



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:02 AM UTC

PDB ID : 8G26 / pdb_00008g26
Title : Crystal Structure of Cathepsin-G and Neutrophil Elastase Inhibited by *S. aureus* EapH2 at pH 8.5
Authors : Mishra, N.B.; Geisbrecht, B.V.
Deposited on : 2023-02-03
Resolution : 1.85 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

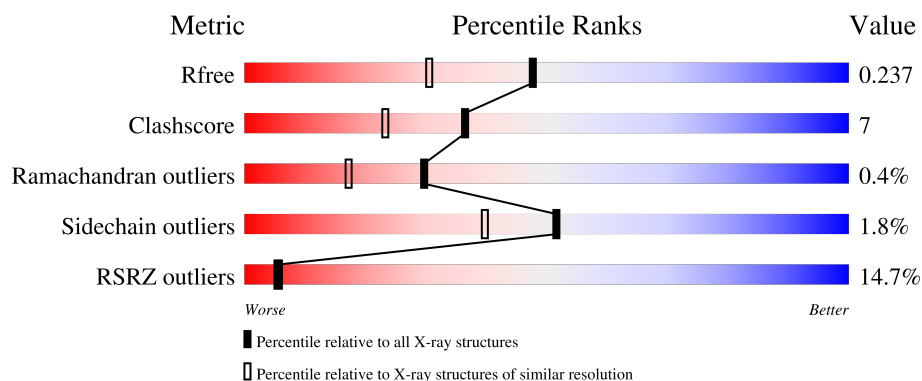
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	223	92% 8%
2	B	218	32% 74% 25% .
3	C	117	7% 73% 14% . 12%
4	D	2	100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8810 atoms, of which 4314 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 Cathepsin-G.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	223	Total	C	H	N	O	S	0	0	0
			3573	1093	1793	369	308	10			

- Molecule 2 is a protein called Neutrophil elastase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	218	Total	C	H	N	O	S	0	0	0
			3285	1026	1650	316	282	11			

- Molecule 3 is a protein called MAP domain-containing protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	103	Total	C	H	N	O	S	0	0	0
			1656	520	836	136	162	2			

There are 3 discrepancies between the modelled and reference sequences:

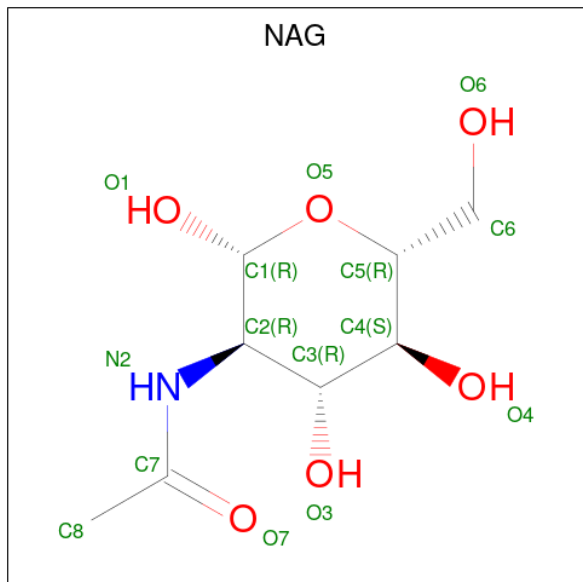
Chain	Residue	Modelled	Actual	Comment	Reference
C	28	GLY	-	expression tag	UNP A0A0H3JUK5
C	29	SER	-	expression tag	UNP A0A0H3JUK5
C	30	THR	-	expression tag	UNP A0A0H3JUK5

- 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	D	2	Total	C	H	N	O		0	0	0
			51	16	23	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	B	1	Total	C	H	N	O	0	0
			26	8	12	1	5		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	132	Total	O	0	0
			132	132		
6	B	32	Total	O	0	0
			32	32		
6	C	55	Total	O	0	0
			55	55		

