



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:19 PM UTC

PDB ID : 6WIF / pdb_00006wif
Title : Class C beta-lactamase from *Acinetobacter baumannii* in complex with 4-(Et hyl(methyl)carbamoyl)phenyl boronic acid
Authors : Chang, C.; Maltseva, N.; Endres, M.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2020-04-09
Resolution : 2.15 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

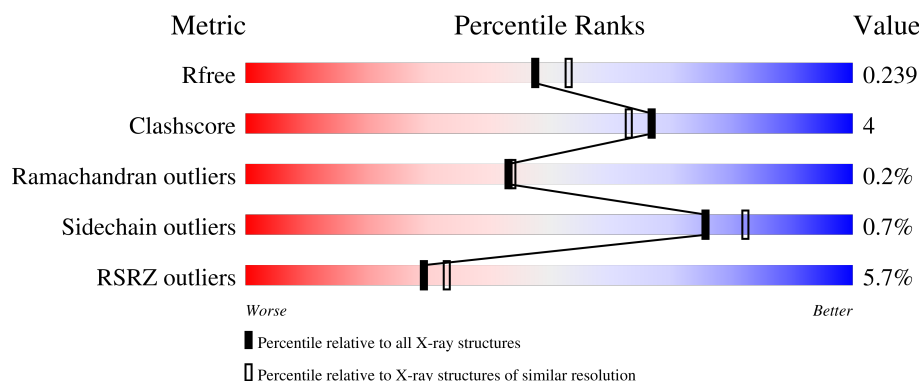
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	360	2% 92% 6% .
1	B	360	2% 91% 8%
1	C	360	17% 86% 13% ..
1	D	360	% 91% 8% .

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	C	407	-	-	X	X

2 Entry composition [i](#)

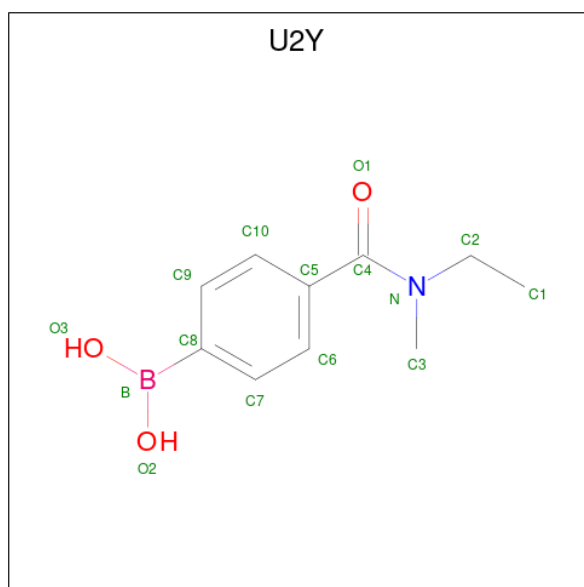
There are 6 unique types of molecules in this entry. The entry contains 12213 atoms, of which 0 are hydrogens and 0 are deuteriums.

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-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	355	Total	C	N	O	S	0	1	0
			2826	1820	467	529	10			
1	B	359	Total	C	N	O	S	0	2	0
			2865	1844	474	538	9			
1	C	357	Total	C	N	O	S	0	2	0
			2837	1829	470	529	9			
1	D	357	Total	C	N	O	S	0	2	0
			2852	1836	473	534	9			

- Molecule 2 is {4-[ethyl(methyl)carbamoyl]phenyl}boronic acid (CCD ID: U2Y) (formula: C₁₀H₁₄BNO₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	B	C	N	O	0
			15	1	10	1	3	0
2	B	1	Total	B	C	N	O	0
			15	1	10	1	3	0

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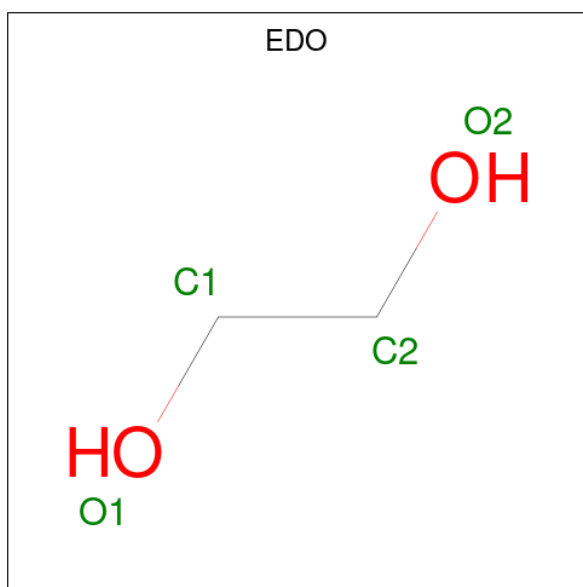
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	B	C	N	O	0	0
			15	1	10	1	3		
2	D	1	Total	B	C	N	O	0	0
			15	1	10	1	3		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	C	2	Total	Cl	0	0
			2	2		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



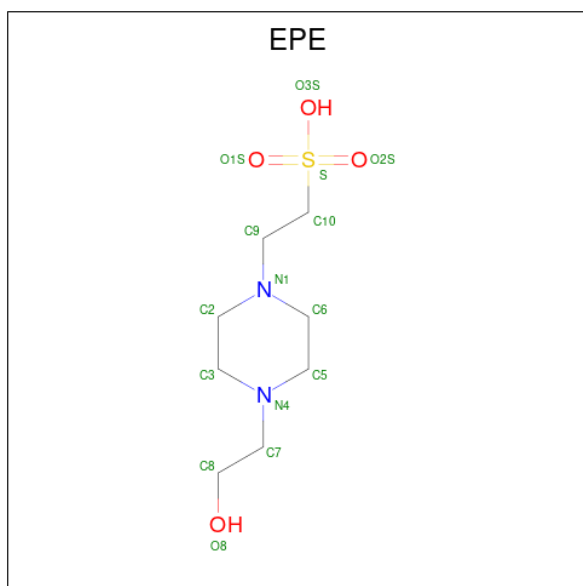
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		
4	C	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		
4	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	C	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
5	D	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

