



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:31 PM UTC

PDB ID : 1JDN / pdb_00001jdn
Title : Crystal Structure of Hormone Receptor
Authors : He, X.-L.; Chow, D.-C.; Martick, M.M.; Garcia, K.C.
Deposited on : 2001-06-14
Resolution : 2.90 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
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

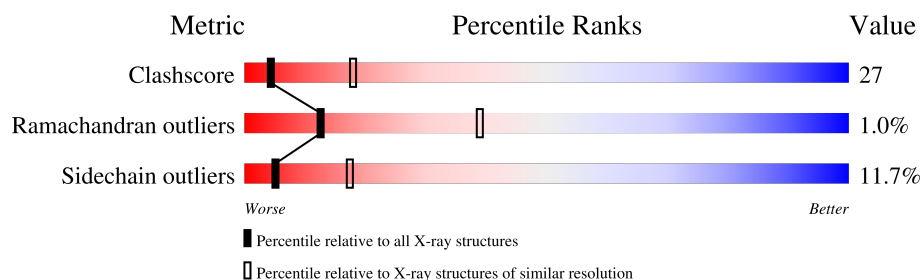
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

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	441	53% 32% 7% 8%
2	B	6	17% 50% 33%
3	C	5	60% 40%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	1	X	-	-	-

2 Entry composition [i](#)

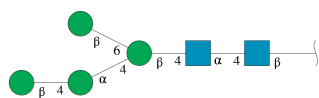
There are 4 unique types of molecules in this entry. The entry contains 3364 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ATRIAL NATRIURETIC PEPTIDE CLEARANCE RECEPTOR.

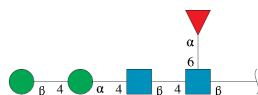
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3230	2048	556	610	16			

- Molecule 2 is an oligosaccharide called beta-D-mannopyranose-(1-4)-alpha-D-mannopyranos e-(1-4)-[beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	6	Total	C	N	O	0	0	0
			72	40	2	30			

- Molecule 3 is an oligosaccharide called beta-D-mannopyranose-(1-4)-alpha-D-mannopyranos e-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	0
			60	34	2	24			

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

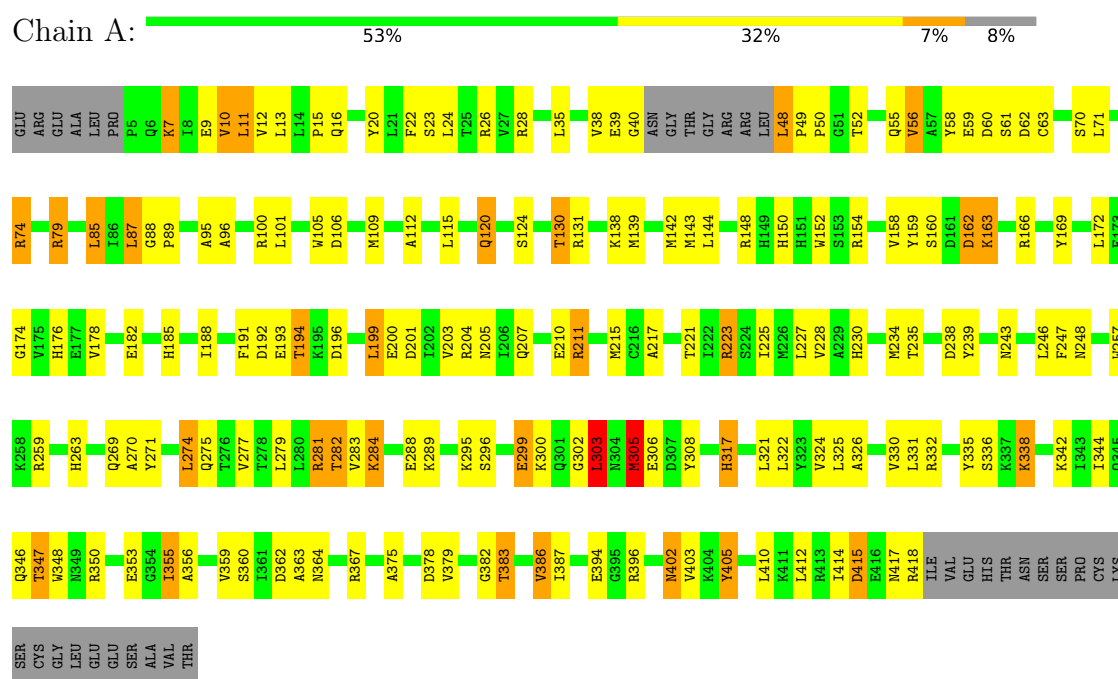
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Cl	0	0
			2	2		

