



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:31 AM UTC

PDB ID : 5W0P / pdb_00005w0p
Title : Crystal structure of rhodopsin bound to visual arrestin determined by X-ray free electron laser
Authors : Zhou, X.E.; He, Y.; de Waal, P.W.; Gao, X.; Kang, Y.; Van Eps, N.; Yin, Y.; Pal, K.; Goswami, D.; White, T.A.; Barty, A.; Latorraca, N.R.; Chapman, H.N.; Hubbell, W.L.; Dror, R.O.; Stevens, R.C.; Cherezov, V.; Gurevich, V.V.; Griffin, P.R.; Ernst, O.P.; Melcher, K.; Xu, H.E.
Deposited on : 2017-05-31
Resolution : 3.01 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)

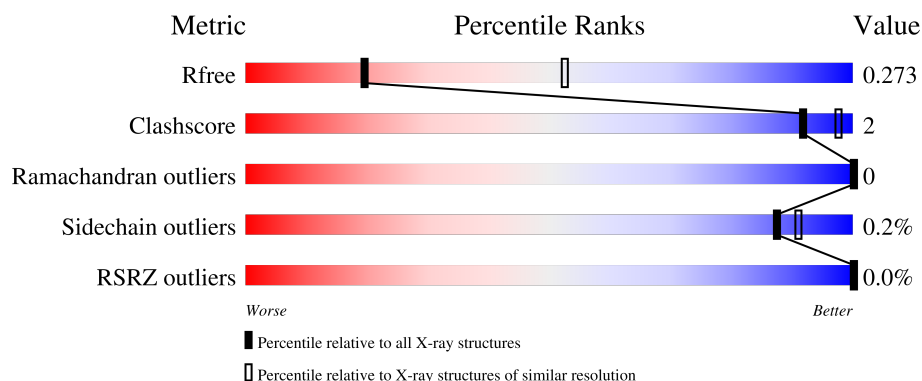
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	906	 88% 5% 6%
1	B	906	 85% 11%
2	C	906	 91% 6%
2	D	906	 81% 15%

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Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
3	E	2	50% 50%
3	F	2	50% 50%
3	G	2	100%
3	H	2	50% 50%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 25976 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 Endolysin,Rhodopsin,S-arrestin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	849	Total	C	N	O	P	S	0	0	0
			6702	4337	1096	1227	2	40			
1	B	804	Total	C	N	O	P	S	0	0	0
			6351	4116	1035	1159	2	39			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-107	THR	CYS	engineered mutation	UNP A0A097J792
A	-64	ALA	CYS	engineered mutation	UNP A0A097J792
A	2	CYS	ASN	engineered mutation	UNP P08100
A	113	GLN	GLU	engineered mutation	UNP P08100
A	257	TYR	MET	engineered mutation	UNP P08100
A	282	CYS	ASN	engineered mutation	UNP P08100
A	1995	GLY	-	linker	UNP P08100
A	1996	SER	-	linker	UNP P08100
A	1997	ALA	-	linker	UNP P08100
A	1998	GLY	-	linker	UNP P08100
A	1999	SER	-	linker	UNP P08100
A	2000	ALA	-	linker	UNP P08100
A	2001	GLY	-	linker	UNP P08100
A	2002	SER	-	linker	UNP P08100
A	2003	ALA	-	linker	UNP P08100
A	2004	GLY	-	linker	UNP P08100
A	2005	SER	-	linker	UNP P08100
A	2006	ALA	-	linker	UNP P08100
A	2007	GLY	-	linker	UNP P08100
A	2008	SER	-	linker	UNP P08100
A	2009	ALA	-	linker	UNP P08100
A	2374	ALA	LEU	engineered mutation	UNP P20443
A	2375	ALA	VAL	engineered mutation	UNP P20443
A	2376	ALA	PHE	engineered mutation	UNP P20443
B	-107	THR	CYS	engineered mutation	UNP A0A097J792

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-64	ALA	CYS	engineered mutation	UNP A0A097J792
B	2	CYS	ASN	engineered mutation	UNP P08100
B	113	GLN	GLU	engineered mutation	UNP P08100
B	257	TYR	MET	engineered mutation	UNP P08100
B	282	CYS	ASN	engineered mutation	UNP P08100
B	1995	GLY	-	linker	UNP P08100
B	1996	SER	-	linker	UNP P08100
B	1997	ALA	-	linker	UNP P08100
B	1998	GLY	-	linker	UNP P08100
B	1999	SER	-	linker	UNP P08100
B	2000	ALA	-	linker	UNP P08100
B	2001	GLY	-	linker	UNP P08100
B	2002	SER	-	linker	UNP P08100
B	2003	ALA	-	linker	UNP P08100
B	2004	GLY	-	linker	UNP P08100
B	2005	SER	-	linker	UNP P08100
B	2006	ALA	-	linker	UNP P08100
B	2007	GLY	-	linker	UNP P08100
B	2008	SER	-	linker	UNP P08100
B	2009	ALA	-	linker	UNP P08100
B	2374	ALA	LEU	engineered mutation	UNP P20443
B	2375	ALA	VAL	engineered mutation	UNP P20443
B	2376	ALA	PHE	engineered mutation	UNP P20443

- Molecule 2 is a protein called Endolysin,Rhodopsin,S-arrestin.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	850	Total	C	N	O	P	S	0	0	0
			6703	4340	1099	1223	1	40			
2	D	774	Total	C	N	O	P	S	0	0	0
			6108	3966	997	1106	1	38			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-107	THR	CYS	engineered mutation	UNP A0A097J792
C	-64	ALA	CYS	engineered mutation	UNP A0A097J792
C	2	CYS	ASN	engineered mutation	UNP P08100
C	113	GLN	GLU	engineered mutation	UNP P08100
C	257	TYR	MET	engineered mutation	UNP P08100
C	282	CYS	ASN	engineered mutation	UNP P08100
C	1995	GLY	-	linker	UNP P08100

