



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:47 PM UTC

PDB ID : 6A94 / pdb_00006a94
Title : Crystal structure of 5-HT2AR in complex with zotepine
Authors : Kimura, T.K.; Asada, H.; Inoue, A.; Kadji, F.M.N.; Im, D.; Mori, C.; Arakawa, T.; Hirata, K.; Nomura, Y.; Nomura, N.; Aoki, J.; Iwata, S.; Shimamura, T.
Deposited on : 2018-07-11
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 ⓘ 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

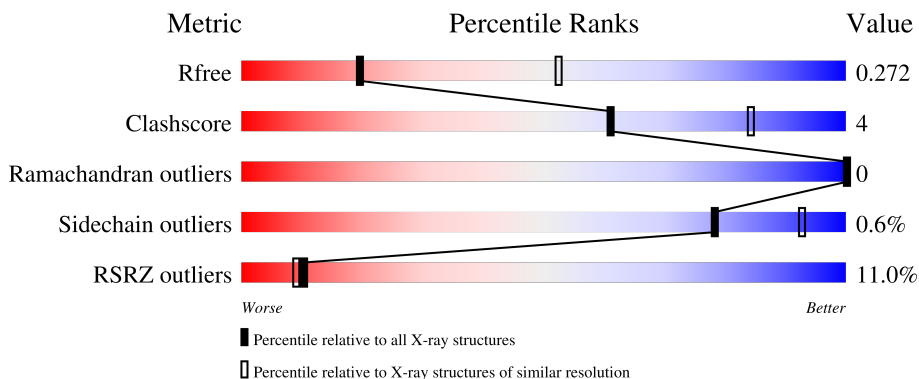
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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 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	376	6% 90% 9% .
1	B	376	15% 82% 13% 5%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5870 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 5-hydroxytryptamine receptor 2A, Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	370	Total	C	N	O	S	0	0	0
			2905	1904	464	519	18			
1	B	359	Total	C	N	O	S	0	0	0
			2818	1851	444	505	18			

There are 28 discrepancies between the modelled and reference sequences:

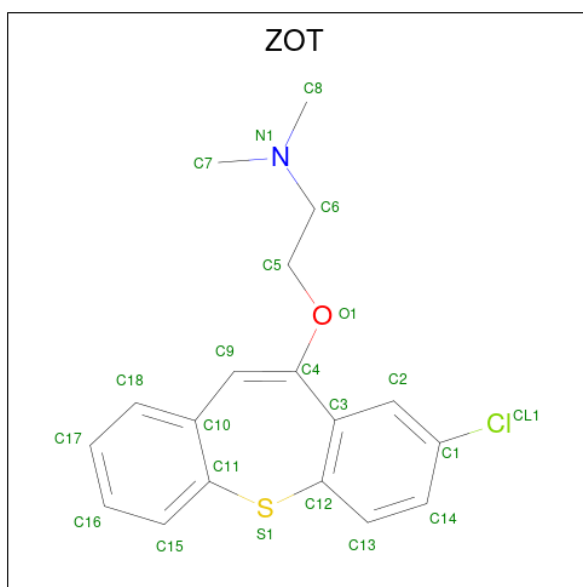
Chain	Residue	Modelled	Actual	Comment	Reference
A	67	GLY	-	expression tag	UNP P28223
A	68	GLY	-	expression tag	UNP P28223
A	69	THR	-	expression tag	UNP P28223
A	162	LYS	SER	engineered mutation	UNP P28223
A	164	TRP	MET	engineered mutation	UNP P28223
A	1007	TRP	MET	engineered mutation	UNP P0ABE7
A	1041	GLY	-	linker	UNP P0ABE7
A	1042	SER	-	linker	UNP P0ABE7
A	1043	GLY	-	linker	UNP P0ABE7
A	1044	SER	-	linker	UNP P0ABE7
A	1045	GLY	-	linker	UNP P0ABE7
A	1098	ILE	ARG	engineered mutation	UNP P0ABE7
A	1102	ILE	HIS	engineered mutation	UNP P0ABE7
A	1106	GLY	ARG	engineered mutation	UNP P0ABE7
B	67	GLY	-	expression tag	UNP P28223
B	68	GLY	-	expression tag	UNP P28223
B	69	THR	-	expression tag	UNP P28223
B	162	LYS	SER	engineered mutation	UNP P28223
B	164	TRP	MET	engineered mutation	UNP P28223
B	1007	TRP	MET	engineered mutation	UNP P0ABE7
B	1041	GLY	-	linker	UNP P0ABE7
B	1062	SER	-	linker	UNP P0ABE7
B	1063	GLY	-	linker	UNP P0ABE7
B	1064	SER	-	linker	UNP P0ABE7
B	1065	GLY	-	linker	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1098	ILE	ARG	engineered mutation	UNP P0ABE7
B	1102	ILE	HIS	engineered mutation	UNP P0ABE7
B	1106	GLY	ARG	engineered mutation	UNP P0ABE7

- Molecule 2 is 2-(3-chloranylbenzo[b][1]benzothiepin-5-yl)oxy-N,N-dimethyl-ethanamine (CCD ID: ZOT) (formula: C₁₈H₁₈ClNOS).



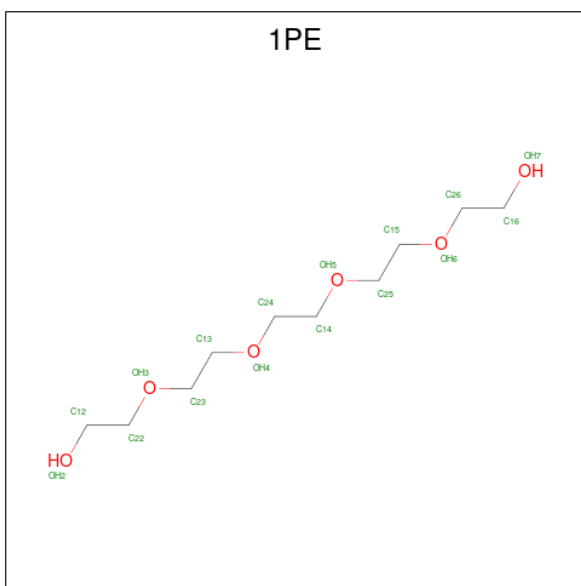
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	S	0	0
			22	18	1	1	1	1		
2	B	1	Total	C	Cl	N	O	S	0	0
			22	18	1	1	1	1		

- Molecule 3 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			28	27	1		
3	B	1	Total	C	O	0	0
			28	27	1		

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).

