



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 02:32 AM UTC

PDB ID : 6DFN / pdb_00006dfn
Title : Crystal structure of estrogen receptor alpha in complex with receptor degrader 16aa
Authors : Kiefer, J.R.; Vinogradova, M.; Liang, J.; Zhang, B.; Ortwine, D.F.; Nettles, K.W.; Nwachukwu, J.C.
Deposited on : 2018-05-15
Resolution : 2.10 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

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>.

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)
Xtriage (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

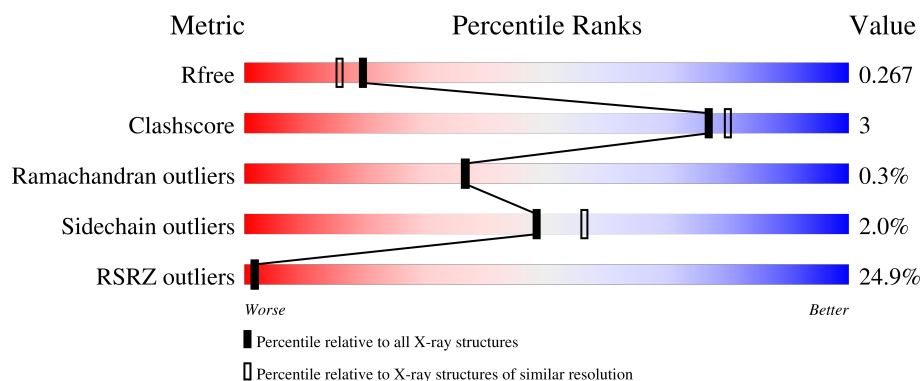
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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 ≥ 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	280	20% 78% 5% 16%
1	B	280	20% 71% 6% 22%
1	C	280	18% 77% • 19%
1	D	280	21% 70% 8% 21%

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
5	GOL	B	604	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7249 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	234	Total	C	N	O	S	0	1	0
			1833	1176	308	330	19			
1	B	218	Total	C	N	O	S	0	2	0
			1690	1076	295	303	16			
1	C	228	Total	C	N	O	S	0	0	0
			1761	1130	301	313	17			
1	D	221	Total	C	N	O	S	0	2	0
			1724	1103	295	307	19			

There are 104 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	274	MET	-	initiating methionine	UNP P03372
A	275	HIS	-	expression tag	UNP P03372
A	276	HIS	-	expression tag	UNP P03372
A	277	HIS	-	expression tag	UNP P03372
A	278	HIS	-	expression tag	UNP P03372
A	279	HIS	-	expression tag	UNP P03372
A	280	HIS	-	expression tag	UNP P03372
A	281	SER	-	expression tag	UNP P03372
A	282	SER	-	expression tag	UNP P03372
A	283	GLY	-	expression tag	UNP P03372
A	284	VAL	-	expression tag	UNP P03372
A	285	ASP	-	expression tag	UNP P03372
A	286	LEU	-	expression tag	UNP P03372
A	287	GLY	-	expression tag	UNP P03372
A	288	THR	-	expression tag	UNP P03372
A	289	GLU	-	expression tag	UNP P03372
A	290	ASN	-	expression tag	UNP P03372
A	291	LEU	-	expression tag	UNP P03372
A	292	TYR	-	expression tag	UNP P03372
A	293	PHE	-	expression tag	UNP P03372
A	294	GLN	-	expression tag	UNP P03372

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Chain	Residue	Modelled	Actual	Comment	Reference
A	295	SER	-	expression tag	UNP P03372
A	296	ASN	-	expression tag	UNP P03372
A	297	ALA	-	expression tag	UNP P03372
A	372	SER	LEU	conflict	UNP P03372
A	536	SER	LEU	conflict	UNP P03372
B	274	MET	-	initiating methionine	UNP P03372
B	275	HIS	-	expression tag	UNP P03372
B	276	HIS	-	expression tag	UNP P03372
B	277	HIS	-	expression tag	UNP P03372
B	278	HIS	-	expression tag	UNP P03372
B	279	HIS	-	expression tag	UNP P03372
B	280	HIS	-	expression tag	UNP P03372
B	281	SER	-	expression tag	UNP P03372
B	282	SER	-	expression tag	UNP P03372
B	283	GLY	-	expression tag	UNP P03372
B	284	VAL	-	expression tag	UNP P03372
B	285	ASP	-	expression tag	UNP P03372
B	286	LEU	-	expression tag	UNP P03372
B	287	GLY	-	expression tag	UNP P03372
B	288	THR	-	expression tag	UNP P03372
B	289	GLU	-	expression tag	UNP P03372
B	290	ASN	-	expression tag	UNP P03372
B	291	LEU	-	expression tag	UNP P03372
B	292	TYR	-	expression tag	UNP P03372
B	293	PHE	-	expression tag	UNP P03372
B	294	GLN	-	expression tag	UNP P03372
B	295	SER	-	expression tag	UNP P03372
B	296	ASN	-	expression tag	UNP P03372
B	297	ALA	-	expression tag	UNP P03372
B	372	SER	LEU	conflict	UNP P03372
B	536	SER	LEU	conflict	UNP P03372
C	274	MET	-	initiating methionine	UNP P03372
C	275	HIS	-	expression tag	UNP P03372
C	276	HIS	-	expression tag	UNP P03372
C	277	HIS	-	expression tag	UNP P03372
C	278	HIS	-	expression tag	UNP P03372
C	279	HIS	-	expression tag	UNP P03372
C	280	HIS	-	expression tag	UNP P03372
C	281	SER	-	expression tag	UNP P03372
C	282	SER	-	expression tag	UNP P03372
C	283	GLY	-	expression tag	UNP P03372
C	284	VAL	-	expression tag	UNP P03372

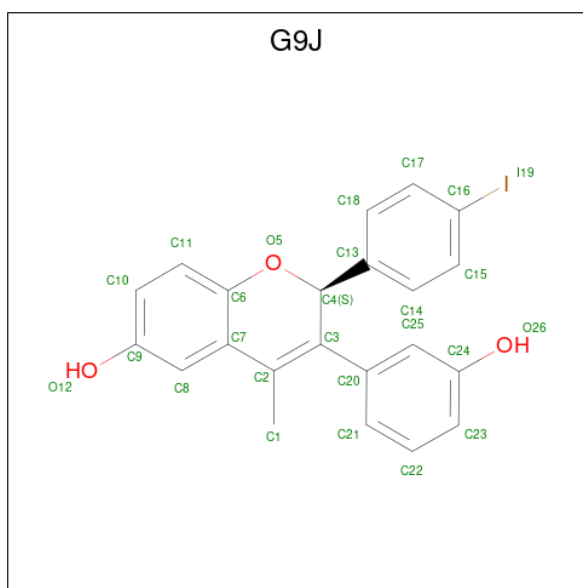
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Chain	Residue	Modelled	Actual	Comment	Reference
C	285	ASP	-	expression tag	UNP P03372
C	286	LEU	-	expression tag	UNP P03372
C	287	GLY	-	expression tag	UNP P03372
C	288	THR	-	expression tag	UNP P03372
C	289	GLU	-	expression tag	UNP P03372
C	290	ASN	-	expression tag	UNP P03372
C	291	LEU	-	expression tag	UNP P03372
C	292	TYR	-	expression tag	UNP P03372
C	293	PHE	-	expression tag	UNP P03372
C	294	GLN	-	expression tag	UNP P03372
C	295	SER	-	expression tag	UNP P03372
C	296	ASN	-	expression tag	UNP P03372
C	297	ALA	-	expression tag	UNP P03372
C	372	SER	LEU	conflict	UNP P03372
C	536	SER	LEU	conflict	UNP P03372
D	274	MET	-	initiating methionine	UNP P03372
D	275	HIS	-	expression tag	UNP P03372
D	276	HIS	-	expression tag	UNP P03372
D	277	HIS	-	expression tag	UNP P03372
D	278	HIS	-	expression tag	UNP P03372
D	279	HIS	-	expression tag	UNP P03372
D	280	HIS	-	expression tag	UNP P03372
D	281	SER	-	expression tag	UNP P03372
D	282	SER	-	expression tag	UNP P03372
D	283	GLY	-	expression tag	UNP P03372
D	284	VAL	-	expression tag	UNP P03372
D	285	ASP	-	expression tag	UNP P03372
D	286	LEU	-	expression tag	UNP P03372
D	287	GLY	-	expression tag	UNP P03372
D	288	THR	-	expression tag	UNP P03372
D	289	GLU	-	expression tag	UNP P03372
D	290	ASN	-	expression tag	UNP P03372
D	291	LEU	-	expression tag	UNP P03372
D	292	TYR	-	expression tag	UNP P03372
D	293	PHE	-	expression tag	UNP P03372
D	294	GLN	-	expression tag	UNP P03372
D	295	SER	-	expression tag	UNP P03372
D	296	ASN	-	expression tag	UNP P03372
D	297	ALA	-	expression tag	UNP P03372
D	372	SER	LEU	conflict	UNP P03372
D	536	SER	LEU	conflict	UNP P03372

- Molecule 2 is (2S)-3-(3-hydroxyphenyl)-2-(4-iodophenyl)-4-methyl-2H-1-benzopyran-6-ol

(CCD ID: G9J) (formula: C₂₂H₁₇IO₃).

