



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:14 AM UTC

PDB ID : 6FQS / pdb_00006fqs
Title : 3.11A complex of S.Aureus gyrase with imidazopyrazinone T3 and DNA
Authors : Bax, B.D.; Germe, T.; Basque, E.; Maxwell, A.
Deposited on : 2018-02-14
Resolution : 3.11 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

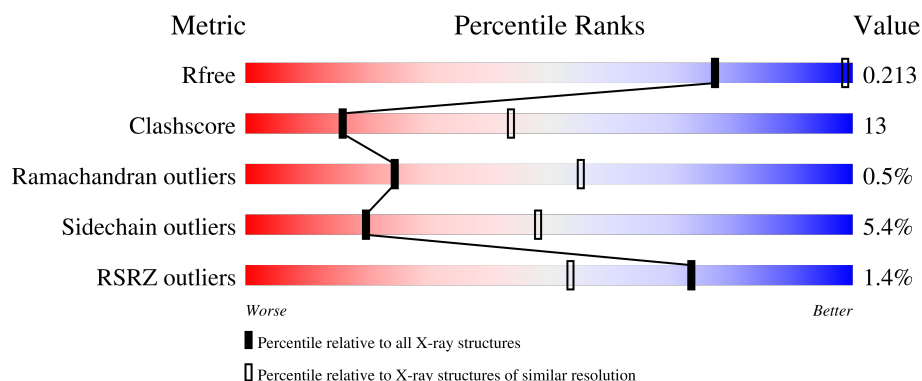
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 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	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)

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	B	202	 7% 65% 23% 6% 6%
1	D	202	 % 66% 23% • 6%
2	A	490	 76% 20% • •
3	C	490	 78% 19% • •
4	E	20	 45% 50% 5%

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Mol	Chain	Length	Quality of chain
4	F	20	

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
9	E3E	E	103[B]	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 11870 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 DNA gyrase subunit B,DNA gyrase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	189	Total	C	N	O	S	0	4	0
			1464	920	252	284	8			
1	D	189	Total	C	N	O	S	0	2	0
			1466	922	252	282	10			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	409	MET	LEU	conflict	UNP P66937
B	544	THR	-	linker	UNP P66937
B	579	GLY	-	linker	UNP P66937
D	409	MET	LEU	conflict	UNP P66937
D	544	THR	-	linker	UNP P66937
D	545	GLY	-	linker	UNP P66937

- Molecule 2 is a protein called DNA gyrase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	481	Total	C	N	O	S	0	6	0
			3883	2413	709	745	16			

- Molecule 3 is a protein called DNA gyrase subunit A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	481	Total	C	N	O	P	S	0	11	0
			3907	2421	708	759	1	18			

- Molecule 4 is a DNA chain called DNA (5'-D(*GP*AP*GP*AP*GP*TP*AP*T*GP*GP*CP*CP*AP*TP*AP*CP*TP*CP*TP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	20	Total	C	N	O	P	0	3	0
			462	223	85	133	21			
4	F	20	Total	C	N	O	P	0	2	0
			448	215	81	131	21			

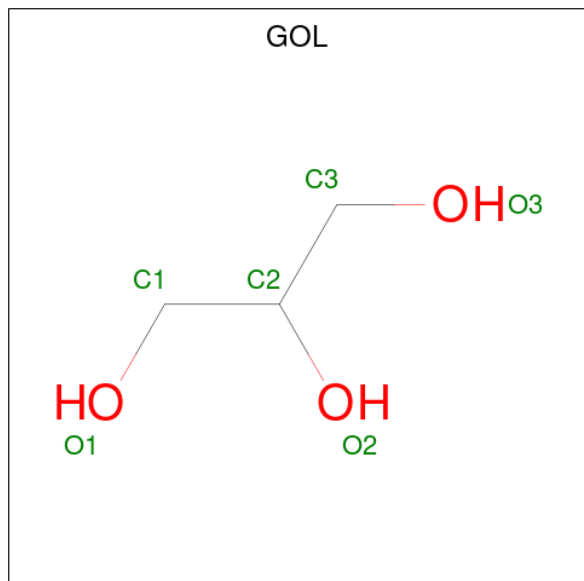
- Molecule 5 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mn	0	0
			1	1		
5	D	1	Total	Mn	0	0
			1	1		

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 7 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		

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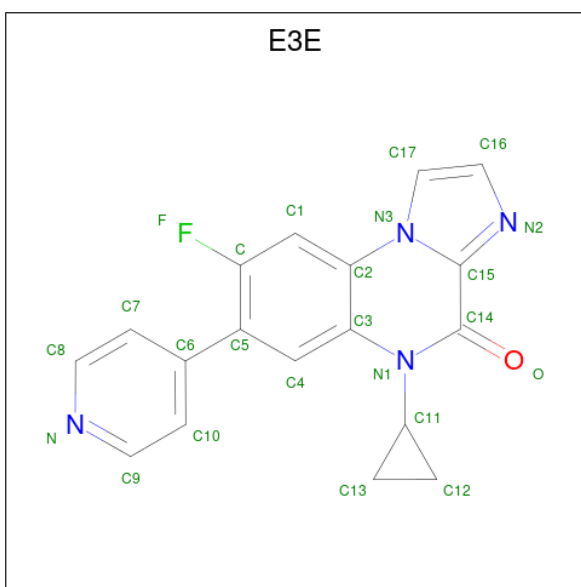
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			6	3	3		
7	A	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	C	1	Total	C	O	0	0
			6	3	3		
7	E	1	Total	C	O	0	0
			6	3	3		