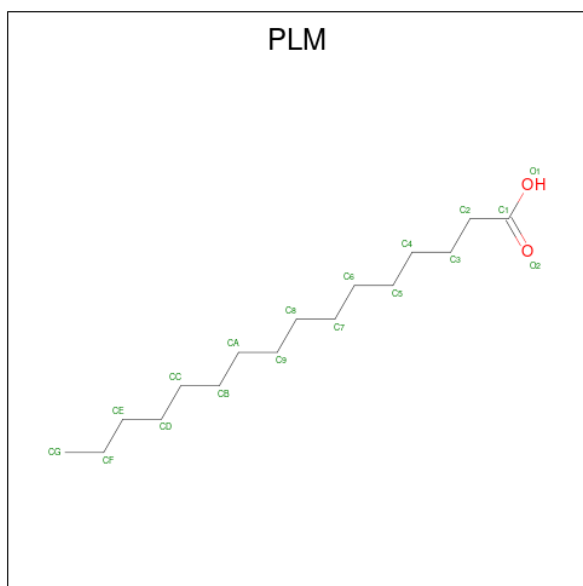


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			16	10	6		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

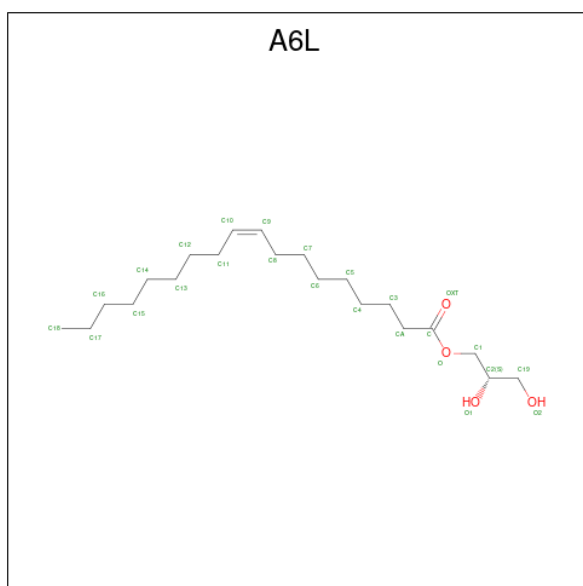
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

- Molecule 6 is PALMITIC ACID (CCD ID: PLM) (formula: $C_{16}H_{32}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			10	9	1		

- Molecule 7 is 2,3-dihydroxypropyl (9Z)-octadec-9-enoate (CCD ID: A6L) (formula: $C_{21}H_{40}O_4$).

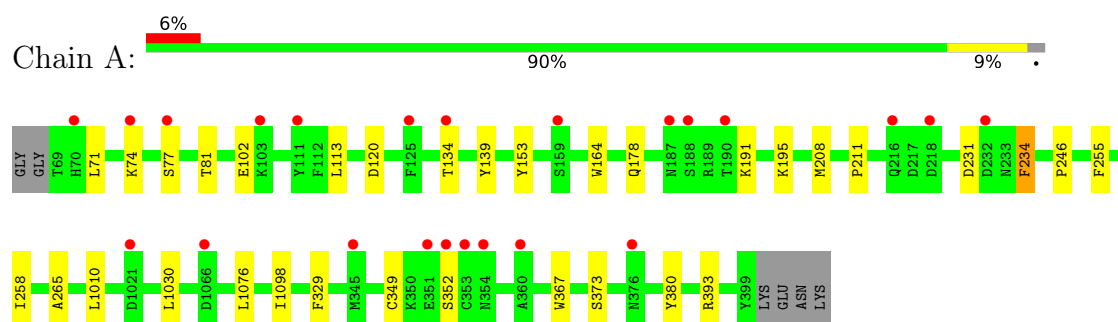


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			20	18	2		

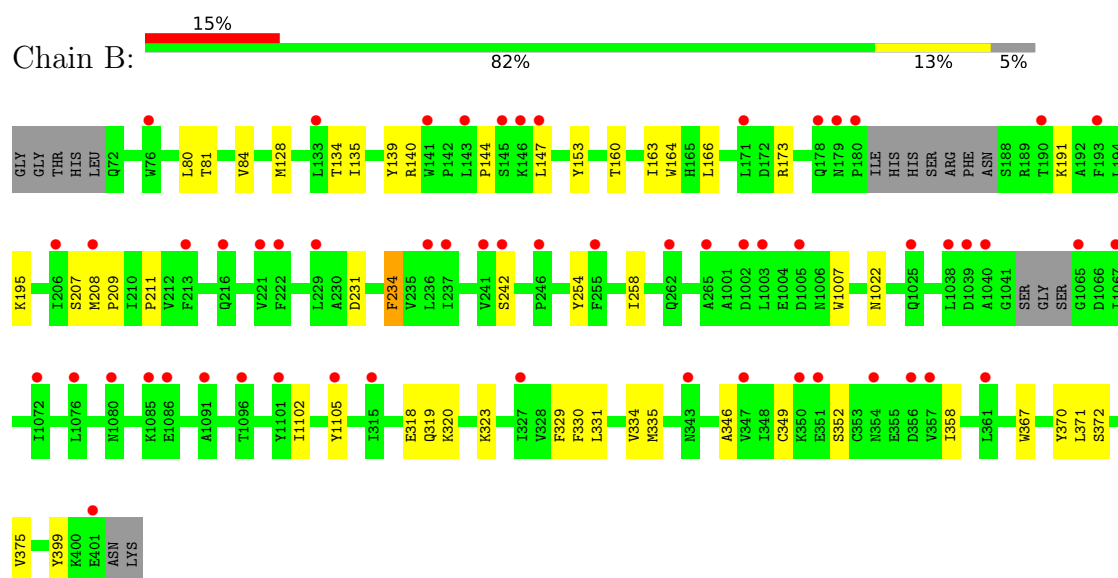
3 Residue-property plots [i](#)

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: 5-hydroxytryptamine receptor 2A,Soluble cytochrome b562



- Molecule 1: 5-hydroxytryptamine receptor 2A,Soluble cytochrome b562



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	279.18Å 42.22Å 91.71Å 90.00° 92.16° 90.00°	Depositor
Resolution (Å)	45.82 – 2.90 45.82 – 2.90	Depositor EDS
% Data completeness (in resolution range)	86.7 (45.82-2.90) 86.7 (45.82-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.13 (at 2.91Å)	Xtriage
Refinement program	PHENIX (1.13_2998)	Depositor
R, R_{free}	0.236 , 0.269 0.238 , 0.272	Depositor DCC
R_{free} test set	1064 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 67.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5870	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.56% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PLM, A6L, ZN, ZOT, CLR, 1PE

