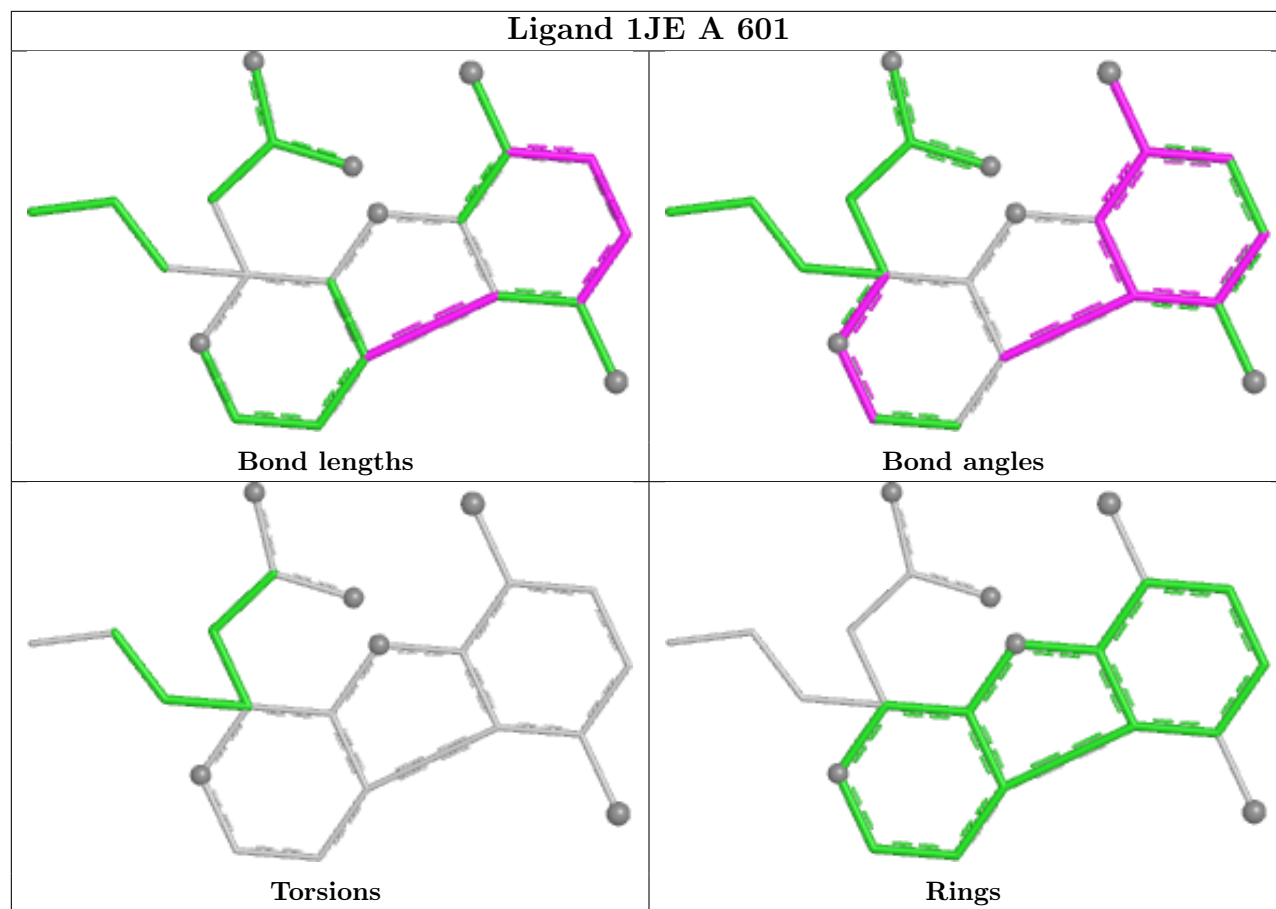
There are no chirality outliers.

There are no torsion outliers.

