Full wwPDB X-ray Structure Validation Report (i)

May 13, 2020 – 05:50 pm BST

PDB ID	:	6D4O
Title	:	Eubacterium eligens beta-glucuronidase bound to an amoxapine-glucuronide conjugate
Authors	:	Pellock, S.J.; Walton, W.G.; Redinbo, M.R.
Deposited on	:	2018-04-18
Resolution	:	2.90 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 (i) symbol.

The following versions of software and data (see references (i)) 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	:	2.11
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)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	Percentile Ranks	Value
Rfree		0.242
Clashscore		9
Ramachandran outliers		0
Sidechain outliers		2.7%
RSRZ outliers		2.7%

Worse ← → Better

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
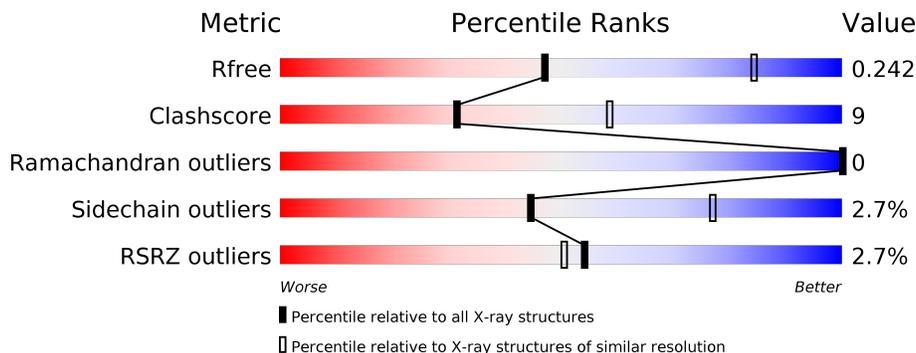
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 on 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 <=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	614	3% / 76% / 19% / •

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	CL	A	702	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4823 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 Beta-glucuronidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	589	Total	C	N	O	S	0	0	0
			4739	3017	783	916	23			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP A0A174ZZA3
A	-1	ASN	-	expression tag	UNP A0A174ZZA3
A	0	ALA	-	expression tag	UNP A0A174ZZA3
A	120	ASP	HIS	conflict	UNP A0A174ZZA3

- Molecule 2 is (5aR,9aR)-2-chloro-11-(4-beta-D-glucopyranuronosylpiperazin-1-yl)-5a,6,9,9a-tetrahydrodibenzo[b,f][1,4]oxazepine (three-letter code: FUV) (formula: $C_{23}H_{28}ClN_3O_7$) (labeled as "Ligand of Interest" by author).
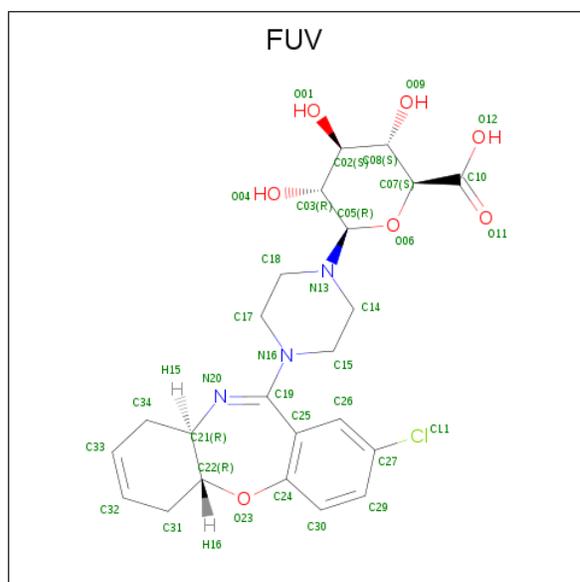
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	1
			34	23	1	3	7		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