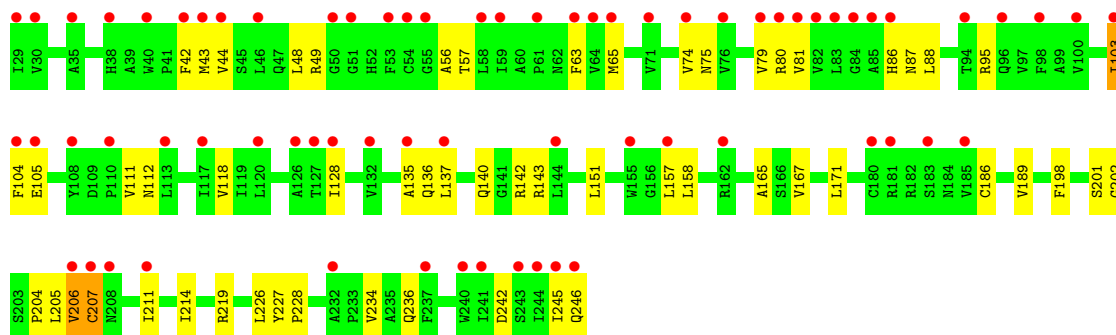
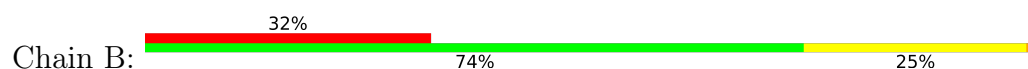
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

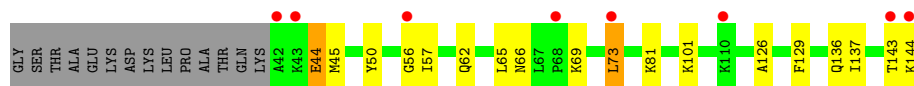
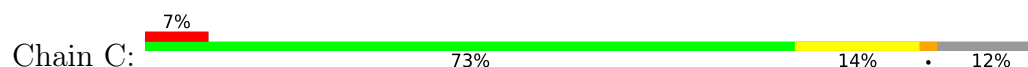
• Molecule 1: Cathepsin-G



• Molecule 2: Neutrophil elastase



• Molecule 3: MAP domain-containing protein



• Molecule 4: 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	49.46Å 68.92Å 82.52Å 90.00° 102.38° 90.00°	Depositor
Resolution (Å)	39.56 – 1.85 39.56 – 1.85	Depositor EDS
% Data completeness (in resolution range)	95.1 (39.56-1.85) 94.8 (39.56-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 1.85Å)	Xtriage
Refinement program	PHENIX v1.19.2	Depositor
R, R_{free}	0.203 , 0.238 0.203 , 0.237	Depositor DCC
R_{free} test set	1987 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtriage
Anisotropy	0.248	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8810	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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: 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	0.36	0/1814	0.59	0/2447
2	B	0.22	0/1665	0.44	0/2263
3	C	0.33	0/832	0.52	0/1120
All	All	0.31	0/4311	0.52	0/5830

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

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	1780	1793	1793	8	0
2	B	1635	1650	1650	45	0
3	C	820	836	836	11	0
4	D	28	23	25	0	0
5	B	14	12	13	0	0
6	A	132	0	0	1	0
6	B	32	0	0	0	0
6	C	55	0	0	0	0
All	All	4496	4314	4317	62	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 7.