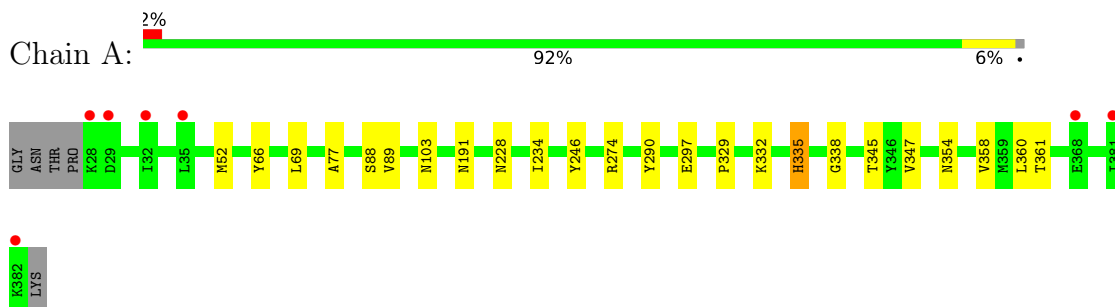
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	175	Total 175	O 175	0	0
6	B	194	Total 194	O 194	0	0
6	C	132	Total 132	O 132	0	0
6	D	165	Total 165	O 165	0	0

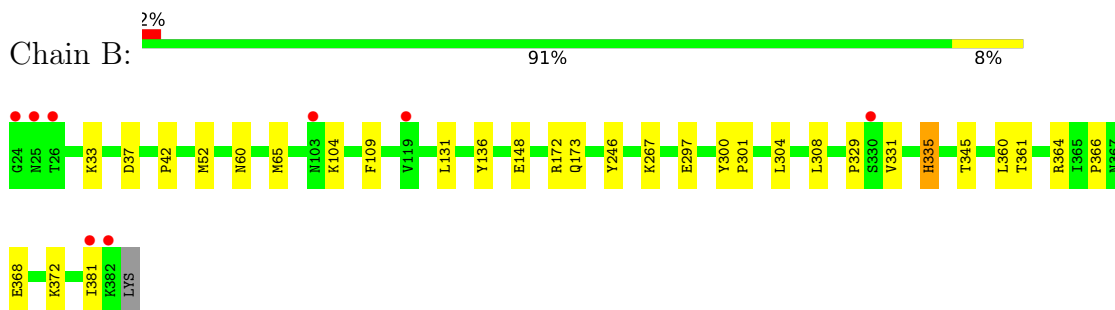
3 Residue-property plots [i](#)

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.

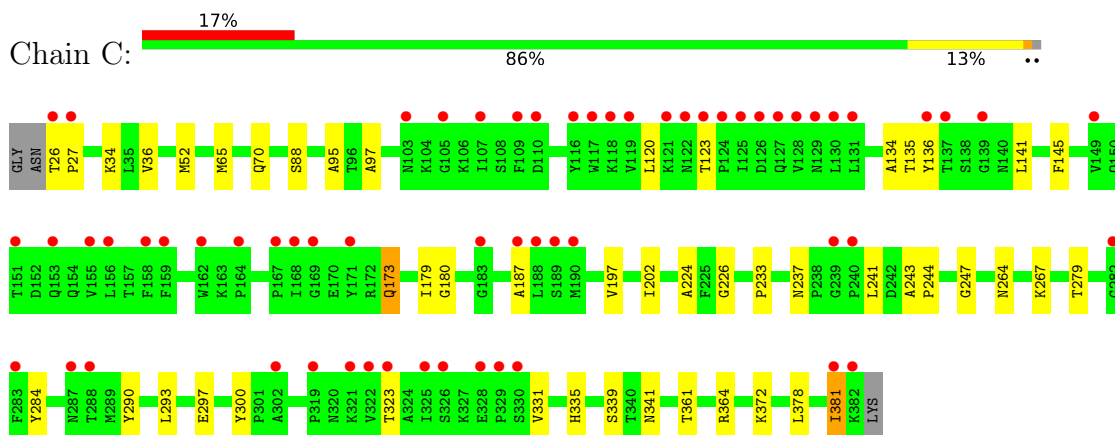
- Molecule 1: Beta-lactamase



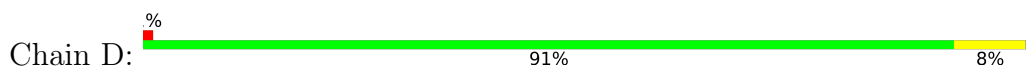
- Molecule 1: Beta-lactamase

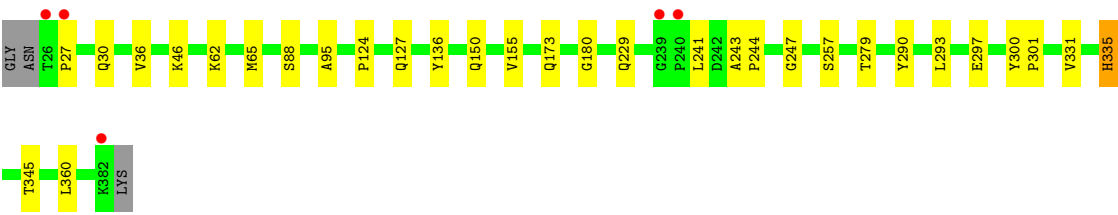


- Molecule 1: Beta-lactamase



- Molecule 1: Beta-lactamase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	93.24Å 80.92Å 104.38Å 90.00° 113.34° 90.00°	Depositor
Resolution (Å)	43.38 – 2.15 43.38 – 2.15	Depositor EDS
% Data completeness (in resolution range)	93.3 (43.38-2.15) 93.3 (43.38-2.15)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.16Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.193 , 0.240 0.193 , 0.239	Depositor DCC
R_{free} test set	3533 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12213	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 30.30 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.3391e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: U2Y, EDO, CL, EPE

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	0.12	0/2894	0.29	0/3925
1	B	0.13	0/2934	0.31	0/3980
1	C	0.12	0/2906	0.30	0/3945
1	D	0.12	0/2921	0.30	0/3962
All	All	0.12	0/11655	0.30	0/15812

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	2826	0	2829	13	0
1	B	2865	0	2870	22	0
1	C	2837	0	2837	30	0
1	D	2852	0	2855	19	0
2	A	15	0	0	1	0
2	B	15	0	0	0	0
2	C	15	0	0	1	0
2	D	15	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
3	C	2	0	0	2	0
4	B	12	0	18	2	0
4	C	12	0	18	1	0
4	D	20	0	30	0	0
5	B	15	0	17	3	0
5	C	30	0	33	4	0
5	D	15	0	17	1	0
6	A	175	0	0	2	0
6	B	194	0	0	3	0
6	C	132	0	0	1	0
6	D	165	0	0	1	0
All	All	12213	0	11524	85	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 4.

