



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 6, 2020 – 08:41 AM BST

PDB ID : 2YD0
Title : Crystal structure of the soluble domain of human endoplasmic reticulum aminopeptidase 1 ERAP1
Authors : Vollmar, M.; Kochan, G.; Krojer, T.; Ugochukwu, E.; Muniz, J.R.C.; Raynor, J.; Chaikuad, A.; Allerston, C.; von Delft, F.; Bountra, C.; Arrowsmith, C.H.; Weigelt, J.; Edwards, A.; Knapp, S.
Deposited on : 2011-03-17
Resolution : 2.70 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 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 : 2.13.1
buster-report : 1.1.7 (2018)
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) : 2.13.1

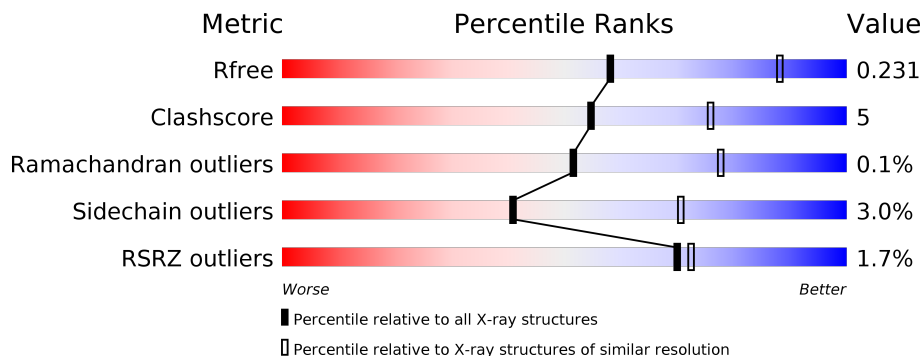
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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	897	 2% 84% 10% . .
2	B	2	 100%
2	C	2	 100%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7239 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 ENDOPLASMIC RETICULUM AMINOPEPTIDASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	858	6852	4422	1132	1264	34	0	4	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	941	LYS	-	expression tag	UNP Q9NZ08
A	942	LYS	-	expression tag	UNP Q9NZ08

- Molecule 2 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
			Total	C	N	O			
2	B	2	28	16	2	10	0	0	0
2	C	2	28	16	2	10	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	1	1	1	0	0

- Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

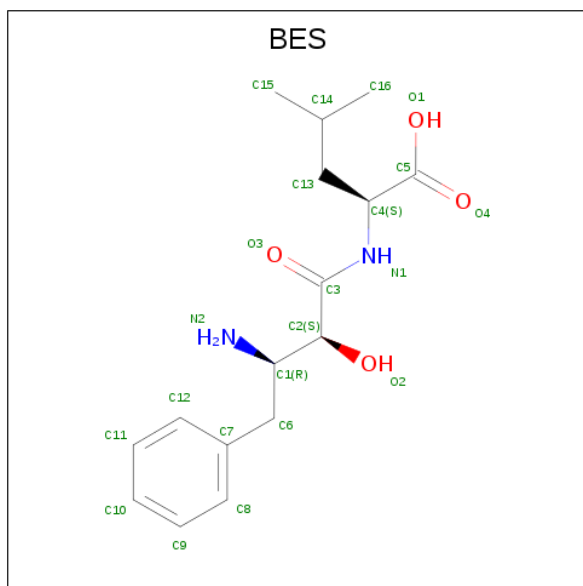
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	K		
5	A	2	2	2	0	0

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 7 is 2-(3-AMINO-2-HYDROXY-4-PHENYL-BUTYRYLAMINO)-4-METHYL-PENTANOIC ACID (three-letter code: BES) (formula: $C_{16}H_{24}N_2O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			22	16	2	4		

