



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 14, 2022 – 04:04 PM EST

PDB ID : 8D4U
Title : Crystal Structure of Neutrophil Elastase Inhibited by Eap2 from *S. aureus*
Authors : Gido, C.D.; Herdendorf, T.J.; Geisbrecht, B.V.
Deposited on : 2022-06-02
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

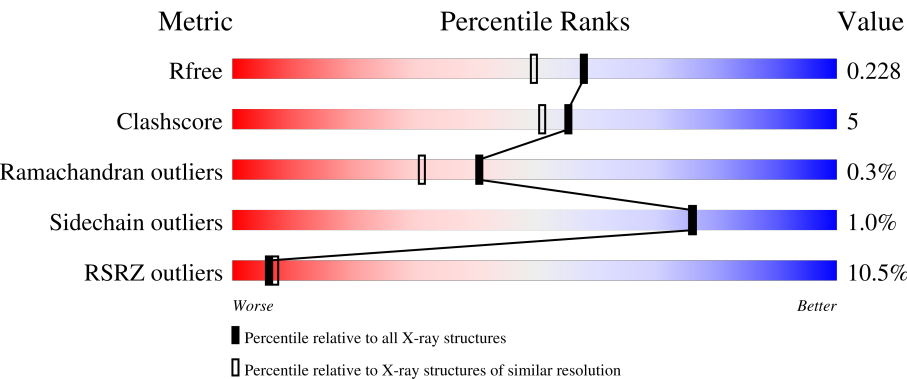
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	218	<div><div>4%</div><div>97%</div><div>.</div></div>
1	B	218	<div><div>19%</div><div>83%</div><div>17%</div></div>
2	C	100	<div><div>8%</div><div>81%</div><div>14%</div><div>.</div><div>.</div></div>
2	D	100	<div><div>8%</div><div>83%</div><div>14%</div><div>.</div></div>
3	E	3	<div><div>33%</div><div>67%</div></div>

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Mol	Chain	Length	Quality of chain
3	F	3	<div><div></div><div>67%</div><div>33%</div></div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5216 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 Neutrophil elastase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1635	1026	316	282	11			
1	B	218	Total	C	N	O	S	0	0	0
			1635	1026	316	282	11			

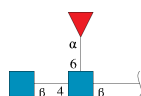
- Molecule 2 is a protein called Extracellular Adherence Protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	97	Total	C	N	O	0	0	0
			757	474	131	152			
2	D	97	Total	C	N	O	0	0	0
			757	474	131	152			

There are 6 discrepancies between the modelled and reference sequences:

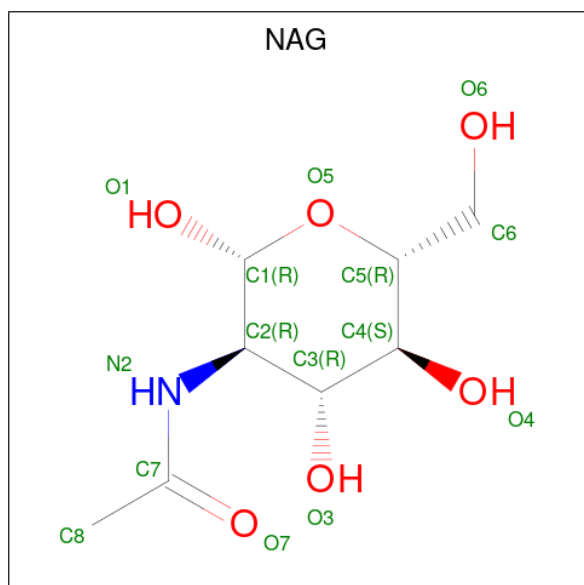
Chain	Residue	Modelled	Actual	Comment	Reference
C	155	GLY	-	expression tag	UNP Q99QS1
C	156	SER	-	expression tag	UNP Q99QS1
C	157	THR	-	expression tag	UNP Q99QS1
D	155	GLY	-	expression tag	UNP Q99QS1
D	156	SER	-	expression tag	UNP Q99QS1
D	157	THR	-	expression tag	UNP Q99QS1