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1996	SER	-	linker	UNP P08100
C	1997	ALA	-	linker	UNP P08100
C	1998	GLY	-	linker	UNP P08100
C	1999	SER	-	linker	UNP P08100
C	2000	ALA	-	linker	UNP P08100
C	2001	GLY	-	linker	UNP P08100
C	2002	SER	-	linker	UNP P08100
C	2003	ALA	-	linker	UNP P08100
C	2004	GLY	-	linker	UNP P08100
C	2005	SER	-	linker	UNP P08100
C	2006	ALA	-	linker	UNP P08100
C	2007	GLY	-	linker	UNP P08100
C	2008	SER	-	linker	UNP P08100
C	2009	ALA	-	linker	UNP P08100
C	2374	ALA	LEU	engineered mutation	UNP P20443
C	2375	ALA	VAL	engineered mutation	UNP P20443
C	2376	ALA	PHE	engineered mutation	UNP P20443
D	-107	THR	CYS	engineered mutation	UNP A0A097J792
D	-64	ALA	CYS	engineered mutation	UNP A0A097J792
D	2	CYS	ASN	engineered mutation	UNP P08100
D	113	GLN	GLU	engineered mutation	UNP P08100
D	257	TYR	MET	engineered mutation	UNP P08100
D	282	CYS	ASN	engineered mutation	UNP P08100
D	1995	GLY	-	linker	UNP P08100
D	1996	SER	-	linker	UNP P08100
D	1997	ALA	-	linker	UNP P08100
D	1998	GLY	-	linker	UNP P08100
D	1999	SER	-	linker	UNP P08100
D	2000	ALA	-	linker	UNP P08100
D	2001	GLY	-	linker	UNP P08100
D	2002	SER	-	linker	UNP P08100
D	2003	ALA	-	linker	UNP P08100
D	2004	GLY	-	linker	UNP P08100
D	2005	SER	-	linker	UNP P08100
D	2006	ALA	-	linker	UNP P08100
D	2007	GLY	-	linker	UNP P08100
D	2008	SER	-	linker	UNP P08100
D	2009	ALA	-	linker	UNP P08100
D	2374	ALA	LEU	engineered mutation	UNP P20443
D	2375	ALA	VAL	engineered mutation	UNP P20443
D	2376	ALA	PHE	engineered mutation	UNP P20443

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-a

cetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	109.24Å 109.24Å 452.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.03 – 3.01 30.03 – 3.01	Depositor EDS
% Data completeness (in resolution range)	70.7 (30.03-3.01) 70.7 (30.03-3.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.91 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.234 , 0.272 0.230 , 0.273	Depositor DCC
R_{free} test set	3761 reflections (3.46%)	wwPDB-VP
Wilson B-factor (Å ²)	113.4	Xtriage
Anisotropy	0.566	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 162.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.35$, $\langle L^2 \rangle = 0.18$	Xtriage
Estimated twinning fraction	0.499 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	25976	wwPDB-VP
Average B, all atoms (Å ²)	201.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.97% 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: SEP, TPO, 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	0.37	0/6837	0.71	3/9285 (0.0%)
1	B	0.39	0/6480	0.77	2/8804 (0.0%)
2	C	0.38	0/6851	0.74	1/9306 (0.0%)
2	D	0.39	0/6248	0.77	5/8495 (0.1%)
All	All	0.38	0/26416	0.75	11/35890 (0.0%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2301	LYS	CB-CA-C	-5.97	109.70	116.63
1	B	170	PRO	N-CA-C	5.87	117.86	110.70
1	B	2097	ALA	N-CA-C	5.86	117.53	111.03
1	A	170	PRO	N-CA-C	5.77	117.74	110.70
1	A	209	VAL	N-CA-C	5.74	116.39	110.82
2	D	170	PRO	N-CA-C	5.73	117.70	110.70
2	D	2301	LYS	CB-CA-C	-5.71	110.01	116.63
2	D	209	VAL	N-CA-C	5.44	116.10	110.82
2	C	170	PRO	N-CA-C	5.20	117.05	110.70
2	D	265	TRP	N-CA-C	5.09	119.64	113.38
2	D	2233	LYS	N-CA-C	5.01	117.91	110.14

