



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:57 PM UTC

PDB ID : 4Y2D / pdb_00004y2d
Title : Crystal structure of the mCD1d/7DW8-5/iNKTCR ternary complex
Authors : Zajonc, D.M.; Yu, E.D.
Deposited on : 2015-02-09
Resolution : 3.05 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) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

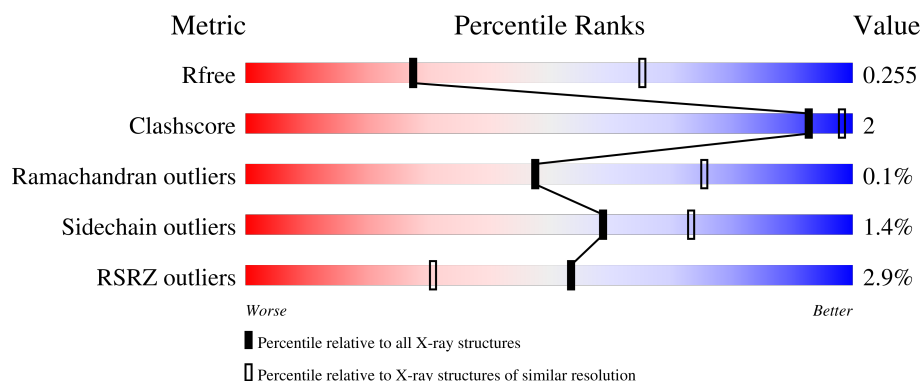
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	285	2% 81% 7% 13%
1	E	285	5% 80% 5% 15%
2	B	99	94%
2	F	99	14% 86% 11%
3	C	209	2% 90% 7%

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Mol	Chain	Length	Quality of chain
3	G	209	% 93%
4	D	241	2% 98%
4	H	241	94% 5%
5	I	2	50% 50%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11943 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 Antigen-presenting glycoprotein CD1d1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1836	1167	308	351	10			
1	E	243	Total	C	N	O	S	0	0	0
			1803	1146	306	340	11			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	HIS	ASP	variant	UNP P11609
A	280	HIS	-	expression tag	UNP P11609
A	281	HIS	-	expression tag	UNP P11609
A	282	HIS	-	expression tag	UNP P11609
A	283	HIS	-	expression tag	UNP P11609
A	284	HIS	-	expression tag	UNP P11609
A	285	HIS	-	expression tag	UNP P11609
E	201	HIS	ASP	variant	UNP P11609
E	280	HIS	-	expression tag	UNP P11609
E	281	HIS	-	expression tag	UNP P11609
E	282	HIS	-	expression tag	UNP P11609
E	283	HIS	-	expression tag	UNP P11609
E	284	HIS	-	expression tag	UNP P11609
E	285	HIS	-	expression tag	UNP P11609

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	97	Total	C	N	O	S	0	0	0
			738	471	126	135	6			
2	F	88	Total	C	N	O	S	0	0	0
			602	378	105	113	6			

- Molecule 3 is a protein called Chimeric TCR Valpha14/Jalpha18 chain (mouse variable do-

main, human constant domain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	202	Total	C	N	O	S	0	0	0
			1501	934	255	305	7			
3	G	202	Total	C	N	O	S	0	0	0
			1491	927	252	304	8			

- Molecule 4 is a protein called Chimeric TCR Vbeta8.2 chain (mouse variable domain, human constant domain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	239	Total	C	N	O	S	0	0	0
			1837	1153	325	353	6			
4	H	239	Total	C	N	O	S	0	0	0
			1819	1142	320	351	6			

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



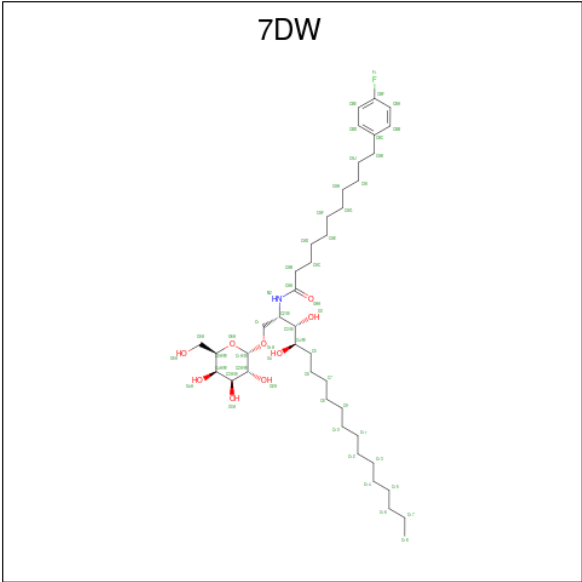
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

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



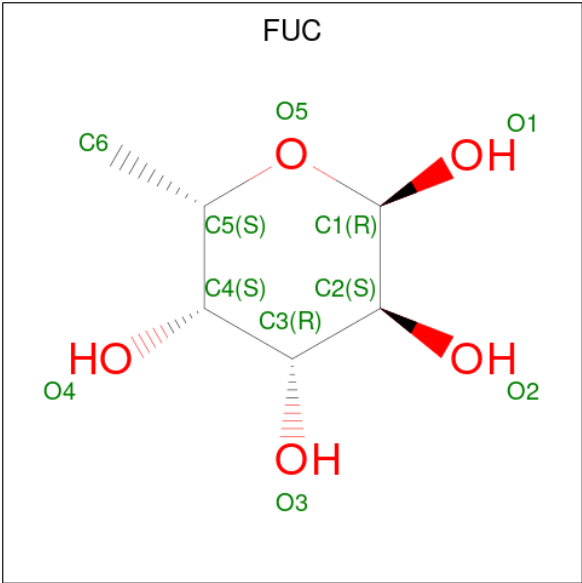
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	E	1	Total	C	N	O	0	0
			14	8	1	5		
6	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 7 is 11-(4-fluorophenyl)-N-[(2S,3S,4R)-1-(alpha-D-galactopyranosyloxy)-3,4-dihydroxyoctadecan-2-yl]undecanamide (CCD ID: 7DW) (formula: C₄₁H₇₂FNO₉).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total 104	C 82	F 2	N 2	O 18	0	1
7	E	1	Total 104	C 82	F 2	N 2	O 18	0	1

- Molecule 8 is alpha-L-fucopyranose (CCD ID: FUC) (formula: C₆H₁₂O₅).

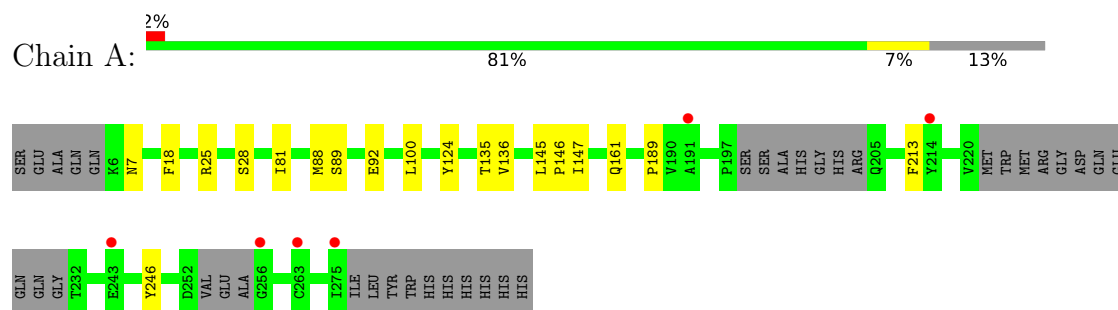


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	E	1	Total	C	O	0	0
			10	6	4		

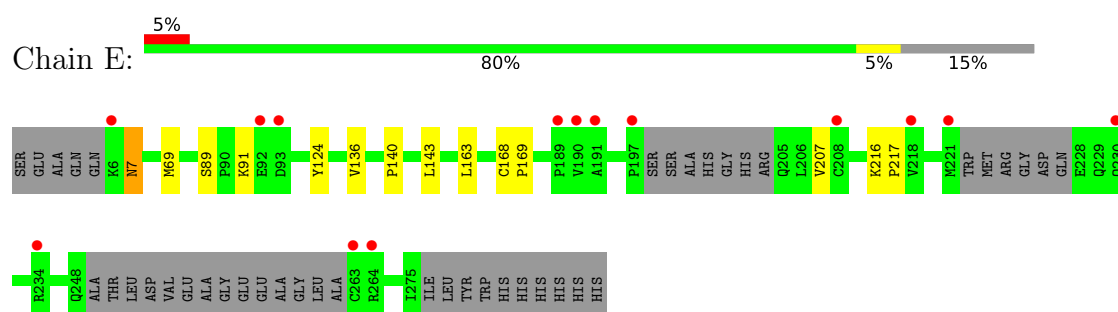
3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

