



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 11:08 AM UTC

PDB ID : 1H3J / pdb_00001h3j
Title : STRUCTURE OF RECOMBINANT COPRINUS CINEREUS PEROXIDASE DETERMINED TO 2.0 Å
Authors : Petersen, J.F.W.; Houborg, K.; Harris, P.; Larsen, S.
Deposited on : 2002-09-05
Resolution : 2.00 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

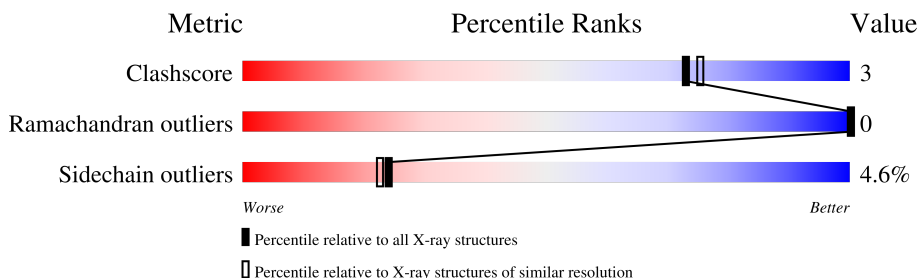
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	342	 86% 9% . .
1	B	342	 84% 12% . .
2	C	2	 100%
2	D	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5591 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 Peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	0	0
			2462	1535	421	491	15			
1	B	336	Total	C	N	O	S	0	0	0
			2462	1535	421	491	15			

- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
2	D	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).

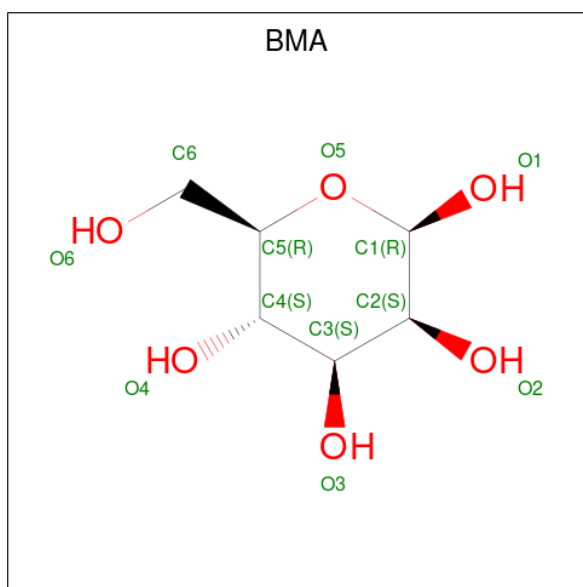


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
3	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Ca 2 2	0	0
4	B	2	Total Ca 2 2	0	0

- Molecule 5 is beta-D-mannopyranose (CCD ID: BMA) (formula: $\text{C}_6\text{H}_{12}\text{O}_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	B	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	236	Total	O	0	0
			236	236		
7	B	262	Total	O	0	0
			262	262		

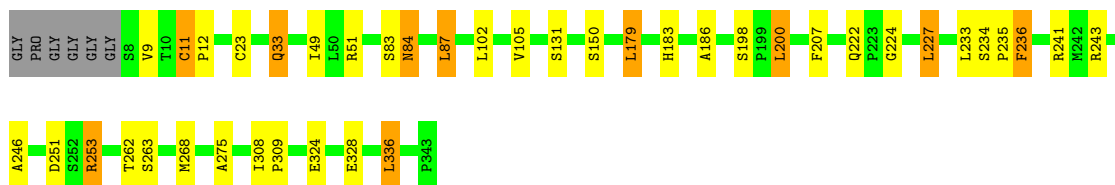
3 Residue-property plots [i](#)

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 was not executed.

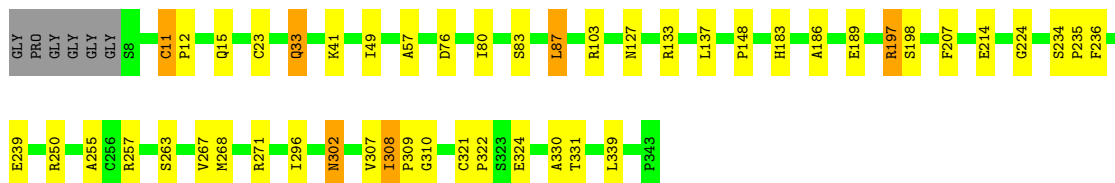
• Molecule 1: Peroxidase

Chain A:  86% 9% . .