3 Residue-property plots

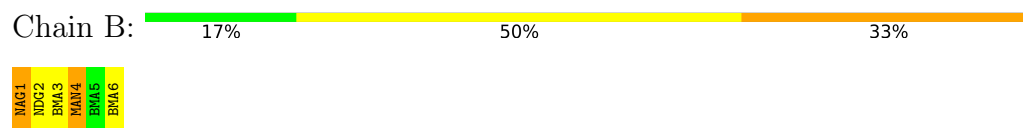
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: ATRIAL NATRIURETIC PEPTIDE CLEARANCE RECEPTOR



• Molecule 2: beta-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-4)-[beta-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-alpha-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



• Molecule 3: beta-D-mannopyranose-(1-4)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	217.19Å 217.19Å 130.79Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.90	Depositor
% Data completeness (in resolution range)	98.1 (50.00-2.90)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.243 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3364	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CL, FUC, NAG, MAN, BMA, NDG

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	0.50	1/3303 (0.0%)	1.01	17/4463 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	305	MET	SD-CE	6.63	1.96	1.79

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	163	LYS	N-CA-C	-7.90	101.33	111.92
1	A	303	LEU	N-CA-C	-7.71	94.39	110.80
1	A	284	LYS	CA-C-N	7.35	126.89	119.24
1	A	284	LYS	C-N-CA	7.35	126.89	119.24
1	A	263	HIS	N-CA-C	7.17	121.62	113.02
1	A	112	ALA	N-CA-C	-6.85	104.50	112.92
1	A	56	VAL	N-CA-C	6.64	117.47	108.17
1	A	402	ASN	N-CA-C	5.91	119.34	111.30
1	A	52	THR	N-CA-C	5.70	119.25	110.42
1	A	317	HIS	N-CA-C	-5.68	104.99	111.07
1	A	405	TYR	CA-C-N	5.40	124.74	118.85
1	A	405	TYR	C-N-CA	5.40	124.74	118.85
1	A	7	LYS	N-CA-C	5.38	118.84	110.17
1	A	162	ASP	N-CA-C	5.15	117.30	111.02
1	A	62	ASP	N-CA-C	-5.14	106.58	112.86
1	A	382	GLY	N-CA-C	-5.10	108.23	115.43
1	A	289	LYS	N-CA-C	-5.10	105.61	111.07

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	3230	0	3132	172	0
2	B	72	0	60	5	0
3	C	60	0	52	6	0
4	A	2	0	0	0	0
All	All	3364	0	3244	177	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 27.

