



Full wwPDB EM Validation Report ⓘ

Apr 5, 2025 – 01:21 PM EDT

PDB ID : 9D37 / pdb_00009d37
EMDB ID : EMD-46526
Title : Nonactive state of Gly-,Glu- bound GluN1a-2B-2D NMDAR
Authors : Hyunook, K.; Hiro, F.
Deposited on : 2024-08-09
Resolution : 3.34 Å(reported)
Based on initial models : 7saa, 8e96

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 : 0.0.1.dev117
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

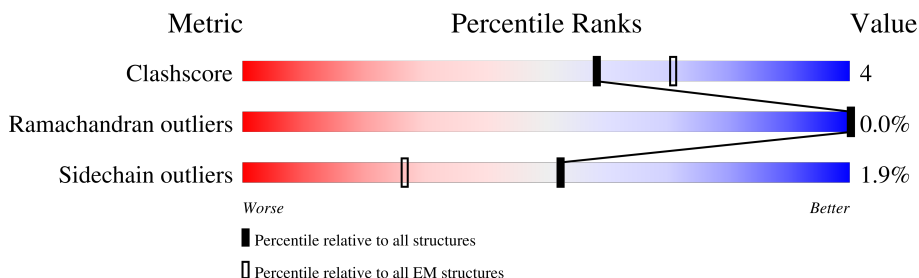
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.34 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	825	 84% 12% •
1	C	825	 83% 14% •
2	B	884	 79% 9% 12%
3	D	861	 76% 12% 11%
4	E	2	 100%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 24274 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 Glutamate receptor ionotropic, NMDA 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	789	Total	C	N	O	S	0	0
			6163	3933	1057	1138	35		
1	C	801	Total	C	N	O	S	0	0
			6246	3985	1066	1160	35		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	844	ASN	ARG	engineered mutation	UNP Q05586
A	845	GLY	ARG	engineered mutation	UNP Q05586
A	846	ALA	LYS	engineered mutation	UNP Q05586
C	844	ASN	ARG	engineered mutation	UNP Q05586
C	845	GLY	ARG	engineered mutation	UNP Q05586
C	846	ALA	LYS	engineered mutation	UNP Q05586

- Molecule 2 is a protein called Glutamate receptor ionotropic, NMDA 2B.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	776	Total	C	N	O	S	0	0
			5880	3795	948	1100	37		

There are 61 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	TRP	-	expression tag	UNP Q13224
B	-7	SER	-	expression tag	UNP Q13224
B	-6	HIS	-	expression tag	UNP Q13224
B	-5	PRO	-	expression tag	UNP Q13224
B	-4	GLN	-	expression tag	UNP Q13224
B	-3	PHE	-	expression tag	UNP Q13224
B	-2	GLU	-	expression tag	UNP Q13224
B	-1	LYS	-	expression tag	UNP Q13224
B	0	GLY	-	expression tag	UNP Q13224

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	-	expression tag	UNP Q13224
B	2	GLY	-	expression tag	UNP Q13224
B	3	SER	-	expression tag	UNP Q13224
B	4	GLY	-	expression tag	UNP Q13224
B	5	GLY	-	expression tag	UNP Q13224
B	6	GLY	-	expression tag	UNP Q13224
B	7	SER	-	expression tag	UNP Q13224
B	8	GLY	-	expression tag	UNP Q13224
B	9	GLY	-	expression tag	UNP Q13224
B	10	SER	-	expression tag	UNP Q13224
B	11	ALA	-	expression tag	UNP Q13224
B	12	TRP	-	expression tag	UNP Q13224
B	13	SER	-	expression tag	UNP Q13224
B	14	HIS	-	expression tag	UNP Q13224
B	15	PRO	-	expression tag	UNP Q13224
B	16	GLN	-	expression tag	UNP Q13224
B	17	PHE	-	expression tag	UNP Q13224
B	18	GLU	-	expression tag	UNP Q13224
B	19	LYS	-	expression tag	UNP Q13224
B	20	GLY	-	expression tag	UNP Q13224
B	21	ALA	-	expression tag	UNP Q13224
B	22	LEU	-	expression tag	UNP Q13224
B	23	VAL	-	expression tag	UNP Q13224
B	24	PRO	-	expression tag	UNP Q13224
B	25	ARG	-	expression tag	UNP Q13224
B	26	GLY	-	expression tag	UNP Q13224
B	588	SER	CYS	engineered mutation	UNP Q13224
B	838	SER	CYS	engineered mutation	UNP Q13224
B	849	SER	CYS	engineered mutation	UNP Q13224
B	853	GLY	-	expression tag	UNP Q13224
B	854	PRO	-	expression tag	UNP Q13224
B	855	GLY	-	expression tag	UNP Q13224
B	856	SER	-	expression tag	UNP Q13224
B	857	GLY	-	expression tag	UNP Q13224
B	858	ALA	-	expression tag	UNP Q13224
B	859	THR	-	expression tag	UNP Q13224
B	860	ASN	-	expression tag	UNP Q13224
B	861	PHE	-	expression tag	UNP Q13224
B	862	SER	-	expression tag	UNP Q13224
B	863	LEU	-	expression tag	UNP Q13224
B	864	LEU	-	expression tag	UNP Q13224
B	865	LYS	-	expression tag	UNP Q13224

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Chain	Residue	Modelled	Actual	Comment	Reference
B	866	GLN	-	expression tag	UNP Q13224
B	867	ALA	-	expression tag	UNP Q13224
B	868	GLY	-	expression tag	UNP Q13224
B	869	ASP	-	expression tag	UNP Q13224
B	870	VAL	-	expression tag	UNP Q13224
B	871	GLU	-	expression tag	UNP Q13224
B	872	GLU	-	expression tag	UNP Q13224
B	873	ASN	-	expression tag	UNP Q13224
B	874	PRO	-	expression tag	UNP Q13224
B	875	GLY	-	expression tag	UNP Q13224

- Molecule 3 is a protein called Glutamate receptor ionotropic, NMDA 2D.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	763	Total	C	N	O	S	0	0
			5870	3774	996	1071	29		

There are 8 discrepancies between the modelled and reference sequences:

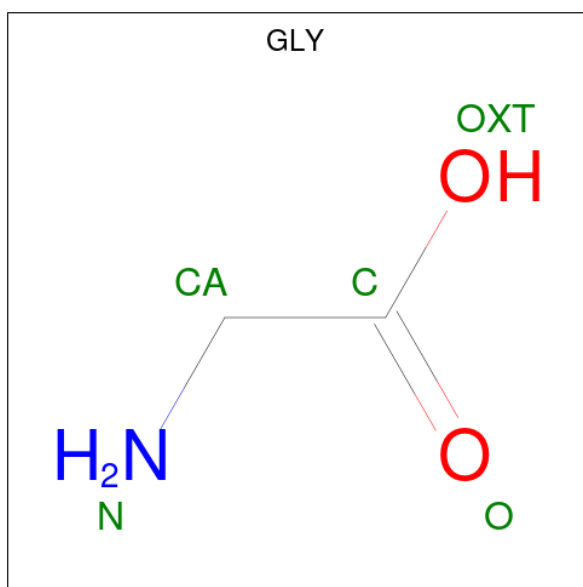
Chain	Residue	Modelled	Actual	Comment	Reference
D	881	GLU	-	expression tag	UNP O15399
D	882	THR	-	expression tag	UNP O15399
D	883	SER	-	expression tag	UNP O15399
D	884	GLN	-	expression tag	UNP O15399
D	885	VAL	-	expression tag	UNP O15399
D	886	ALA	-	expression tag	UNP O15399
D	887	PRO	-	expression tag	UNP O15399
D	888	ALA	-	expression tag	UNP O15399