- Molecule 8 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 9 is 5-cyclopropyl-8-fluoranyl-7-pyridin-4-yl-imidazo[1,2-a]quinoxalin-4-one (CCD ID: E3E) (formula: C₁₈H₁₃FN₄O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	E	1	Total	C	F	N	O	0	0
			24	18	1	4	1		
9	E	1	Total	C	F	N	O	0	1
			48	36	2	8	2		

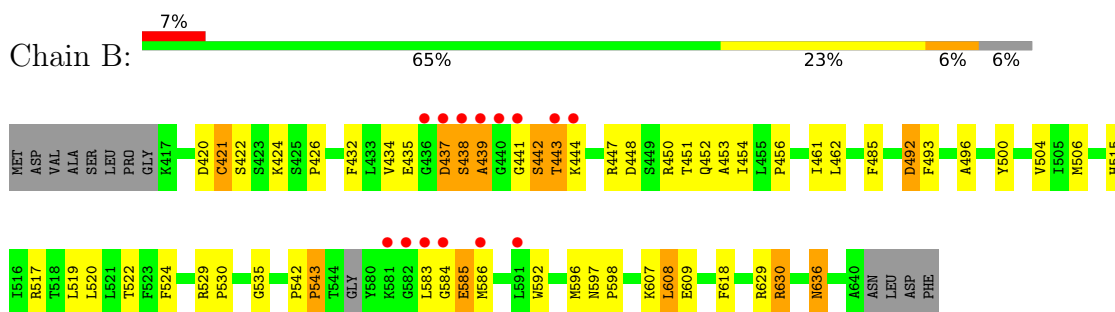
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	8	Total	O	0	0
			8	8		
10	A	46	Total	O	0	0
			46	46		
10	D	4	Total	O	0	0
			4	4		
10	C	39	Total	O	0	0
			39	39		
10	E	4	Total	O	0	0
			4	4		
10	F	11	Total	O	0	0
			11	11		

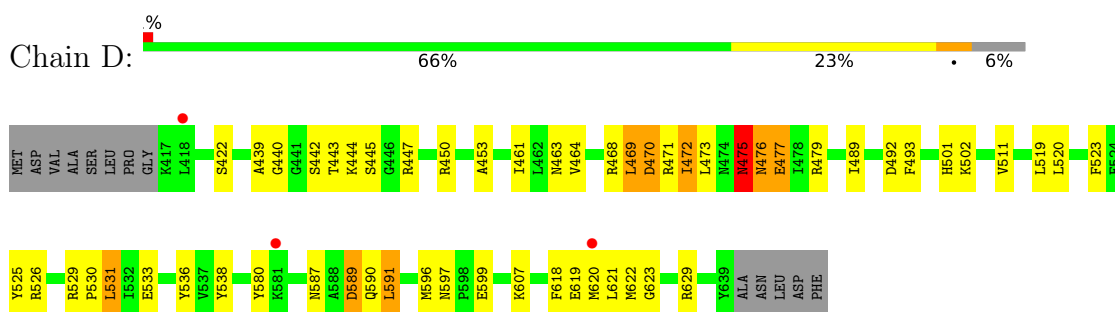
3 Residue-property plots [i](#)

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.

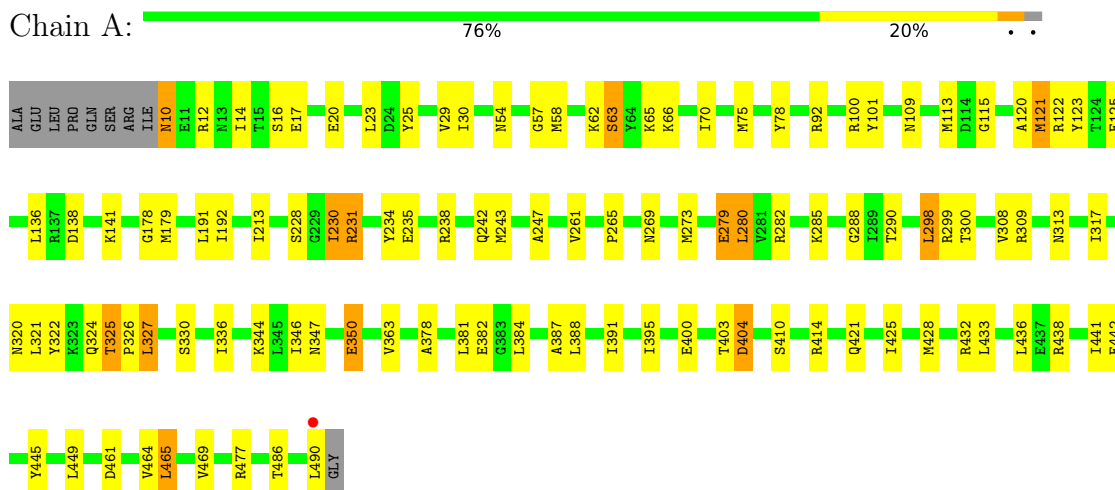
- Molecule 1: DNA gyrase subunit B,DNA gyrase subunit B



