



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:27 AM UTC

PDB ID : 1C3E / pdb_00001c3e
Title : NEW INSIGHTS INTO INHIBITOR DESIGN FROM THE CRYSTAL STRUCTURE AND NMR STUDIES OF E. COLI GAR TRANSFORMYLATE IN COMPLEX WITH BETA-GAR AND 10-FORMYL-5,8,10-TRIDE AZAFOLIC ACID.
Authors : Greasley, S.E.; Yamashita, M.M.; Cai, H.; Benkovic, S.J.; Boger, D.L.; Wilson, I.A.
Deposited on : 1999-07-27
Resolution : 2.10 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
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)	:	2.49

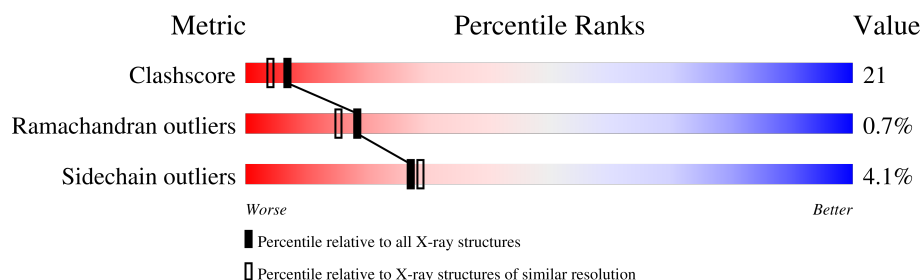
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	209	
1	B	209	

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	GAR	B	223	-	-	X	-

2 Entry composition [i](#)

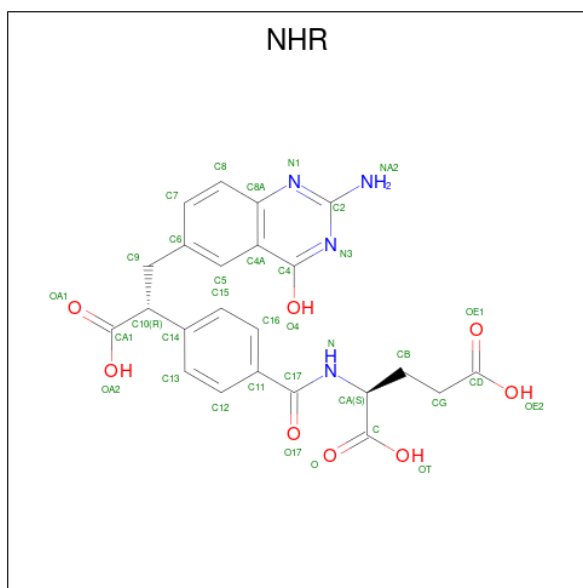
There are 4 unique types of molecules in this entry. The entry contains 3539 atoms, of which 0 are hydrogens and 0 are deuteriums.

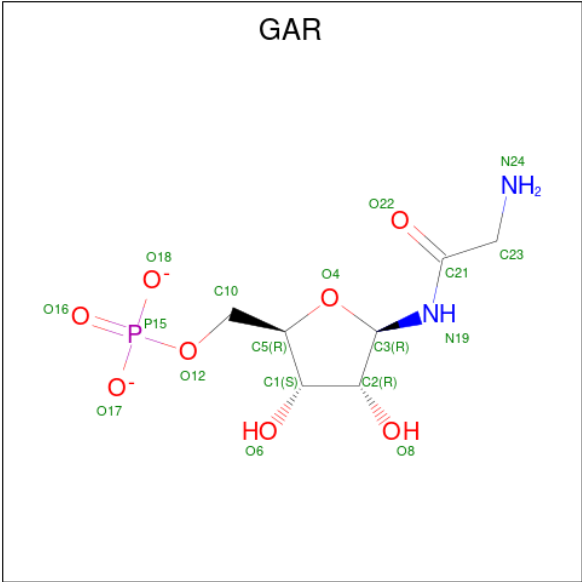
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GLYCINAMIDE RIBONUCLEOTIDE TRANSFORMYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	209	Total	C	N	O	S	0	0	0
			1618	1024	287	302	5			
1	B	209	Total	C	N	O	S	0	0	0
			1618	1024	287	302	5			

- Molecule 2 is 2-{4-[2-(2-AMINO-4-HYDROXY-QUINAZOLIN-6-YL)-1-CARBOXY-ETHYL]-BENZOYLAMINO}-PENTANEDIOIC ACID (CCD ID: NHR) (formula: C₂₃H₂₂N₄O₈).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			18	7	2	8	1		
3	B	1	Total	C	N	O	P	0	0
			18	7	2	8	1		

- Molecule 4 is water.

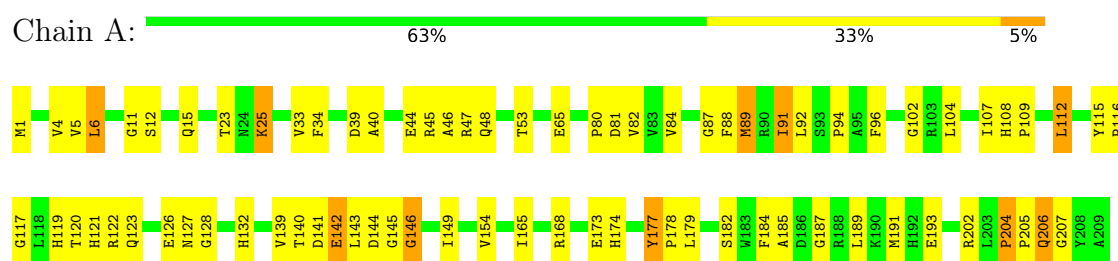
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	94	Total	O	0	0
			94	94		
4	B	103	Total	O	0	0
			103	103		

