



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 11:19 PM BST

PDB ID : 1TCR  
Title : MURINE T-CELL ANTIGEN RECEPTOR 2C CLONE  
Authors : Garcia, K.C.; Degano, M.; Stanfield, R.L.; Wilson, I.A.  
Deposited on : 1996-09-12  
Resolution : 2.50 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

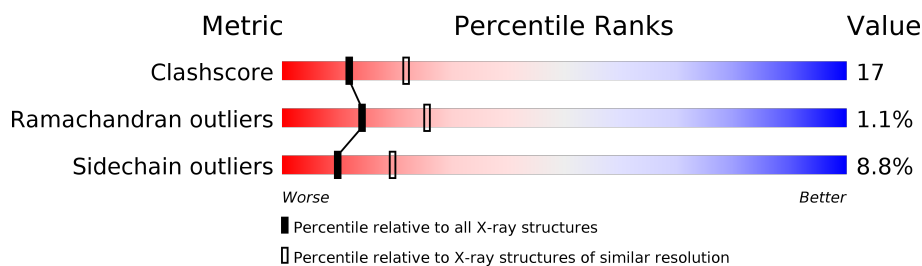
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	202	
2	B	237	
3	C	4	
4	D	3	
5	E	2	

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 3589 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 ALPHA, BETA T-CELL RECEPTOR (VB8.2DB2JB2.4CB2\;VA3JA58CA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1570	999	253	310	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	ALA	GLN	conflict	EMBL X01134
A	165	ALA	LYS	conflict	EMBL X01134

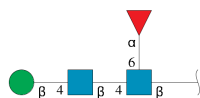
- Molecule 2 is a protein called ALPHA, BETA T-CELL RECEPTOR (VB8.2DB2JB2.4CB2\;VA3JA58CA).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	237	Total	C	N	O	S	0	0	0
			1853	1160	331	355	7			

There are 8 discrepancies between the modelled and reference sequences:

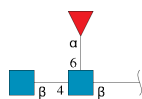
Chain	Residue	Modelled	Actual	Comment	Reference
B	97	GLY	GLN	conflict	GB 1791255
B	?	-	ARG	deletion	GB 1791255
B	?	-	ALA	deletion	GB 1791255
B	105	THR	GLU	conflict	GB 1791255
B	106	LEU	GLN	conflict	GB 1791255
B	107	TYR	PHE	conflict	GB 1791255
B	110	ALA	PRO	conflict	GB 1791255
B	115	SER	THR	conflict	GB 1791255

- Molecule 3 is an oligosaccharide called beta-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.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	4	Total	C	N	O	0	0	0
			49	28	2	19			

- Molecule 4 is an oligosaccharide called 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
4	D	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



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

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 7 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		
7	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 8 is water.

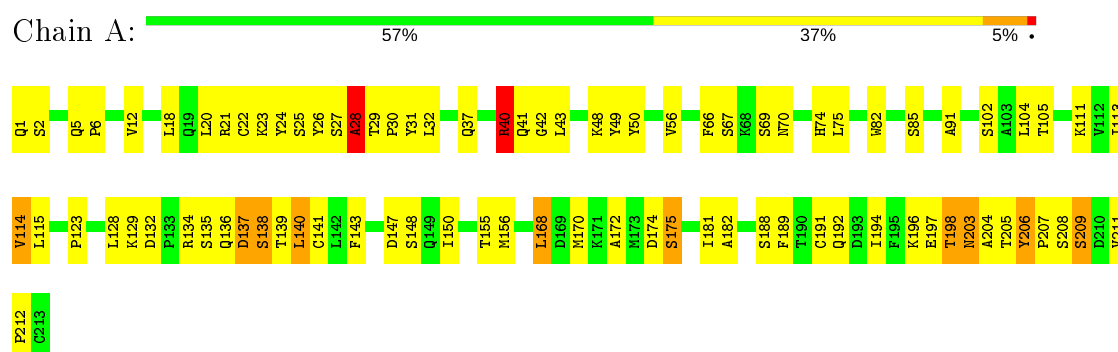
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	9	Total 9	O 9	0	0
8	B	13	Total 13	O 13	0	0

