



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 08:41 AM UTC

PDB ID : 7Q0D / pdb_00007q0d
Title : Human carbonic anhydrase I in complex with Methyl 2-(benzenesulfonyl)-4-chloro-5-sulfamoylbenzoate
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Deposited on : 2021-10-14
Resolution : 1.24 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

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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

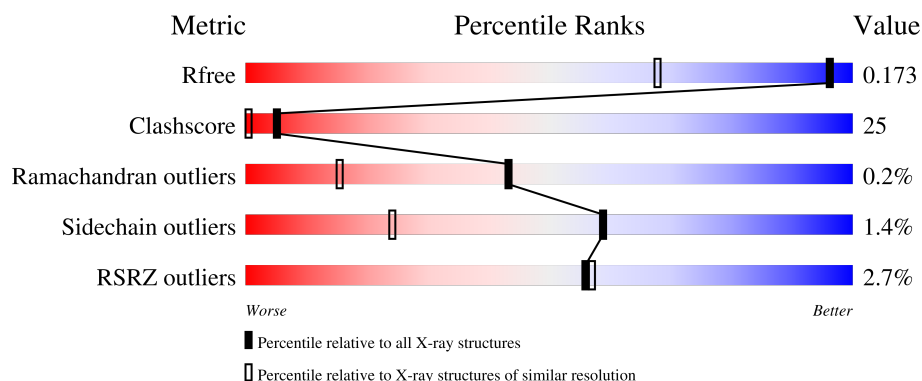
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.24 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	1630 (1.26-1.22)
Clashscore	190562	1668 (1.26-1.22)
Ramachandran outliers	187476	1635 (1.26-1.22)
Sidechain outliers	187428	1633 (1.26-1.22)
RSRZ outliers	180081	1630 (1.26-1.22)

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	261	2% 82% 16% ..
1	B	261	3% 75% 21% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	84Z	A	302[A]	-	-	X	-
3	84Z	B	302[A]	-	-	X	-
4	EDO	A	305	-	-	X	-
4	EDO	A	311	-	-	X	-
4	EDO	A	312	-	-	X	-
4	EDO	A	314	-	-	X	-
4	EDO	B	311	-	-	X	-
4	EDO	B	314	-	-	X	-
4	EDO	B	316	-	-	X	-
4	EDO	B	317	-	-	X	-
5	ACT	A	306	-	-	X	-
5	ACT	A	307	-	-	X	-
5	ACT	B	305	-	-	X	-
6	PEG	A	308	-	-	X	-
6	PEG	A	310	-	-	X	-
6	PEG	B	303	-	-	X	-
6	PEG	B	306	-	-	X	-
6	PEG	B	308	-	-	X	-
6	PEG	B	309	-	-	X	-
6	PEG	B	310	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5464 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.

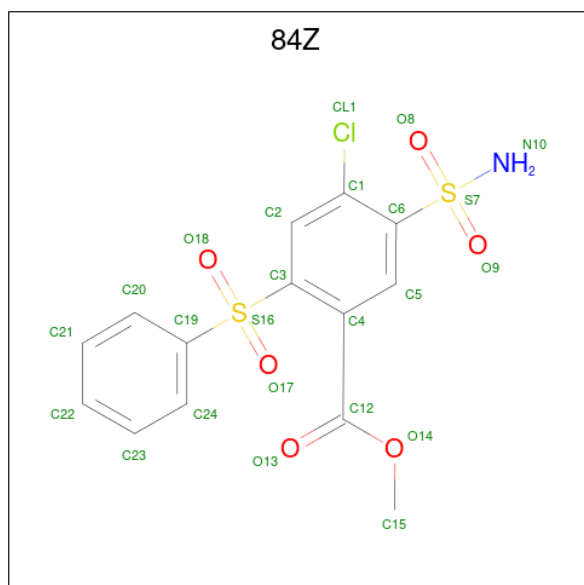
- Molecule 1 is a protein called Carbonic anhydrase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	32	0
			2280	1438	393	446	3			
1	B	258	Total	C	N	O	S	0	14	0
			2114	1331	365	415	3			

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is methyl 4-chloranyl-2-(phenylsulfonyl)-5-sulfamoyl-benzoate (CCD ID: 84Z) (formula: C₁₄H₁₂ClNO₆S₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	S	0	1
			48	28	2	2	12	4		
3	B	1	Total	C	Cl	N	O	S	0	1
			48	28	2	2	12	4		

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



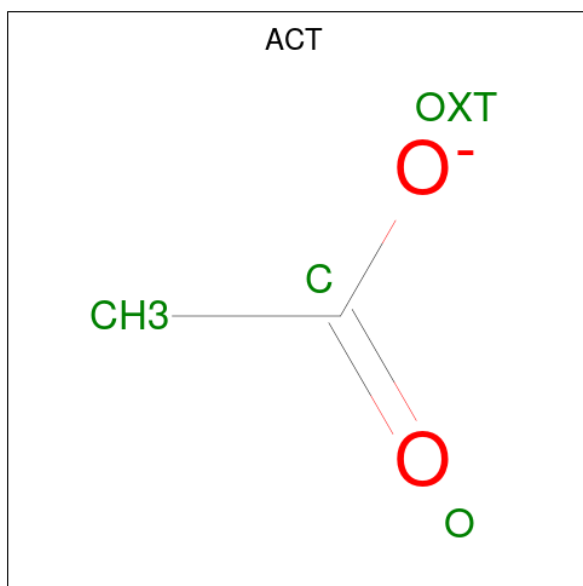
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total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

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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	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		
6	A	1	Total	C	O	0	0
			4	2	2		
6	A	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		
6	B	1	Total	C	O	0	0
			7	4	3		