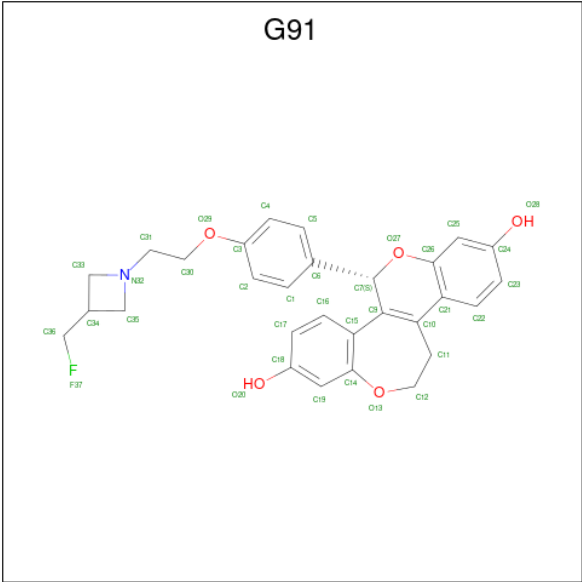


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	I	O	0	0
			26	22	1	3		
2	B	1	Total	C	I	O	0	1
			26	22	1	3		
2	C	1	Total	C	I	O	0	0
			26	22	1	3		
2	D	1	Total	C	I	O	0	1
			26	22	1	3		

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

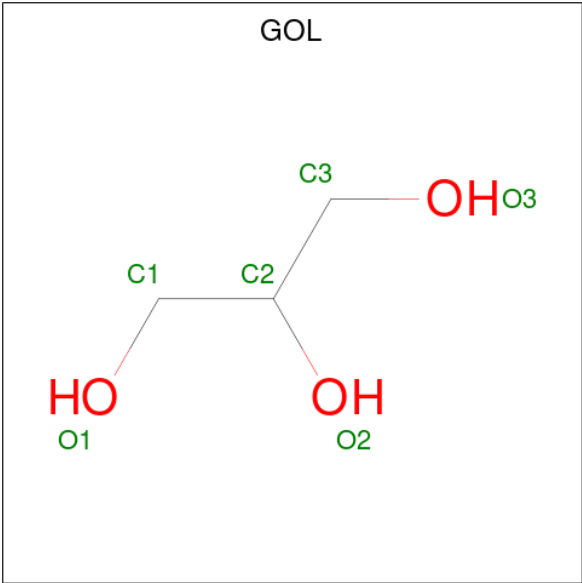
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Ni	0	0
			1	1		

- Molecule 4 is (8S)-8-(4-{2-[3-(fluoromethyl)azetidin-1-yl]ethoxy}phenyl)-1,8-dihydro-2H-[1]benzopyrano[4,3-d][1]benzoxepine-5,11-diol (CCD ID: G91) (formula: C₂₉H₂₈FNO₅).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	F	N	O	0	1
			36	29	1	1	5		
4	D	1	Total	C	F	N	O	0	1
			36	29	1	1	5		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			6	3	3		

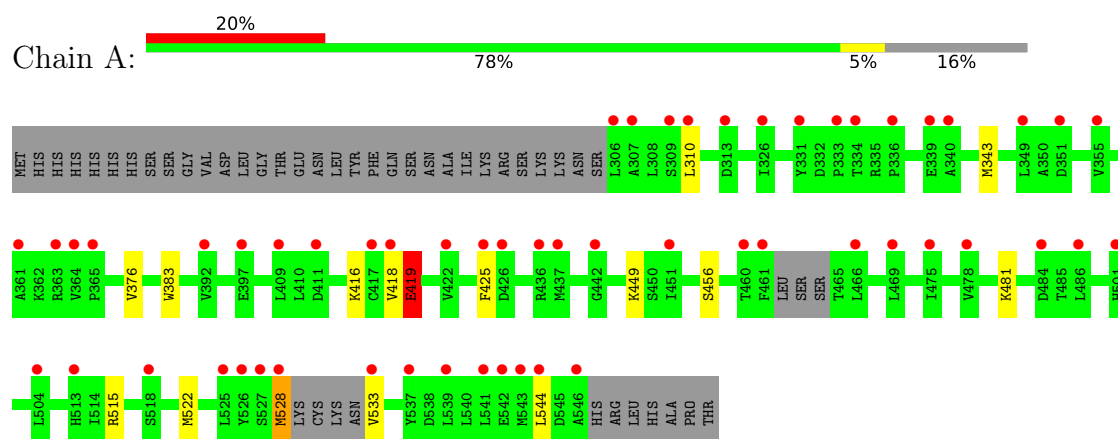
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	16	Total	O	0	1
			17	17		
6	B	9	Total	O	0	0
			9	9		
6	C	10	Total	O	0	0
			10	10		
6	D	10	Total	O	0	0
			10	10		

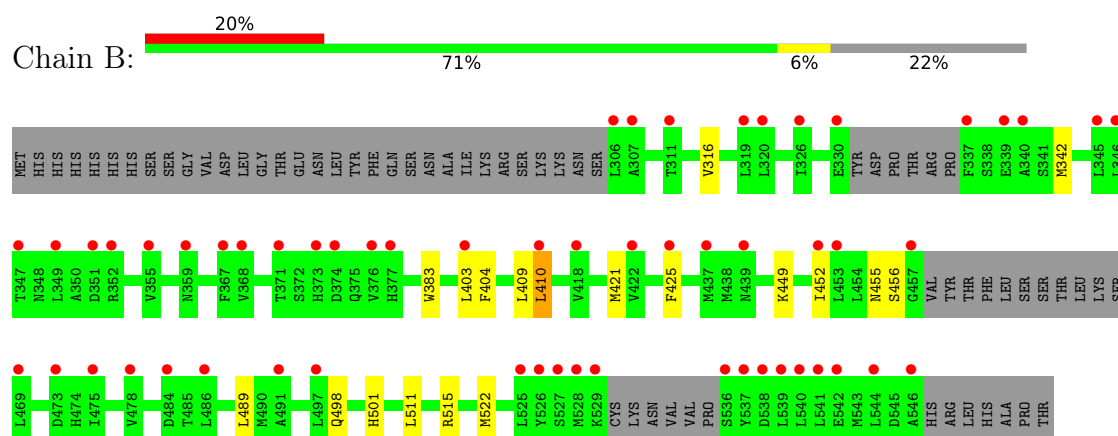
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

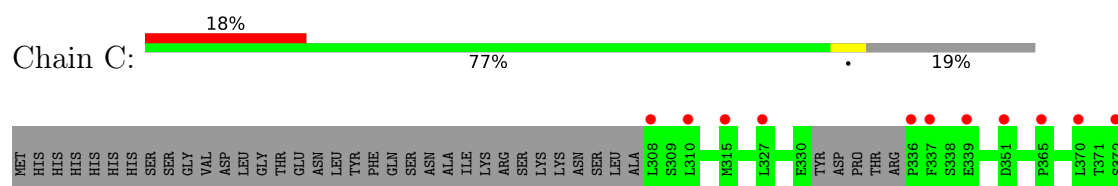
• Molecule 1: Estrogen receptor

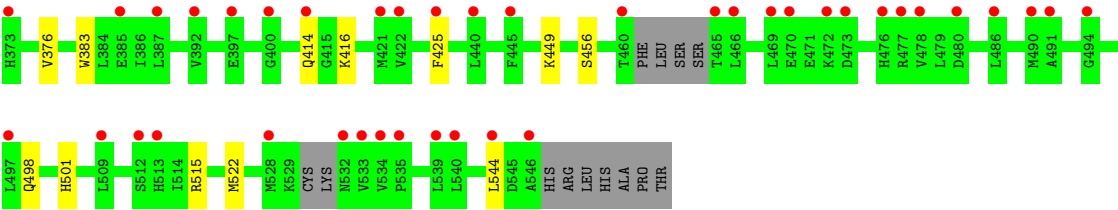


• Molecule 1: Estrogen receptor

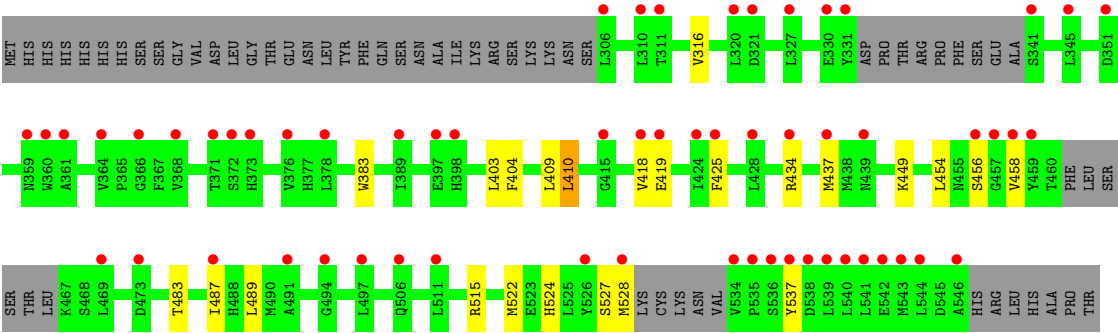


• Molecule 1: Estrogen receptor





● Molecule 1: Estrogen receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.09Å 59.13Å 94.18Å 86.05° 74.92° 63.34°	Depositor
Resolution (Å)	29.47 – 2.10 29.47 – 2.10	Depositor EDS
% Data completeness (in resolution range)	89.2 (29.47-2.10) 94.0 (29.47-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.35 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.247 , 0.265 0.255 , 0.267	Depositor DCC
R_{free} test set	2737 reflections (4.28%)	wwPDB-VP
Wilson B-factor (Å ²)	49.4	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.40$	Xtriage
Estimated twinning fraction	0.148 for h,h-k,h-l	Xtriage
Reported twinning fraction	0.839 for H, K, L 0.161 for H, H-K, H-L	Depositor
Outliers	0 of 54118 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7249	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: G9J, NI, G91, GOL