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



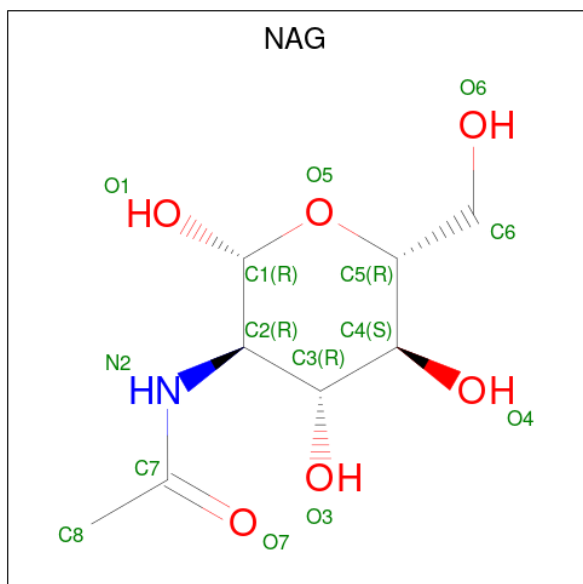
Mol	Chain	Residues	Atoms				AltConf	Trace
4	E	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is GLYCINE (CCD ID: GLY) (formula: C₂H₅NO₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			5	2	1	2	
5	C	1	Total	C	N	O	0
			5	2	1	2	

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



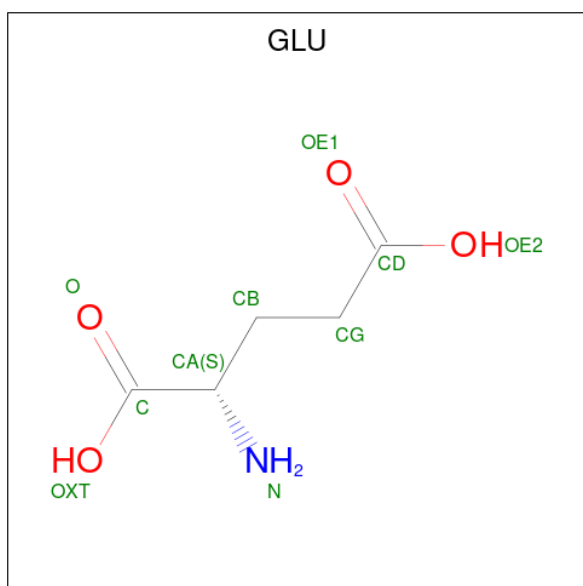
Mol	Chain	Residues	Atoms				AltConf
6	A	1	Total	C	N	O	0
			14	8	1	5	

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Mol	Chain	Residues	Atoms				AltConf
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	C	1	Total	C	N	O	0
			14	8	1	5	
6	D	1	Total	C	N	O	0
			14	8	1	5	

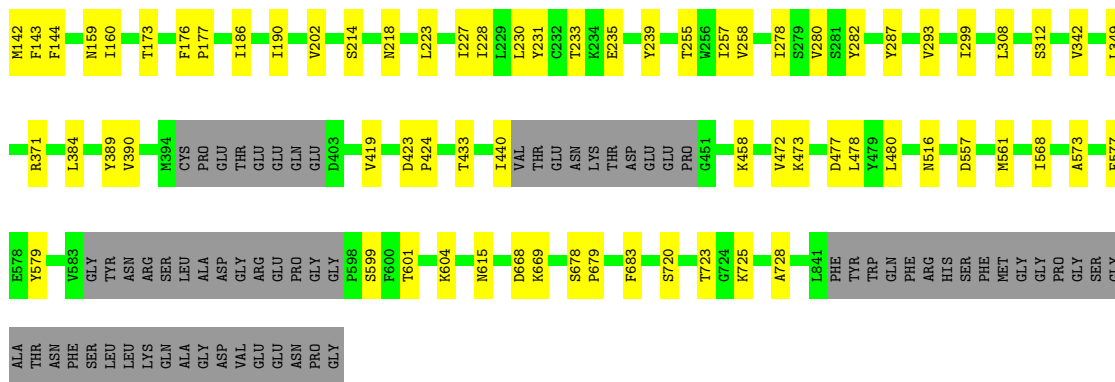
- Molecule 7 is GLUTAMIC ACID (CCD ID: GLU) (formula: $C_5H_9NO_4$) (labeled as "Ligand of Interest" by depositor).



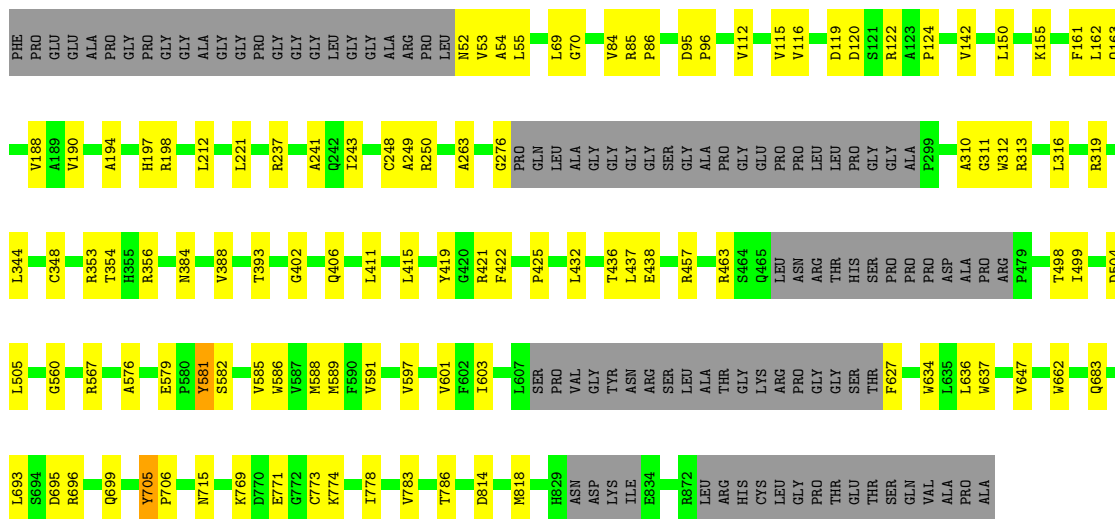
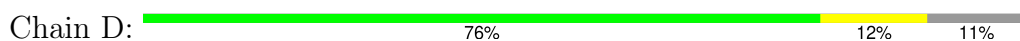
Mol	Chain	Residues	Atoms				AltConf
7	B	1	Total	C	N	O	0
			10	5	1	4	
7	D	1	Total	C	N	O	0
			10	5	1	4	

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		AltConf
8	B	1	Total	O	0
			1	1	



- Molecule 3: Glutamate receptor ionotropic, NMDA 2D



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	143193	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	63.3	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (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: 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	0.24	0/6301	0.47	0/8547
1	C	0.24	0/6388	0.47	0/8672
2	B	0.24	0/6007	0.44	0/8168
3	D	0.24	0/6008	0.47	0/8179
All	All	0.24	0/24704	0.46	0/33566

There are no bond length outliers.