- Molecule 1: DNA gyrase subunit B,DNA gyrase subunit B

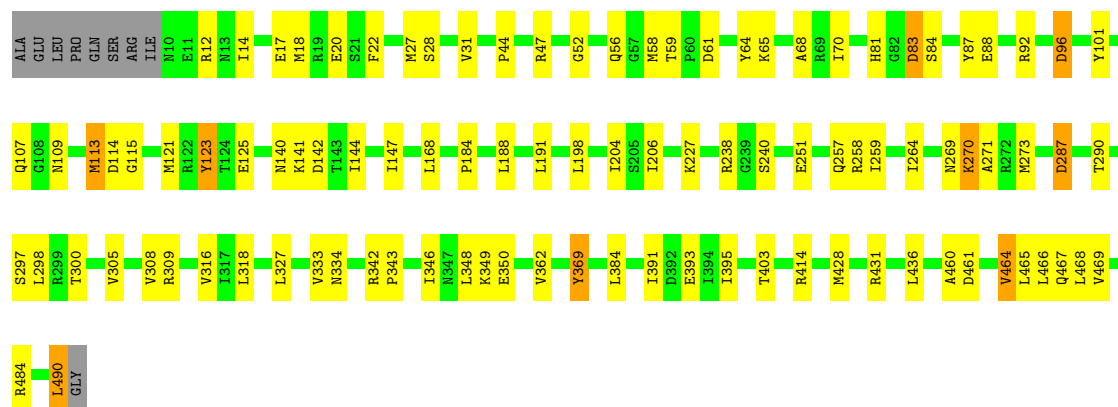


- Molecule 2: DNA gyrase subunit A



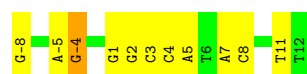
• Molecule 3: DNA gyrase subunit A

Chain C:  78% 19% ..



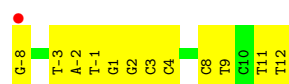
• Molecule 4: DNA (5'-D(*GP*AP*GP*AP*GP*TP*AP*T*GP*GP*CP*CP*AP*TP*AP*CP*TP*CP*TP*T)-3')

Chain E:  45% 50% 5%



• Molecule 4: DNA (5'-D(*GP*AP*GP*AP*GP*TP*AP*T*GP*GP*CP*CP*AP*TP*AP*CP*TP*CP*TP*T)-3')

Chain F:  5% 40% 60%



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	94.03Å 94.03Å 420.47Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.01 – 3.11 47.01 – 3.11	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.01-3.11) 99.9 (47.01-3.11)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 3.12Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.179 , 0.210 0.183 , 0.213	Depositor DCC
R_{free} test set	1843 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	85.0	Xtriage
Anisotropy	0.009	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 70.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.078 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11870	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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: MN, GOL, NA, PTR, E3E, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	B	0.49	0/1487	0.82	4/2014 (0.2%)
1	D	0.71	8/1490 (0.5%)	0.98	6/2017 (0.3%)
2	A	0.45	3/3932 (0.1%)	0.65	2/5295 (0.0%)
3	C	0.46	1/3937 (0.0%)	0.66	2/5301 (0.0%)
4	E	0.61	0/517	0.85	1/794 (0.1%)
4	F	0.51	0/500	0.86	0/766
All	All	0.51	12/11863 (0.1%)	0.74	15/16187 (0.1%)

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	B	0	1

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	184	PRO	CA-C	9.68	1.61	1.52
1	D	477	GLU	CB-CG	-8.03	1.28	1.52
1	D	476[A]	ASN	N-CA	6.92	1.55	1.46
1	D	476[B]	ASN	N-CA	6.92	1.55	1.46
1	D	475	ASN	CB-CG	6.43	1.68	1.52

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	475	ASN	N-CA-C	14.81	143.39	111.84
1	D	475	ASN	CA-C-O	-13.10	101.07	119.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	475	ASN	CB-CA-C	-9.45	91.62	110.42
1	B	608	LEU	CA-C-N	-8.96	105.32	122.53
1	B	608	LEU	C-N-CA	-8.96	105.32	122.53

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	439[B]	ALA	Peptide

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	B	1464	0	1398	68	0
1	D	1466	0	1411	49	0
2	A	3883	0	3928	88	0
3	C	3907	0	3914	80	0
4	E	462	0	257	30	0
4	F	448	0	246	30	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
6	A	1	0	0	0	0
7	A	24	0	32	1	0
7	C	18	0	24	3	0
7	E	6	0	8	2	0
8	C	5	0	0	0	0
9	E	72	0	0	12	0
10	A	46	0	0	0	0
10	B	8	0	0	0	0
10	C	39	0	0	0	0
10	D	4	0	0	0	0
10	E	4	0	0	2	0
10	F	11	0	0	1	0
All	All	11870	0	11218	302	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 13.