All (177) 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:130:THR:HG21	1:A:347:THR:HG21	1.28	1.15
1:A:79:ARG:HH11	1:A:79:ARG:HB3	1.23	1.01
1:A:144:LEU:HD11	1:A:182:GLU:HG3	1.39	1.01
1:A:130:THR:HG21	1:A:347:THR:CG2	1.90	1.00
1:A:230:HIS:CD2	1:A:235:THR:HG21	1.97	0.98
1:A:159:TYR:HB3	1:A:172:LEU:HD12	1.45	0.96
1:A:130:THR:HG22	1:A:348:TRP:HE1	1.33	0.92
1:A:305:MET:HA	1:A:305:MET:HE3	1.52	0.92
1:A:74:ARG:HH11	1:A:74:ARG:HG2	1.34	0.91
1:A:415:ASP:HB3	1:A:418:ARG:HH21	1.36	0.86
1:A:200:GLU:O	1:A:204:ARG:HG3	1.79	0.83
1:A:346:GLN:O	1:A:350:ARG:NH1	2.15	0.80
1:A:221:THR:O	1:A:225:ILE:HG12	1.83	0.78
1:A:79:ARG:HB3	1:A:79:ARG:NH1	1.98	0.78
1:A:344:ILE:O	1:A:347:THR:HG22	1.86	0.74
1:A:9:GLU:OE2	1:A:55:GLN:HG2	1.87	0.74
1:A:130:THR:HG23	1:A:344:ILE:HD12	1.71	0.73
1:A:281:ARG:HD2	1:A:386:VAL:HG11	1.71	0.73
1:A:71:LEU:HD12	1:A:101:LEU:HD13	1.72	0.71
1:A:174:GLY:O	1:A:178:VAL:HG23	1.91	0.71
1:A:305:MET:HA	1:A:305:MET:CE	2.20	0.71
1:A:10:VAL:HG22	1:A:56:VAL:HG12	1.73	0.70
1:A:79:ARG:HH11	1:A:79:ARG:CB	2.04	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ARG:HG2	1:A:74:ARG:NH1	2.07	0.67
1:A:26:ARG:HH11	1:A:303:LEU:HD21	1.59	0.67
1:A:223:ARG:NH2	1:A:259:ARG:HG2	2.10	0.66
1:A:330:VAL:HG12	1:A:335:TYR:HB2	1.76	0.65
1:A:144:LEU:HD12	1:A:178:VAL:HG12	1.79	0.65
1:A:405:TYR:CE2	1:A:410:LEU:HB2	2.30	0.65
1:A:154:ARG:NH1	1:A:210:GLU:HG3	2.11	0.65
1:A:230:HIS:HD2	1:A:235:THR:HG21	1.56	0.64
1:A:378:ASP:HB3	1:A:383:THR:HB	1.79	0.64
1:A:275:GLN:HE21	1:A:387:ILE:HD11	1.62	0.64
1:A:162:ASP:HB2	1:A:166:ARG:HA	1.80	0.64
1:A:154:ARG:NH1	1:A:154:ARG:HB3	2.12	0.64
1:A:130:THR:CG2	1:A:348:TRP:HE1	2.10	0.63
1:A:160:SER:HA	1:A:191:PHE:O	1.98	0.63
1:A:326:ALA:O	1:A:330:VAL:HG23	1.98	0.63
1:A:23:SER:OG	1:A:26:ARG:HG2	1.99	0.62
1:A:415:ASP:CB	1:A:418:ARG:HH21	2.10	0.62
1:A:7:LYS:HD3	1:A:55:GLN:HB2	1.80	0.61
1:A:223:ARG:NH2	1:A:257:TRP:O	2.30	0.61
1:A:394:GLU:HB3	1:A:396:ARG:NH1	2.15	0.60
1:A:215:MET:HE3	1:A:225:ILE:HG21	1.82	0.60
1:A:130:THR:CG2	1:A:344:ILE:HD12	2.30	0.60
3:C:1:NAG:H3	3:C:1:NAG:H83	1.84	0.60
1:A:415:ASP:HB3	1:A:418:ARG:NH2	2.11	0.59
1:A:335:TYR:CZ	1:A:342:LYS:HE2	2.38	0.59
1:A:230:HIS:HA	1:A:235:THR:CG2	2.33	0.58
1:A:203:VAL:HG21	1:A:228:VAL:CG1	2.33	0.58
1:A:321:LEU:O	1:A:325:LEU:HD13	2.03	0.58
3:C:2:NAG:H3	3:C:2:NAG:H82	1.85	0.58
1:A:193:GLU:OE2	1:A:217:ALA:HB1	2.03	0.58
1:A:56:VAL:HG23	1:A:58:TYR:HE1	1.69	0.58
1:A:143:MET:HE1	1:A:277:VAL:HG21	1.86	0.58
1:A:148:ARG:HH21	1:A:148:ARG:HG2	1.68	0.58
1:A:211:ARG:HG2	1:A:414:ILE:HG23	1.86	0.58
1:A:204:ARG:HH11	1:A:204:ARG:HG2	1.70	0.57