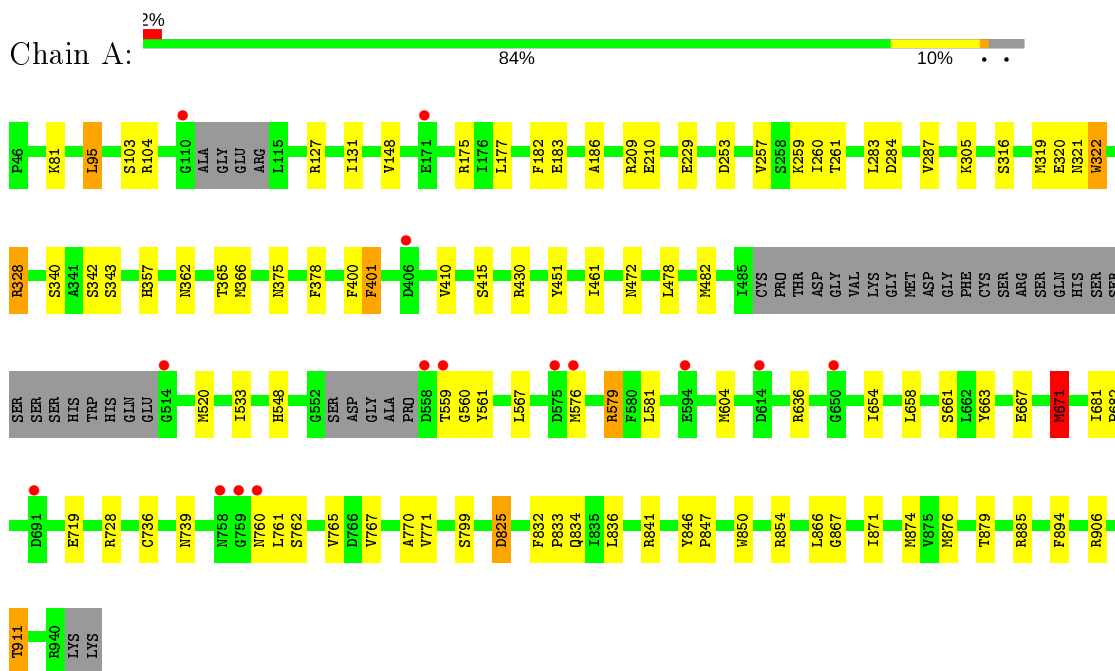
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	288	Total 288	O 288	0	0

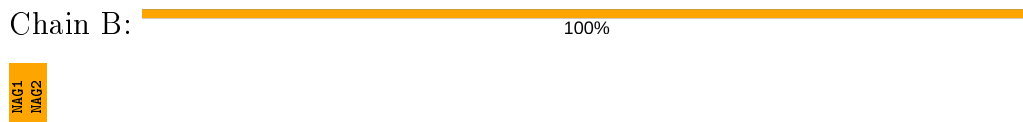
3 Residue-property plots i

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.

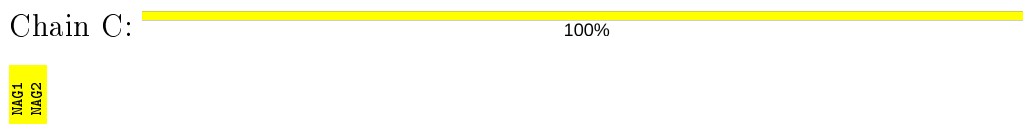
- Molecule 1: ENDOPLASMIC RETICULUM AMINOPEPTIDASE 1



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



- Molecule 2: 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 6 2 2	Depositor
Cell constants a, b, c, α , β , γ	200.95Å 200.95Å 114.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.94 – 2.70 19.92 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.94-2.70) 99.6 (19.92-2.70)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.02 (at 2.71Å)	Xtrriage
Refinement program	REFMAC 5.5.0110	Depositor
R, R_{free}	0.152 , 0.215 0.181 , 0.231	Depositor DCC
R_{free} test set	1880 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	36.8	Xtrriage
Anisotropy	0.001	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7239	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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: K, BES, ZN, NAG, EDO

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	0.78	0/7038	0.82	9/9554 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	430	ARG	NE-CZ-NH2	-6.63	116.99	120.30
1	A	579	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	A	430	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	885	ARG	NE-CZ-NH1	5.51	123.06	120.30
1	A	825	ASP	CB-CG-OD1	5.51	123.26	118.30
1	A	209	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	A	104	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	A	671	MET	CG-SD-CE	5.22	108.55	100.20
1	A	328	ARG	NE-CZ-NH1	5.07	122.83	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	866	LEU	Peptide

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	6852	0	6694	69	0
2	B	28	0	25	3	0
2	C	28	0	25	0	0
3	A	14	0	13	0	0
4	A	1	0	0	0	0
5	A	2	0	0	0	0
6	A	4	0	6	3	0
7	A	22	0	22	8	0
8	A	288	0	0	3	0
All	All	7239	0	6785	72	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 5.