All (62) 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)
2:B:57:THR:HG21	2:B:204:PRO:HB3	1.73	0.69
2:B:48:LEU:HD13	2:B:79:VAL:HG22	1.78	0.66
2:B:65:MET:HE1	2:B:234:VAL:HG13	1.78	0.65
2:B:43:MET:HE1	2:B:204:PRO:HD3	1.81	0.63
2:B:43:MET:HE1	2:B:204:PRO:CD	2.29	0.62
2:B:206:VAL:HG13	2:B:207:CYS:N	2.16	0.61
2:B:206:VAL:O	2:B:207:CYS:SG	2.60	0.58
2:B:202:GLY:HA2	2:B:214:ILE:HG22	1.86	0.58
2:B:63:PHE:CG	2:B:245:ILE:HG22	2.40	0.56
1:A:136:LEU:HD13	1:A:160:ARG:CZ	2.36	0.56
2:B:87:ASN:O	2:B:95:ARG:NH2	2.39	0.55
2:B:103:ILE:HD12	2:B:104:PHE:N	2.22	0.55
2:B:43:MET:HE3	2:B:43:MET:HA	1.88	0.55
3:C:56:GLY:C	3:C:57:ILE:HD12	2.33	0.54
2:B:44:VAL:HB	2:B:56:ALA:HB3	1.91	0.53
2:B:137:LEU:HD12	2:B:234:VAL:HG11	1.91	0.52
2:B:151:LEU:O	2:B:206:VAL:HG12	2.10	0.52
2:B:42:PHE:HB2	2:B:135:ALA:HB2	1.92	0.52
3:C:45:MET:HE3	3:C:66:ASN:HB3	1.92	0.52
1:A:28:PRO:HG2	1:A:120:ASN:OD1	2.10	0.52
2:B:171:LEU:HD21	2:B:189:VAL:HG21	1.90	0.52
3:C:50:TYR:HA	3:C:137:ILE:O	2.10	0.52
3:C:73:LEU:HD12	3:C:129:PHE:CE2	2.45	0.51
2:B:137:LEU:CD1	2:B:234:VAL:HG11	2.41	0.51
3:C:136:GLN:HG3	3:C:137:ILE:N	2.26	0.51
2:B:226:LEU:HD11	2:B:227:TYR:CD2	2.46	0.50
2:B:205:LEU:O	2:B:206:VAL:HG12	2.11	0.50
3:C:65:LEU:HD21	3:C:81:LYS:HZ2	1.78	0.49
2:B:88:LEU:HA	2:B:95:ARG:NH2	2.27	0.49
2:B:105:GLU:HG3	2:B:118:VAL:HG23	1.94	0.49
2:B:103:ILE:HD12	2:B:103:ILE:C	2.38	0.48
2:B:142:ARG:NH1	2:B:143:ARG:O	2.47	0.48
2:B:157:LEU:HD23	2:B:198:PHE:O	2.13	0.48
2:B:63:PHE:CD2	2:B:245:ILE:HG22	2.49	0.48
2:B:206:VAL:HG22	2:B:207:CYS:H	1.80	0.47
2:B:206:VAL:O	2:B:207:CYS:CB	2.63	0.47
3:C:44:GLU:HG3	3:C:69:LYS:HB3	1.96	0.47
2:B:206:VAL:HA	2:B:211:ILE:HA	1.98	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:202:GLY:HA2	2:B:214:ILE:CG2	2.46	0.46
1:A:144:ARG:HD3	3:C:62:GLN:OE1	2.16	0.45
2:B:43:MET:HE1	2:B:204:PRO:HD2	1.96	0.45
2:B:158:LEU:HD21	2:B:165:ALA:HB2	1.97	0.45
3:C:101:LYS:HD3	3:C:144:LYS:HB2	1.99	0.45
2:B:74:VAL:HG12	2:B:75:ASN:N	2.31	0.45
2:B:128:ILE:H	2:B:128:ILE:HD12	1.82	0.44
2:B:42:PHE:CB	2:B:135:ALA:HB2	2.47	0.43
2:B:111:VAL:HG13	2:B:112:ASN:CG	2.44	0.43
2:B:140:GLN:HE22	2:B:236:GLN:C	2.27	0.43
1:A:132:ARG:HG3	1:A:133:PRO:HD2	2.00	0.42
1:A:168:LEU:HD23	1:A:169:ARG:HH21	1.83	0.42
2:B:44:VAL:HG11	2:B:81:VAL:HG13	2.01	0.42
2:B:219:ARG:HG2	2:B:227:TYR:CD2	2.54	0.42
2:B:242:ASP:O	2:B:246:GLN:HG2	2.19	0.42
2:B:245:ILE:O	2:B:246:GLN:C	2.62	0.42
2:B:186:CYS:HB3	2:B:228:PRO:HB2	2.03	0.41
1:A:125:PRO:HD3	1:A:206:ALA:O	2.20	0.41
1:A:208:GLY:HA2	1:A:224:THR:O	2.21	0.41
2:B:79:VAL:O	2:B:80:ARG:NH1	2.54	0.41
6:A:332:HOH:O	3:C:45:MET:HE2	2.19	0.41
2:B:86:HIS:CE1	2:B:167:VAL:CG2	3.03	0.41
2:B:201:SER:HB3	3:C:126:ALA:HB3	2.03	0.40
1:A:127:ALA:HA	1:A:230:LEU:HD12	2.03	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	221/223 (99%)	215 (97%)	6 (3%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	216/218 (99%)	207 (96%)	7 (3%)	2 (1%)	14	4
3	C	101/117 (86%)	100 (99%)	1 (1%)	0	100	100
All	All	538/558 (96%)	522 (97%)	14 (3%)	2 (0%)	30	17