### 3 Residue-property plots

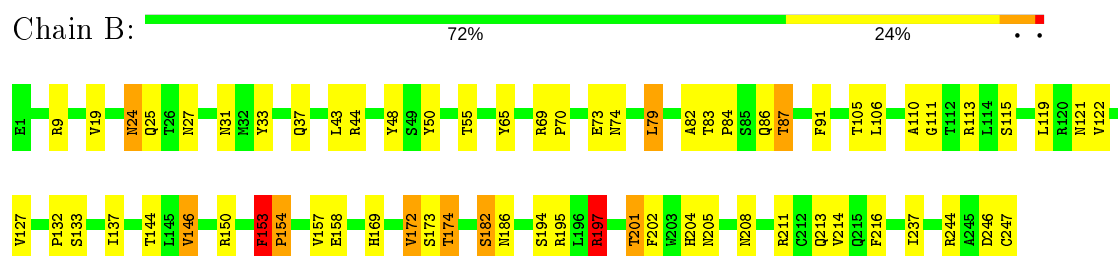
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: ALPHA, BETA T-CELL RECEPTOR (VB8.2DB2JB2.4CB2\;VA3JA58CA)



- Molecule 2: ALPHA, BETA T-CELL RECEPTOR (VB8.2DB2JB2.4CB2\;VA3JA58CA)



- Molecule 3: beta-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



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



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E:

100%

MOL  
MOL2



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.00 Å   72.90 Å   57.30 Å 90.00°   101.20°   90.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	93.4 ((Not available)-2.50)	Depositor
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.208 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3589	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	45.0	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: FUC, BMA, SO4, 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	0.73	3/1611 (0.2%)	0.94	4/2193 (0.2%)
2	B	0.63	0/1904	0.90	5/2586 (0.2%)
All	All	0.67	3/3515 (0.1%)	0.92	9/4779 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	28	ALA	C-N	-7.29	1.17	1.34
1	A	29	THR	N-CA	-7.05	1.32	1.46
1	A	29	THR	C-N	-5.63	1.23	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	153	PHE	O-C-N	-9.66	102.75	121.10
1	A	40	ARG	NE-CZ-NH2	8.57	124.59	120.30
2	B	197	ARG	NE-CZ-NH2	7.15	123.87	120.30
1	A	21	ARG	NE-CZ-NH2	6.76	123.68	120.30
2	B	44	ARG	NE-CZ-NH2	6.69	123.65	120.30
2	B	195	ARG	NE-CZ-NH2	6.65	123.63	120.30
2	B	153	PHE	CA-C-N	6.23	134.54	117.10
1	A	140	LEU	CA-CB-CG	5.92	128.91	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	SER	N-CA-C	-5.37	96.50	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	153	PHE	Peptide

## 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	1570	0	1502	72	0
2	B	1853	0	1762	59	0
3	C	49	0	43	2	0
4	D	38	0	34	2	0
5	E	28	0	25	0	0
6	A	14	0	13	0	0
7	B	15	0	0	1	0
8	A	9	0	0	0	0
8	B	13	0	0	0	0
All	All	3589	0	3379	119	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 17.