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	0.56	0/1866	0.89	0/2524
1	B	0.55	0/1715	0.89	0/2317
1	C	0.56	0/1791	0.89	0/2422
1	D	0.58	0/1751	0.90	0/2366
All	All	0.56	0/7123	0.89	0/9629

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1833	0	1839	10	0
1	B	1690	0	1686	13	0
1	C	1761	0	1772	4	0
1	D	1724	0	1733	13	0
2	A	26	0	0	1	0
2	B	26	0	0	0	0
2	C	26	0	0	0	0
2	D	26	0	0	1	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	36	0	0	0	0
4	D	36	0	0	0	0
5	B	12	0	16	6	0
5	D	6	0	8	0	0
6	A	17	0	0	0	0
6	B	9	0	0	0	0
6	C	10	0	0	0	0
6	D	10	0	0	0	0
All	All	7249	0	7054	41	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 3.

All (41) 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:343:MET:HE2	1:A:528[A]:MET:HE1	1.62	0.82
1:D:483:THR:O	1:D:487:ILE:HD12	1.81	0.80
1:A:310:LEU:O	1:A:481:LYS:HE3	1.96	0.65
1:A:310:LEU:O	1:A:481:LYS:CE	2.47	0.62
1:B:452:ILE:HG12	5:B:604:GOL:C3	2.34	0.57
1:D:404:PHE:CD2	1:D:410:LEU:HD22	2.45	0.52
1:B:452:ILE:HG12	5:B:604:GOL:H31	1.91	0.52
1:B:404:PHE:CD2	1:B:410:LEU:HD22	2.45	0.52
1:A:418:VAL:CG1	1:A:528[B]:MET:HE1	2.41	0.50
1:B:455:ASN:HD22	5:B:604:GOL:C1	2.24	0.50
1:D:483:THR:O	1:D:487:ILE:CD1	2.56	0.50
1:A:418:VAL:HG13	1:A:528[B]:MET:HE1	1.94	0.49
1:B:455:ASN:HD22	5:B:604:GOL:H12	1.76	0.49
1:D:418:VAL:HG13	1:D:528:MET:HE1	1.96	0.48
1:B:403:LEU:HD12	1:B:409:LEU:HD13	1.94	0.48
1:B:511:LEU:HB3	5:B:604:GOL:O2	2.13	0.48
1:D:403:LEU:HD12	1:D:409:LEU:HD13	1.95	0.47
2:D:601[B]:G9J:C21	2:D:601[B]:G9J:C1	2.94	0.46
1:A:383:TRP:CE2	1:A:522:MET:HE1	2.52	0.45
1:B:383:TRP:CE2	1:B:522:MET:HE1	2.52	0.45
1:C:383:TRP:CE2	1:C:522:MET:HE1	2.52	0.45
1:B:342:MET:CE	1:B:421:MET:CE	2.95	0.44
1:D:383:TRP:CE2	1:D:522:MET:HE1	2.52	0.44
1:B:452:ILE:HG12	5:B:604:GOL:H32	1.99	0.44
1:D:418:VAL:CG1	1:D:528:MET:HE1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:454:LEU:O	1:D:458:VAL:CG2	2.66	0.43
1:B:498:GLN:HA	1:B:501:HIS:CE1	2.53	0.43
1:C:498:GLN:HA	1:C:501:HIS:CE1	2.53	0.43
1:B:456:SER:HA	1:B:515:ARG:NH2	2.34	0.42
1:D:456:SER:HA	1:D:515:ARG:NH2	2.35	0.42
1:A:376:VAL:HG22	1:A:544:LEU:HD12	2.02	0.41
1:D:524:HIS:O	1:D:527:SER:OG	2.33	0.41
1:A:418:VAL:O	1:A:419:GLU:CB	2.68	0.41
1:B:316:VAL:HG21	1:B:489:LEU:HD21	2.03	0.41
1:A:533:VAL:O	2:A:601:G9J:I19	3.09	0.41
1:A:456:SER:HA	1:A:515:ARG:NH2	2.36	0.41
1:C:376:VAL:HG22	1:C:544:LEU:HD12	2.04	0.40
1:D:383:TRP:CZ2	1:D:522:MET:HE1	2.56	0.40
1:D:434:ARG:HA	1:D:437[B]:MET:HG2	2.03	0.40
1:C:456:SER:HA	1:C:515:ARG:NH2	2.36	0.40
1:D:316:VAL:HG21	1:D:489:LEU:HD21	2.04	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	228/280 (81%)	225 (99%)	2 (1%)	1 (0%)	30	28
1	B	212/280 (76%)	211 (100%)	1 (0%)	0	100	100
1	C	220/280 (79%)	218 (99%)	2 (1%)	0	100	100
1	D	215/280 (77%)	210 (98%)	3 (1%)	2 (1%)	14	10
All	All	875/1120 (78%)	864 (99%)	8 (1%)	3 (0%)	36	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	419	GLU
1	D	419	GLU
1	D	537	TYR

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	201/252 (80%)	195 (97%)	6 (3%)	36	41
1	B	180/252 (71%)	177 (98%)	3 (2%)	53	62
1	C	191/252 (76%)	187 (98%)	4 (2%)	47	54
1	D	187/252 (74%)	184 (98%)	3 (2%)	55	64
All	All	759/1008 (75%)	743 (98%)	16 (2%)	48	54

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	416	LYS
1	A	419	GLU
1	A	425	PHE
1	A	449	LYS
1	A	528[A]	MET
1	A	528[B]	MET
1	B	410	LEU
1	B	425	PHE
1	B	449	LYS
1	C	414	GLN
1	C	416	LYS
1	C	425	PHE
1	C	449	LYS
1	D	410	LEU
1	D	425	PHE
1	D	449	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	476	HIS
1	A	488	HIS
1	A	519	ASN
1	B	375	GLN
1	B	439	ASN
1	B	455	ASN
1	B	476	HIS
1	B	501	HIS
1	B	516	HIS
1	C	488	HIS
1	C	516	HIS
1	D	413	ASN
1	D	439	ASN
1	D	476	HIS
1	D	501	HIS
1	D	519	ASN
1	D	524	HIS

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 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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
4	G9I	D	602[A]	-	38,41,41	0.22	0	44,59,59	0.85	1 (2%)
5	GOL	B	603	-	5,5,5	0.36	0	5,5,5	0.26	0
5	GOL	D	603	-	5,5,5	0.34	0	5,5,5	0.15	0
2	G9J	A	601	-	29,29,29	0.81	1 (3%)	39,42,42	1.00	0
4	G9I	B	601[A]	-	38,41,41	0.23	0	44,59,59	0.48	1 (2%)
5	GOL	B	604	-	5,5,5	0.22	0	5,5,5	0.50	0
2	G9J	C	601	-	29,29,29	0.88	1 (3%)	39,42,42	1.21	4 (10%)
2	G9J	B	602[B]	-	29,29,29	0.50	0	39,42,42	1.22	4 (10%)
2	G9J	D	601[B]	-	29,29,29	0.50	0	39,42,42	1.20	4 (10%)

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
4	G9I	D	602[A]	-	-	1/8/46/46	0/6/6/6
5	GOL	B	603	-	-	2/4/4/4	-
5	GOL	D	603	-	-	2/4/4/4	-
2	G9J	A	601	-	-	0/8/24/24	0/4/4/4
4	G9I	B	601[A]	-	-	0/8/46/46	0/6/6/6
5	GOL	B	604	-	-	2/4/4/4	-
2	G9J	C	601	-	-	0/8/24/24	0/4/4/4
2	G9J	B	602[B]	-	-	2/8/24/24	0/4/4/4
2	G9J	D	601[B]	-	-	0/8/24/24	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	601	G9J	C7-C2	2.71	1.50	1.46
2	A	601	G9J	C7-C2	2.09	1.49	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	602[A]	G9I	C6-C7-C9	-5.08	105.96	114.48
2	B	602[B]	G9J	C13-C4-C3	-3.94	107.88	114.48
2	D	601[B]	G9J	C13-C4-C3	-3.31	108.93	114.48
2	D	601[B]	G9J	C1-C2-C3	-3.08	120.57	124.43
2	B	602[B]	G9J	C1-C2-C3	-2.68	121.07	124.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	G9J	C13-C4-C3	-2.58	110.15	114.48
2	C	601	G9J	O5-C6-C7	-2.58	119.16	122.16
2	B	602[B]	G9J	O5-C6-C11	2.42	120.62	116.20
2	C	601	G9J	C21-C20-C3	-2.28	117.95	120.91
2	D	601[B]	G9J	O5-C6-C11	2.21	120.24	116.20
2	B	602[B]	G9J	O5-C6-C7	-2.16	119.65	122.16
2	C	601	G9J	C20-C3-C4	-2.08	113.48	116.18
4	B	601[A]	G91	C6-C7-C9	-2.04	111.05	114.48
2	D	601[B]	G9J	C1-C2-C7	2.04	120.81	118.49

