



Full wwPDB EM Validation Report ⓘ

Mar 19, 2026 – 08:38 PM UTC

PDB ID : 8HGM / pdb_00008hgm
EMDB ID : EMD-34742
Title : Structure of SARS-CoV-2 spike RBD in complex with neutralizing antibody NIV-11
Authors : Moriyama, S.; Anraku, Y.; Muranishi, S.; Adachi, Y.; Kuroda, D.; Higuchi, Y.; Kotaki, R.; Tonouchi, K.; Yumoto, K.; Suzuki, T.; Kita, S.; Someya, T.; Fukuhara, H.; Kuroda, Y.; Yamamoto, T.; Onodera, T.; Fukushi, S.; Maeda, K.; Nakamura-Uchiyama, F.; Hashiguchi, T.; Hoshino, A.; Maenaka, K.; Takahashi, Y.
Deposited on : 2022-11-15
Resolution : 3.40 Å(reported)
Based on initial model : 6M0J

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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
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)

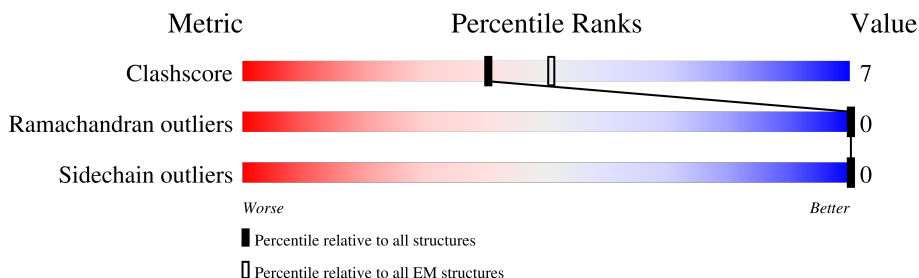
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	B	1288	
2	C	223	
3	D	215	
4	A	2	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4886 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	194	Total	C	N	O	S	0	0
			1532	981	256	287	8		

There are 89 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	817	PRO	PHE	engineered mutation	UNP P0DTC2
B	892	PRO	ALA	engineered mutation	UNP P0DTC2
B	899	PRO	ALA	engineered mutation	UNP P0DTC2
B	942	PRO	ALA	engineered mutation	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	1209	GLY	-	expression tag	UNP P0DTC2
B	1210	SER	-	expression tag	UNP P0DTC2
B	1211	GLY	-	expression tag	UNP P0DTC2
B	1212	TYR	-	expression tag	UNP P0DTC2
B	1213	ILE	-	expression tag	UNP P0DTC2
B	1214	PRO	-	expression tag	UNP P0DTC2
B	1215	GLU	-	expression tag	UNP P0DTC2
B	1216	ALA	-	expression tag	UNP P0DTC2
B	1217	PRO	-	expression tag	UNP P0DTC2
B	1218	ARG	-	expression tag	UNP P0DTC2
B	1219	ASP	-	expression tag	UNP P0DTC2
B	1220	GLY	-	expression tag	UNP P0DTC2
B	1221	GLN	-	expression tag	UNP P0DTC2
B	1222	ALA	-	expression tag	UNP P0DTC2
B	1223	TYR	-	expression tag	UNP P0DTC2
B	1224	VAL	-	expression tag	UNP P0DTC2
B	1225	ARG	-	expression tag	UNP P0DTC2
B	1226	LYS	-	expression tag	UNP P0DTC2
B	1227	ASP	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1228	GLY	-	expression tag	UNP P0DTC2
B	1229	GLU	-	expression tag	UNP P0DTC2
B	1230	TRP	-	expression tag	UNP P0DTC2
B	1231	VAL	-	expression tag	UNP P0DTC2