All (119) 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:26:TYR:CE2	1:A:28:ALA:HB3	1.75	1.20
2:B:153:PHE:O	2:B:154:PRO:O	1.72	1.08
1:A:27:SER:O	1:A:28:ALA:HB2	1.55	1.04
1:A:123:PRO:O	1:A:204:ALA:HB3	1.65	0.97
1:A:27:SER:O	1:A:28:ALA:CB	2.10	0.93
2:B:153:PHE:O	2:B:154:PRO:C	1.98	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:MET:HB2	1:A:175:SER:HB3	1.55	0.88
1:A:40:ARG:HD3	1:A:40:ARG:O	1.73	0.87
2:B:84:PRO:O	2:B:87:THR:HG23	1.79	0.82
1:A:28:ALA:O	1:A:30:PRO:HD3	1.79	0.81
1:A:91:ALA:HB1	1:A:104:LEU:HD22	1.60	0.81
2:B:174:THR:HB	2:B:194:SER:HB2	1.62	0.80
1:A:192:GLN:HG3	1:A:205:THR:HG21	1.69	0.75
1:A:26:TYR:CE2	1:A:28:ALA:CB	2.64	0.74
2:B:87:THR:HB	2:B:115:SER:HA	1.70	0.71
1:A:143:PHE:CZ	1:A:198:THR:HG21	2.26	0.70
1:A:26:TYR:CD2	1:A:28:ALA:HB3	2.26	0.70
1:A:67:SER:HB3	4:D:1:NAG:H82	1.73	0.70
2:B:205:ASN:HB3	2:B:208:ASN:ND2	2.06	0.69
1:A:128:LEU:HD12	2:B:146:VAL:HG13	1.75	0.68
2:B:133:SER:O	2:B:137:ILE:HG13	1.94	0.66
1:A:49:TYR:HB2	1:A:56:VAL:HG21	1.77	0.66
1:A:22:CYS:H	1:A:74:HIS:HD2	1.43	0.66
1:A:170:MET:HB2	1:A:175:SER:CB	2.26	0.66
2:B:127:VAL:HG13	2:B:237:ILE:HG22	1.77	0.65
2:B:174:THR:HB	2:B:194:SER:CB	2.26	0.65
2:B:246:ASP:O	2:B:247:CYS:HB2	1.97	0.65
2:B:37:GLN:HB2	2:B:43:LEU:CD2	2.26	0.65
1:A:48:LYS:O	1:A:56:VAL:HG11	1.96	0.65
1:A:172:ALA:HB3	1:A:175:SER:OG	1.98	0.64
1:A:132:ASP:HB3	1:A:138:SER:HB3	1.79	0.64
2:B:65:TYR:HD1	2:B:79:LEU:HD22	1.63	0.62
2:B:24:ASN:HA	2:B:73:GLU:O	2.00	0.62
1:A:22:CYS:H	1:A:74:HIS:CD2	2.19	0.60
2:B:169:HIS:O	2:B:172:VAL:HG13	2.02	0.60
1:A:42:GLY:HA2	2:B:91:PHE:CE2	2.36	0.60
2:B:83:THR:H	2:B:86:GLN:HE21	1.49	0.59
2:B:82:ALA:HA	2:B:86:GLN:NE2	2.17	0.59
2:B:204:HIS:HA	2:B:244:ARG:O	2.02	0.59
1:A:182:ALA:HB1	1:A:194:ILE:CD1	2.32	0.59
1:A:2:SER:HB3	1:A:25:SER:HB3	1.85	0.58
1:A:26:TYR:HE2	1:A:28:ALA:HB3	1.57	0.57
2:B:65:TYR:CD1	2:B:79:LEU:HD22	2.37	0.57
2:B:9:ARG:NH1	2:B:110:ALA:HB3	2.20	0.57
1:A:18:LEU:HD11	1:A:20:LEU:HD21	1.86	0.57
1:A:168:LEU:HB3	2:B:173:SER:CB	2.36	0.56
1:A:129:LYS:HG2	1:A:139:THR:HG22	1.89	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:69:ARG:HD2	2:B:74:ASN:O	2.05	0.55
1:A:82:TRP:HA	1:A:114:VAL:HG22	1.89	0.55
1:A:40:ARG:O	1:A:40:ARG:CD	2.49	0.54
1:A:67:SER:CB	4:D:1:NAG:H82	2.35	0.54
1:A:128:LEU:HD12	2:B:146:VAL:CG1	2.38	0.54
1:A:182:ALA:HB1	1:A:194:ILE:HD11	1.90	0.53
1:A:12:VAL:O	1:A:114:VAL:HA	2.08	0.53
1:A:111:LYS:HD3	1:A:113:ILE:HD11	1.89	0.53
1:A:115:LEU:HB3	1:A:148:SER:HB3	1.89	0.52
2:B:82:ALA:HA	2:B:86:GLN:HE22	1.73	0.52
1:A:147:ASP:O	1:A:150:ILE:HG22	2.09	0.52
2:B:48:TYR:HE2	2:B:50:TYR:CE2	2.27	0.52
1:A:28:ALA:O	1:A:30:PRO:CD	2.54	0.52
2:B:119:LEU:O	2:B:122:VAL:HG23	2.10	0.51