3 Residue-property plots

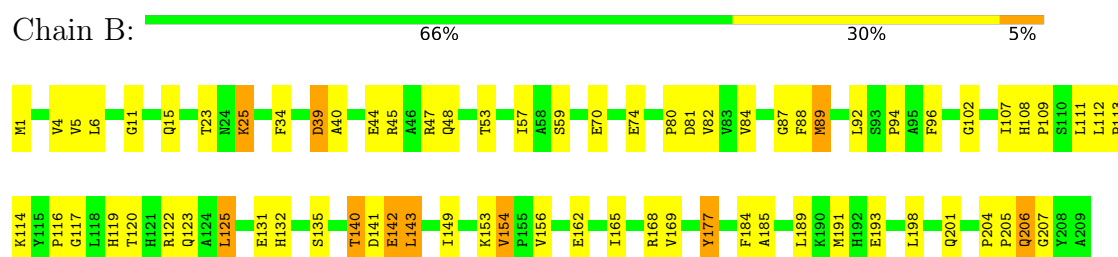
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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 was not executed.

• Molecule 1: GLYCINAMIDE RIBONUCLEOTIDE TRANSFORMYLASE



• Molecule 1: GLYCINAMIDE RIBONUCLEOTIDE TRANSFORMYLASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.25 Å 112.79 Å 46.96 Å 90.00° 101.50° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10	Depositor
% Data completeness (in resolution range)	78.9 (20.00-2.10)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.3	Depositor
R, R_{free}	0.227 , 0.263	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3539	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GAR, NHR

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	0.63	1/1655 (0.1%)	1.06	8/2248 (0.4%)
1	B	0.54	0/1655	1.05	7/2248 (0.3%)
All	All	0.59	1/3310 (0.0%)	1.05	15/4496 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	204	PRO	CA-C	5.51	1.57	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	LYS	N-CA-C	-8.14	102.40	111.28
1	B	25	LYS	N-CA-C	-8.10	102.45	111.28
1	B	116	PRO	N-CA-C	-6.91	101.05	111.41
1	A	140	THR	N-CA-C	-6.83	99.03	109.41
1	B	193	GLU	N-CA-C	-6.40	103.10	111.74
1	B	81	ASP	N-CA-C	-6.24	105.50	113.23
1	A	146	GLY	CA-C-N	6.15	127.11	119.98
1	A	146	GLY	C-N-CA	6.15	127.11	119.98
1	A	81	ASP	N-CA-C	-5.96	106.17	113.50
1	A	84	VAL	N-CA-C	5.53	115.81	107.80
1	B	140	THR	N-CA-C	-5.27	101.70	109.18
1	A	116	PRO	N-CA-C	-5.21	103.10	111.38
1	A	91	ILE	CB-CA-C	-5.10	103.73	111.33
1	B	205	PRO	CA-C-N	-5.10	114.56	122.67
1	B	205	PRO	C-N-CA	-5.10	114.56	122.67

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	1618	0	1592	75	0
1	B	1618	0	1592	64	0
2	A	35	0	20	1	0
2	B	35	0	19	3	0
3	A	18	0	13	3	0
3	B	18	0	13	9	0
4	A	94	0	0	5	0
4	B	103	0	0	3	0
All	All	3539	0	3249	140	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 21.