- Molecule 3 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
3	E	3	Total	C	N	O	0	0	0
			38	22	2	14			
3	F	3	Total	C	N	O	0	0	0
			38	22	2	14			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

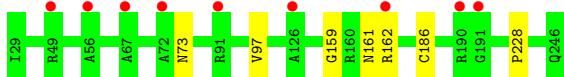
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	157	Total	O	0	0
			157	157		
5	C	84	Total	O	0	0
			84	84		
5	B	34	Total	O	0	0
			34	34		
5	D	67	Total	O	0	0
			67	67		

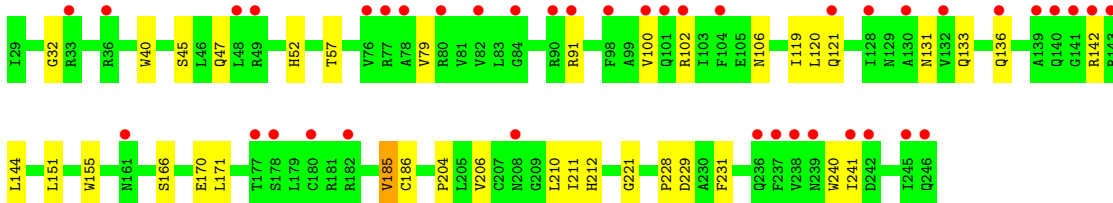
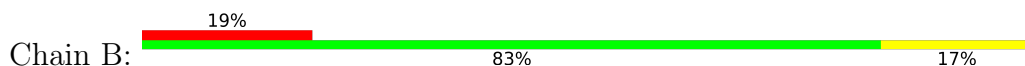
3 Residue-property plots [i](#)

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.

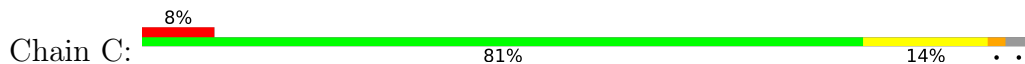
- Molecule 1: Neutrophil elastase



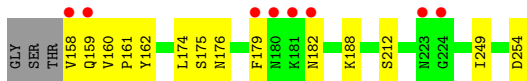
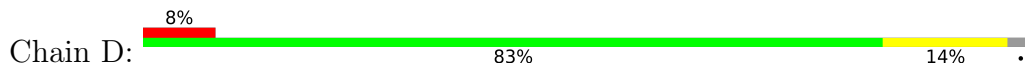
- Molecule 1: Neutrophil elastase



- Molecule 2: Extracellular Adherence Protein



- Molecule 2: Extracellular Adherence Protein



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





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

Chain F:  67% 33%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	152.51Å 56.01Å 86.04Å 90.00° 95.05° 90.00°	Depositor
Resolution (Å)	37.98 – 1.90 37.98 – 1.90	Depositor EDS
% Data completeness (in resolution range)	91.8 (37.98-1.90) 91.5 (37.98-1.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.89Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.200 , 0.230 0.199 , 0.228	Depositor DCC
R_{free} test set	2000 reflections (3.56%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.768	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5216	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.61% 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: 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	0.40	0/1665	0.64	0/2263
1	B	0.34	0/1665	0.60	0/2263
2	C	0.37	0/763	0.62	0/1030
2	D	0.38	0/763	0.58	0/1030
All	All	0.37	0/4856	0.61	0/6586

There are no bond length outliers.

There are no bond angle outliers.

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	1635	0	1650	5	0
1	B	1635	0	1651	22	0
2	C	757	0	785	15	0
2	D	757	0	785	8	0
3	E	38	0	34	0	0
3	F	38	0	34	1	0
4	B	14	0	13	0	0
5	A	157	0	0	1	0
5	B	34	0	0	4	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	C	84	0	0	3	0
5	D	67	0	0	3	1
All	All	5216	0	4952	50	1

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 5.