The worst 5 of 302 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)
4:F:3:DC:H2''	4:F:4:DC:H5'	1.25	1.17
4:E:5[A]:DA:N1	4:F:-1[A]:DT:N3	1.94	1.16
2:A:321:LEU:O	2:A:325:THR:OG1	1.63	1.15
1:B:447:ARG:NH2	1:B:452:GLN:O	1.79	1.14
1:B:438[B]:SER:HA	1:B:441:GLY:HA3	1.30	1.08

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	B	189/202 (94%)	176 (93%)	10 (5%)	3 (2%)	7	29
1	D	189/202 (94%)	182 (96%)	6 (3%)	1 (0%)	24	55
2	A	485/490 (99%)	472 (97%)	12 (2%)	1 (0%)	43	71
3	C	489/490 (100%)	474 (97%)	14 (3%)	1 (0%)	43	71
All	All	1352/1384 (98%)	1304 (96%)	42 (3%)	6 (0%)	24	60

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	470	ASP
2	A	141	LYS
1	B	443	THR
1	B	496	ALA
1	B	543	PRO

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	B	147/168 (88%)	133 (90%)	14 (10%)	8	29
1	D	150/168 (89%)	141 (94%)	9 (6%)	17	45
2	A	421/423 (100%)	402 (96%)	19 (4%)	24	54
3	C	422/422 (100%)	401 (95%)	21 (5%)	22	50
All	All	1140/1181 (96%)	1077 (94%)	63 (6%)	20	47

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	404	ASP
3	C	298	LEU
1	D	475	ASN
3	C	290	THR
3	C	369	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	10	ASN
1	D	480	GLN
1	D	587	ASN
1	D	590	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	PTR	C	123	3,4	15,16,17	1.31	1 (6%)	17,22,24	0.63	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
3	PTR	C	123	3,4	-	1/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	123	PTR	OH-CZ	-4.29	1.31	1.40

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	123	PTR	N-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	123	PTR	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 15 ligands modelled in this entry, 3 are monoatomic - leaving 12 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$
9	E3E	E	103[A]	-	28,28,28	0.56	0	36,42,42	1.35	6 (16%)
8	SO4	C	501	-	4,4,4	0.22	0	6,6,6	0.11	0
9	E3E	E	102	-	28,28,28	0.59	0	36,42,42	1.31	5 (13%)
7	GOL	A	505	-	5,5,5	0.25	0	5,5,5	0.48	0
7	GOL	C	504	-	5,5,5	0.37	0	5,5,5	0.28	0
9	E3E	E	103[B]	-	28,28,28	0.70	0	36,42,42	1.70	7 (19%)
7	GOL	A	504	-	5,5,5	0.38	0	5,5,5	0.55	0
7	GOL	E	101	-	5,5,5	0.34	0	5,5,5	0.46	0
7	GOL	C	503	-	5,5,5	0.35	0	5,5,5	0.19	0
7	GOL	A	503	-	5,5,5	0.30	0	5,5,5	0.40	0
7	GOL	C	502	-	5,5,5	0.43	0	5,5,5	0.56	0
7	GOL	A	502	-	5,5,5	0.37	0	5,5,5	0.27	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
9	E3E	E	103[A]	-	-	4/8/10/10	0/5/5/5
9	E3E	E	102	-	-	0/8/10/10	0/5/5/5
7	GOL	A	505	-	-	2/4/4/4	-
7	GOL	C	504	-	-	0/4/4/4	-
9	E3E	E	103[B]	-	-	6/8/10/10	0/5/5/5
7	GOL	A	504	-	-	3/4/4/4	-
7	GOL	E	101	-	-	1/4/4/4	-
7	GOL	C	503	-	-	4/4/4/4	-
7	GOL	A	503	-	-	0/4/4/4	-
7	GOL	C	502	-	-	2/4/4/4	-
7	GOL	A	502	-	-	0/4/4/4	-

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	E	103[B]	E3E	C17-N3-C15	4.57	108.27	106.21
9	E	102	E3E	C17-N3-C15	4.11	108.07	106.21
9	E	103[B]	E3E	C12-C11-N1	3.87	122.20	118.29
9	E	103[A]	E3E	C12-C11-N1	3.82	122.15	118.29
9	E	103[B]	E3E	N3-C15-N2	-3.77	109.38	111.38

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	504	GOL	O1-C1-C2-C3
7	A	505	GOL	O1-C1-C2-O2
7	C	503	GOL	O1-C1-C2-C3
9	E	103[B]	E3E	C4-C5-C6-C7
9	E	103[B]	E3E	C4-C5-C6-C10

