



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:13 AM UTC

PDB ID : 5HVG / pdb_00005hvg
Title : Crystal Structure of Thrombin-activatable Fibrinolysis Inhibitor in Complex with an Inhibitory Nanobody (VHH-a204)
Authors : Zhou, X.; Weeks, S.D.; Strelkov, S.V.; Declerck, P.J.
Deposited on : 2016-01-28
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
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

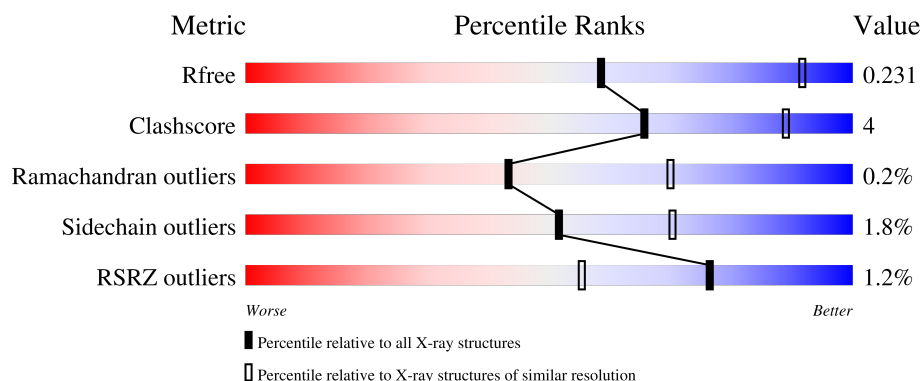
1 Overall quality at a glance

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	401	2% 90% 9%
1	C	401	89% 10%
2	B	128	2% 81% 12% • 5%
2	D	128	• 80% 10% • 7%
3	E	5	40% 60%

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Mol	Chain	Length	Quality of chain
4	F	2	50% 50%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8485 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 Carboxypeptidase B2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	0	0
			3253	2089	552	599	13			
1	C	400	Total	C	N	O	S	0	0	0
			3242	2080	551	598	13			

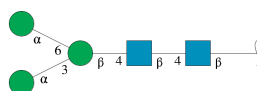
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	CYS	SER	engineered mutation	UNP Q96IY4
A	329	ILE	THR	engineered mutation	UNP Q96IY4
A	333	TYR	HIS	engineered mutation	UNP Q96IY4
A	335	GLN	HIS	engineered mutation	UNP Q96IY4
C	305	CYS	SER	engineered mutation	UNP Q96IY4
C	329	ILE	THR	engineered mutation	UNP Q96IY4
C	333	TYR	HIS	engineered mutation	UNP Q96IY4
C	335	GLN	HIS	engineered mutation	UNP Q96IY4

- Molecule 2 is a protein called VHH-a204.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	122	Total	C	N	O	S	0	0	0
			928	576	162	186	4			
2	D	119	Total	C	N	O	S	0	0	0
			907	565	158	180	4			

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



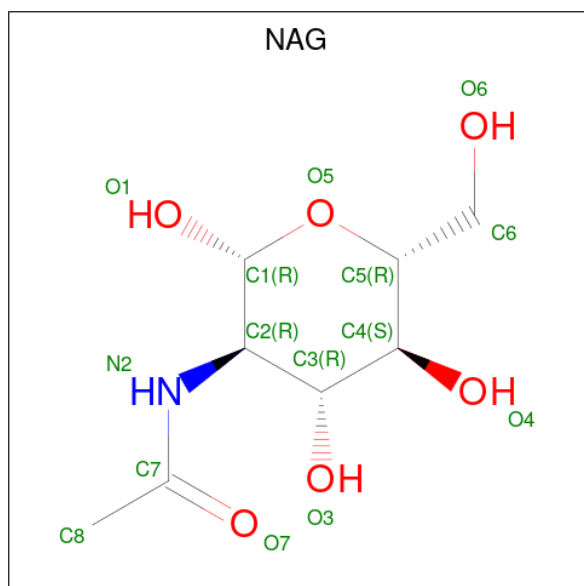
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	5	Total	C	N	O	0	0	0
			61	34	2	25			

- 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				ZeroOcc	AltConf	Trace
4	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

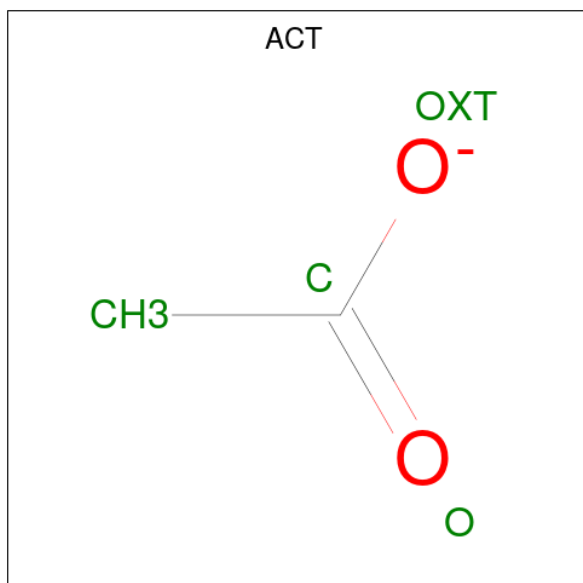


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Zn	0	0
			1	1		
6	C	1	Total	Zn	0	0
			1	1		

- Molecule 7 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).