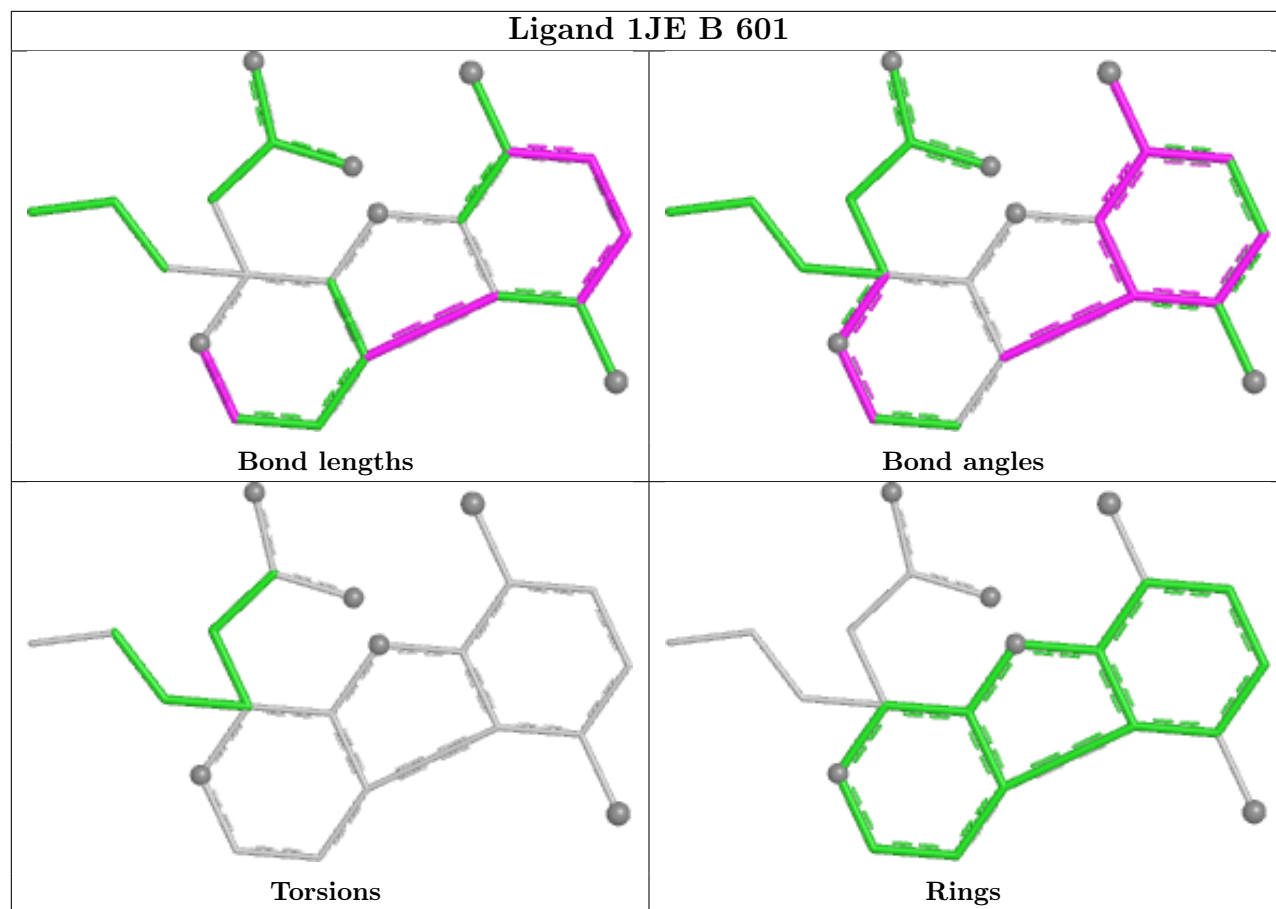
There are no ring outliers.