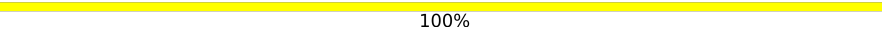


• Molecule 1: Peroxidase

Chain B:  84% 12% . .

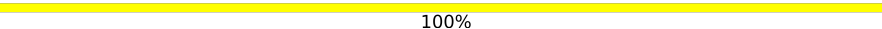


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:  100%



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:  100%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	127.18Å 75.53Å 76.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	98.0 (8.00-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.186 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5591	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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: HEM, CA, BMA, NAG, MG

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	0.77	0/2518	1.11	16/3432 (0.5%)
1	B	0.80	1/2518 (0.0%)	1.13	20/3432 (0.6%)
All	All	0.78	1/5036 (0.0%)	1.12	36/6864 (0.5%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	183	HIS	CG-CD2	5.01	1.41	1.35

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	308	ILE	N-CA-C	-11.64	96.97	107.56
1	B	308	ILE	N-CA-C	-11.03	97.52	107.56
1	A	263	SER	N-CA-C	8.62	123.92	113.23
1	A	224	GLY	CA-C-N	7.86	127.92	119.28
1	A	224	GLY	C-N-CA	7.86	127.92	119.28
1	B	309	PRO	N-CA-C	7.81	122.77	111.13
1	B	310	GLY	N-CA-C	7.23	124.04	113.48
1	B	296	ILE	N-CA-C	7.23	114.85	108.63
1	B	236	PHE	N-CA-C	7.04	114.56	108.22
1	B	263	SER	N-CA-C	6.55	121.36	113.23
1	A	309	PRO	N-CA-C	6.37	120.14	111.22
1	B	57	ALA	N-CA-C	6.30	118.22	111.36
1	B	224	GLY	CA-C-N	6.06	125.94	119.28
1	B	224	GLY	C-N-CA	6.06	125.94	119.28
1	A	262	THR	N-CA-C	6.03	117.93	111.36
1	A	236	PHE	N-CA-C	5.90	113.53	108.22
1	B	214	GLU	N-CA-C	5.81	118.39	111.71
1	B	186	ALA	N-CA-C	5.78	117.86	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	255	ALA	N-CA-C	5.74	117.54	111.28
1	A	183	HIS	ND1-CE1-NE2	5.71	114.11	108.40
1	B	76	ASP	N-CA-C	5.71	120.37	113.17
1	A	11	CYS	CA-C-N	5.65	126.91	119.84
1	A	11	CYS	C-N-CA	5.65	126.91	119.84
1	B	148	PRO	N-CA-C	-5.42	104.09	110.70
1	A	23	CYS	N-CA-C	5.39	117.16	111.28
1	B	198	SER	N-CA-C	-5.34	101.66	109.50
1	A	243	ARG	N-CA-C	5.29	117.46	111.11
1	B	23	CYS	N-CA-C	5.26	117.02	111.28
1	A	150	SER	N-CA-C	5.25	118.83	111.74
1	B	250	ARG	N-CA-C	5.20	119.90	113.50
1	A	198	SER	N-CA-C	-5.20	101.86	109.50
1	B	302	ASN	N-CA-C	-5.10	100.21	108.52
1	A	131	SER	N-CA-C	5.06	116.26	109.83
1	A	51	ARG	N-CA-C	-5.03	105.71	111.14
1	B	11	CYS	CA-C-N	5.02	126.12	119.84
1	B	11	CYS	C-N-CA	5.02	126.12	119.84