All (140) 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:202:ARG:NH2	1:B:113:PRO:HG3	1.76	0.98
1:A:202:ARG:CZ	1:B:113:PRO:HG3	1.93	0.97
1:A:91:ILE:HD12	1:A:143:LEU:HD11	1.47	0.95
1:B:89:MET:CE	3:B:223:GAR:H241	1.81	0.93
1:B:89:MET:HE3	3:B:223:GAR:N24	1.83	0.92
1:B:87:GLY:HA2	3:B:223:GAR:H19	1.36	0.91
1:B:140:THR:HG22	1:B:142:GLU:HG2	1.58	0.86
1:B:89:MET:HE3	3:B:223:GAR:H241	1.38	0.83
1:A:154:VAL:HG21	1:A:168:ARG:HG2	1.64	0.80
1:A:112:LEU:HD21	1:A:144:ASP:HB3	1.61	0.79
1:B:23:THR:OG1	1:B:25:LYS:HG3	1.82	0.77
1:A:23:THR:OG1	1:A:25:LYS:HG3	1.85	0.77
1:A:89:MET:HA	1:A:89:MET:HE2	1.67	0.76
1:A:11:GLY:HA2	4:A:225:HOH:O	1.86	0.76
1:B:132:HIS:HB3	1:B:165:ILE:HD11	1.69	0.74
1:B:15:GLN:HE21	1:B:45:ARG:HH11	1.34	0.73
1:A:119:HIS:O	1:A:123:GLN:HG3	1.89	0.72
1:A:109:PRO:HG2	1:A:120:THR:HG21	1.72	0.71
1:A:206:GLN:HE21	1:A:206:GLN:CA	2.03	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:11:GLY:HA2	4:B:291:HOH:O	1.91	0.70
1:B:131:GLU:OE2	1:B:153:LYS:HD3	1.91	0.69
1:A:112:LEU:HD21	1:A:144:ASP:O	1.94	0.68
1:A:91:ILE:CD1	1:A:143:LEU:HD11	2.22	0.67
1:A:15:GLN:HE21	1:A:45:ARG:HH11	1.40	0.67
1:A:126:GLU:C	1:A:128:GLY:H	2.04	0.66
1:A:112:LEU:CD2	1:A:144:ASP:O	2.43	0.65
1:A:122:ARG:O	1:A:126:GLU:HG3	1.97	0.65
1:B:102:GLY:HA2	1:B:191:MET:HE2	1.78	0.65
1:A:115:TYR:CE2	1:A:123:GLN:HB3	2.31	0.64
1:B:162:GLU:HG2	4:B:263:HOH:O	1.97	0.64
1:B:89:MET:HE2	1:B:89:MET:HA	1.80	0.63
1:B:23:THR:HG21	1:B:25:LYS:NZ	2.13	0.63
1:A:94:PRO:HA	1:A:141:ASP:OD1	1.98	0.63
1:A:102:GLY:HA2	1:A:191:MET:HE2	1.81	0.63
1:B:206:GLN:O	1:B:206:GLN:HG3	1.97	0.63
1:A:1:MET:HE2	1:A:185:ALA:HB2	1.81	0.62
1:B:156:VAL:HG22	1:B:165:ILE:HD12	1.82	0.62
1:A:91:ILE:HD12	1:A:143:LEU:CD1	2.26	0.62
1:A:154:VAL:CG2	1:A:168:ARG:HG2	2.30	0.61
1:A:23:THR:HG21	1:A:25:LYS:NZ	2.15	0.61
1:A:89:MET:CE	3:A:221:GAR:N24	2.65	0.60
1:B:119:HIS:O	1:B:123:GLN:HG3	2.02	0.60
1:A:132:HIS:O	1:A:154:VAL:HG12	2.03	0.59
1:B:47:ARG:NH1	1:B:53:THR:OG1	2.36	0.58
1:A:87:GLY:HA2	3:A:221:GAR:H19	1.68	0.58
1:B:132:HIS:CB	1:B:165:ILE:HD11	2.32	0.58
1:B:4:VAL:HG23	1:B:80:PRO:HB3	1.84	0.57
1:A:206:GLN:HE21	1:A:206:GLN:HA	1.67	0.57
1:A:132:HIS:HB3	1:A:165:ILE:HD11	1.86	0.57
1:A:47:ARG:NH1	1:A:53:THR:OG1	2.38	0.56
2:B:222:NHR:H151	3:B:223:GAR:N24	2.20	0.56
1:B:6:LEU:HD22	1:B:34:PHE:HB2	1.87	0.55
1:A:108:HIS:HE1	1:A:117:GLY:O	1.89	0.55
1:A:206:GLN:HB2	4:A:278:HOH:O	2.07	0.55
1:A:132:HIS:CB	1:A:165:ILE:HD11	2.37	0.55
1:B:94:PRO:HA	1:B:141:ASP:OD1	2.07	0.55
1:B:107:ILE:HG23	1:B:107:ILE:O	2.07	0.55
1:A:23:THR:HG21	1:A:25:LYS:HZ1	1.73	0.54
1:B:149:ILE:HD13	1:B:189:LEU:HD21	1.88	0.54
1:B:82:VAL:HB	1:B:184:PHE:CE2	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:PHE:CE2	1:A:92:LEU:HD21	2.44	0.53
1:B:15:GLN:NE2	1:B:45:ARG:HH11	2.06	0.52
1:A:107:ILE:O	1:A:107:ILE:HG23	2.08	0.52
1:A:88:PHE:HE2	1:A:92:LEU:HD21	1.73	0.52
1:B:89:MET:CE	3:B:223:GAR:N24	2.51	0.51
1:A:126:GLU:C	1:A:128:GLY:N	2.69	0.51
1:B:140:THR:CG2	1:B:142:GLU:HG2	2.37	0.50
1:B:1:MET:HE2	1:B:185:ALA:HB2	1.94	0.50
1:B:88:PHE:HE2	1:B:92:LEU:HD21	1.77	0.49
1:A:65:GLU:HA	4:A:247:HOH:O	2.12	0.49