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	604	GOL	O1-C1-C2-C3
5	D	603	GOL	C1-C2-C3-O3
5	D	603	GOL	O2-C2-C3-O3
5	B	603	GOL	C1-C2-C3-O3
5	B	603	GOL	O2-C2-C3-O3
5	B	604	GOL	O1-C1-C2-O2
2	B	602[B]	G9J	C25-C20-C3-C2
2	B	602[B]	G9J	C21-C20-C3-C2
4	D	602[A]	G91	O29-C30-C31-N32

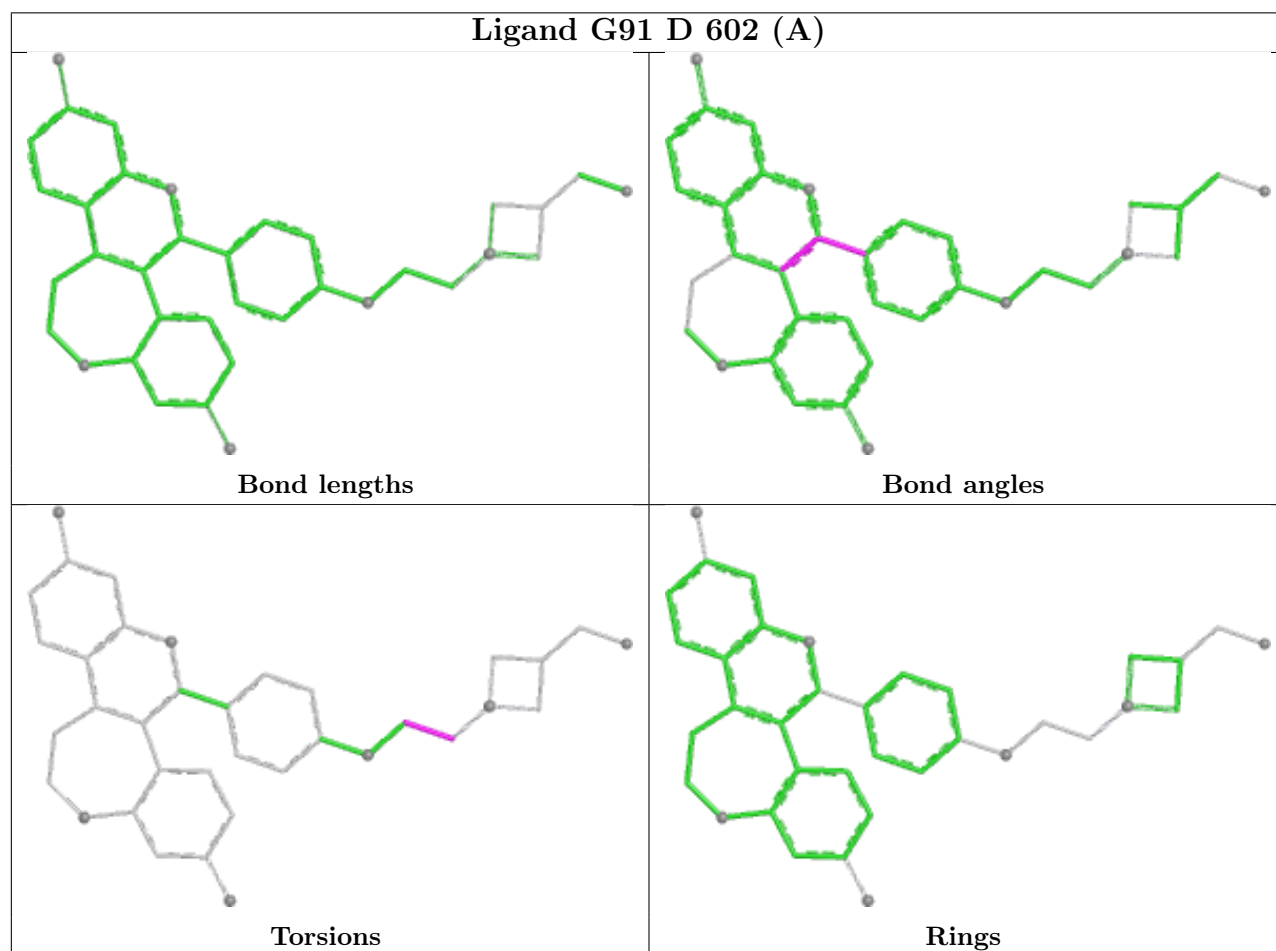
There are no ring outliers.

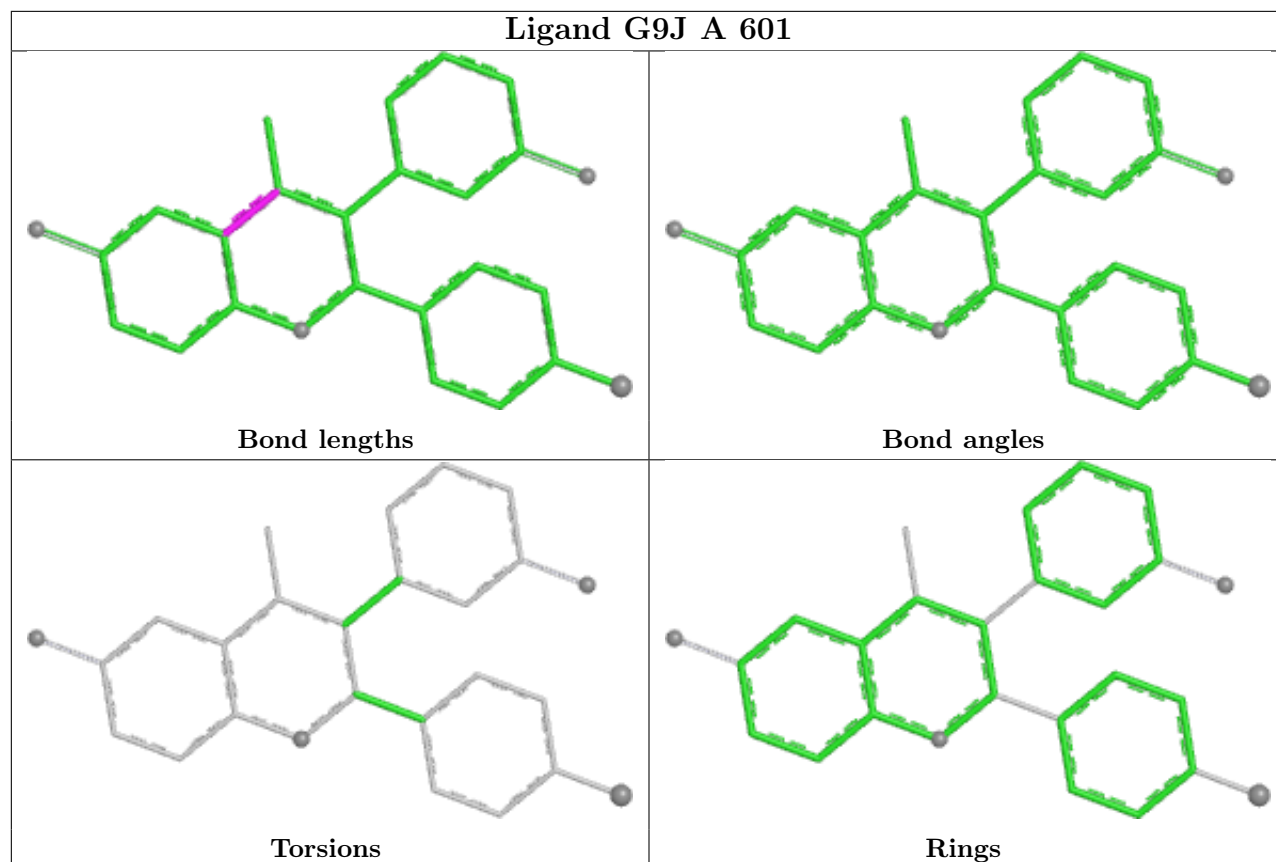
3 monomers are involved in 8 short contacts:

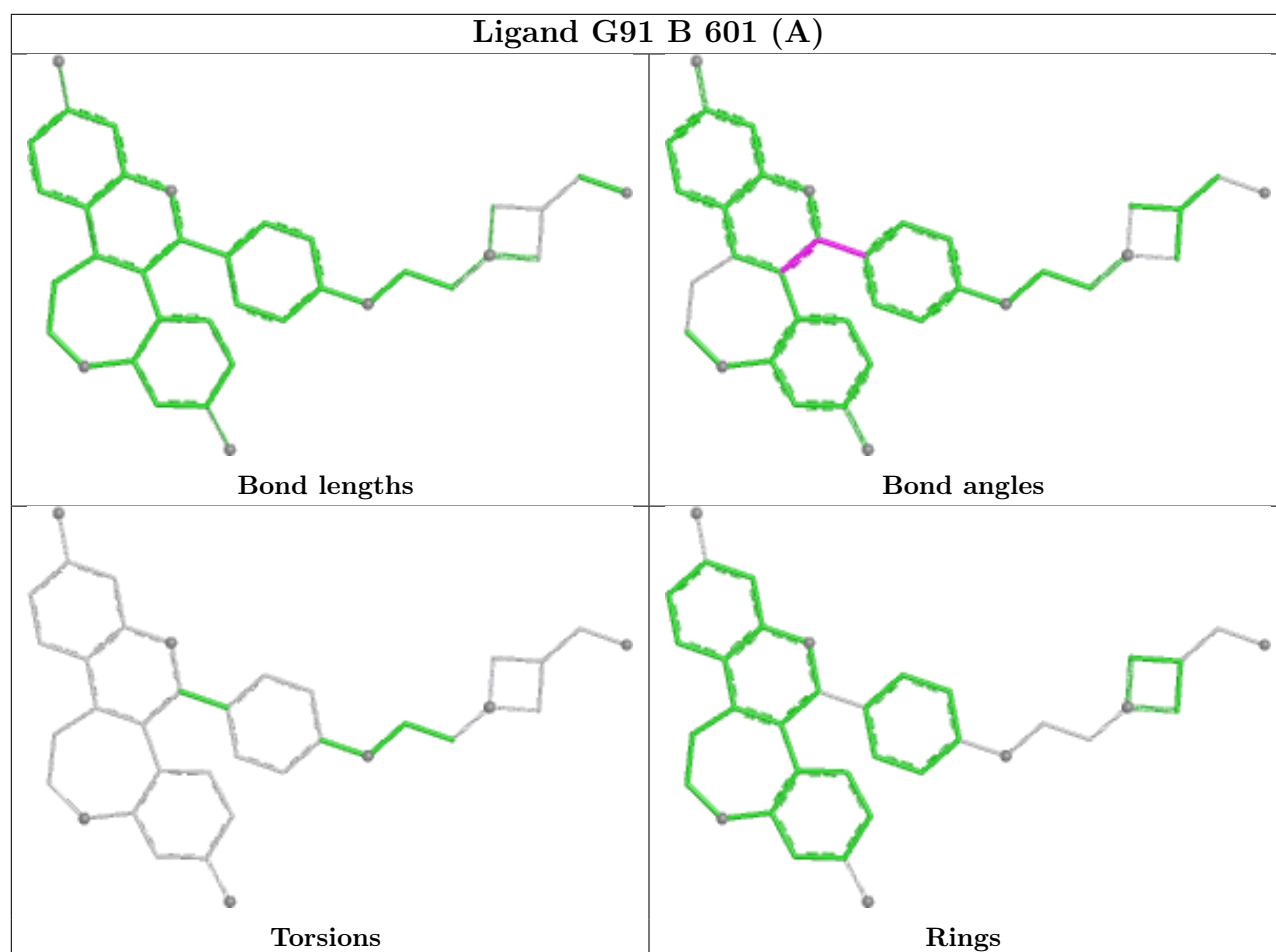
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	G9J	1	0
5	B	604	GOL	6	0
2	D	601[B]	G9J	1	0

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.

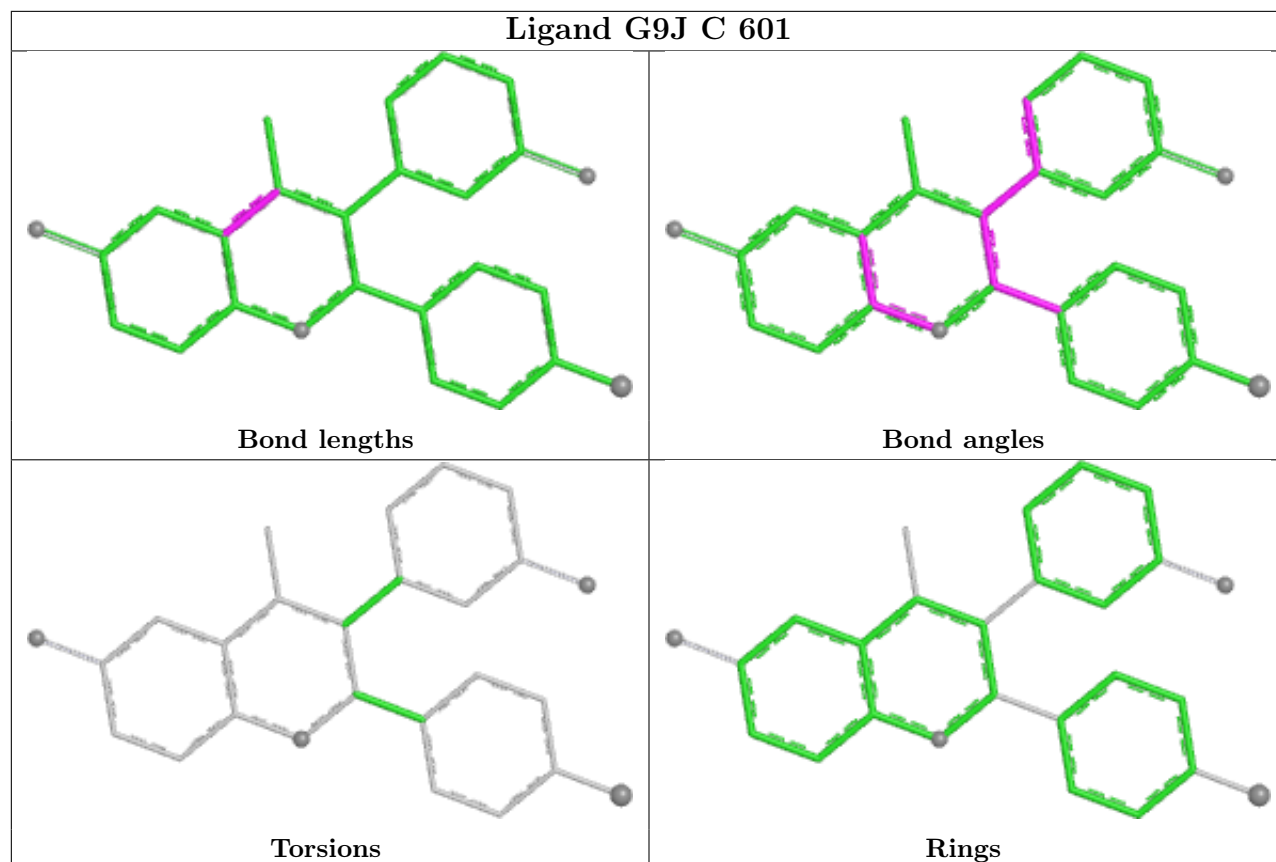
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