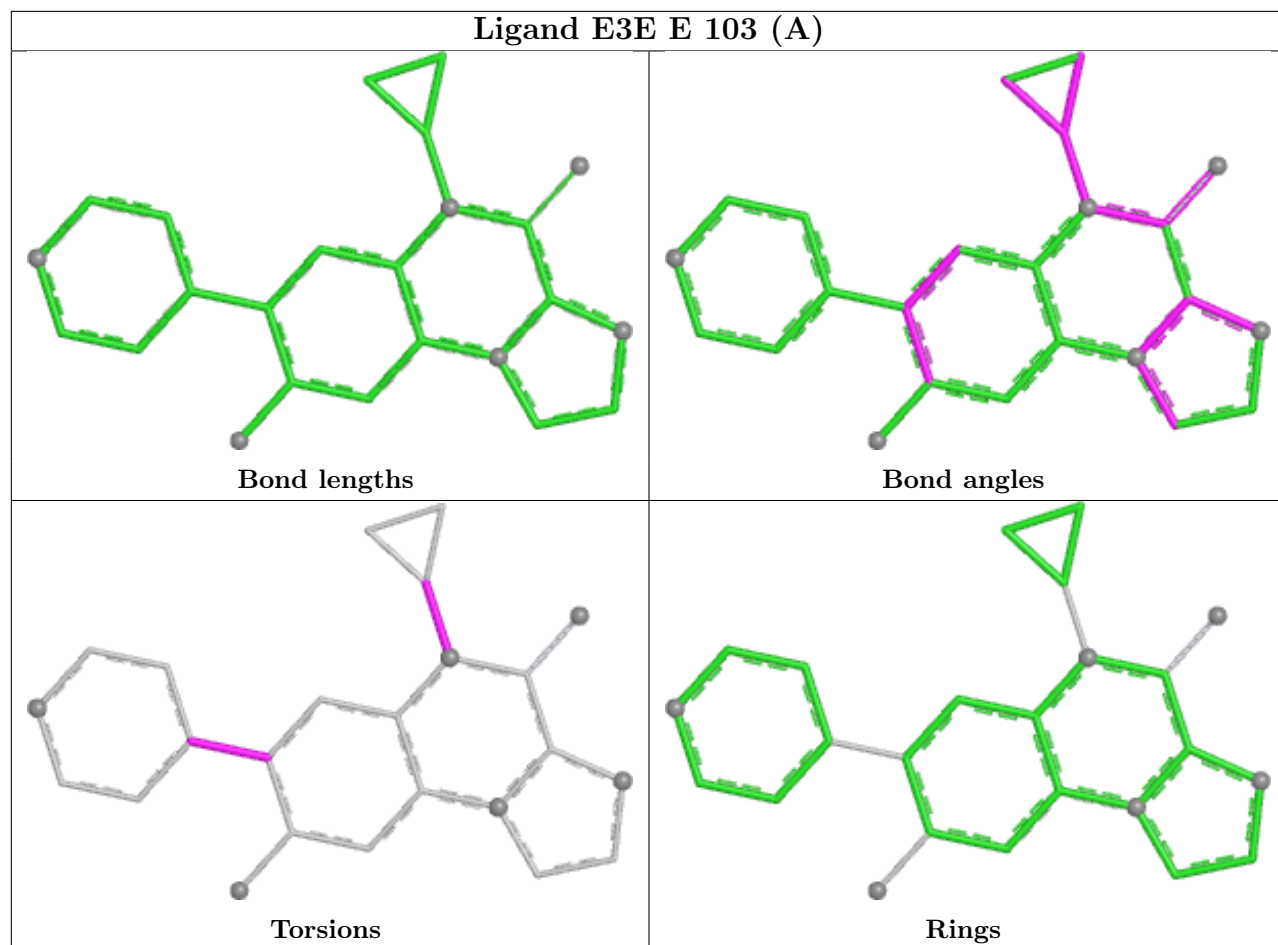
There are no ring outliers.