1:A:211:ARG:HG3	1:A:238:ASP:O	2.05	0.56
1:A:162:ASP:O	1:A:163:LYS:HB2	2.05	0.56
1:A:284:LYS:HE2	1:A:353:GLU:OE1	2.05	0.56
1:A:88:GLY:O	1:A:109:MET:HE3	2.04	0.56
1:A:139:MET:HE3	1:A:142:MET:HB3	1.87	0.56
1:A:207:GLN:HB3	1:A:234:MET:CE	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:ARG:NH1	1:A:74:ARG:CG	2.68	0.56
1:A:56:VAL:HG23	1:A:58:TYR:CE1	2.40	0.55
1:A:166:ARG:HB3	1:A:169:TYR:HB3	1.89	0.55
1:A:288:GLU:HG3	2:B:4:MAN:O2	2.06	0.54
1:A:26:ARG:NH1	1:A:303:LEU:HD21	2.22	0.54
1:A:154:ARG:HH12	1:A:210:GLU:HG3	1.71	0.54
1:A:96:ALA:O	1:A:100:ARG:HG3	2.07	0.54
1:A:223:ARG:HG3	1:A:223:ARG:HH21	1.72	0.53
1:A:336:SER:C	1:A:338:LYS:H	2.16	0.53
1:A:355:ILE:H	1:A:355:ILE:HD12	1.73	0.53
1:A:281:ARG:HG3	1:A:281:ARG:HH11	1.73	0.53
1:A:139:MET:HE3	1:A:139:MET:HA	1.90	0.53
1:A:13:LEU:HD23	1:A:59:GLU:HB2	1.92	0.52
1:A:305:MET:O	1:A:306:GLU:HB2	2.10	0.52
1:A:355:ILE:HD12	1:A:355:ILE:N	2.25	0.52
1:A:85:LEU:CD1	1:A:87:LEU:HD13	2.40	0.52
1:A:150:HIS:HD2	1:A:152:TRP:CH2	2.28	0.51
1:A:234:MET:HB3	1:A:239:TYR:CD1	2.45	0.51
1:A:257:TRP:HB3	1:A:271:TYR:CG	2.45	0.51
1:A:20:TYR:O	1:A:26:ARG:HD2	2.09	0.51
1:A:211:ARG:NH1	1:A:239:TYR:OH	2.43	0.51
1:A:16:GLN:HB2	1:A:60:ASP:CG	2.36	0.51
1:A:367:ARG:HH11	1:A:367:ARG:HG2	1.76	0.51
1:A:26:ARG:HH11	1:A:303:LEU:CD2	2.22	0.50
1:A:158:VAL:O	1:A:215:MET:HA	2.10	0.50
1:A:235:THR:OG1	1:A:270:ALA:HA	2.12	0.50
1:A:336:SER:C	1:A:338:LYS:N	2.70	0.49
1:A:148:ARG:HG2	1:A:148:ARG:NH2	2.28	0.49
1:A:154:ARG:HH12	1:A:210:GLU:CG	2.25	0.48
1:A:89:PRO:HD2	1:A:95:ALA:HA	1.95	0.48
1:A:363:ALA:HB2	3:C:1:NAG:H82	1.95	0.48
1:A:211:ARG:HH21	1:A:418:ARG:HG3	1.77	0.48
1:A:295:LYS:O	1:A:299:GLU:HB2	2.13	0.48
1:A:70:SER:O	1:A:74:ARG:HB2	2.14	0.48
1:A:405:TYR:CZ	1:A:410:LEU:HB2	2.48	0.47
1:A:48:LEU:N	1:A:49:PRO:HD3	2.28	0.47
1:A:38:VAL:C	1:A:40:GLY:H	2.21	0.47
1:A:282:THR:O	2:B:2:NDG:H6C2	2.14	0.47
1:A:71:LEU:CD1	1:A:101:LEU:HD13	2.41	0.47
1:A:199:LEU:HD12	1:A:200:GLU:H	1.79	0.47
1:A:144:LEU:HD23	1:A:144:LEU:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:LEU:O	1:A:48:LEU:HD13	2.14	0.47
1:A:85:LEU:HD13	1:A:87:LEU:HD13	1.97	0.46
1:A:154:ARG:HH12	1:A:210:GLU:CD	2.23	0.46
1:A:154:ARG:HA	1:A:185:HIS:O	2.16	0.46
1:A:281:ARG:NH1	2:B:2:NDG:H2	2.30	0.46
1:A:246:LEU:HD13	1:A:247:PHE:CZ	2.51	0.46
1:A:355:ILE:H	1:A:355:ILE:CD1	2.29	0.46
1:A:38:VAL:HG11	1:A:324:VAL:HG21	1.97	0.45
1:A:144:LEU:HD23	1:A:144:LEU:C	2.41	0.45
1:A:207:GLN:HB3	1:A:234:MET:HE3	1.97	0.45
1:A:282:THR:HG21	1:A:356:ALA:C	2.41	0.45
1:A:322:LEU:HG	1:A:347:THR:OG1	2.17	0.45
1:A:188:ILE:HD12	1:A:188:ILE:N	2.31	0.45