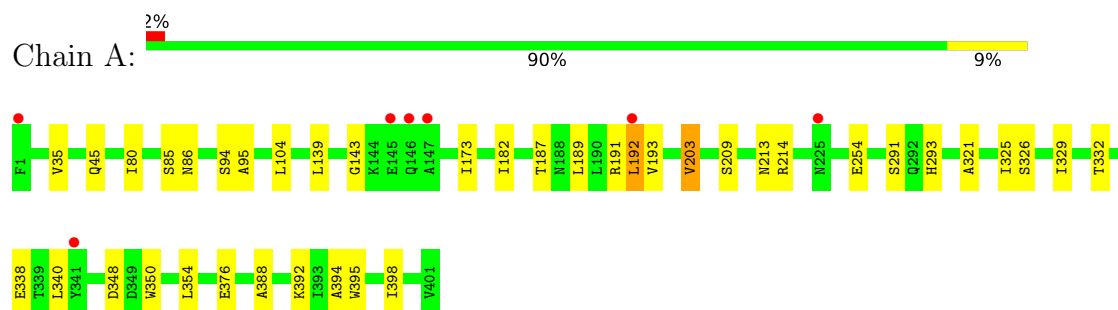


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	C	1	Total	C	O	0	0
			4	2	2		

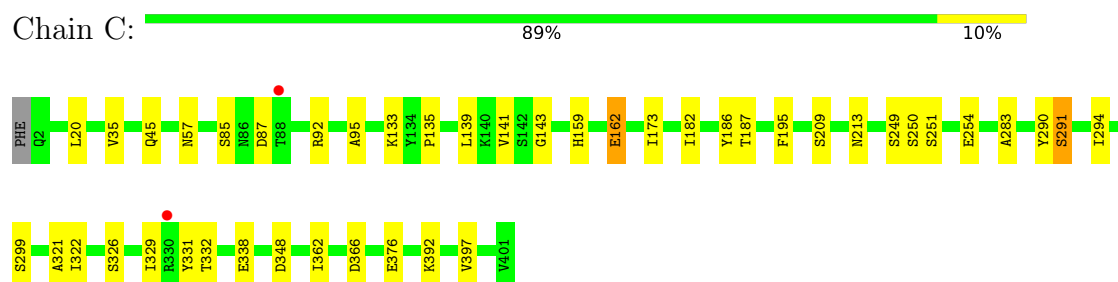
3 Residue-property plots [i](#)

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.

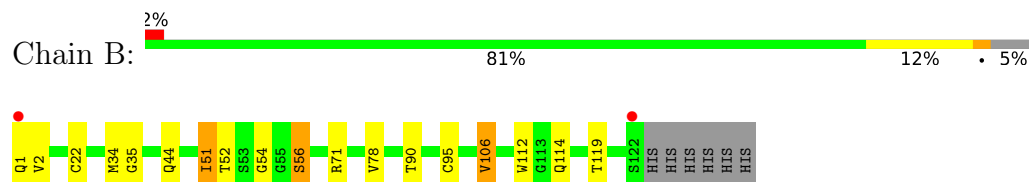
- Molecule 1: Carboxypeptidase B2



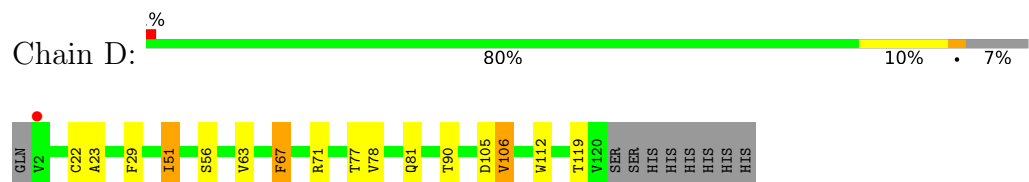
- Molecule 1: Carboxypeptidase B2



- Molecule 2: VHH-a204



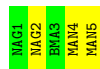
- Molecule 2: VHH-a204



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

nose

Chain E:  40% 60%



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

Chain F:  50% 50%



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	193.27 Å 193.27 Å 111.77 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.38 – 3.05 48.38 – 3.05	Depositor EDS
% Data completeness (in resolution range)	100.0 (48.38-3.05) 99.9 (48.38-3.05)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 3.07 Å)	Xtriage
Refinement program	BUSTER-TNT 2.10.2	Depositor
R, R_{free}	0.179 , 0.212 0.201 , 0.231	Depositor DCC
R_{free} test set	2006 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å ²)	66.7	Xtriage
Anisotropy	0.484	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 72.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.046 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8485	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.13% 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

5.1 Standard geometry

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

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	0.82	0/3341	1.28	19/4538 (0.4%)
1	C	0.86	1/3329 (0.0%)	1.30	18/4522 (0.4%)
2	B	0.84	0/949	1.22	0/1289
2	D	0.83	0/928	1.21	3/1261 (0.2%)
All	All	0.84	1/8547 (0.0%)	1.27	40/11610 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	87	ASP	CA-C	5.50	1.60	1.52