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	6702	0	6749	27	0
1	B	6351	0	6385	19	0
2	C	6703	0	6755	16	0
2	D	6108	0	6152	21	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
3	G	28	0	25	0	0
3	H	28	0	25	2	0
All	All	25976	0	26141	83	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 (83) 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:B:2301:LYS:HG3	1:B:2302:HIS:H	1.51	0.74
2:D:2176:ARG:HG3	2:D:2300:ILE:HD11	1.70	0.72
1:B:72:LEU:HD12	1:B:2073:ILE:HD12	1.72	0.72
1:A:72:LEU:HB2	1:A:2073:ILE:HD11	1.74	0.68
2:C:-74:VAL:HA	2:C:-39:GLN:OE1	1.93	0.68
1:B:2027:LEU:HD12	1:B:2173:LEU:HD23	1.77	0.65
2:C:57:LEU:HB3	2:C:317:MET:HE1	1.80	0.64
1:A:2306:ASN:HD21	1:A:2358:HIS:CE1	2.15	0.64
1:B:-150:GLU:HA	1:B:-16:ARG:NH2	2.14	0.61
2:D:2070:GLN:HB3	2:D:2073:ILE:HG22	1.83	0.61
1:A:312:GLN:HB3	1:A:2076:MET:SD	2.41	0.60
2:D:72:LEU:HB2	2:D:2073:ILE:HD11	1.82	0.60
1:B:-74:VAL:HA	1:B:-39:GLN:OE1	2.05	0.56
2:C:146:PHE:HZ	2:C:2135:PRO:HA	1.70	0.55
1:A:2176:ARG:HG3	1:A:2300:ILE:HD11	1.89	0.55
2:C:34:PRO:HB2	2:D:318:LEU:HD21	1.90	0.54
2:D:21:ARG:HA	3:H:1:NAG:H83	1.88	0.53
1:B:70:THR:HG21	1:B:2073:ILE:HD13	1.89	0.53
2:C:2282:VAL:HG13	2:C:2282:VAL:O	2.09	0.52
1:A:2070:GLN:HB2	1:A:2073:ILE:HG22	1.92	0.52
2:D:253:MET:HB2	2:D:2078:LEU:HD21	1.92	0.51
2:D:2030:ARG:HD3	2:D:2300:ILE:HG21	1.92	0.51
1:B:72:LEU:HD21	1:B:138:VAL:HG21	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:PRO:HA	1:A:102:TYR:HB3	1.93	0.50
2:D:-58:VAL:HG22	2:D:-50:VAL:HG11	1.93	0.50
1:A:-71:SER:HB2	1:A:-39:GLN:HE21	1.76	0.50
1:B:2302:HIS:O	1:B:2302:HIS:CG	2.64	0.49
2:C:146:PHE:CZ	2:C:2135:PRO:HA	2.47	0.49
1:A:332:GLU:HG3	1:A:333:ALA:N	2.27	0.49
2:C:257:TYR:HE2	2:C:2078:LEU:HD21	1.78	0.48
1:B:145:ASN:ND2	1:B:2069:GLY:HA3	2.29	0.48
2:D:27:PRO:HA	2:D:102:TYR:HB3	1.95	0.47
1:A:-19:THR:O	1:A:-19:THR:HG23	2.14	0.47
1:A:-150:GLU:HA	1:A:-16:ARG:NH2	2.30	0.47
2:D:-71:SER:HB2	2:D:-39:GLN:OE1	2.15	0.47
2:D:-19:THR:O	2:D:-19:THR:HG23	2.15	0.47
2:D:-77:LEU:HD21	2:D:-50:VAL:HG13	1.97	0.46
1:A:-158:ILE:HG12	1:A:-64:ALA:HB1	1.98	0.46
1:A:52:PHE:HB3	1:A:53:PRO:HD3	1.98	0.46
2:C:2053:VAL:O	2:C:2053:VAL:HG12	2.15	0.46
1:A:-45:ASN:HB3	1:A:-29:ASN:HD21	1.81	0.46
1:B:70:THR:HG21	1:B:2073:ILE:HG21	1.98	0.46
1:A:253:MET:HB2	1:A:2078:LEU:HD11	1.99	0.45
2:C:2301:LYS:HG3	2:C:2302:HIS:H	1.82	0.45
1:A:2014:PHE:CZ	1:A:2030:ARG:HG3	2.52	0.45
2:D:52:PHE:HB3	2:D:53:PRO:HD3	1.98	0.45
1:B:10:TYR:CE1	1:B:192:TYR:HE1	2.34	0.45
1:B:2053:VAL:HG12	1:B:2053:VAL:O	2.16	0.45
1:B:52:PHE:HB3	1:B:53:PRO:HD3	1.99	0.44
1:A:70:THR:HG21	1:A:2073:ILE:HD13	1.98	0.44
1:A:271:VAL:HG21	1:A:291:PRO:HG3	1.99	0.44
2:D:2014:PHE:CZ	2:D:2030:ARG:HG3	2.52	0.44
1:A:-158:ILE:HG12	1:A:-64:ALA:CB	2.48	0.44
2:D:250:VAL:HG22	2:D:2078:LEU:HD13	1.99	0.44
1:B:2014:PHE:HE1	1:B:2029:LYS:HA	1.83	0.43
1:B:2301:LYS:HG3	1:B:2302:HIS:N	2.26	0.43
2:D:2242:VAL:HG23	2:D:2281:LEU:HD22	2.01	0.43
1:A:72:LEU:HD21	1:A:138:VAL:HG21	2.00	0.43
1:A:209:VAL:O	1:A:214:ILE:HG12	2.17	0.43
1:B:2082:ARG:HB3	1:B:2250:LEU:HD11	2.00	0.43
2:C:2027:LEU:HD12	2:C:2173:LEU:HD23	2.01	0.43
1:A:33:GLU:HA	1:A:34:PRO:HD3	1.92	0.43
2:C:52:PHE:HB3	2:C:53:PRO:HD3	2.00	0.42
1:A:2285:LEU:HD13	1:A:2296:LEU:HD21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2206:LEU:HD13	1:A:2334:LEU:HD11	2.02	0.42
2:D:72:LEU:HD21	2:D:138:VAL:HG21	2.01	0.42
2:C:2014:PHE:HE1	2:C:2029:LYS:HA	1.84	0.42
2:D:-41:MET:HB3	2:D:-36:ARG:HB2	2.01	0.42
1:A:2206:LEU:CD1	1:A:2334:LEU:HD11	2.50	0.42
2:C:209:VAL:O	2:C:214:ILE:HG12	2.20	0.42
2:D:214:ILE:HB	2:D:215:PRO:HD3	2.02	0.41
2:C:72:LEU:HD21	2:C:138:VAL:HG21	2.03	0.41
2:C:2077:GLY:O	2:C:2078:LEU:HB2	2.19	0.41
3:H:1:NAG:O3	3:H:1:NAG:C7	2.69	0.41
1:A:2242:VAL:HG23	1:A:2281:LEU:HD22	2.03	0.41
1:B:126:TRP:HB2	1:B:160:THR:HG23	2.03	0.41
1:B:2188:GLN:HA	1:B:2189:PRO:HD3	1.87	0.41
1:A:2077:GLY:O	1:A:2078:LEU:HB3	2.20	0.40
2:D:2057:LYS:HE3	2:D:2158:THR:HA	2.03	0.40
1:B:33:GLU:HA	1:B:34:PRO:HD3	1.92	0.40
2:D:2231:THR:O	2:D:2271:PRO:HB3	2.20	0.40
1:A:-155:MET:HG2	1:A:0:TYR:CD1	2.56	0.40
2:C:310:ASN:HB3	2:C:2076:MET:HG3	2.03	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	841/906 (93%)	827 (98%)	14 (2%)	0	100	100
1	B	794/906 (88%)	784 (99%)	10 (1%)	0	100	100
2	C	843/906 (93%)	831 (99%)	12 (1%)	0	100	100
2	D	767/906 (85%)	759 (99%)	8 (1%)	0	100	100
All	All	3245/3624 (90%)	3201 (99%)	44 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	736/776 (95%)	735 (100%)	1 (0%)	88	92
1	B	698/776 (90%)	696 (100%)	2 (0%)	86	90
2	C	737/777 (95%)	736 (100%)	1 (0%)	88	92
2	D	673/777 (87%)	671 (100%)	2 (0%)	86	90
All	All	2844/3106 (92%)	2838 (100%)	6 (0%)	87	91

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	LEU
1	B	57	LEU
1	B	2343	LEU
2	C	172	LEU
2	D	2078	LEU
2	D	2340	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-39	GLN
1	A	36	GLN
1	A	199	ASN
1	A	200	ASN
1	A	278	HIS
1	A	312	GLN
1	A	2217	HIS
1	A	2244	GLN
1	A	2247	ASN
1	A	2358	HIS
1	B	152	HIS

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Mol	Chain	Res	Type
1	B	2244	GLN
1	B	2247	ASN
1	B	2270	GLN
1	B	2306	ASN
1	B	2358	HIS
2	C	184	GLN
2	C	278	HIS
2	C	2244	GLN
2	C	2247	ASN
2	C	2266	GLN
2	C	2306	ASN
2	D	2090	GLN
2	D	2217	HIS
2	D	2244	GLN
2	D	2247	ASN
2	D	2266	GLN
2	D	2358	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	SEP	A	338	1	8,9,10	1.54	1 (12%)	7,12,14	0.84	0
1	SEP	B	338	1	8,9,10	1.52	1 (12%)	7,12,14	0.66	0
1	TPO	A	336	1	8,10,11	1.16	0	10,14,16	1.70	1 (10%)
1	TPO	B	336	1	8,10,11	1.69	1 (12%)	10,14,16	1.77	1 (10%)
2	SEP	D	338	2	8,9,10	1.53	1 (12%)	7,12,14	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SEP	C	338	2	8,9,10	1.52	1 (12%)	7,12,14	0.89	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
1	SEP	A	338	1	-	0/6/8/10	-
1	SEP	B	338	1	-	0/6/8/10	-
1	TPO	A	336	1	-	4/9/11/13	-
1	TPO	B	336	1	-	1/9/11/13	-
2	SEP	D	338	2	-	0/6/8/10	-
2	SEP	C	338	2	-	0/6/8/10	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	336	TPO	P-O1P	3.41	1.61	1.50
1	A	338	SEP	P-O1P	3.35	1.60	1.50
2	D	338	SEP	P-O1P	3.32	1.60	1.50
1	B	338	SEP	P-O1P	3.31	1.60	1.50
2	C	338	SEP	P-O1P	3.28	1.60	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	336	TPO	P-OG1-CB	-5.07	109.56	123.33
1	A	336	TPO	P-OG1-CB	-4.73	110.48	123.33