All (72) 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:559:THR:HG23	1:A:561:TYR:H	1.32	0.93
1:A:366:MET:HE3	1:A:375:ASN:OD1	1.72	0.88
1:A:95:LEU:HD11	1:A:131:ILE:HD11	1.55	0.85
1:A:879:THR:OG1	1:A:911:THR:HG21	1.75	0.85
1:A:95:LEU:HD12	1:A:95:LEU:C	1.97	0.84
1:A:366:MET:HE3	1:A:375:ASN:CG	2.05	0.77
1:A:366:MET:CE	1:A:375:ASN:CG	2.55	0.75
1:A:183:GLU:OE1	7:A:1950:BES:N2	2.22	0.73
1:A:175:ARG:NH1	1:A:253:ASP:OD2	2.24	0.71
1:A:319:MET:SD	7:A:1950:BES:H61	2.31	0.70
1:A:579:ARG:HB3	6:A:1949:EDO:H12	1.76	0.67
1:A:316:SER:O	1:A:328:ARG:HD2	1.97	0.64
1:A:95:LEU:C	1:A:95:LEU:CD1	2.67	0.61
1:A:548:HIS:CB	1:A:559:THR:HG21	2.30	0.61
1:A:671:MET:HA	1:A:671:MET:CE	2.31	0.60
1:A:451:TYR:HA	6:A:1949:EDO:H22	1.83	0.60
1:A:559:THR:HG23	1:A:560:GLY:N	2.17	0.60
1:A:182:PHE:HA	1:A:186:ALA:HB3	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:GLU:HG2	2:B:1:NAG:H83	1.85	0.58
1:A:95:LEU:HD11	1:A:131:ILE:CD1	2.31	0.58
1:A:366:MET:HE1	1:A:375:ASN:CG	2.24	0.58
1:A:867:GLY:HA2	8:A:2274:HOH:O	2.07	0.53
1:A:671:MET:HA	1:A:671:MET:HE2	1.90	0.53
1:A:854:ARG:HG2	1:A:894:PHE:CD1	2.43	0.53
1:A:719:GLU:O	1:A:728:ARG:NH2	2.40	0.53
1:A:257:VAL:HG23	1:A:283:LEU:HD22	1.92	0.52
1:A:836:LEU:HD23	1:A:874:MET:HG2	1.93	0.51
1:A:316:SER:HB3	7:A:1950:BES:O1	2.10	0.51
1:A:850:TRP:CZ2	1:A:854:ARG:HD2	2.46	0.51
1:A:867:GLY:CA	8:A:2274:HOH:O	2.58	0.51
1:A:559:THR:CG2	1:A:560:GLY:N	2.74	0.50
1:A:260:ILE:HG22	1:A:261:THR:O	2.12	0.50
1:A:736[B]:CYS:SG	1:A:770:ALA:HB1	2.51	0.50
2:B:2:NAG:O7	2:B:2:NAG:C3	2.60	0.49
1:A:846:TYR:CG	1:A:847:PRO:HD3	2.47	0.49
1:A:520:MET:CE	1:A:581:LEU:HD11	2.42	0.49
1:A:183:GLU:HB3	7:A:1950:BES:H12	1.95	0.48
1:A:365:THR:O	1:A:472:ASN:HA	2.13	0.48
1:A:259:LYS:HD3	1:A:287:VAL:HG21	1.96	0.48
1:A:357:HIS:CD2	7:A:1950:BES:O2	2.66	0.48
1:A:548:HIS:HB2	1:A:559:THR:HG21	1.96	0.47
1:A:871:ILE:HA	1:A:874:MET:HE3	1.95	0.47
1:A:81:LYS:HG2	1:A:148:VAL:HG22	1.96	0.47
1:A:850:TRP:CH2	1:A:854:ARG:HD2	2.50	0.47
1:A:415:SER:O	1:A:906:ARG:NH1	2.46	0.47
1:A:461:ILE:HG22	1:A:482:MET:CE	2.44	0.47
1:A:340:SER:HA	1:A:765:VAL:HG11	1.97	0.46
1:A:559:THR:HG23	1:A:561:TYR:N	2.15	0.45
1:A:183:GLU:O	7:A:1950:BES:H11	2.17	0.45
1:A:320:GLU:OE1	7:A:1950:BES:N2	2.51	0.44
1:A:658:LEU:O	1:A:661:SER:HB2	2.17	0.44
1:A:579:ARG:HD3	6:A:1949:EDO:H21	1.99	0.44
1:A:366:MET:HE1	1:A:375:ASN:ND2	2.33	0.44
1:A:322:TRP:CD2	1:A:362:ASN:HB3	2.52	0.44
1:A:95:LEU:O	1:A:95:LEU:HD12	2.15	0.44
1:A:520:MET:HE2	1:A:581:LEU:HD11	2.00	0.43
1:A:876:MET:HG2	1:A:911:THR:HG23	1.99	0.43
1:A:548:HIS:ND1	1:A:559:THR:HG21	2.32	0.43
2:B:2:NAG:O7	2:B:2:NAG:O3	2.29	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:PHE:O	1:A:401:PHE:C	2.57	0.43
1:A:681:ILE:N	1:A:682:PRO:HD2	2.35	0.42
7:A:1950:BES:H163	7:A:1950:BES:H4	1.91	0.42
1:A:825:ASP:N	8:A:2261:HOH:O	2.52	0.42
1:A:533:ILE:HG13	1:A:567:LEU:HD21	2.02	0.42
1:A:478:LEU:HD11	1:A:482:MET:HE3	2.01	0.41
1:A:832:PHE:HB3	1:A:833:PRO:HD3	2.02	0.41
1:A:761:LEU:HD12	1:A:762:SER:H	1.86	0.41
1:A:366:MET:CE	1:A:375:ASN:ND2	2.84	0.41
1:A:320:GLU:O	1:A:321:ASN:C	2.60	0.40
1:A:767:VAL:O	1:A:771:VAL:HG23	2.21	0.40
1:A:636:ARG:HD2	1:A:667:GLU:OE1	2.22	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	854/897 (95%)	816 (96%)	37 (4%)	1 (0%)	51 78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	401	PHE

