



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 10:12 PM EDT

PDB ID : 1ZFK / pdb_00001zfk
Title : carbonic anhydrase II in complex with N-4-sulfonamidphenyl-N'-4-methylbenzotranssulfonylurease as sulfonamide inhibitor
Authors : Honndorf, V.S.; Heine, A.; Klebe, G.; Supuran, C.T.
Deposited on : 2005-04-20
Resolution : 1.56 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 : **FAILED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

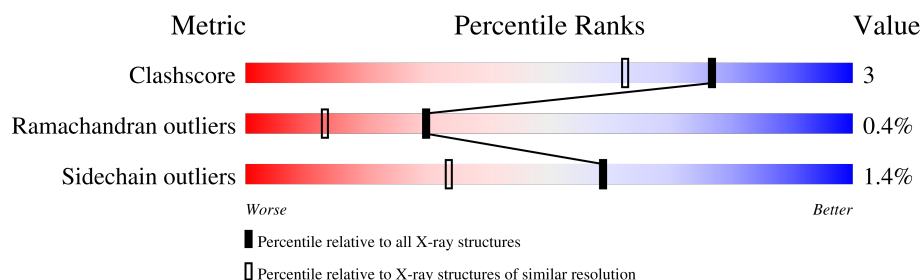
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.56 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))
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)

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 $\leq 5\%$.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	259	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 2367 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 II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	256	Total	C	N	O	S	0	0	0
			2031	1304	348	377	2			

- 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		

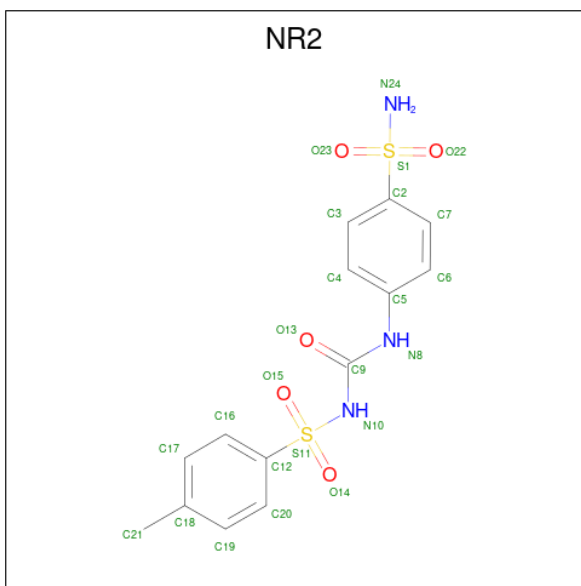
- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

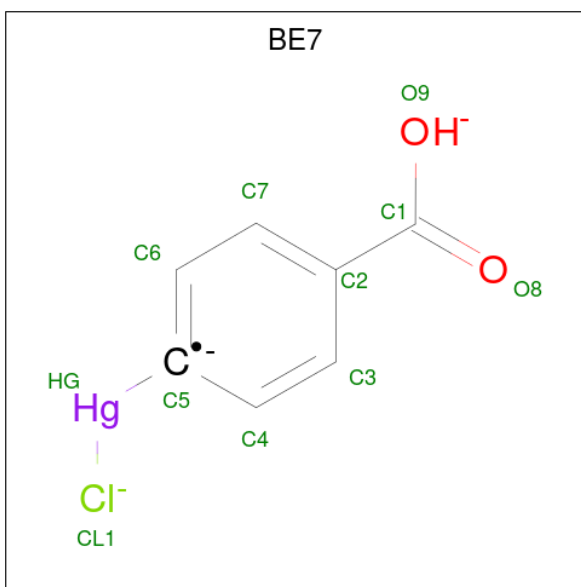
- Molecule 4 is N-([4-(AMINOSULFONYL)PHENYL]AMINO)CARBONYL-4-METHYLB

ENZENESULFONAMIDE (CCD ID: NR2) (formula: $C_{14}H_{15}N_3O_5S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			24	14	3	5	2		
4	A	1	Total	C	N	O	S	0	0
			24	14	3	5	2		

- Molecule 5 is (4-CARBOXYPHENYL)(CHLORO)MERCURY (CCD ID: BE7) (formula: $C_7H_5ClHgO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	Hg	O	0	0
			10	7	1	2		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	266	Total	O	0	0
			266	266		

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. 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. 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.

Note EDS failed to run properly.