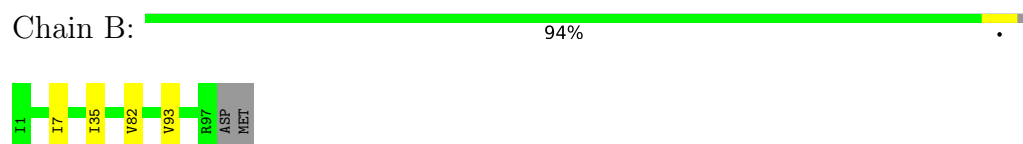
- Molecule 1: Antigen-presenting glycoprotein CD1d1



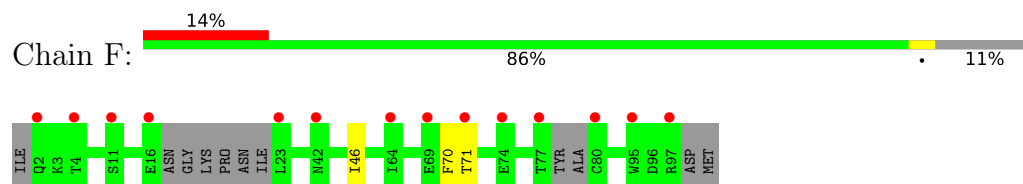
- Molecule 1: Antigen-presenting glycoprotein CD1d1



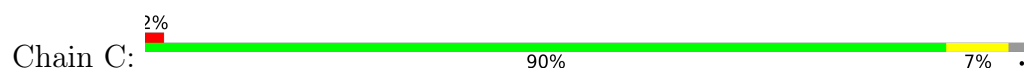
- Molecule 2: Beta-2-microglobulin



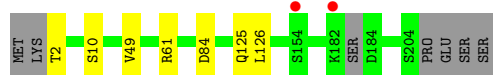
- Molecule 2: Beta-2-microglobulin



- Molecule 3: Chimeric TCR Valpha14/Jalpha18 chain (mouse variable domain, human constant domain)



- Molecule 3: Chimeric TCR Valpha14/Jalpha18 chain (mouse variable domain, human constant domain)



- Molecule 4: Chimeric TCR Vbeta8.2 chain (mouse variable domain, human constant domain)



- Molecule 4: Chimeric TCR Vbeta8.2 chain (mouse variable domain, human constant domain)



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.42Å 150.26Å 100.80Å 90.00° 96.24° 90.00°	Depositor
Resolution (Å)	49.41 – 3.05 49.41 – 3.05	Depositor EDS
% Data completeness (in resolution range)	99.2 (49.41-3.05) 99.2 (49.41-3.05)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 3.07Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.217 , 0.257 0.216 , 0.255	Depositor DCC
R_{free} test set	1388 reflections (3.10%)	wwPDB-VP
Wilson B-factor (Å ²)	67.6	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11943	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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: 7DW, NAG, FUC

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	0.45	0/1888	0.71	0/2586
1	E	0.44	0/1853	0.69	0/2536
2	B	0.44	0/764	0.69	0/1050
2	F	0.48	0/620	0.86	4/851 (0.5%)
3	C	0.45	0/1528	0.67	0/2086
3	G	0.45	0/1518	0.66	0/2076
4	D	0.41	0/1888	0.64	0/2582
4	H	0.43	0/1870	0.66	0/2562
All	All	0.44	0/11929	0.69	4/16329 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	46	ILE	CA-C-N	9.17	128.51	118.97
2	F	46	ILE	C-N-CA	9.17	128.51	118.97
2	F	71	THR	CA-C-N	5.88	125.82	119.76
2	F	71	THR	C-N-CA	5.88	125.82	119.76

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	1836	0	1579	9	0
1	E	1803	0	1576	6	0
2	B	738	0	646	2	0
2	F	602	0	425	0	0
3	C	1501	0	1383	7	0
3	G	1491	0	1345	3	0
4	D	1837	0	1700	1	0
4	H	1819	0	1663	5	0
5	I	28	0	25	0	0
6	A	42	0	39	2	0
6	E	28	0	26	0	0
7	A	104	0	144	0	0
7	E	104	0	144	2	0
8	E	10	0	10	0	0
All	All	11943	0	10705	34	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 2.

All (34) 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)
3:G:61:ARG:NH2	3:G:84:ASP:OD2	2.37	0.58
1:E:7:ASN:N	1:E:7:ASN:OD1	2.37	0.57
3:C:61:ARG:NH2	3:C:84:ASP:OD2	2.39	0.56
7:E:506[A]:7DW:CAI	7:E:506[A]:7DW:H69	2.38	0.52
3:G:2:THR:O	3:G:2:THR:HG23	2.10	0.52
1:A:189:PRO:HB3	1:A:213:PHE:HB3	1.93	0.51
2:B:7:ILE:HB	2:B:93:VAL:HG21	1.94	0.50
4:H:126:GLU:OE2	4:H:239:ARG:NH2	2.45	0.49
1:A:161:GLN:HB3	6:A:302:NAG:H82	1.94	0.48
3:G:125:GLN:C	3:G:126:LEU:HD12	2.38	0.48
4:H:78:LEU:HD23	4:H:85:GLN:CD	2.39	0.47
4:H:21:LEU:HD22	4:H:106:THR:HG21	1.95	0.47
3:C:2:THR:O	3:C:2:THR:HG23	2.15	0.46
4:H:9:ARG:NH2	4:H:104:PRO:HB2	2.31	0.46
3:C:125:GLN:C	3:C:126:LEU:HD12	2.41	0.46
1:A:124:TYR:CZ	1:A:136:VAL:HG11	2.52	0.45
1:A:18:PHE:CE1	1:A:81:ILE:HG21	2.53	0.44
1:A:135:THR:HG23	1:A:147:ILE:HG13	2.00	0.44
1:A:88:MET:CB	1:A:92:GLU:HG2	2.49	0.43
1:A:25:ARG:HB3	6:A:303:NAG:H82	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:506[A]:7DW:CAI	7:E:506[A]:7DW:CBB	2.94	0.42
4:H:140:LEU:N	4:H:140:LEU:HD12	2.35	0.42
3:C:179:TRP:CZ3	4:D:143:LEU:HD11	2.55	0.41
2:B:35:ILE:HD11	2:B:82:VAL:HG11	2.02	0.41
3:C:58:SER:HA	3:C:63:SER:HA	2.02	0.41
3:C:20:VAL:C	3:C:21:LEU:HD12	2.45	0.41
1:E:124:TYR:CZ	1:E:136:VAL:HG11	2.55	0.41
3:C:37:LYS:HB2	3:C:47:LEU:HD11	2.02	0.41
1:A:246:TYR:C	1:A:246:TYR:CD1	2.98	0.41
1:E:216:LYS:N	1:E:217:PRO:HD2	2.36	0.41
1:E:140:PRO:HD2	1:E:143:LEU:HD12	2.02	0.41
1:A:145:LEU:HB3	1:A:146:PRO:HD3	2.03	0.40
1:E:69:MET:HE1	1:E:163:LEU:HD21	2.03	0.40
1:E:168:CYS:HB3	1:E:169:PRO:CD	2.52	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	241/285 (85%)	232 (96%)	9 (4%)	0	100	100
1	E	235/285 (82%)	224 (95%)	10 (4%)	1 (0%)	30	57
2	B	95/99 (96%)	92 (97%)	3 (3%)	0	100	100
2	F	82/99 (83%)	77 (94%)	5 (6%)	0	100	100
3	C	198/209 (95%)	186 (94%)	11 (6%)	1 (0%)	24	52
3	G	198/209 (95%)	189 (96%)	9 (4%)	0	100	100
4	D	237/241 (98%)	233 (98%)	4 (2%)	0	100	100
4	H	237/241 (98%)	228 (96%)	9 (4%)	0	100	100
All	All	1523/1668 (91%)	1461 (96%)	60 (4%)	2 (0%)	48	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	91	LYS
3	C	42	LYS