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	559/576 (97%)	-0.06	23 (4%)	42	40	14, 25, 44, 76	0
1	B	558/576 (96%)	0.38	63 (11%)	11	10	15, 29, 62, 79	0
All	All	1117/1152 (96%)	0.16	86 (7%)	21	19	14, 27, 55, 79	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	27	SER	5.4
1	A	563	SER	5.1
1	A	149	PRO	5.0
1	B	153	GLY	4.7
1	B	24	ASN	4.7
1	A	545	LEU	4.6
1	B	563	SER	4.6
1	A	81	LYS	4.6
1	B	26	LEU	4.5
1	B	23	ILE	4.5
1	B	545	LEU	4.5
1	B	25	PRO	4.3
1	B	534	LEU	4.2
1	B	532	THR	4.2
1	B	513	SER	4.0
1	B	29	SER	4.0
1	B	548	SER	4.0
1	B	542	ALA	3.9
1	A	542	ALA	3.6
1	A	366	CYS	3.6
1	A	547	LEU	3.5
1	B	544	GLN	3.4
1	B	154	ARG	3.3
1	B	367	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	402	HIS	3.2
1	B	547	LEU	3.1
1	B	538	PRO	3.0
1	B	540	PRO	3.0
1	B	535	LYS	3.0
1	B	530	VAL	3.0
1	B	536	LEU	2.8
1	A	381	VAL	2.8
1	B	543	SER	2.6
1	B	515	GLY	2.6
1	A	352	ASP	2.6
1	B	512	LEU	2.6
1	B	381	VAL	2.6
1	A	148	GLN	2.6
1	A	82	LEU	2.6
1	A	544	GLN	2.5
1	B	453	SER	2.5
1	B	366	CYS	2.5
1	B	531	ARG	2.5
1	B	546	ASP	2.5
1	B	57	LEU	2.4
1	B	523	ARG	2.4
1	A	541	ALA	2.4
1	B	524	TYR	2.4
1	B	522	GLY	2.4
1	B	549	GLY	2.4
1	B	310	ASP	2.4
1	B	537	THR	2.4
1	A	562	HIS	2.3
1	B	448	TYR	2.3
1	B	452	TYR	2.3
1	B	562	HIS	2.3
1	A	404	PRO	2.3
1	A	548	SER	2.3
1	B	365	SER	2.3
1	B	28	ASN	2.3
1	B	541	ALA	2.3
1	B	516	GLY	2.2
1	B	436	GLN	2.2
1	B	439	LEU	2.2
