



Full wwPDB EM Validation Report ⓘ

Apr 28, 2026 – 02:22 PM JST

PDB ID : 9L1Y / pdb_00009l1y
EMDB ID : EMD-62758
Title : Vitamin K-dependent gamma-carboxylase apo status
Authors : Yao, D.; Wu, K.; Lan, P.
Deposited on : 2024-12-16
Resolution : 3.46 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : **FAILED**
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

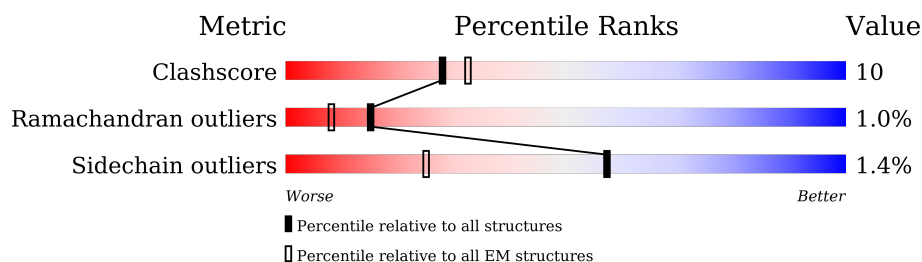
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.46 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	758	
2	B	2	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5267 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Vitamin K-dependent gamma-carboxylase.

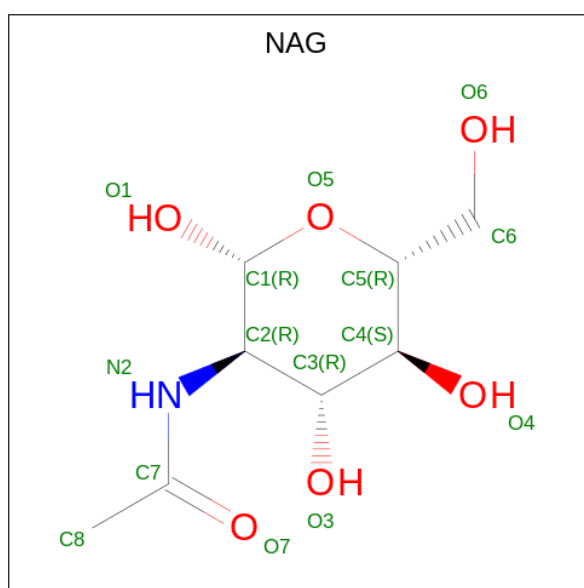
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	624	5148	3362	874	886	26	0	0

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



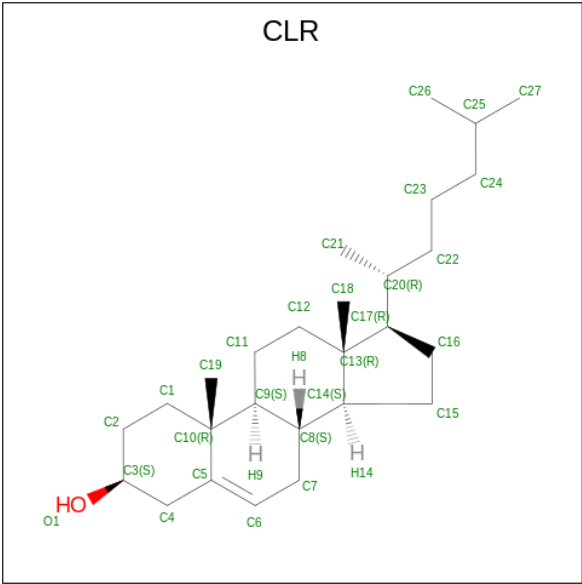
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	B	2	28	16	2	10	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