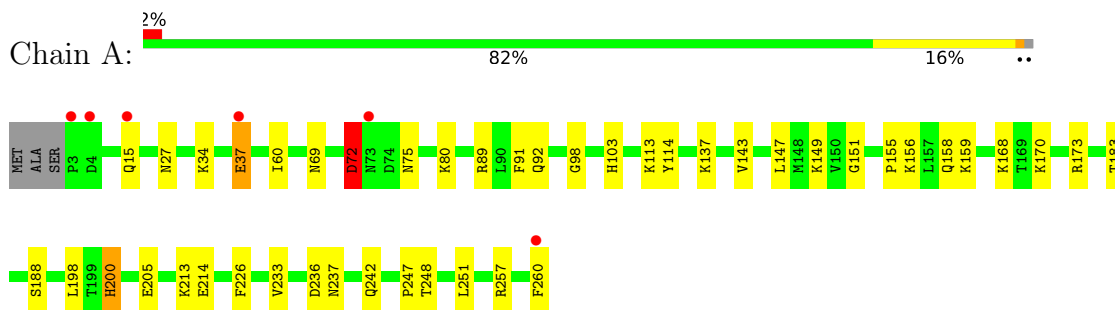
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	442	Total	O	0	0
			442	442		
7	B	394	Total	O	0	0
			394	394		

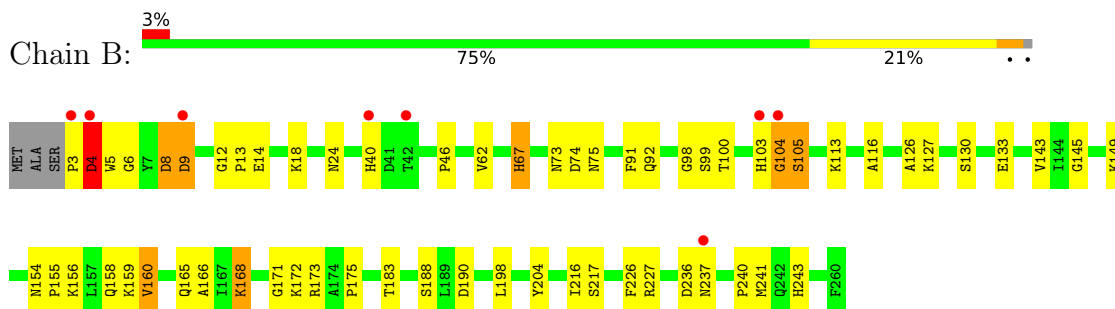
3 Residue-property plots [i](#)

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: Carbonic anhydrase 1



- Molecule 1: Carbonic anhydrase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	62.04Å 73.23Å 120.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	55.16 – 1.24 55.16 – 1.24	Depositor EDS
% Data completeness (in resolution range)	98.3 (55.16-1.24) 98.3 (55.16-1.24)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.50 (at 1.24Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.131 , 0.158 (Not available) , 0.173	Depositor DCC
R_{free} test set	15031 reflections (9.73%)	wwPDB-VP
Wilson B-factor (Å ²)	10.7	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	5464	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.74% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, ACT, ZN, PEG, 84Z

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	1.25	6/2343 (0.3%)	1.13	3/3180 (0.1%)
1	B	1.46	14/2175 (0.6%)	1.32	10/2961 (0.3%)
All	All	1.35	20/4518 (0.4%)	1.22	13/6141 (0.2%)

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	1

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	200	HIS	ND1-CE1	8.20	1.40	1.32
1	A	251	LEU	CB-CG	-7.28	1.38	1.53
1	B	100	THR	N-CA	6.79	1.54	1.45
1	A	103	HIS	C-O	6.73	1.31	1.23
1	B	145	GLY	CA-C	-6.31	1.47	1.52

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	105	SER	N-CA-C	-12.53	90.10	109.52
1	B	168	LYS	N-CA-C	6.98	119.73	111.71
1	A	72[A]	ASP	O-C-N	-6.97	115.25	122.64
1	A	72[B]	ASP	O-C-N	-6.97	115.25	122.64
1	B	105	SER	N-CA-CB	6.70	123.21	111.55

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	72[A]	ASP	Mainchain

CLOSE-CONTACTS INFOmissingINFO

5.2 Torsion angles [i](#)

5.2.1 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	287/261 (110%)	277 (96%)	10 (4%)	0	100	100
1	B	270/261 (103%)	259 (96%)	10 (4%)	1 (0%)	30	9
All	All	557/522 (107%)	536 (96%)	20 (4%)	1 (0%)	43	15

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	104	GLY

5.2.2 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	253/226 (112%)	249 (98%)	4 (2%)	55	20
1	B	230/226 (102%)	226 (98%)	4 (2%)	53	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	483/452 (107%)	475 (98%)	8 (2%)	59 17

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	92[B]	GLN
1	B	92[A]	GLN
1	B	4	ASP
1	A	168	LYS
1	B	9	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	249	GLN
1	B	73	ASN
1	B	24	ASN
1	A	73	ASN
1	B	40	HIS

5.2.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.4 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.5 Ligand geometry ⓘ