1	B	511	LEU	2.2
1	A	543	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	377	SER	2.2
1	A	113	SER	2.1
1	A	535	LYS	2.1
1	B	359	ASP	2.1
1	A	367	SER	2.1
1	B	404	PRO	2.1
1	B	501	ARG	2.1
1	A	86	GLU	2.1
1	B	403	THR	2.1
1	B	454	ILE	2.1
1	B	309	GLN	2.1
1	A	540	PRO	2.0
1	B	376	ALA	2.0
1	B	380	ARG	2.0
1	B	533	LYS	2.0
1	B	539	ILE	2.0
1	B	435	ALA	2.0
1	B	550	TRP	2.0
1	B	14	CYS	2.0
1	B	147	VAL	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(Å <sup>2</sup> )	Q<0.9
4	NA	B	603	1/1	0.78	0.17	39,39,39,39	0
3	SO4	B	602	5/5	0.79	0.17	68,68,68,68	0
3	SO4	A	602	5/5	0.82	0.20	73,73,74,74	0

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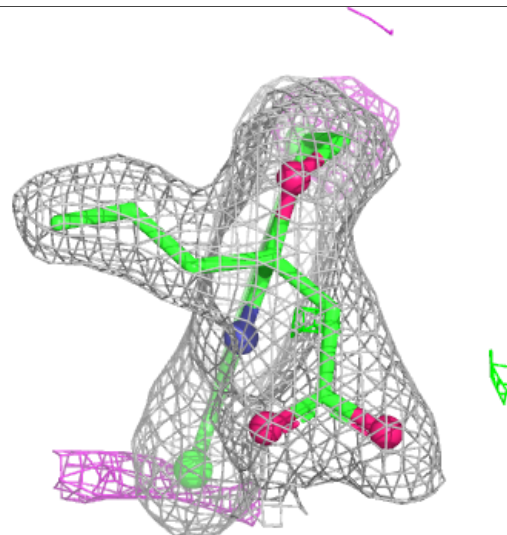
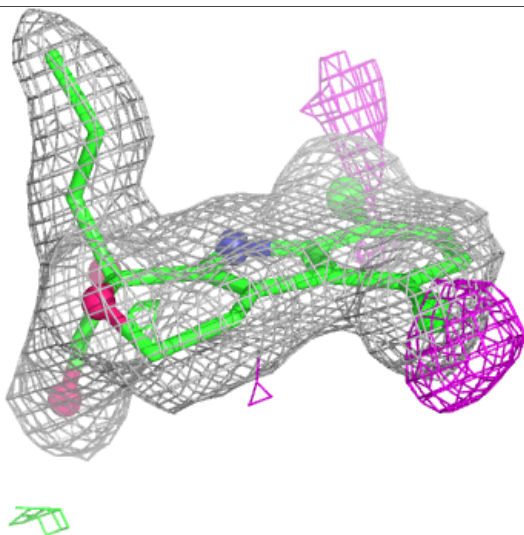
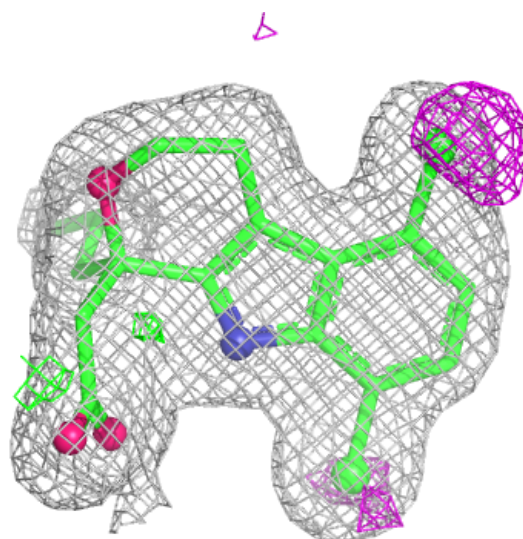
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	1JE	B	601	22/22	0.90	0.10	31,35,38,42	0
4	NA	A	603	1/1	0.92	0.10	36,36,36,36	0
2	1JE	A	601	22/22	0.95	0.08	23,26,31,32	0

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.

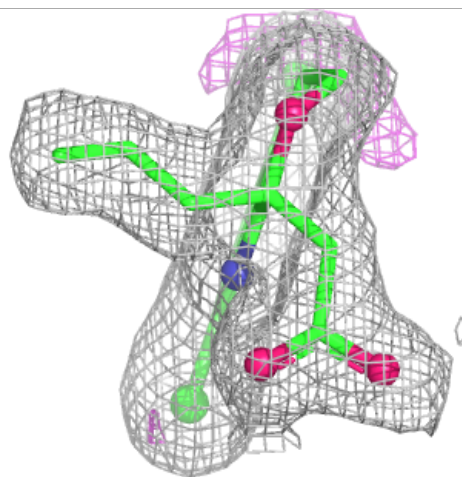
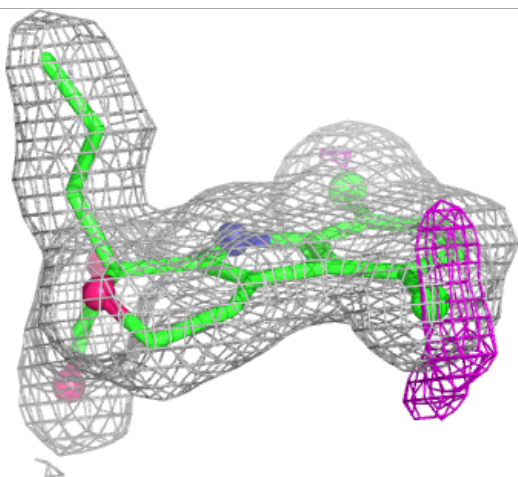
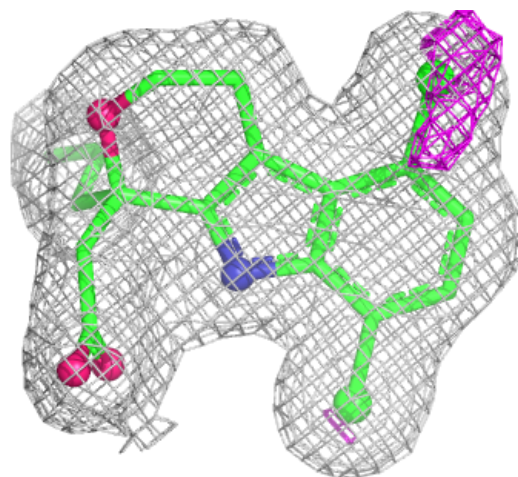
**Electron density around 1JE B 601:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 1JE 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)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.