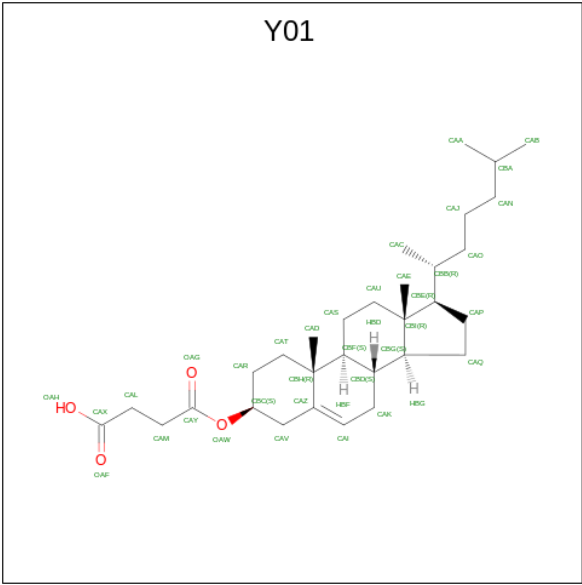
Mol	Chain	Residues	Atoms				AltConf
3	A	1	Total	C	N	O	0
			14	8	1	5	
3	A	1	Total	C	N	O	0
			14	8	1	5	

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total	C	O		0
			28	27	1		

- Molecule 5 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: C₃₁H₅₀O₄).



Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			35	31	4	

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	166899	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	1700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor

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: Y01, CLR, NAG

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	0.25	1/5299 (0.0%)	0.46	4/7196 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	308	PRO	C-O	-5.61	1.16	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	309	LEU	N-CA-C	-7.62	102.19	113.61
1	A	527	THR	CB-CA-C	-5.88	100.89	114.41
1	A	310	PHE	N-CA-C	-5.23	106.13	112.88
1	A	306	SER	N-CA-C	-5.01	107.22	113.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5148	0	5110	99	0
2	B	28	0	25	0	0
3	A	28	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	28	0	46	2	0
5	A	35	0	49	9	0
All	All	5267	0	5256	101	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 10.