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	176/249 (71%)	172 (98%)	4 (2%)	44	66
1	E	177/249 (71%)	174 (98%)	3 (2%)	53	71
2	B	74/93 (80%)	74 (100%)	0	100	100
2	F	46/93 (50%)	45 (98%)	1 (2%)	45	67
3	C	163/188 (87%)	162 (99%)	1 (1%)	78	81
3	G	158/188 (84%)	156 (99%)	2 (1%)	61	74
4	D	193/208 (93%)	191 (99%)	2 (1%)	68	77
4	H	189/208 (91%)	186 (98%)	3 (2%)	55	72
All	All	1176/1476 (80%)	1160 (99%)	16 (1%)	59	73

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	28	SER
1	A	89	SER
1	A	100	LEU
3	C	10	SER
4	D	25	GLN
4	D	132	ILE
1	E	7	ASN
1	E	89	SER
1	E	207	VAL
2	F	70	PHE
3	G	10	SER

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Mol	Chain	Res	Type
3	G	49	VAL
4	H	25	GLN
4	H	116	ASN
4	H	172	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	67	HIS
3	C	22	GLN
3	C	24	ASN
3	C	38	GLN
4	D	37	GLN
4	D	136	GLN
4	D	222	GLN
1	E	68	HIS
2	F	31	HIS
3	G	38	GLN
4	H	37	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

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
5	NAG	I	1	1,5	14,14,15	0.53	0	17,19,21	0.94	0
5	NAG	I	2	5	14,14,15	0.44	0	17,19,21	1.12	1 (5%)

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	NAG	I	1	1,5	-	2/6/23/26	0/1/1/1
5	NAG	I	2	5	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	2	NAG	C1-O5-C5	3.05	116.27	112.19

There are no chirality outliers.

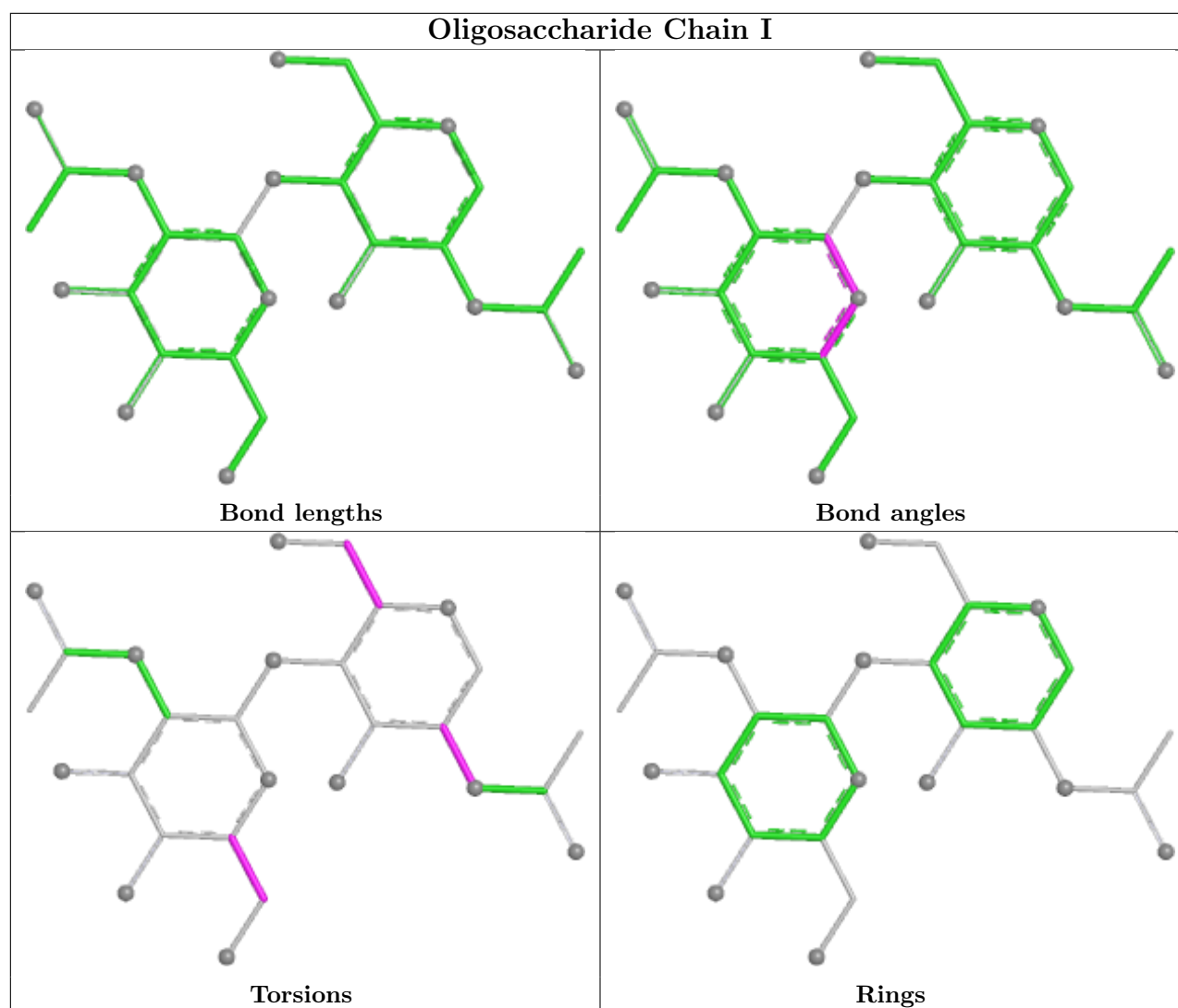
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	I	2	NAG	O5-C5-C6-O6
5	I	2	NAG	C4-C5-C6-O6
5	I	1	NAG	O5-C5-C6-O6
5	I	1	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 [i](#)

10 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	7DW	E	506[B]	-	53,53,53	0.96	3 (5%)	62,65,65	1.33	5 (8%)
6	NAG	E	504	1	14,14,15	0.51	0	17,19,21	1.49	1 (5%)
6	NAG	A	301	1	14,14,15	0.50	0	17,19,21	1.74	5 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	7DW	A	304[B]	-	53,53,53	0.96	3 (5%)	62,65,65	1.27	5 (8%)
7	7DW	A	304[A]	-	53,53,53	0.87	2 (3%)	62,65,65	1.37	7 (11%)
7	7DW	E	506[A]	-	53,53,53	0.85	2 (3%)	62,65,65	1.40	7 (11%)
8	FUC	E	503	-	10,10,11	0.68	0	14,14,16	0.80	0
6	NAG	E	505	1	14,14,15	0.54	0	17,19,21	1.14	1 (5%)
6	NAG	A	303	1	14,14,15	0.53	0	17,19,21	1.45	1 (5%)
6	NAG	A	302	1	14,14,15	0.56	0	17,19,21	1.02	1 (5%)

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
7	7DW	E	506[B]	-	-	19/46/66/66	0/2/2/2
6	NAG	E	504	1	-	2/6/23/26	0/1/1/1
6	NAG	A	301	1	-	6/6/23/26	0/1/1/1
7	7DW	A	304[B]	-	-	20/46/66/66	0/2/2/2
7	7DW	A	304[A]	-	-	22/46/66/66	0/2/2/2
7	7DW	E	506[A]	-	-	18/46/66/66	0/2/2/2
8	FUC	E	503	-	-	-	0/1/1/1
6	NAG	E	505	1	-	2/6/23/26	0/1/1/1
6	NAG	A	303	1	-	2/6/23/26	0/1/1/1
6	NAG	A	302	1	-	1/6/23/26	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	506[B]	7DW	CAK-CBC	-4.63	1.38	1.51
7	A	304[A]	7DW	CAK-CBC	-4.51	1.39	1.51
7	A	304[B]	7DW	CAK-CBC	-4.47	1.39	1.51
7	E	506[A]	7DW	CAK-CBC	-4.36	1.39	1.51
7	E	506[B]	7DW	F1-CBF	-3.19	1.28	1.36
7	A	304[A]	7DW	O1A-C1A	3.06	1.45	1.40
7	A	304[B]	7DW	O1A-C1A	3.01	1.45	1.40
7	E	506[A]	7DW	O1A-C1A	2.99	1.45	1.40
7	E	506[B]	7DW	O1A-C1A	2.78	1.44	1.40
7	A	304[B]	7DW	F1-CBF	-2.71	1.29	1.36