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	336	TPO	N-CA-CB-OG1
1	B	336	TPO	N-CA-CB-OG1
1	A	336	TPO	CB-OG1-P-O2P
1	A	336	TPO	O-C-CA-CB
1	A	336	TPO	CB-OG1-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

8 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	1,3	14,14,15	0.90	1 (7%)	17,19,21	0.98	1 (5%)
3	NAG	E	2	3	14,14,15	0.58	0	17,19,21	0.51	0
3	NAG	F	1	1,3	14,14,15	0.75	0	17,19,21	0.89	0
3	NAG	F	2	3	14,14,15	0.97	1 (7%)	17,19,21	1.65	2 (11%)
3	NAG	G	1	3,2	14,14,15	0.93	0	17,19,21	0.96	2 (11%)
3	NAG	G	2	3	14,14,15	0.93	1 (7%)	17,19,21	0.86	1 (5%)
3	NAG	H	1	3,2	14,14,15	1.00	1 (7%)	17,19,21	1.27	1 (5%)
3	NAG	H	2	3	14,14,15	0.82	1 (7%)	17,19,21	0.73	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	1,3	-	4/6/23/26	0/1/1/1
3	NAG	E	2	3	-	1/6/23/26	0/1/1/1
3	NAG	F	1	1,3	-	4/6/23/26	0/1/1/1
3	NAG	F	2	3	-	3/6/23/26	0/1/1/1
3	NAG	G	1	3,2	-	5/6/23/26	0/1/1/1
3	NAG	G	2	3	-	5/6/23/26	0/1/1/1
3	NAG	H	1	3,2	-	3/6/23/26	0/1/1/1
3	NAG	H	2	3	-	4/6/23/26	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	2	NAG	O5-C1	-2.89	1.38	1.43
3	H	1	NAG	C2-N2	-2.48	1.42	1.46
3	G	2	NAG	C1-C2	2.29	1.55	1.52
3	H	2	NAG	C1-C2	2.27	1.55	1.52
3	E	1	NAG	C1-C2	2.13	1.55	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	2	NAG	C1-C2-N2	-5.46	101.83	110.43
3	H	1	NAG	C2-N2-C7	3.60	127.72	122.90
3	F	2	NAG	C2-N2-C7	2.87	126.74	122.90
3	G	1	NAG	C4-C3-C2	2.16	114.18	111.02
3	G	2	NAG	C4-C3-C2	2.15	114.17	111.02
3	E	1	NAG	C4-C3-C2	2.06	114.04	111.02
3	G	1	NAG	C2-N2-C7	2.02	125.61	122.90

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	1	NAG	O7-C7-N2-C2
3	F	2	NAG	O7-C7-N2-C2
3	H	1	NAG	C8-C7-N2-C2
3	F	2	NAG	C8-C7-N2-C2
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
3	G	2	NAG	O7-C7-N2-C2
3	F	1	NAG	O7-C7-N2-C2
3	E	2	NAG	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	E	1	NAG	C8-C7-N2-C2
3	H	2	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C1-C2-N2-C7
3	F	1	NAG	C1-C2-N2-C7
3	G	1	NAG	C1-C2-N2-C7
3	G	2	NAG	C1-C2-N2-C7
3	H	2	NAG	C1-C2-N2-C7
3	G	2	NAG	C8-C7-N2-C2

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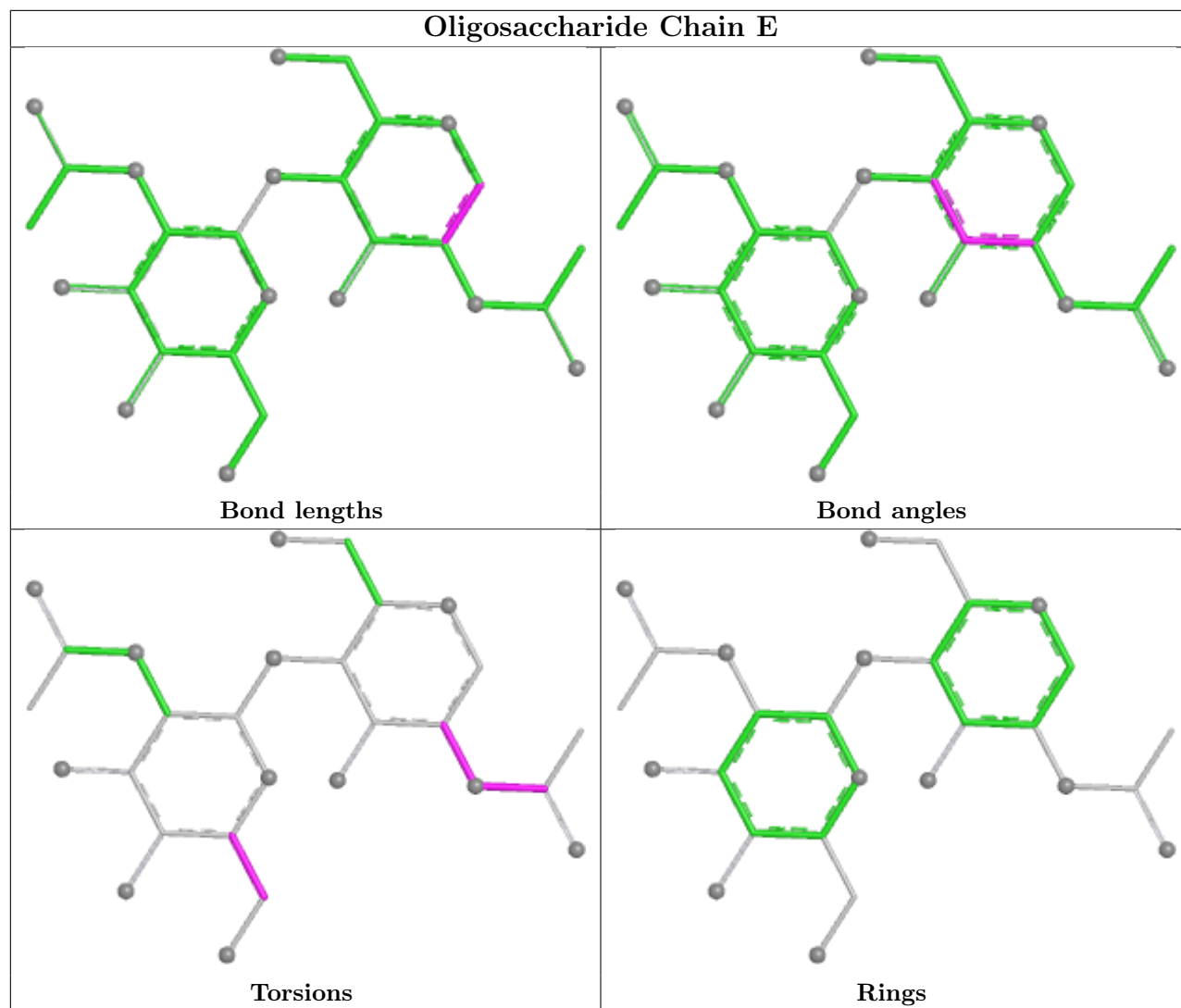
Mol	Chain	Res	Type	Atoms
3	F	1	NAG	C8-C7-N2-C2
3	E	1	NAG	C3-C2-N2-C7
3	F	1	NAG	C3-C2-N2-C7
3	G	1	NAG	C3-C2-N2-C7
3	G	2	NAG	C3-C2-N2-C7
3	H	1	NAG	C3-C2-N2-C7
3	H	2	NAG	C3-C2-N2-C7
3	H	2	NAG	O7-C7-N2-C2