All (101) 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:696:PHE:CD2	5:A:804:Y01:HAQ1	1.89	1.07
1:A:696:PHE:CE2	5:A:804:Y01:HAQ1	2.01	0.94
1:A:696:PHE:CE2	5:A:804:Y01:CAQ	2.62	0.82
1:A:696:PHE:HD2	5:A:804:Y01:HAE3	1.48	0.79
1:A:317:ARG:HG2	1:A:334:LYS:HG2	1.68	0.74
1:A:389:ASN:ND2	1:A:392:ASN:O	2.23	0.72
1:A:207:ILE:HD13	1:A:306:SER:HB3	1.72	0.71
1:A:403:VAL:HG11	1:A:406:ARG:HH21	1.58	0.69
1:A:320:VAL:O	1:A:328:GLN:NE2	2.26	0.69
1:A:347:ARG:HH21	1:A:354:GLN:HA	1.59	0.68
1:A:211:TYR:HH	1:A:287:HIS:HE2	1.43	0.67
1:A:77:LEU:O	1:A:81:GLN:NE2	2.29	0.66
1:A:408:HIS:NE2	1:A:438:LYS:HB3	2.12	0.65
1:A:60:ASP:OD2	1:A:317:ARG:NH1	2.30	0.65
1:A:693:ARG:O	1:A:697:LEU:HG	1.98	0.64
1:A:203:LEU:HB3	1:A:309:LEU:HD21	1.79	0.64
1:A:696:PHE:CD2	5:A:804:Y01:HAE3	2.33	0.62
1:A:483:ASP:OD1	1:A:503:GLN:NE2	2.30	0.62
1:A:571:GLN:NE2	1:A:572:THR:O	2.32	0.62
1:A:588:LYS:HB3	1:A:590:TYR:HE1	1.66	0.60
1:A:325:ARG:HG3	1:A:328:GLN:HG3	1.84	0.59
1:A:266:ALA:O	1:A:270:LEU:HB2	2.03	0.58
1:A:317:ARG:HH12	1:A:337:PRO:HG3	1.69	0.57
1:A:211:TYR:OH	1:A:287:HIS:NE2	2.35	0.56
1:A:520:LYS:HA	1:A:523:LEU:HG	1.88	0.56
1:A:49:ARG:HH22	1:A:50:ARG:HD3	1.71	0.55
1:A:534:ASP:HB3	1:A:591:THR:HG21	1.88	0.55
1:A:573:LEU:HD23	1:A:577:GLU:HB3	1.89	0.54
1:A:269:LEU:O	1:A:275:SER:OG	2.26	0.53
1:A:679:GLU:H	1:A:679:GLU:CD	2.17	0.52
1:A:331:LEU:H	1:A:331:LEU:HD23	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:LYS:HD2	1:A:519:ILE:HD13	1.92	0.51
1:A:515:LYS:HA	1:A:518:GLU:HB3	1.91	0.51
1:A:704:ARG:NH2	1:A:719:GLU:OE1	2.33	0.51
1:A:551:THR:HG22	1:A:603:TYR:HB3	1.93	0.51
1:A:696:PHE:HE2	5:A:804:Y01:HAP1	1.76	0.51
1:A:219:LEU:HG	1:A:260:LEU:HD21	1.93	0.50
1:A:345:TYR:N	1:A:354:GLN:OE1	2.38	0.50
1:A:86:SER:O	1:A:694:ARG:NH2	2.45	0.50
1:A:460:VAL:HG12	1:A:461:THR:H	1.77	0.50
1:A:555:LEU:HD21	1:A:559:GLU:HA	1.92	0.50
1:A:160:HIS:HB3	1:A:299:PHE:HB2	1.95	0.49
1:A:544:VAL:HG13	1:A:584:GLY:H	1.78	0.49
4:A:803:CLR:H161	4:A:803:CLR:H221	1.78	0.49
1:A:315:TRP:CG	1:A:316:PRO:HD3	2.47	0.48
1:A:528:GLU:HB3	1:A:603:TYR:CE1	2.48	0.48
1:A:351:LYS:HG3	1:A:352:SER:N	2.28	0.48
1:A:476:ARG:O	1:A:531:PHE:HB2	2.12	0.48
1:A:60:ASP:HB3	1:A:313:PRO:O	2.13	0.47
1:A:431:PHE:HE2	1:A:454:LEU:HD22	1.79	0.47
1:A:483:ASP:HB3	1:A:486:VAL:HG22	1.97	0.46