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

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	48	Total	O	0	0
			48	48		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Beta-glucuronidase
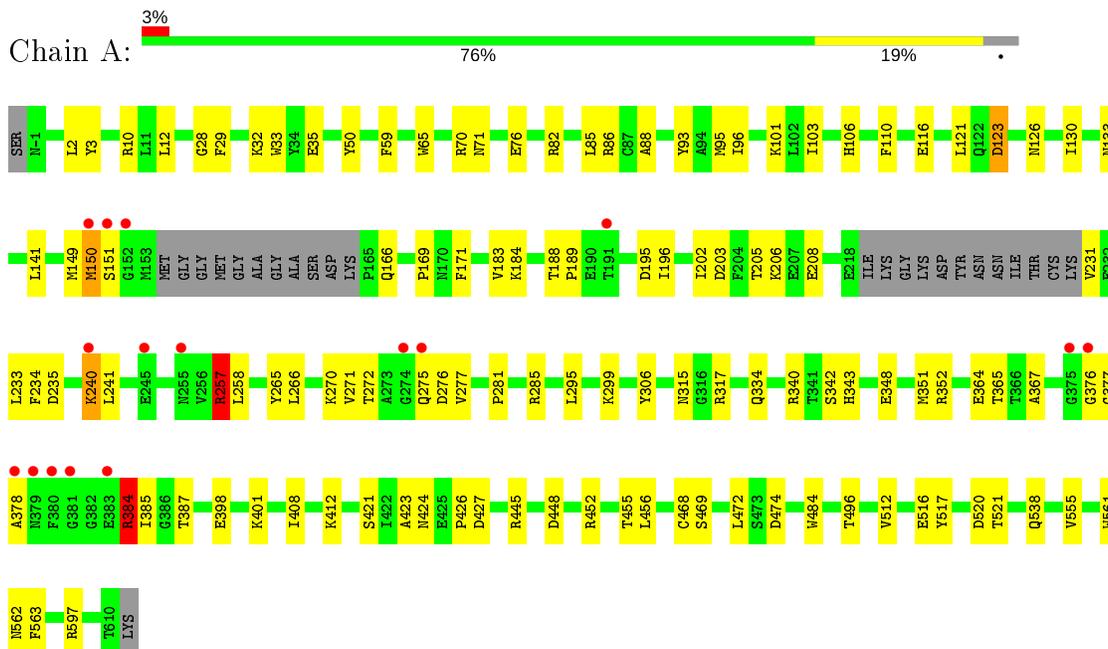
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 64 2 2	Depositor
Cell constants a, b, c, α, β, γ	179.95Å 179.95Å 134.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.45 – 2.90 29.45 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.45-2.90) 100.0 (29.45-2.90)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	5.15 (at 2.90Å)	Xtriage
Refinement program	PHENIX (1.13_2998)	Depositor
R, R_{free}	0.199 , 0.244 0.199 , 0.242	Depositor DCC
R_{free} test set	2000 reflections (6.89%)	wwPDB-VP
Wilson B-factor (Å²)	51.8	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol}(e/Å³), B_{sol}(Å²)	0.32 , 48.2	EDS
L-test for twinning[2]	$<|L|> = 0.46$, $<L^2> = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4823	wwPDB-VP
Average B, all atoms (Å²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.04% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ 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: FUV, NA, CL

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	0.40	0/4859	0.57	1/6588 (0.0%)

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

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	517	TYR	CB-CA-C	5.11	120.63	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	257	ARG	Sidechain
1	A	384	ARG	Sidechain

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	4739	0	4526	84	0
2	A	34	0	0	0	0
3	A	1	0	0	2	0
4	A	1	0	0	0	0
5	A	48	0	0	3	0
All	All	4823	0	4526	84	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 9.