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	E	506[A]	7DW	C6-C5-C4	-6.43	103.57	114.11
7	E	506[B]	7DW	C6-C5-C4	-5.90	104.45	114.11
7	A	304[A]	7DW	C6-C5-C4	-5.62	104.90	114.11
6	E	504	NAG	C1-O5-C5	5.30	119.28	112.19
6	A	303	NAG	C1-O5-C5	5.10	119.03	112.19
7	A	304[B]	7DW	C6-C5-C4	-5.01	105.90	114.11
6	A	301	NAG	C2-N2-C7	3.62	127.75	122.90
6	A	301	NAG	C8-C7-N2	3.21	121.44	116.12
6	E	505	NAG	C4-C3-C2	3.08	115.53	111.02
7	E	506[B]	7DW	C5-C4-C3	-3.07	109.11	113.97
7	E	506[A]	7DW	C5-C4-C3	-2.87	109.42	113.97
7	E	506[B]	7DW	C1A-O6A-C5A	-2.69	108.47	113.72
7	E	506[A]	7DW	O5A-C6A-C5A	-2.66	102.28	111.33
7	A	304[B]	7DW	C5-C4-C3	-2.62	109.82	113.97
7	A	304[B]	7DW	C7-C6-C5	-2.61	103.79	113.62
6	A	301	NAG	C4-C3-C2	-2.58	107.24	111.02
7	A	304[A]	7DW	O5A-C6A-C5A	-2.56	102.61	111.33
6	A	301	NAG	O5-C1-C2	-2.51	107.40	111.29
7	A	304[A]	7DW	C7-C6-C5	-2.50	104.19	113.62
7	E	506[B]	7DW	C7-C6-C5	-2.48	104.27	113.62
7	A	304[A]	7DW	C5-C4-C3	-2.43	110.12	113.97
7	E	506[A]	7DW	C7-C6-C5	-2.42	104.48	113.62
7	E	506[A]	7DW	CBE-CBF-CBA	-2.33	119.75	122.80
7	A	304[A]	7DW	CBE-CBF-CBA	-2.31	119.77	122.80
7	A	304[B]	7DW	C1-C2-C3	-2.29	108.21	112.71
6	A	302	NAG	O7-C7-C8	-2.16	118.21	122.05
7	A	304[B]	7DW	CBE-CBF-CBA	-2.12	120.02	122.80
7	E	506[A]	7DW	C1-O1A-C1A	-2.11	109.28	113.80
7	A	304[A]	7DW	C6-C7-C8	-2.10	103.76	114.37
6	A	301	NAG	C1-O5-C5	2.10	114.99	112.19
7	E	506[A]	7DW	C6-C7-C8	-2.09	103.80	114.37
7	A	304[A]	7DW	C1-C2-C3	-2.06	108.65	112.71
7	E	506[B]	7DW	C6-C7-C8	-2.06	103.97	114.37

There are no chirality outliers.

All (92) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	304[A]	7DW	O4-C4-C5-C6
7	A	304[A]	7DW	N2-C2-C3-O3
7	A	304[B]	7DW	O4-C4-C5-C6

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Mol	Chain	Res	Type	Atoms
7	E	506[A]	7DW	O4-C4-C5-C6
7	E	506[B]	7DW	O4-C4-C5-C6
7	E	506[A]	7DW	CAA-CAB-CAC-CAD
7	E	506[B]	7DW	CAA-CAB-CAC-CAD
7	A	304[B]	7DW	O6A-C5A-C6A-O5A
7	E	506[B]	7DW	O6A-C5A-C6A-O5A
7	A	304[B]	7DW	C4A-C5A-C6A-O5A
6	A	301	NAG	O5-C5-C6-O6
6	E	504	NAG	O5-C5-C6-O6
7	A	304[A]	7DW	CAA-CAB-CAC-CAD
6	A	301	NAG	C4-C5-C6-O6
6	E	504	NAG	C4-C5-C6-O6
7	A	304[B]	7DW	CAI-CAJ-CAK-CBC
6	A	301	NAG	C8-C7-N2-C2
6	A	301	NAG	O7-C7-N2-C2
7	E	506[B]	7DW	C4A-C5A-C6A-O5A
6	A	303	NAG	C4-C5-C6-O6
6	E	505	NAG	O5-C5-C6-O6
6	E	505	NAG	C4-C5-C6-O6
7	E	506[B]	7DW	CAI-CAJ-CAK-CBC
6	A	303	NAG	O5-C5-C6-O6
7	A	304[B]	7DW	CAA-CAB-CAC-CAD
7	A	304[A]	7DW	C12-C13-C14-C15
7	A	304[A]	7DW	CAC-CAD-CAE-CAF
7	A	304[B]	7DW	CAF-CAG-CAH-CAI
7	E	506[A]	7DW	CAG-CAH-CAI-CAJ
7	A	304[A]	7DW	C14-C15-C16-C17
7	E	506[B]	7DW	CAD-CAE-CAF-CAG
7	A	304[B]	7DW	CAH-CAI-CAJ-CAK
7	E	506[B]	7DW	CAB-CAC-CAD-CAE
7	A	304[B]	7DW	CAC-CAD-CAE-CAF
7	A	304[A]	7DW	CAB-CAC-CAD-CAE
7	E	506[A]	7DW	CAH-CAI-CAJ-CAK
7	E	506[A]	7DW	CAB-CAC-CAD-CAE
7	A	304[B]	7DW	C12-C13-C14-C15
7	E	506[A]	7DW	C5-C6-C7-C8
7	E	506[A]	7DW	CAF-CAG-CAH-CAI
7	E	506[A]	7DW	C7-C8-C9-C10
7	A	304[A]	7DW	CAI-CAJ-CAK-CBC
7	E	506[B]	7DW	C7-C8-C9-C10
7	E	506[B]	7DW	C5-C6-C7-C8
7	A	304[B]	7DW	CAD-CAE-CAF-CAG

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Mol	Chain	Res	Type	Atoms
7	A	304[A]	7DW	C7-C8-C9-C10
7	E	506[B]	7DW	C9-C10-C11-C12
7	A	304[B]	7DW	C14-C15-C16-C17
7	E	506[A]	7DW	C14-C15-C16-C17
7	E	506[B]	7DW	C14-C15-C16-C17
7	E	506[A]	7DW	C9-C10-C11-C12
7	A	304[A]	7DW	C5-C6-C7-C8
7	E	506[B]	7DW	CAH-CAI-CAJ-CAK
7	E	506[A]	7DW	C11-C12-C13-C14
7	A	304[B]	7DW	C7-C8-C9-C10
7	A	304[A]	7DW	CAF-CAG-CAH-CAI
7	A	304[B]	7DW	C9-C10-C11-C12
7	A	304[B]	7DW	C11-C10-C9-C8
7	E	506[B]	7DW	C12-C13-C14-C15
7	E	506[B]	7DW	C11-C12-C13-C14
7	A	304[A]	7DW	C11-C10-C9-C8
7	A	304[A]	7DW	C9-C10-C11-C12
7	E	506[A]	7DW	C12-C13-C14-C15
7	A	304[A]	7DW	C13-C14-C15-C16
7	A	304[A]	7DW	C3-C4-C5-C6
7	E	506[B]	7DW	CAE-CAF-CAG-CAH
7	A	304[B]	7DW	C5-C6-C7-C8
7	E	506[B]	7DW	CAF-CAG-CAH-CAI
7	A	304[B]	7DW	C6-C7-C8-C9
6	A	302	NAG	C4-C5-C6-O6
7	E	506[A]	7DW	C13-C14-C15-C16
7	E	506[A]	7DW	CAC-CAD-CAE-CAF
7	A	304[A]	7DW	CAG-CAH-CAI-CAJ
7	A	304[B]	7DW	CAB-CAC-CAD-CAE
7	A	304[B]	7DW	CAG-CAH-CAI-CAJ
7	A	304[A]	7DW	C10-C11-C12-C13
7	E	506[B]	7DW	C13-C14-C15-C16
7	E	506[A]	7DW	C3-C4-C5-C6
7	A	304[A]	7DW	C11-C12-C13-C14
6	A	301	NAG	C1-C2-N2-C7
7	A	304[A]	7DW	CAJ-CAK-CBC-CBB
7	A	304[B]	7DW	C2-C3-C4-C5
7	E	506[A]	7DW	CAJ-CAK-CBC-CBB
6	A	301	NAG	C3-C2-N2-C7
7	E	506[A]	7DW	CAJ-CAK-CBC-CBD
7	A	304[A]	7DW	CAJ-CAK-CBC-CBD
7	E	506[B]	7DW	C3-C4-C5-C6