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	0.18	0/2966	0.34	0/4030
1	B	0.15	0/2873	0.31	0/3900
All	All	0.17	0/5839	0.33	0/7930

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2905	0	2986	18	0
1	B	2818	0	2906	31	0
2	A	22	0	0	0	0
2	B	22	0	0	0	0
3	A	28	0	46	1	0
3	B	28	0	46	0	0
4	A	16	0	22	2	0
5	A	1	0	0	0	0
6	B	10	0	14	0	0
7	B	20	0	0	0	0
All	All	5870	0	6020	50	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 (50) 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:319:GLN:HG2	1:B:323:LYS:HE3	1.73	0.69
1:A:231:ASP:HB3	1:A:234:PHE:HB2	1.76	0.68
1:B:231:ASP:HB3	1:B:234:PHE:HB2	1.78	0.65
1:B:1105:TYR:N	1:B:1105:TYR:HD1	2.03	0.57
1:B:346:ALA:HB2	1:B:358:ILE:HG21	1.86	0.57
1:B:1007:TRP:HD1	1:B:1102:ILE:HG13	1.70	0.56
1:B:331:LEU:HD22	1:B:335:MET:HE3	1.88	0.55
1:B:371:LEU:O	1:B:375:VAL:HG13	2.07	0.55
1:A:71:LEU:HA	1:A:74:LYS:HE3	1.89	0.54
1:B:1105:TYR:N	1:B:1105:TYR:CD1	2.74	0.54
1:A:349:CYS:HB2	1:A:352:SER:HB3	1.90	0.53
1:B:349:CYS:HB2	1:B:352:SER:HB3	1.91	0.52
1:A:164:TRP:CZ2	1:A:246:PRO:HG3	2.45	0.51
1:A:191:LYS:HG3	1:A:195:LYS:HE3	1.93	0.51
1:A:102:GLU:OE2	1:A:393:ARG:NH2	2.37	0.50
1:B:207:SER:O	1:B:211:PRO:HD2	2.12	0.50
1:A:153:TYR:HB2	1:A:211:PRO:HG3	1.94	0.49
1:A:265:ALA:HB1	4:A:3003:1PE:H141	1.95	0.48
1:B:135:ILE:HD11	1:B:367:TRP:HE1	1.78	0.48
1:B:320:LYS:HA	1:B:323:LYS:HD2	1.96	0.48
1:A:255:PHE:O	1:A:258:ILE:HG12	2.15	0.47
1:B:128:MET:HE3	1:B:370:TYR:HB3	1.95	0.47
1:A:120:ASP:OD1	1:A:373:SER:OG	2.32	0.46
1:B:173:ARG:NH1	1:B:318:GLU:OE1	2.49	0.46
1:B:134:THR:HG22	1:B:139:TYR:HA	1.98	0.45
1:B:153:TYR:HB2	1:B:211:PRO:HD3	1.99	0.45
1:A:1010:LEU:HD13	1:A:1098:ILE:HG23	1.98	0.45
1:B:144:PRO:HD2	1:B:147:LEU:HD12	1.97	0.45
1:B:191:LYS:HG2	1:B:195:LYS:HE3	1.99	0.45
1:B:372:SER:O	1:B:375:VAL:HG22	2.16	0.45
1:A:1030:LEU:HB3	1:A:1076:LEU:HG	1.98	0.44
1:B:160:THR:HA	1:B:163:ILE:HG22	1.99	0.44
1:B:254:TYR:O	1:B:258:ILE:HG23	2.19	0.43
1:B:331:LEU:HD23	1:B:331:LEU:HA	1.88	0.43
1:B:166:LEU:HD22	1:B:329:PHE:HE1	1.84	0.42
1:A:113:LEU:HD22	1:A:380:TYR:OH	2.19	0.42
1:B:208:MET:N	1:B:209:PRO:HD2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:81:THR:HB	1:A:367:TRP:CH2	2.55	0.42
1:B:80:LEU:O	1:B:84:VAL:HG23	2.21	0.41
4:A:3003:1PE:H121	4:A:3003:1PE:H232	1.84	0.41
1:B:163:ILE:HG21	1:B:242:SER:O	2.20	0.41
3:A:3002:CLR:H211	3:A:3002:CLR:H232	1.85	0.41
1:A:134:THR:HG22	1:A:139:TYR:HA	2.03	0.41
1:A:178:GLN:HG2	1:B:399:TYR:HB2	2.03	0.41
1:B:160:THR:HG22	1:B:164:TRP:HD1	1.86	0.41
1:B:1022:ASN:OD1	1:B:1022:ASN:N	2.54	0.41
1:B:330:PHE:CZ	1:B:334:VAL:HG21	2.56	0.41
1:B:81:THR:HB	1:B:367:TRP:CH2	2.56	0.40
1:A:77:SER:O	1:A:81:THR:HG23	2.21	0.40
1:A:208:MET:O	1:A:211:PRO:HD2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	368/376 (98%)	360 (98%)	8 (2%)	0	100	100
1	B	353/376 (94%)	348 (99%)	5 (1%)	0	100	100
All	All	721/752 (96%)	708 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	318/322 (99%)	316 (99%)	2 (1%)	78	93
1	B	308/322 (96%)	306 (99%)	2 (1%)	78	93
All	All	626/644 (97%)	622 (99%)	4 (1%)	78	93

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	PHE
1	A	329	PHE
1	B	140	ARG
1	B	234	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	ASN
1	B	317	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 1 is monoatomic - leaving 7 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
3	CLR	A	3002	-	31,31,31	0.68	0	48,48,48	0.98	2 (4%)
7	A6L	B	3004	-	19,19,24	1.25	2 (10%)	19,19,25	1.19	2 (10%)
2	ZOT	B	3001	-	23,24,24	2.76	4 (17%)	27,33,33	2.14	7 (25%)
2	ZOT	A	3001	-	23,24,24	2.61	3 (13%)	27,33,33	2.03	7 (25%)
6	PLM	B	3002	1	8,9,17	0.64	0	7,8,17	0.56	0
4	1PE	A	3003	-	15,15,15	0.58	0	14,14,14	0.45	0
3	CLR	B	3003	-	31,31,31	0.72	0	48,48,48	1.20	4 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CLR	A	3002	-	-	7/10/68/68	0/4/4/4
7	A6L	B	3004	-	-	7/17/17/24	-
2	ZOT	B	3001	-	-	4/6/18/18	0/2/3/3
2	ZOT	A	3001	-	-	4/6/18/18	0/2/3/3
6	PLM	B	3002	1	-	0/7/7/15	-
4	1PE	A	3003	-	-	5/13/13/13	-
3	CLR	B	3003	-	-	6/10/68/68	0/4/4/4