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	739/799 (92%)	717 (97%)	22 (3%)	41 70

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	95	LEU
1	A	103	SER
1	A	127	ARG
1	A	177	LEU
1	A	229	GLU
1	A	305	LYS
1	A	322	TRP
1	A	342	SER
1	A	343	SER
1	A	378	PHE
1	A	410	VAL
1	A	576	MET
1	A	604	MET
1	A	654	ILE
1	A	663	TYR
1	A	671	MET
1	A	739	ASN
1	A	760	ASN
1	A	799	SER
1	A	834	GLN
1	A	841	ARG
1	A	911	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates i

4 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
2	NAG	B	1	1,2	14,14,15	0.92	1 (7%)	17,19,21	2.18	5 (29%)
2	NAG	B	2	2	14,14,15	0.54	0	17,19,21	2.58	6 (35%)
2	NAG	C	1	1,2	14,14,15	0.97	1 (7%)	17,19,21	2.62	8 (47%)
2	NAG	C	2	2	14,14,15	0.95	1 (7%)	17,19,21	1.98	5 (29%)

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
2	NAG	B	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	2	2	-	3/6/23/26	0/1/1/1
2	NAG	C	1	1,2	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	NAG	O5-C1	-2.41	1.39	1.43
2	C	2	NAG	C1-C2	2.09	1.55	1.52
2	C	1	NAG	C2-N2	2.08	1.49	1.46

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	NAG	O4-C4-C3	5.48	123.03	110.35
2	B	2	NAG	O5-C5-C6	5.20	115.36	107.20
2	C	1	NAG	O7-C7-C8	-5.13	112.53	122.06

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2	NAG	O5-C1-C2	4.65	118.63	111.29
2	B	2	NAG	C1-O5-C5	4.45	118.23	112.19
2	C	1	NAG	C1-O5-C5	4.34	118.07	112.19
2	C	1	NAG	C1-C2-N2	4.29	117.81	110.49
2	C	1	NAG	C8-C7-N2	4.27	123.32	116.10
2	C	2	NAG	O5-C5-C6	4.14	113.69	107.20
2	C	2	NAG	C1-O5-C5	-4.10	106.63	112.19
2	B	1	NAG	C4-C3-C2	-3.54	105.83	111.02
2	B	2	NAG	O3-C3-C2	3.44	116.59	109.47
2	B	2	NAG	C1-C2-N2	-3.40	104.69	110.49
2	B	1	NAG	O5-C5-C6	3.06	112.00	107.20
2	B	1	NAG	O5-C1-C2	2.82	115.74	111.29
2	B	1	NAG	O4-C4-C5	-2.77	102.42	109.30
2	C	2	NAG	C3-C4-C5	-2.73	105.38	110.24
2	C	1	NAG	O4-C4-C3	-2.59	104.36	110.35
2	C	1	NAG	C4-C3-C2	2.56	114.77	111.02
2	C	2	NAG	C8-C7-N2	2.48	120.30	116.10
2	C	1	NAG	O6-C6-C5	2.38	119.45	111.29
2	C	2	NAG	O4-C4-C5	2.22	114.82	109.30
2	C	1	NAG	O5-C5-C6	2.17	110.60	107.20
2	B	2	NAG	O7-C7-C8	-2.15	118.06	122.06

There are no chirality outliers.