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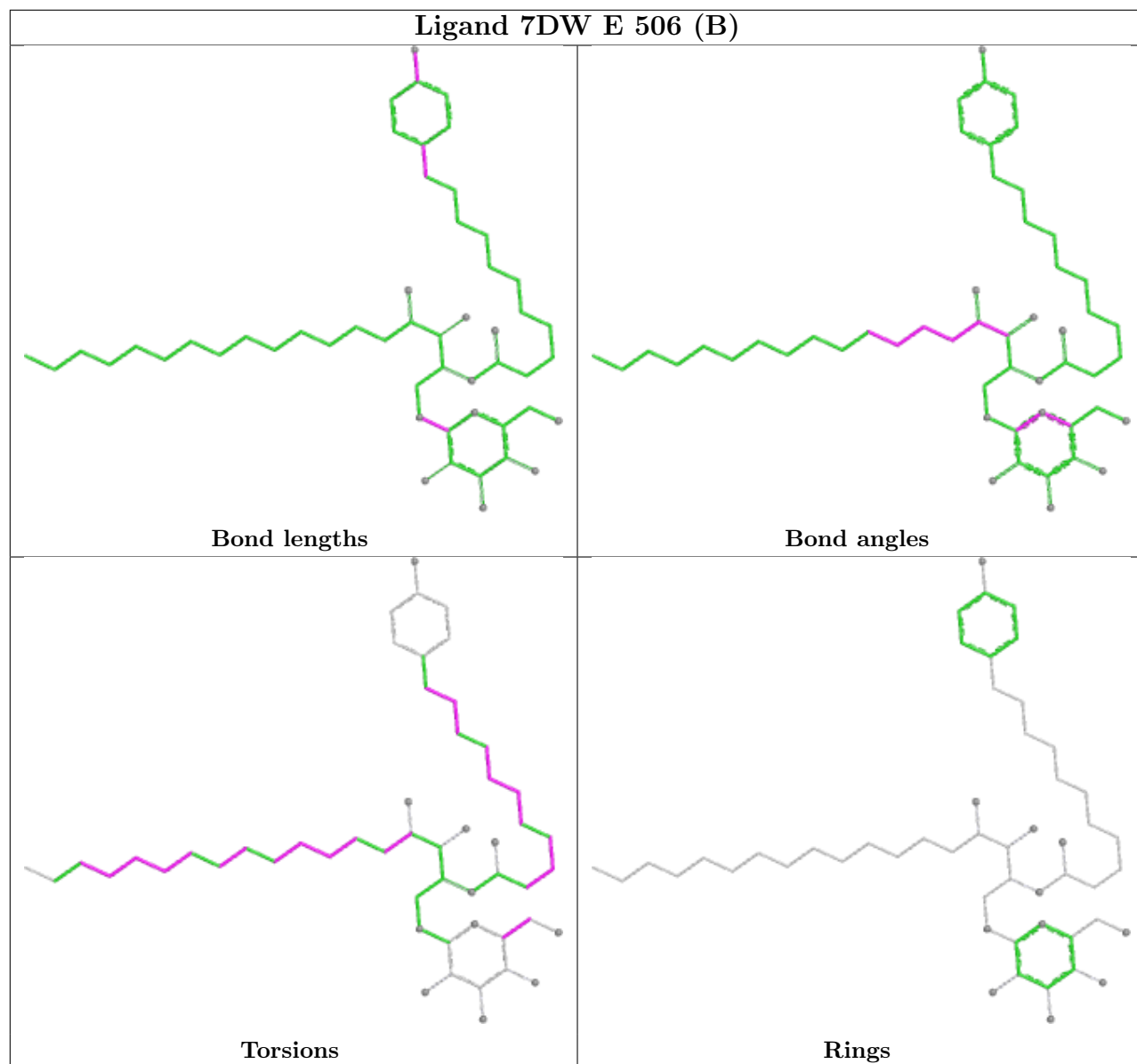
Mol	Chain	Res	Type	Atoms
7	E	506[A]	7DW	C15-C16-C17-C18
7	E	506[B]	7DW	C6-C7-C8-C9
7	A	304[A]	7DW	C4-C5-C6-C7
7	A	304[B]	7DW	OAA-CAA-CAB-CAC
7	A	304[A]	7DW	C6-C7-C8-C9

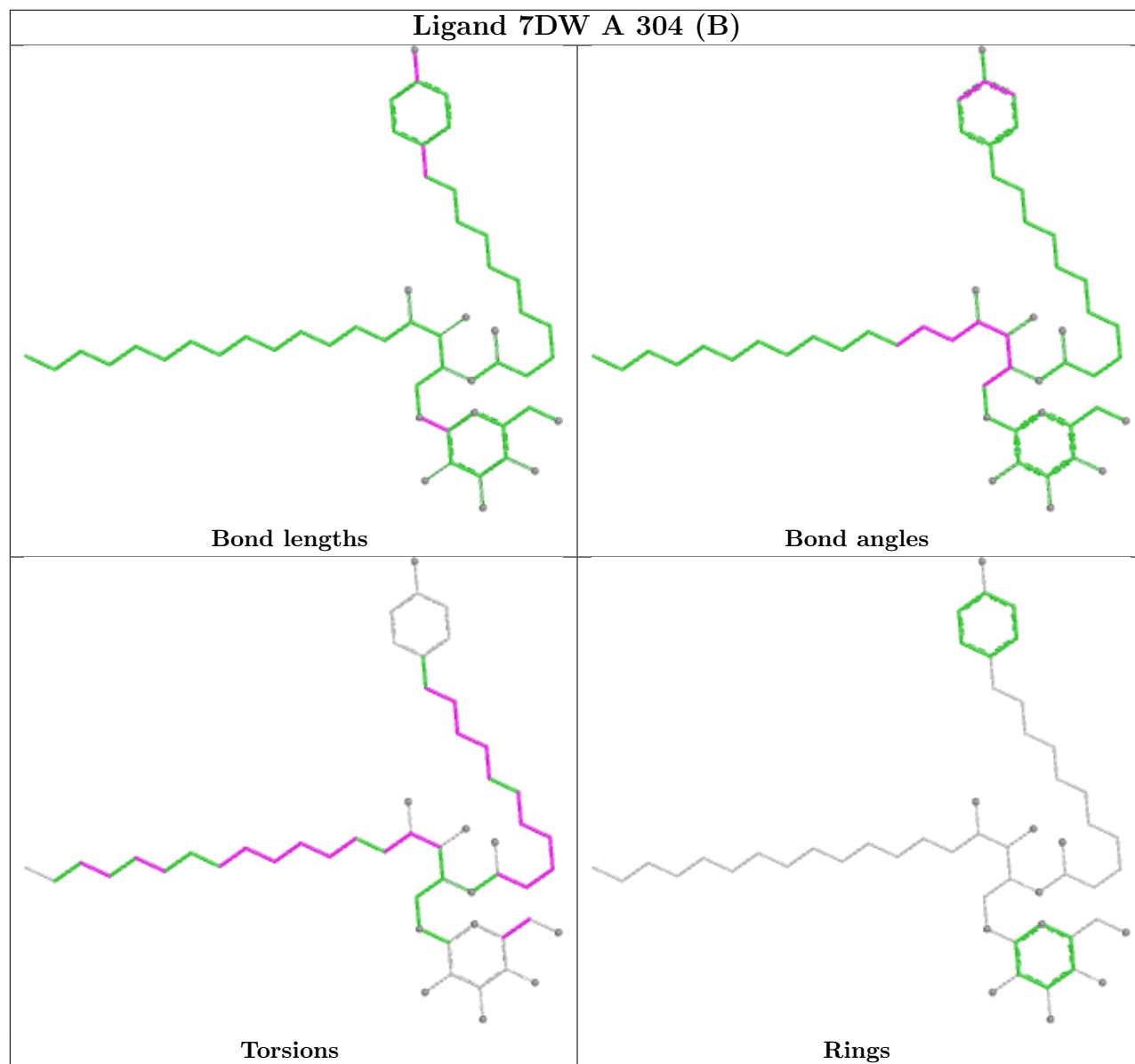
There are no ring outliers.