Of 34 ligands modelled in this entry, 2 are monoatomic - leaving 32 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	$\# Z > 2$
5	ACT	B	305	-	3,3,3	0.82	0	3,3,3	0.74	0
4	EDO	A	314	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	316	-	3,3,3	0.42	0	2,2,2	0.38	0
6	PEG	B	308	-	6,6,6	0.44	0	5,5,5	0.31	0
4	EDO	A	304	-	3,3,3	0.43	0	2,2,2	0.38	0
6	PEG	A	310	-	6,6,6	0.44	0	5,5,5	0.31	0
4	EDO	B	312	-	3,3,3	0.42	0	2,2,2	0.38	0
3	84Z	B	302[B]	2	25,25,25	2.70	9 (36%)	38,38,38	1.76	10 (26%)
6	PEG	A	308	-	6,6,6	0.44	0	5,5,5	0.31	0
6	PEG	B	309	-	6,6,6	0.43	0	5,5,5	0.30	0
6	PEG	A	309	-	3,3,6	0.40	0	2,2,5	0.39	0
4	EDO	A	312	-	3,3,3	0.43	0	2,2,2	0.38	0
3	84Z	A	302[B]	2	25,25,25	2.13	7 (28%)	38,38,38	2.40	12 (31%)
4	EDO	A	305	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	315	-	3,3,3	0.42	0	2,2,2	0.38	0
6	PEG	B	307	-	6,6,6	0.43	0	5,5,5	0.31	0
4	EDO	B	311	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	314	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	A	315	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	317	-	3,3,3	0.43	0	2,2,2	0.39	0
6	PEG	B	303	-	6,6,6	0.44	0	5,5,5	0.31	0
5	ACT	A	307	-	3,3,3	0.82	0	3,3,3	0.74	0
4	EDO	B	313	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	B	304	-	3,3,3	0.43	0	2,2,2	0.39	0
3	84Z	B	302[A]	2	25,25,25	2.61	10 (40%)	38,38,38	2.75	17 (44%)
4	EDO	A	311	-	3,3,3	0.42	0	2,2,2	0.38	0
6	PEG	B	310	-	6,6,6	0.44	0	5,5,5	0.31	0
4	EDO	A	313	-	3,3,3	0.43	0	2,2,2	0.38	0
3	84Z	A	302[A]	2	25,25,25	2.66	8 (32%)	38,38,38	3.33	21 (55%)
4	EDO	A	303	-	3,3,3	0.43	0	2,2,2	0.38	0
6	PEG	B	306	-	6,6,6	0.44	0	5,5,5	0.31	0
5	ACT	A	306	-	3,3,3	0.81	0	3,3,3	0.73	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
4	EDO	A	314	-	-	0/1/1/1	-
4	EDO	B	316	-	-	0/1/1/1	-
6	PEG	B	308	-	-	2/4/4/4	-
4	EDO	A	304	-	-	1/1/1/1	-
6	PEG	A	310	-	-	1/4/4/4	-
4	EDO	B	312	-	-	1/1/1/1	-
3	84Z	B	302[B]	2	-	4/24/24/24	0/2/2/2
6	PEG	A	308	-	-	0/4/4/4	-
6	PEG	B	309	-	-	2/4/4/4	-
6	PEG	A	309	-	-	1/1/1/4	-
4	EDO	A	312	-	-	1/1/1/1	-
3	84Z	A	302[B]	2	-	7/24/24/24	0/2/2/2
4	EDO	A	305	-	-	1/1/1/1	-
4	EDO	B	315	-	-	1/1/1/1	-
6	PEG	B	307	-	-	4/4/4/4	-
4	EDO	B	311	-	-	0/1/1/1	-
4	EDO	B	314	-	-	0/1/1/1	-
4	EDO	A	315	-	-	1/1/1/1	-
4	EDO	B	317	-	-	0/1/1/1	-
6	PEG	B	303	-	-	2/4/4/4	-
4	EDO	B	313	-	-	0/1/1/1	-
4	EDO	B	304	-	-	0/1/1/1	-
3	84Z	B	302[A]	2	-	2/24/24/24	0/2/2/2
4	EDO	A	311	-	-	1/1/1/1	-
6	PEG	B	310	-	-	2/4/4/4	-
4	EDO	A	313	-	-	0/1/1/1	-
3	84Z	A	302[A]	2	-	0/24/24/24	0/2/2/2
4	EDO	A	303	-	-	0/1/1/1	-
6	PEG	B	306	-	-	3/4/4/4	-

The worst 5 of 34 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302[A]	84Z	C19-S16	-7.54	1.65	1.77
3	B	302[B]	84Z	C4-C3	6.71	1.47	1.40
3	B	302[B]	84Z	O18-S16	6.51	1.55	1.44
3	B	302[B]	84Z	C3-S16	6.20	1.86	1.78
3	B	302[A]	84Z	S7-N10	6.15	1.72	1.60

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302[A]	84Z	O18-S16-C19	9.14	119.20	107.96
3	A	302[A]	84Z	O17-S16-O18	-7.44	104.21	119.25
3	A	302[A]	84Z	C23-C24-C19	7.20	126.31	118.95
3	A	302[A]	84Z	C22-C23-C24	-6.47	112.26	120.24
3	A	302[B]	84Z	O18-S16-C19	6.46	115.90	107.96

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302[B]	84Z	C4-C12-O14-C15
3	A	302[B]	84Z	O13-C12-O14-C15
3	B	302[A]	84Z	C4-C12-O14-C15
6	A	310	PEG	C1-C2-O2-C3
3	B	302[A]	84Z	O13-C12-O14-C15

There are no ring outliers.

28 monomers are involved in 165 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	305	ACT	4	0
4	A	314	EDO	5	0
4	B	316	EDO	4	0
6	B	308	PEG	6	0
6	A	310	PEG	14	0
4	B	312	EDO	2	0
3	B	302[B]	84Z	5	0
6	A	308	PEG	10	0
6	B	309	PEG	16	0
6	A	309	PEG	3	0
4	A	312	EDO	10	0
3	A	302[B]	84Z	5	0
4	A	305	EDO	6	0
4	B	315	EDO	3	0
6	B	307	PEG	3	0
4	B	311	EDO	5	0
4	B	314	EDO	4	0
4	A	315	EDO	2	0
4	B	317	EDO	4	0
6	B	303	PEG	10	0
5	A	307	ACT	6	0
3	B	302[A]	84Z	9	0