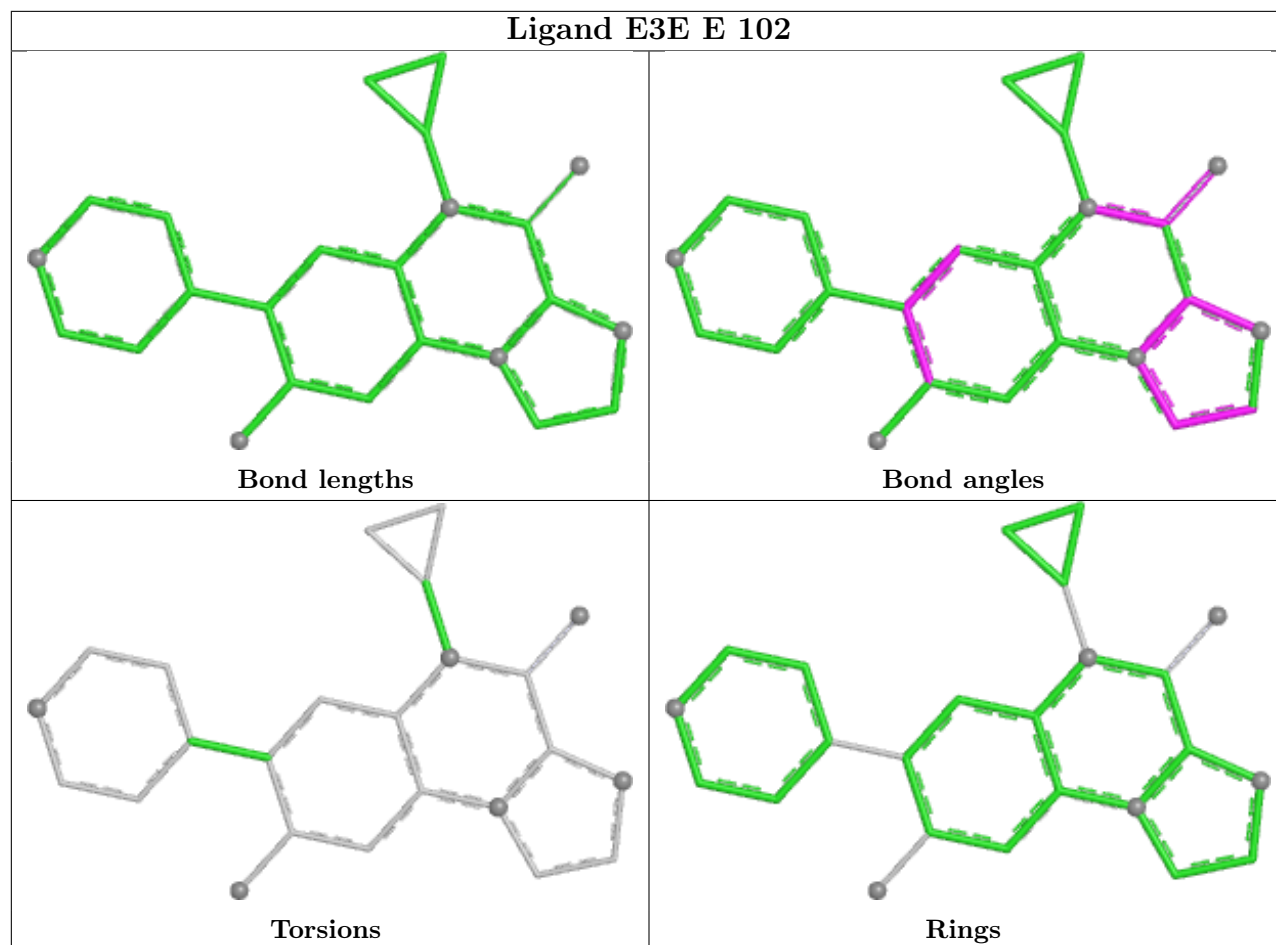
6 monomers are involved in 18 short contacts:

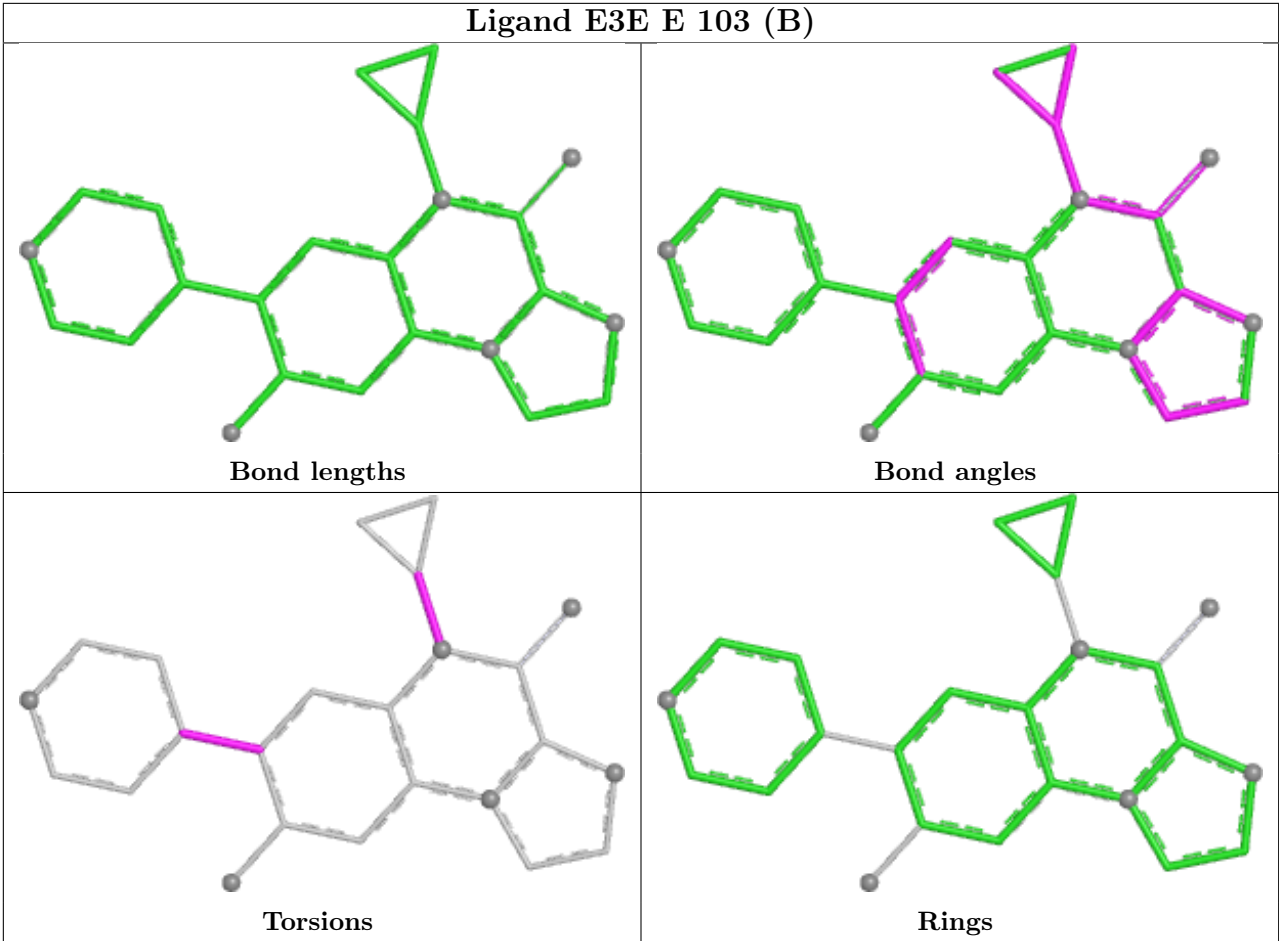
Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	E	103[A]	E3E	2	0
9	E	103[B]	E3E	10	0
7	E	101	GOL	2	0
7	C	503	GOL	1	0
7	A	503	GOL	1	0
7	C	502	GOL	2	0