There are no bond angle outliers.

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	6163	0	6100	56	0
1	C	6246	0	6162	62	0
2	B	5880	0	5685	42	0
3	D	5870	0	5771	61	0
4	E	28	0	25	0	0
5	A	5	0	2	1	0
5	C	5	0	2	0	0
6	A	14	0	13	0	0
6	B	14	0	13	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	14	0	13	0	0
6	D	14	0	13	1	0
7	B	10	0	5	0	0
7	D	10	0	5	0	0
8	B	1	0	0	0	0
All	All	24274	0	23809	215	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 4.

All (215) 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:C:254:ILE:HD11	1:C:268:GLY:HA3	1.70	0.74
1:A:831:ILE:HG21	3:D:603:ILE:HD11	1.70	0.72
1:A:298:LYS:HB2	1:A:301:ILE:HD11	1.76	0.68
2:B:299:ILE:HG23	2:B:342:VAL:HG21	1.75	0.68
1:C:307:GLY:O	1:C:311:ASN:ND2	2.28	0.67
3:D:122:ARG:HH22	3:D:312:TRP:HH2	1.44	0.66
1:A:828:ILE:HA	1:A:831:ILE:HD12	1.77	0.66
1:C:365:GLY:HA2	1:C:374:PRO:HD2	1.77	0.66
1:A:70:ASN:ND2	1:A:73:GLN:OE1	2.29	0.65
1:C:148:SER:HB3	1:C:179:ARG:HD2	1.78	0.64
2:B:227:ILE:HG22	2:B:255:THR:HB	1.80	0.64
3:D:344:LEU:HG	3:D:356:ARG:HH21	1.63	0.64
1:C:796:GLN:NE2	1:C:798:CYS:O	2.31	0.63
3:D:212:LEU:O	3:D:457:ARG:NH1	2.32	0.63
3:D:155:LYS:NZ	3:D:161:PHE:O	2.33	0.62
1:C:124:ARG:NH2	1:C:251:GLU:OE1	2.33	0.60
3:D:194:ALA:H	3:D:197:HIS:HD2	1.48	0.60
2:B:101:ASP:OD1	2:B:102:ASP:N	2.35	0.60
1:C:68:LYS:HG2	1:C:73:GLN:HB2	1.84	0.59
1:A:119:LEU:HD23	1:A:138:LEU:HB2	1.84	0.59
3:D:69:LEU:HD11	3:D:316:LEU:HD21	1.83	0.58
2:B:214:SER:O	2:B:218:ASN:ND2	2.34	0.58
1:C:335:THR:OG1	1:C:337:ARG:NH1	2.34	0.58
1:A:290:GLN:NE2	1:A:328:SER:OG	2.36	0.58
2:B:573:ALA:HA	2:B:577:PHE:HD2	1.68	0.58
2:B:88:LEU:HB3	2:B:94:ILE:HD11	1.86	0.58
1:A:578:TYR:OH	1:A:582:ARG:NH1	2.37	0.57
1:C:637:ALA:HB3	3:D:637:TRP:HH2	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:GLU:HG3	1:A:216:ALA:HB2	1.87	0.57
2:B:599:SER:O	2:B:604:LYS:NZ	2.29	0.57
1:A:505:LEU:O	1:A:763:ARG:NH1	2.37	0.57
3:D:311:GLY:O	3:D:319:ARG:NH2	2.38	0.57
1:C:112:GLY:O	1:C:115:ARG:NH1	2.38	0.57
1:A:732:ASP:OD2	5:A:901:GLY:N	2.38	0.56
1:C:696:GLN:HB2	1:C:699:LEU:HD11	1.88	0.56
2:B:419:VAL:HG21	2:B:480:LEU:HD21	1.87	0.56
3:D:705:TYR:CD1	3:D:706:PRO:HD3	2.40	0.56
1:A:264:ASP:HA	1:A:356:LEU:HD22	1.87	0.56
1:A:48:GLN:HG3	1:A:52:ARG:HD3	1.87	0.56
1:C:142:PRO:HD3	1:C:346:ARG:HB3	1.87	0.56
1:A:338:VAL:HG13	1:A:346:ARG:HD3	1.87	0.56
1:C:263:PRO:HD2	1:C:266:ILE:HD11	1.88	0.55
3:D:384:ASN:OD1	3:D:406:GLN:NE2	2.39	0.55
1:C:663:ARG:HH21	1:C:747:VAL:HG21	1.71	0.55
1:A:170:ASP:OD1	1:A:171:HIS:N	2.36	0.55
1:A:253:GLU:N	1:A:253:GLU:OE1	2.40	0.55
1:C:28:ASN:OD1	1:C:61:ASN:ND2	2.39	0.55
1:C:220:ILE:HG12	1:C:248:LEU:HB2	1.89	0.55
2:B:173:THR:HG23	2:B:231:TYR:HB3	1.90	0.54
3:D:142:VAL:HG22	3:D:162:LEU:HB2	1.89	0.54
1:A:305:PRO:HB3	1:A:311:ASN:HB2	1.89	0.53
3:D:693:LEU:O	3:D:699:GLN:NE2	2.41	0.53
1:A:101:HIS:HD2	1:A:125:MET:HG3	1.74	0.53
1:C:73:GLN:OE1	1:C:73:GLN:N	2.42	0.53
1:C:165:LEU:HD21	1:C:194:VAL:HG22	1.91	0.53
3:D:119:ASP:OD1	3:D:120:ASP:N	2.42	0.53
3:D:695:ASP:OD1	3:D:696:ARG:N	2.42	0.53
1:A:132:SER:HB2	2:B:177:PRO:HB3	1.91	0.53
3:D:150:LEU:O	3:D:163:GLN:NE2	2.41	0.52
3:D:579:GLU:O	3:D:581:TYR:N	2.40	0.52
1:A:140:THR:HG22	1:A:340:PHE:HZ	1.74	0.52
1:C:264:ASP:OD1	1:C:359:ARG:NH2	2.42	0.52
3:D:188:VAL:HG23	3:D:241:ALA:HB3	1.91	0.52
1:C:343:ASP:OD1	1:C:344:GLY:N	2.36	0.52
2:B:135:ALA:HB2	2:B:177:PRO:HB2	1.91	0.52
2:B:678:SER:HB2	2:B:679:PRO:HD2	1.91	0.52
1:A:363:GLN:NE2	1:A:365:GLY:O	2.44	0.52
3:D:194:ALA:H	3:D:197:HIS:CD2	2.26	0.51
3:D:636:LEU:O	3:D:662:TRP:NE1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:235:GLU:OE1	2:B:235:GLU:N	2.43	0.51
1:C:205:THR:HG22	1:C:234:ALA:HB1	1.93	0.51
3:D:248:CYS:SG	3:D:249:ALA:N	2.84	0.51
3:D:188:VAL:N	3:D:243:ILE:O	2.44	0.51
1:A:125:MET:HB2	1:A:128:TYR:HE1	1.77	0.50
1:C:332:ASP:OD1	1:C:333:GLY:N	2.44	0.50
3:D:250:ARG:NH1	3:D:276:GLY:O	2.44	0.50
1:C:59:GLN:O	1:C:61:ASN:ND2	2.45	0.50
2:B:123:ILE:HG23	2:B:143:PHE:HD2	1.77	0.50
1:C:97:THR:OG1	1:C:99:ASN:OD1	2.27	0.50
2:B:299:ILE:HD11	2:B:349:LEU:HD22	1.94	0.49
1:C:49:ALA:HA	1:C:52:ARG:HD2	1.94	0.49
1:C:33:LEU:HD12	1:C:39:GLU:HG2	1.94	0.49
1:A:30:GLY:HA3	1:A:82:LEU:HD11	1.95	0.49
1:C:138:LEU:HA	1:C:344:GLY:HA3	1.93	0.49
1:A:49:ALA:HA	1:A:52:ARG:HB2	1.94	0.49
1:C:355:ASN:HD21	1:C:379:ILE:HG23	1.78	0.49
1:C:135:LEU:O	1:C:322:LYS:NZ	2.46	0.49
1:C:681:TYR:HB3	1:C:728:ALA:HB3	1.94	0.49
3:D:437:LEU:HG	3:D:438:GLU:H	1.78	0.48
1:A:105:THR:HG22	1:A:106:PRO:HD3	1.94	0.48
3:D:771:GLU:OE1	3:D:771:GLU:N	2.47	0.48
2:B:477:ASP:OD1	2:B:477:ASP:N	2.47	0.48
1:A:557:PRO:HB3	1:A:650:ASN:HD22	1.79	0.47
1:A:152:PHE:HE1	1:A:187:ARG:HH11	1.62	0.47
2:B:577:PHE:HA	1:C:831:ILE:HD11	1.96	0.47
1:C:163:ILE:HD12	1:C:220:ILE:HD12	1.96	0.47
3:D:237:ARG:HH22	3:D:263:ALA:HB1	1.78	0.47
1:C:341:ASN:ND2	1:C:343:ASP:H	2.12	0.47
3:D:55:LEU:HD13	3:D:116:VAL:HB	1.95	0.47
2:B:723:THR:HG21	2:B:725:LYS:HE3	1.97	0.47
2:B:601:THR:HG22	2:B:604:LYS:HE2	1.96	0.47
1:C:436:CYS:O	1:C:453:GLN:N	2.45	0.47
3:D:463:ARG:NH2	3:D:504:ASP:OD2	2.47	0.47
3:D:560:GLY:HA3	3:D:783:VAL:HG13	1.97	0.47
3:D:310:ALA:H	3:D:388:VAL:HG22	1.79	0.47
2:B:124:LEU:HD22	2:B:144:PHE:HB2	1.97	0.47
1:C:105:THR:HB	1:C:106:PRO:HD3	1.97	0.46