All (85) 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)
3:C:407:CL:CL	6:C:590:HOH:O	2.33	0.83
1:D:290:TYR:HB2	1:D:297:GLU:HB3	1.66	0.77
1:B:364:ARG:HB3	5:B:404:EPE:H51	1.67	0.76
1:C:290:TYR:HB2	1:C:297:GLU:HB3	1.69	0.75
1:C:341:ASN:ND2	3:C:407:CL:CL	2.58	0.72
1:C:36:VAL:HG21	1:C:65:MET:HE3	1.74	0.68
1:B:33:LYS:HD3	1:B:65:MET:HG2	1.76	0.66
1:B:308:LEU:HD22	1:B:368[B]:GLU:HG3	1.77	0.66
1:B:172:ARG:HH12	4:B:405:EDO:H21	1.59	0.66
1:C:339:SER:HB2	5:C:404:EPE:H101	1.77	0.65
1:B:109:PHE:HB3	1:B:131:LEU:HB2	1.81	0.62
1:D:62:LYS:NZ	1:D:257:SER:OG	2.33	0.62
1:D:36:VAL:HG21	1:D:65:MET:HE3	1.83	0.61
1:B:297:GLU:OE2	6:B:501:HOH:O	2.17	0.60
1:C:120:LEU:O	1:C:123:THR:OG1	2.20	0.59
1:B:300:TYR:HB3	1:B:331:VAL:HG12	1.86	0.58
1:C:279:THR:HA	1:C:293:LEU:HB3	1.86	0.58
1:B:60:ASN:OD1	1:B:267:LYS:NZ	2.34	0.56
1:D:300:TYR:HB3	1:D:331:VAL:HG12	1.90	0.54
1:C:26:THR:N	1:C:27:PRO:HD2	2.22	0.54
1:B:172:ARG:NH1	4:B:405:EDO:H21	2.23	0.53
1:C:180:GLY:HA2	1:C:244:PRO:HG2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:264:ASN:HB3	1:C:267:LYS:HD3	1.90	0.52
1:C:300:TYR:HB3	1:C:331:VAL:HG12	1.90	0.52
1:D:124:PRO:O	1:D:127[B]:GLN:HG2	2.09	0.52
1:C:364:ARG:HE	5:C:404:EPE:H81	1.75	0.51
1:A:347:VAL:HG12	1:A:358:VAL:HG22	1.93	0.51
1:C:237:ASN:O	5:C:403:EPE:H61	2.11	0.51
1:A:335:HIS:C	1:A:335:HIS:CD2	2.89	0.50
1:D:46:LYS:NZ	6:D:605:HOH:O	2.43	0.50
1:A:66:TYR:O	6:A:501:HOH:O	2.19	0.50
1:B:335:HIS:CD2	1:B:335:HIS:C	2.90	0.49
1:B:148:GLU:OE1	6:B:502:HOH:O	2.19	0.49
1:C:145:PHE:HZ	1:C:241:LEU:HD23	1.76	0.49
1:D:229[B]:GLN:H	1:D:229[B]:GLN:CD	2.21	0.48
1:D:180:GLY:HA2	1:D:244:PRO:HG2	1.94	0.48
1:A:52:MET:HG3	1:A:361:THR:HG22	1.95	0.48
1:A:103:ASN:OD1	1:A:274:ARG:HD2	2.14	0.48
1:C:134:ALA:HA	1:C:179[B]:ILE:HG12	1.95	0.48
1:A:329:PRO:HG2	1:A:332:LYS:HG2	1.95	0.48
1:A:345:THR:HG23	1:A:360:LEU:HD23	1.96	0.48
1:B:52:MET:HG3	1:B:361:THR:HG22	1.95	0.48
1:D:155:VAL:HG11	1:D:241:LEU:HD13	1.96	0.47
1:B:366:PRO:HA	5:B:404:EPE:H32	1.96	0.47
1:D:335:HIS:CD2	1:D:335:HIS:C	2.91	0.47
1:D:88:SER:CB	2:D:401:U2Y:O2	2.60	0.47
1:A:88:SER:CB	2:A:401:U2Y:O2	2.63	0.47
1:B:345:THR:HG23	1:B:360:LEU:HD23	1.96	0.46
1:C:136:TYR:HB3	1:C:173:GLN:O	2.16	0.46
1:B:381[B]:ILE:H	1:B:381[B]:ILE:HG12	1.50	0.46
1:C:141:LEU:O	1:C:173:GLN:HG2	2.16	0.46
1:C:97:ALA:HB2	1:C:202:ILE:HG13	1.99	0.45
1:D:345:THR:HG23	1:D:360:LEU:HD23	1.99	0.44
1:B:300:TYR:CD1	1:B:301:PRO:HA	2.52	0.44
1:C:34:LYS:HG3	4:C:402:EDO:H12	1.98	0.44
1:C:243:ALA:HA	1:C:247:GLY:HA3	1.99	0.44
1:D:279:THR:HA	1:D:293:LEU:HB3	2.00	0.44
1:D:150:GLN:OE1	5:D:404:EPE:H52	2.16	0.44
1:A:228:ASN:HB3	1:A:234:ILE:HD13	1.99	0.44
1:A:191:ASN:ND2	6:A:513:HOH:O	2.42	0.44
1:B:136:TYR:HB3	1:B:173:GLN:O	2.18	0.44
1:C:335:HIS:CD2	1:C:335:HIS:C	2.94	0.44
1:D:136:TYR:HB3	1:D:173:GLN:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:290:TYR:HB2	1:A:297:GLU:HB3	1.99	0.43
1:A:69:LEU:HA	1:A:77:ALA:HA	2.00	0.43
1:C:135:THR:HB	1:C:284:TYR:HE2	1.84	0.43
1:B:37:ASP:O	1:B:42:PRO:HD3	2.19	0.43
1:D:95:ALA:HB1	1:D:293:LEU:HG	2.00	0.43
1:A:89:VAL:HG23	1:A:338:GLY:HA3	2.01	0.42
1:C:187:ALA:HA	1:C:197:VAL:HG21	2.02	0.42
1:B:364:ARG:HD2	5:B:404:EPE:H51	2.00	0.42
1:C:70:GLN:HG3	1:C:224:ALA:HA	2.01	0.41
1:C:88:SER:CB	2:C:401:U2Y:O2	2.60	0.41
1:D:300:TYR:CD1	1:D:301:PRO:HA	2.55	0.41
1:C:95:ALA:HB1	1:C:293:LEU:HG	2.01	0.41
1:B:104:LYS:HE2	1:B:104:LYS:HB3	1.91	0.41
1:B:329:PRO:HD2	6:B:501:HOH:O	2.20	0.41
1:C:52:MET:HG3	1:C:361:THR:HG22	2.03	0.41
1:C:145:PHE:CZ	1:C:241:LEU:HD23	2.55	0.41
1:C:378:LEU:HA	1:C:381:ILE:HD11	2.02	0.41
1:C:226:GLY:O	1:C:233:PRO:HA	2.22	0.40
1:C:364:ARG:HG2	5:C:404:EPE:H52	1.75	0.40
1:D:243:ALA:HA	1:D:247:GLY:HA3	2.03	0.40
1:D:293:LEU:HD12	1:D:293:LEU:HA	1.94	0.40
1:B:304:LEU:HD21	1:B:372:LYS:HG2	2.02	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	354/360 (98%)	342 (97%)	11 (3%)	1 (0%)	36	34
1	B	359/360 (100%)	349 (97%)	9 (2%)	1 (0%)	36	34
1	C	357/360 (99%)	344 (96%)	13 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	357/360 (99%)	348 (98%)	8 (2%)	1 (0%)	36	34
All	All	1427/1440 (99%)	1383 (97%)	41 (3%)	3 (0%)	43	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	27	PRO
1	A	246	TYR
1	B	246	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	311/315 (99%)	309 (99%)	2 (1%)	78	84
1	B	316/315 (100%)	315 (100%)	1 (0%)	86	91
1	C	311/315 (99%)	307 (99%)	4 (1%)	61	68
1	D	314/315 (100%)	312 (99%)	2 (1%)	78	84
All	All	1252/1260 (99%)	1243 (99%)	9 (1%)	76	82