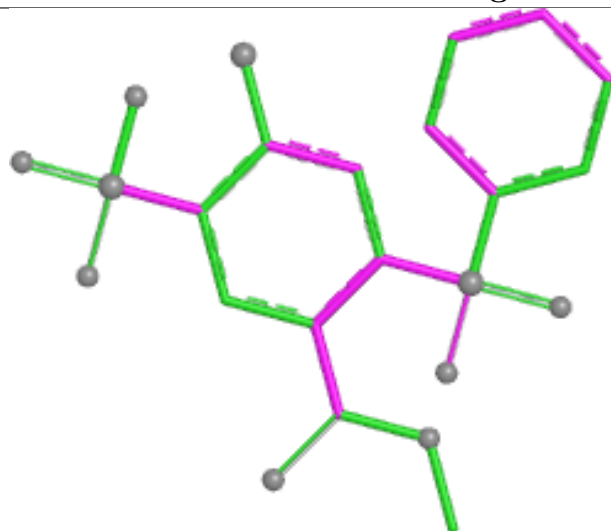
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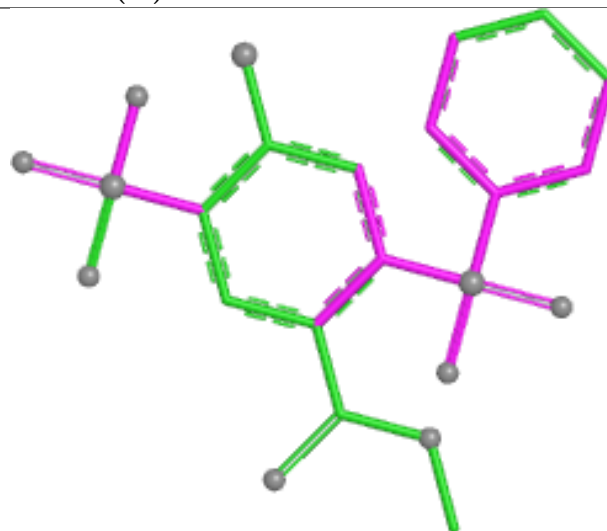
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	311	EDO	5	0
6	B	310	PEG	7	0
4	A	313	EDO	2	0
3	A	302[A]	84Z	8	0
6	B	306	PEG	5	0
5	A	306	ACT	5	0

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.

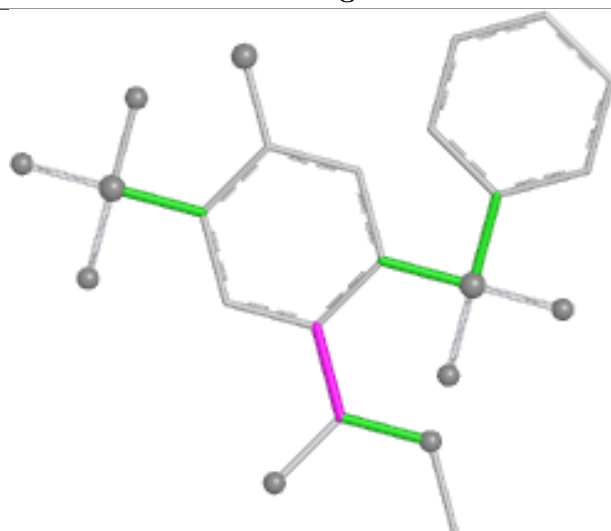
Ligand 84Z B 302 (B)