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	2462	0	2366	16	0
1	B	2462	0	2366	16	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
3	A	43	0	30	0	0
3	B	43	0	30	0	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	11	0	10	0	0
5	B	11	0	10	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	236	0	0	0	0
7	B	262	0	0	0	0
All	All	5591	0	4862	32	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 (32) 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:33:GLN:HE21	1:A:33:GLN:HA	1.36	0.91
1:B:33:GLN:HA	1:B:33:GLN:HE21	1.42	0.85
1:B:33:GLN:HE22	1:B:127:ASN:HD21	1.26	0.83
1:A:251:ASP:OD1	1:A:253:ARG:HD3	1.96	0.66
1:A:83:SER:HB2	1:A:87:LEU:HD22	1.78	0.66
1:B:257:ARG:NH2	1:B:271:ARG:HD2	2.12	0.65
1:B:80:ILE:O	1:B:103:ARG:NH2	2.31	0.62
1:B:267:VAL:O	1:B:271:ARG:HG3	2.00	0.61
1:B:207:PHE:CE2	1:B:268:MET:HE3	2.38	0.58
1:B:307:VAL:HG12	1:B:330:ALA:HB3	1.87	0.56
1:A:234:SER:HB2	1:A:235:PRO:HD2	1.89	0.55
1:A:33:GLN:HA	1:A:33:GLN:NE2	2.16	0.54
1:A:236:PHE:HB3	1:A:336:LEU:HG	1.94	0.50
1:B:189:GLU:OE1	1:B:197:ARG:HD3	2.10	0.50
1:A:222:GLN:HG3	1:A:227:LEU:HD13	1.94	0.49
1:A:84:ASN:HD22	1:A:84:ASN:H	1.60	0.49
1:B:33:GLN:HA	1:B:33:GLN:NE2	2.20	0.49
1:B:308:ILE:HB	1:B:331:THR:HG22	1.96	0.47
1:A:179:LEU:HD13	1:A:275:ALA:CB	2.45	0.46
1:B:234:SER:HB2	1:B:235:PRO:HD2	1.97	0.45
1:B:11:CYS:HB3	1:B:12:PRO:HD2	1.99	0.45
1:B:83:SER:HB2	1:B:87:LEU:HD22	2.01	0.42
1:A:11:CYS:HB3	1:A:12:PRO:HD2	2.01	0.42
1:B:307:VAL:HA	1:B:330:ALA:O	2.19	0.42
1:A:207:PHE:CE2	1:A:268:MET:HE3	2.55	0.42
1:A:179:LEU:HD13	1:A:275:ALA:HB1	2.02	0.41
1:A:241:ARG:HD3	1:A:246:ALA:HB2	2.02	0.41
1:B:321:CYS:HA	1:B:322:PRO:HD2	1.89	0.41
1:A:186:ALA:CB	1:A:200:LEU:HD22	2.51	0.41
1:A:84:ASN:HD22	1:A:84:ASN:N	2.19	0.40
1:A:83:SER:O	1:A:87:LEU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:GLU:HB2	1:B:339:LEU:HD22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	334/342 (98%)	320 (96%)	14 (4%)	0	100	100
1	B	334/342 (98%)	326 (98%)	8 (2%)	0	100	100
All	All	668/684 (98%)	646 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	270/272 (99%)	255 (94%)	15 (6%)	19	16
1	B	270/272 (99%)	260 (96%)	10 (4%)	30	30
All	All	540/544 (99%)	515 (95%)	25 (5%)	24	22

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	VAL
1	A	33	GLN
1	A	49	ILE
1	A	84	ASN
1	A	87	LEU
1	A	102	LEU
1	A	105	VAL
1	A	179	LEU
1	A	200	LEU
1	A	227	LEU
1	A	233	LEU
1	A	253	ARG
1	A	324	GLU
1	A	328	GLU
1	A	336	LEU
1	B	15	GLN
1	B	33	GLN
1	B	41	LYS
1	B	49	ILE
1	B	87	LEU
1	B	133	ARG
1	B	137	LEU
1	B	197	ARG
1	B	302	ASN
1	B	324	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	84	ASN
1	A	108	ASN
1	A	127	ASN
1	A	205	GLN
1	A	270	GLN
1	A	302	ASN
1	B	15	GLN
1	B	33	GLN
1	B	205	GLN
1	B	302	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 ⓘ

4 monosaccharides 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
2	NAG	C	1	2,1	14,14,15	1.64	2 (14%)	17,19,21	1.44	3 (17%)
2	NAG	C	2	2	14,14,15	1.48	2 (14%)	17,19,21	2.00	7 (41%)
2	NAG	D	1	2,1	14,14,15	1.51	2 (14%)	17,19,21	1.53	3 (17%)
2	NAG	D	2	2	14,14,15	1.79	4 (28%)	17,19,21	2.45	6 (35%)

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
2	NAG	C	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	C	2	2	-	1/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	1/6/23/26	0/1/1/1
2	NAG	D	2	2	-	0/6/23/26	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	NAG	C4-C5	-4.81	1.42	1.53
2	D	2	NAG	O4-C4	3.69	1.52	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	NAG	C4-C5	-3.65	1.45	1.53
2	C	2	NAG	C4-C3	3.47	1.61	1.52
2	D	2	NAG	O5-C1	-3.19	1.38	1.43
2	C	2	NAG	O4-C4	3.07	1.50	1.43
2	D	2	NAG	C4-C3	2.92	1.59	1.52
2	D	2	NAG	C4-C5	2.46	1.58	1.53
2	C	1	NAG	O5-C5	2.37	1.48	1.43
2	D	1	NAG	O3-C3	-2.09	1.37	1.43