1:A:581:LEU:HD23	1:A:587:HIS:CD2	2.51	0.46
1:A:696:PHE:HE2	5:A:804:Y01:CAP	2.29	0.46
1:A:435:ARG:HG3	1:A:438:LYS:HE3	1.98	0.46
1:A:346:LYS:HB2	1:A:349:ARG:HH12	1.81	0.45
1:A:556:LEU:HB2	1:A:598:CYS:HB3	1.98	0.45
1:A:695:SER:O	1:A:699:THR:OG1	2.27	0.45
1:A:696:PHE:CE2	5:A:804:Y01:CAP	3.00	0.45
1:A:563:GLU:HG2	1:A:569:LYS:O	2.16	0.45
1:A:351:LYS:HG3	1:A:352:SER:H	1.81	0.45
1:A:460:VAL:HG12	1:A:461:THR:N	2.32	0.45
1:A:260:LEU:O	1:A:264:LEU:HD12	2.17	0.44
1:A:307:SER:C	1:A:309:LEU:H	2.26	0.44
1:A:540:LEU:HB3	1:A:589:VAL:HG22	1.98	0.44
1:A:394:LEU:HD23	1:A:394:LEU:HA	1.73	0.44
1:A:405:SER:C	1:A:406:ARG:HG2	2.43	0.44
1:A:536:PRO:HB3	1:A:593:SER:O	2.17	0.44
1:A:408:HIS:CD2	1:A:438:LYS:HB3	2.52	0.44
1:A:468:ASP:OD1	1:A:484:PRO:HB3	2.17	0.44
1:A:571:GLN:HE22	1:A:573:LEU:HG	1.83	0.43
1:A:455:LEU:N	1:A:456:PRO:HD2	2.34	0.43
4:A:803:CLR:H213	4:A:803:CLR:H231	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:ILE:HD12	1:A:601:TYR:CD2	2.54	0.43
1:A:541:GLU:HG2	1:A:588:LYS:HZ3	1.84	0.43
1:A:563:GLU:HA	1:A:569:LYS:O	2.18	0.43
1:A:548:LEU:HD22	1:A:603:TYR:HB2	1.99	0.43
1:A:471:VAL:O	1:A:478:GLN:HA	2.18	0.43
1:A:325:ARG:HG2	1:A:327:LEU:N	2.33	0.43
1:A:371:LEU:HD23	1:A:371:LEU:HA	1.93	0.43
1:A:551:THR:HA	1:A:602:VAL:O	2.19	0.43
1:A:96:LEU:HD12	1:A:96:LEU:HA	1.90	0.42
1:A:219:LEU:HG	1:A:260:LEU:HD11	2.01	0.42
1:A:355:LYS:HA	1:A:355:LYS:HD2	1.77	0.42
1:A:478:GLN:H	1:A:478:GLN:HG2	1.70	0.42
1:A:528:GLU:HB3	1:A:603:TYR:HE1	1.85	0.42
1:A:605:ASN:CG	1:A:608:GLU:HB2	2.45	0.42
1:A:431:PHE:CE2	1:A:454:LEU:HD22	2.55	0.41
1:A:703:LEU:HD23	1:A:703:LEU:HA	1.91	0.41
1:A:83:ARG:HA	1:A:83:ARG:HD2	1.73	0.41
1:A:127:LEU:HA	1:A:127:LEU:HD12	1.80	0.41
1:A:524:ASP:HB3	1:A:525:ASN:H	1.67	0.41
1:A:456:PRO:HA	1:A:460:VAL:O	2.21	0.41
1:A:696:PHE:CE2	5:A:804:Y01:HAP1	2.54	0.41
1:A:548:LEU:HD13	1:A:603:TYR:CG	2.56	0.41
1:A:262:LEU:O	1:A:266:ALA:CB	2.69	0.40
1:A:303:MET:HA	1:A:306:SER:HB2	2.03	0.40
1:A:455:LEU:HD23	1:A:455:LEU:HA	1.87	0.40
1:A:470:TRP:CZ2	1:A:540:LEU:HD12	2.56	0.40
1:A:503:GLN:OE1	1:A:503:GLN:HA	2.21	0.40
1:A:203:LEU:CB	1:A:309:LEU:HD21	2.51	0.40
1:A:690:TYR:O	1:A:693:ARG:HG2	2.21	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 PDB entries followed by that with respect to all EM entries.