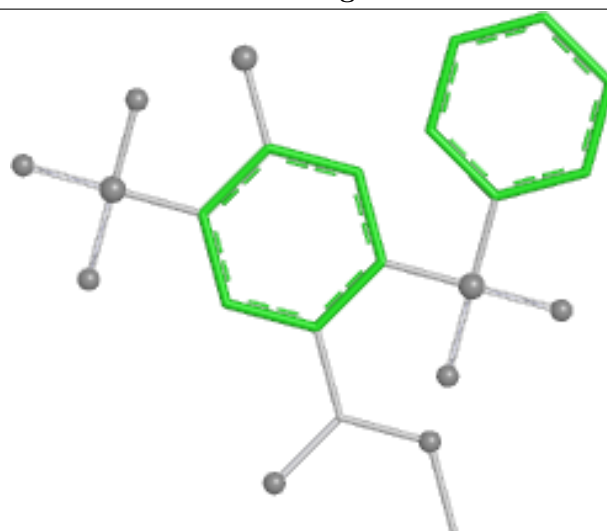
Bond lengths



Bond angles

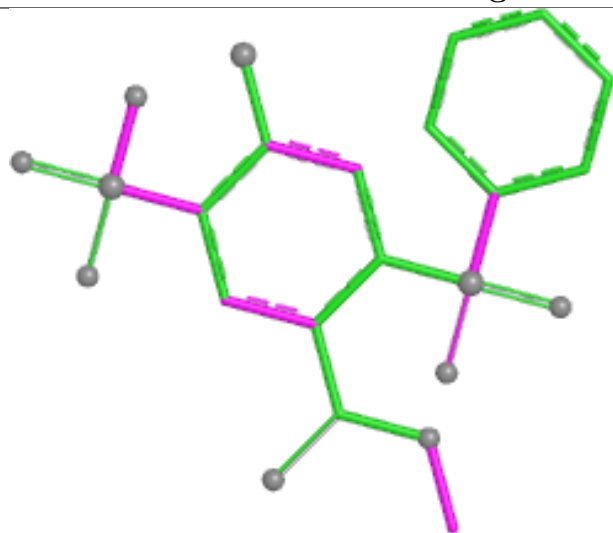


Torsions

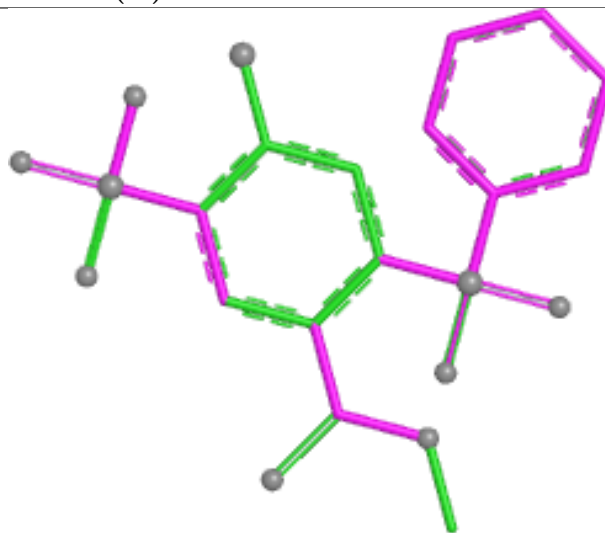


Rings

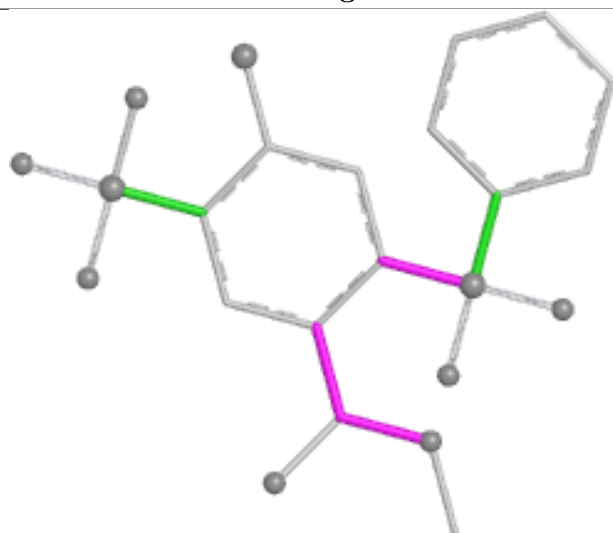
Ligand 84Z A 302 (B)



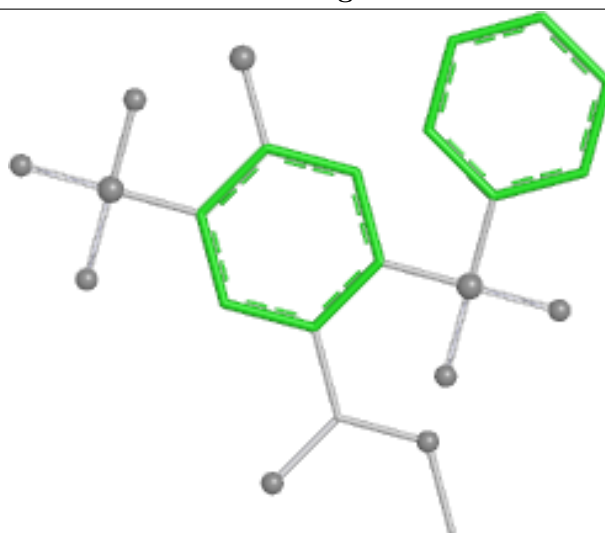
Bond lengths



Bond angles

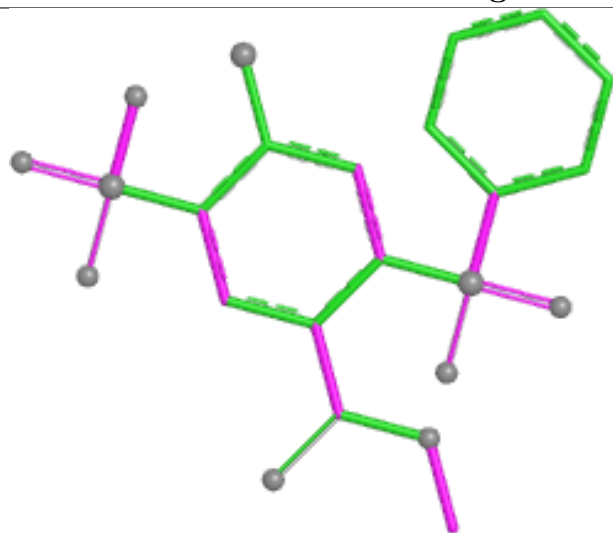


Torsions

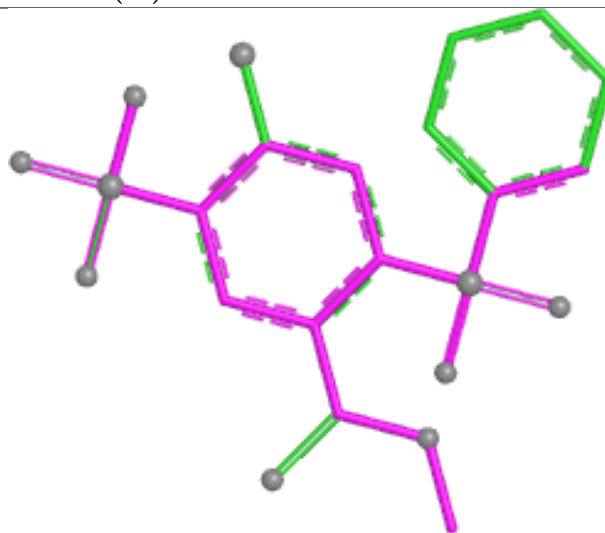


Rings

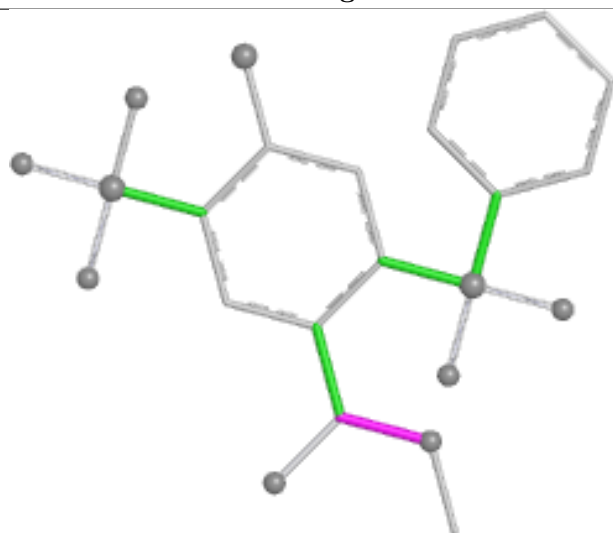
Ligand 84Z B 302 (A)