All (5) torsion outliers are listed below:

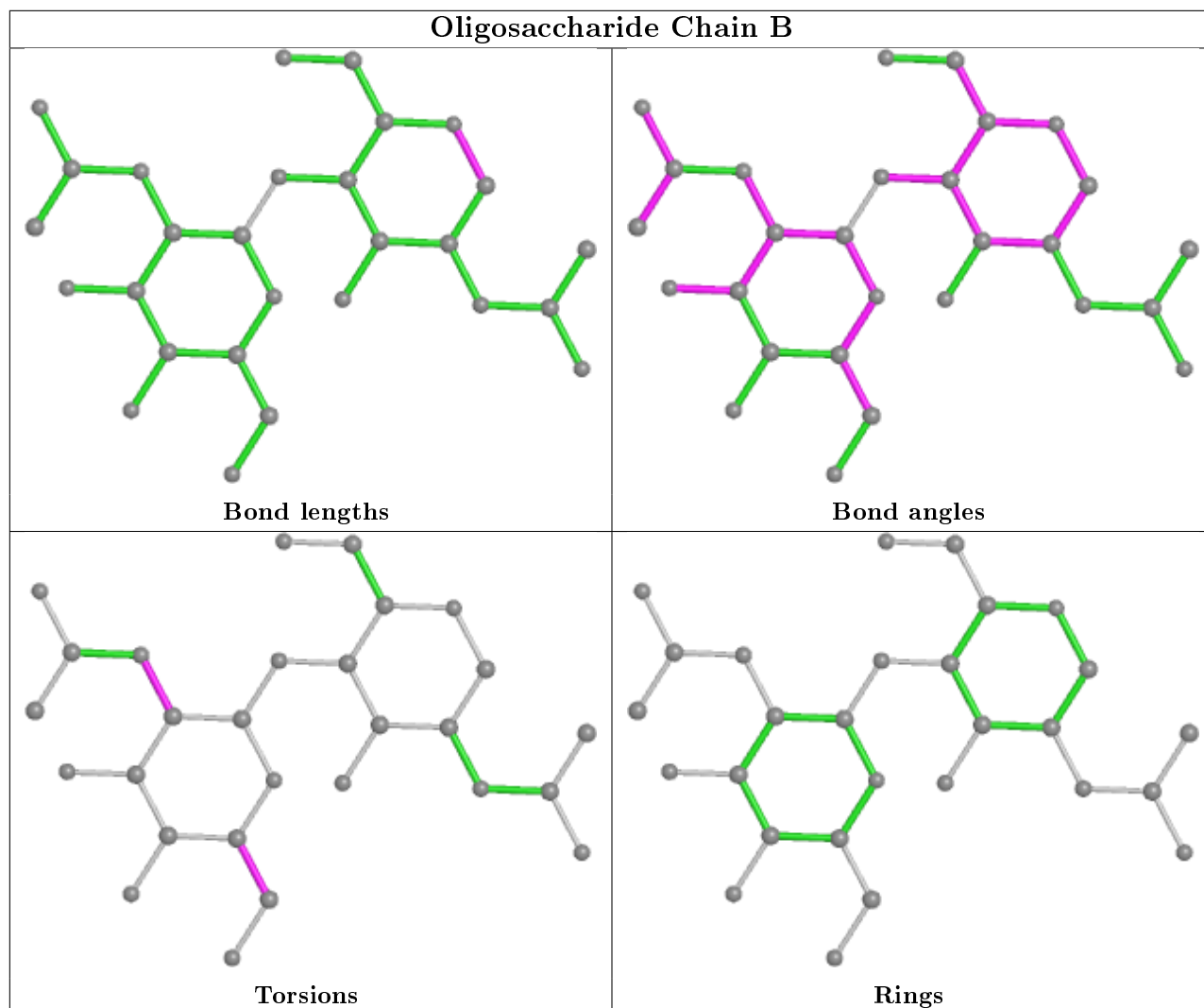
Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C3-C2-N2-C7
2	B	2	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6