1:C:157:VAL:HG23	1:C:158:TYR:HD1	1.81	0.46
3:D:582:SER:HB3	3:D:585:VAL:HG23	1.97	0.46
2:B:389:TYR:HD2	2:B:390:VAL:HG23	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:433:THR:HG22	2:B:458:LYS:HB3	1.97	0.46
1:C:357:GLN:HG2	1:C:380:ILE:HG22	1.98	0.46
1:C:152:PHE:HE2	1:C:184:LEU:HA	1.81	0.45
1:A:27:VAL:HG22	1:A:88:TYR:HE2	1.81	0.45
1:A:198:ASP:O	1:A:201:THR:OG1	2.32	0.45
3:D:124:PRO:HB3	3:D:150:LEU:HD13	1.99	0.45
3:D:498:THR:HG23	3:D:499:ILE:HG13	1.98	0.45
1:A:140:THR:HG22	1:A:340:PHE:CZ	2.52	0.45
1:A:225:GLU:HB3	1:A:252:ARG:HB3	1.98	0.45
1:C:701:THR:OG1	1:C:704:ARG:NH2	2.50	0.45
1:A:287:VAL:HG12	1:A:330:TYR:HB3	1.99	0.45
1:C:338:VAL:HG22	1:C:346:ARG:HH12	1.81	0.45
1:C:130:ASP:OD1	1:C:130:ASP:N	2.50	0.45
1:C:355:ASN:ND2	1:C:379:ILE:HG23	2.31	0.45
1:C:414:THR:OG1	1:C:419:THR:O	2.33	0.45
1:C:90:ILE:HB	1:C:118:VAL:HG23	1.99	0.44
3:D:504:ASP:N	3:D:504:ASP:OD1	2.50	0.44
3:D:586:TRP:HA	3:D:589:MET:HB2	1.98	0.44
3:D:634:TRP:CD1	3:D:647:VAL:HG12	2.52	0.44
1:C:219:ILE:HD12	1:C:219:ILE:H	1.83	0.44
1:A:704:ARG:O	1:A:708:LYS:NZ	2.51	0.44
3:D:54:ALA:HB3	3:D:115:VAL:HG22	1.98	0.44
1:A:254:ILE:HD13	1:A:268:GLY:HA3	1.99	0.44
1:C:269:LEU:HD12	1:C:351:TYR:HB3	2.00	0.44
3:D:814:ASP:O	3:D:818:MET:HG2	2.18	0.44
1:A:143:PRO:HD2	1:A:146:HIS:CD2	2.52	0.44
1:A:436:CYS:O	1:A:453:GLN:N	2.50	0.44
1:C:337:ARG:HD2	1:C:348:PHE:HB2	1.99	0.44
1:A:541:LEU:HD21	1:A:746:LEU:HD13	2.00	0.44
1:A:79:CYS:O	1:A:308:CYS:HB2	2.18	0.43
1:A:371:HIS:O	1:A:371:HIS:ND1	2.50	0.43
1:A:808:LEU:HD21	1:A:813:MET:HG3	2.00	0.43
3:D:769:LYS:HE3	3:D:769:LYS:HB3	1.90	0.43
1:C:198:ASP:OD1	1:C:198:ASP:N	2.50	0.43
1:C:555:MET:HG2	1:C:563:TRP:CZ3	2.53	0.43
3:D:70:GLY:HA2	3:D:86:PRO:HB2	1.99	0.43
1:A:133:ILE:HG23	1:A:134:HIS:ND1	2.33	0.43
1:A:813:MET:O	1:A:816:VAL:HG12	2.18	0.43
2:B:683:PHE:HB3	2:B:728:ALA:HB3	2.01	0.43
1:C:425:THR:HG23	1:C:427:ASN:H	1.84	0.43
1:A:31:ALA:HB1	1:A:91:LEU:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:831:ILE:HD13	3:D:603:ILE:HG12	2.00	0.43
2:B:668:ASP:OD1	2:B:669:LYS:N	2.52	0.43
1:A:116:ILE:HD11	1:A:304:PRO:HB3	2.02	0.42
1:C:693:PHE:HD1	1:C:699:LEU:HD13	1.84	0.42
1:C:830:LEU:HD13	1:C:833:ILE:HD11	2.00	0.42
3:D:597:VAL:HG12	3:D:636:LEU:HD12	2.01	0.42
1:A:265:GLY:HA3	1:A:382:PRO:HG3	1.99	0.42
1:A:481:ASP:N	1:A:481:ASP:OD1	2.50	0.42
2:B:186:ILE:O	2:B:190:ILE:HG12	2.18	0.42
2:B:257:ILE:HG12	2:B:278:ILE:HG23	2.01	0.42
1:C:580:LEU:HD23	1:C:629:ALA:HA	2.00	0.42
1:C:94:HIS:ND1	1:C:95:PRO:O	2.52	0.42
3:D:54:ALA:HB2	3:D:112:VAL:HG21	2.01	0.42
3:D:155:LYS:HB3	3:D:155:LYS:HE2	1.80	0.42
3:D:188:VAL:HG12	3:D:190:VAL:HG13	2.00	0.42
3:D:567:ARG:NH2	3:D:773:CYS:O	2.43	0.42
1:A:79:CYS:HB3	1:A:110:THR:HG21	2.02	0.42
2:B:230:LEU:HB3	2:B:258:VAL:HG12	2.02	0.42
3:D:52:ASN:OD1	3:D:53:VAL:N	2.52	0.42
3:D:313:ARG:O	3:D:319:ARG:NH2	2.52	0.42
1:A:300:ASN:O	1:A:300:ASN:ND2	2.53	0.42
2:B:223:LEU:HD13	2:B:228:ILE:HG12	2.02	0.42
2:B:308:LEU:HD12	2:B:312:SER:HA	1.99	0.42
1:C:440:ASN:HD22	1:C:451:VAL:HG11	1.84	0.42
1:C:722:ARG:NH1	1:C:743:LYS:HD2	2.34	0.42
1:C:139:ARG:HH21	1:C:143:PRO:HG3	1.85	0.42
3:D:84:VAL:HG22	3:D:86:PRO:HD3	2.01	0.42
3:D:715:ASN:HD22	6:D:902:NAG:H83	1.83	0.42
1:A:539:THR:HG23	1:A:736:LEU:HD12	2.02	0.42
3:D:95:ASP:HA	3:D:96:PRO:HD3	1.92	0.42
3:D:505:LEU:H	3:D:505:LEU:HD12	1.84	0.42
3:D:601:VAL:HG22	3:D:627:PHE:HD1	1.85	0.41
2:B:160:ILE:HG22	2:B:384:LEU:HD21	2.01	0.41
2:B:478:LEU:HD12	2:B:478:LEU:H	1.84	0.41
1:A:31:ALA:O	1:A:64:SER:HA	2.21	0.41
1:A:34:SER:OG	1:A:35:THR:N	2.54	0.41
1:C:771:ASN:OD1	1:C:771:ASN:N	2.53	0.41
3:D:421:ARG:HG3	3:D:422:PHE:HD1	1.85	0.41
3:D:783:VAL:HG12	3:D:786:THR:HG22	2.02	0.41
2:B:516:ASN:OD1	2:B:516:ASN:N	2.53	0.41
3:D:198:ARG:H	3:D:198:ARG:HD2	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:389:TYR:CD2	2:B:390:VAL:HG23	2.56	0.41
3:D:419:TYR:HB3	3:D:425:PRO:HG3	2.03	0.41
2:B:720:SER:HB3	2:B:725:LYS:HB2	2.03	0.41
1:C:177:GLN:NE2	1:C:194:VAL:HG11	2.36	0.41
1:A:441:ASP:N	1:A:441:ASP:OD1	2.53	0.41
2:B:176:PHE:CG	2:B:177:PRO:HD2	2.55	0.41
2:B:440:ILE:HD12	2:B:440:ILE:HA	1.87	0.41
2:B:472:VAL:C	2:B:473:LYS:HG2	2.42	0.41
2:B:557:ASP:OD2	1:C:810:PHE:HB2	2.21	0.41
1:C:143:PRO:HD2	1:C:146:HIS:ND1	2.36	0.41
3:D:402:GLY:HA3	3:D:411:LEU:HD13	2.02	0.41
3:D:576:ALA:HA	3:D:579:GLU:HB3	2.03	0.41
1:C:249:VAL:O	1:C:268:GLY:HA2	2.21	0.41
1:A:254:ILE:HG21	1:A:268:GLY:HA3	2.03	0.40
1:A:433:LYS:HG2	1:A:456:TYR:HB3	2.02	0.40
2:B:39:VAL:HG11	2:B:293:VAL:HG13	2.02	0.40
2:B:423:ASP:HA	2:B:424:PRO:HD3	1.94	0.40
2:B:568:ILE:HD13	2:B:568:ILE:HA	1.97	0.40
3:D:588:MET:O	3:D:591:VAL:HG22	2.21	0.40
3:D:778:ILE:HD13	3:D:778:ILE:HA	1.96	0.40
1:A:27:VAL:O	1:A:60:LEU:HA	2.20	0.40
2:B:123:ILE:HG23	2:B:143:PHE:CD2	2.56	0.40
1:A:215:GLU:OE2	1:A:395:SER:N	2.55	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 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	783/825 (95%)	735 (94%)	48 (6%)	0	100	100
1	C	797/825 (97%)	748 (94%)	49 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	768/884 (87%)	730 (95%)	37 (5%)	1 (0%)	48	76
3	D	753/861 (88%)	716 (95%)	37 (5%)	0	100	100
All	All	3101/3395 (91%)	2929 (94%)	171 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	615	ASN