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	207	CYS
2	B	206	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	190/190 (100%)	188 (99%)	2 (1%)	65	57
2	B	172/172 (100%)	169 (98%)	3 (2%)	53	42
3	C	92/103 (89%)	89 (97%)	3 (3%)	33	18
All	All	454/465 (98%)	446 (98%)	8 (2%)	51	40

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ARG
1	A	36	GLN
2	B	49	ARG
2	B	103	ILE
2	B	136	GLN
3	C	44	GLU
3	C	73	LEU
3	C	143	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	GLN
1	A	102	ASN
1	A	118	ASN
2	B	86	HIS
2	B	112	ASN
2	B	131	ASN
2	B	169	GLN
2	B	236	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

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	$\# Z > 2$
4	NAG	D	1	4,2	14,14,15	0.23	0	17,19,21	0.56	0
4	NAG	D	2	4	14,14,15	0.40	0	17,19,21	0.39	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	D	1	4,2	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

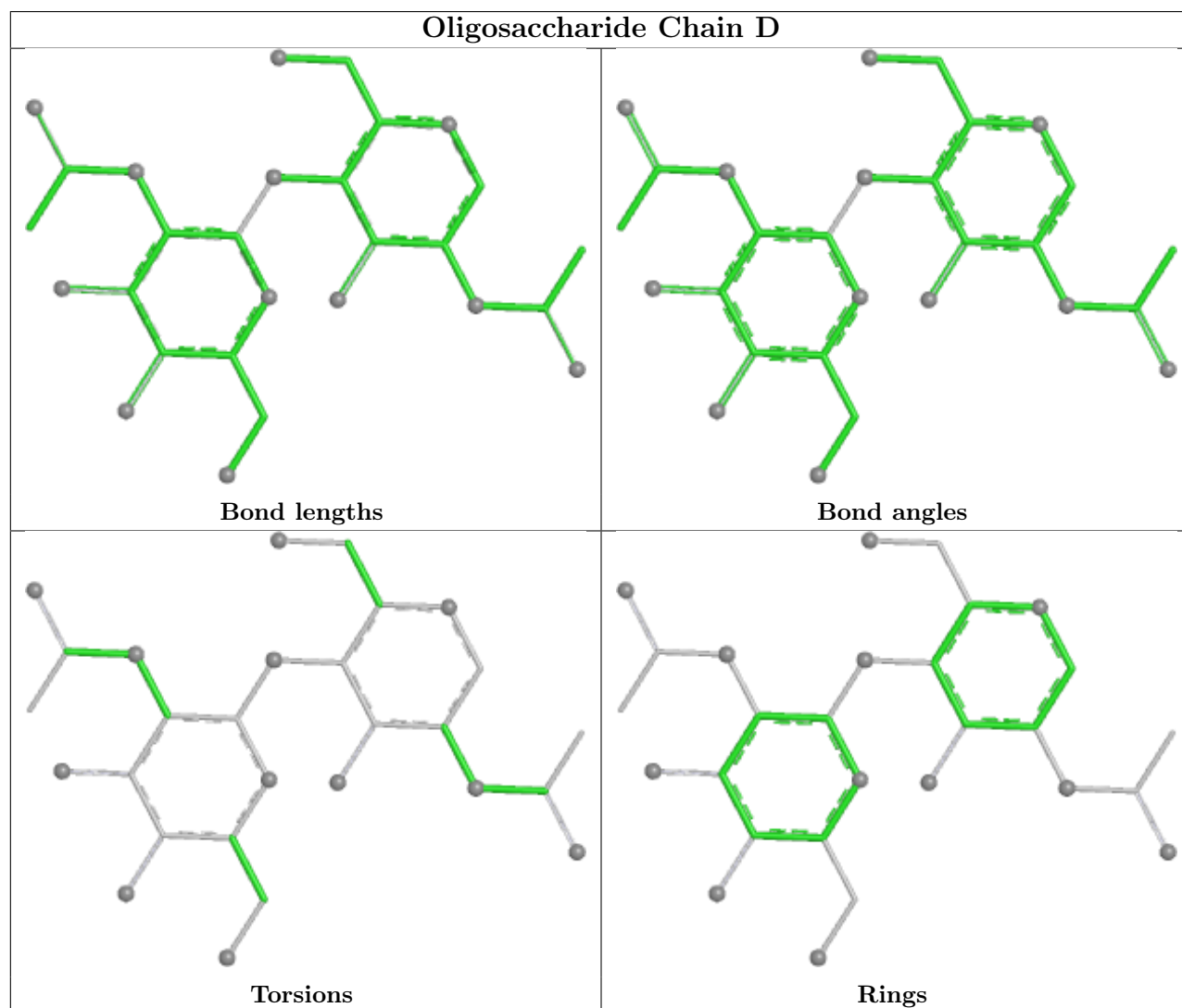
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	$\# Z > 2$
5	NAG	B	301	2	14,14,15	0.34	0	17,19,21	0.39	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	B	301	2	-	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	223/223 (100%)	0.02	3 (1%) 75 79	20, 35, 76, 89	0
2	B	218/218 (100%)	1.77	69 (31%) 1 1	51, 82, 114, 143	0
3	C	103/117 (88%)	0.55	8 (7%) 19 20	26, 49, 96, 149	0
All	All	544/558 (97%)	0.82	80 (14%) 6 5	20, 57, 107, 149	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	241	ILE	4.3