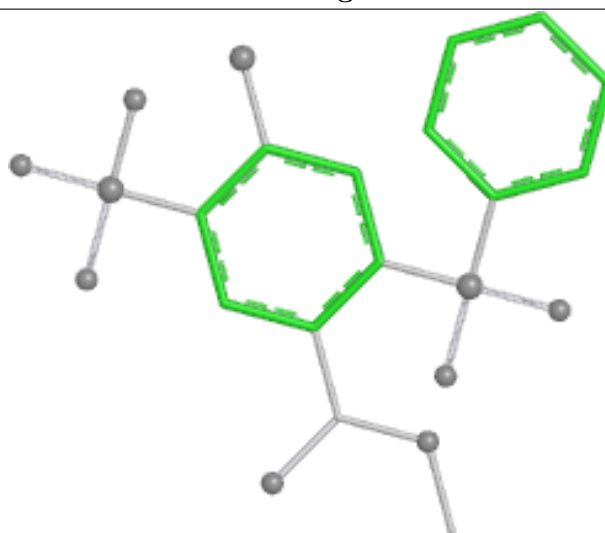
Bond lengths



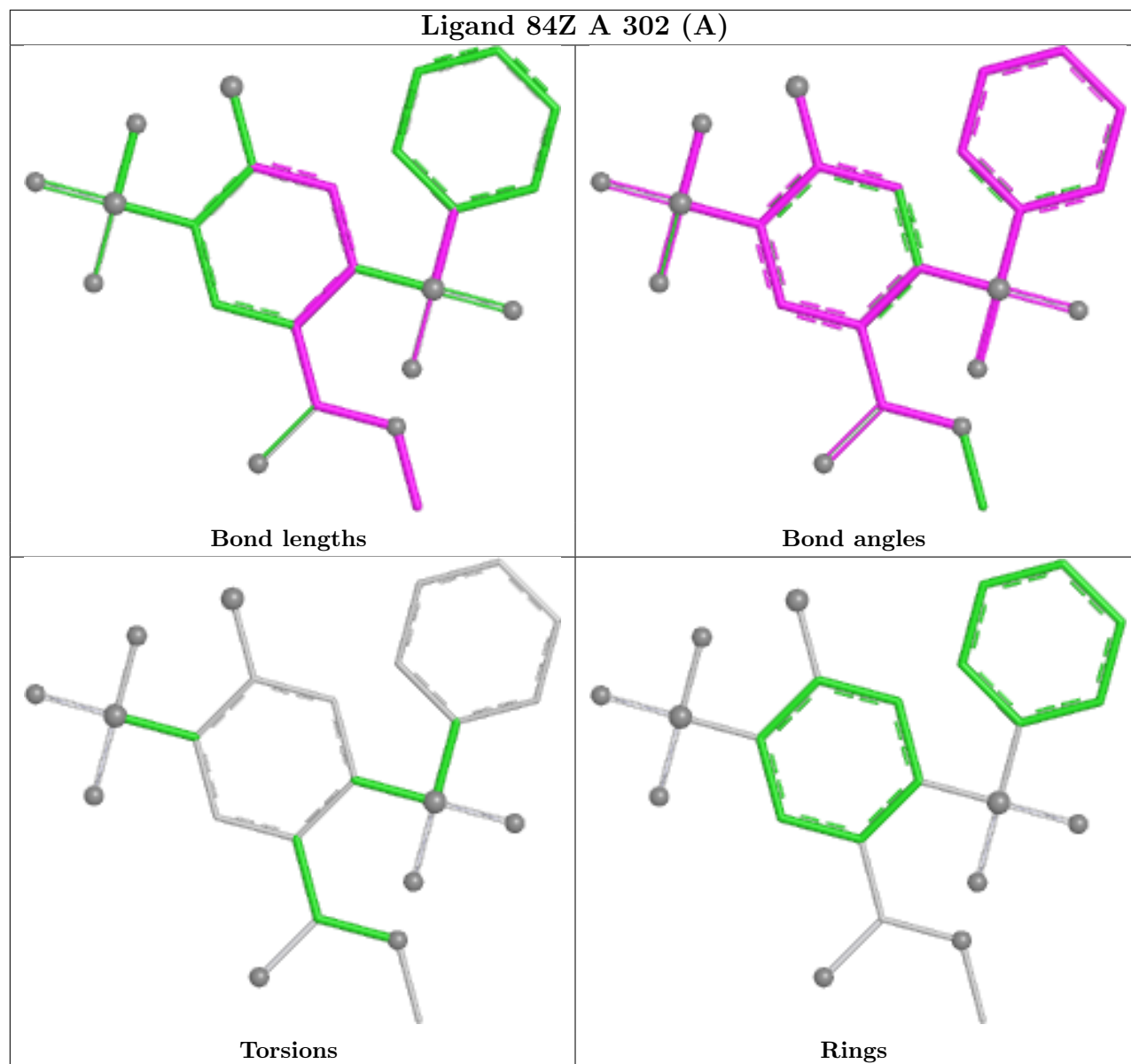
Bond angles



Torsions



Rings



5.6 Other polymers [i](#)

There are no such residues in this entry.

5.7 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	258/261 (98%)	-0.39	6 (2%) 61 62	4, 11, 23, 39	32 (12%)
1	B	258/261 (98%)	-0.25	8 (3%) 51 52	5, 14, 30, 66	14 (5%)
All	All	516/522 (98%)	-0.32	14 (2%) 56 57	4, 12, 26, 66	46 (8%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	260[A]	PHE	10.4
1	B	3	PRO	7.2
1	B	104	GLY	7.1
1	A	3	PRO	3.8
1	B	4	ASP	3.3

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](#)