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 E3E E 103 (A)







5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
4	F	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	-1[A]:DT	O3'	1[A]:DG	P	5.71

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	B	189/202 (93%)	0.18	14 (7%)	20 11	47, 111, 198, 218	4 (2%)
1	D	189/202 (93%)	0.23	3 (1%)	70 49	57, 131, 177, 198	2 (1%)
2	A	481/490 (98%)	-0.52	1 (0%)	91 83	33, 72, 107, 168	6 (1%)
3	C	480/490 (97%)	-0.60	0	100 100	28, 69, 102, 175	11 (2%)
4	E	20/20 (100%)	-0.32	0	100 100	60, 72, 121, 135	3 (15%)
4	F	20/20 (100%)	-0.09	1 (5%)	34 18	46, 71, 129, 158	2 (10%)
All	All	1379/1424 (96%)	-0.34	19 (1%)	73 53	28, 78, 163, 218	28 (2%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	437[A]	ASP	5.2
1	B	438[A]	SER	5.2
1	B	583	LEU	4.3
1	B	440	GLY	3.7
1	B	443	THR	3.5

6.2 Non-standard residues in protein, DNA, RNA chains [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
3	PTR	C	123	16/17	0.92	0.14	61,89,119,130	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

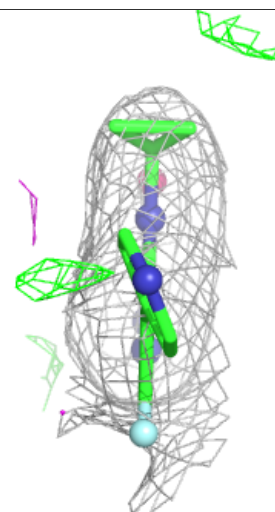
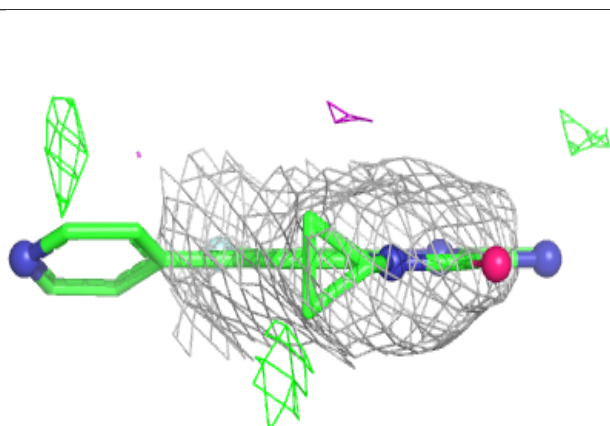
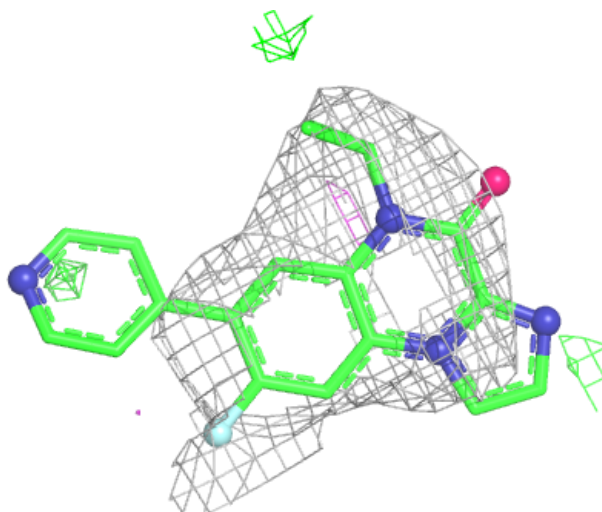
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	SO4	C	501	5/5	0.72	0.10	140,145,151,160	0
7	GOL	E	101	6/6	0.74	0.15	95,100,118,118	0
7	GOL	C	504	6/6	0.76	0.16	87,102,110,115	0
7	GOL	A	503	6/6	0.81	0.15	92,109,114,120	0
7	GOL	A	505	6/6	0.82	0.20	99,104,105,112	0
7	GOL	A	504	6/6	0.88	0.15	101,114,119,121	0
9	E3E	E	103[A]	24/24	0.88	0.22	110,124,166,173	24
9	E3E	E	103[B]	24/24	0.88	0.22	112,127,170,178	24
7	GOL	C	503	6/6	0.90	0.19	158,158,163,167	0
7	GOL	A	502	6/6	0.90	0.26	120,135,146,149	0
7	GOL	C	502	6/6	0.90	0.23	107,117,122,141	0
9	E3E	E	102	24/24	0.93	0.10	74,97,108,114	0
5	MN	D	701	1/1	0.97	0.06	153,153,153,153	0
6	NA	A	501	1/1	0.97	0.04	105,105,105,105	0
5	MN	B	701	1/1	0.98	0.07	114,114,114,114	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.