3	C	42	ALA	4.1
2	B	144	LEU	3.9
2	B	127	THR	3.8
2	B	85	ALA	3.8
2	B	240	TRP	3.8
2	B	132	VAL	3.7
2	B	117	ILE	3.7
2	B	83	LEU	3.6
2	B	82	VAL	3.5
2	B	206	VAL	3.5
2	B	207	CYS	3.5
2	B	58	LEU	3.3
2	B	79	VAL	3.3
2	B	42	PHE	3.3
2	B	244	ILE	3.2
2	B	120	LEU	3.2
2	B	86	HIS	3.2
2	B	76	VAL	3.1
2	B	61	PRO	3.1
2	B	71	VAL	3.0
2	B	104	PHE	3.0
2	B	64	VAL	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	81	VAL	3.0
2	B	54	CYS	3.0
2	B	105	GLU	3.0
2	B	108	TYR	2.9
2	B	35	ALA	2.9
2	B	245	ILE	2.9
3	C	68	PRO	2.9
2	B	128	ILE	2.8
2	B	135	ALA	2.8
2	B	211	ILE	2.8
2	B	237	PHE	2.7
2	B	246	GLN	2.7
2	B	137	LEU	2.7
2	B	65	MET	2.7
2	B	46	LEU	2.6
2	B	43	MET	2.6
2	B	208	ASN	2.6
2	B	126	ALA	2.6
2	B	243	SER	2.6
2	B	29	ILE	2.6
2	B	59	ILE	2.5
2	B	155	TRP	2.5
2	B	30	VAL	2.5
2	B	94	THR	2.5
3	C	110	LYS	2.5
2	B	40	TRP	2.5
2	B	74	VAL	2.5
3	C	73	LEU	2.4
2	B	183	SER	2.4
2	B	53	PHE	2.4
2	B	162	ARG	2.4
2	B	113	LEU	2.3
2	B	50	GLY	2.3
1	A	188	ARG	2.3
2	B	80	ARG	2.3
2	B	44	VAL	2.3
2	B	185	VAL	2.3
3	C	56	GLY	2.3
2	B	96	GLN	2.3
1	A	117	ARG	2.2
2	B	181	ARG	2.2
2	B	63	PHE	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	98	PHE	2.2
3	C	143	THR	2.2
2	B	55	GLY	2.2
2	B	157	LEU	2.2
2	B	84	GLY	2.1
2	B	110	PRO	2.1
3	C	43	LYS	2.1
2	B	103	ILE	2.1
2	B	38	HIS	2.1
2	B	51	GLY	2.1
2	B	232	ALA	2.1
1	A	169	ARG	2.1
3	C	144	LYS	2.0
2	B	100	VAL	2.0
2	B	180	CYS	2.0