All (50) 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:185:VAL:HG23	1:B:231:PHE:HB2	1.56	0.85
2:C:165:THR:HA	2:C:170:SER:HB2	1.67	0.77
2:C:248:SER:OG	5:C:301:HOH:O	2.11	0.69
2:C:169:THR:O	2:C:169:THR:OG1	2.10	0.66
2:D:182:ASN:ND2	5:D:301:HOH:O	2.22	0.66
2:D:188:LYS:NZ	5:D:303:HOH:O	2.29	0.66
2:C:170:SER:OG	2:C:202:ARG:NH1	2.31	0.64
2:C:166:VAL:H	2:C:170:SER:HB2	1.63	0.62
2:D:161:PRO:HB2	2:D:174:LEU:HD11	1.80	0.61
2:C:170:SER:O	2:C:171:GLN:HB2	2.03	0.57
1:B:186:CYS:HB3	1:B:228:PRO:HB2	1.86	0.57
1:B:57:THR:HG21	1:B:204:PRO:HB3	1.86	0.56
2:C:182:ASN:ND2	5:C:303:HOH:O	2.38	0.56
1:B:119:ILE:HD11	1:B:241:ILE:HG12	1.88	0.54
1:B:144:LEU:HD11	1:B:212:HIS:CD2	2.43	0.54
2:C:166:VAL:N	2:C:170:SER:HB2	2.24	0.52
1:A:186:CYS:HB3	1:A:228:PRO:HB2	1.92	0.51
1:B:47:GLN:N	5:B:401:HOH:O	2.27	0.51
1:B:206:VAL:HG12	1:B:211:ILE:HD13	1.93	0.50
2:C:163:THR:HB	2:C:171:GLN:OE1	2.13	0.48
2:D:159:GLN:O	2:D:176:ASN:HB3	2.13	0.48
1:A:97:VAL:HG11	3:F:2:NAG:H81	1.96	0.47
2:D:212:SER:HB2	2:D:254:ASP:OD1	2.13	0.47
1:B:47:GLN:HG2	1:B:52:HIS:HA	1.97	0.46
2:C:183:GLN:O	2:C:243:SER:OG	2.31	0.46
1:B:45:SER:HB2	1:B:155:TRP:CZ3	2.51	0.46
2:C:162:TYR:HA	2:C:249:ILE:O	2.16	0.46
2:D:162:TYR:HA	2:D:249:ILE:O	2.17	0.45
1:A:161:ASN:O	1:A:162:ARG:HB2	2.17	0.44
2:C:170:SER:O	2:C:171:GLN:CB	2.65	0.44
2:C:175:SER:N	5:C:311:HOH:O	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:ASN:OD1	5:A:301:HOH:O	2.21	0.44
2:C:170:SER:HB3	2:C:202:ARG:NH2	2.34	0.43
1:B:131:ASN:ND2	5:B:407:HOH:O	2.50	0.43
1:B:102:ARG:H	1:B:121:GLN:HB3	1.84	0.42
2:D:158:VAL:HG22	2:D:179:PHE:HB2	2.00	0.42
1:B:32:GLY:HA2	1:B:171:LEU:HD13	2.01	0.42
1:B:151:LEU:O	1:B:206:VAL:HG22	2.19	0.42
1:B:142:ARG:HH22	1:B:210:LEU:HD12	1.83	0.42
2:D:162:TYR:CZ	2:D:175:SER:HB2	2.55	0.42
1:B:91:ARG:NH2	5:B:410:HOH:O	2.52	0.42
1:B:100:VAL:HG13	1:B:120:LEU:HB3	2.02	0.42
2:C:158:VAL:N	2:C:179:PHE:O	2.52	0.42
1:B:186:CYS:HA	1:B:229:ASP:O	2.20	0.42
1:B:221:GLY:N	5:D:303:HOH:O	2.54	0.41
1:B:40:TRP:NE1	1:B:170:GLU:OE1	2.43	0.41
1:B:79:VAL:HG13	5:B:401:HOH:O	2.20	0.40
1:B:106:ASN:HB2	1:B:240:TRP:CE2	2.57	0.40
1:B:204:PRO:HB2	1:B:211:ILE:HD12	2.03	0.40
1:A:159:GLY:O	1:A:161:ASN:O	2.40	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:434:HOH:O	5:D:367:HOH:O[1_565]	2.17	0.03