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	335	HIS
1	A	354	ASN
1	B	335	HIS
1	C	173	GLN
1	C	323	THR
1	C	372	LYS
1	C	381	ILE
1	D	30	GLN
1	D	335	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	166	ASN
1	B	39	ASN
1	B	210	HIS
1	B	222	ASN
1	B	229	GLN
1	B	311	ASN
1	C	39	ASN
1	C	231	ASN
1	C	287	ASN
1	C	314	GLN
1	C	320	ASN
1	D	30	GLN
1	D	60	ASN
1	D	153	GLN
1	D	196	GLN
1	D	222	ASN
1	D	367	ASN

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 22 ligands modelled in this entry, 3 are monoatomic - leaving 19 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	U2Y	D	401	1	14,15,15	4.05	2 (14%)	17,20,20	0.99	1 (5%)
2	U2Y	C	401	1	14,15,15	4.02	2 (14%)	17,20,20	0.94	0
4	EDO	B	403	-	3,3,3	0.42	0	2,2,2	0.38	0
4	EDO	B	405	-	3,3,3	0.37	0	2,2,2	0.40	0
4	EDO	D	407	-	3,3,3	0.43	0	2,2,2	0.37	0
4	EDO	D	402	-	3,3,3	0.43	0	2,2,2	0.35	0
4	EDO	C	402	-	3,3,3	0.42	0	2,2,2	0.38	0
5	EPE	C	403	-	15,15,15	0.84	1 (6%)	19,20,20	1.91	4 (21%)
5	EPE	D	404	-	15,15,15	0.86	1 (6%)	19,20,20	1.67	5 (26%)
4	EDO	D	406	-	3,3,3	0.41	0	2,2,2	0.33	0
4	EDO	D	403	-	3,3,3	0.42	0	2,2,2	0.42	0
5	EPE	B	404	-	15,15,15	0.78	1 (6%)	19,20,20	1.66	3 (15%)
5	EPE	C	404	-	15,15,15	0.81	1 (6%)	19,20,20	1.59	5 (26%)
2	U2Y	B	401	1	14,15,15	4.05	2 (14%)	17,20,20	1.00	1 (5%)
2	U2Y	A	401	1	14,15,15	4.04	2 (14%)	17,20,20	1.11	1 (5%)
4	EDO	C	405	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	402	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	D	405	-	3,3,3	0.42	0	2,2,2	0.37	0
4	EDO	C	406	-	3,3,3	0.45	0	2,2,2	0.30	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	U2Y	D	401	1	-	4/14/14/14	0/1/1/1
2	U2Y	C	401	1	-	4/14/14/14	0/1/1/1
4	EDO	B	403	-	-	0/1/1/1	-
4	EDO	B	405	-	-	0/1/1/1	-
4	EDO	D	407	-	-	0/1/1/1	-
4	EDO	D	402	-	-	0/1/1/1	-
4	EDO	C	402	-	-	0/1/1/1	-
5	EPE	C	403	-	-	7/9/19/19	0/1/1/1
5	EPE	D	404	-	-	1/9/19/19	0/1/1/1
4	EDO	D	406	-	-	0/1/1/1	-
4	EDO	D	403	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EPE	B	404	-	-	2/9/19/19	0/1/1/1
5	EPE	C	404	-	-	6/9/19/19	0/1/1/1
2	U2Y	B	401	1	-	3/14/14/14	0/1/1/1
2	U2Y	A	401	1	-	4/14/14/14	0/1/1/1
4	EDO	C	405	-	-	0/1/1/1	-
4	EDO	B	402	-	-	0/1/1/1	-
4	EDO	D	405	-	-	0/1/1/1	-
4	EDO	C	406	-	-	0/1/1/1	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	U2Y	B-O3	10.81	1.54	1.36
2	D	401	U2Y	B-O3	10.71	1.54	1.36
2	C	401	U2Y	B-O2	10.69	1.54	1.36
2	A	401	U2Y	B-O2	10.68	1.54	1.36
2	A	401	U2Y	B-O3	10.65	1.53	1.36
2	D	401	U2Y	B-O2	10.62	1.53	1.36
2	B	401	U2Y	B-O2	10.54	1.53	1.36
2	C	401	U2Y	B-O3	10.51	1.53	1.36
5	D	404	EPE	C10-S	2.94	1.81	1.77
5	C	403	EPE	C10-S	2.62	1.81	1.77
5	C	404	EPE	C10-S	2.56	1.81	1.77
5	B	404	EPE	C10-S	2.55	1.81	1.77