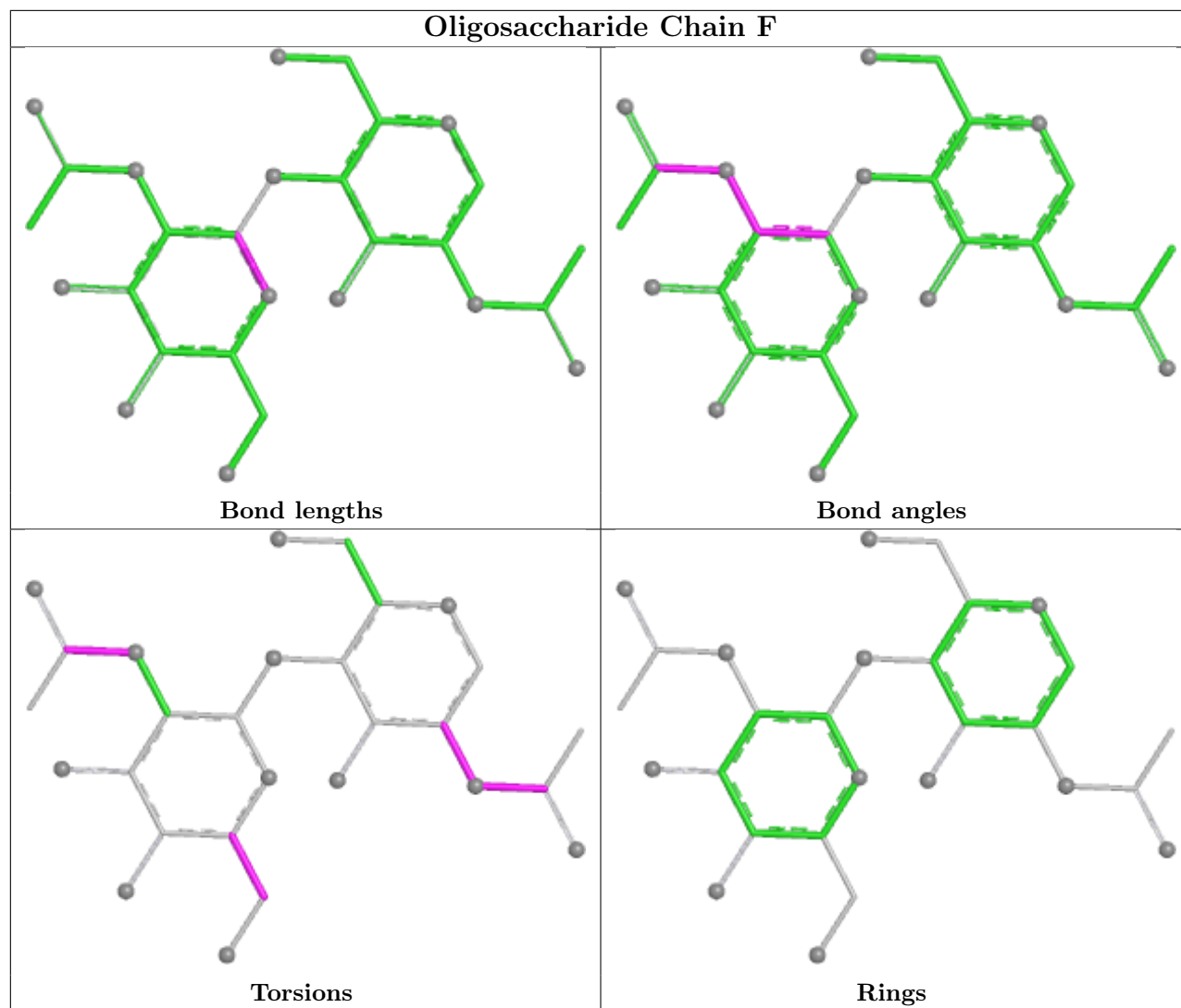
There are no ring outliers.