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	666/710 (94%)	655 (98%)	11 (2%)	56	75
1	C	675/710 (95%)	662 (98%)	13 (2%)	52	72
2	B	618/760 (81%)	606 (98%)	12 (2%)	52	72
3	D	615/701 (88%)	602 (98%)	13 (2%)	48	70
All	All	2574/2881 (89%)	2525 (98%)	49 (2%)	52	72

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ARG
1	A	79	CYS
1	A	105	THR
1	A	113	PHE
1	A	152	PHE
1	A	204	VAL
1	A	306	ARG
1	A	312	THR
1	A	315	TRP
1	A	321	PHE
1	A	475	GLU

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Mol	Chain	Res	Type
2	B	86	CYS
2	B	142	MET
2	B	159	ASN
2	B	202	VAL
2	B	233	THR
2	B	239	TYR
2	B	280	VAL
2	B	282	TYR
2	B	287	TYR
2	B	371	ARG
2	B	561	MET
2	B	579	TYR
1	C	57	LYS
1	C	79	CYS
1	C	103	THR
1	C	119	LEU
1	C	260	ARG
1	C	302	THR
1	C	315	TRP
1	C	392	TYR
1	C	601	LEU
1	C	602	THR
1	C	696	GLN
1	C	699	LEU
1	C	748	THR
3	D	85	ARG
3	D	221	LEU
3	D	348	CYS
3	D	353	ARG
3	D	354	THR
3	D	393	THR
3	D	415	LEU
3	D	432	LEU
3	D	436	THR
3	D	581	TYR
3	D	683	GLN
3	D	705	TYR
3	D	774	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	290	GLN
1	C	70	ASN
3	D	197	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	$\# Z > 2$
4	NAG	E	1	1,4	14,14,15	0.27	0	17,19,21	0.44	0
4	NAG	E	2	4	14,14,15	0.36	0	17,19,21	0.56	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	NAG	E	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