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	95	ALA	CA-C-N	8.49	131.65	120.28
1	A	95	ALA	C-N-CA	8.49	131.65	120.28
2	D	67	PHE	CA-CB-CG	7.81	121.61	113.80
1	C	182	ILE	N-CA-C	-7.29	105.86	111.62
1	C	254	GLU	CB-CG-CD	6.94	124.40	112.60
1	C	250	SER	CA-C-N	6.52	133.99	121.54
1	C	250	SER	C-N-CA	6.52	133.99	121.54
1	C	366	ASP	CA-CB-CG	6.47	119.07	112.60
1	A	376	GLU	CB-CG-CD	6.42	123.51	112.60
1	C	85	SER	N-CA-C	6.29	118.13	111.28
1	A	86	ASN	OD1-CG-ND2	6.22	128.82	122.60
1	C	95	ALA	CA-C-N	6.22	129.24	120.28
1	C	95	ALA	C-N-CA	6.22	129.24	120.28
1	A	182	ILE	N-CA-C	-6.19	106.73	111.62
1	C	376	GLU	CB-CG-CD	6.02	122.83	112.60
1	A	85	SER	N-CA-C	5.91	117.72	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	338	GLU	CA-C-N	5.89	128.10	120.44
1	A	338	GLU	C-N-CA	5.89	128.10	120.44
2	D	105	ASP	CA-CB-CG	5.71	118.31	112.60
2	D	29	PHE	N-CA-C	5.71	117.36	111.03
1	C	348	ASP	CA-CB-CG	5.70	118.30	112.60
1	A	94	SER	N-CA-C	-5.68	103.20	110.53
1	C	187	THR	CA-C-N	5.54	127.97	120.38
1	C	187	THR	C-N-CA	5.54	127.97	120.38
1	A	86	ASN	CA-CB-CG	5.48	118.08	112.60
1	A	192	LEU	CD1-CG-CD2	-5.45	98.80	110.80
1	C	299	SER	N-CA-C	-5.45	107.00	113.97
1	A	348	ASP	CA-CB-CG	5.45	118.05	112.60
1	C	143	GLY	CA-C-N	5.40	127.78	120.38
1	C	143	GLY	C-N-CA	5.40	127.78	120.38
1	A	143	GLY	CA-C-N	5.40	127.77	120.38
1	A	143	GLY	C-N-CA	5.40	127.77	120.38
1	C	35	VAL	N-CA-C	5.37	115.58	110.42
1	A	254	GLU	CB-CG-CD	5.33	121.66	112.60
1	A	86	ASN	CB-CG-ND2	-5.20	108.60	116.40
1	A	35	VAL	N-CA-C	5.12	115.33	110.42
1	C	162	GLU	CB-CG-CD	5.10	121.27	112.60
1	A	340	LEU	CA-C-N	5.09	130.21	121.87
1	A	340	LEU	C-N-CA	5.09	130.21	121.87
1	C	57	ASN	CA-CB-CG	5.02	117.62	112.60