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2	NAG	O7-C7-C8	-4.30	114.41	122.05
2	D	2	NAG	C1-O5-C5	4.05	117.61	112.19
2	D	2	NAG	C2-N2-C7	4.03	128.30	122.90
2	D	2	NAG	C8-C7-N2	3.80	122.43	116.12
2	C	2	NAG	O7-C7-C8	-3.62	115.61	122.05
2	C	2	NAG	C3-C4-C5	-3.45	103.97	110.23
2	D	1	NAG	C8-C7-N2	-3.38	110.51	116.12
2	C	2	NAG	C8-C7-N2	3.23	121.47	116.12
2	C	2	NAG	C1-O5-C5	3.06	116.28	112.19
2	C	1	NAG	O3-C3-C2	2.72	115.05	109.40
2	D	2	NAG	C3-C4-C5	-2.68	105.37	110.23
2	D	1	NAG	O7-C7-C8	2.51	126.53	122.05
2	C	1	NAG	O4-C4-C5	-2.42	103.36	109.32
2	C	1	NAG	C2-N2-C7	2.33	126.02	122.90
2	C	2	NAG	C4-C3-C2	2.25	114.31	111.02
2	D	2	NAG	O6-C6-C5	-2.25	103.69	111.33
2	C	2	NAG	O4-C4-C3	2.09	115.31	110.38
2	C	2	NAG	O5-C1-C2	-2.08	108.08	111.29
2	D	1	NAG	C2-N2-C7	2.04	125.64	122.90

There are no chirality outliers.

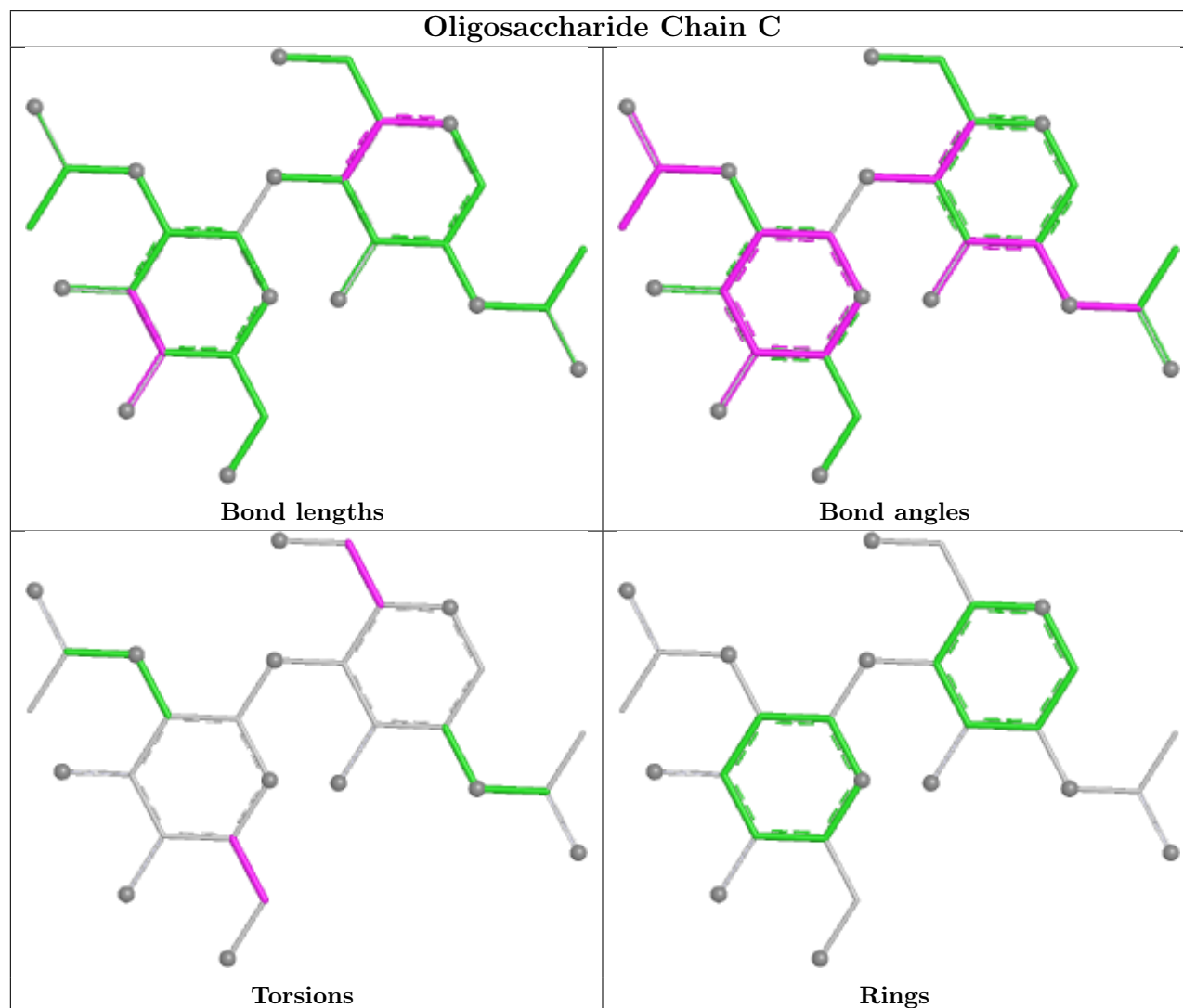
All (3) torsion outliers are listed below:

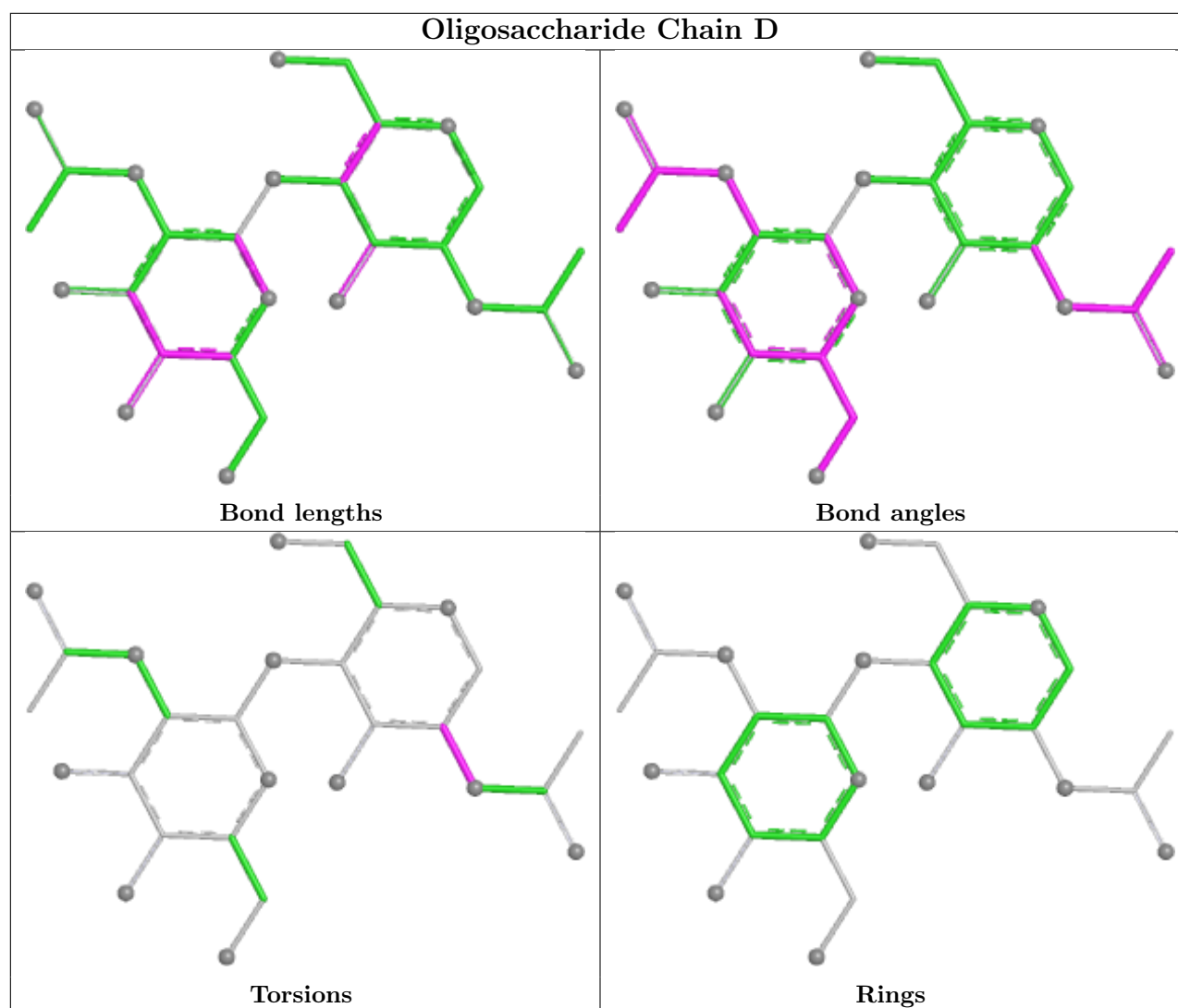
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	O5-C5-C6-O6
2	D	1	NAG	C1-C2-N2-C7
2	C	2	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 5 are monoatomic - leaving 4 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	BMA	B	404	-	11,11,12	1.99	3 (27%)	15,15,17	3.05	8 (53%)
3	HEM	A	401	1,7	50,50,50	1.46	9 (18%)	67,82,82	1.23	6 (8%)
5	BMA	A	404	-	11,11,12	1.84	5 (45%)	15,15,17	3.08	8 (53%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	HEM	B	401	1,7	50,50,50	1.53	9 (18%)	67,82,82	1.00	1 (1%)