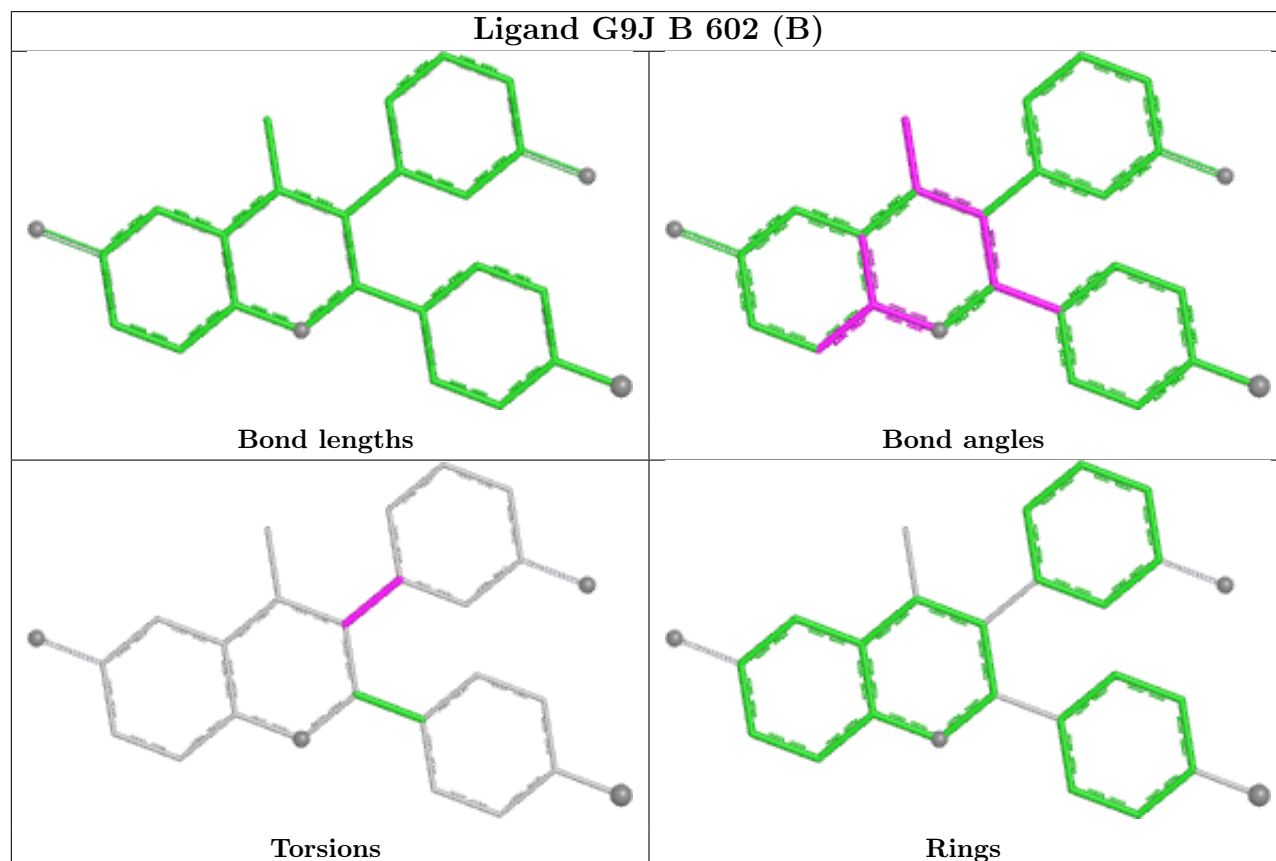


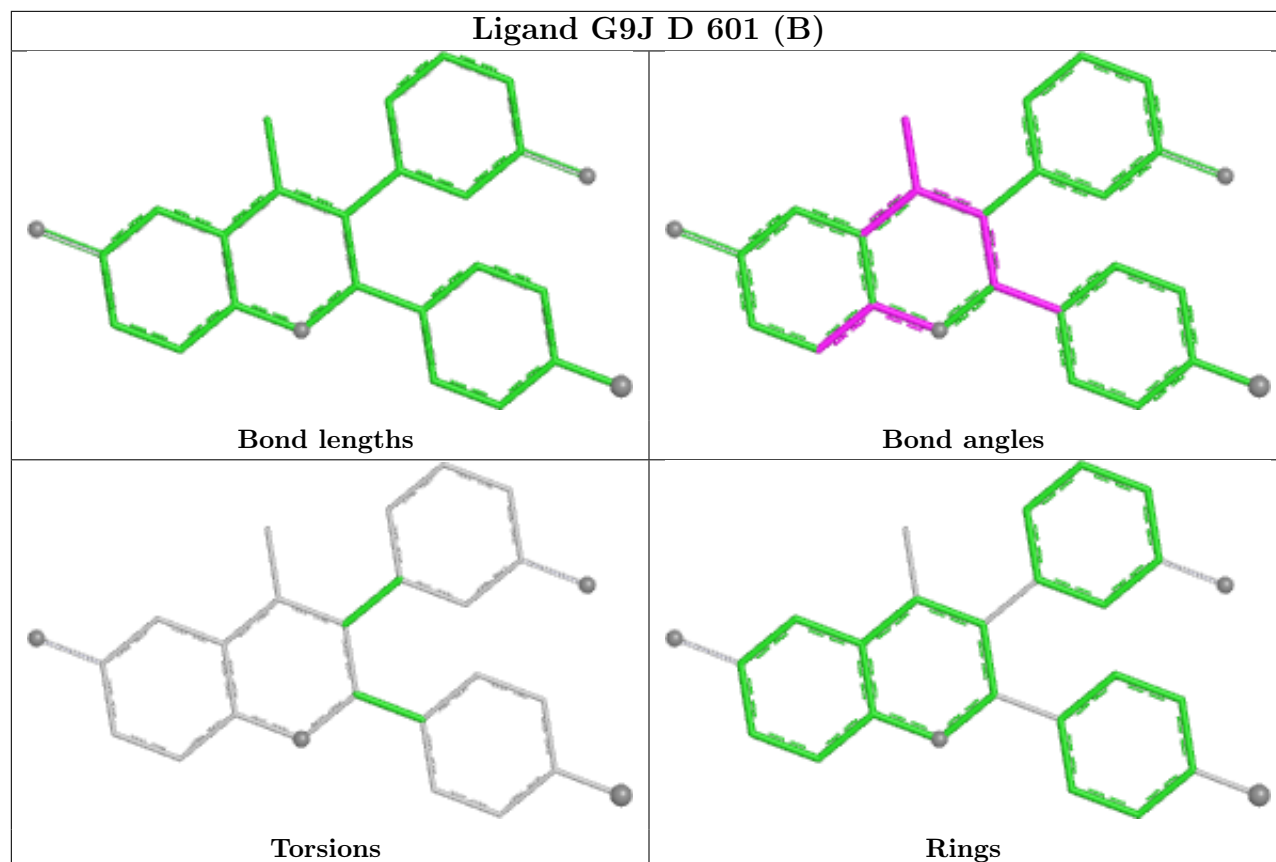


Ligand G9J C 601



Ligand G9J B 602 (B)





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, 95th 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 ²)	Q<0.9
1	A	234/280 (83%)	1.43	56 (23%)	2 2	41, 63, 96, 119	1 (0%)
1	B	218/280 (77%)	1.63	57 (26%)	1 1	28, 61, 106, 131	2 (0%)
1	C	228/280 (81%)	1.53	51 (22%)	2 2	42, 66, 90, 114	0
1	D	221/280 (78%)	1.58	60 (27%)	1 1	28, 60, 100, 122	2 (0%)
All	All	901/1120 (80%)	1.54	224 (24%)	2 2	28, 62, 97, 131	5 (0%)