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	618/758 (82%)	564 (91%)	48 (8%)	6 (1%)	12	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	ASP
1	A	275	SER
1	A	525	ASN
1	A	566	ALA
1	A	509	LEU
1	A	308	PRO

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 PDB entries followed by that with respect to all EM entries.

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	560/681 (82%)	552 (99%)	8 (1%)	59	72

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	ASP
1	A	254	VAL
1	A	304	LEU
1	A	307	SER
1	A	309	LEU
1	A	375	LEU
1	A	525	ASN
1	A	526	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	170	GLN
1	A	187	ASN

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Mol	Chain	Res	Type
1	A	526	HIS
1	A	554	GLN
1	A	678	HIS

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 ⓘ

2 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	B	1	2,1	14,14,15	0.23	0	17,19,21	0.36	0
2	NAG	B	2	2	14,14,15	0.20	0	17,19,21	0.44	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
2	NAG	B	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	B	2	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

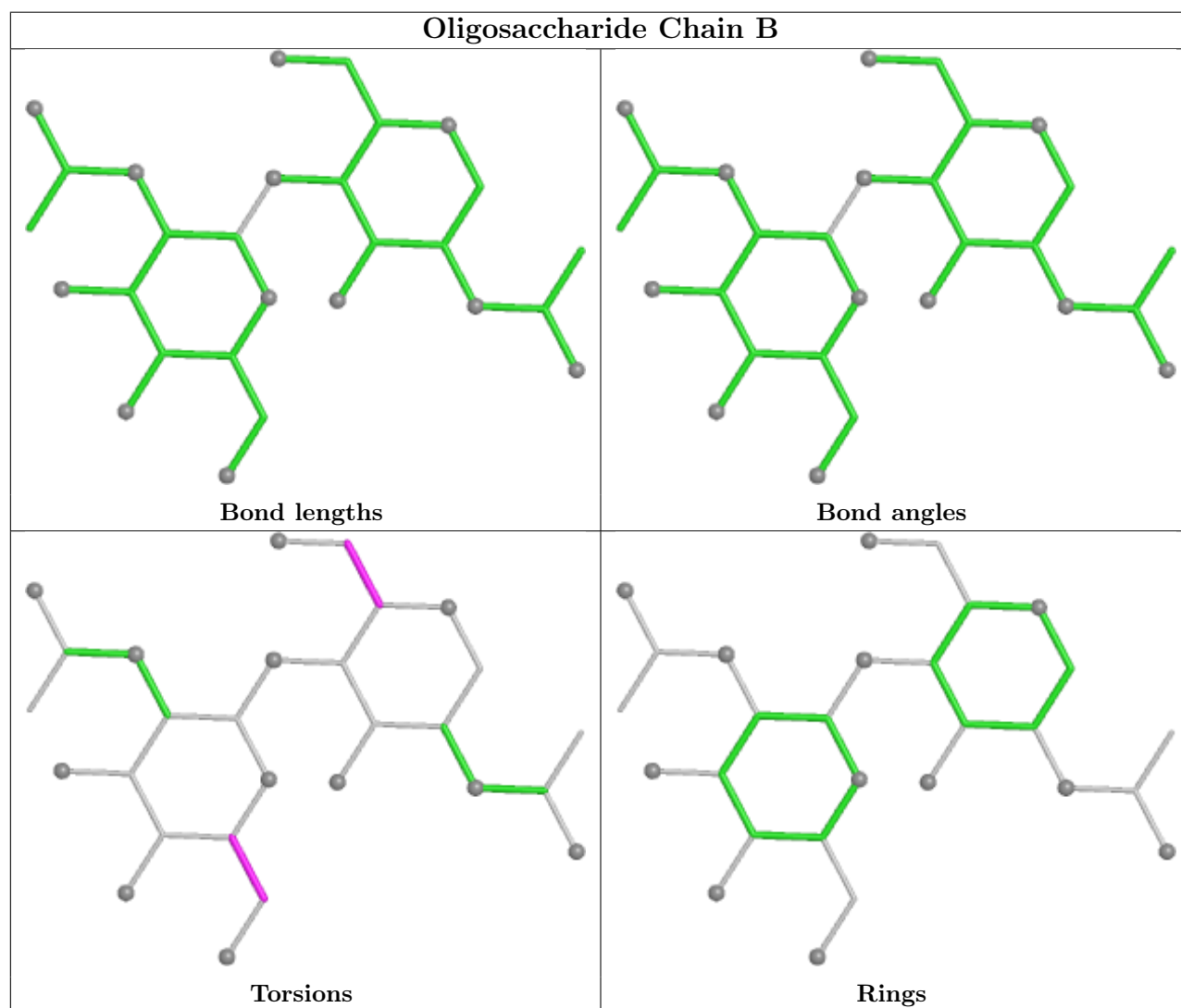
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1	NAG	C4-C5-C6-O6
2	B	1	NAG	O5-C5-C6-O6
2	B	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

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
5	Y01	A	804	-	38,38,38	1.18	3 (7%)	57,57,57	1.93	9 (15%)
4	CLR	A	803	-	31,31,31	1.07	1 (3%)	48,48,48	1.27	7 (14%)
3	NAG	A	802	1	14,14,15	0.29	0	17,19,21	0.41	0
3	NAG	A	801	1	14,14,15	0.22	0	17,19,21	0.40	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
5	Y01	A	804	-	-	10/19/77/77	0/4/4/4
4	CLR	A	803	-	-	7/10/68/68	0/4/4/4
3	NAG	A	802	1	-	2/6/23/26	0/1/1/1
3	NAG	A	801	1	-	1/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	804	Y01	CAK-CAI	-4.20	1.41	1.50
5	A	804	Y01	CAI-CAZ	2.61	1.38	1.33
4	A	803	CLR	C18-C13	-2.36	1.50	1.54
5	A	804	Y01	CAL-CAX	2.05	1.55	1.50