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	403	EPE	C5-N4-C3	4.49	118.52	108.84
5	C	403	EPE	O1S-S-C10	4.11	112.94	106.73
5	D	404	EPE	C5-N4-C3	4.07	117.60	108.84
5	B	404	EPE	C5-N4-C3	3.76	116.94	108.84
5	B	404	EPE	C7-N4-C3	3.60	120.84	111.24
5	C	403	EPE	C7-N4-C3	3.35	120.16	111.24
5	C	404	EPE	C7-N4-C5	3.10	119.51	111.24
5	C	404	EPE	C5-N4-C3	3.01	115.33	108.84
5	C	403	EPE	C7-N4-C5	2.95	119.10	111.24
5	B	404	EPE	C7-N4-C5	2.86	118.85	111.24
5	D	404	EPE	C7-N4-C3	2.83	118.79	111.24
5	C	404	EPE	C7-N4-C3	2.78	118.64	111.24
5	D	404	EPE	O1S-S-C10	2.76	110.90	106.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	U2Y	C9-C8-C7	2.55	119.79	116.86
2	B	401	U2Y	C9-C8-C7	2.40	119.62	116.86
5	C	404	EPE	O1S-S-C10	2.24	110.12	106.73
2	D	401	U2Y	C9-C8-C7	2.20	119.39	116.86
5	C	404	EPE	C6-N1-C2	2.17	113.53	108.84
5	D	404	EPE	C9-N1-C6	-2.16	105.50	111.24
5	D	404	EPE	C7-N4-C5	2.09	116.81	111.24

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	U2Y	O2-B-C8-C7
2	A	401	U2Y	O2-B-C8-C9
2	A	401	U2Y	O3-B-C8-C7
2	A	401	U2Y	O3-B-C8-C9
5	C	403	EPE	C9-C10-S-O1S
5	C	403	EPE	C9-C10-S-O3S
5	C	404	EPE	C10-C9-N1-C2
5	C	404	EPE	C10-C9-N1-C6
5	C	404	EPE	C9-C10-S-O2S
5	C	403	EPE	N4-C7-C8-O8
5	C	404	EPE	C8-C7-N4-C5
2	D	401	U2Y	O2-B-C8-C7
2	D	401	U2Y	O2-B-C8-C9
2	D	401	U2Y	O3-B-C8-C9
2	D	401	U2Y	O3-B-C8-C7
2	C	401	U2Y	O2-B-C8-C9
2	C	401	U2Y	O2-B-C8-C7
2	C	401	U2Y	O3-B-C8-C9
5	B	404	EPE	C10-C9-N1-C2
5	B	404	EPE	C10-C9-N1-C6
2	C	401	U2Y	O3-B-C8-C7
5	C	403	EPE	C9-C10-S-O2S
5	C	404	EPE	C9-C10-S-O1S
5	C	403	EPE	C8-C7-N4-C5
2	B	401	U2Y	O2-B-C8-C7
5	C	403	EPE	C10-C9-N1-C2
5	C	403	EPE	C10-C9-N1-C6
5	C	404	EPE	C9-C10-S-O3S
5	D	404	EPE	C8-C7-N4-C5
2	B	401	U2Y	O2-B-C8-C9

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Mol	Chain	Res	Type	Atoms
2	B	401	U2Y	O3-B-C8-C7

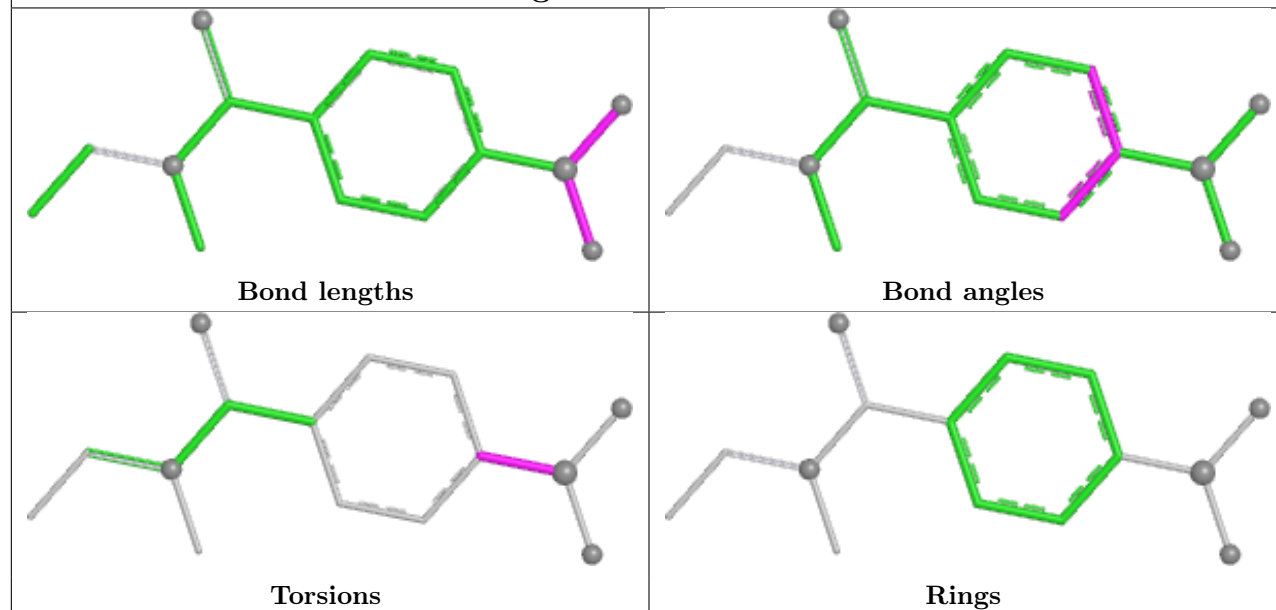
There are no ring outliers.