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	3001	ZOT	C3-C4	-11.35	1.39	1.48
2	A	3001	ZOT	C3-C4	-11.01	1.39	1.48
7	B	3004	A6L	OXT-C	4.60	1.37	1.22
2	A	3001	ZOT	C10-C9	-4.28	1.39	1.46
2	B	3001	ZOT	C10-C9	-4.28	1.39	1.46
2	B	3001	ZOT	C11-S1	-3.96	1.74	1.78
7	B	3004	A6L	O-C	-2.33	1.23	1.30
2	A	3001	ZOT	C11-S1	-2.32	1.76	1.78
2	B	3001	ZOT	C12-S1	-2.26	1.76	1.78

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	3001	ZOT	C2-C3-C4	-7.05	109.64	118.97
2	A	3001	ZOT	C2-C3-C4	-6.83	109.93	118.97
2	B	3001	ZOT	C18-C10-C9	-4.23	110.04	117.53
2	A	3001	ZOT	C18-C10-C9	-4.05	110.36	117.53
7	B	3004	A6L	O-C-CA	3.84	126.12	114.00
3	B	3003	CLR	C13-C17-C20	-3.49	114.11	119.50
2	B	3001	ZOT	C15-C11-S1	-3.43	109.99	118.28
2	B	3001	ZOT	C13-C12-S1	-3.36	110.15	118.28
2	B	3001	ZOT	C10-C11-S1	3.22	129.77	121.45
2	B	3001	ZOT	C3-C12-S1	3.11	130.18	121.71
2	A	3001	ZOT	C15-C11-S1	-3.08	110.84	118.28
2	A	3001	ZOT	C13-C12-S1	-2.99	111.06	118.28
2	A	3001	ZOT	C10-C11-S1	2.97	129.12	121.45
7	B	3004	A6L	OXT-C-CA	-2.81	114.19	123.09
2	A	3001	ZOT	C3-C12-S1	2.73	129.15	121.71
3	B	3003	CLR	C3-C4-C5	-2.35	108.31	112.05
3	B	3003	CLR	C8-C7-C6	-2.27	109.61	112.76
2	B	3001	ZOT	O1-C4-C9	-2.23	119.33	123.13
2	A	3001	ZOT	O1-C4-C9	-2.23	119.33	123.13
3	B	3003	CLR	C17-C13-C14	2.15	102.56	100.10
3	A	3002	CLR	C13-C17-C20	-2.03	116.36	119.50
3	A	3002	CLR	C3-C4-C5	-2.01	108.85	112.05

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	3001	ZOT	C3-C4-O1-C5
2	A	3001	ZOT	C9-C4-O1-C5
2	B	3001	ZOT	C3-C4-O1-C5
2	B	3001	ZOT	C9-C4-O1-C5
3	B	3003	CLR	C17-C20-C22-C23
2	A	3001	ZOT	O1-C5-C6-N1
3	A	3002	CLR	C21-C20-C22-C23
2	A	3001	ZOT	C6-C5-O1-C4
2	B	3001	ZOT	C6-C5-O1-C4
7	B	3004	A6L	C11-C12-C13-C14
3	B	3003	CLR	C21-C20-C22-C23
7	B	3004	A6L	C15-C16-C17-C18
3	B	3003	CLR	C13-C17-C20-C22
7	B	3004	A6L	C12-C13-C14-C15

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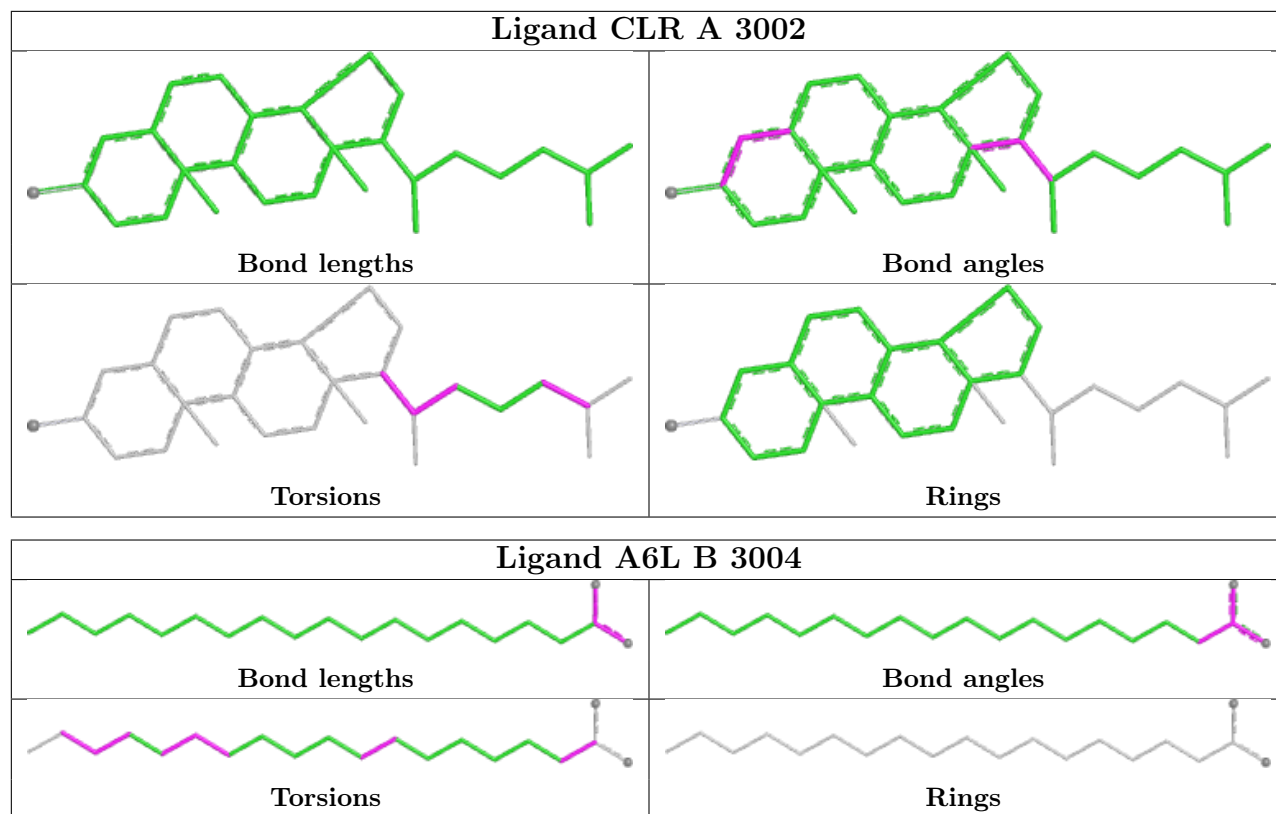
Mol	Chain	Res	Type	Atoms
3	B	3003	CLR	C13-C17-C20-C21
4	A	3003	1PE	C24-C14-OH5-C25
3	A	3002	CLR	C13-C17-C20-C21
3	A	3002	CLR	C13-C17-C20-C22
7	B	3004	A6L	C14-C15-C16-C17
4	A	3003	1PE	C16-C26-OH6-C15
3	A	3002	CLR	C23-C24-C25-C27
3	B	3003	CLR	C16-C17-C20-C22
3	A	3002	CLR	C16-C17-C20-C22
4	A	3003	1PE	C12-C22-OH3-C23
7	B	3004	A6L	C6-C7-C8-C9
3	A	3002	CLR	C23-C24-C25-C26
4	A	3003	1PE	OH6-C15-C25-OH5
2	B	3001	ZOT	O1-C5-C6-N1
4	A	3003	1PE	OH5-C14-C24-OH4
3	A	3002	CLR	C16-C17-C20-C21
3	B	3003	CLR	C16-C17-C20-C21
7	B	3004	A6L	O-C-CA-C3
7	B	3004	A6L	OXT-C-CA-C3