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	3253	0	3169	32	0
1	C	3242	0	3159	19	0
2	B	928	0	877	11	0
2	D	907	0	856	8	0
3	E	61	0	52	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	28	0	25	0	0
5	A	42	0	39	0	0
5	C	14	0	13	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
7	A	4	0	3	0	0
7	C	4	0	3	0	0
All	All	8485	0	8196	64	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (64) 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:192:LEU:HD23	1:C:133:LYS:HG3	1.19	1.15
1:A:192:LEU:HD13	1:A:398:ILE:CD1	1.92	1.00
1:A:192:LEU:HD23	1:C:133:LYS:CG	1.97	0.93
1:A:192:LEU:HD22	1:A:398:ILE:HD13	1.55	0.88
1:A:192:LEU:HD13	1:A:398:ILE:HD11	1.58	0.85
1:A:192:LEU:CD2	1:C:133:LYS:HG3	2.11	0.76
2:B:52:THR:HG22	2:B:54:GLY:H	1.50	0.75
1:A:192:LEU:HD12	1:A:193:VAL:HG22	1.71	0.72
1:A:192:LEU:CD2	1:A:398:ILE:HD13	2.20	0.71
1:A:192:LEU:HD13	1:A:398:ILE:HD13	1.70	0.71
2:B:1:GLN:HG2	2:B:2:VAL:H	1.53	0.71
1:A:104:LEU:HD21	1:A:203:VAL:HG13	1.74	0.69
1:A:192:LEU:CD1	1:A:398:ILE:CD1	2.73	0.66
1:A:187:THR:HG22	1:A:191:ARG:NH2	2.14	0.63
1:A:139:LEU:HD12	1:A:173:ILE:HD13	1.82	0.62
1:A:192:LEU:CD1	1:A:398:ILE:HD13	2.32	0.59
1:A:192:LEU:CD1	1:A:193:VAL:HG22	2.34	0.58
2:D:63:VAL:HG11	2:D:67:PHE:CG	2.39	0.57
1:C:139:LEU:HD12	1:C:173:ILE:HD13	1.85	0.57
1:A:187:THR:HG22	1:A:191:ARG:HH22	1.68	0.56
1:A:192:LEU:CD1	1:A:398:ILE:HD11	2.34	0.56
1:A:350:TRP:O	1:A:354:LEU:HD23	2.06	0.55
1:A:104:LEU:CD2	1:A:203:VAL:HG13	2.35	0.55
1:C:159:HIS:HB2	1:C:162:GLU:CD	2.33	0.54
1:A:394:ALA:O	1:A:398:ILE:HD12	2.08	0.53
2:B:90:THR:HG23	2:B:119:THR:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:321:ALA:HB2	1:A:392:LYS:HG3	1.91	0.51
1:C:290:TYR:O	1:C:291:SER:HB3	2.10	0.51
1:C:326:SER:HB3	1:C:329:ILE:HD13	1.92	0.51
2:B:114:GLN:HG3	1:C:92:ARG:HB2	1.92	0.50
1:A:395:TRP:CZ3	1:C:133:LYS:HG2	2.47	0.49
2:D:90:THR:HG23	2:D:119:THR:HA	1.94	0.49
1:A:192:LEU:HD12	1:A:193:VAL:N	2.28	0.49
1:A:326:SER:HB3	1:A:329:ILE:HD13	1.94	0.49
2:D:63:VAL:HG11	2:D:67:PHE:CD2	2.48	0.48
1:A:209:SER:HA	1:A:213:ASN:O	2.15	0.46
1:C:209:SER:HA	1:C:213:ASN:O	2.14	0.46
1:C:141:VAL:HB	1:C:195:PHE:HB2	1.98	0.46
1:A:80:ILE:HG12	1:A:214:ARG:HG2	1.98	0.46
1:C:186:TYR:N	1:C:186:TYR:CD2	2.83	0.46
1:C:186:TYR:N	1:C:186:TYR:HD2	2.13	0.46
1:A:191:ARG:CZ	1:C:135:PRO:HD3	2.45	0.46
2:B:52:THR:HB	2:B:56:SER:H	1.80	0.46
1:A:325:ILE:HG13	1:A:388:ALA:HB2	1.99	0.45
2:B:1:GLN:HG2	2:B:2:VAL:N	2.28	0.45
2:D:23:ALA:HA	2:D:77:THR:HG22	1.98	0.45
2:B:34:MET:HB2	2:B:78:VAL:HG11	1.98	0.45
2:D:106:VAL:HG12	2:D:112:TRP:HZ2	1.82	0.45
1:C:294:ILE:HG12	1:C:362:ILE:HG12	1.99	0.44
1:A:192:LEU:HD22	1:A:398:ILE:HG21	1.99	0.44
1:A:189:LEU:HD12	1:A:192:LEU:HD11	2.01	0.43
2:D:67:PHE:HA	2:D:81:GLN:O	2.18	0.43
2:B:106:VAL:HG12	2:B:112:TRP:HZ2	1.81	0.43
1:C:321:ALA:HB2	1:C:392:LYS:HG3	2.00	0.43
2:D:51:ILE:HD12	2:D:71:ARG:HG2	2.02	0.42
1:C:322:ILE:HG21	1:C:331:TYR:CD1	2.54	0.41
1:A:293:HIS:CE1	1:A:332:THR:OG1	2.73	0.41
2:B:51:ILE:HD12	2:B:71:ARG:HG2	2.02	0.41
2:B:35:GLY:O	2:B:95:CYS:HA	2.21	0.41
2:B:106:VAL:HG12	2:B:112:TRP:CZ2	2.56	0.41
1:C:283:ALA:HB2	1:C:397:VAL:HG21	2.02	0.40
1:A:187:THR:CG2	1:A:191:ARG:HH22	2.31	0.40
2:D:71:ARG:HB3	2:D:78:VAL:HG12	2.02	0.40
1:C:20:LEU:HD23	1:C:20:LEU:HA	1.97	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	399/401 (100%)	386 (97%)	12 (3%)	1 (0%)	36	63
1	C	398/401 (99%)	383 (96%)	14 (4%)	1 (0%)	36	63
2	B	120/128 (94%)	114 (95%)	6 (5%)	0	100	100
2	D	117/128 (91%)	110 (94%)	7 (6%)	0	100	100
All	All	1034/1058 (98%)	993 (96%)	39 (4%)	2 (0%)	43	70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	291	SER
1	C	291	SER

5.3.2 Protein sidechains [i](#)

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	354/354 (100%)	352 (99%)	2 (1%)	78	81
1	C	353/354 (100%)	348 (99%)	5 (1%)	59	73
2	B	98/104 (94%)	93 (95%)	5 (5%)	21	48
2	D	95/104 (91%)	91 (96%)	4 (4%)	26	54
All	All	900/916 (98%)	884 (98%)	16 (2%)	51	70

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

Mol	Chain	Res	Type
1	A	45	GLN
1	A	203	VAL
2	B	22	CYS
2	B	44	GLN
2	B	51	ILE
2	B	56	SER
2	B	106	VAL
1	C	45	GLN
1	C	249	SER
1	C	251	SER
1	C	332	THR
1	C	338	GLU
2	D	22	CYS
2	D	51	ILE
2	D	56	SER
2	D	106	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	ASN
1	A	82	GLN
1	A	146	GLN
2	B	1	GLN
2	B	3	GLN
2	B	83	ASN
1	C	82	GLN
1	C	105	ASN
2	D	3	GLN
2	D	83	ASN