B	1232	LEU	-	expression tag	UNP P0DTC2
B	1233	LEU	-	expression tag	UNP P0DTC2
B	1234	SER	-	expression tag	UNP P0DTC2
B	1235	THR	-	expression tag	UNP P0DTC2
B	1236	PHE	-	expression tag	UNP P0DTC2
B	1237	LEU	-	expression tag	UNP P0DTC2
B	1238	GLY	-	expression tag	UNP P0DTC2
B	1239	ARG	-	expression tag	UNP P0DTC2
B	1240	SER	-	expression tag	UNP P0DTC2
B	1241	LEU	-	expression tag	UNP P0DTC2
B	1242	GLU	-	expression tag	UNP P0DTC2
B	1243	VAL	-	expression tag	UNP P0DTC2
B	1244	LEU	-	expression tag	UNP P0DTC2
B	1245	PHE	-	expression tag	UNP P0DTC2
B	1246	GLN	-	expression tag	UNP P0DTC2
B	1247	GLY	-	expression tag	UNP P0DTC2
B	1248	PRO	-	expression tag	UNP P0DTC2
B	1249	GLY	-	expression tag	UNP P0DTC2
B	1250	HIS	-	expression tag	UNP P0DTC2
B	1251	HIS	-	expression tag	UNP P0DTC2
B	1252	HIS	-	expression tag	UNP P0DTC2
B	1253	HIS	-	expression tag	UNP P0DTC2
B	1254	HIS	-	expression tag	UNP P0DTC2
B	1255	HIS	-	expression tag	UNP P0DTC2
B	1256	HIS	-	expression tag	UNP P0DTC2
B	1257	HIS	-	expression tag	UNP P0DTC2
B	1258	SER	-	expression tag	UNP P0DTC2
B	1259	ALA	-	expression tag	UNP P0DTC2
B	1260	TRP	-	expression tag	UNP P0DTC2
B	1261	SER	-	expression tag	UNP P0DTC2
B	1262	HIS	-	expression tag	UNP P0DTC2
B	1263	PRO	-	expression tag	UNP P0DTC2
B	1264	GLN	-	expression tag	UNP P0DTC2
B	1265	PHE	-	expression tag	UNP P0DTC2
B	1266	GLU	-	expression tag	UNP P0DTC2
B	1267	LYS	-	expression tag	UNP P0DTC2
B	1268	GLY	-	expression tag	UNP P0DTC2
B	1269	GLY	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1270	GLY	-	expression tag	UNP P0DTC2
B	1271	SER	-	expression tag	UNP P0DTC2
B	1272	GLY	-	expression tag	UNP P0DTC2
B	1273	GLY	-	expression tag	UNP P0DTC2
B	1274	GLY	-	expression tag	UNP P0DTC2
B	1275	GLY	-	expression tag	UNP P0DTC2
B	1276	SER	-	expression tag	UNP P0DTC2
B	1277	GLY	-	expression tag	UNP P0DTC2
B	1278	GLY	-	expression tag	UNP P0DTC2
B	1279	SER	-	expression tag	UNP P0DTC2
B	1280	ALA	-	expression tag	UNP P0DTC2
B	1281	TRP	-	expression tag	UNP P0DTC2
B	1282	SER	-	expression tag	UNP P0DTC2
B	1283	HIS	-	expression tag	UNP P0DTC2
B	1284	PRO	-	expression tag	UNP P0DTC2
B	1285	GLN	-	expression tag	UNP P0DTC2
B	1286	PHE	-	expression tag	UNP P0DTC2
B	1287	GLU	-	expression tag	UNP P0DTC2
B	1288	LYS	-	expression tag	UNP P0DTC2