9 monomers are involved in 14 short contacts:

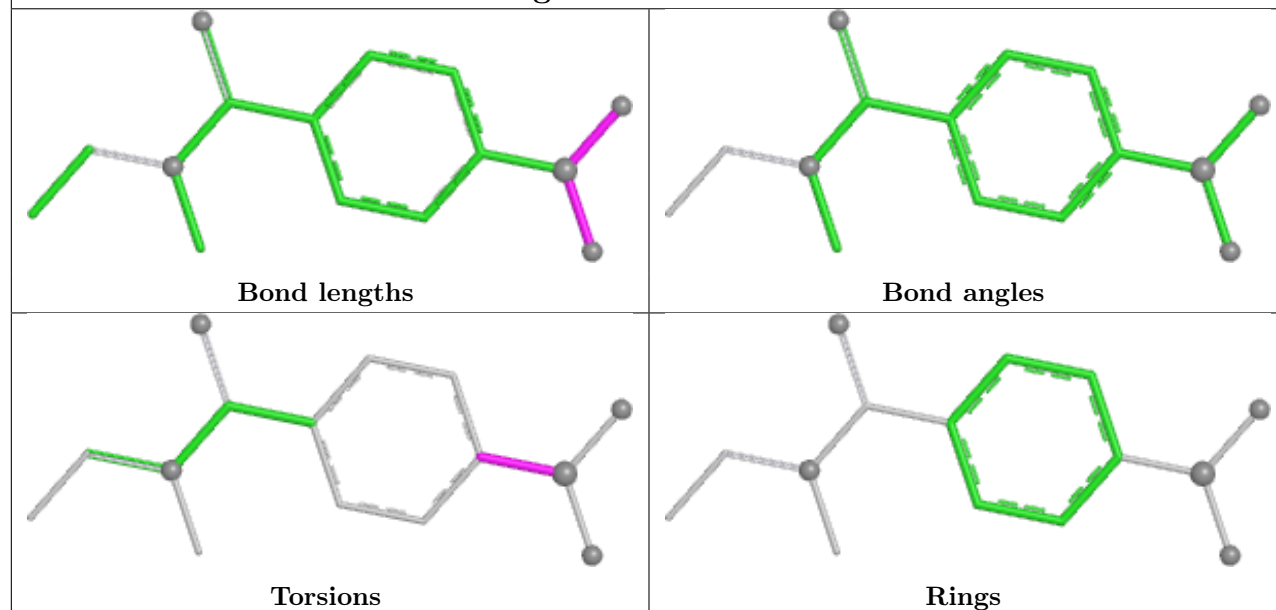
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	U2Y	1	0
2	C	401	U2Y	1	0
4	B	405	EDO	2	0
4	C	402	EDO	1	0
5	C	403	EPE	1	0
5	D	404	EPE	1	0
5	B	404	EPE	3	0
5	C	404	EPE	3	0
2	A	401	U2Y	1	0

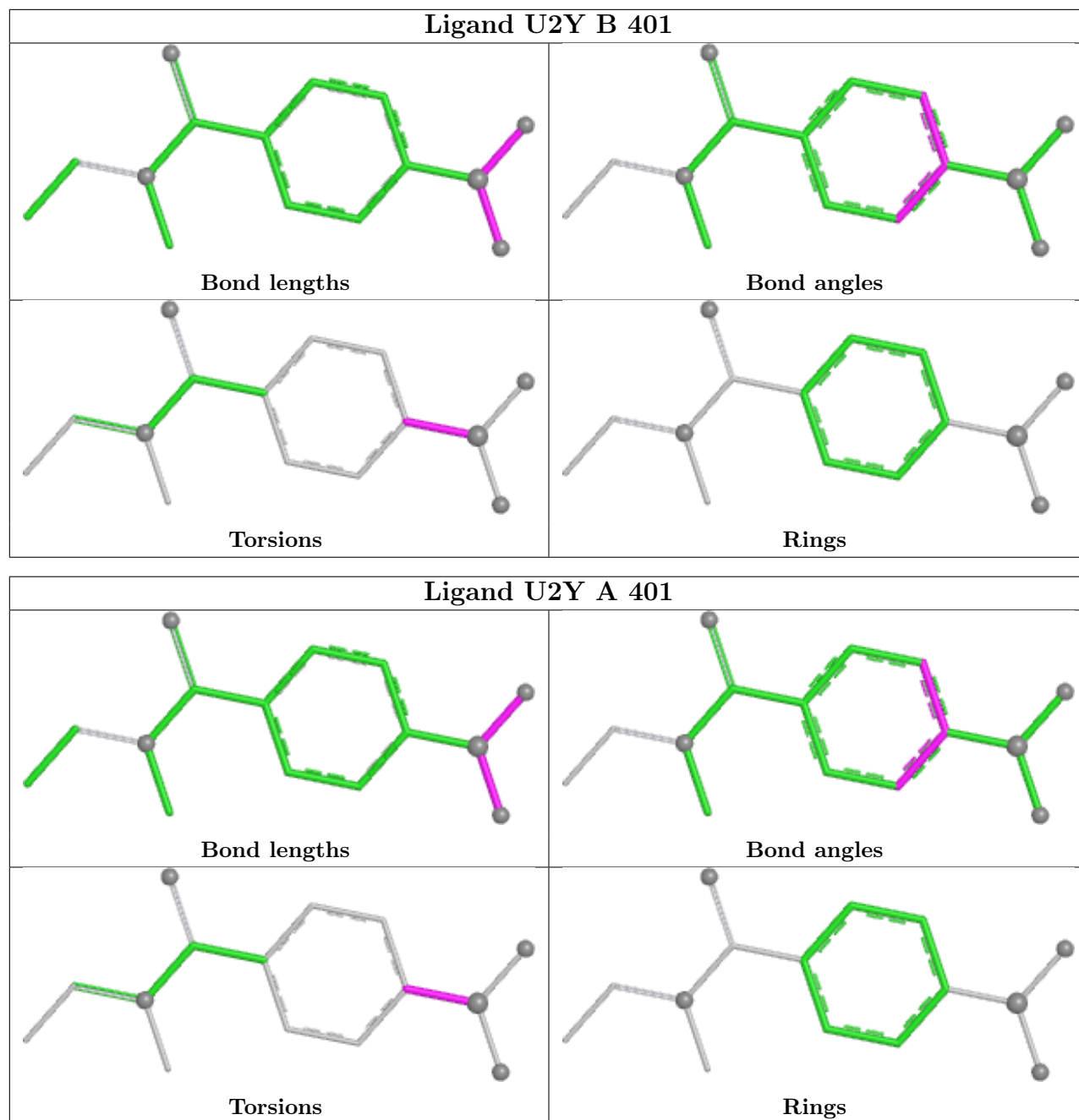
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 U2Y D 401