There are no ring outliers.

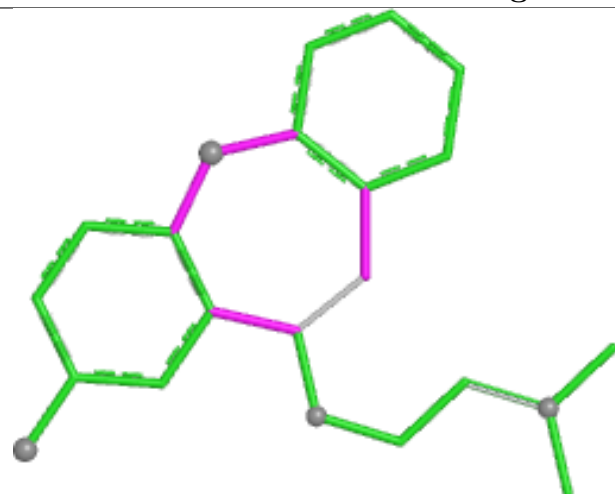
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3002	CLR	1	0
4	A	3003	1PE	2	0

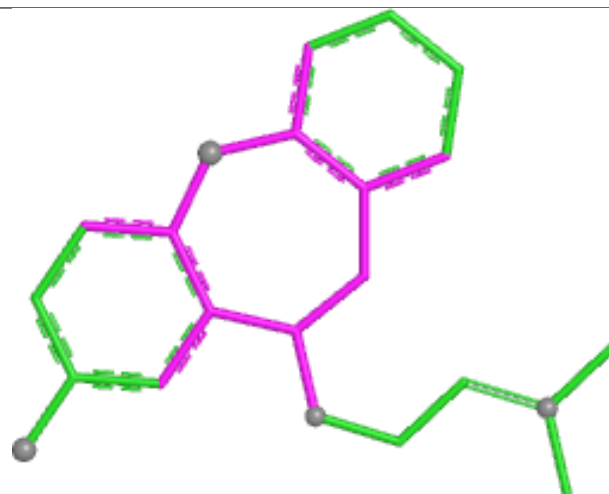
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