- Molecule 2 is a protein called NIV-11 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	223	Total	C	N	O	S	0	0
			1668	1050	281	328	9		

- Molecule 3 is a protein called NIV-11 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	215	Total	C	N	O	S	0	0
			1658	1038	281	334	5		

- 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	A	2	Total	C	N	O		0	0
			28	16	2	10			

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	80132	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.41	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2300	Depositor
Magnification	130000	Depositor
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	B	0.16	0/1576	0.30	0/2145
2	C	0.14	0/1708	0.29	0/2323
3	D	0.14	0/1695	0.32	0/2302
All	All	0.15	0/4979	0.30	0/6770

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	B	1532	0	1438	15	0
2	C	1668	0	1637	24	0
3	D	1658	0	1609	28	0
4	A	28	0	25	0	0
All	All	4886	0	4709	67	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 7.

All (67) 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)
2:C:179:GLN:NE2	2:C:183:LEU:O	2.23	0.71
1:B:391:CYS:HA	1:B:525:CYS:HB3	1.75	0.69
3:D:8:PRO:HB2	3:D:11:LEU:HD11	1.73	0.68
3:D:152:ASP:OD2	3:D:190:HIS:ND1	2.26	0.67
2:C:37:GLN:HB2	2:C:43:LEU:HD23	1.77	0.67
3:D:137:LEU:HB2	3:D:176:LEU:HB3	1.79	0.65
1:B:457:ARG:NH1	1:B:459:SER:O	2.36	0.57
2:C:201:THR:HG23	2:C:218:LYS:HE3	1.87	0.57
3:D:182:LEU:HD11	3:D:186:ASP:HB3	1.87	0.57
3:D:109:ARG:NH1	3:D:171:ASP:OD1	2.38	0.56
3:D:117:PHE:HD2	3:D:136:LEU:HD23	1.72	0.54
1:B:371:SER:OG	1:B:373:SER:OG	2.18	0.54
2:C:105:TYR:HD2	2:C:107:GLY:H	1.57	0.52
3:D:95:SER:OG	3:D:96:PRO:HD3	2.09	0.51
1:B:491:PRO:HB2	1:B:492:LEU:HD12	1.92	0.51
2:C:163:ASN:HB3	2:C:166:ALA:HB3	1.91	0.51
3:D:124:GLU:HA	3:D:127:LYS:HE2	1.93	0.51
3:D:114:PRO:HB3	3:D:140:PHE:HB3	1.92	0.50
3:D:187:TYR:O	3:D:212:ARG:NH1	2.45	0.50
3:D:182:LEU:HD12	3:D:183:SER:N	2.27	0.49
2:C:152:ASP:HA	2:C:183:LEU:HB3	1.94	0.49
2:C:155:PRO:HD2	2:C:208:HIS:CE1	2.47	0.49
3:D:6:GLN:O	3:D:101:GLN:NE2	2.46	0.48
3:D:17:ASP:O	3:D:79:LEU:HD23	2.13	0.48
2:C:154:PHE:HB3	2:C:155:PRO:HD3	1.95	0.48
2:C:207:ASN:OD1	2:C:208:HIS:N	2.46	0.48
3:D:6:GLN:HE22	3:D:88:TYR:HA	1.79	0.48
2:C:2:LEU:HD12	2:C:20:CYS:SG	2.55	0.47
1:B:346:ARG:HB3	1:B:346:ARG:NH1	2.30	0.47
1:B:414:GLN:HA	1:B:414:GLN:OE1	2.14	0.47
2:C:39:ARG:HH11	2:C:39:ARG:HA	1.80	0.46
3:D:16:GLY:HA2	3:D:78:ARG:HG3	1.98	0.46
3:D:94:SER:O	3:D:97:TRP:NE1	2.45	0.45
3:D:126:LEU:HA	3:D:184:LYS:NZ	2.31	0.45
3:D:182:LEU:HD12	3:D:183:SER:H	1.81	0.45
3:D:159:ASN:N	3:D:159:ASN:OD1	2.50	0.45
2:C:60:GLN:H	2:C:60:GLN:CD	2.25	0.45
1:B:458:LYS:HA	1:B:458:LYS:HD3	1.76	0.45
3:D:184:LYS:HD3	3:D:184:LYS:HA	1.79	0.44
1:B:506:GLN:OE1	1:B:507:PRO:HD2	2.18	0.44
3:D:149:TRP:CG	3:D:180:LEU:HD13	2.52	0.44
1:B:393:THR:HA	1:B:522:ALA:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:462:LYS:N	1:B:465:GLU:OE2	2.51	0.43
3:D:165:THR:HG22	3:D:175:SER:H	1.83	0.43
1:B:439:ASN:CG	1:B:506:GLN:HE22	2.27	0.43
3:D:109:ARG:NH2	3:D:110:THR:OG1	2.51	0.43
1:B:377:PHE:CD1	1:B:434:ILE:HG12	2.54	0.43
2:C:162:TRP:CH2	2:C:204:CYS:HB3	2.53	0.43
1:B:457:ARG:NE	1:B:467:ASP:OD1	2.39	0.42
3:D:187:TYR:HE1	3:D:193:TYR:HE1	1.67	0.42
3:D:194:ALA:HA	3:D:209:SER:HA	2.02	0.42
1:B:447:GLY:HA2	1:B:497:PHE:O	2.19	0.42
2:C:153:TYR:OH	2:C:186:LEU:HD23	2.20	0.42
2:C:30:SER:O	2:C:51:VAL:HG12	2.20	0.42
2:C:108:PHE:O	2:C:111:TRP:NE1	2.52	0.42
2:C:127:PRO:HD3	2:C:208:HIS:ND1	2.36	0.41
2:C:32:VAL:HG12	2:C:96:ALA:HB2	2.01	0.41
2:C:200:GLN:NE2	2:C:201:THR:O	2.54	0.41
2:C:203:ILE:HG13	2:C:217:LYS:C	2.45	0.41
3:D:149:TRP:HB3	3:D:156:GLN:NE2	2.36	0.41
1:B:518:LEU:HD23	1:B:518:LEU:HA	1.91	0.41
2:C:163:ASN:HB2	2:C:167:LEU:H	1.86	0.41
2:C:171:VAL:HA	2:C:190:VAL:HG23	2.03	0.41
3:D:4:LEU:HD12	3:D:23:CYS:SG	2.61	0.40
3:D:186:ASP:HA	3:D:189:LYS:NZ	2.36	0.40
2:C:70:ARG:HD2	2:C:72:MET:HE1	2.04	0.40
2:C:178:LEU:HD11	2:C:182:GLY:HA2	2.02	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	B	192/1288 (15%)	184 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	221/223 (99%)	216 (98%)	5 (2%)	0	100	100
3	D	213/215 (99%)	199 (93%)	14 (7%)	0	100	100
All	All	626/1726 (36%)	599 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	B	165/1116 (15%)	165 (100%)	0	100	100
2	C	187/187 (100%)	187 (100%)	0	100	100
3	D	187/187 (100%)	187 (100%)	0	100	100
All	All	539/1490 (36%)	539 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