Ligand U2Y C 401





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	355/360 (98%)	0.19	7 (1%) 65 69	15, 32, 57, 88	1 (0%)
1	B	359/360 (99%)	-0.07	8 (2%) 62 66	9, 27, 50, 83	2 (0%)
1	C	357/360 (99%)	0.62	61 (17%) 4 5	11, 39, 77, 89	2 (0%)
1	D	357/360 (99%)	0.00	5 (1%) 73 77	14, 31, 54, 92	2 (0%)
All	All	1428/1440 (99%)	0.18	81 (5%) 29 33	9, 31, 64, 92	7 (0%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	382	LYS	5.1
1	C	125	ILE	5.0
1	B	24	GLY	4.7
1	C	127[A]	GLN	4.7
1	A	381	ILE	4.6
1	C	168	ILE	4.1
1	A	28	LYS	4.1
1	C	117	TRP	3.9
1	D	26	THR	3.6
1	C	171	TYR	3.6
1	A	29	ASP	3.3
1	C	167	PRO	3.3
1	C	330	SER	3.2
1	C	103	ASN	3.1
1	D	382	LYS	3.1
1	C	162	TRP	3.0
1	C	322	VAL	2.9
1	B	382	LYS	2.9
1	C	26	THR	2.9
1	C	282	GLY	2.8
1	D	27	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	159	PHE	2.8
1	C	325	ILE	2.8
1	C	130	LEU	2.7
1	C	128	VAL	2.7
1	C	323	THR	2.7
1	C	107	ILE	2.7
1	C	381	ILE	2.7
1	C	105	GLY	2.7
1	C	328	GLU	2.7
1	C	239	GLY	2.6
1	C	129	ASN	2.6
1	C	326	SER	2.6
1	C	288	THR	2.6
1	C	302	ALA	2.6
1	C	119	VAL	2.5
1	B	25	ASN	2.5
1	A	368	GLU	2.5
1	C	319	PRO	2.5
1	C	188	LEU	2.5
1	C	149	VAL	2.5
1	C	287	ASN	2.5
1	D	240	PRO	2.4
1	C	109	PHE	2.4
1	C	169	GLY	2.4
1	A	32	ILE	2.4
1	A	382	LYS	2.4
1	C	126	ASP	2.3
1	C	158	PHE	2.3
1	B	103	ASN	2.3
1	C	156	LEU	2.3
1	C	153	GLN	2.3
1	C	240	PRO	2.3
1	A	35	LEU	2.3
1	C	190	MET	2.3
1	B	381[A]	ILE	2.2
1	C	164	PRO	2.2
1	C	116	TYR	2.2
1	C	122	ASN	2.2
1	C	124	PRO	2.2
1	C	27	PRO	2.2
1	C	123	THR	2.2
1	C	110	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	119	VAL	2.2
1	C	131	LEU	2.2
1	C	189	SER	2.2
1	C	137	THR	2.2
1	C	151	THR	2.2
1	C	187	ALA	2.1
1	C	329	PRO	2.1
1	C	139	GLY	2.1
1	C	155	VAL	2.1
1	C	321	LYS	2.1
1	B	330	SER	2.1
1	C	283	PHE	2.1
1	B	26	THR	2.0
1	C	118	LYS	2.0
1	C	183	GLY	2.0
1	D	239	GLY	2.0
1	C	121	LYS	2.0
1	C	136	TYR	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 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(Å ²)	Q<0.9
5	EPE	C	404	15/15	0.56	0.28	45,54,89,90	15
3	CL	C	407	1/1	0.65	0.49	165,165,165,165	0
5	EPE	C	403	15/15	0.68	0.24	50,68,72,73	0
4	EDO	D	406	4/4	0.68	0.20	49,50,51,54	0
5	EPE	B	404	15/15	0.70	0.28	40,50,73,73	15

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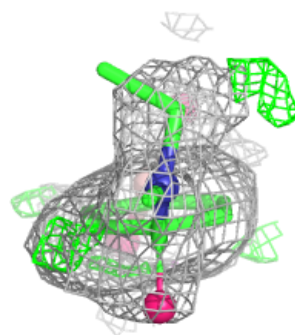
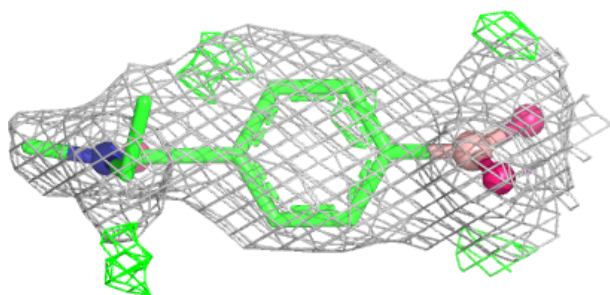
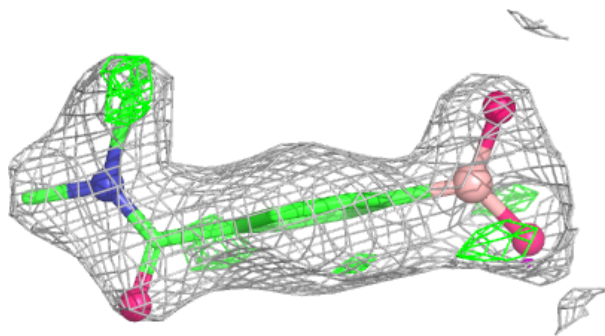
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	D	403	4/4	0.71	0.32	74,74,75,75	0
4	EDO	B	402	4/4	0.74	0.16	51,52,53,54	0
4	EDO	C	402	4/4	0.82	0.21	61,62,63,64	0
4	EDO	D	405	4/4	0.82	0.14	50,50,51,53	0
2	U2Y	A	401	15/15	0.83	0.16	27,38,49,49	0
4	EDO	C	405	4/4	0.83	0.10	51,53,55,56	0
4	EDO	C	406	4/4	0.83	0.21	46,46,46,47	0
5	EPE	D	404	15/15	0.83	0.16	44,51,55,58	0
2	U2Y	D	401	15/15	0.85	0.12	23,29,35,36	0
4	EDO	D	402	4/4	0.85	0.16	60,61,62,62	0
4	EDO	B	405	4/4	0.85	0.29	56,56,57,58	0
3	CL	C	408	1/1	0.86	0.10	65,65,65,65	0
4	EDO	D	407	4/4	0.87	0.12	48,48,49,50	0
2	U2Y	C	401	15/15	0.88	0.11	29,40,48,50	0
2	U2Y	B	401	15/15	0.90	0.11	16,26,36,37	0
3	CL	A	402	1/1	0.90	0.16	75,75,75,75	0
4	EDO	B	403	4/4	0.91	0.15	43,43,46,46	0