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

7 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	E	1	3,1	14,14,15	0.31	0	17,19,21	0.46	0
3	NAG	E	2	3	14,14,15	0.48	0	17,19,21	1.80	3 (17%)
3	BMA	E	3	3	11,11,12	0.37	0	15,15,17	0.68	0
3	MAN	E	4	3	11,11,12	0.42	0	15,15,17	1.26	1 (6%)
3	MAN	E	5	3	11,11,12	0.57	0	15,15,17	1.52	1 (6%)
4	NAG	F	1	4,1	14,14,15	0.38	0	17,19,21	1.24	2 (11%)
4	NAG	F	2	4	14,14,15	0.33	0	17,19,21	0.59	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	E	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	BMA	E	3	3	-	0/2/19/22	0/1/1/1
3	MAN	E	4	3	-	0/2/19/22	1/1/1/1
3	MAN	E	5	3	-	2/2/19/22	1/1/1/1
4	NAG	F	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	F	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	5	MAN	C1-O5-C5	5.38	119.39	112.19
3	E	2	NAG	C1-C2-N2	5.18	118.60	110.43
3	E	4	MAN	C1-O5-C5	4.54	118.27	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	2	NAG	C2-N2-C7	4.33	128.71	122.90
4	F	1	NAG	O5-C1-C2	-3.80	105.41	111.29
3	E	2	NAG	C1-O5-C5	2.12	115.02	112.19
4	F	1	NAG	O4-C4-C3	-2.01	105.63	110.38

There are no chirality outliers.

All (8) torsion outliers are listed below:

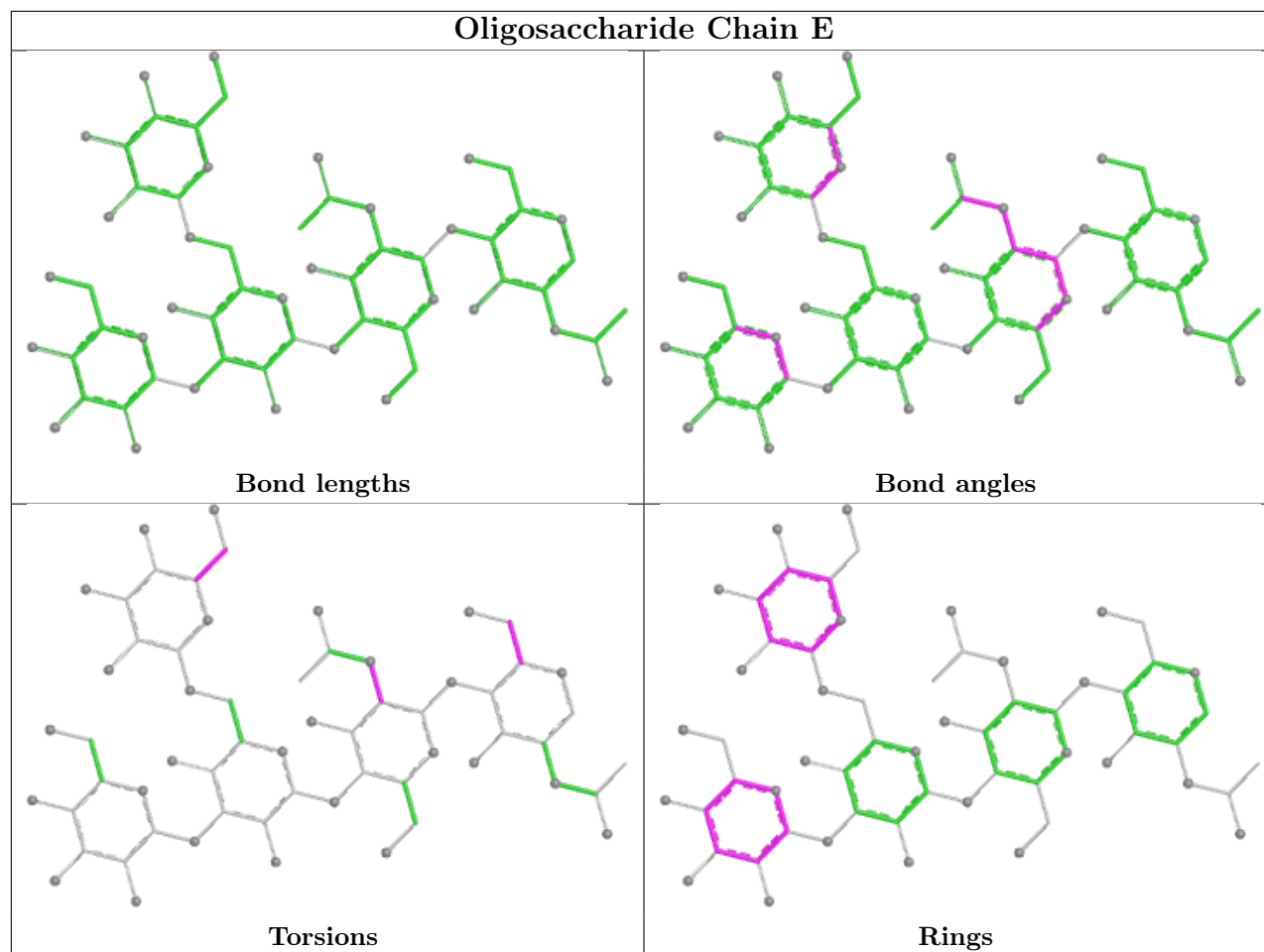
Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C1-C2-N2-C7
3	E	5	MAN	O5-C5-C6-O6
3	E	5	MAN	C4-C5-C6-O6
4	F	2	NAG	O5-C5-C6-O6
4	F	1	NAG	C4-C5-C6-O6
4	F	1	NAG	O5-C5-C6-O6
4	F	2	NAG	C1-C2-N2-C7
3	E	1	NAG	O5-C5-C6-O6