Mol	Chain	Res	Type
1	B	493	GLN
3	D	6	GLN
3	D	27	GLN
3	D	125	GLN
3	D	200	GLN

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	A	1	1,4	14,14,15	0.24	0	17,19,21	0.46	0
4	NAG	A	2	4	14,14,15	0.19	0	17,19,21	0.45	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	A	1	1,4	-	2/6/23/26	0/1/1/1
4	NAG	A	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

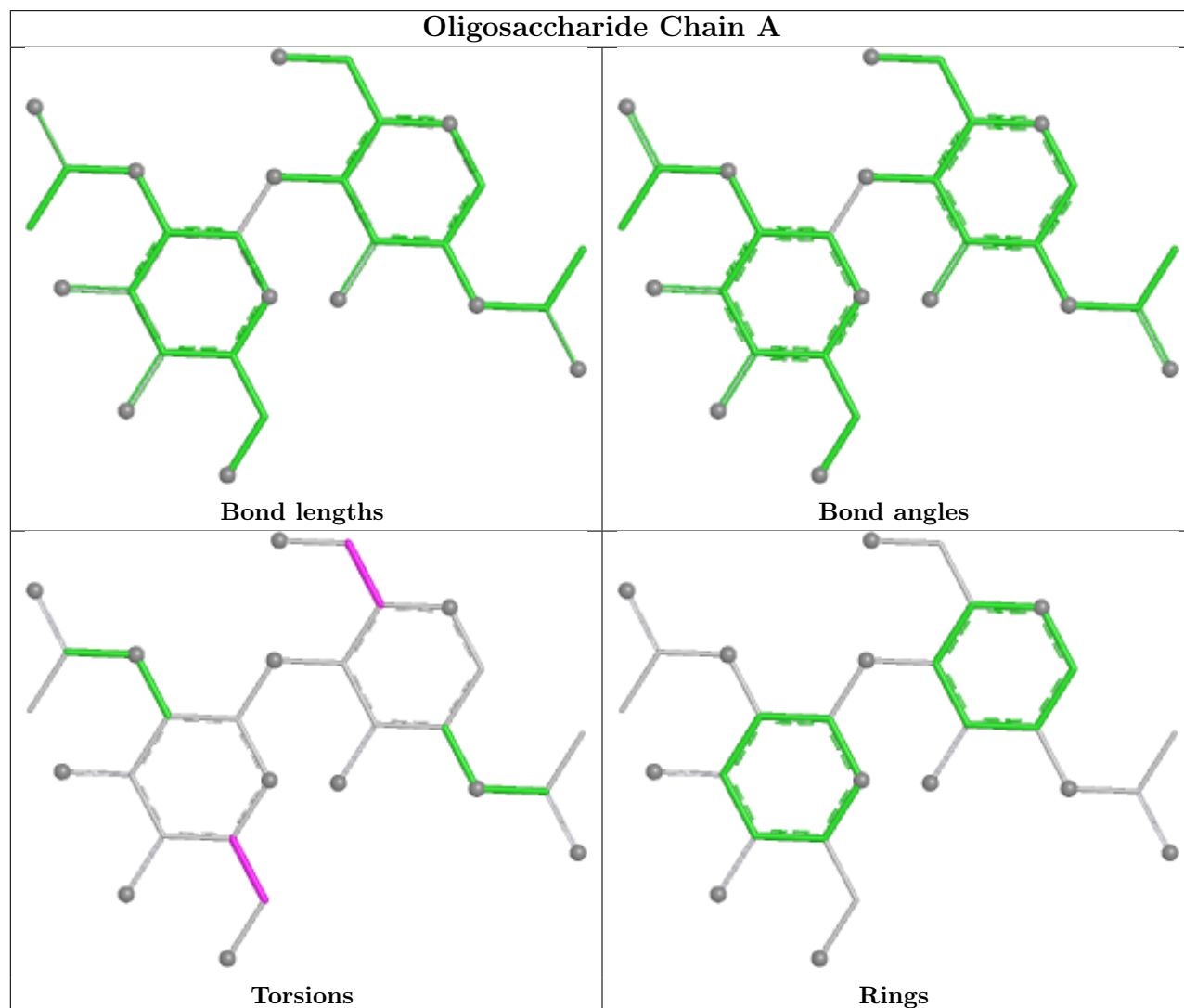
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1	NAG	O5-C5-C6-O6
4	A	1	NAG	C4-C5-C6-O6
4	A	2	NAG	C4-C5-C6-O6
4	A	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](#)

There are no ligands in this entry.

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-34742. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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.