1:A:168:LEU:HD12	1:A:168:LEU:C	2.30	0.51
1:A:42:GLY:HA2	2:B:91:PHE:HE2	1.73	0.51
2:B:132:PRO:HB2	2:B:137:ILE:HD11	1.91	0.51
2:B:121:ASN:O	2:B:153:PHE:CB	2.58	0.51
1:A:31:TYR:O	1:A:32:LEU:HD23	2.11	0.51
2:B:37:GLN:CB	2:B:43:LEU:HD23	2.41	0.51
2:B:144:THR:OG1	2:B:197:ARG:HD3	2.12	0.50
1:A:192:GLN:CG	1:A:205:THR:HG21	2.41	0.50
1:A:141:CYS:HG	1:A:191:CYS:CB	2.18	0.50
1:A:203:ASN:OD1	1:A:203:ASN:N	2.44	0.50
1:A:43:LEU:HD11	2:B:43:LEU:HD12	1.94	0.49
1:A:43:LEU:HD11	2:B:43:LEU:CD1	2.41	0.49
1:A:70:ASN:OD1	1:A:70:ASN:N	2.45	0.49
2:B:37:GLN:HB2	2:B:43:LEU:HD23	1.93	0.49
2:B:84:PRO:O	2:B:87:THR:CG2	2.57	0.49
2:B:9:ARG:NH1	2:B:111:GLY:O	2.46	0.49
1:A:212:PRO:HB3	2:B:247:CYS:O	2.14	0.48
2:B:121:ASN:O	2:B:153:PHE:HB3	2.14	0.47
1:A:168:LEU:CB	2:B:173:SER:HB2	2.45	0.47
1:A:168:LEU:HB3	2:B:173:SER:HB3	1.96	0.47
2:B:150:ARG:HH21	3:C:4:FUC:H5	1.79	0.47
1:A:182:ALA:HB1	1:A:194:ILE:HD13	1.97	0.47
1:A:85:SER:OG	1:A:114:VAL:HG13	2.15	0.47
1:A:155:THR:HG22	1:A:156:MET:N	2.31	0.46
1:A:197:GLU:O	1:A:198:THR:HG23	2.16	0.46
1:A:205:THR:O	1:A:207:PRO:HD3	2.15	0.46
1:A:20:LEU:HD12	1:A:75:LEU:HD23	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:LEU:N	1:A:128:LEU:HD23	2.31	0.45
2:B:201:THR:HG22	2:B:202:PHE:N	2.31	0.45
1:A:136:GLN:HE21	1:A:137:ASP:H	1.64	0.45
1:A:5:GLN:HA	1:A:6:PRO:HD2	1.74	0.45
2:B:246:ASP:O	2:B:247:CYS:CB	2.65	0.45
2:B:25:GLN:OE1	2:B:27:ASN:HB2	2.17	0.44
1:A:37:GLN:HB2	1:A:43:LEU:HD22	1.99	0.44
1:A:168:LEU:HB3	2:B:173:SER:HB2	2.00	0.43
1:A:48:LYS:HD2	1:A:50:TYR:CE2	2.53	0.43
1:A:91:ALA:HA	1:A:105:THR:O	2.17	0.43
2:B:246:ASP:CG	2:B:247:CYS:N	2.71	0.43
2:B:31:ASN:OD1	2:B:50:TYR:CD1	2.72	0.43
2:B:19:VAL:HB	2:B:79:LEU:HG	2.00	0.42
1:A:170:MET:CB	1:A:175:SER:HB3	2.39	0.42
2:B:182:SER:HB3	3:C:4:FUC:O3	2.19	0.42
2:B:113:ARG:NH2	2:B:158:GLU:OE2	2.53	0.41
2:B:157:VAL:HG12	2:B:216:PHE:HA	2.02	0.41
1:A:188:SER:C	1:A:189:PHE:HD1	2.24	0.41
1:A:26:TYR:CD2	1:A:30:PRO:HB3	2.56	0.41
2:B:79:LEU:N	2:B:79:LEU:HD23	2.35	0.41
1:A:24:TYR:C	1:A:24:TYR:CD1	2.93	0.41
1:A:32:LEU:HD12	1:A:66:PHE:CD1	2.55	0.41
2:B:174:THR:HA	2:B:194:SER:HA	2.02	0.41
1:A:196:LYS:HG2	1:A:196:LYS:O	2.20	0.41
2:B:211:ARG:HD3	7:B:251:SO4:O3	2.20	0.41
2:B:205:ASN:HB3	2:B:208:ASN:HD22	1.81	0.41
1:A:104:LEU:HD12	2:B:106:LEU:HG	2.03	0.40
1:A:206:TYR:HA	1:A:207:PRO:HD2	1.90	0.40
2:B:213:GLN:HG2	2:B:214:VAL:N	2.35	0.40
2:B:70:PRO:HG2	2:B:74:ASN:HB2	2.02	0.40
1:A:141:CYS:SG	1:A:191:CYS:CB	3.09	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	200/202 (99%)	177 (88%)	20 (10%)	3 (2%)	10	18
2	B	235/237 (99%)	222 (94%)	11 (5%)	2 (1%)	17	31
All	All	435/439 (99%)	399 (92%)	31 (7%)	5 (1%)	14	26