All (84) 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:377:GLY:CA	1:A:384:ARG:NH1	1.79	1.41
1:A:377:GLY:HA3	1:A:384:ARG:NH1	0.95	1.26
1:A:377:GLY:CA	1:A:384:ARG:HH11	1.44	1.14
1:A:257:ARG:HD2	1:A:265:TYR:CD2	2.07	0.90
1:A:377:GLY:HA3	1:A:384:ARG:HH12	1.12	0.83
1:A:10:ARG:HD3	1:A:188:THR:HG22	1.59	0.83
1:A:377:GLY:CA	1:A:384:ARG:HH12	1.66	0.81
1:A:376:GLY:C	1:A:384:ARG:HH12	1.88	0.76
1:A:376:GLY:O	1:A:384:ARG:NH1	2.23	0.70
1:A:377:GLY:HA2	1:A:384:ARG:NH1	2.03	0.70
1:A:202:ILE:HD11	1:A:258:LEU:HD21	1.75	0.68
1:A:150:MET:HG3	1:A:150:MET:O	1.92	0.68
1:A:340:ARG:HD2	1:A:364:GLU:OE2	1.97	0.65
1:A:121:LEU:HD12	1:A:126:ASN:ND2	2.11	0.65
1:A:70:ARG:NH1	1:A:71:ASN:O	2.29	0.65
1:A:340:ARG:NE	3:A:702:CL:CL	2.66	0.63
1:A:377:GLY:N	1:A:384:ARG:HH12	1.96	0.63
1:A:340:ARG:HB3	3:A:702:CL:CL	2.36	0.62
1:A:88:ALA:O	5:A:801:HOH:O	2.16	0.62
1:A:266:LEU:HD13	1:A:281:PRO:HB2	1.81	0.61
1:A:377:GLY:HA3	1:A:384:ARG:HH11	0.78	0.60
1:A:29:PHE:CE1	1:A:95:MET:HE3	2.36	0.60
1:A:456:LEU:HD22	1:A:469:SER:HB2	1.83	0.60
1:A:240:LYS:O	1:A:241:LEU:HD23	2.01	0.59
1:A:351:MET:HE3	5:A:817:HOH:O	2.03	0.58
1:A:272:THR:HG23	1:A:277:VAL:HG22	1.85	0.57
1:A:110:PHE:HE1	1:A:317:ARG:CD	2.17	0.56
1:A:82:ARG:NH2	1:A:116:GLU:OE2	2.38	0.56
1:A:295:LEU:HA	1:A:299:LYS:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:GLU:OE1	1:A:401:LYS:NZ	2.40	0.55
1:A:484:TRP:CZ2	1:A:520:ASP:HB2	2.44	0.53
1:A:110:PHE:HE1	1:A:317:ARG:HD2	1.74	0.53
1:A:378:ALA:HB1	1:A:385:ILE:HD12	1.90	0.53
1:A:348:GLU:O	1:A:352:ARG:HG3	2.09	0.53
1:A:233:LEU:HD22	1:A:241:LEU:HB2	1.92	0.52
1:A:512:VAL:O	1:A:555:VAL:HA	2.10	0.51
1:A:189:PRO:HD2	1:A:276:ASP:OD2	2.11	0.51
1:A:169:PRO:HB3	1:A:171:PHE:CZ	2.46	0.51
1:A:516:GLU:HG2	1:A:561:TRP:HB2	1.93	0.51
1:A:364:GLU:OE1	1:A:424:ASN:HB2	2.11	0.50
1:A:521:THR:OG1	1:A:538:GLN:HB2	2.12	0.50
1:A:334:GLN:HA	1:A:597:ARG:HG3	1.93	0.50
1:A:317:ARG:HH11	1:A:317:ARG:HG3	1.78	0.49
1:A:65:TRP:CH2	1:A:95:MET:HE2	2.48	0.48
1:A:257:ARG:HD2	1:A:265:TYR:CG	2.47	0.48
1:A:377:GLY:HA2	1:A:384:ARG:HH11	1.59	0.48
1:A:65:TRP:CH2	1:A:95:MET:CE	2.97	0.48
1:A:189:PRO:HG3	1:A:275:GLN:O	2.15	0.47
1:A:342:SER:HA	1:A:343:HIS:HA	1.69	0.46
1:A:76:GLU:HG3	1:A:123:ASP:OD2	2.15	0.46
1:A:85:LEU:HD11	1:A:183:VAL:HG13	1.96	0.46
1:A:445:ARG:NH2	1:A:472:LEU:O	2.49	0.46
1:A:240:LYS:C	1:A:241:LEU:HD23	2.36	0.45
1:A:234:PHE:HE2	1:A:270:LYS:HB3	1.81	0.45
1:A:50:TYR:O	1:A:59:PHE:HE1	1.98	0.45
1:A:445:ARG:NH1	1:A:474:ASP:OD1	2.43	0.45
1:A:65:TRP:CZ3	1:A:95:MET:HE2	2.51	0.45
1:A:29:PHE:HE1	1:A:95:MET:HE3	1.78	0.45
1:A:101:LYS:O	1:A:103:ILE:HG23	2.17	0.44
1:A:408:ILE:O	1:A:412:LYS:HB3	2.18	0.44
1:A:445:ARG:HH12	1:A:474:ASP:CG	2.21	0.44
1:A:412:LYS:O	1:A:452:ARG:NH2	2.43	0.44
1:A:203:ASP:OD1	1:A:205:THR:OG1	2.35	0.43
1:A:561:TRP:HA	1:A:562:ASN:HA	1.67	0.43
1:A:455:THR:OG1	1:A:456:LEU:N	2.50	0.43
1:A:12:LEU:HD11	1:A:184:LYS:HD3	2.01	0.43
1:A:32:LYS:HD2	1:A:35:GLU:CD	2.39	0.43
1:A:448:ASP:OD2	1:A:452:ARG:HB2	2.19	0.43
1:A:387:THR:OG1	1:A:427:ASP:OD2	2.28	0.42
1:A:423:ALA:HB3	1:A:426:PRO:HG3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:562:ASN:OD1	1:A:563:PHE:N	2.53	0.41
1:A:96:ILE:HG12	1:A:130:ILE:HG12	2.01	0.41
1:A:93:TYR:HB3	1:A:133:ASN:HB3	2.01	0.41
1:A:257:ARG:CD	1:A:265:TYR:CG	3.04	0.41
1:A:365:THR:HG23	1:A:421:SER:O	2.20	0.41
1:A:231:VAL:HA	1:A:271:VAL:HA	2.01	0.41
1:A:3:TYR:CD2	1:A:352:ARG:HD2	2.55	0.41
1:A:195:ASP:OD1	1:A:196:ILE:N	2.54	0.41
1:A:2:LEU:O	1:A:86:ARG:NH2	2.44	0.41
1:A:206:LYS:HG3	1:A:208:GLU:H	1.86	0.41
1:A:141:LEU:HD22	1:A:367:ALA:HA	2.02	0.41
1:A:106:HIS:HD2	5:A:816:HOH:O	2.04	0.40
1:A:110:PHE:CE1	1:A:317:ARG:HD2	2.54	0.40
1:A:28:GLY:HA2	1:A:33:TRP:CE2	2.57	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	583/614 (95%)	548 (94%)	35 (6%)	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	515/533 (97%)	501 (97%)	14 (3%)	44	77