1:A:15:GLN:NE2	1:A:45:ARG:HH11	2.10	0.49
1:A:82:VAL:HB	1:A:184:PHE:CE2	2.48	0.49
1:A:115:TYR:CE2	1:A:123:GLN:CB	2.95	0.49
1:A:112:LEU:HD23	1:A:144:ASP:O	2.14	0.48
1:A:187:GLY:HA2	4:A:276:HOH:O	2.13	0.48
1:B:112:LEU:HD12	1:B:135:SER:HB2	1.95	0.48
1:B:39:ASP:O	1:B:40:ALA:C	2.55	0.48
1:B:88:PHE:CE2	1:B:92:LEU:HD21	2.49	0.48
1:A:142:GLU:O	1:A:145:GLY:N	2.36	0.47
1:A:204:PRO:HG2	1:A:207:GLY:O	2.13	0.47
1:A:132:HIS:C	1:A:154:VAL:HG12	2.39	0.47
1:B:198:LEU:O	1:B:201:GLN:HG2	2.15	0.47
1:B:57:ILE:HG22	1:B:59:SER:H	1.79	0.47
1:A:132:HIS:O	1:A:154:VAL:N	2.48	0.47
1:B:109:PRO:HG2	1:B:120:THR:HG21	1.97	0.46
1:A:142:GLU:HB2	1:A:145:GLY:HA3	1.97	0.46
1:A:89:MET:HA	1:A:89:MET:CE	2.41	0.46
1:B:87:GLY:HA2	3:B:223:GAR:H232	1.97	0.46
1:B:132:HIS:O	1:B:154:VAL:N	2.49	0.46
1:B:156:VAL:HG22	1:B:165:ILE:CD1	2.44	0.46
1:A:6:LEU:HD22	1:A:34:PHE:HB2	1.98	0.46
1:B:140:THR:HG22	1:B:142:GLU:CG	2.38	0.46
1:A:104:LEU:HG	1:A:139:VAL:HB	1.98	0.45
1:A:108:HIS:HD1	2:A:220:NHR:CA1	2.26	0.45
1:A:149:ILE:HD13	1:A:189:LEU:HD21	1.98	0.45
1:B:154:VAL:HG13	1:B:168:ARG:HD2	1.97	0.45
2:B:222:NHR:H151	3:B:223:GAR:H242	1.80	0.45
1:B:108:HIS:HE1	1:B:117:GLY:O	2.00	0.45
1:B:165:ILE:O	1:B:169:VAL:HG23	2.16	0.45
1:A:107:ILE:HD11	1:A:173:GLU:HG2	1.99	0.45
1:A:177:TYR:HB3	1:A:178:PRO:HD3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:THR:HG21	1:B:25:LYS:HZ1	1.79	0.44
1:B:89:MET:CE	1:B:89:MET:HA	2.47	0.44
1:B:87:GLY:CA	3:B:223:GAR:H232	2.48	0.44
1:A:120:THR:OG1	1:A:121:HIS:N	2.50	0.44
1:B:4:VAL:CG2	1:B:80:PRO:HB3	2.47	0.44
1:B:114:LYS:HG3	4:B:268:HOH:O	2.18	0.44
1:A:5:VAL:C	1:A:6:LEU:HD23	2.43	0.43
1:A:126:GLU:O	1:A:128:GLY:N	2.51	0.43
1:B:204:PRO:HG2	1:B:207:GLY:O	2.18	0.43
1:B:84:VAL:HG13	1:B:177:TYR:OH	2.19	0.43
1:A:109:PRO:HG2	1:A:120:THR:CG2	2.46	0.43
1:B:70:GLU:O	1:B:74:GLU:HG2	2.19	0.43
1:A:108:HIS:CD2	1:A:112:LEU:HD13	2.54	0.42
1:A:4:VAL:HG23	1:A:80:PRO:HB3	2.01	0.42
1:A:44:GLU:O	1:A:48:GLN:HG2	2.19	0.42
1:A:142:GLU:H	1:A:142:GLU:HG2	1.37	0.42
1:A:143:LEU:HD12	1:A:143:LEU:HA	1.54	0.42
1:B:142:GLU:HG2	1:B:142:GLU:H	1.27	0.42
1:A:89:MET:HE2	1:A:89:MET:CA	2.39	0.42
1:B:111:LEU:O	1:B:114:LYS:HB2	2.19	0.42
1:B:142:GLU:O	1:B:143:LEU:C	2.63	0.42
1:A:39:ASP:O	1:A:40:ALA:C	2.62	0.42
1:A:87:GLY:HA2	3:A:221:GAR:N19	2.33	0.41
1:B:122:ARG:HH11	1:B:122:ARG:HG3	1.85	0.41
1:B:39:ASP:OD1	1:B:39:ASP:N	2.53	0.41
1:B:44:GLU:O	1:B:48:GLN:HG2	2.21	0.41
1:B:125:LEU:HB3	1:B:162:GLU:OE2	2.20	0.41
1:A:96:PHE:C	1:A:96:PHE:CD1	2.98	0.41
1:A:193:GLU:HB2	4:A:311:HOH:O	2.20	0.41
1:B:96:PHE:CD1	1:B:96:PHE:C	2.99	0.41
1:A:33:VAL:HG21	1:A:46:ALA:HB2	2.02	0.41
1:A:112:LEU:HA	1:A:112:LEU:HD12	1.84	0.41
1:A:179:LEU:O	1:A:182:SER:OG	2.38	0.41
1:B:125:LEU:HD22	1:B:162:GLU:CD	2.45	0.41
1:A:108:HIS:CD2	1:A:112:LEU:CD1	3.04	0.40
1:B:5:VAL:C	1:B:6:LEU:HD23	2.45	0.40
1:B:122:ARG:HG3	1:B:122:ARG:NH1	2.35	0.40
2:B:222:NHR:O17	2:B:222:NHR:HB2	2.22	0.40
1:A:12:SER:OG	1:A:174:HIS:NE2	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	207/209 (99%)	194 (94%)	11 (5%)	2 (1%)	12	9
1	B	207/209 (99%)	200 (97%)	6 (3%)	1 (0%)	24	22
All	All	414/418 (99%)	394 (95%)	17 (4%)	3 (1%)	18	15