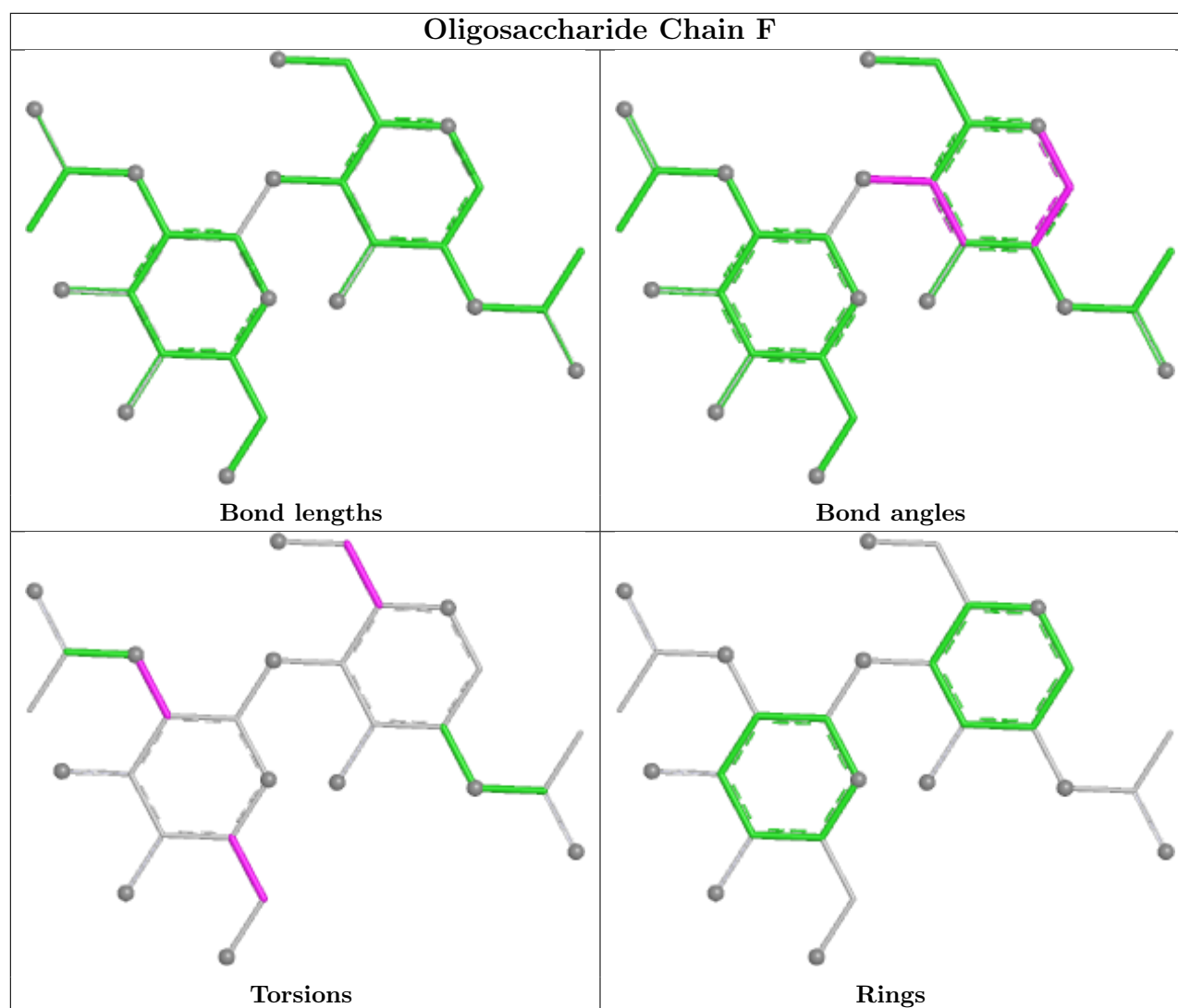
All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	4	MAN	C1-C2-C3-C4-C5-O5
3	E	5	MAN	C1-C2-C3-C4-C5-O5

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](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	ACT	C	505	-	3,3,3	0.94	0	3,3,3	1.22	0
7	ACT	A	510	6	3,3,3	1.53	0	3,3,3	0.68	0
5	NAG	A	506	1	14,14,15	0.41	0	17,19,21	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	A	507	1	14,14,15	0.47	0	17,19,21	0.80	1 (5%)
5	NAG	C	503	1	14,14,15	0.42	0	17,19,21	1.41	3 (17%)
5	NAG	A	508	1	14,14,15	0.37	0	17,19,21	0.75	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
5	NAG	A	506	1	-	1/6/23/26	0/1/1/1
5	NAG	A	507	1	-	1/6/23/26	0/1/1/1
5	NAG	C	503	1	-	2/6/23/26	0/1/1/1
5	NAG	A	508	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	503	NAG	O5-C1-C2	-3.96	105.16	111.29
5	C	503	NAG	C1-O5-C5	3.19	116.47	112.19
5	A	507	NAG	C1-O5-C5	2.30	115.27	112.19
5	C	503	NAG	C1-C2-N2	2.03	113.63	110.43