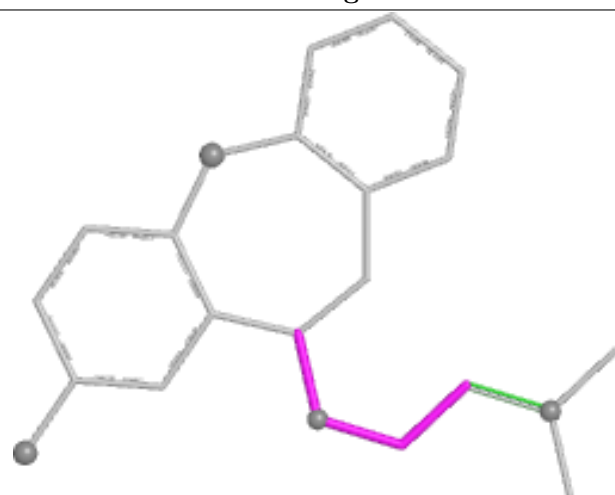
Ligand ZOT B 3001



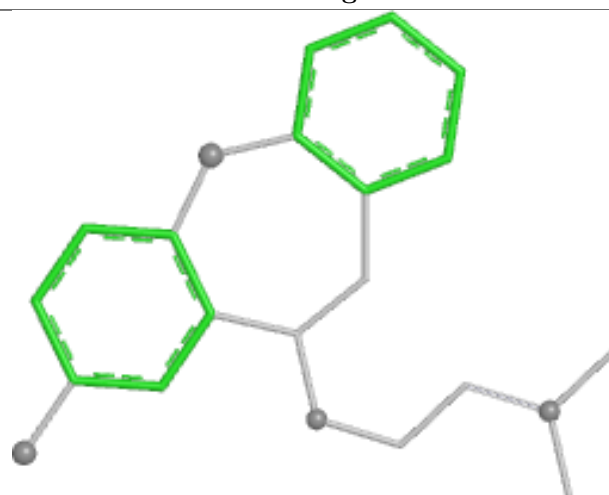
Bond lengths



Bond angles

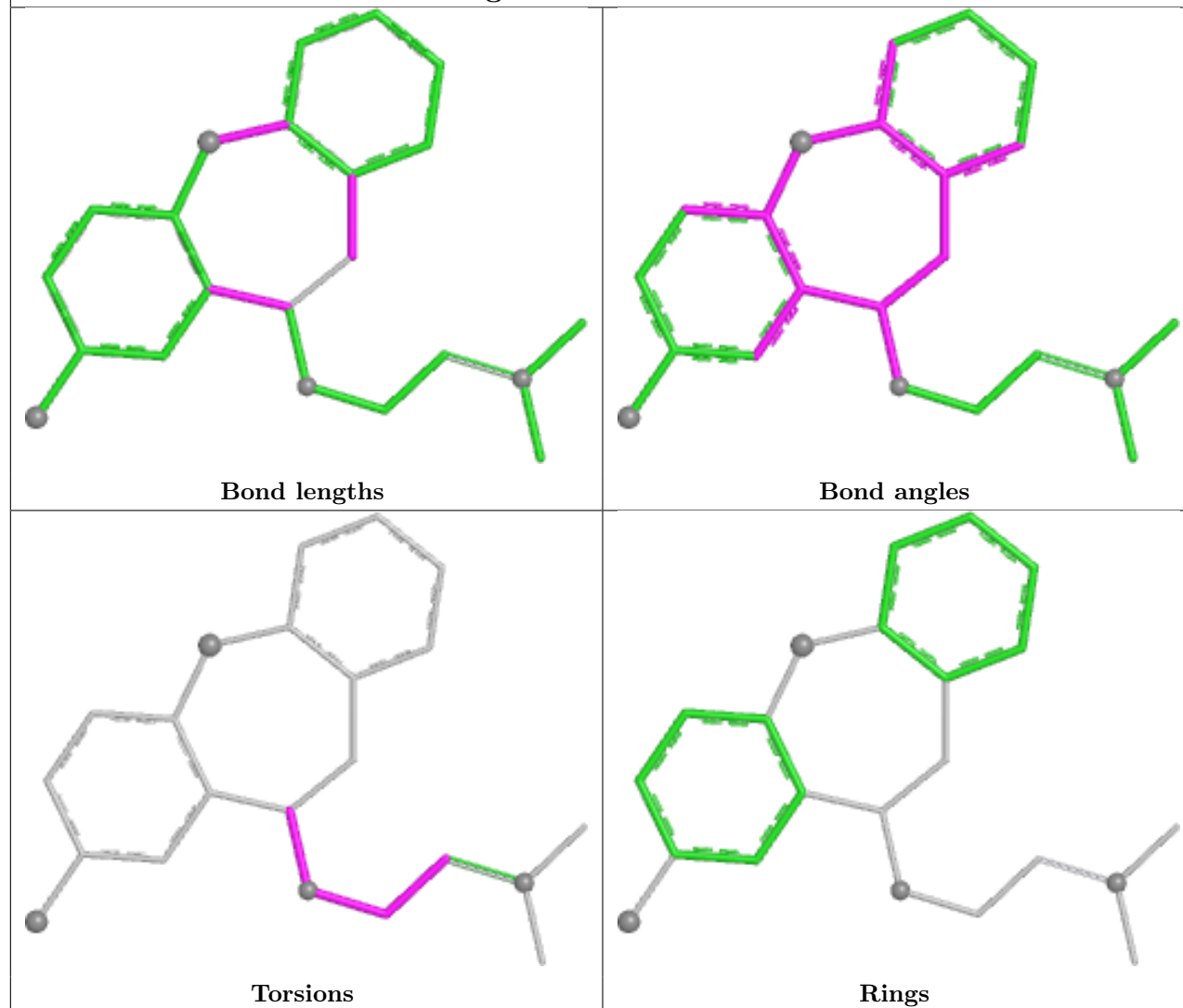


Torsions

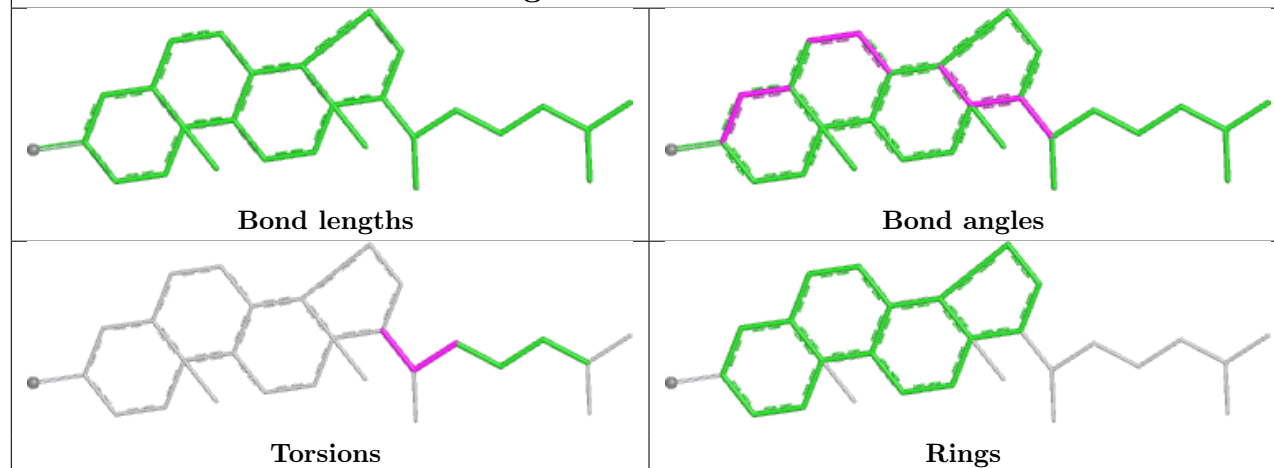


Rings

Ligand ZOT A 3001



Ligand CLR B 3003



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	370/376 (98%)	0.52	23 (6%) 26 21	12, 65, 117, 172	0
1	B	359/376 (95%)	1.14	57 (15%) 5 4	35, 86, 124, 159	0
All	All	729/752 (96%)	0.83	80 (10%) 10 9	12, 77, 121, 172	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1105	TYR	4.6
1	B	147	LEU	4.5
1	B	350	LYS	4.0
1	B	146	LYS	3.8
1	B	255	PHE	3.7
1	B	343	ASN	3.7
1	B	213	PHE	3.5
1	B	351	GLU	3.5
1	B	1002	ASP	3.4
1	B	1096	THR	3.4
1	B	354	ASN	3.4
1	B	208	MET	3.3
1	B	76	TRP	3.3
1	A	1066	ASP	3.2
1	B	1091	ALA	3.2
1	B	1067	ILE	3.2
1	B	180	PRO	3.2
1	A	376	ASN	3.1
1	B	1086	GLU	3.1
1	A	351	GLU	3.1
1	B	356	ASP	3.0
1	B	357	VAL	3.0
1	B	206	ILE	2.9
1	B	1101	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	190	THR	2.9
1	B	141	TRP	2.8
1	A	232	ASP	2.8
1	B	1065	GLY	2.8
1	B	178	GLN	2.7
1	B	145	SER	2.7
1	A	70	HIS	2.7
1	B	1039	ASP	2.7
1	A	216	GLN	2.7
1	B	143	LEU	2.7
1	B	246	PRO	2.6
1	A	352	SER	2.5
1	B	265	ALA	2.5
1	A	354	ASN	2.5
1	B	241	VAL	2.5
1	B	1038	LEU	2.4
1	B	1085	LYS	2.4
1	A	187	ASN	2.4
1	A	360	ALA	2.4
1	B	327	ILE	2.4
1	A	125	PHE	2.4
1	A	188	SER	2.4
1	B	179	ASN	2.3
1	A	159	SER	2.3
1	B	221	VAL	2.3
1	B	229	LEU	2.3
1	B	1005	ASP	2.3
1	B	1025	GLN	2.3
1	A	77	SER	2.3
1	A	190	THR	2.3
1	A	1021	ASP	2.2
1	B	347	VAL	2.2
1	A	134	THR	2.2
1	B	315	ILE	2.2
1	B	193	PHE	2.2
1	B	237	ILE	2.1
1	A	74	LYS	2.1
1	B	401	GLU	2.1
1	B	216	GLN	2.1
1	B	1076	LEU	2.1
1	B	242	SER	2.1
1	B	1072	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	133	LEU	2.1
1	B	361	LEU	2.1
1	B	222	PHE	2.1
1	A	111	TYR	2.1
1	B	1080	ASN	2.1
1	B	1003	LEU	2.1
1	A	353	CYS	2.0
1	B	171	LEU	2.0
1	B	236	LEU	2.0
1	A	218	ASP	2.0
1	A	103	LYS	2.0
1	B	262	GLN	2.0
1	B	1040	ALA	2.0
1	A	345	MET	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](#)