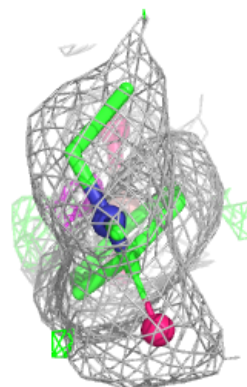
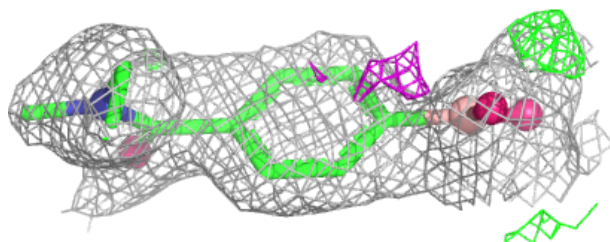
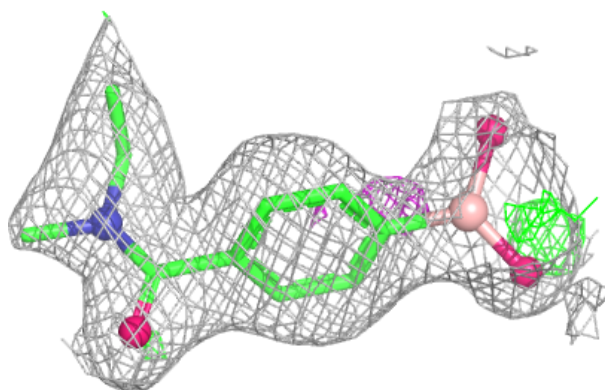
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around U2Y A 401:

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

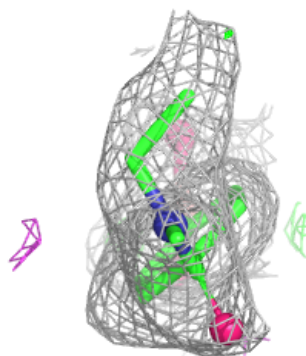
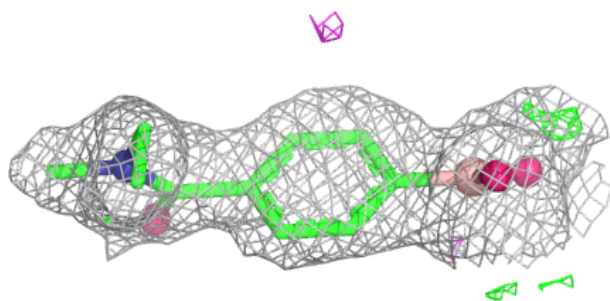
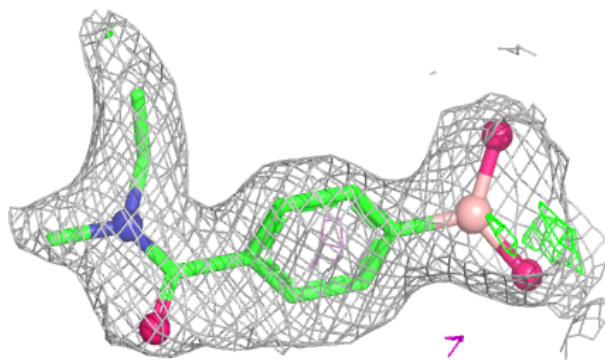
**Electron density around U2Y D 401:**

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

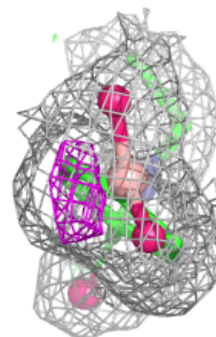
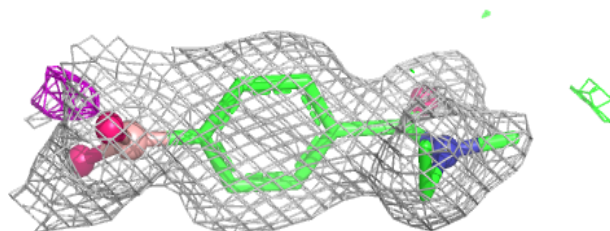
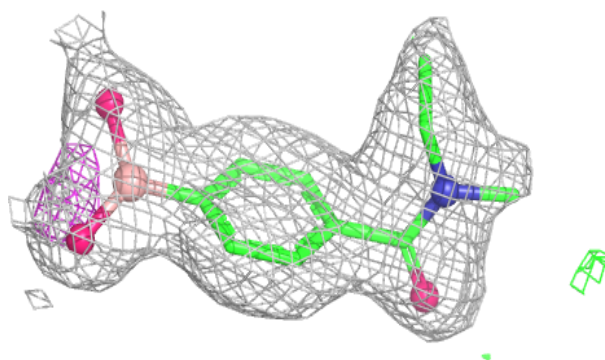


Electron density around U2Y C 401:

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

**Electron density around U2Y B 401:**

$2mF_o - DF_c$ (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.