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	503	NAG	O5-C5-C6-O6
5	C	503	NAG	C4-C5-C6-O6
5	A	508	NAG	C8-C7-N2-C2
5	A	508	NAG	O7-C7-N2-C2
5	A	507	NAG	C1-C2-N2-C7
5	A	506	NAG	C8-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	401/401 (100%)	-0.02	7 (1%) 69 46	57, 83, 120, 162	0
1	C	400/401 (99%)	-0.32	2 (0%) 87 72	44, 69, 111, 137	0
2	B	122/128 (95%)	-0.17	2 (1%) 70 47	59, 79, 120, 141	0
2	D	119/128 (92%)	0.09	1 (0%) 82 63	66, 108, 146, 161	0
All	All	1042/1058 (98%)	-0.14	12 (1%) 76 55	44, 81, 124, 162	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	PHE	3.9
1	A	147	ALA	3.6
2	B	122	SER	3.4
1	C	88	THR	3.0
1	A	225	ASN	3.0
1	A	341	TYR	2.5
2	D	2	VAL	2.4
1	A	146	GLN	2.4
1	A	192	LEU	2.3
2	B	1	GLN	2.3
1	A	145	GLU	2.1
1	C	330	ARG	2.0

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

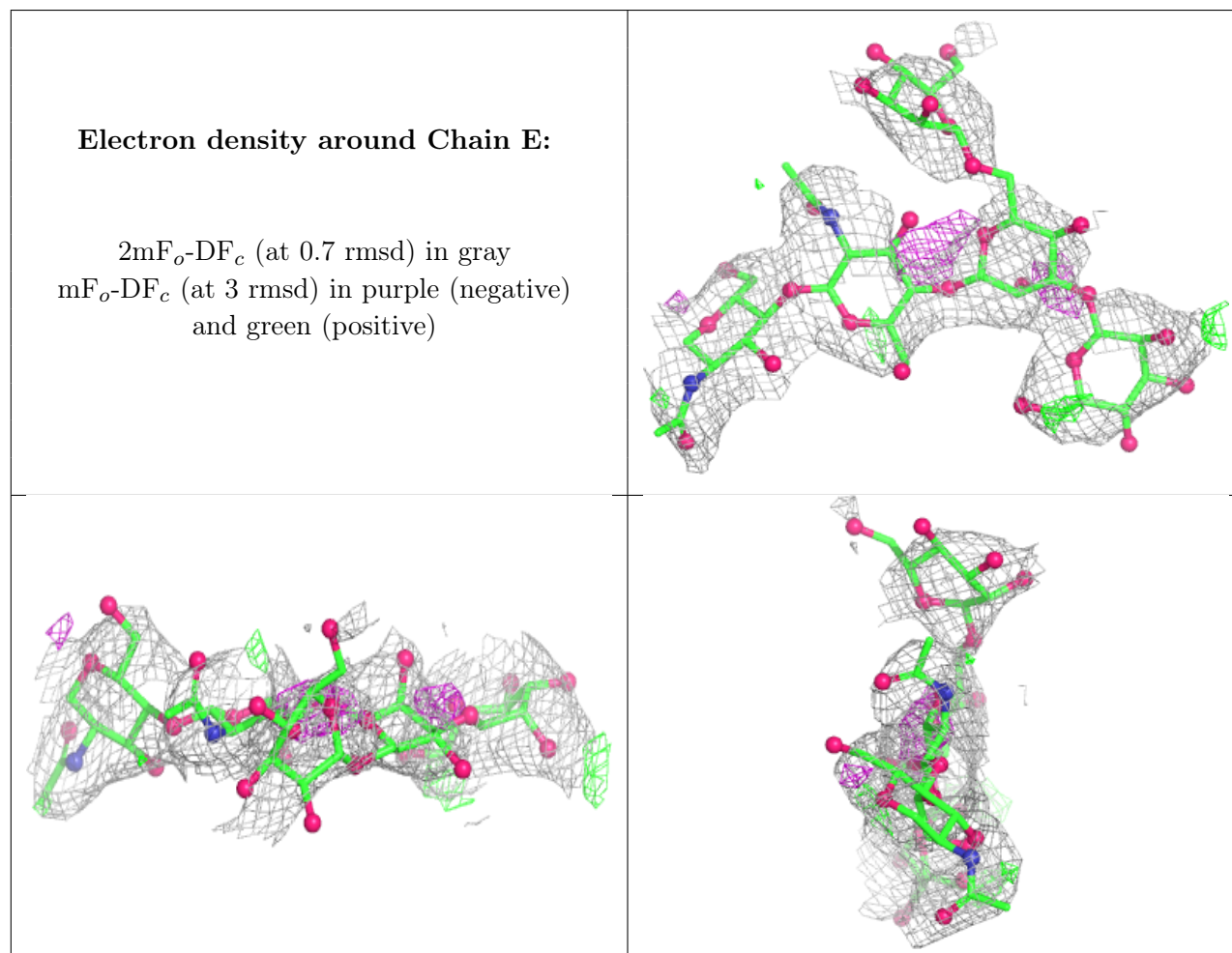
There are no non-standard protein/DNA/RNA residues in this entry.