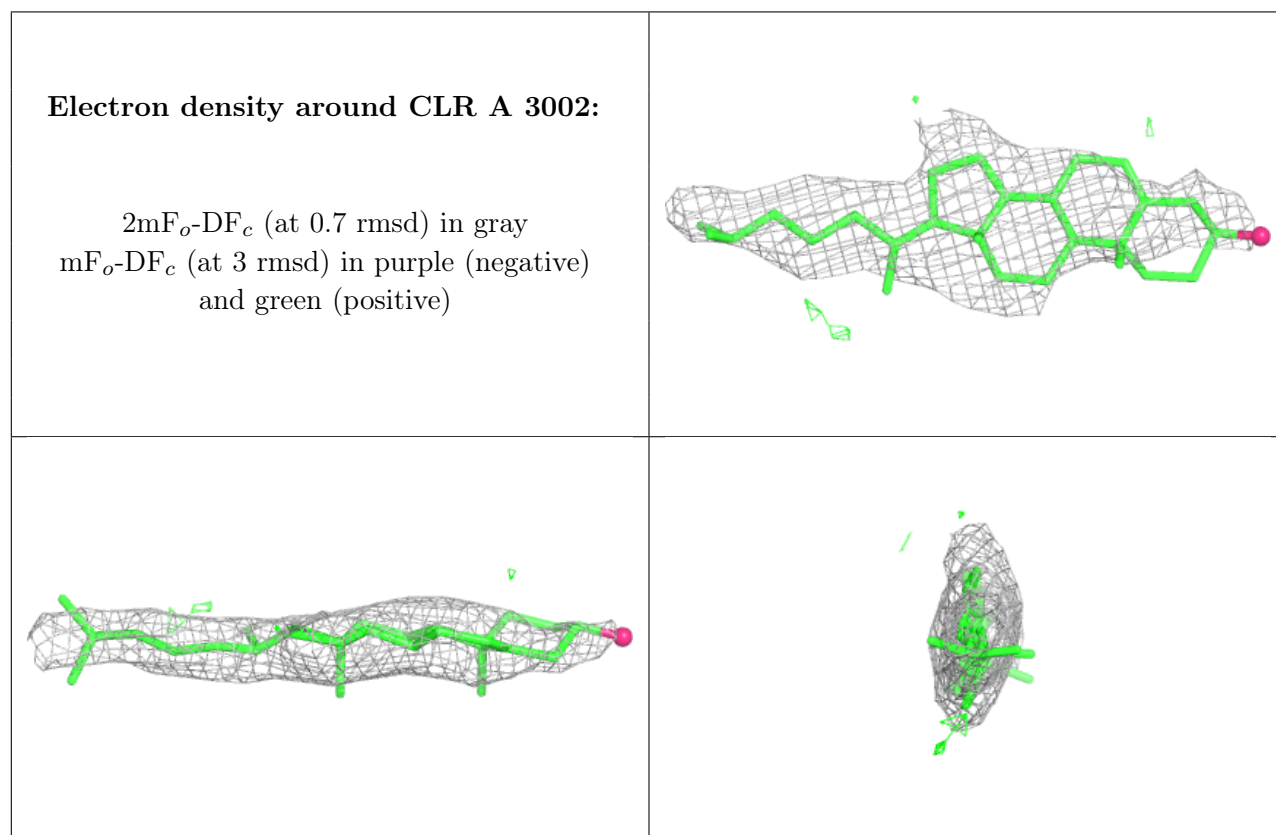
There are no oligosaccharides in this entry.

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.

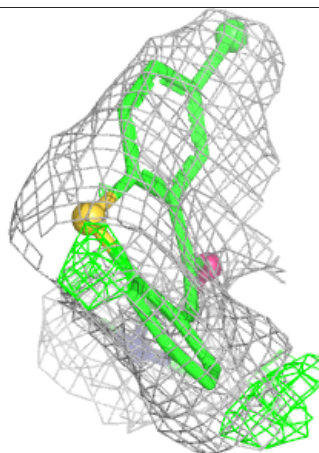
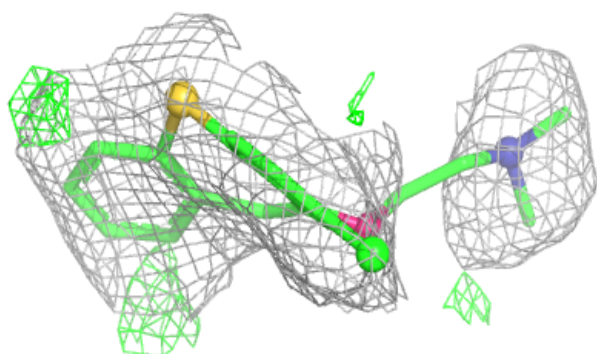
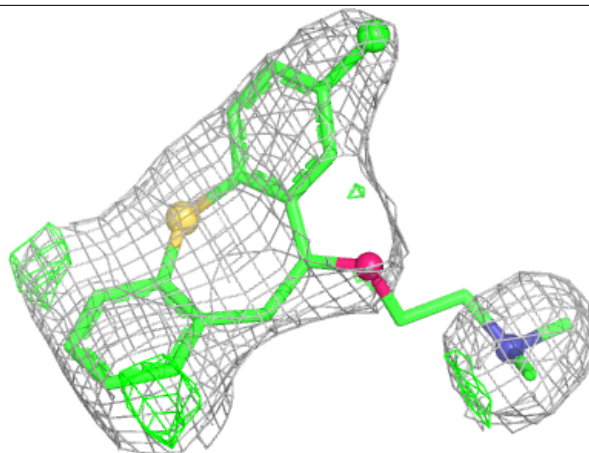
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CLR	A	3002	28/28	0.79	0.22	54,77,87,89	0
2	ZOT	B	3001	22/22	0.81	0.20	64,85,100,114	0
3	CLR	B	3003	28/28	0.89	0.12	34,52,61,62	0
4	1PE	A	3003	16/16	0.92	0.13	32,51,74,75	0
6	PLM	B	3002	10/18	0.92	0.12	29,38,46,48	0
2	ZOT	A	3001	22/22	0.93	0.11	41,55,61,63	0
7	A6L	B	3004	20/25	0.94	0.11	1,44,55,65	0
5	ZN	A	3004	1/1	1.00	0.03	27,27,27,27	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.