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	216/218 (99%)	206 (95%)	10 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	216/218 (99%)	203 (94%)	13 (6%)	0	100	100
2	C	95/100 (95%)	93 (98%)	1 (1%)	1 (1%)	14	5
2	D	95/100 (95%)	93 (98%)	1 (1%)	1 (1%)	14	5
All	All	622/636 (98%)	595 (96%)	25 (4%)	2 (0%)	41	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	171	GLN
2	D	160	VAL

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	172/172 (100%)	172 (100%)	0	100	100
1	B	172/172 (100%)	168 (98%)	4 (2%)	50	45
2	C	90/92 (98%)	89 (99%)	1 (1%)	73	73
2	D	90/92 (98%)	90 (100%)	0	100	100
All	All	524/528 (99%)	519 (99%)	5 (1%)	76	76

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	169	THR
1	B	133	GLN
1	B	136	GLN
1	B	166	SER
1	B	185	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	212	HIS

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 ⓘ

6 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	0.51	0
3	NAG	E	2	3	14,14,15	0.30	0	17,19,21	0.73	1 (5%)
3	FUC	E	3	3	10,10,11	1.23	1 (10%)	14,14,16	1.25	2 (14%)
3	NAG	F	1	3,1	14,14,15	0.37	0	17,19,21	0.45	0
3	NAG	F	2	3	14,14,15	0.39	0	17,19,21	0.60	0
3	FUC	F	3	3	10,10,11	0.82	0	14,14,16	0.81	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	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	FUC	E	3	3	-	-	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1
3	FUC	F	3	3	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	3	FUC	C1-C2	3.42	1.60	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	3	FUC	O2-C2-C1	2.56	114.39	109.15
3	E	2	NAG	C1-O5-C5	2.51	115.60	112.19
3	E	3	FUC	O5-C1-C2	2.04	113.93	110.77

There are no chirality outliers.

All (6) torsion outliers are listed below:

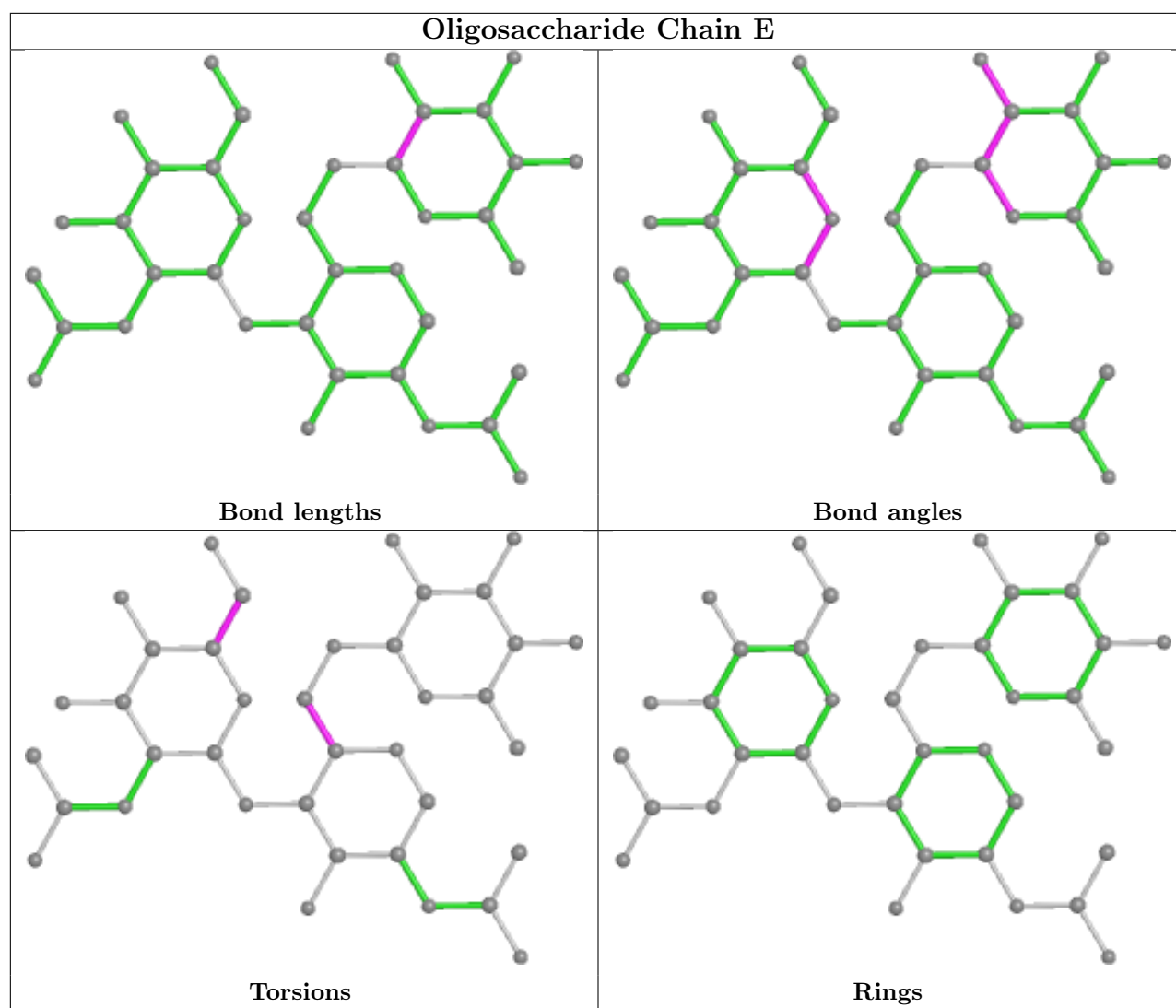
Mol	Chain	Res	Type	Atoms
3	F	2	NAG	O5-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	E	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6