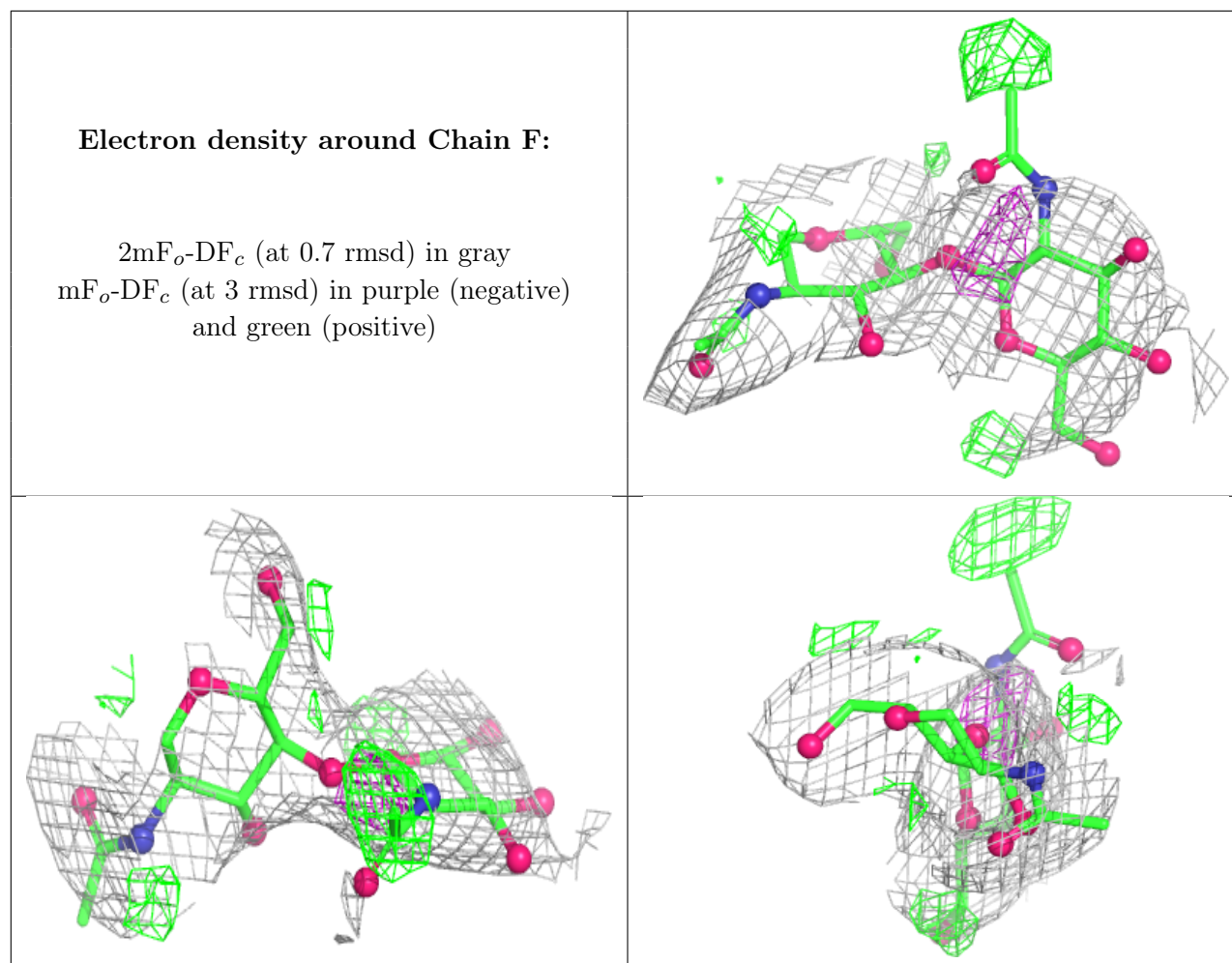
6.3 Carbohydrates [i](#)

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(Å ²)	Q<0.9
3	MAN	E	4	11/12	0.09	0.18	159,165,166,166	0
3	MAN	E	5	11/12	0.40	0.15	158,164,164,164	0
4	NAG	F	2	14/15	0.42	0.17	147,150,153,154	0
3	NAG	E	2	14/15	0.72	0.17	134,146,153,158	0
4	NAG	F	1	14/15	0.80	0.14	115,131,139,146	0
3	BMA	E	3	11/12	0.81	0.16	161,162,164,166	0
3	NAG	E	1	14/15	0.85	0.14	116,122,129,137	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(Å ²)	Q<0.9
5	NAG	A	506	14/15	0.38	0.20	103,113,116,117	0
5	NAG	A	507	14/15	0.57	0.15	130,131,132,134	0
5	NAG	A	508	14/15	0.75	0.16	146,151,154,155	0
5	NAG	C	503	14/15	0.79	0.15	126,129,132,132	0
7	ACT	A	510	4/4	0.87	0.18	89,90,91,93	0
7	ACT	C	505	4/4	0.94	0.15	79,81,83,87	0
6	ZN	A	509	1/1	1.00	0.04	71,71,71,71	0
6	ZN	C	504	1/1	1.00	0.06	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.