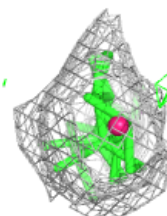
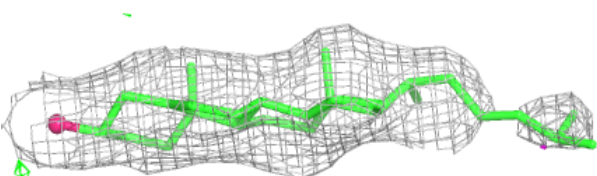
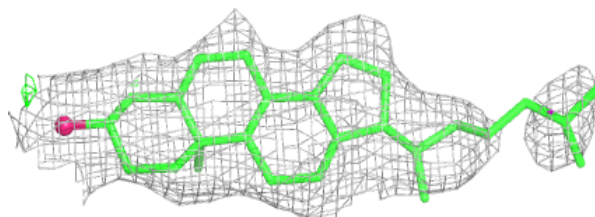


Electron density around ZOT B 3001:

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

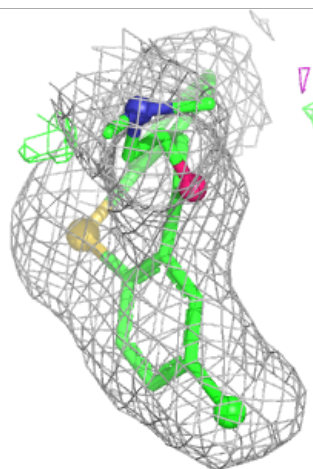
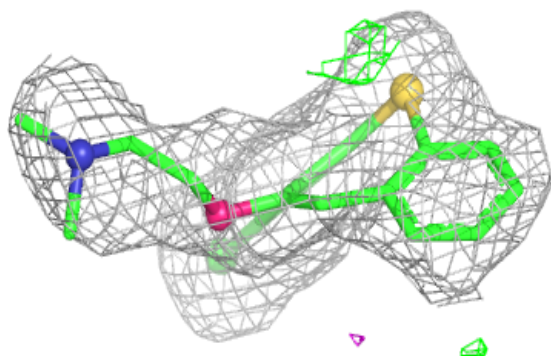
**Electron density around CLR B 3003:**

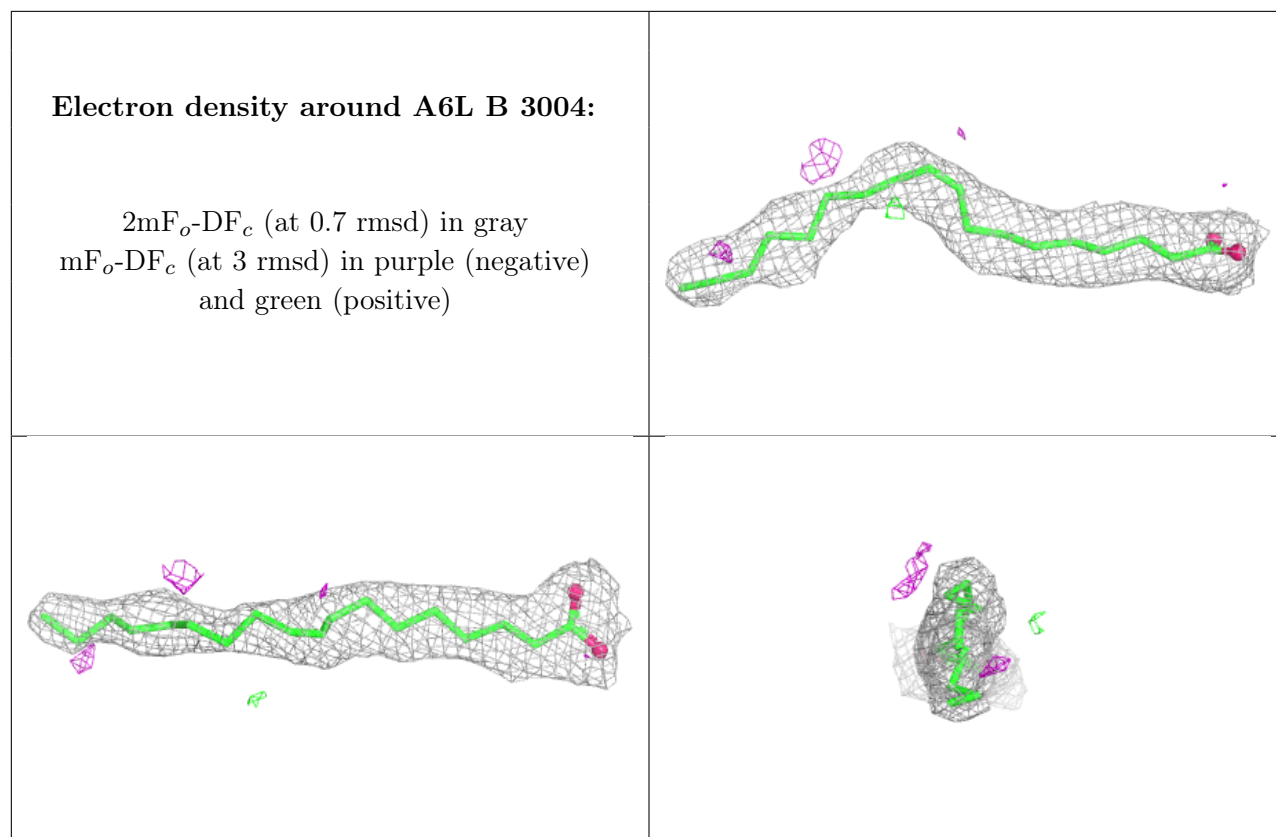
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZOT A 3001:

$2mF_o-DF_c$ (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.