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	127	ASN
1	A	146	GLY
1	B	143	LEU

5.3.2 Protein sidechains

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	169/169 (100%)	162 (96%)	7 (4%)	27	29
1	B	169/169 (100%)	162 (96%)	7 (4%)	27	29
All	All	338/338 (100%)	324 (96%)	14 (4%)	27	29

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	89	MET
1	A	112	LEU

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Mol	Chain	Res	Type
1	A	142	GLU
1	A	177	TYR
1	A	205	PRO
1	A	206	GLN
1	B	39	ASP
1	B	89	MET
1	B	125	LEU
1	B	142	GLU
1	B	154	VAL
1	B	177	TYR
1	B	206	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	99	HIS
1	A	123	GLN
1	A	172	GLN
1	A	194	ASN
1	A	206	GLN
1	B	2	ASN
1	B	15	GLN
1	B	24	ASN
1	B	99	HIS
1	B	123	GLN
1	B	172	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 ligands are 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	GAR	A	221	-	17,18,18	1.36	3 (17%)	22,26,26	1.71	5 (22%)
2	NHR	A	220	-	37,37,37	2.54	15 (40%)	52,52,52	1.89	13 (25%)
3	GAR	B	223	-	17,18,18	1.46	3 (17%)	22,26,26	1.34	3 (13%)
2	NHR	B	222	-	37,37,37	2.52	17 (45%)	52,52,52	1.92	13 (25%)

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	GAR	A	221	-	-	4/12/28/28	0/1/1/1
2	NHR	A	220	-	-	10/29/29/29	0/3/3/3
3	GAR	B	223	-	-	8/12/28/28	0/1/1/1
2	NHR	B	222	-	-	10/29/29/29	0/3/3/3

All (38) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	222	NHR	C8A-N1	6.54	1.47	1.37
2	A	220	NHR	C2-N3	6.50	1.46	1.35
2	B	222	NHR	C2-N3	6.42	1.46	1.35
2	A	220	NHR	C14-C10	6.09	1.61	1.52
2	A	220	NHR	C8A-N1	5.74	1.46	1.37
2	B	222	NHR	C14-C10	4.17	1.58	1.52
2	A	220	NHR	C4-C4A	4.07	1.53	1.43
2	A	220	NHR	C13-C14	3.72	1.45	1.39
2	B	222	NHR	CA-N	3.59	1.53	1.45
2	B	222	NHR	C4-C4A	3.41	1.51	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	223	GAR	P15-O18	-3.41	1.42	1.54
2	A	220	NHR	C12-C11	3.25	1.44	1.39
2	B	222	NHR	C15-C14	3.22	1.44	1.39
3	A	221	GAR	P15-O18	-3.18	1.43	1.54
2	B	222	NHR	C12-C11	3.05	1.44	1.39
2	B	222	NHR	C8-C7	2.90	1.42	1.36
2	B	222	NHR	C16-C11	2.82	1.43	1.39
3	B	223	GAR	C3-N19	2.72	1.46	1.43
2	A	220	NHR	C13-C12	2.71	1.43	1.38
2	A	220	NHR	CA-C	2.67	1.59	1.52
2	A	220	NHR	C4A-C8A	2.61	1.46	1.42
3	B	223	GAR	P15-O16	2.60	1.58	1.50
3	A	221	GAR	P15-O16	2.57	1.58	1.50
2	A	220	NHR	OA2-CA1	-2.53	1.22	1.30
2	B	222	NHR	C4A-C8A	2.51	1.46	1.42
2	A	220	NHR	C15-C14	2.35	1.42	1.39
2	B	222	NHR	C17-N	2.33	1.39	1.34
2	B	222	NHR	C13-C14	2.26	1.42	1.39
3	A	221	GAR	P15-O12	-2.26	1.53	1.60
2	B	222	NHR	C7-C6	2.26	1.43	1.38
2	B	222	NHR	C13-C12	2.23	1.42	1.38
2	A	220	NHR	C9-C10	2.20	1.62	1.54
2	B	222	NHR	OA2-CA1	-2.12	1.23	1.30
2	A	220	NHR	OE2-CD	2.11	1.37	1.30
2	B	222	NHR	C11-C17	2.11	1.54	1.50
2	A	220	NHR	C11-C17	2.06	1.54	1.50
2	A	220	NHR	C8-C7	2.04	1.41	1.36
2	B	222	NHR	CA-C	2.03	1.57	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	222	NHR	OA2-CA1-OA1	-4.64	113.56	124.08
2	B	222	NHR	N1-C2-N3	-4.52	121.46	127.21
2	A	220	NHR	OA2-CA1-OA1	-4.49	113.88	124.08
2	A	220	NHR	N1-C2-N3	-4.46	121.54	127.21
3	A	221	GAR	O4-C3-N19	-4.40	105.24	110.22
2	A	220	NHR	C-CA-N	4.39	120.75	110.57
2	B	222	NHR	C-CA-N	4.27	120.48	110.57
2	B	222	NHR	C9-C10-CA1	4.15	119.73	110.94
2	A	220	NHR	CG-CB-CA	4.02	120.57	113.16
2	B	222	NHR	CA-N-C17	3.86	130.81	121.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	222	NHR	C4-C4A-C8A	3.56	117.11	114.77
2	B	222	NHR	C4A-C4-N3	-3.51	117.87	124.44
2	A	220	NHR	C4A-C4-N3	-3.48	117.92	124.44
2	A	220	NHR	C14-C10-CA1	3.42	116.15	109.67
2	B	222	NHR	CG-CB-CA	3.42	119.46	113.16
3	A	221	GAR	O12-P15-O16	-3.41	97.23	106.44
2	A	220	NHR	CA-N-C17	3.35	129.60	121.56
2	A	220	NHR	O4-C4-C4A	3.08	123.28	116.68
2	A	220	NHR	C4-C4A-C8A	3.07	116.79	114.77
2	B	222	NHR	C2-N3-C4	2.97	122.71	116.31
2	A	220	NHR	OA1-CA1-C10	-2.96	114.03	122.35
2	A	220	NHR	C2-N3-C4	2.80	122.35	116.31
2	B	222	NHR	O4-C4-C4A	2.77	122.61	116.68
2	B	222	NHR	C4A-C8A-N1	-2.75	119.89	122.80
3	B	223	GAR	O12-P15-O16	-2.73	99.05	106.44
2	A	220	NHR	C4A-C8A-N1	-2.67	119.97	122.80
3	A	221	GAR	C3-N19-C21	2.54	127.03	122.54
3	B	223	GAR	C1-C2-C3	2.53	106.25	101.46
3	B	223	GAR	O18-P15-O12	2.52	113.24	106.67
3	A	221	GAR	O18-P15-O12	2.38	112.87	106.67
2	B	222	NHR	OA1-CA1-C10	-2.35	115.75	122.35
2	A	220	NHR	C2-N1-C8A	2.15	121.42	116.35
3	A	221	GAR	O6-C1-C5	-2.05	105.21	111.08
2	B	222	NHR	C14-C10-CA1	2.00	113.47	109.67