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	ALA
1	A	175	SER
2	B	153	PHE
1	A	135	SER
2	B	154	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 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	176/176 (100%)	156 (89%)	20 (11%)	5	11
2	B	200/200 (100%)	187 (94%)	13 (6%)	17	33
All	All	376/376 (100%)	343 (91%)	33 (9%)	10	19

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLN
1	A	23	LYS
1	A	40	ARG
1	A	41	GLN
1	A	69	SER
1	A	102	SER
1	A	114	VAL
1	A	134	ARG

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Mol	Chain	Res	Type
1	A	137	ASP
1	A	138	SER
1	A	140	LEU
1	A	168	LEU
1	A	174	ASP
1	A	181	ILE
1	A	198	THR
1	A	203	ASN
1	A	206	TYR
1	A	208	SER
1	A	209	SER
1	A	211	VAL
2	B	24	ASN
2	B	33	TYR
2	B	55	THR
2	B	79	LEU
2	B	87	THR
2	B	105	THR
2	B	146	VAL
2	B	172	VAL
2	B	174	THR
2	B	182	SER
2	B	186	ASN
2	B	197	ARG
2	B	201	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1	GLN
1	A	60	ASN
1	A	74	HIS
1	A	136	GLN
2	B	74	ASN
2	B	86	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 ⓘ

9 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$
3	NAG	C	1	1,3	14,14,15	0.85	0	17,19,21	0.67	0
3	NAG	C	2	3	14,14,15	0.59	0	17,19,21	0.65	0
3	BMA	C	3	3	11,11,12	1.40	2 (18%)	15,15,17	0.82	0
3	FUC	C	4	3	10,10,11	1.03	1 (10%)	14,14,16	1.87	2 (14%)
4	NAG	D	1	1,4	14,14,15	1.08	1 (7%)	17,19,21	0.60	0
4	NAG	D	2	4	14,14,15	0.88	0	17,19,21	0.54	0
4	FUC	D	3	4	10,10,11	1.19	1 (10%)	14,14,16	1.35	2 (14%)
5	NAG	E	1	2,5	14,14,15	0.61	0	17,19,21	0.49	0
5	NAG	E	2	5	14,14,15	0.63	0	17,19,21	0.78	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
3	NAG	C	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	1/2/19/22	0/1/1/1
3	FUC	C	4	3	-	-	0/1/1/1
4	NAG	D	1	1,4	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	FUC	D	3	4	-	-	0/1/1/1
5	NAG	E	1	2,5	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	2/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	3	FUC	C2-C3	2.78	1.56	1.52
4	D	1	NAG	C1-C2	2.70	1.56	1.52
3	C	3	BMA	C2-C3	2.66	1.56	1.52
3	C	3	BMA	C1-C2	2.44	1.57	1.52
3	C	4	FUC	C4-C3	2.18	1.57	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	4	FUC	C6-C5-C4	4.85	122.04	113.07
3	C	4	FUC	C3-C4-C5	3.89	115.83	109.77
4	D	3	FUC	C1-C2-C3	3.38	113.82	109.67
4	D	3	FUC	C6-C5-C4	3.10	118.79	113.07

There are no chirality outliers.