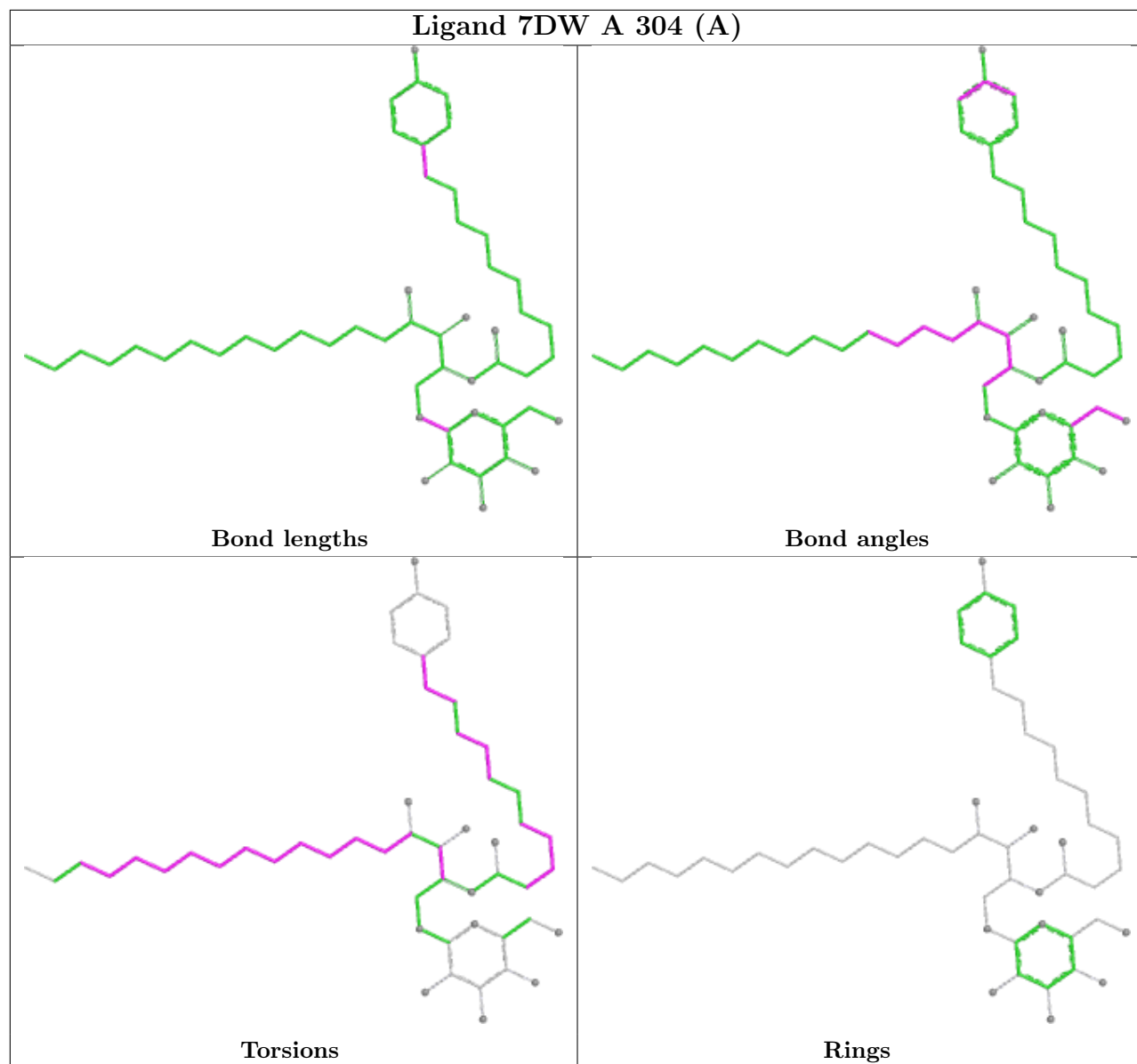
3 monomers are involved in 4 short contacts:

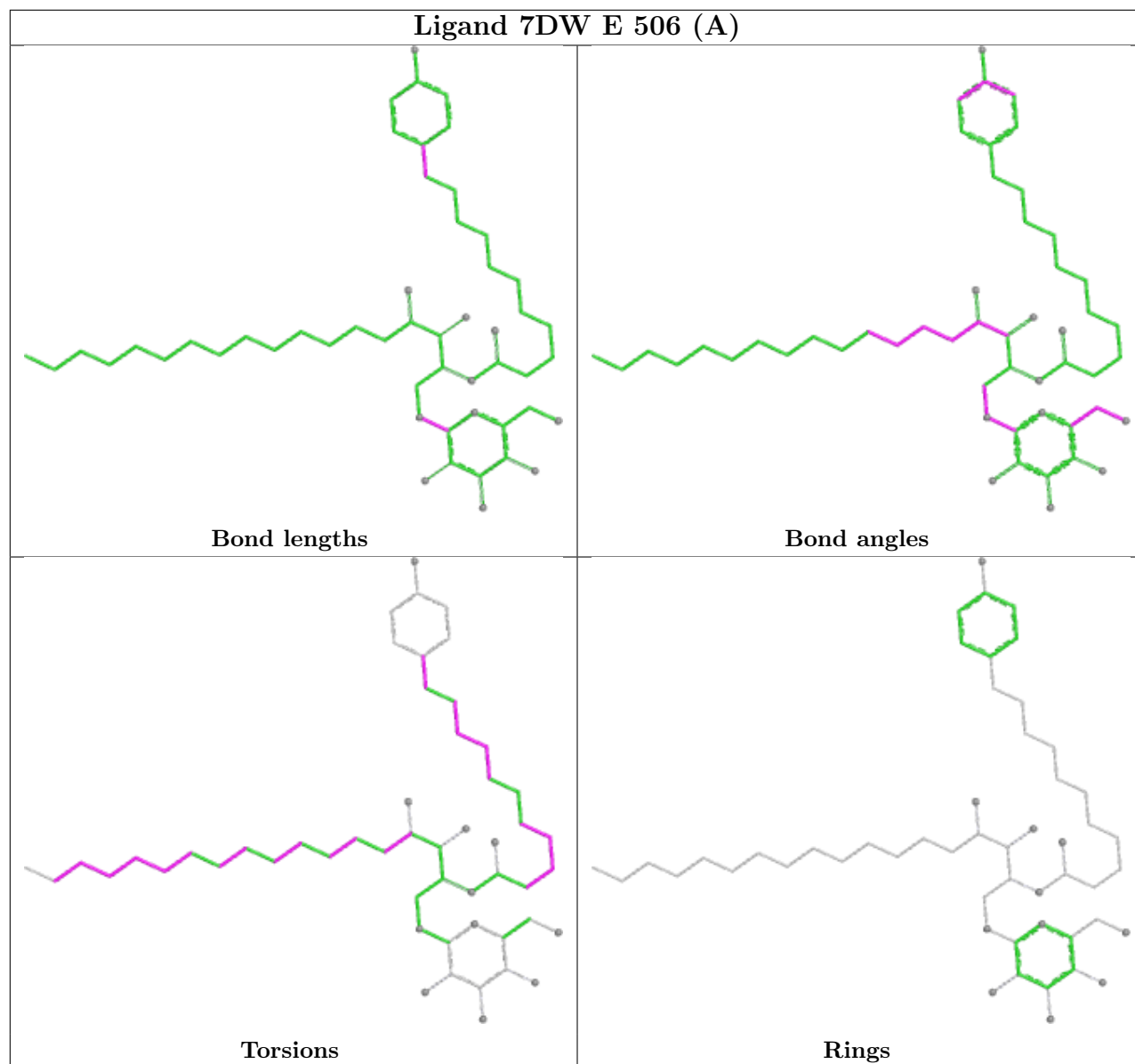
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	506[A]	7DW	2	0
6	A	303	NAG	1	0
6	A	302	NAG	1	0