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	220	NHR	CA-CB-CG-CD
3	A	221	GAR	C10-O12-P15-O16
3	A	221	GAR	C10-O12-P15-O17
3	A	221	GAR	C10-O12-P15-O18
3	B	223	GAR	O4-C3-N19-C21
3	B	223	GAR	C10-O12-P15-O16
3	B	223	GAR	C10-O12-P15-O17
3	B	223	GAR	C10-O12-P15-O18
2	B	222	NHR	CB-CA-N-C17
2	A	220	NHR	N-CA-CB-CG
2	B	222	NHR	CA-CB-CG-CD
3	B	223	GAR	O22-C21-C23-N24
2	A	220	NHR	C-CA-CB-CG

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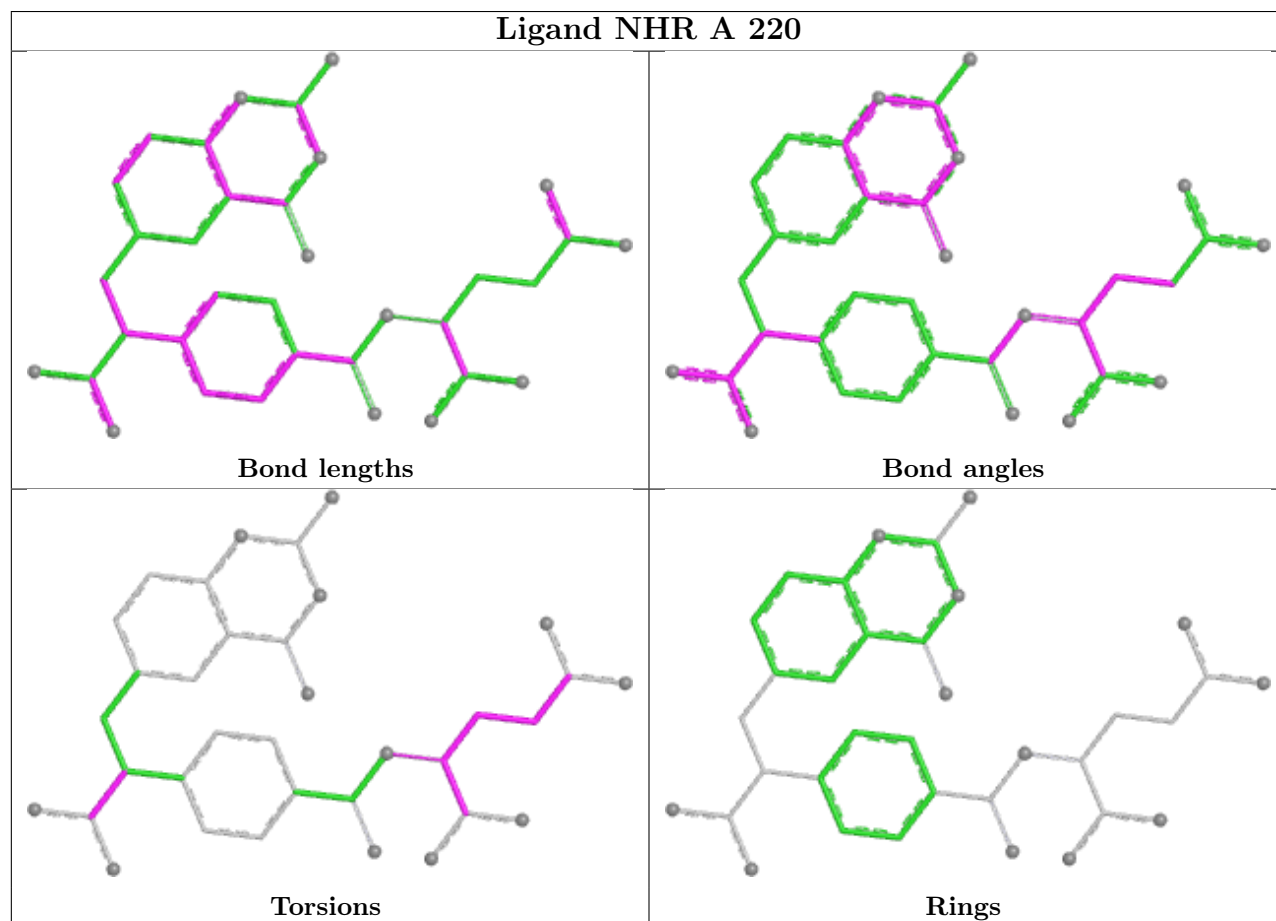
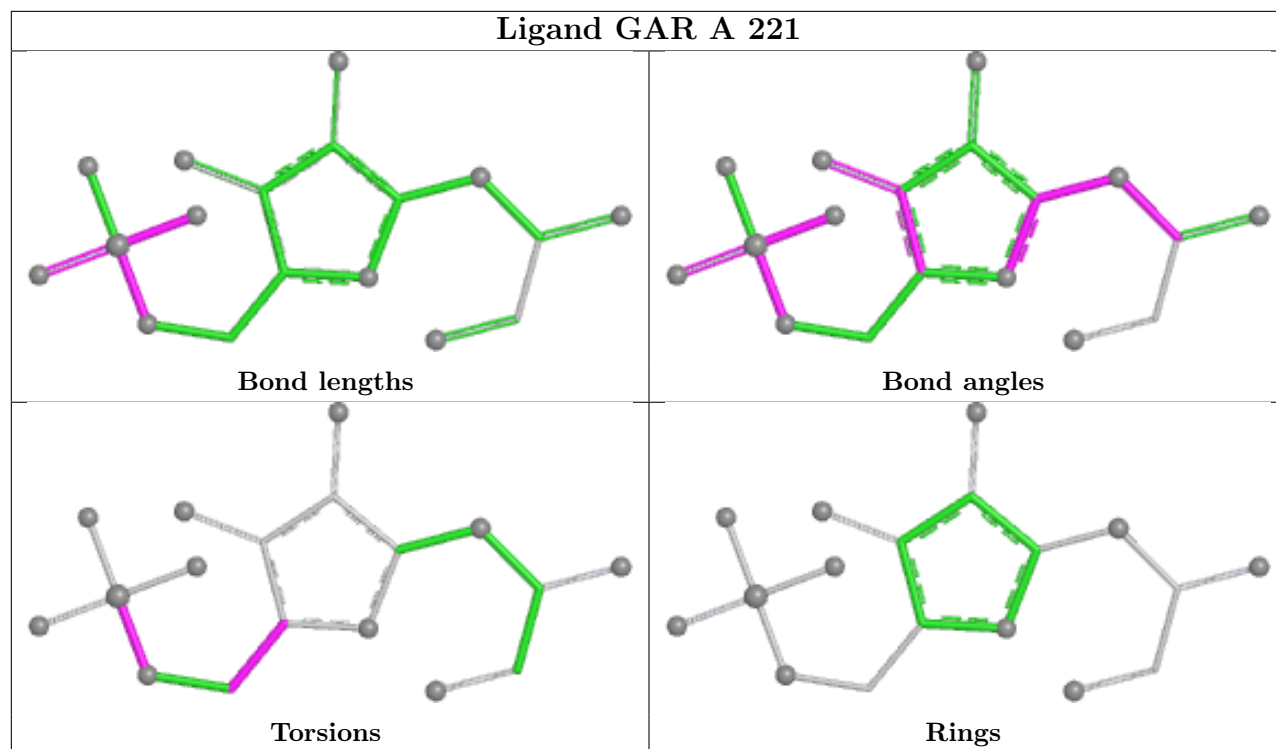
Mol	Chain	Res	Type	Atoms
3	B	223	GAR	O12-C10-C5-O4
3	B	223	GAR	N19-C21-C23-N24
2	B	222	NHR	C-CA-CB-CG
3	A	221	GAR	O12-C10-C5-O4
2	A	220	NHR	CB-CA-N-C17
3	B	223	GAR	O12-C10-C5-C1
2	A	220	NHR	C14-C10-CA1-OA2
2	B	222	NHR	C14-C10-CA1-OA1
2	B	222	NHR	C14-C10-CA1-OA2
2	B	222	NHR	C14-C10-C9-C6
2	B	222	NHR	OT-C-CA-N
2	B	222	NHR	O-C-CA-N
2	B	222	NHR	OE1-CD-CG-CB
2	A	220	NHR	C14-C10-CA1-OA1
2	B	222	NHR	OE2-CD-CG-CB
2	A	220	NHR	OE1-CD-CG-CB
2	A	220	NHR	OE2-CD-CG-CB
2	A	220	NHR	C9-C10-CA1-OA1
2	A	220	NHR	O-C-CA-N