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

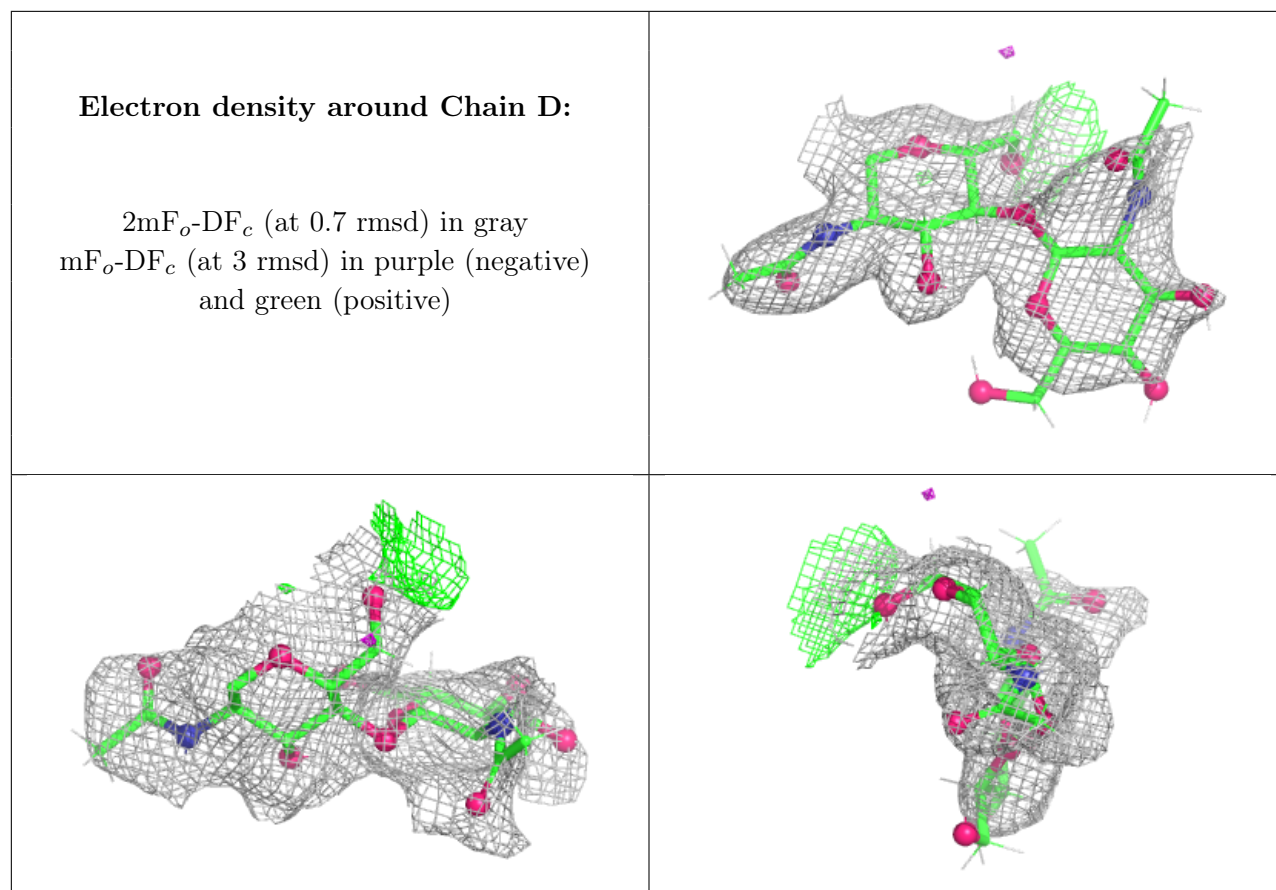
There are no non-standard protein/DNA/RNA residues in this entry.

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($\text{\AA}^2$)	Q<0.9
4	NAG	D	2	14/15	0.62	0.13	91,106,127,134	0
4	NAG	D	1	14/15	0.76	0.13	69,81,95,102	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 [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($\text{\AA}^2$)	Q<0.9
5	NAG	B	301	14/15	0.66	0.15	88,98,113,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.