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	123	ASP
1	A	149	MET
1	A	150	MET
1	A	151	SER
1	A	166	GLN
1	A	235	ASP
1	A	240	LYS
1	A	257	ARG
1	A	285	ARG
1	A	306	TYR
1	A	315	ASN
1	A	384	ARG
1	A	468	CYS
1	A	496	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	FUV	A	701[A]	-	33,38,38	3.85	17 (51%)	40,56,56	2.60	15 (37%)

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	FUV	A	701[A]	-	-	2/8/65/65	0/4/5/5

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701[A]	FUV	C21-N20	-10.23	1.36	1.47
2	A	701[A]	FUV	C19-N20	7.53	1.45	1.29
2	A	701[A]	FUV	C31-C22	-7.02	1.40	1.51
2	A	701[A]	FUV	C19-N16	6.20	1.50	1.37
2	A	701[A]	FUV	C25-C19	6.16	1.67	1.48
2	A	701[A]	FUV	O23-C22	-5.85	1.37	1.45
2	A	701[A]	FUV	O23-C24	5.55	1.50	1.38
2	A	701[A]	FUV	O06-C07	4.46	1.49	1.44
2	A	701[A]	FUV	C34-C33	-4.00	1.41	1.49
2	A	701[A]	FUV	C31-C32	-3.97	1.41	1.49
2	A	701[A]	FUV	C25-C24	3.87	1.48	1.40
2	A	701[A]	FUV	O06-C05	3.81	1.48	1.42
2	A	701[A]	FUV	C33-C32	3.61	1.43	1.32
2	A	701[A]	FUV	C29-C27	2.58	1.42	1.38
2	A	701[A]	FUV	C03-C05	2.51	1.55	1.52
2	A	701[A]	FUV	C34-C21	-2.35	1.40	1.54
2	A	701[A]	FUV	C27-CL1	2.32	1.79	1.74

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	701[A]	FUV	C25-C19-N16	9.74	122.91	115.48
2	A	701[A]	FUV	C02-C03-C05	5.79	117.49	108.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701[A]	FUV	C25-C19-N20	-5.64	120.95	125.85
2	A	701[A]	FUV	O06-C05-C03	3.78	115.99	110.15
2	A	701[A]	FUV	O06-C07-C08	3.53	114.72	108.91
2	A	701[A]	FUV	N16-C19-N20	-3.09	115.97	118.30
2	A	701[A]	FUV	O23-C24-C30	-2.95	110.33	116.53
2	A	701[A]	FUV	C22-C31-C32	-2.54	105.09	110.81
2	A	701[A]	FUV	C25-C26-C27	2.53	123.89	119.64
2	A	701[A]	FUV	C24-C25-C19	2.36	130.05	123.03
2	A	701[A]	FUV	C15-C14-N13	2.29	114.97	110.59
2	A	701[A]	FUV	C15-N16-C19	2.23	126.01	119.34
2	A	701[A]	FUV	O23-C24-C25	2.19	128.36	122.80
2	A	701[A]	FUV	C26-C25-C24	-2.13	115.31	118.29
2	A	701[A]	FUV	C14-C15-N16	2.12	114.97	110.44

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701[A]	FUV	C25-C19-N16-C15
2	A	701[A]	FUV	N20-C19-N16-C15

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 then 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 FUV A 701 (A)