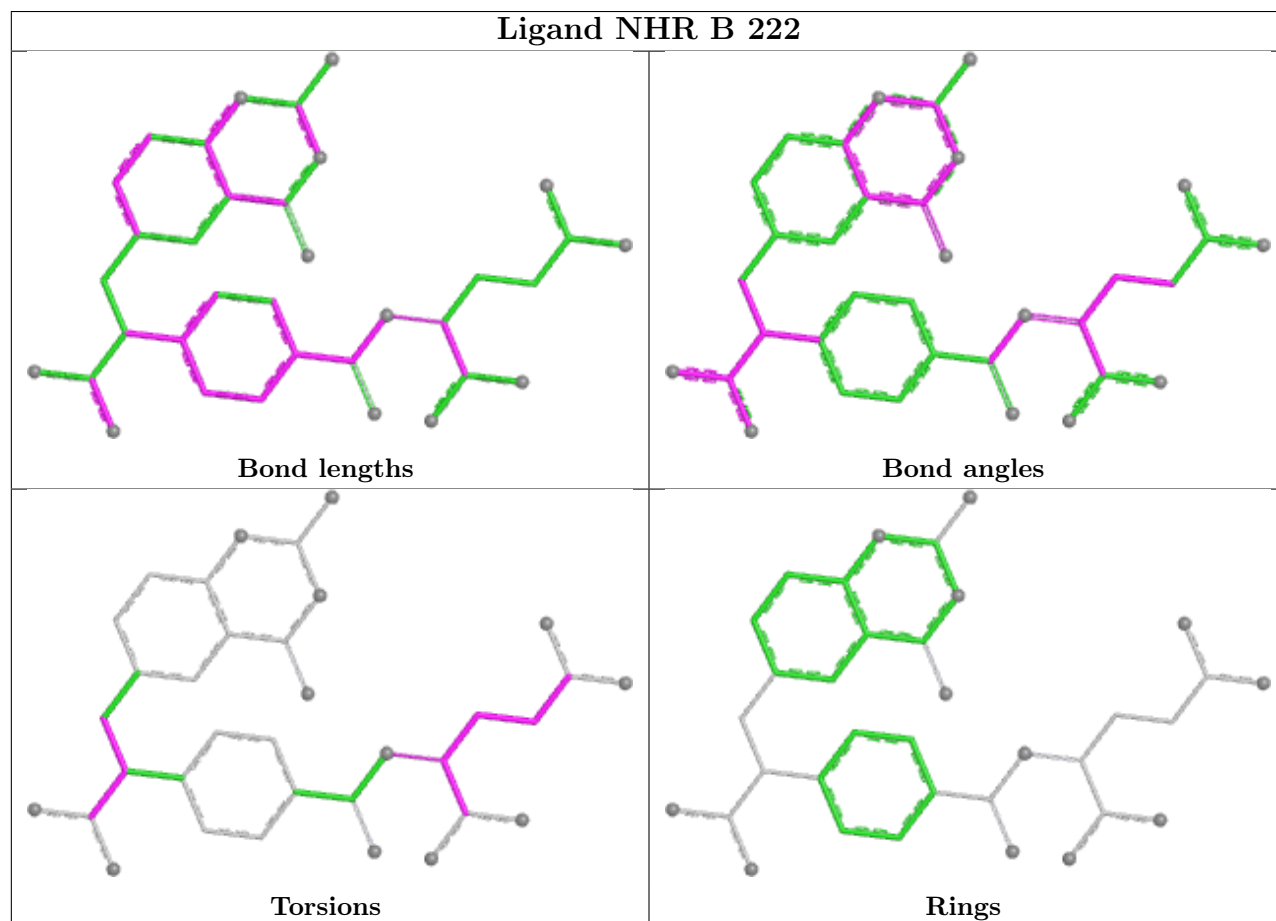
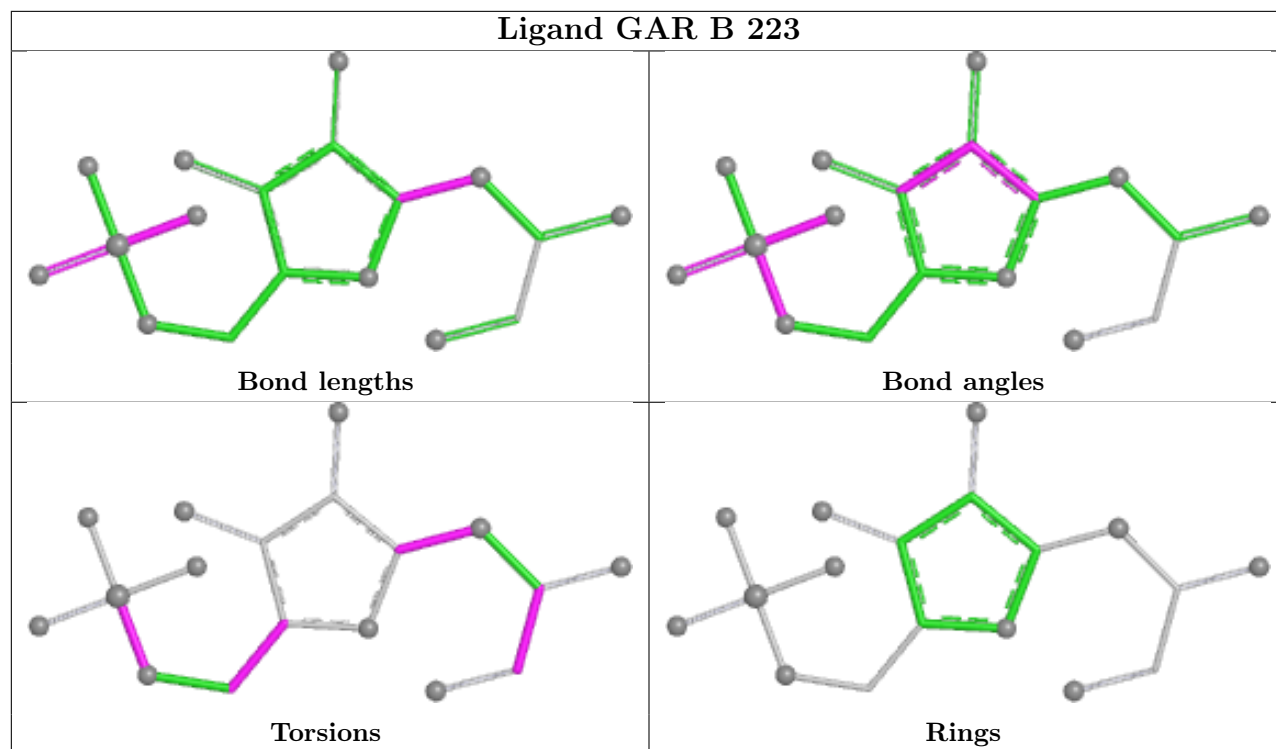
There are no ring outliers.

4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	221	GAR	3	0
2	A	220	NHR	1	0
3	B	223	GAR	9	0
2	B	222	NHR	3	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

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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.