All (3) torsion outliers are listed below:

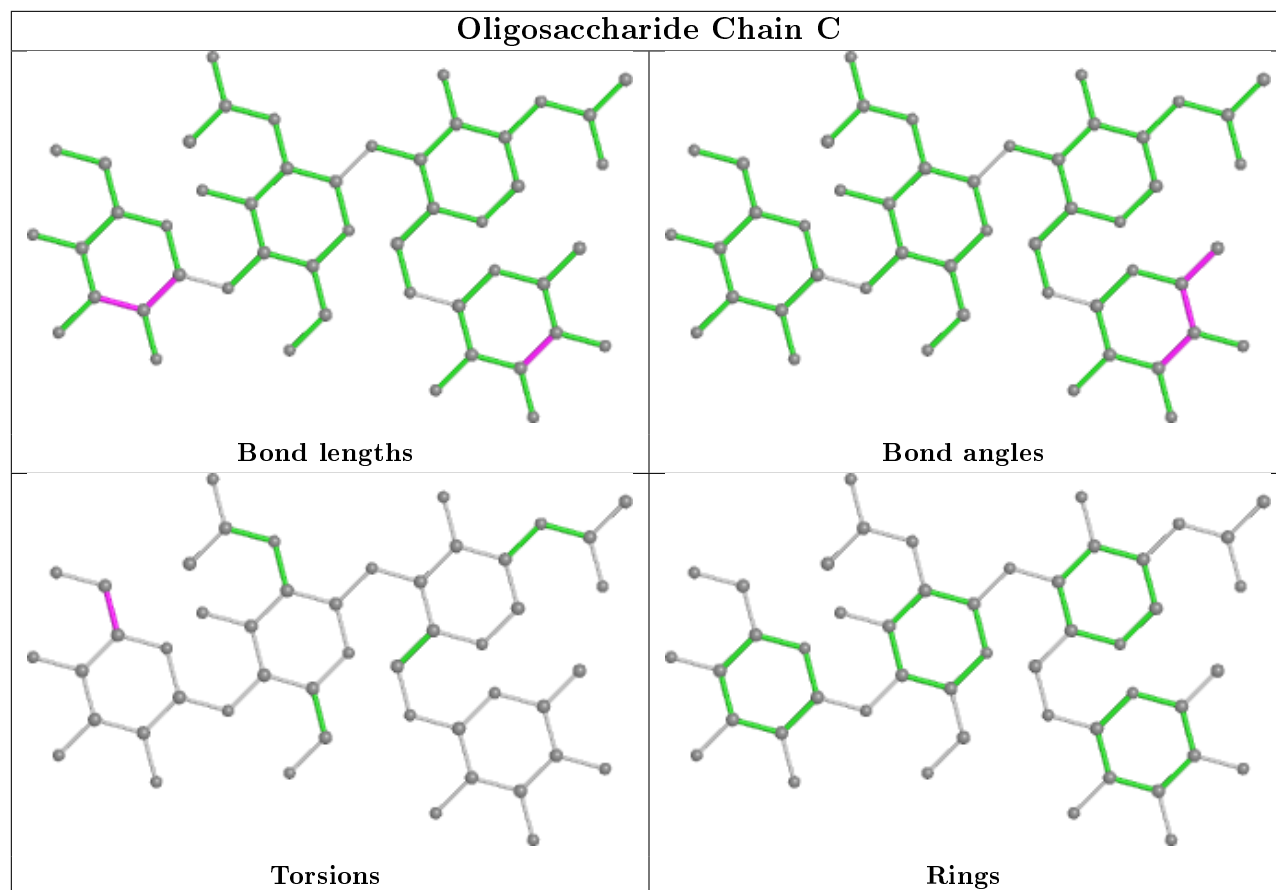
Mol	Chain	Res	Type	Atoms
5	E	2	NAG	O5-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
3	C	3	BMA	O5-C5-C6-O6