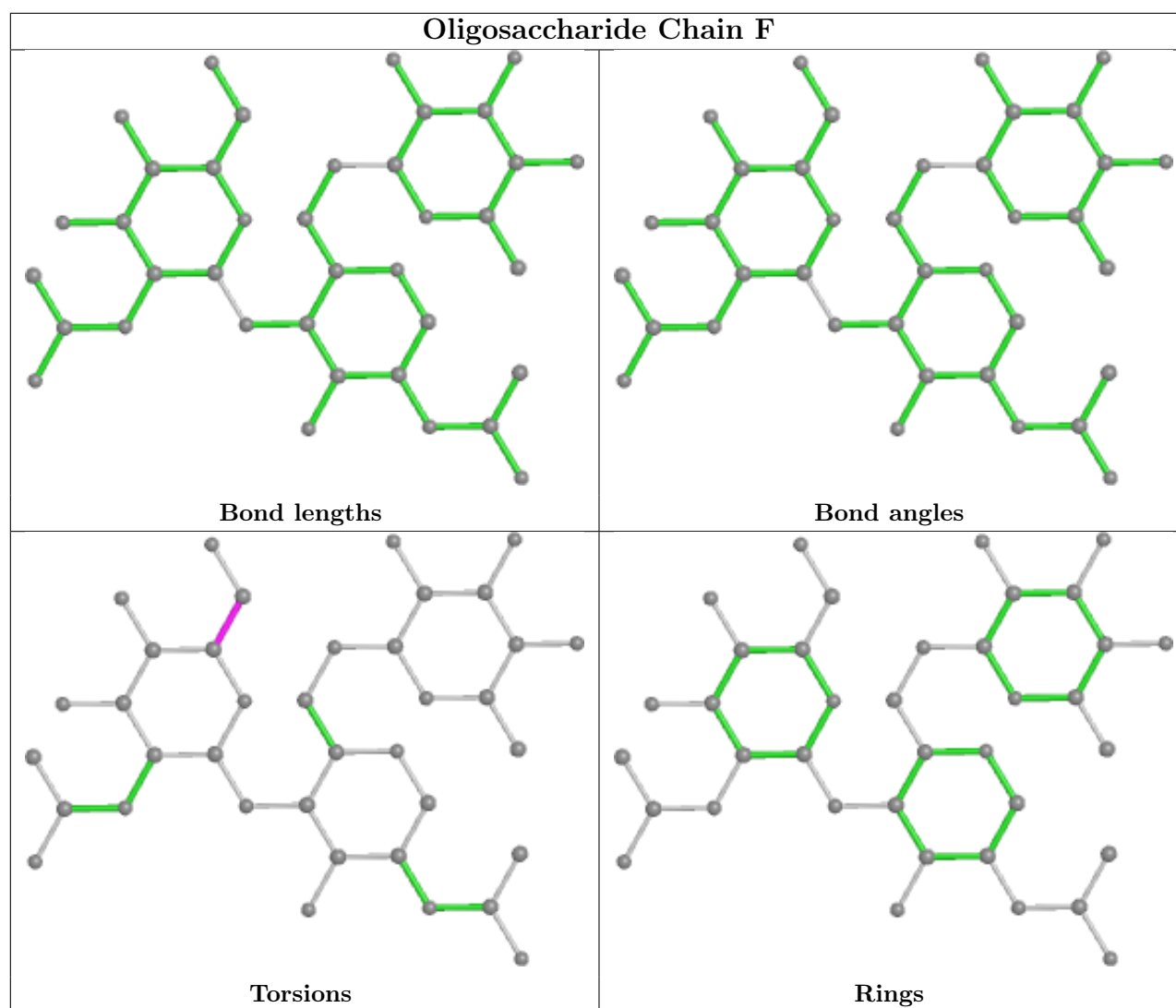
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	2	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 oligosaccharide.