- Molecule 1: Carbonic anhydrase II

Chain A:  88% 11%



4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.49Å 41.51Å 72.41Å 90.00° 104.45° 90.00°	Depositor
Resolution (Å)	10.00 – 1.56	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-1.56)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.56 (at 1.56Å)	Xtriage
Refinement program	SHELXL-97, CNS	Depositor
R, R_{free}	0.161 , 0.224	Depositor
Wilson B-factor (Å ²)	2.6	Xtriage
Anisotropy	0.771	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.30$, $\langle L^2 \rangle = 0.14$	Xtriage
Estimated twinning fraction	0.216 for h,-k,-h-l	Xtriage
Total number of atoms	2367	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.84% 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: BE7, NR2, GOL, SO4, ZN

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	0.61	0/2092	1.47	19/2842 (0.7%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1252	LYS	CA-C-N	9.41	139.51	121.54
1	A	1252	LYS	C-N-CA	9.41	139.51	121.54
1	A	1189	LEU	CA-C-N	7.42	131.28	120.82
1	A	1189	LEU	C-N-CA	7.42	131.28	120.82
1	A	1189	LEU	O-C-N	-7.07	113.66	122.35
1	A	1093	PHE	CA-CB-CG	6.81	120.61	113.80
1	A	1027	ARG	CA-CB-CG	6.50	127.09	114.10
1	A	1188	SER	CA-C-O	-6.38	113.58	120.92
1	A	1231	PHE	CA-CB-CG	6.27	120.07	113.80
1	A	1226	PHE	CA-CB-CG	6.12	119.92	113.80
1	A	1057	LEU	CA-C-O	5.77	126.56	119.81
1	A	1227	ARG	CD-NE-CZ	5.72	132.41	124.40
1	A	1158	GLN	CA-C-N	-5.67	112.12	120.28
1	A	1158	GLN	C-N-CA	-5.67	112.12	120.28
1	A	1190	ASP	CA-C-N	5.63	131.11	121.87
1	A	1190	ASP	C-N-CA	5.63	131.11	121.87
1	A	1103	GLN	OE1-CD-NE2	-5.31	117.29	122.60
1	A	1190	ASP	CA-CB-CG	5.18	117.78	112.60
1	A	1107	HIS	CA-CB-CG	-5.08	108.72	113.80

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	2031	0	1972	11	0
2	A	1	0	0	0	0
3	A	5	0	0	0	0
4	A	48	0	29	4	0
5	A	10	0	4	1	0
6	A	6	0	8	0	0
7	A	266	0	0	4	0
All	All	2367	0	2013	12	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 3.

All (12) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1206:CYS:SG	5:A:1700:BE7:HG	1.89	0.91
1:A:1252:LYS:HE2	7:A:3093:HOH:O	1.99	0.62
1:A:1159:LYS:HD2	7:A:3071:HOH:O	2.05	0.56
1:A:1131:PHE:HE2	4:A:1400:NR2:H16	1.74	0.51
1:A:1221:GLU:O	1:A:1225:LYS:HG3	2.12	0.50
1:A:1135:VAL:HG21	4:A:1400:NR2:H17	1.96	0.47
4:A:1500:NR2:O13	4:A:1500:NR2:H4	2.14	0.47
1:A:1161:VAL:CG1	1:A:1225:LYS:HD2	2.46	0.45
1:A:1187:GLU:HG3	7:A:3256:HOH:O	2.16	0.45
1:A:1175:ASP:HB3	7:A:3189:HOH:O	2.17	0.44
1:A:1071:ASP:HA	4:A:1500:NR2:H10	1.82	0.43
1:A:1009:LYS:O	1:A:1015:HIS:NE2	2.52	0.42

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	254/259 (98%)	241 (95%)	12 (5%)	1 (0%)	30	13

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1076	LYS

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	219/224 (98%)	216 (99%)	3 (1%)	59	33

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1004	HIS
1	A	1045	LYS
1	A	1074	GLN

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	1103	GLN
1	A	1178	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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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$
4	NR2	A	1500	-	25,25,25	1.91	3 (12%)	37,37,37	2.02	9 (24%)
6	GOL	A	1900	-	5,5,5	0.80	0	5,5,5	1.53	1 (20%)
4	NR2	A	1400	2	25,25,25	1.86	3 (12%)	37,37,37	1.58	6 (16%)
3	SO4	A	1600	-	4,4,4	0.64	0	6,6,6	1.30	0
5	BE7	A	1700	1	7,10,11	1.58	2 (28%)	8,13,14	1.31	1 (12%)