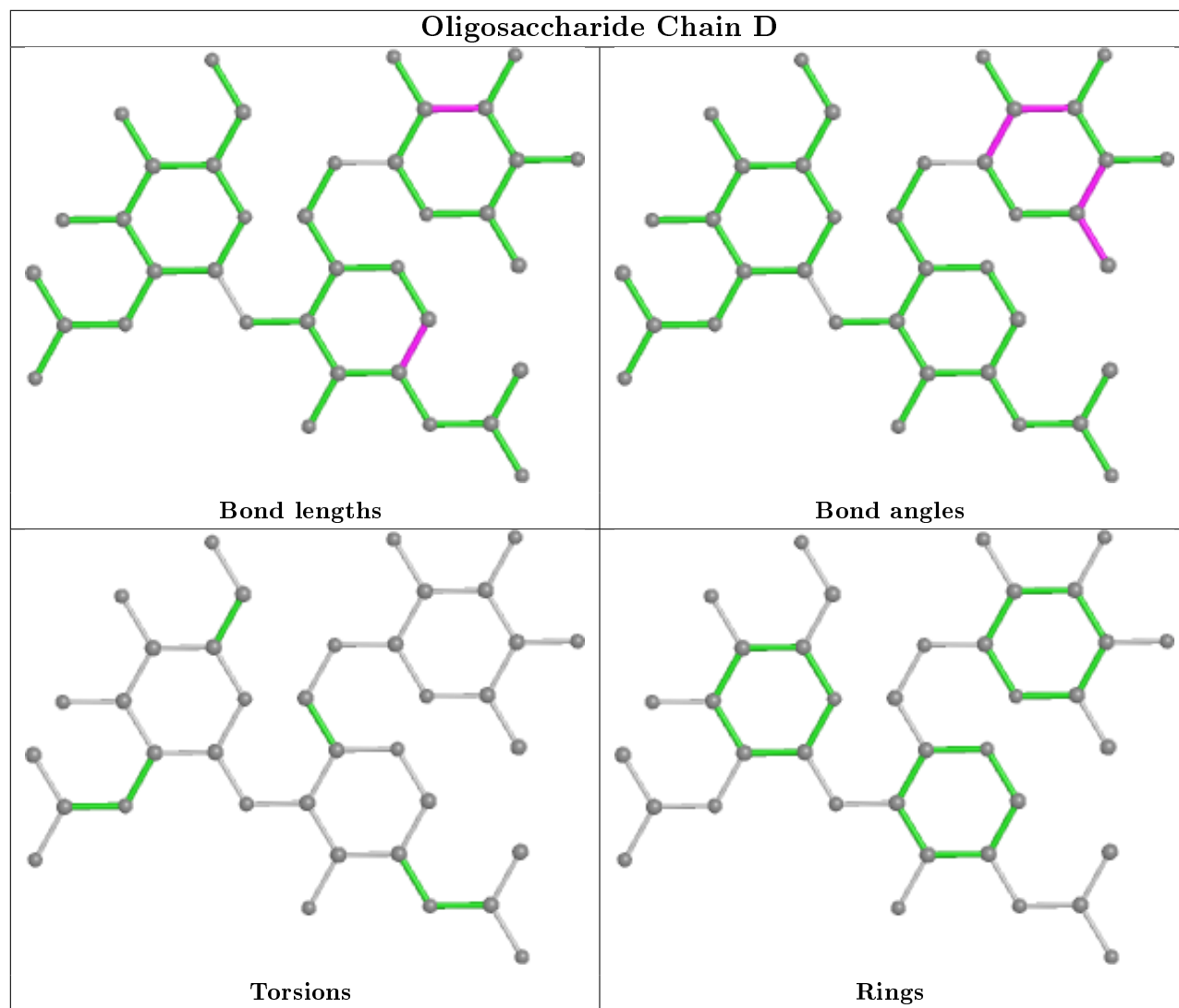
There are no ring outliers.