3:C:3:MAN:H62	3:C:4:BMA:O5	2.16	0.45
1:A:288:GLU:N	1:A:288:GLU:OE2	2.49	0.45
1:A:230:HIS:CG	1:A:235:THR:HG21	2.49	0.45
1:A:367:ARG:HG2	1:A:367:ARG:NH1	2.32	0.45
1:A:176:HIS:CD2	1:A:176:HIS:C	2.95	0.44
3:C:2:NAG:H82	3:C:2:NAG:C3	2.47	0.44
3:C:1:NAG:H3	3:C:1:NAG:C8	2.45	0.44
1:A:15:PRO:HG2	1:A:22:PHE:CE1	2.52	0.44
1:A:24:LEU:HD22	1:A:58:TYR:HB3	2.00	0.44
1:A:279:LEU:HB3	2:B:1:NAG:H82	1.99	0.44
1:A:10:VAL:CG2	1:A:56:VAL:HG12	2.44	0.44
1:A:347:THR:HG22	1:A:348:TRP:CD1	2.52	0.44
1:A:223:ARG:NH2	1:A:223:ARG:HG3	2.32	0.44
1:A:281:ARG:HG3	1:A:281:ARG:NH1	2.33	0.44
1:A:192:ASP:OD2	1:A:194:THR:HG23	2.18	0.43
1:A:283:VAL:O	1:A:283:VAL:HG12	2.17	0.43
1:A:162:ASP:HB2	1:A:166:ARG:CA	2.48	0.43
1:A:211:ARG:HA	1:A:211:ARG:HE	1.84	0.43
1:A:279:LEU:CB	2:B:1:NAG:H82	2.48	0.43
1:A:11:LEU:HD12	1:A:71:LEU:HD23	2.00	0.43
1:A:199:LEU:HD12	1:A:200:GLU:N	2.34	0.43
1:A:317:HIS:CE1	1:A:355:ILE:HG13	2.53	0.43
1:A:230:HIS:HA	1:A:235:THR:HG22	1.99	0.43
1:A:154:ARG:CB	1:A:154:ARG:HH11	2.32	0.43
1:A:362:ASP:OD1	1:A:364:ASN:N	2.48	0.43
1:A:120:GLN:HE21	1:A:120:GLN:HB2	1.50	0.42
1:A:247:PHE:O	1:A:248:ASN:C	2.62	0.42
1:A:120:GLN:HB3	1:A:131:ARG:HH22	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:THR:HG22	1:A:348:TRP:NE1	2.16	0.42
1:A:360:SER:O	1:A:367:ARG:HD2	2.19	0.42
1:A:61:SER:C	1:A:63:CYS:N	2.74	0.42
1:A:295:LYS:HA	1:A:308:TYR:CD2	2.54	0.42
1:A:199:LEU:HD13	1:A:228:VAL:HG21	2.01	0.42
1:A:85:LEU:HD11	1:A:87:LEU:CD1	2.50	0.42
1:A:403:VAL:O	1:A:403:VAL:HG23	2.19	0.42
1:A:105:TRP:O	1:A:106:ASP:C	2.62	0.42
1:A:295:LYS:HG3	1:A:308:TYR:CE1	2.55	0.42
1:A:12:VAL:O	1:A:12:VAL:HG12	2.20	0.42
1:A:162:ASP:CB	1:A:166:ARG:H	2.32	0.42
1:A:299:GLU:HA	1:A:299:GLU:OE1	2.19	0.42
1:A:207:GLN:CB	1:A:234:MET:HE3	2.50	0.41
1:A:308:TYR:CD1	1:A:308:TYR:N	2.88	0.41
1:A:227:LEU:HD23	1:A:227:LEU:HA	1.92	0.41
1:A:58:TYR:CD1	1:A:58:TYR:N	2.89	0.41
1:A:204:ARG:O	1:A:207:GLN:HG2	2.20	0.41
1:A:28:ARG:HG3	1:A:58:TYR:CE2	2.56	0.41
1:A:63:CYS:O	1:A:63:CYS:SG	2.79	0.41
1:A:204:ARG:HG2	1:A:204:ARG:NH1	2.33	0.41
1:A:274:LEU:HD22	1:A:275:GLN:N	2.36	0.41
1:A:130:THR:HG22	1:A:344:ILE:HG23	2.02	0.41
1:A:324:VAL:O	1:A:325:LEU:C	2.64	0.41
1:A:375:ALA:HB3	1:A:387:ILE:HD13	2.03	0.41
1:A:120:GLN:HB3	1:A:131:ARG:NH2	2.36	0.40
1:A:138:LYS:HA	1:A:138:LYS:HD3	1.78	0.40
1:A:163:LYS:H	1:A:166:ARG:HG3	1.86	0.40
1:A:375:ALA:HB1	1:A:410:LEU:HD11	2.02	0.40
1:A:281:ARG:NH2	1:A:283:VAL:HG21	2.36	0.40
1:A:296:SER:O	1:A:300:LYS:HG3	2.22	0.40
1:A:317:HIS:ND1	1:A:317:HIS:C	2.79	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	403/441 (91%)	370 (92%)	29 (7%)	4 (1%)	12	39