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	NR2	A	1500	-	-	4/21/21/21	0/2/2/2
6	GOL	A	1900	-	-	2/4/4/4	-
5	BE7	A	1700	1	-	0/4/14/16	0/1/1/1
4	NR2	A	1400	2	-	7/21/21/21	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1500	NR2	S1-N24	-5.85	1.49	1.60
4	A	1400	NR2	S11-N10	-5.73	1.50	1.64
4	A	1500	NR2	S11-N10	-5.46	1.51	1.64
4	A	1400	NR2	S1-N24	-5.38	1.50	1.60
5	A	1700	BE7	C4-C3	2.96	1.42	1.35
4	A	1400	NR2	O14-S11	2.37	1.46	1.43
4	A	1500	NR2	C9-N10	-2.33	1.34	1.39
5	A	1700	BE7	C2-C1	2.29	1.52	1.48

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1500	NR2	C12-S11-N10	-6.08	96.37	106.06
4	A	1500	NR2	C2-S1-N24	-6.05	99.98	108.40
4	A	1400	NR2	C12-S11-N10	-4.60	98.73	106.06
4	A	1400	NR2	C3-C2-S1	4.36	125.65	119.72
4	A	1500	NR2	C7-C2-S1	-3.79	114.58	119.72
4	A	1400	NR2	C7-C2-S1	-3.24	115.32	119.72
4	A	1400	NR2	O22-S1-N24	2.73	111.28	107.35
6	A	1900	GOL	O2-C2-C3	2.71	120.42	109.18
4	A	1500	NR2	O23-S1-C2	-2.65	104.35	107.35
4	A	1400	NR2	O15-S11-N10	2.65	114.34	106.77
4	A	1500	NR2	O14-S11-C12	2.51	111.15	107.98
4	A	1500	NR2	O22-S1-N24	2.48	110.93	107.35
4	A	1500	NR2	O23-S1-N24	2.31	110.69	107.35
4	A	1500	NR2	C4-C3-C2	-2.30	117.20	119.44
5	A	1700	BE7	O9-C1-O8	-2.15	118.79	123.90
4	A	1500	NR2	C3-C2-C7	2.08	123.17	120.47
4	A	1400	NR2	O22-S1-C2	-2.01	105.08	107.35

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1900	GOL	O1-C1-C2-C3
6	A	1900	GOL	O2-C2-C3-O3
4	A	1400	NR2	C9-N10-S11-O15
4	A	1500	NR2	C3-C2-S1-O22
4	A	1500	NR2	C7-C2-S1-O22
4	A	1400	NR2	C16-C12-S11-O14
4	A	1400	NR2	C7-C2-S1-O22