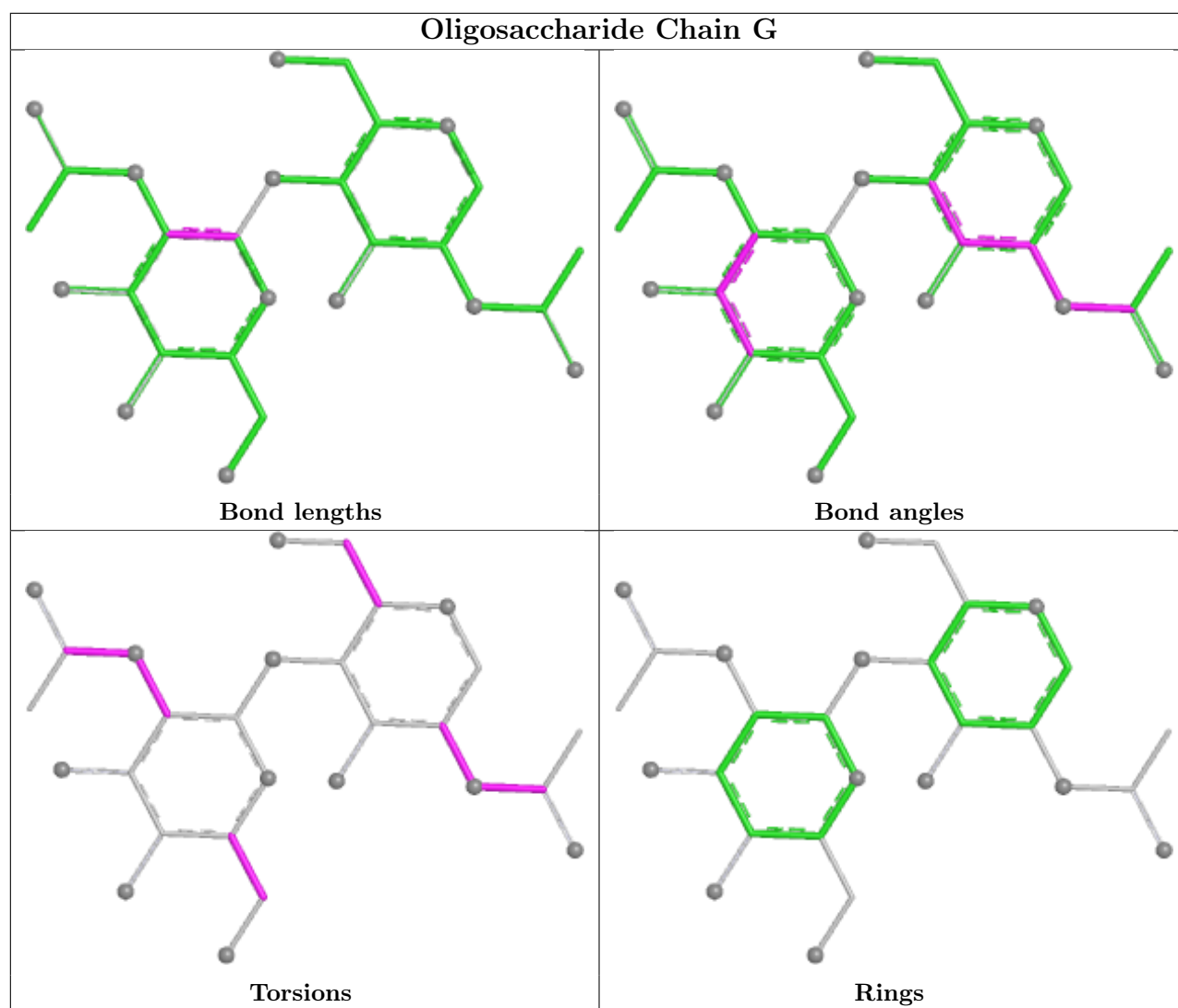
1 monomer is involved in 2 short contacts:

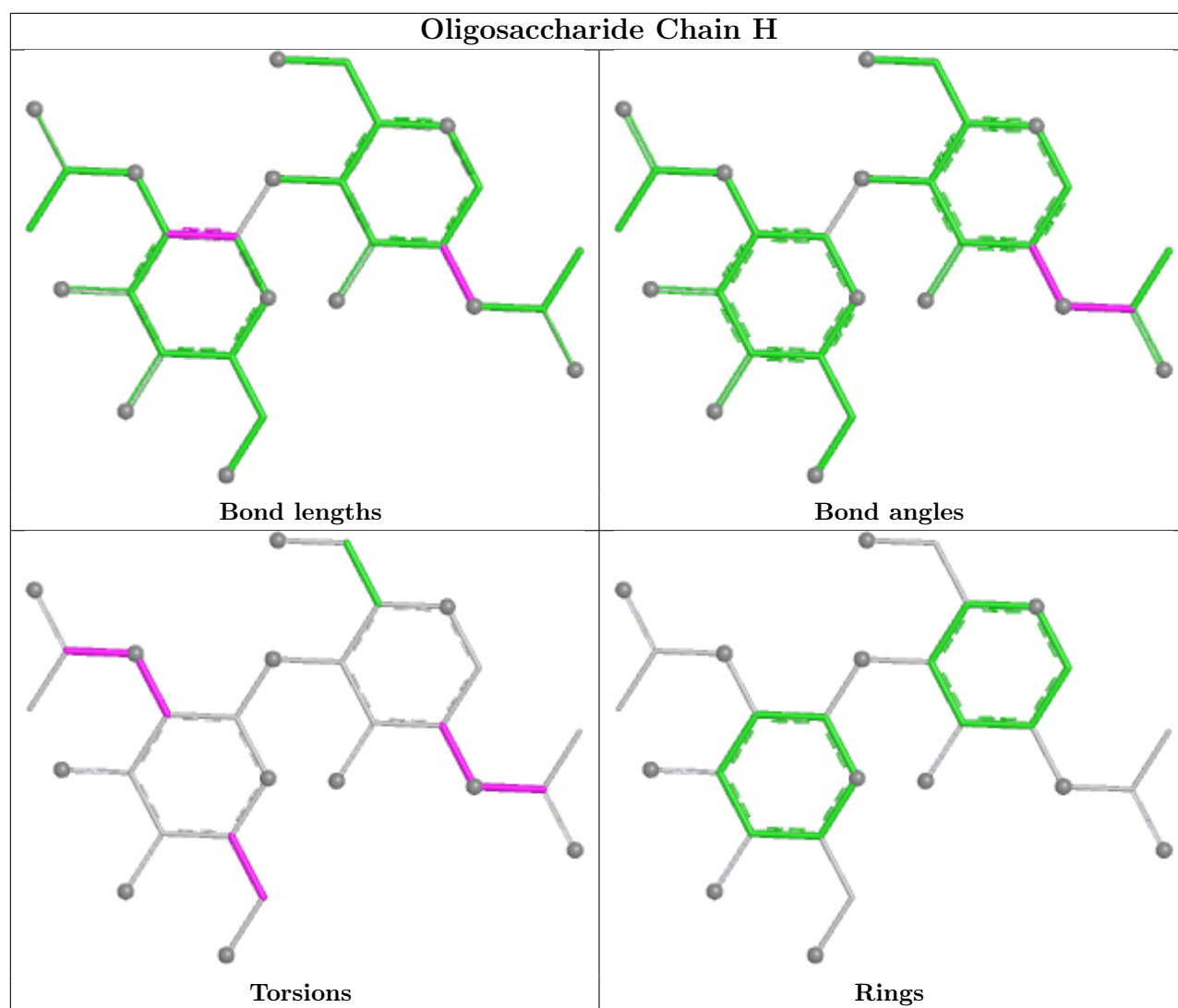
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	1	NAG	2	0

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	847/906 (93%)	-1.62	0 100 100	115, 194, 307, 335	0
1	B	802/906 (88%)	-1.60	0 100 100	116, 196, 297, 321	0
2	C	849/906 (93%)	-1.61	0 100 100	119, 190, 323, 347	0
2	D	773/906 (85%)	-1.57	1 (0%) 92 86	83, 171, 341, 370	0
All	All	3271/3624 (90%)	-1.60	1 (0%) 100 100	83, 188, 311, 370	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	2336	VAL	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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.