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	540	LEU	6.5
1	D	425	PHE	5.9
1	B	306	LEU	5.8
1	C	546	ALA	5.6
1	B	340	ALA	5.5
1	C	336	PRO	5.4
1	A	546	ALA	4.9
1	C	308	LEU	4.8
1	D	368	VAL	4.7
1	A	437	MET	4.7
1	C	460	THR	4.6
1	D	458	VAL	4.2
1	B	541	LEU	4.2
1	C	532	ASN	4.2
1	B	544	LEU	4.2
1	C	544	LEU	4.2
1	D	546	ALA	4.1
1	D	306	LEU	4.1
1	C	351	ASP	4.0
1	B	337	PHE	4.0
1	B	537	TYR	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	533	VAL	4.0
1	A	542	GLU	3.9
1	B	527	SER	3.9
1	B	539	LEU	3.9
1	D	437[A]	MET	3.9
1	D	526	TYR	3.9
1	B	536	SER	3.9
1	D	439	ASN	3.8
1	B	469	LEU	3.8
1	B	351	ASP	3.8
1	D	535	PRO	3.7
1	C	470	GLU	3.7
1	B	377	HIS	3.7
1	D	537	TYR	3.7
1	A	307	ALA	3.7
1	A	528[A]	MET	3.6
1	C	469	LEU	3.5
1	C	497	LEU	3.5
1	D	320	LEU	3.5
1	D	542	GLU	3.5
1	B	425	PHE	3.5
1	B	546	ALA	3.5
1	B	320	LEU	3.5
1	B	473	ASP	3.5
1	A	336	PRO	3.4
1	D	341	SER	3.4
1	D	539	LEU	3.4
1	B	457	GLY	3.4
1	B	418	VAL	3.4
1	D	473	ASP	3.3
1	D	345	LEU	3.3
1	D	540	LEU	3.3
1	B	359	ASN	3.2
1	A	392	VAL	3.1
1	D	491	ALA	3.1
1	D	424	ILE	3.1
1	A	409	LEU	3.1
1	D	541	LEU	3.1
1	A	397	GLU	3.1
1	A	461	PHE	3.1
1	D	434	ARG	3.1
1	A	339	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	422	VAL	3.1
1	D	373	HIS	3.1
1	B	376	VAL	3.0
1	D	536	SER	3.0
1	B	475	ILE	3.0
1	A	537	TYR	3.0
1	D	321	ASP	3.0
1	C	337	PHE	3.0
1	A	486	LEU	3.0
1	C	440	LEU	3.0
1	D	378	LEU	3.0
1	B	528	MET	3.0
1	A	422	VAL	2.9
1	A	533	VAL	2.9
1	D	538	ASP	2.9
1	B	410	LEU	2.9
1	D	494	GLY	2.9
1	C	534	VAL	2.9
1	D	506	GLN	2.9
1	A	544	LEU	2.9
1	B	307	ALA	2.9
1	C	476	HIS	2.9
1	D	351	ASP	2.8
1	D	528	MET	2.8
1	B	349	LEU	2.8
1	B	311	THR	2.8
1	D	330	GLU	2.8
1	C	466	LEU	2.8
1	D	310	LEU	2.8
1	C	392	VAL	2.8
1	D	534	VAL	2.8
1	D	543	MET	2.8
1	D	371	THR	2.8
1	B	330	GLU	2.7
1	C	494	GLY	2.7
1	A	349	LEU	2.7
1	B	346	LEU	2.7
1	D	544	LEU	2.7
1	C	414	GLN	2.7
1	D	372	SER	2.7
1	C	400	GLY	2.7
1	C	491	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	361	ALA	2.7
1	A	460	THR	2.7
1	A	469	LEU	2.7
1	C	540	LEU	2.7
1	D	469	LEU	2.7
1	C	480	ASP	2.7
1	D	397	GLU	2.6
1	C	539	LEU	2.6
1	D	398	HIS	2.6
1	D	511	LEU	2.6
1	B	526	TYR	2.6
1	C	387	LEU	2.6
1	C	445	PHE	2.6
1	D	497	LEU	2.6
1	C	473	ASP	2.6
1	A	331	TYR	2.6
1	C	397	GLU	2.6
1	B	373	HIS	2.6
1	A	355	VAL	2.6
1	B	355	VAL	2.6
1	B	439	ASN	2.6
1	A	504	LEU	2.6
1	C	372	SER	2.6
1	B	542	GLU	2.5
1	B	374	ASP	2.5
1	C	465	THR	2.5
1	A	340	ALA	2.5
1	C	478	VAL	2.5
1	A	417	CYS	2.5
1	D	459	TYR	2.5
1	A	306	LEU	2.5
1	B	453	LEU	2.5
1	B	486	LEU	2.5
1	C	486	LEU	2.5
1	B	352[A]	ARG	2.5
1	C	513	HIS	2.5
1	D	389	ILE	2.5
1	B	339	GLU	2.4
1	B	452	ILE	2.4
1	A	365	PRO	2.4
1	A	539	LEU	2.4
1	B	367	PHE	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	472	LYS	2.4
1	A	475	ILE	2.4
1	A	436	ARG	2.4
1	C	315	MET	2.4
1	B	491	ALA	2.3
1	A	525	LEU	2.3
1	B	319	LEU	2.3
1	D	327	LEU	2.3
1	A	313	ASP	2.3
1	A	425	PHE	2.3
1	D	456	SER	2.3
1	A	513	HIS	2.3
1	C	535	PRO	2.3
1	A	526	TYR	2.3
1	A	442	GLY	2.3
1	C	310	LEU	2.3
1	D	457	GLY	2.3
1	A	364	VAL	2.3
1	C	422	VAL	2.3
1	D	376	VAL	2.3
1	A	333	PRO	2.3
1	A	310	LEU	2.3
1	B	345	LEU	2.3
1	D	366	GLY	2.3
1	C	490	MET	2.3
1	A	418	VAL	2.3
1	B	368	VAL	2.3
1	D	364	VAL	2.3
1	C	365	PRO	2.3
1	A	543	MET	2.3
1	B	437	MET	2.3
1	C	339	GLU	2.2
1	D	419	GLU	2.2
1	B	403	LEU	2.2
1	B	326	ILE	2.2
1	B	529	LYS	2.2
1	B	538	ASP	2.2
1	C	421	MET	2.2
1	C	528	MET	2.2
1	D	415	GLY	2.2
1	A	466	LEU	2.2
1	C	370	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	309	SER	2.2
1	A	351	ASP	2.2
1	C	385	GLU	2.2
1	A	411	ASP	2.2
1	A	426	ASP	2.2
1	A	451	ILE	2.1
1	D	360	TRP	2.1
1	C	373	HIS	2.1
1	A	541	LEU	2.1
1	B	497	LEU	2.1
1	D	428	LEU	2.1
1	A	334	THR	2.1
1	B	347	THR	2.1
1	A	326	ILE	2.1
1	A	363	ARG	2.1
1	D	487	ILE	2.1
1	C	425	PHE	2.1
1	B	478	VAL	2.1
1	C	327	LEU	2.1
1	A	501	HIS	2.1
1	C	477	ARG	2.1
1	A	478	VAL	2.1
1	A	361	ALA	2.1
1	A	527	SER	2.1
1	C	509	LEU	2.0
1	A	484	ASP	2.0
1	D	311	THR	2.0
1	D	331	TYR	2.0
1	D	418	VAL	2.0
1	A	518	SER	2.0
1	C	512	SER	2.0
1	D	359	ASN	2.0
1	B	525	LEU	2.0
1	B	484	ASP	2.0
1	B	371	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

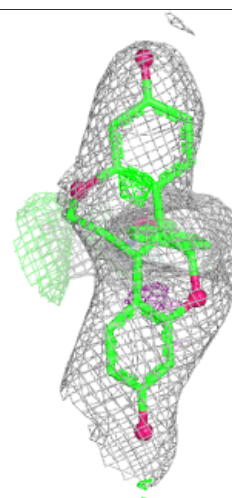
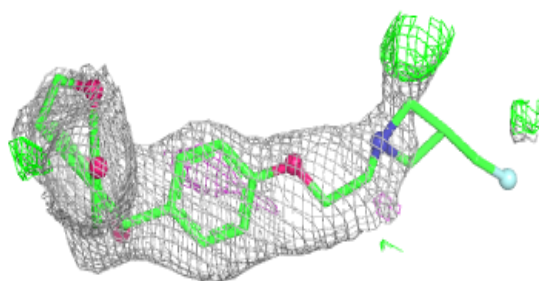
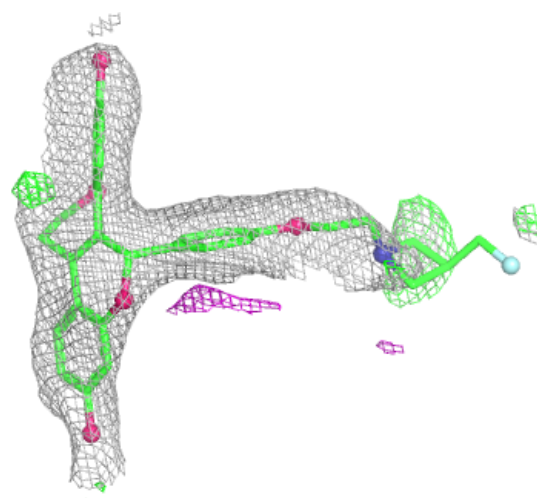
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
5	GOL	B	603	6/6	0.44	0.20	85,86,87,87	0
3	NI	A	602	1/1	0.54	0.17	159,159,159,159	0
5	GOL	B	604	6/6	0.73	0.21	73,74,76,77	0
4	G9I	B	601[A]	36/36	0.76	0.16	42,50,61,61	36
4	G9I	D	602[A]	36/36	0.80	0.17	57,60,69,70	36
5	GOL	D	603	6/6	0.84	0.11	64,66,68,69	0
2	G9J	B	602[B]	26/26	0.91	0.15	60,64,71,82	26
2	G9J	A	601	26/26	0.92	0.14	48,53,64,68	0
2	G9J	C	601	26/26	0.92	0.15	49,56,68,73	0
2	G9J	D	601[B]	26/26	0.93	0.13	53,55,61,71	26

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.

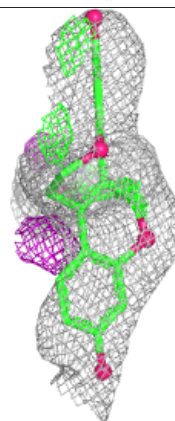
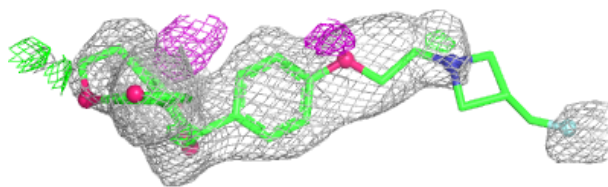
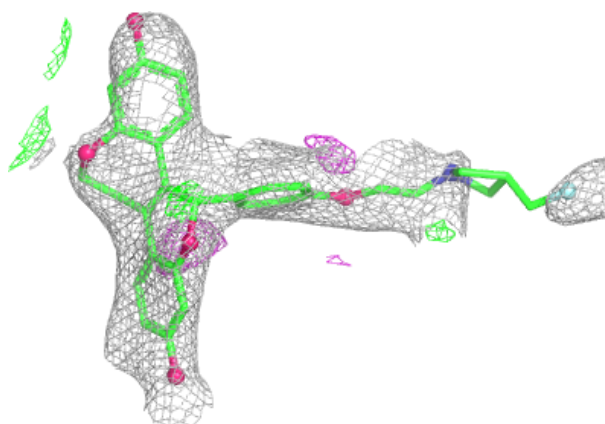
Electron density around G91 B 601 (A):