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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	249/285 (87%)	0.21	6 (2%) 59 37	46, 76, 138, 178	0
1	E	243/285 (85%)	0.27	14 (5%) 29 15	46, 80, 132, 157	0
2	B	97/99 (97%)	-0.06	0 100 100	57, 76, 112, 115	0
2	F	88/99 (88%)	1.11	14 (15%) 5 2	88, 118, 145, 154	0
3	C	202/209 (96%)	-0.03	4 (1%) 65 42	44, 60, 107, 124	0
3	G	202/209 (96%)	-0.11	2 (0%) 79 59	42, 62, 117, 134	0
4	D	239/241 (99%)	-0.09	4 (1%) 69 46	48, 66, 100, 134	0
4	H	239/241 (99%)	-0.14	1 (0%) 88 75	44, 64, 96, 120	0
All	All	1559/1668 (93%)	0.08	45 (2%) 53 31	42, 70, 127, 178	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	191	ALA	4.7
1	A	263	CYS	3.8
2	F	42	ASN	3.7
1	E	6	LYS	3.6
1	E	208	CYS	3.5
4	H	2	ALA	3.4
1	A	256	GLY	3.2
1	A	191	ALA	3.2
2	F	16	GLU	3.2
1	E	197	PRO	3.0
2	F	71	THR	3.0
2	F	77	THR	3.0
4	D	179	ALA	3.0
2	F	80	CYS	3.0
4	D	181	ASN	2.8
1	E	189	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
2	F	74	GLU	2.8
4	D	2	ALA	2.7
2	F	4	THR	2.7
3	C	184	ASP	2.7
1	E	234	ARG	2.6
2	F	23	LEU	2.5
4	D	182	ASP	2.5
1	E	264	ARG	2.5
3	C	153	ASP	2.5
2	F	97	ARG	2.4
1	E	263	CYS	2.4
1	E	190	VAL	2.3
2	F	95	TRP	2.3
1	E	93	ASP	2.2
2	F	64	ILE	2.2
2	F	11	SER	2.2
2	F	69	GLU	2.2
3	G	154	SER	2.1
1	A	214	TYR	2.1
3	C	152	LYS	2.1
1	A	275	ILE	2.1
1	E	221	MET	2.1
2	F	2	GLN	2.1
1	E	218	VAL	2.0
3	C	53	GLN	2.0
1	A	243	GLU	2.0
1	E	92	GLU	2.0
3	G	182	LYS	2.0
1	E	230	GLN	2.0

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

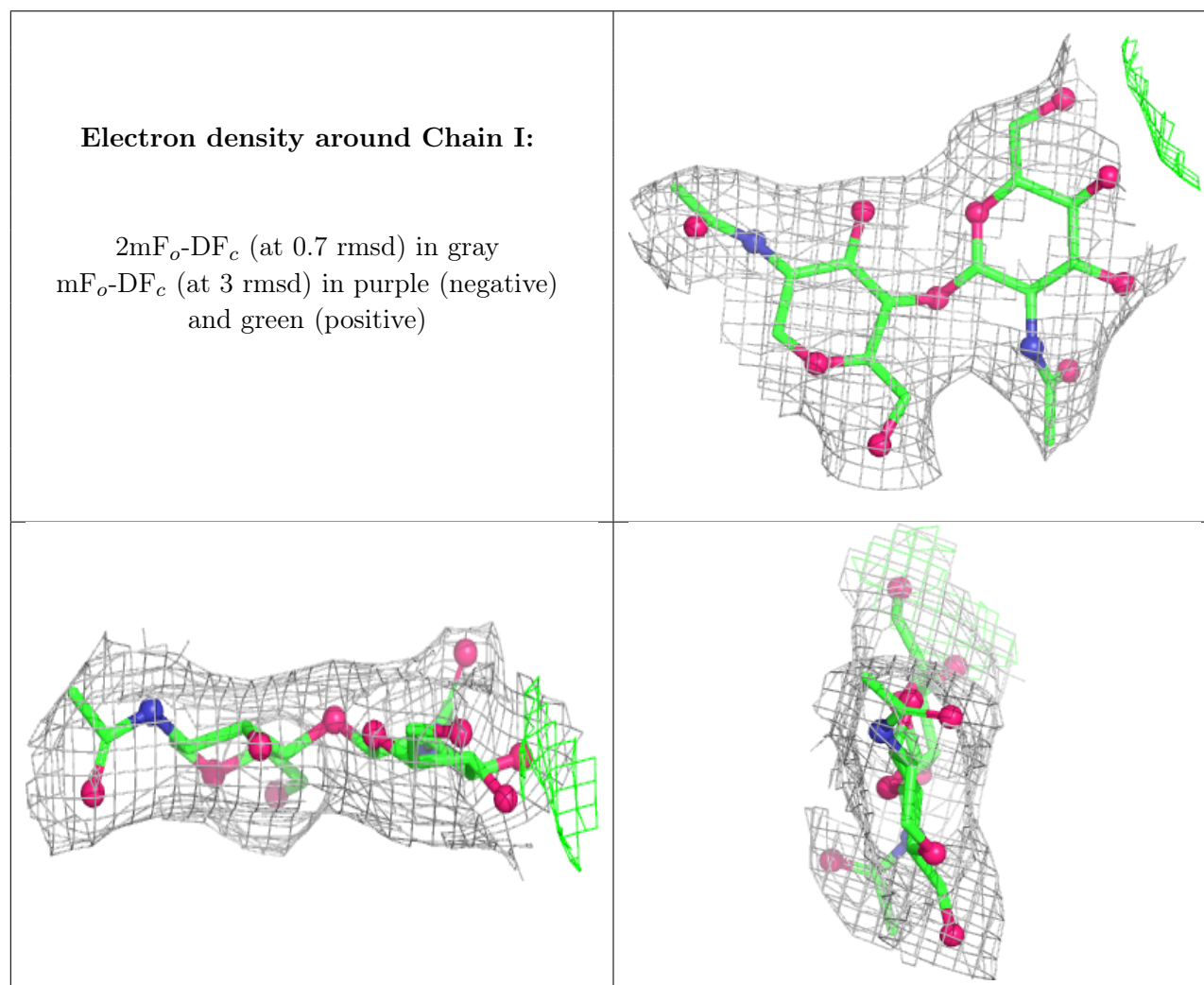
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	I	2	14/15	0.83	0.10	80,83,89,91	0
5	NAG	I	1	14/15	0.95	0.07	73,75,77,78	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.



6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

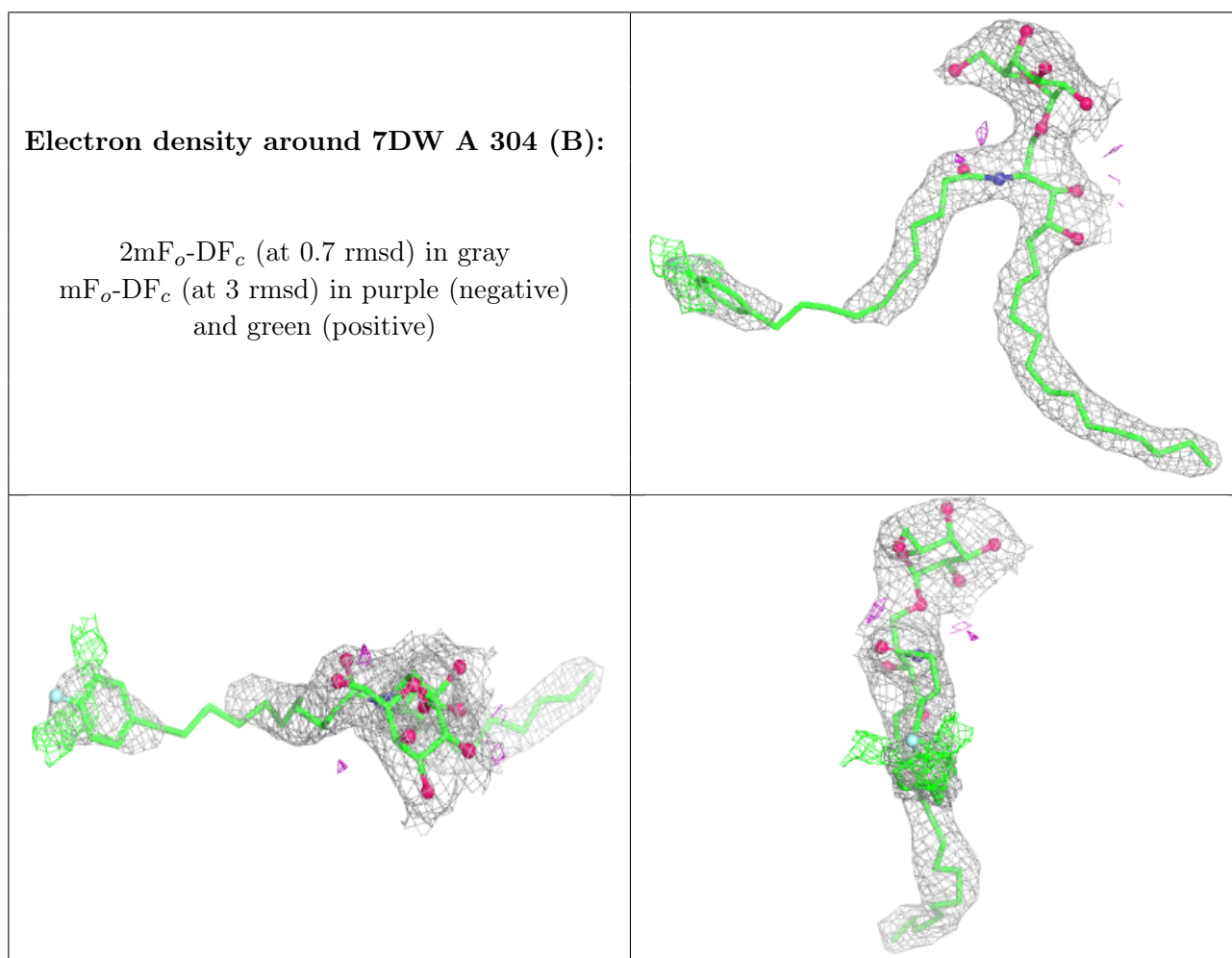
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	E	505	14/15	0.72	0.16	151,161,173,177	0
6	NAG	A	301	14/15	0.76	0.14	128,137,149,154	0