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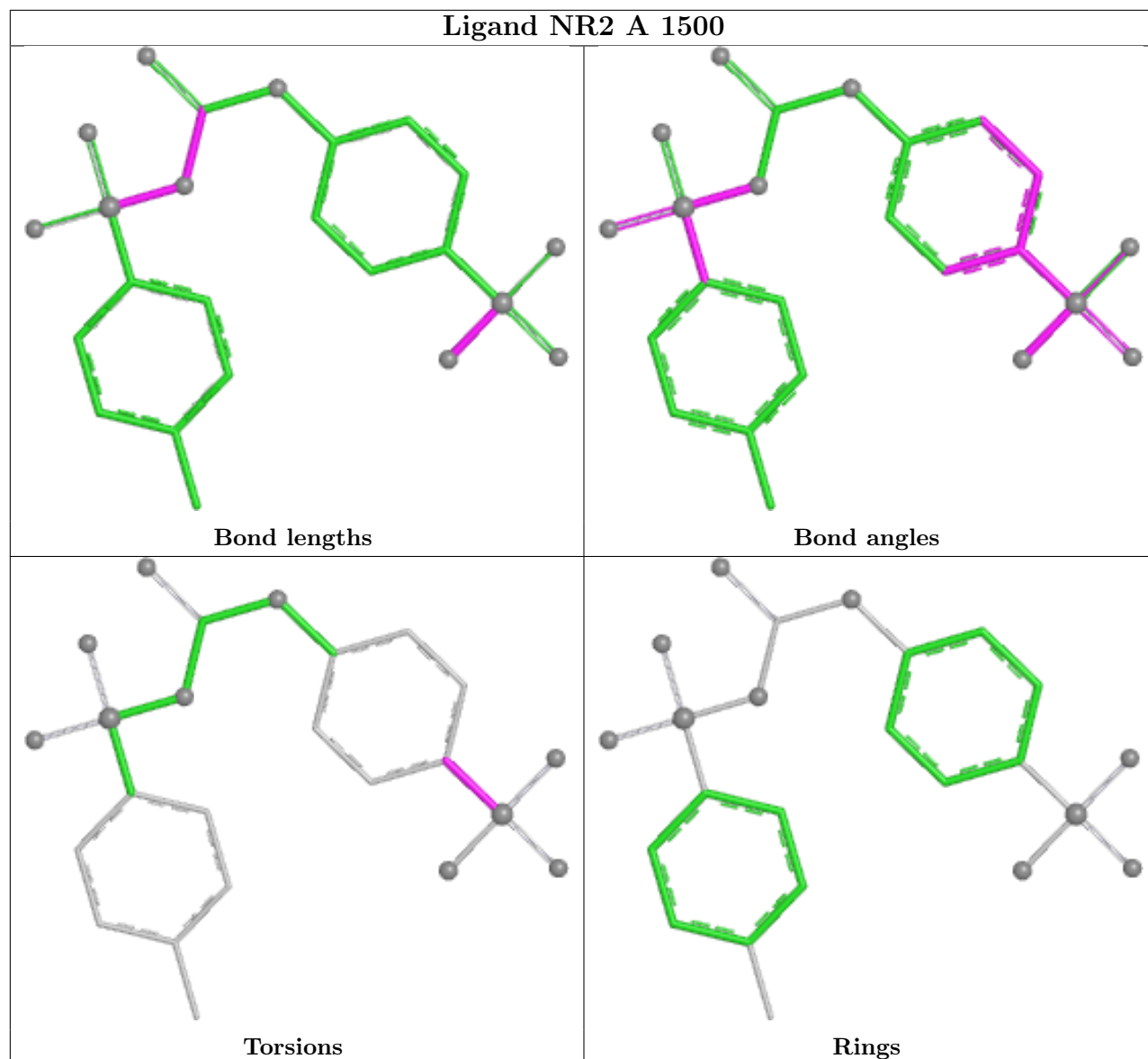
Mol	Chain	Res	Type	Atoms
4	A	1500	NR2	C3-C2-S1-N24
4	A	1400	NR2	C9-N10-S11-O14
4	A	1400	NR2	C3-C2-S1-O22
4	A	1400	NR2	C20-C12-S11-O14
4	A	1500	NR2	C7-C2-S1-N24
4	A	1400	NR2	C9-N10-S11-C12

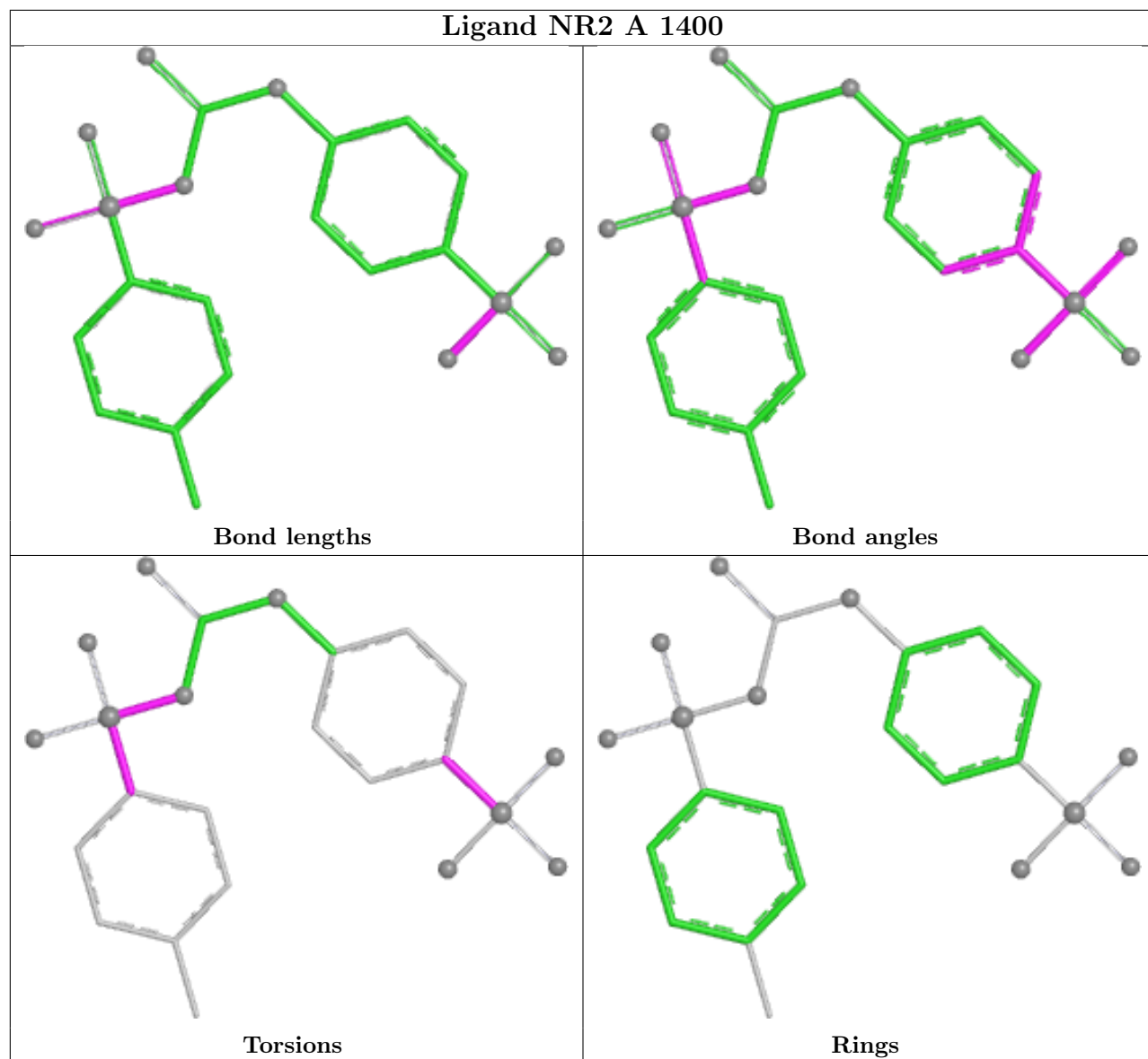
There are no ring outliers.