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	804	Y01	CAV-CAZ-CBH	7.55	126.46	116.42
5	A	804	Y01	OAW-CAY-CAM	5.23	122.78	111.50
5	A	804	Y01	OAW-CAY-OAG	-5.10	111.38	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	804	Y01	CAV-CAZ-CAI	-4.93	113.50	120.61
4	A	803	CLR	C22-C20-C17	-2.73	104.65	110.28
5	A	804	Y01	OAW-CBC-CAV	-2.66	102.68	108.12
5	A	804	Y01	CAP-CBE-CBB	-2.33	108.53	112.15
5	A	804	Y01	OAW-CBC-CAR	2.29	113.86	108.33
4	A	803	CLR	C18-C13-C12	2.27	114.17	110.59
4	A	803	CLR	C13-C17-C20	-2.27	115.94	119.49
4	A	803	CLR	C7-C8-C14	-2.25	107.65	110.91
5	A	804	Y01	CAS-CBF-CBD	-2.18	108.61	111.75
5	A	804	Y01	OAF-CAX-CAL	-2.15	116.17	123.08
4	A	803	CLR	C16-C17-C13	-2.13	101.28	103.84
4	A	803	CLR	C24-C23-C22	-2.08	103.67	113.24
4	A	803	CLR	C11-C12-C13	-2.04	109.28	112.78

There are no chirality outliers.

All (20) torsion outliers are listed below:

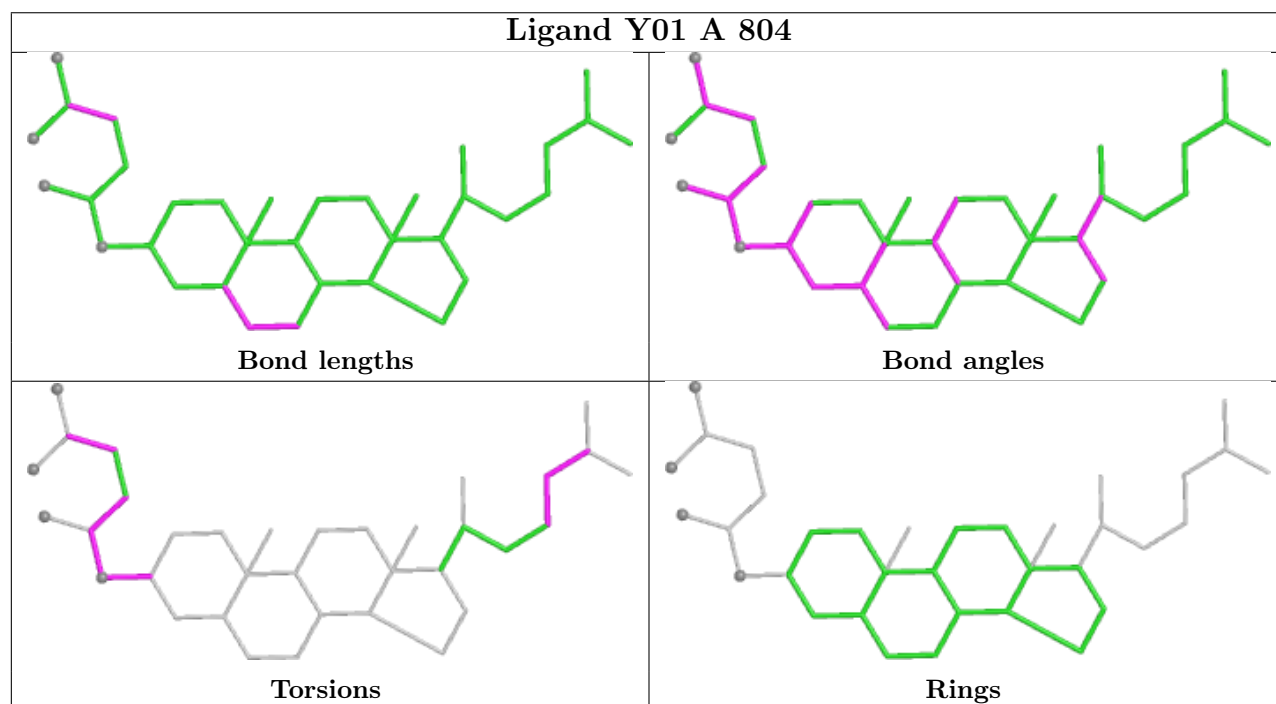
Mol	Chain	Res	Type	Atoms
5	A	804	Y01	OAG-CAY-OAW-CBC
4	A	803	CLR	C21-C20-C22-C23
5	A	804	Y01	CAM-CAY-OAW-CBC
5	A	804	Y01	CAR-CBC-OAW-CAY
4	A	803	CLR	C20-C22-C23-C24
4	A	803	CLR	C17-C20-C22-C23
5	A	804	Y01	CAV-CBC-OAW-CAY
5	A	804	Y01	CAJ-CAN-CBA-CAB
3	A	801	NAG	O5-C5-C6-O6
4	A	803	CLR	C13-C17-C20-C21
3	A	802	NAG	C4-C5-C6-O6
5	A	804	Y01	CAJ-CAN-CBA-CAA
3	A	802	NAG	O5-C5-C6-O6
5	A	804	Y01	CAO-CAJ-CAN-CBA
4	A	803	CLR	C13-C17-C20-C22
5	A	804	Y01	CAM-CAL-CAX-OAF
4	A	803	CLR	C23-C24-C25-C27
5	A	804	Y01	CAM-CAL-CAX-OAH
4	A	803	CLR	C23-C24-C25-C26
5	A	804	Y01	CAL-CAM-CAY-OAW