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
5	BMA	B	404	-	-	0/2/19/22	0/1/1/1
3	HEM	A	401	1,7	-	5/14/54/54	-
5	BMA	A	404	-	-	0/2/19/22	0/1/1/1
3	HEM	B	401	1,7	-	6/14/54/54	-

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	404	BMA	C4-C3	4.48	1.64	1.52
3	B	401	HEM	CAB-C3B	-4.17	1.36	1.47
3	A	401	HEM	FE-NC	4.07	2.08	1.95
5	B	404	BMA	C4-C5	3.63	1.60	1.53
5	A	404	BMA	C4-C3	3.24	1.60	1.52
3	A	401	HEM	FE-NB	3.00	2.04	1.94
3	A	401	HEM	C1B-C2B	-3.00	1.38	1.44
3	A	401	HEM	CHA-C4D	2.94	1.44	1.38
5	A	404	BMA	C4-C5	2.87	1.59	1.53
3	B	401	HEM	FE-NB	2.79	2.03	1.94
3	B	401	HEM	C4A-NA	2.64	1.44	1.39
3	B	401	HEM	CMB-C2B	2.64	1.56	1.50
3	B	401	HEM	CHC-C1C	2.59	1.43	1.38
3	B	401	HEM	C1B-C2B	-2.42	1.39	1.44
3	A	401	HEM	CAB-C3B	-2.33	1.41	1.47
3	B	401	HEM	C4B-NB	-2.33	1.34	1.38
5	A	404	BMA	O4-C4	-2.31	1.37	1.43
3	A	401	HEM	CBB-CAB	2.27	1.41	1.30
3	A	401	HEM	C4A-NA	2.24	1.43	1.39
3	A	401	HEM	CHC-C1C	2.21	1.42	1.38
3	B	401	HEM	CMD-C2D	2.21	1.55	1.50
3	B	401	HEM	CHA-C4D	2.20	1.42	1.38
5	B	404	BMA	O5-C5	2.13	1.47	1.43
5	A	404	BMA	O5-C5	2.12	1.47	1.43
5	A	404	BMA	C1-C2	-2.04	1.47	1.52
3	A	401	HEM	CMC-C2C	2.00	1.54	1.50

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	404	BMA	C1-C2-C3	-7.13	99.26	109.64
5	A	404	BMA	C1-C2-C3	-6.63	100.00	109.64
5	A	404	BMA	C3-C4-C5	5.18	119.63	110.23
5	B	404	BMA	C1-O5-C5	-4.57	106.06	112.19
5	A	404	BMA	C2-C3-C4	-4.27	103.35	110.86
5	B	404	BMA	C2-C3-C4	-3.92	103.96	110.86
3	A	401	HEM	CMB-C2B-C1B	3.80	130.97	125.03
5	B	404	BMA	C6-C5-C4	3.65	121.99	113.02
5	A	404	BMA	C1-O5-C5	-3.56	107.41	112.19
3	A	401	HEM	C1A-CHA-C4D	-3.48	118.05	126.25
5	B	404	BMA	O2-C2-C3	3.35	117.08	110.15
5	A	404	BMA	O2-C2-C3	2.99	116.33	110.15
5	A	404	BMA	O3-C3-C4	2.91	117.24	110.38
3	A	401	HEM	C4C-C3C-C2C	-2.71	104.46	106.81
3	A	401	HEM	CMD-C2D-C1D	2.66	129.19	125.03
5	B	404	BMA	C3-C4-C5	2.65	115.04	110.23
5	A	404	BMA	O4-C4-C5	-2.61	102.89	109.32
3	B	401	HEM	C1A-CHA-C4D	-2.47	120.44	126.25
5	B	404	BMA	O3-C3-C4	2.32	115.84	110.38
5	A	404	BMA	O5-C5-C6	2.23	112.00	107.66
3	A	401	HEM	CBA-CAA-C2A	-2.11	106.70	112.53
5	B	404	BMA	O3-C3-C2	2.05	114.24	110.05
3	A	401	HEM	CMB-C2B-C3B	-2.04	123.48	128.43

There are no chirality outliers.