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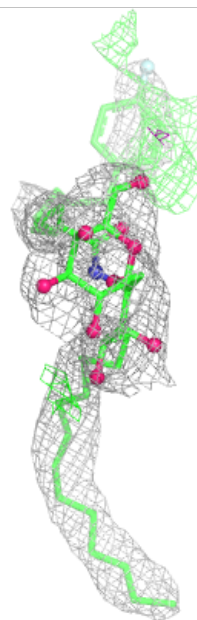
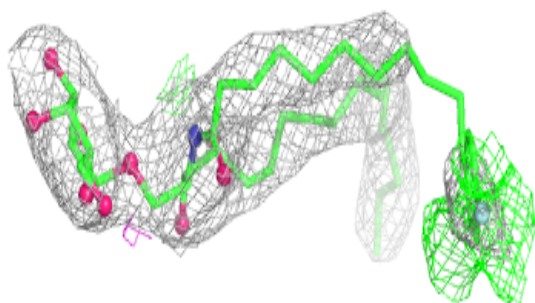
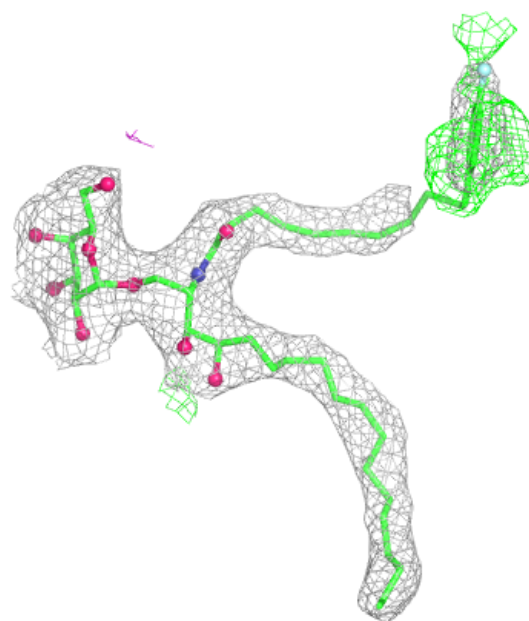
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	NAG	A	303	14/15	0.87	0.10	64,67,70,70	0
6	NAG	E	504	14/15	0.88	0.09	74,77,84,84	0
6	NAG	A	302	14/15	0.88	0.09	66,67,69,71	0
8	FUC	E	503	10/11	0.89	0.13	86,91,96,100	0
7	7DW	A	304[B]	52/52	0.90	0.19	47,50,58,62	52
7	7DW	E	506[A]	52/52	0.90	0.17	43,48,59,61	52
7	7DW	E	506[B]	52/52	0.90	0.17	43,47,58,61	52
7	7DW	A	304[A]	52/52	0.90	0.19	47,52,57,60	52

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



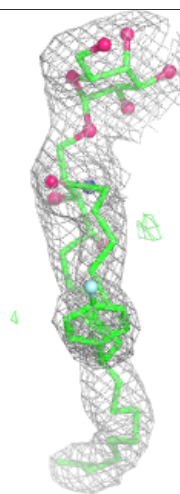
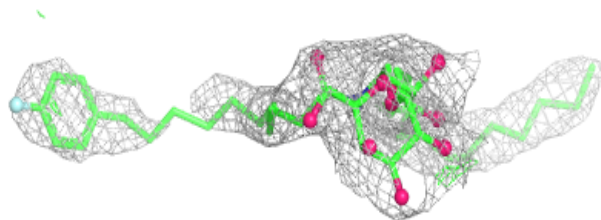
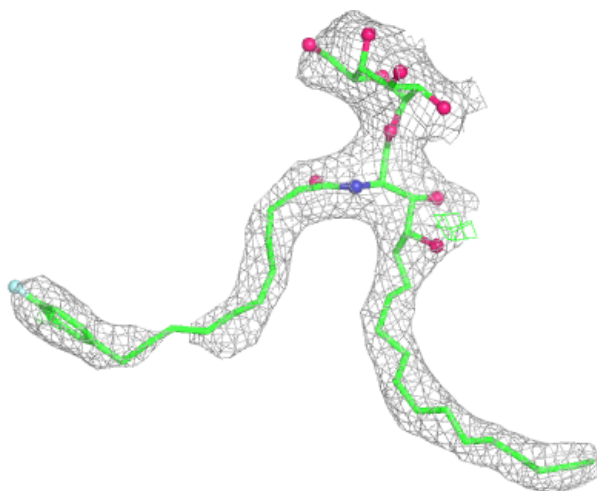
Electron density around 7DW E 506 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



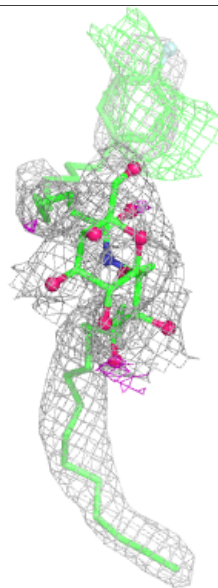
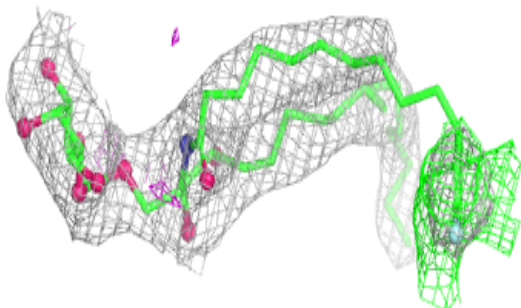
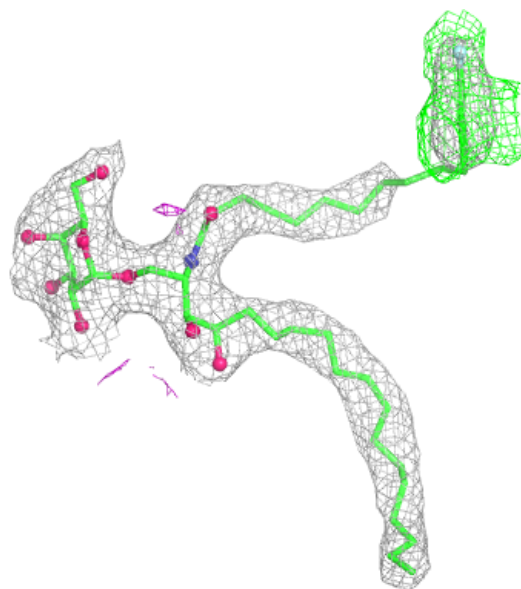
Electron density around 7DW E 506 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around 7DW A 304 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.