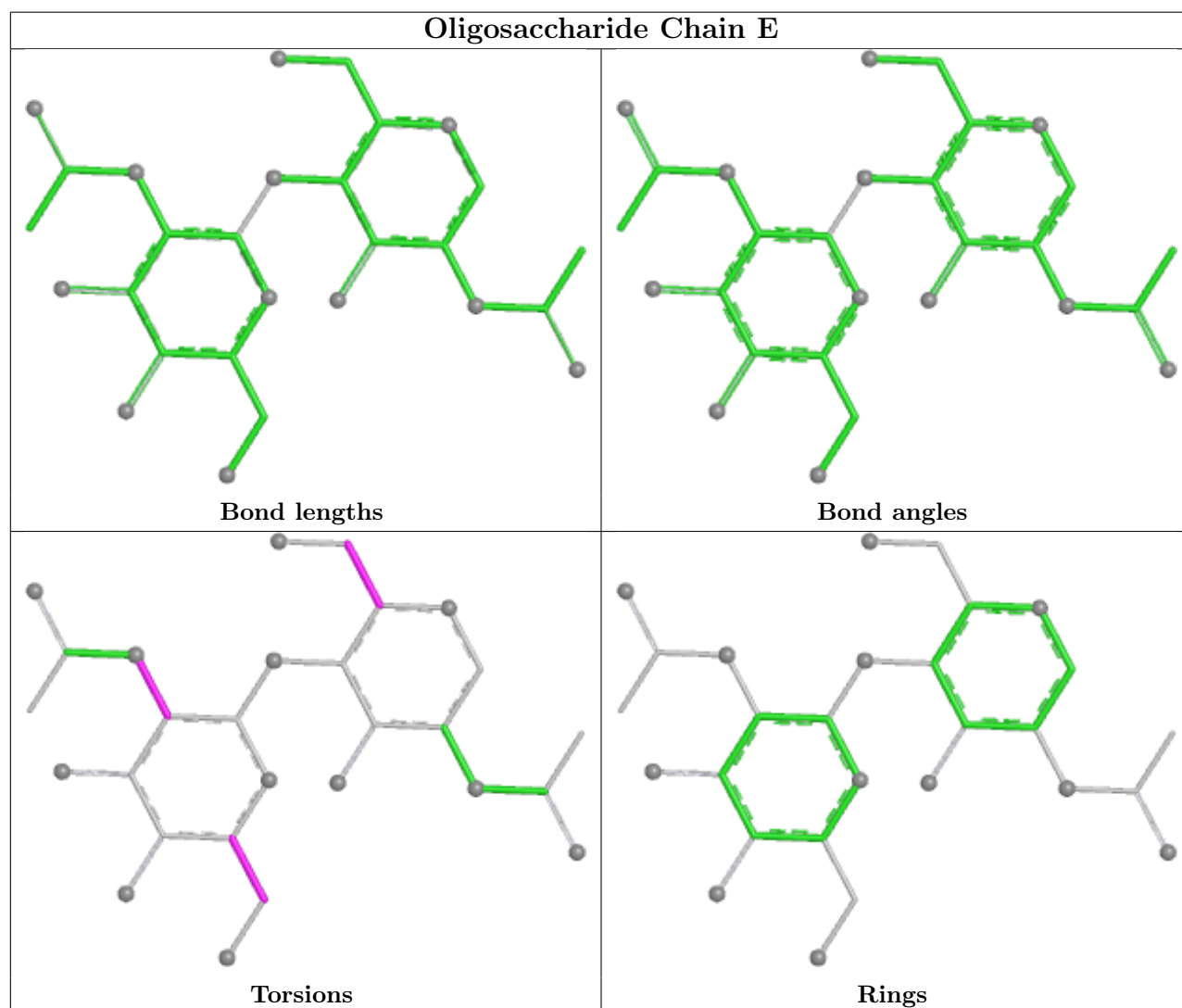
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	2	NAG	O5-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6
4	E	1	NAG	C4-C5-C6-O6
4	E	1	NAG	O5-C5-C6-O6
4	E	2	NAG	C3-C2-N2-C7
4	E	2	NAG	C1-C2-N2-C7

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

8 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	GLY	C	901	-	4,4,4	1.17	1 (25%)	3,4,4	1.68	2 (66%)
6	NAG	C	902	1	14,14,15	0.19	0	17,19,21	0.44	0
7	GLU	B	901	-	8,9,9	1.12	1 (12%)	8,11,11	1.21	1 (12%)
6	NAG	D	902	3	14,14,15	0.25	0	17,19,21	0.46	0
6	NAG	B	902	2	14,14,15	0.21	0	17,19,21	0.62	0
6	NAG	A	902	1	14,14,15	0.43	0	17,19,21	0.37	0
7	GLU	D	901	-	8,9,9	1.11	1 (12%)	8,11,11	1.23	1 (12%)
5	GLY	A	901	-	4,4,4	1.18	1 (25%)	3,4,4	1.67	1 (33%)

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	GLY	C	901	-	-	0/2/2/2	-
6	NAG	C	902	1	-	2/6/23/26	0/1/1/1
7	GLU	B	901	-	-	1/9/9/9	-
6	NAG	D	902	3	-	3/6/23/26	0/1/1/1
6	NAG	B	902	2	-	2/6/23/26	0/1/1/1
6	NAG	A	902	1	-	4/6/23/26	0/1/1/1
7	GLU	D	901	-	-	2/9/9/9	-
5	GLY	A	901	-	-	0/2/2/2	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	901	GLU	OXT-C	-2.33	1.23	1.30
7	D	901	GLU	OXT-C	-2.29	1.23	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	901	GLY	OXT-C	-2.25	1.23	1.30
5	C	901	GLY	OXT-C	-2.23	1.23	1.30

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	D	901	GLU	OXT-C-O	-2.79	117.75	124.08
7	B	901	GLU	OXT-C-O	-2.71	117.94	124.08
5	A	901	GLY	OXT-C-O	-2.07	118.00	123.33
5	C	901	GLY	OXT-C-O	-2.04	118.09	123.33
5	C	901	GLY	OXT-C-CA	2.03	121.45	113.38

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	902	NAG	C4-C5-C6-O6
6	C	902	NAG	O5-C5-C6-O6
6	C	902	NAG	C4-C5-C6-O6
6	A	902	NAG	O5-C5-C6-O6
6	A	902	NAG	C8-C7-N2-C2
6	A	902	NAG	O7-C7-N2-C2
6	D	902	NAG	C8-C7-N2-C2
6	D	902	NAG	O7-C7-N2-C2
6	D	902	NAG	O5-C5-C6-O6
6	B	902	NAG	C3-C2-N2-C7
7	D	901	GLU	O-C-CA-CB
7	D	901	GLU	OXT-C-CA-CB
6	B	902	NAG	C1-C2-N2-C7
7	B	901	GLU	OXT-C-CA-N