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



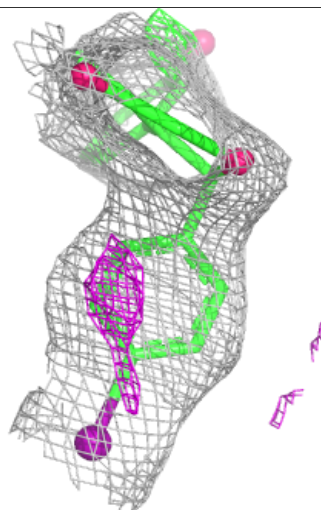
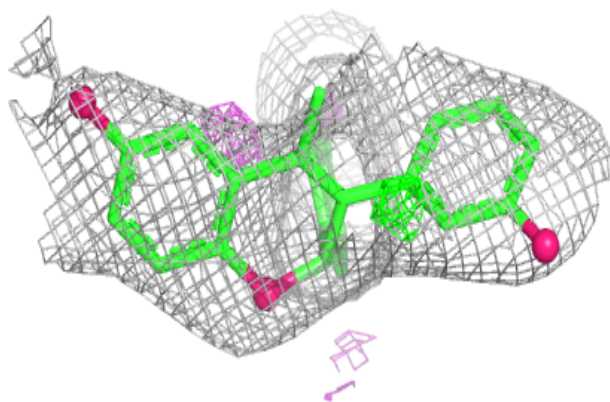
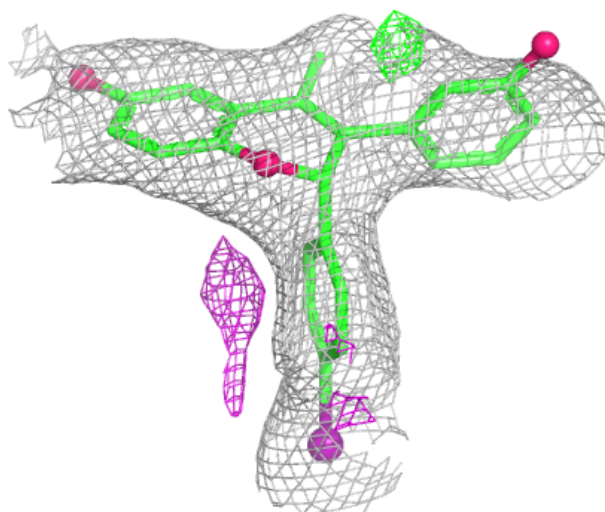
Electron density around G91 D 602 (A):

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



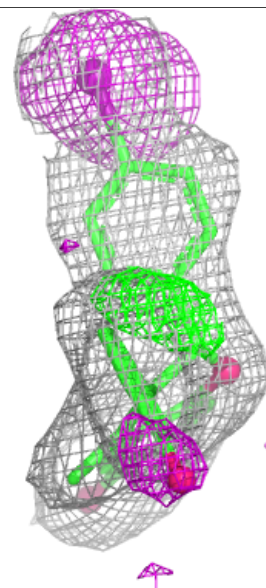
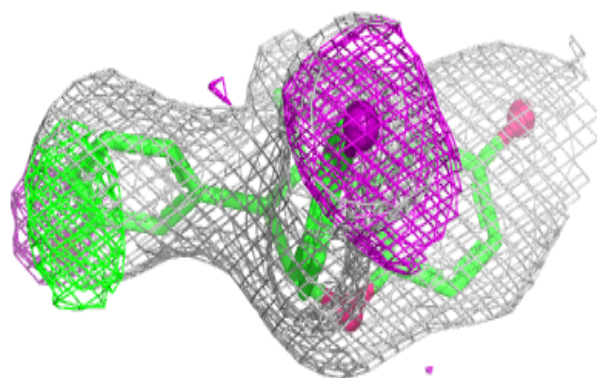
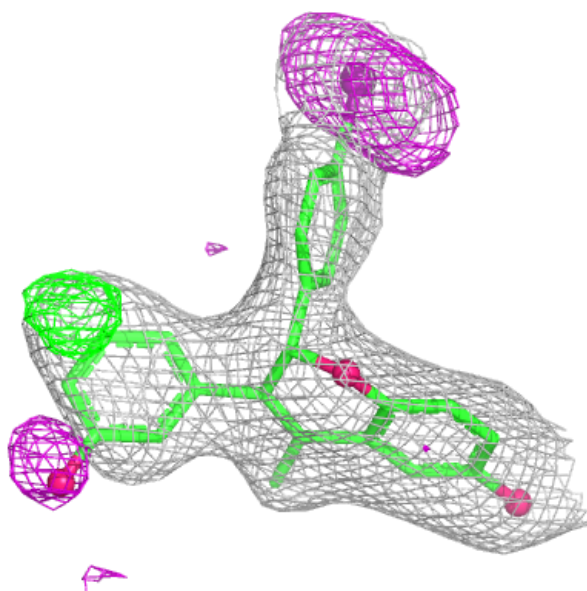
Electron density around G9J B 602 (B):

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



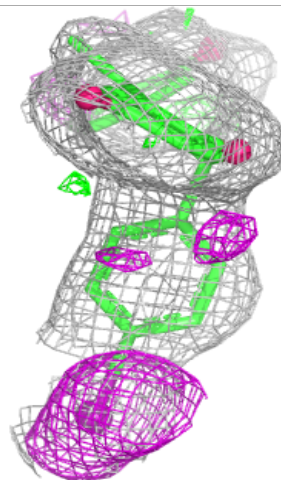
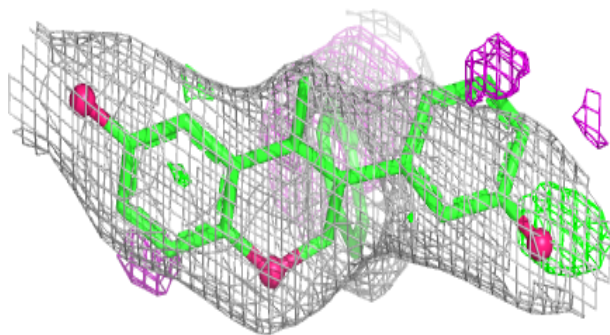
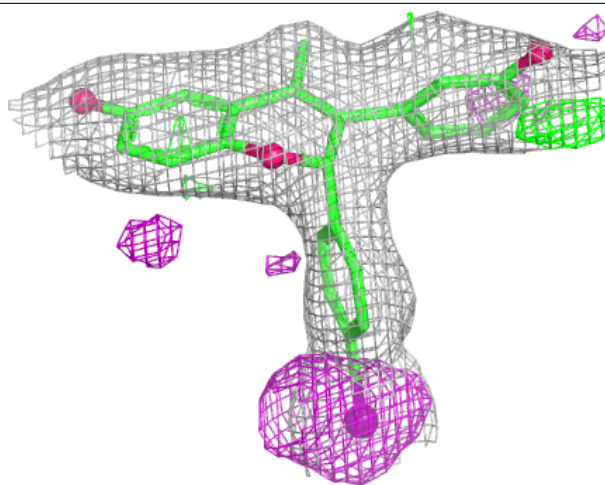
Electron density around G9J A 601:

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



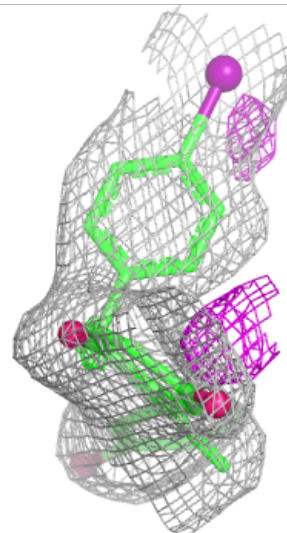
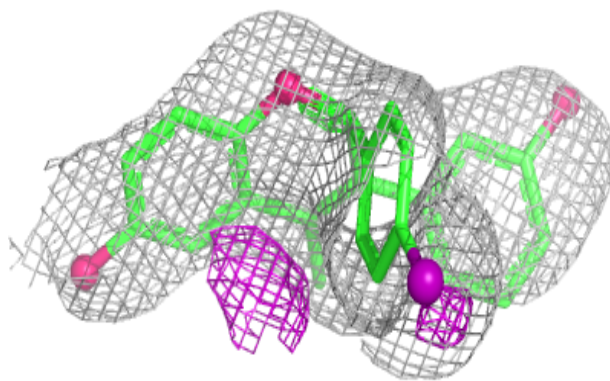
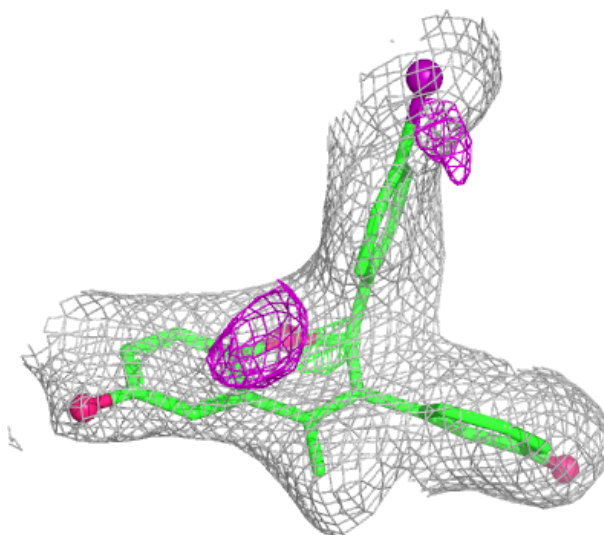
Electron density around G9J C 601:

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



Electron density around G9J D 601 (B):

$2mF_o-DF_c$ (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.