5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
4	NAG	B	301	1	14,14,15	0.51	0	17,19,21	0.47	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
4	NAG	B	301	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [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	218/218 (100%)	0.42	9 (4%) 37 40	17, 31, 52, 88	0
1	B	218/218 (100%)	1.22	41 (18%) 1 1	35, 71, 93, 106	0
2	C	97/100 (97%)	0.46	8 (8%) 11 13	19, 32, 56, 97	0
2	D	97/100 (97%)	0.29	8 (8%) 11 13	20, 32, 59, 68	0
All	All	630/636 (99%)	0.68	66 (10%) 6 7	17, 41, 85, 106	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	173	ILE	7.4
1	B	49	ARG	6.6
2	C	172	ASN	6.5
2	C	175	SER	6.2
1	B	33	ARG	5.1
1	B	130	ALA	4.7
1	B	77	ARG	4.6
1	B	139	ALA	4.5
1	B	36	ARG	4.4
2	C	171	GLN	4.2
1	B	242	ASP	4.1
2	C	174	LEU	4.1
2	D	179	PHE	3.9
1	B	141	GLY	3.8
1	B	143	ARG	3.7
1	B	246	GLN	3.7
1	B	84	GLY	3.7
1	B	102	ARG	3.7
1	B	100	VAL	3.6
1	B	239	ASN	3.6
1	A	190	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	142	ARG	3.6
1	B	241	ILE	3.5
1	B	98	PHE	3.4
1	B	80	ARG	3.4
2	D	224	GLY	3.3
1	A	91	ARG	3.2
1	B	104	PHE	3.2
1	B	78	ALA	3.2
2	D	158	VAL	3.2
1	B	237	PHE	3.1
1	B	121	GLN	3.0
1	A	49	ARG	3.0
2	C	170	SER	3.0
1	B	238	VAL	3.0
2	C	169	THR	2.9
2	D	180	ASN	2.9
2	D	182	ASN	2.9
1	B	48	LEU	2.7
2	D	181	LYS	2.7
1	B	132	VAL	2.7
1	B	177	THR	2.6
1	B	180	CYS	2.6
1	B	91	ARG	2.6
1	B	128	ILE	2.6
1	B	245	ILE	2.5
1	A	191	GLY	2.5
1	B	178	SER	2.5
1	B	76	VAL	2.5
1	B	182	ARG	2.4
1	B	208	ASN	2.4
2	D	223	ASN	2.4
1	B	136	GLN	2.4
1	A	67	ALA	2.3
1	B	161	ASN	2.3
1	A	72	ALA	2.3
1	A	56	ALA	2.2
2	C	254	ASP	2.2
1	B	236	GLN	2.2
1	A	126	ALA	2.2
1	B	90	ARG	2.2
1	B	82	VAL	2.2
2	D	159	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	162	ARG	2.1
1	B	140	GLN	2.1
1	B	101	GLN	2.1