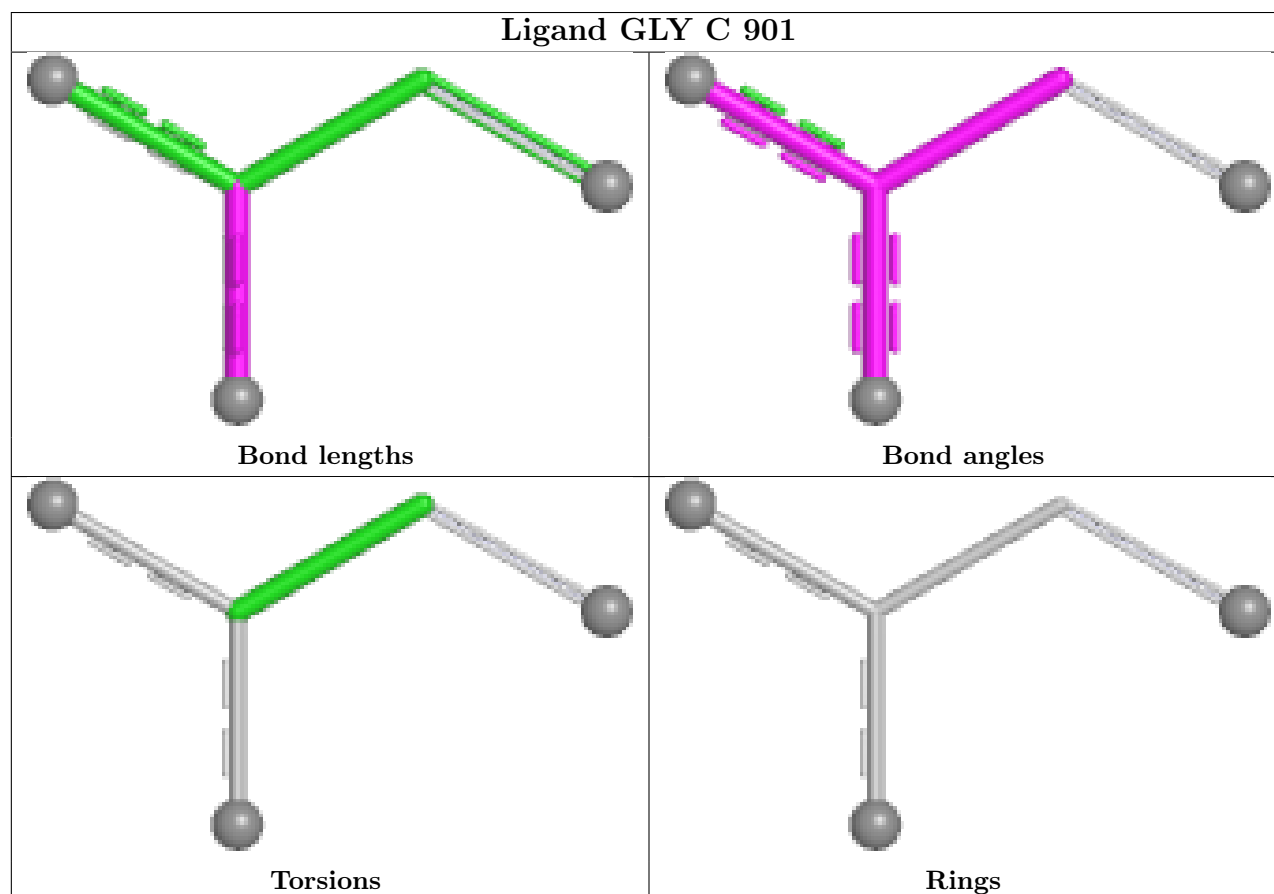
There are no ring outliers.

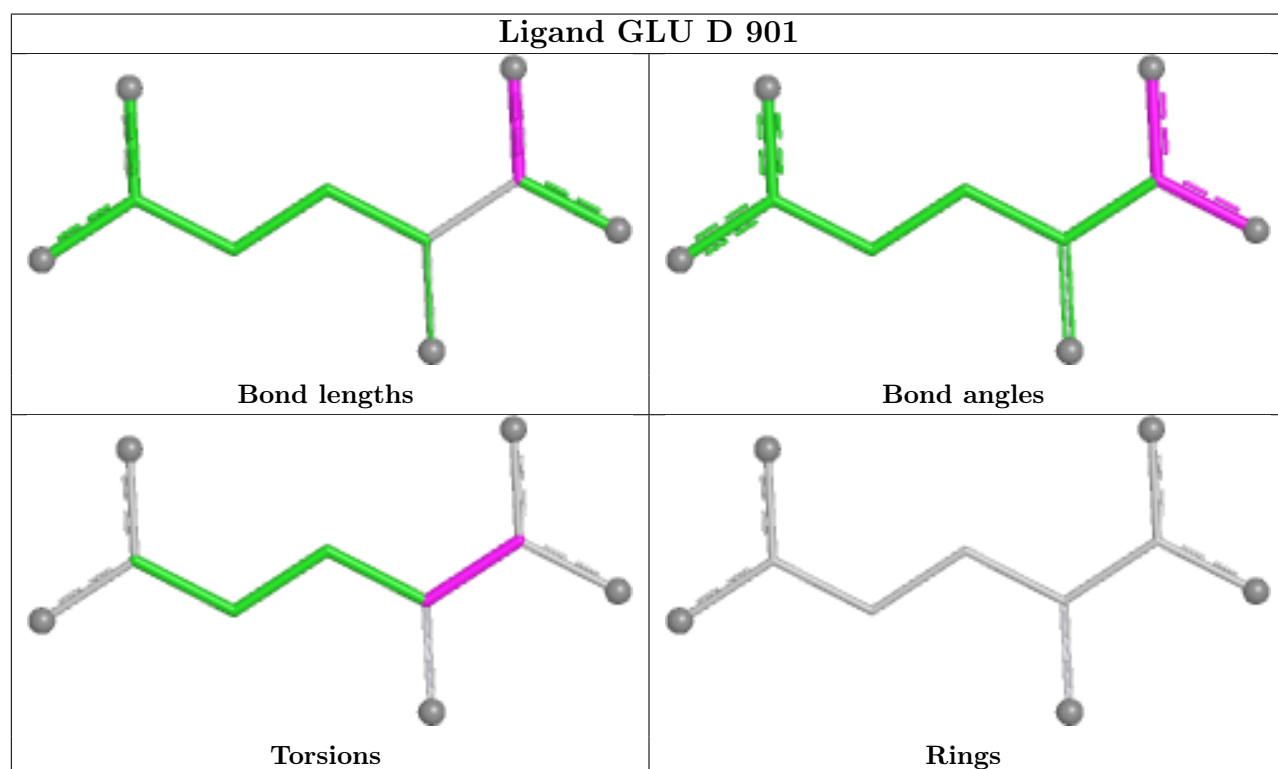
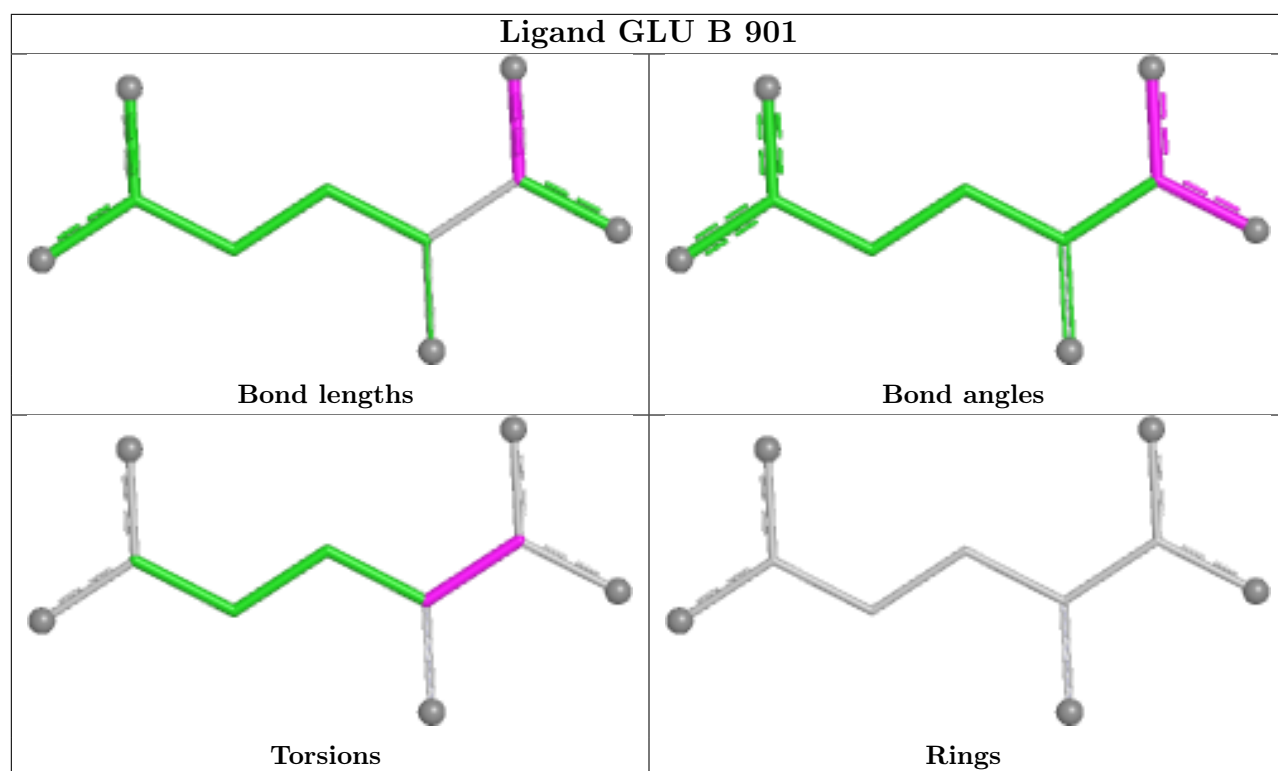
2 monomers are involved in 2 short contacts:

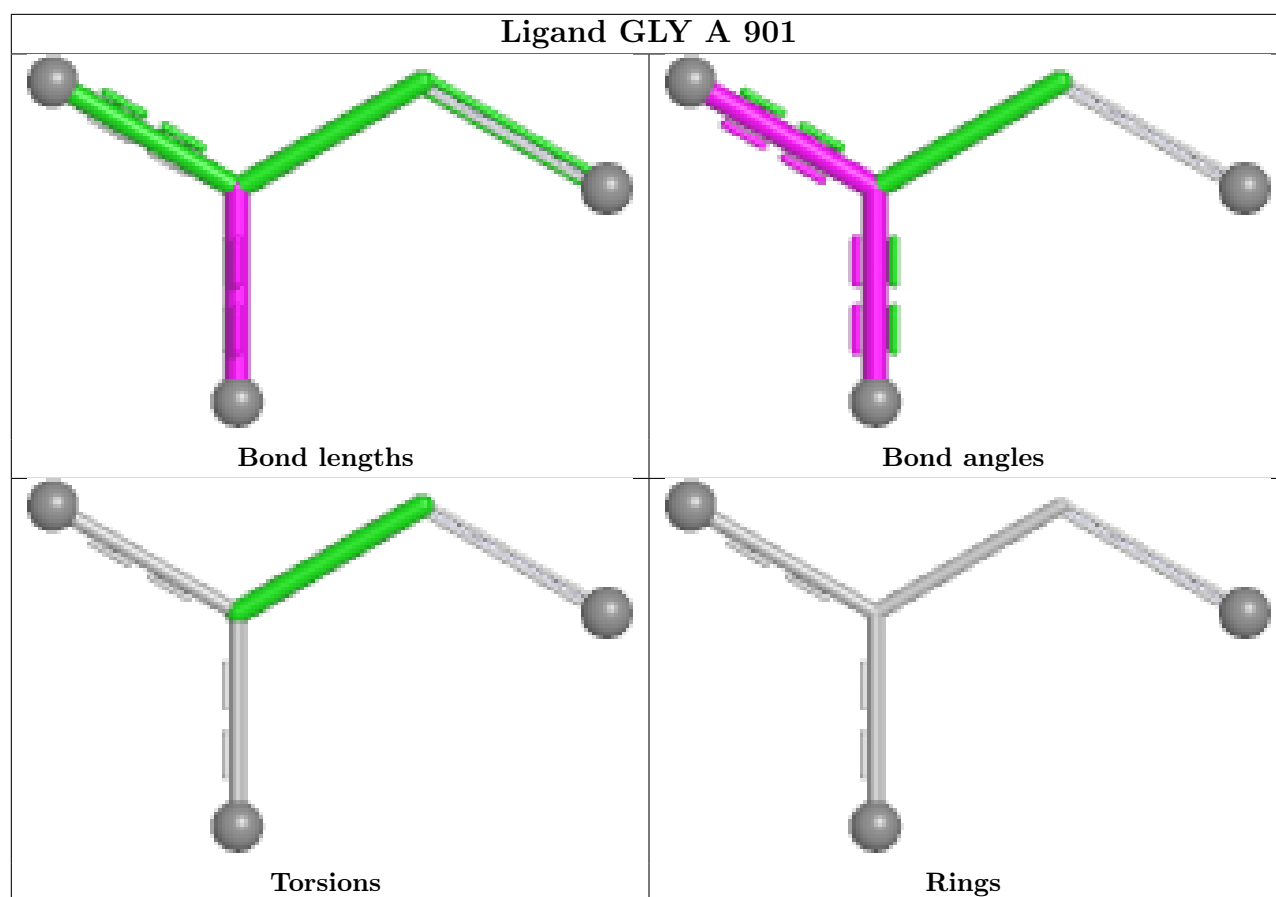
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	902	NAG	1	0
5	A	901	GLY	1	0

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 Map visualisation

This section contains visualisations of the EMDB entry EMD-46526. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.