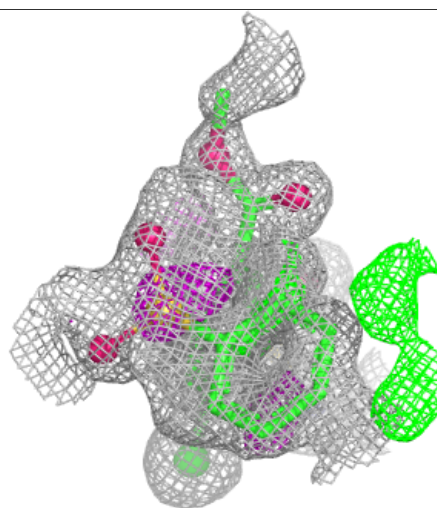
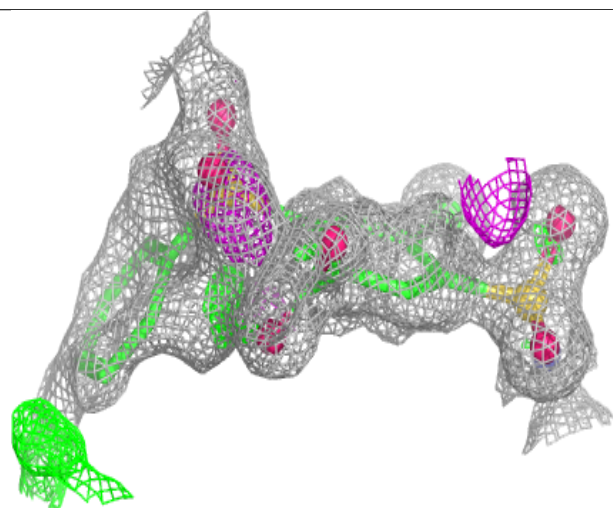
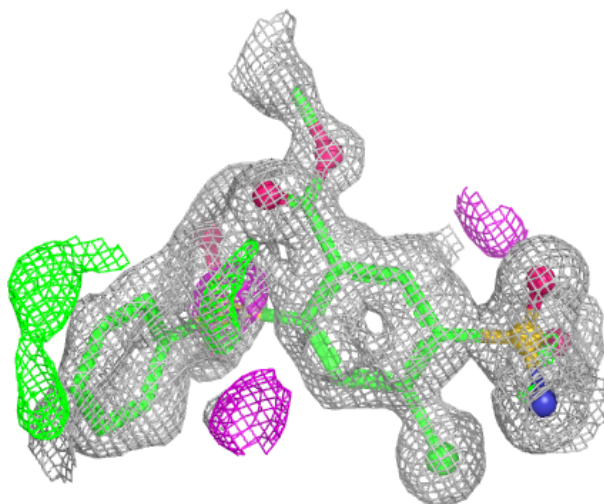
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists 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
6	PEG	A	310	7/7	0.55	0.20	20,20,20,20	0
6	PEG	B	310	7/7	0.69	0.17	20,20,20,20	0
6	PEG	B	303	7/7	0.74	0.21	24,27,45,97	0
6	PEG	A	308	7/7	0.76	0.18	26,31,48,56	0
6	PEG	B	309	7/7	0.76	0.16	20,20,20,20	0
4	EDO	B	311	4/4	0.76	0.16	25,29,39,52	0
4	EDO	B	317	4/4	0.77	0.16	20,20,20,20	0
4	EDO	B	315	4/4	0.78	0.16	20,20,25,26	0
6	PEG	B	306	7/7	0.78	0.16	52,63,76,90	0
5	ACT	A	306	4/4	0.79	0.15	23,31,33,40	0
5	ACT	A	307	4/4	0.79	0.13	27,28,31,35	0
4	EDO	A	315	4/4	0.80	0.14	23,24,27,27	0
5	ACT	B	305	4/4	0.80	0.15	17,23,26,34	0
4	EDO	A	304	4/4	0.81	0.13	27,32,33,55	0
4	EDO	B	316	4/4	0.81	0.14	20,20,20,20	0
4	EDO	A	314	4/4	0.83	0.13	23,26,29,30	0
6	PEG	A	309	4/7	0.84	0.23	47,86,93,98	0
4	EDO	B	312	4/4	0.84	0.13	40,42,49,51	0
4	EDO	A	312	4/4	0.84	0.12	18,20,30,37	0
4	EDO	B	314	4/4	0.87	0.12	29,30,37,37	0
4	EDO	B	313	4/4	0.89	0.11	21,25,31,36	0
4	EDO	A	311	4/4	0.90	0.11	21,25,27,28	0
6	PEG	B	308	7/7	0.90	0.13	20,23,42,53	0
6	PEG	B	307	7/7	0.92	0.11	20,34,48,66	0
4	EDO	A	313	4/4	0.92	0.11	17,21,23,25	0
3	84Z	B	302[B]	24/24	0.94	0.11	8,11,20,21	24
3	84Z	B	302[A]	24/24	0.94	0.11	9,16,23,29	24
3	84Z	A	302[B]	24/24	0.95	0.19	5,15,33,38	24
4	EDO	A	303	4/4	0.95	0.10	21,28,35,35	0
3	84Z	A	302[A]	24/24	0.95	0.19	11,14,22,691	24
4	EDO	B	304	4/4	0.96	0.08	19,20,22,33	0
4	EDO	A	305	4/4	0.96	0.07	19,22,28,33	0
2	ZN	A	301	1/1	1.00	0.01	7,7,7,7	0
2	ZN	B	301	1/1	1.00	0.00	8,8,8,8	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.

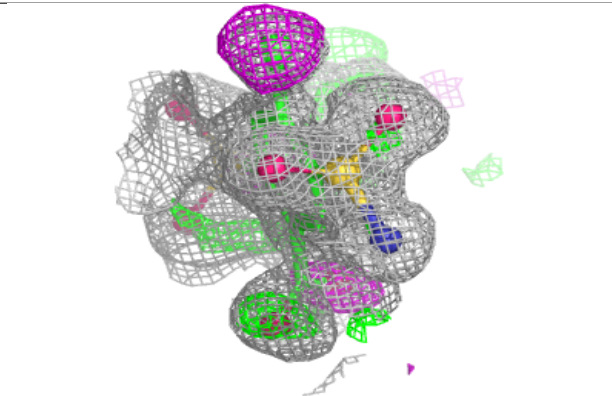
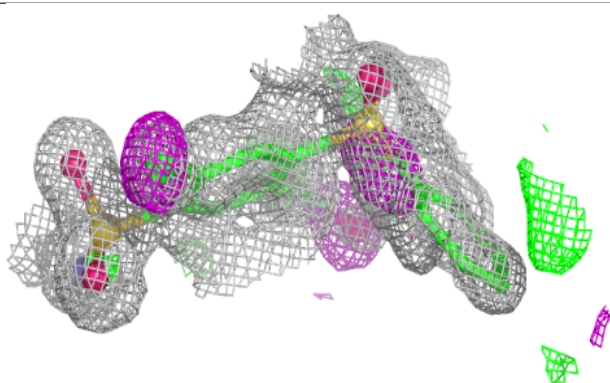
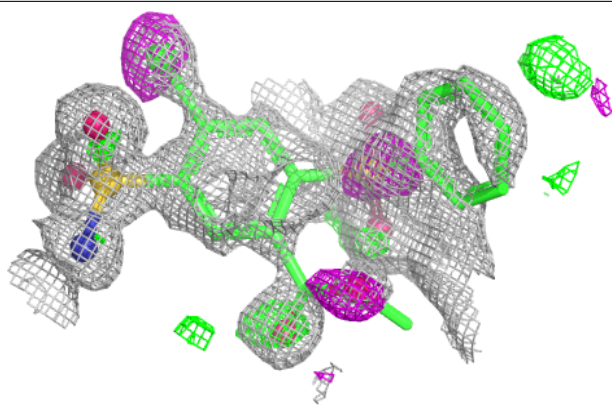
Electron density around 84Z B 302 (B):