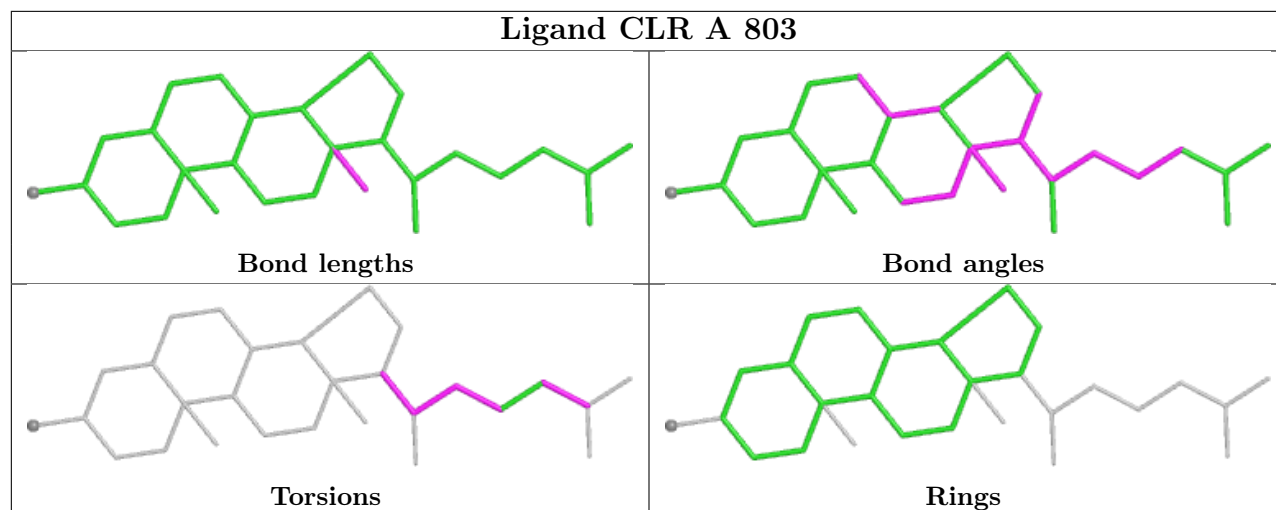
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	804	Y01	9	0
4	A	803	CLR	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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.