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	50	PRO
1	A	302	GLY
1	A	124	SER
1	A	303	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	342/371 (92%)	302 (88%)	40 (12%)	5	17

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	11	LEU
1	A	35	LEU
1	A	39	GLU
1	A	48	LEU
1	A	74	ARG
1	A	79	ARG
1	A	85	LEU
1	A	87	LEU
1	A	115	LEU
1	A	120	GLN
1	A	130	THR
1	A	194	THR
1	A	196	ASP
1	A	199	LEU

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Mol	Chain	Res	Type
1	A	201	ASP
1	A	205	ASN
1	A	211	ARG
1	A	223	ARG
1	A	243	ASN
1	A	269	GLN
1	A	274	LEU
1	A	281	ARG
1	A	282	THR
1	A	299	GLU
1	A	303	LEU
1	A	305	MET
1	A	331	LEU
1	A	332	ARG
1	A	338	LYS
1	A	347	THR
1	A	355	ILE
1	A	359	VAL
1	A	379	VAL
1	A	383	THR
1	A	386	VAL
1	A	402	ASN
1	A	412	LEU
1	A	415	ASP
1	A	417	ASN

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	120	GLN
1	A	176	HIS
1	A	180	GLN
1	A	207	GLN
1	A	275	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 ⓘ

11 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	1,2	14,14,15	1.18	1 (7%)	17,19,21	1.48	4 (23%)
2	NDG	B	2	2	14,14,15	0.61	0	17,19,21	0.84	0
2	BMA	B	3	2	11,11,12	0.98	0	15,15,17	0.76	1 (6%)
2	MAN	B	4	2	11,11,12	0.94	0	15,15,17	0.91	1 (6%)
2	BMA	B	5	2	11,11,12	0.85	0	15,15,17	0.53	0
2	BMA	B	6	2	11,11,12	1.01	0	15,15,17	0.97	1 (6%)
3	NAG	C	1	1,3	14,14,15	1.11	1 (7%)	17,19,21	1.64	4 (23%)
3	NAG	C	2	3	14,14,15	0.78	0	17,19,21	0.84	0
3	MAN	C	3	3	11,11,12	0.83	0	15,15,17	0.91	1 (6%)
3	BMA	C	4	3	11,11,12	0.62	0	15,15,17	0.39	0
3	FUC	C	5	3	10,10,11	0.97	1 (10%)	14,14,16	2.02	2 (14%)

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	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NDG	B	2	2	-	3/6/23/26	0/1/1/1
2	BMA	B	3	2	-	0/2/19/22	1/1/1/1
2	MAN	B	4	2	-	2/2/19/22	0/1/1/1
2	BMA	B	5	2	-	2/2/19/22	0/1/1/1
2	BMA	B	6	2	-	1/2/19/22	1/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	1	1,3	-	5/6/23/26	0/1/1/1
3	NAG	C	2	3	-	5/6/23/26	0/1/1/1
3	MAN	C	3	3	-	0/2/19/22	0/1/1/1
3	BMA	C	4	3	-	0/2/19/22	0/1/1/1
3	FUC	C	5	3	-	-	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	C1-C2	3.82	1.57	1.52
3	C	1	NAG	C1-C2	-2.64	1.48	1.52
3	C	5	FUC	C1-C2	2.19	1.57	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	5	FUC	C1-C2-C3	6.51	119.12	109.64
3	C	1	NAG	C3-C4-C5	4.11	117.69	110.23
2	B	1	NAG	C3-C4-C5	-3.29	104.26	110.23
2	B	6	BMA	C1-O5-C5	3.11	116.35	112.19
2	B	1	NAG	O5-C1-C2	3.02	115.97	111.29
3	C	1	NAG	O5-C1-C2	-2.64	107.21	111.29
2	B	1	NAG	C2-N2-C7	-2.46	119.61	122.90
2	B	4	MAN	C1-C2-C3	2.43	113.18	109.64
3	C	1	NAG	O4-C4-C3	-2.39	104.74	110.38
3	C	3	MAN	C1-C2-C3	2.32	113.02	109.64
2	B	1	NAG	C1-O5-C5	2.27	115.23	112.19
2	B	3	BMA	C2-C3-C4	-2.26	106.89	110.86
3	C	1	NAG	C4-C3-C2	2.08	114.06	111.02
3	C	5	FUC	C2-C3-C4	2.04	114.45	110.86