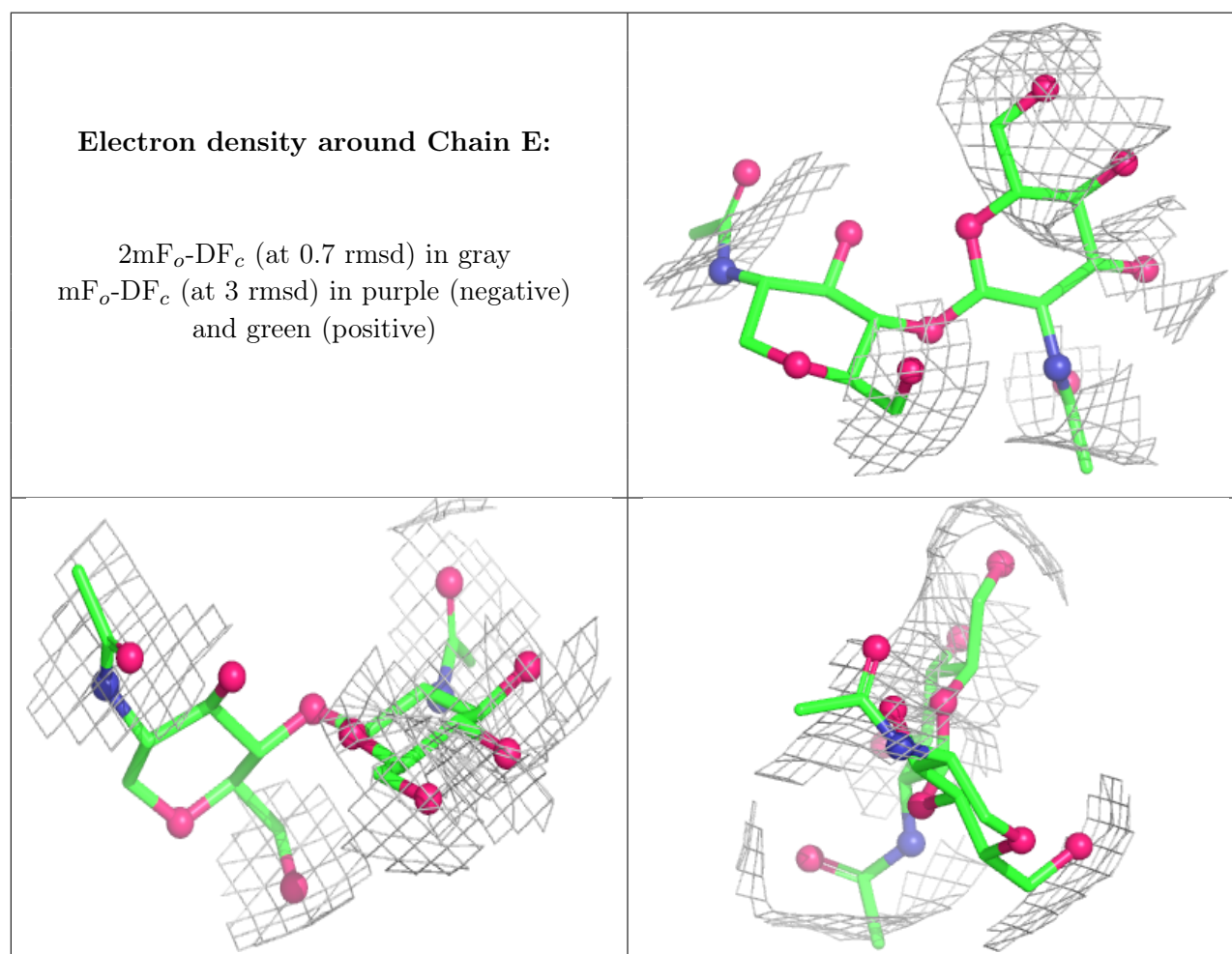
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	SEP	A	338	10/11	0.96	0.03	161,177,223,236	0
1	TPO	B	336	11/12	0.96	0.03	290,319,323,323	0
1	TPO	A	336	11/12	0.98	0.02	213,238,258,261	0
1	SEP	B	338	10/11	0.98	0.02	244,270,302,307	0
2	SEP	C	338	10/11	0.99	0.02	209,224,261,294	0
2	SEP	D	338	10/11	0.99	0.02	171,190,205,216	0

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.

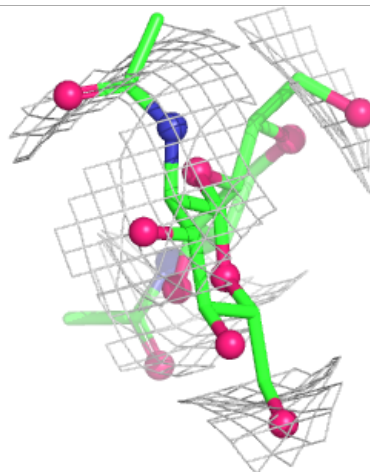
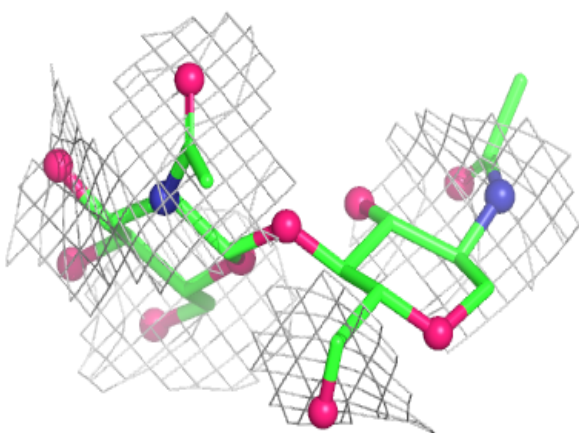
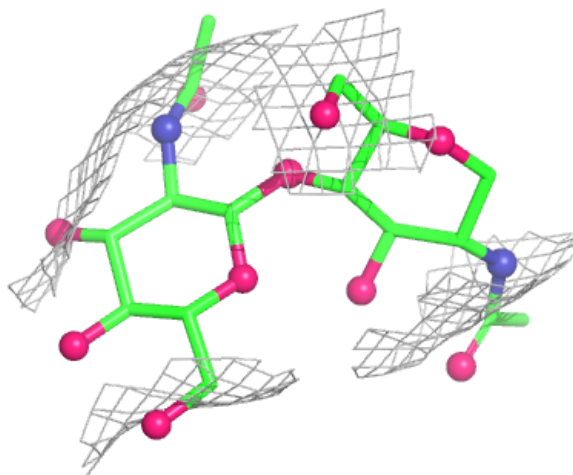
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	E	2	14/15	0.98	0.02	237,270,293,298	0
3	NAG	F	2	14/15	0.98	0.03	320,341,347,347	0
3	NAG	G	2	14/15	0.98	0.02	221,271,296,319	0
3	NAG	H	2	14/15	0.98	0.02	153,186,215,232	0
3	NAG	G	1	14/15	0.99	0.03	261,289,303,307	0
3	NAG	F	1	14/15	0.99	0.03	264,287,315,325	0
3	NAG	H	1	14/15	0.99	0.02	123,171,181,188	0
3	NAG	E	1	14/15	0.99	0.03	217,244,266,290	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.