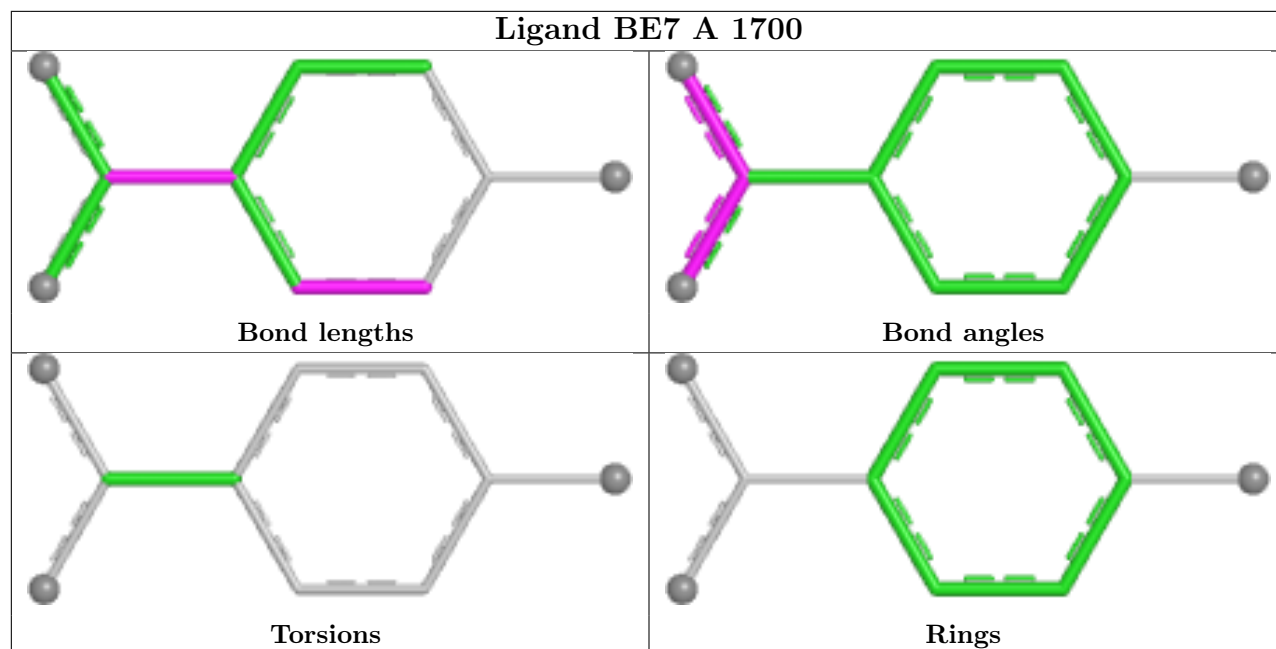
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1500	NR2	2	0
4	A	1400	NR2	2	0
5	A	1700	BE7	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.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

6.4 Ligands

EDS failed to run properly - this section is therefore empty.

6.5 Other polymers

EDS failed to run properly - this section is therefore empty.