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	1	NAG	C1

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1	NAG	C3-C2-N2-C7
3	C	1	NAG	C8-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	C	1	NAG	O7-C7-N2-C2
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
2	B	5	BMA	C4-C5-C6-O6
2	B	5	BMA	O5-C5-C6-O6
2	B	4	MAN	C4-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
2	B	4	MAN	O5-C5-C6-O6
2	B	2	NDG	C8-C7-N2-C2
3	C	1	NAG	O5-C5-C6-O6
2	B	2	NDG	O7-C7-N2-C2
2	B	6	BMA	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
2	B	2	NDG	O5-C5-C6-O6
3	C	2	NAG	C3-C2-N2-C7
3	C	2	NAG	C1-C2-N2-C7

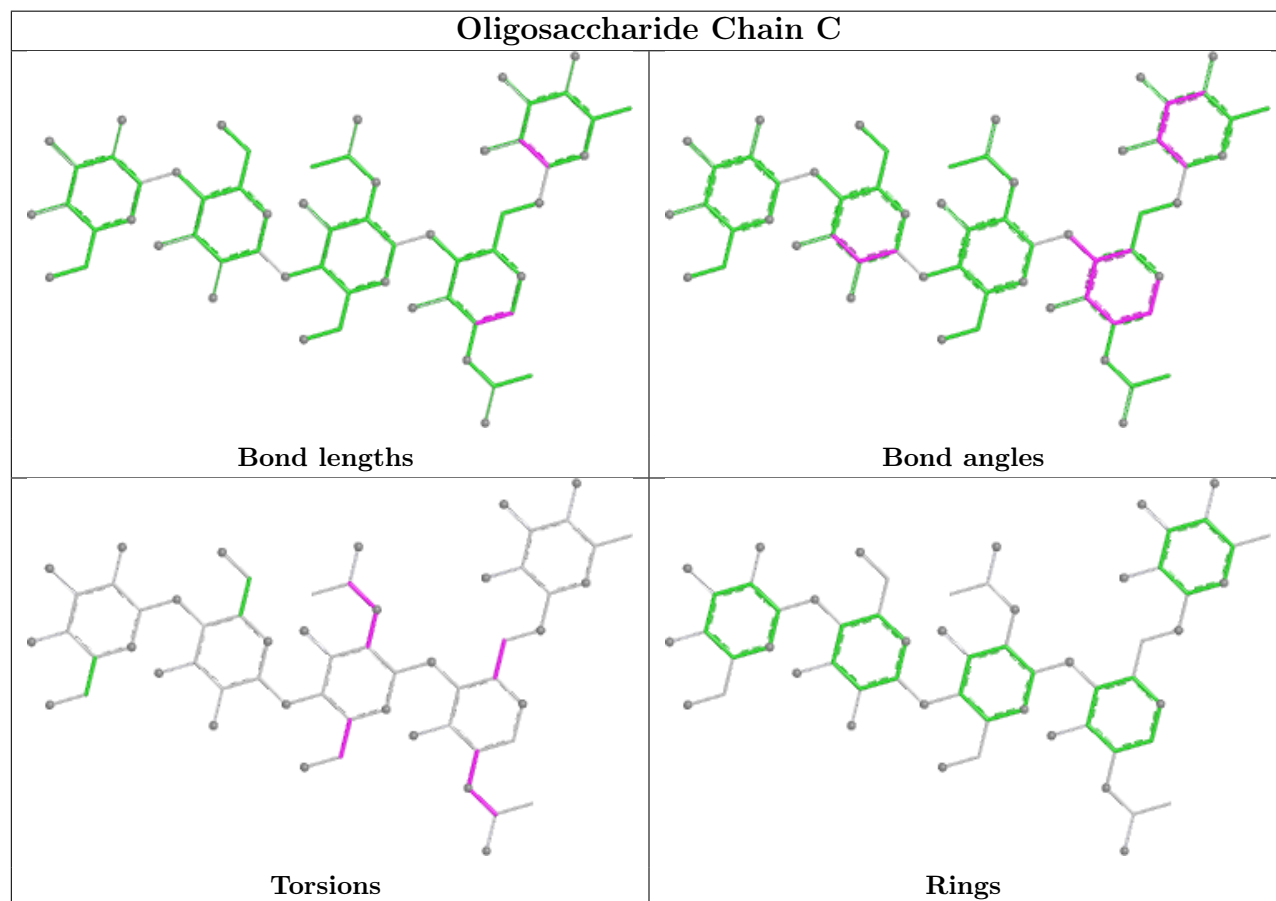
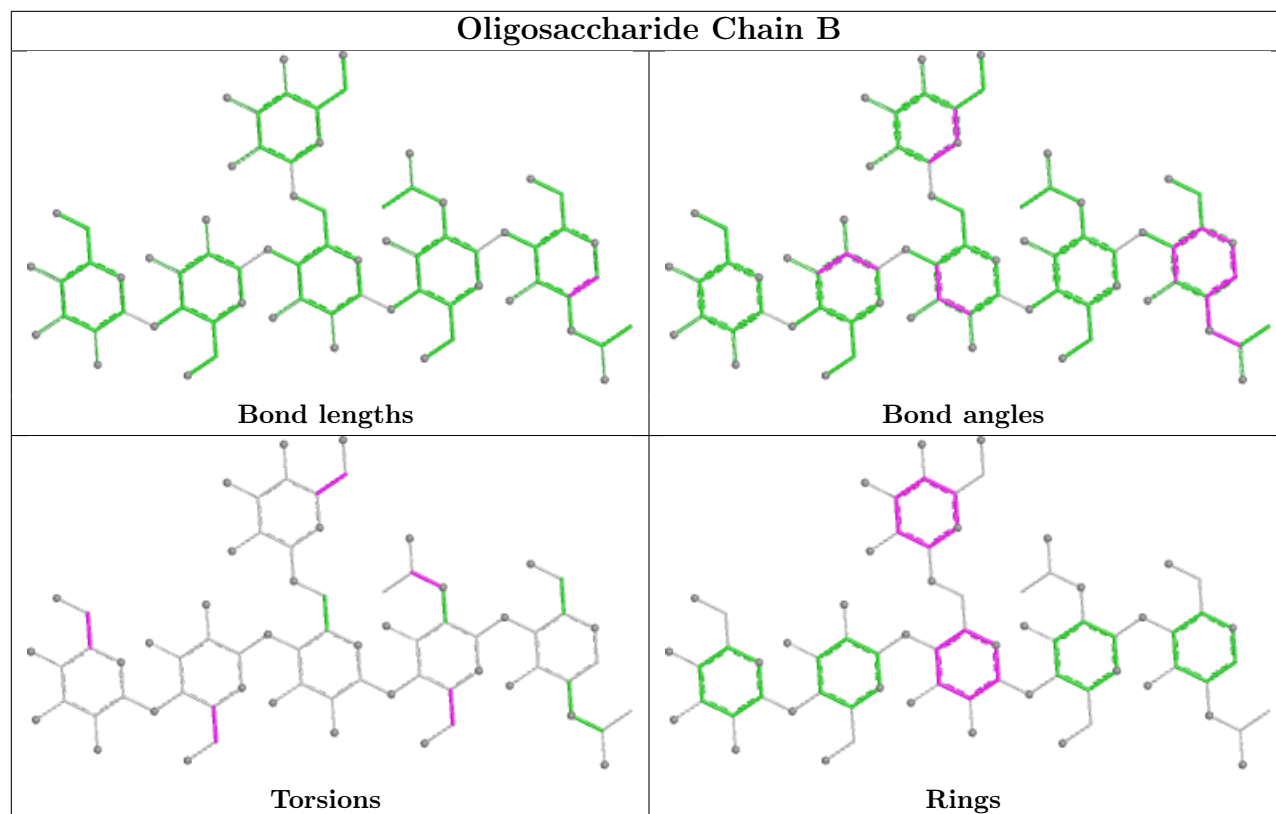
All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	6	BMA	C1-C2-C3-C4-C5-O5
2	B	3	BMA	C1-C2-C3-C4-C5-O5

7 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	4	BMA	1	0
2	B	4	MAN	1	0
3	C	1	NAG	3	0
3	C	3	MAN	1	0
2	B	1	NAG	2	0
3	C	2	NAG	2	0
2	B	2	NDG	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 oligosaccharide.



5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.