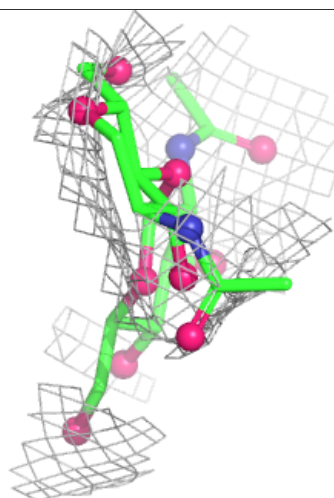
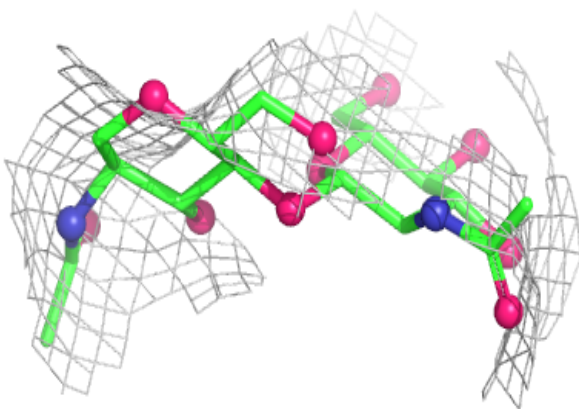
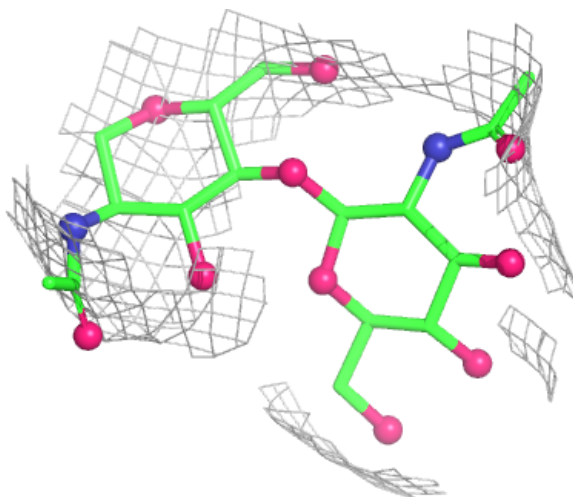
Electron density around Chain F:

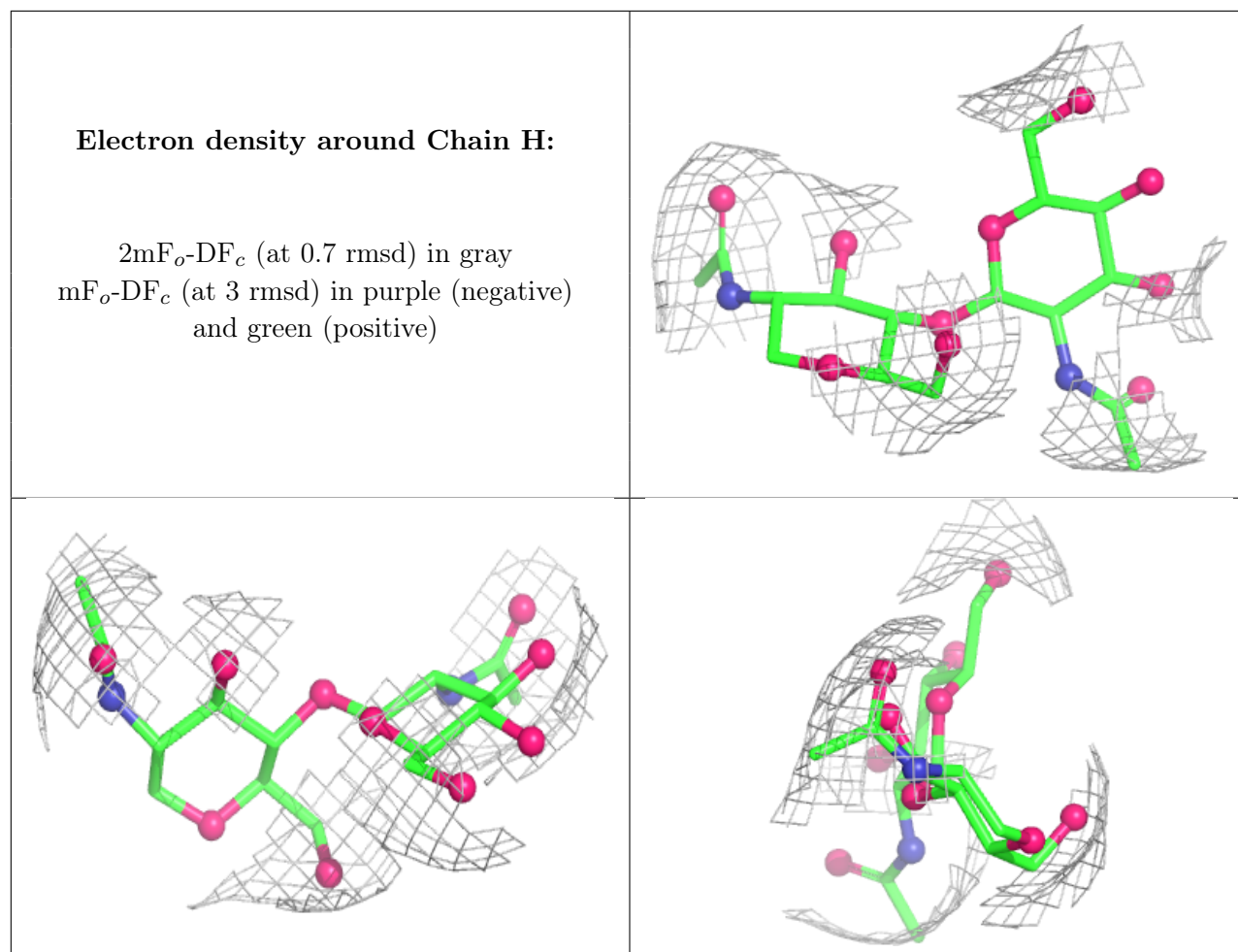
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain G:

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.