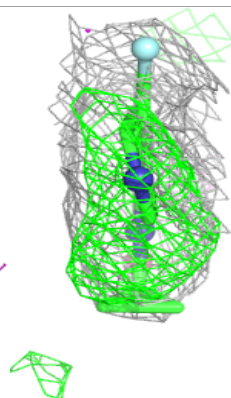
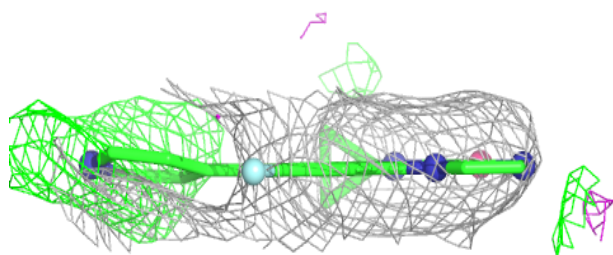
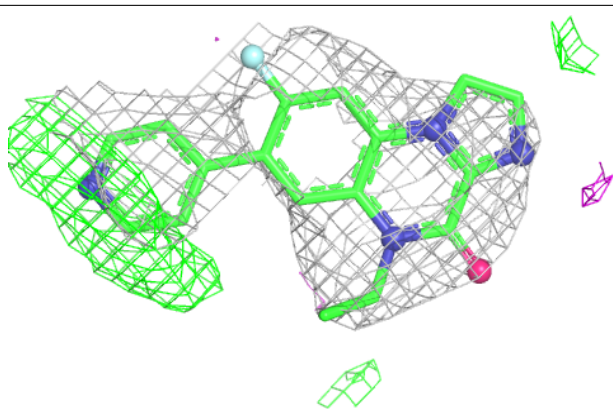
Electron density around E3E E 103 (A):

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

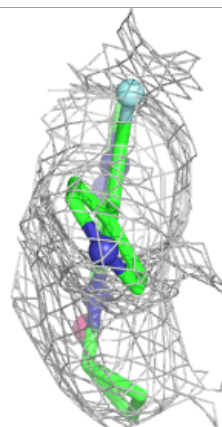
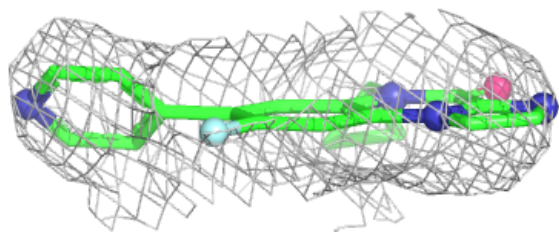
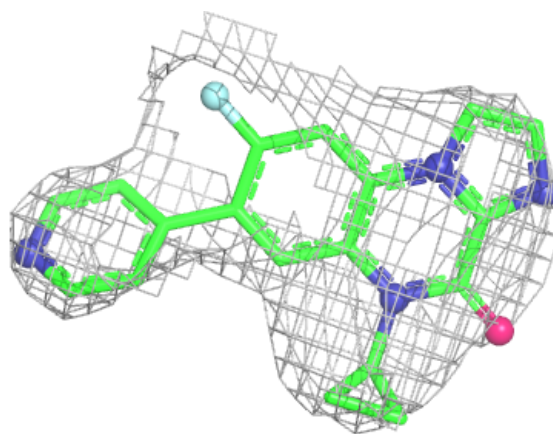


Electron density around E3E E 103 (B):

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

**Electron density around E3E E 102:**

$2mF_o-DF_c$ (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.