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](#)

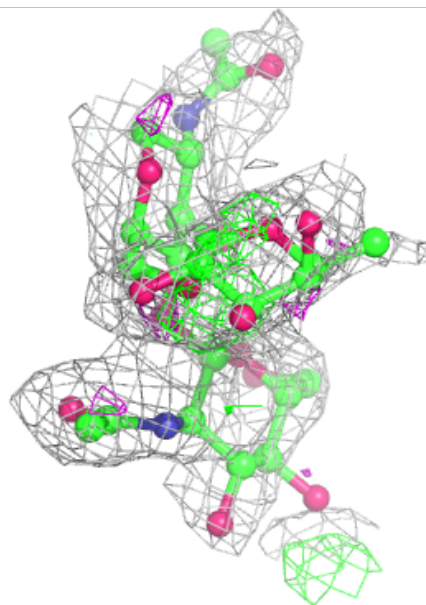
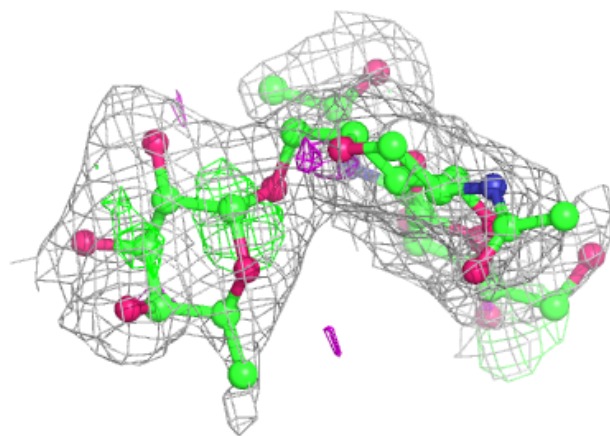
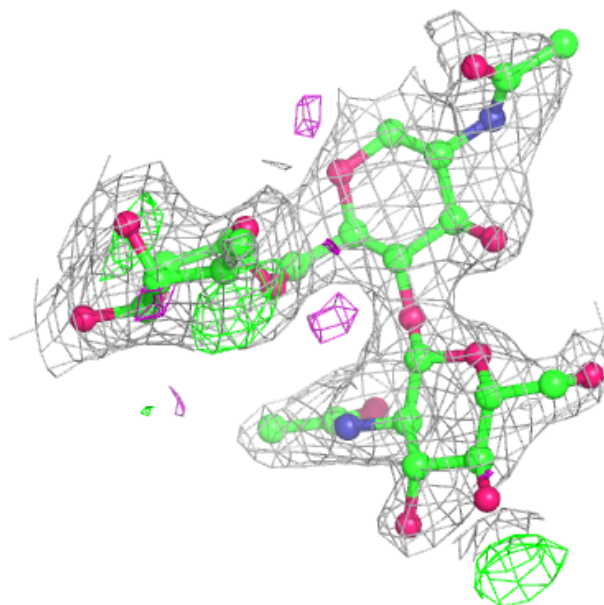
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