Bond lengths — Bond angles — Torsions — Rings
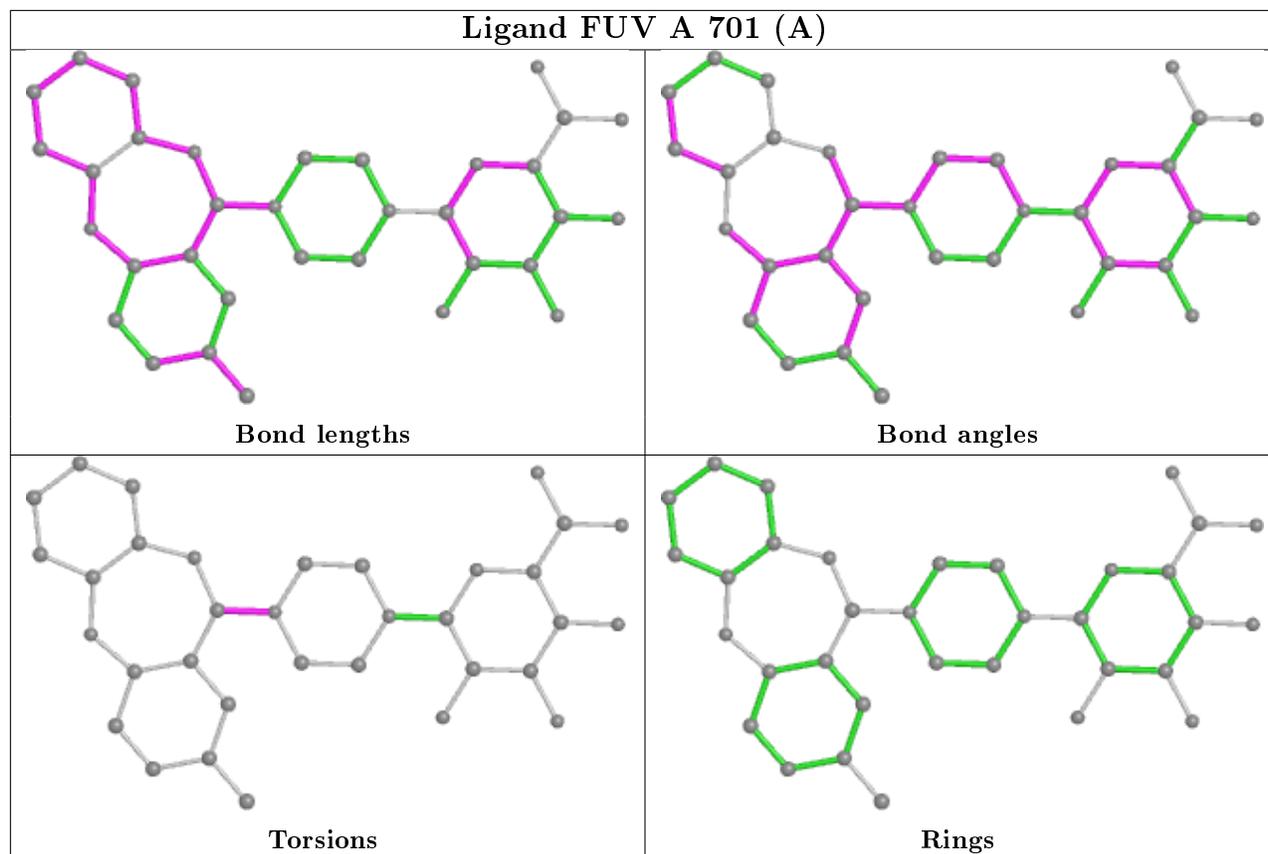
5.7 Other polymers (i)

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, 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	589/614 (95%)	-0.33	16 (2%)	54	50	22, 49, 89, 104	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	240	LYS	3.4
1	A	275	GLN	3.2
1	A	380	PHE	3.2
1	A	150	MET	3.1
1	A	375	GLY	3.1
1	A	151	SER	2.8
1	A	152	GLY	2.7
1	A	255	ASN	2.6
1	A	274	GLY	2.5
1	A	381	GLY	2.5
1	A	191	THR	2.5
1	A	379	ASN	2.4
1	A	378	ALA	2.3
1	A	383	GLU	2.3
1	A	245	GLU	2.2
1	A	376	GLY	2.1

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 ⓘ

There are no carbohydrates 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(Å^2)	Q<0.9
2	FUV	A	701[A]	34/34	0.86	0.23	32,55,82,82	0
3	CL	A	702	1/1	0.95	0.13	55,55,55,55	0
4	NA	A	703	1/1	0.96	0.16	34,34,34,34	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 FUV A 701 (A):

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

6.5 Other polymers (i)

There are no such residues in this entry.