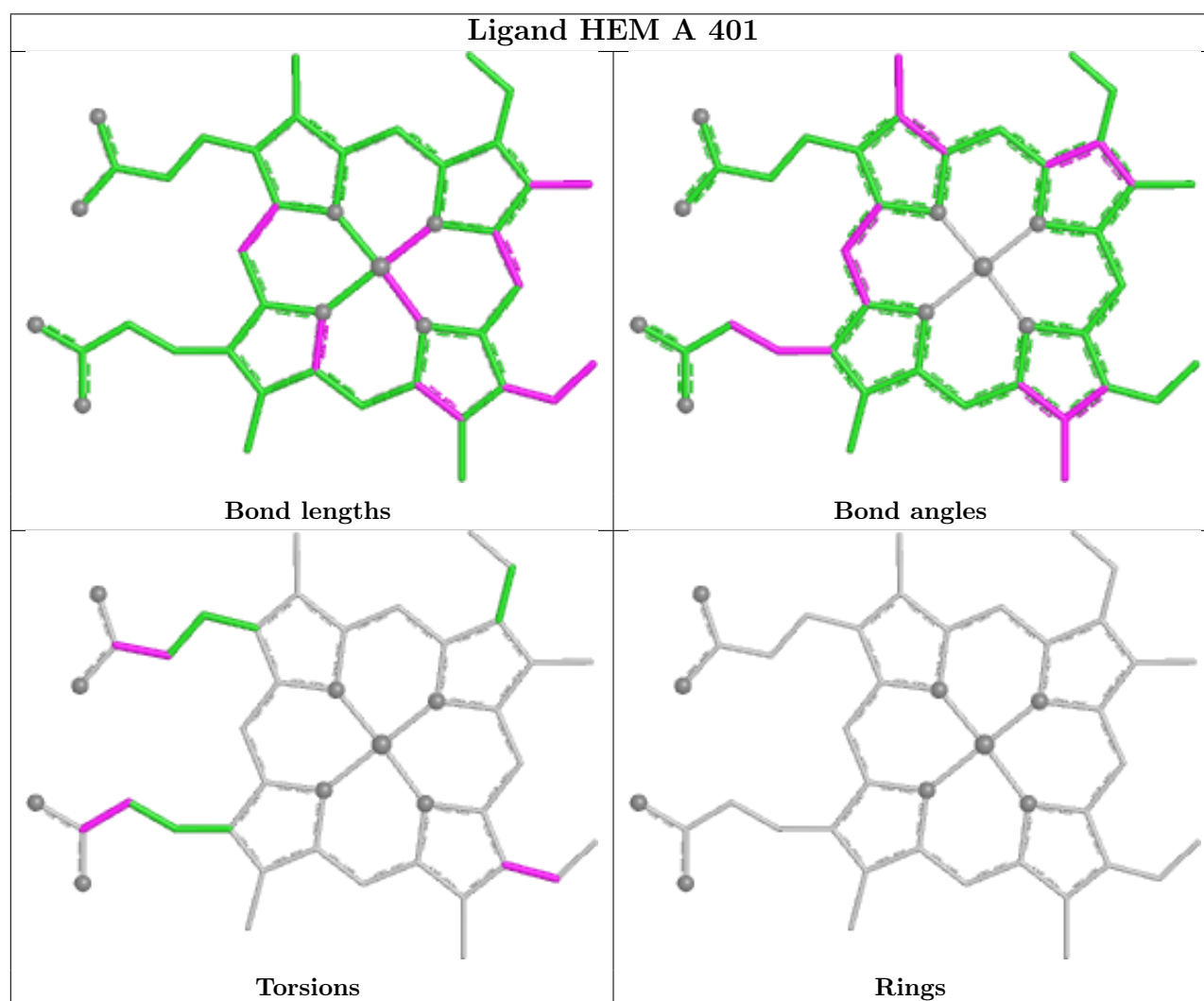
All (11) torsion outliers are listed below:

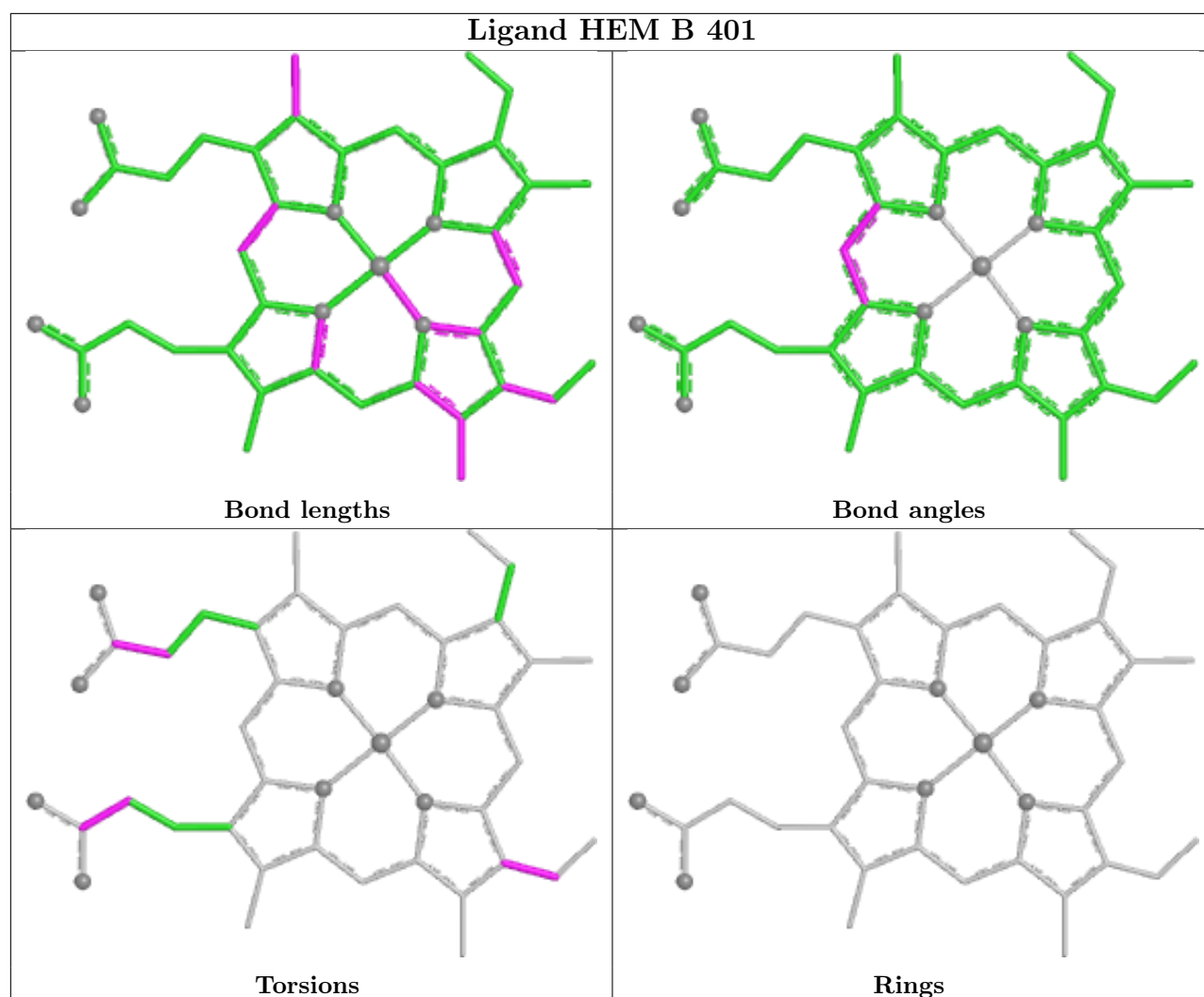
Mol	Chain	Res	Type	Atoms
3	A	401	HEM	C2B-C3B-CAB-CBB
3	A	401	HEM	C4B-C3B-CAB-CBB
3	B	401	HEM	C2B-C3B-CAB-CBB
3	B	401	HEM	C4B-C3B-CAB-CBB
3	B	401	HEM	CAA-CBA-CGA-O2A
3	A	401	HEM	CAA-CBA-CGA-O2A
3	B	401	HEM	CAA-CBA-CGA-O1A
3	B	401	HEM	CAD-CBD-CGD-O2D
3	B	401	HEM	CAD-CBD-CGD-O1D
3	A	401	HEM	CAA-CBA-CGA-O1A
3	A	401	HEM	CAD-CBD-CGD-O2D

There are no ring outliers.

No monomer is involved in short contacts.

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 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.