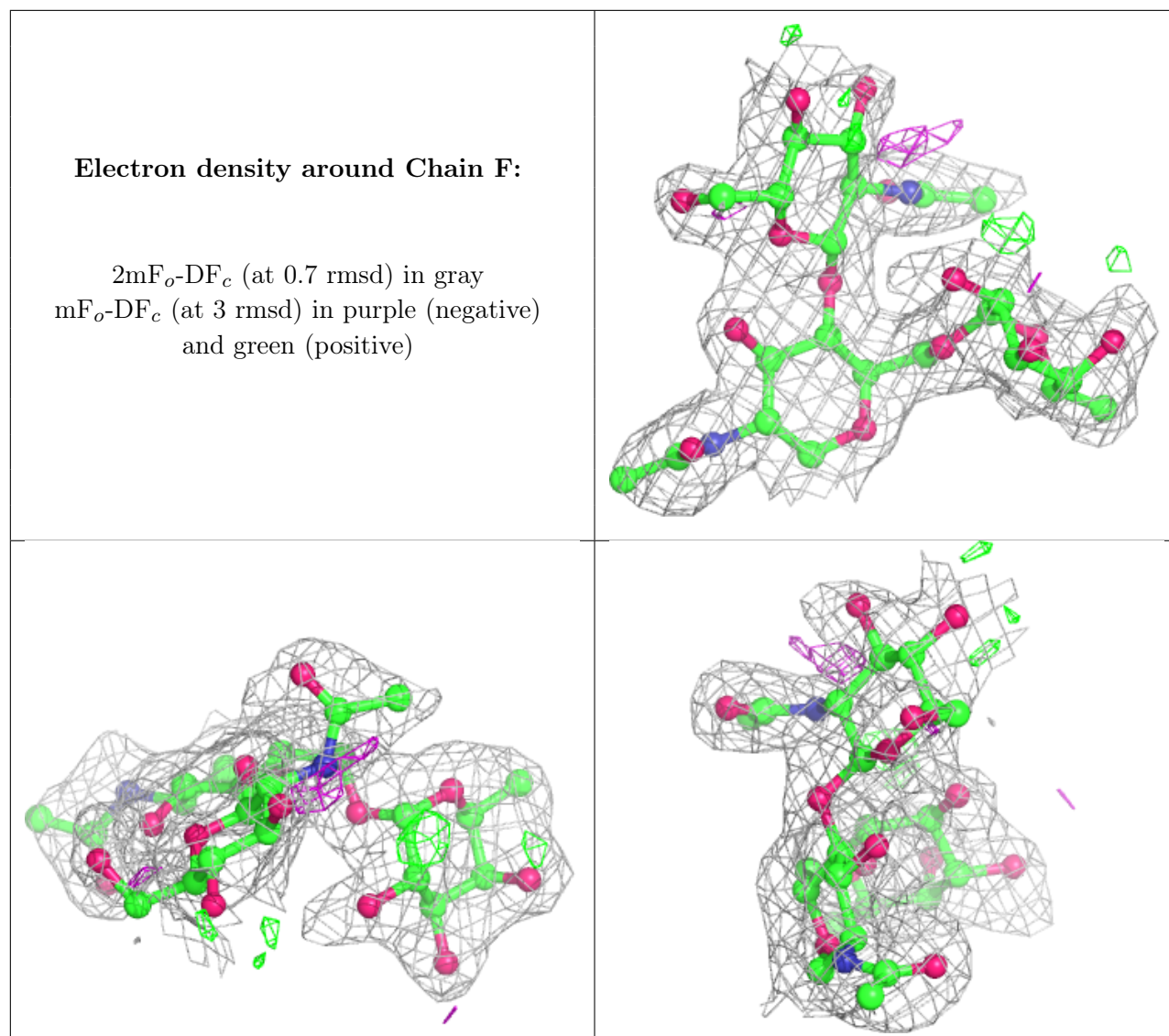
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	E	2	14/15	0.69	0.30	54,67,75,77	0
3	FUC	E	3	10/11	0.71	0.23	42,54,59,61	0
3	NAG	F	2	14/15	0.81	0.22	45,50,56,62	0
3	NAG	E	1	14/15	0.82	0.20	51,58,64,66	0
3	FUC	F	3	10/11	0.87	0.15	34,46,50,53	0
3	NAG	F	1	14/15	0.94	0.09	30,33,38,39	0

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 E:

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





6.4 Ligands [i](#)

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
4	NAG	B	301	14/15	0.64	0.27	82,89,94,96	0

6.5 Other polymers [i](#)

There are no such residues in this entry.