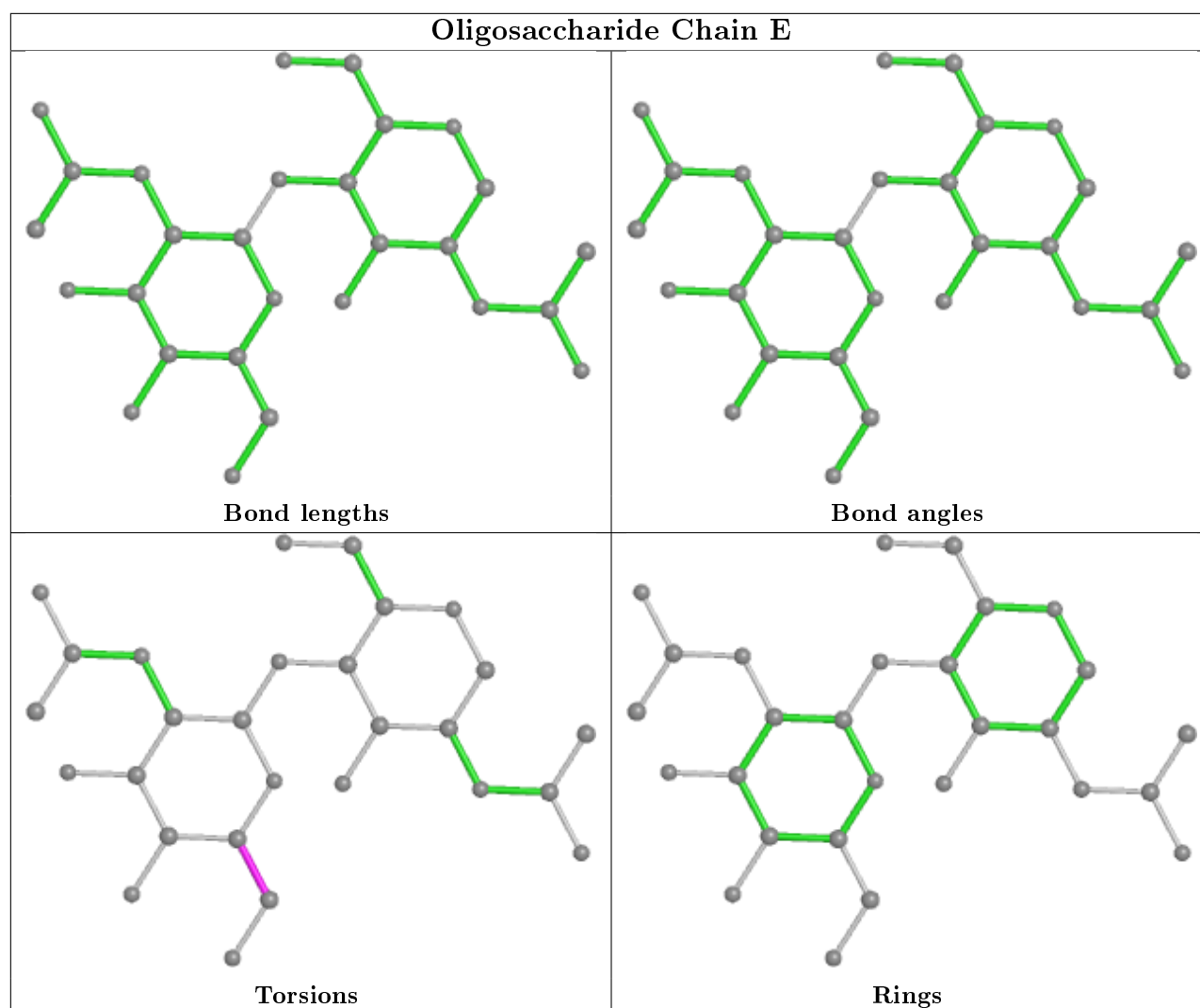
2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1	NAG	2	0
3	C	4	FUC	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 [i](#)

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	$\# Z  > 2$
7	SO4	B	252	-	4,4,4	0.34	0	6,6,6	0.90	0
7	SO4	B	251	-	4,4,4	0.39	0	6,6,6	0.50	0
7	SO4	B	250	-	4,4,4	0.63	0	6,6,6	0.72	0
6	NAG	A	200	1	14,14,15	1.18	2 (14%)	17,19,21	0.85	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
6	NAG	A	200	1	-	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	200	NAG	C1-C2	3.19	1.57	1.52
6	A	200	NAG	C3-C2	2.58	1.58	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	200	NAG	C1-C2-N2-C7
6	A	200	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	251	SO4	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	28:ALA	C	29:THR	N	1.17

## 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.