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

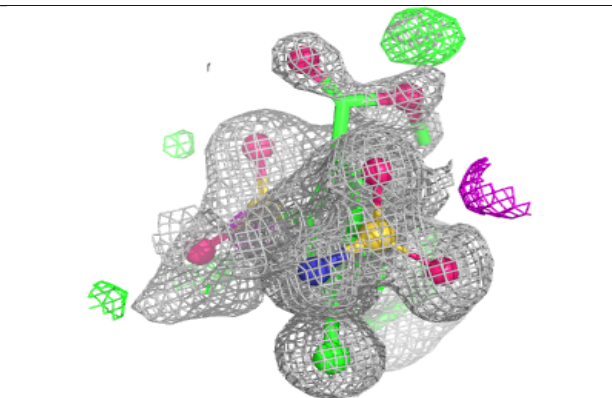
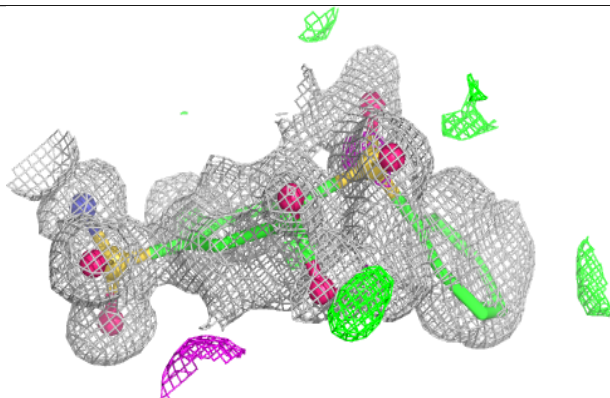
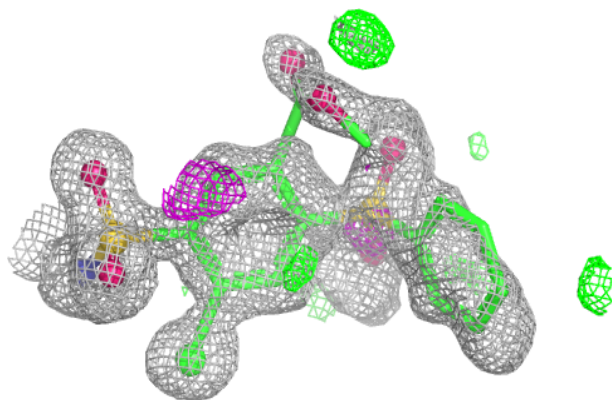


Electron density around 84Z B 302 (A):

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

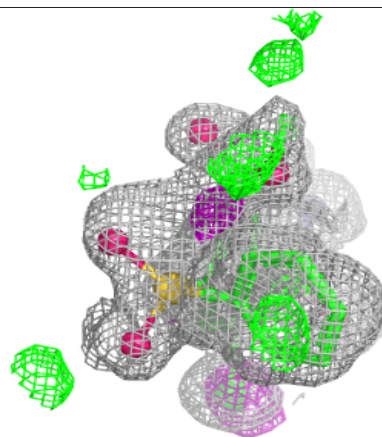
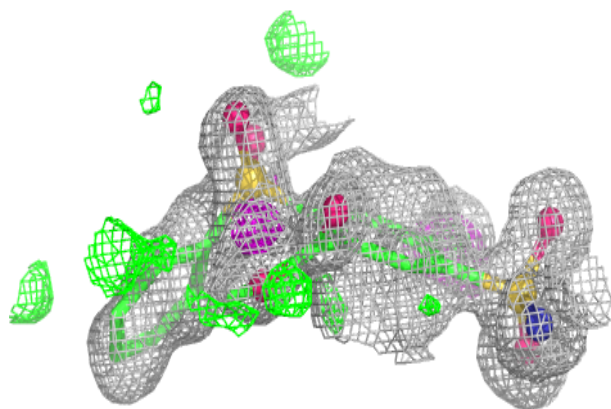
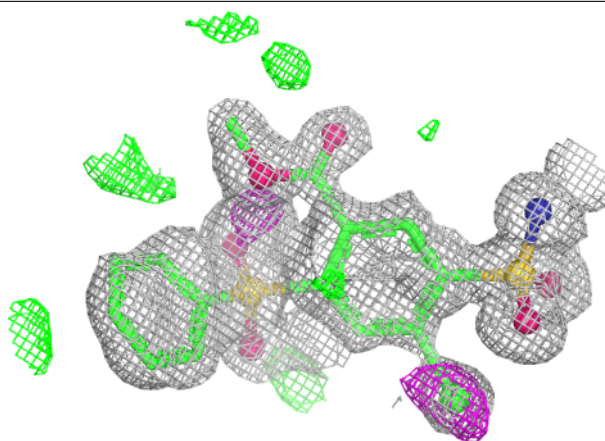
**Electron density around 84Z A 302 (B):**

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



Electron density around 84Z A 302 (A):

$2mF_o-DF_c$ (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.