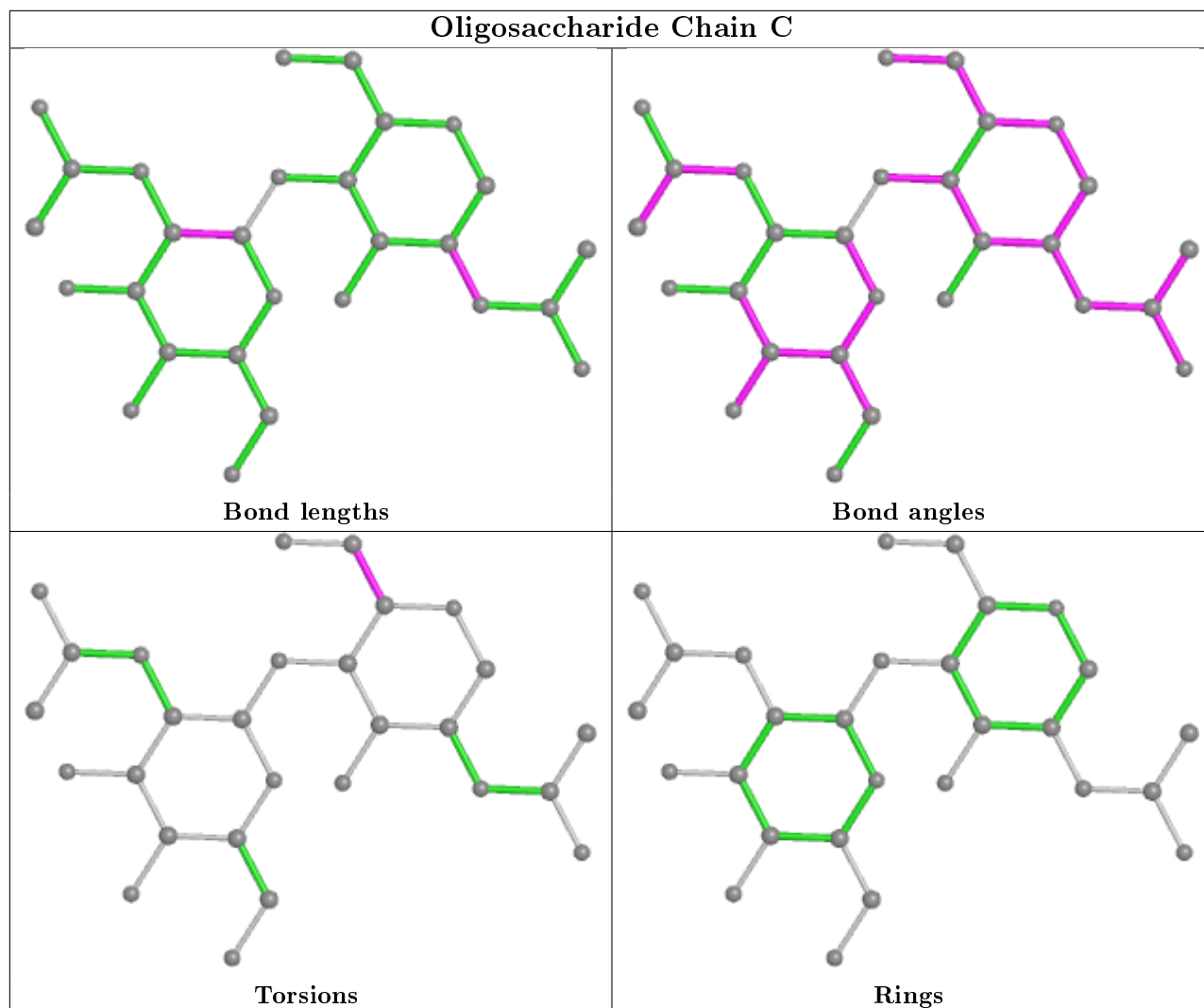
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	NAG	2	0
2	B	1	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](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	$\# Z > 2$
3	NAG	A	1943	1	14,14,15	0.94	0	17,19,21	2.39	6 (35%)
6	EDO	A	1949	-	3,3,3	0.83	0	2,2,2	0.30	0
7	BES	A	1950	4	19,22,22	1.28	2 (10%)	23,29,29	2.22	6 (26%)

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	A	1943	1	-	0/6/23/26	0/1/1/1
6	EDO	A	1949	-	-	0/1/1/1	-
7	BES	A	1950	4	-	9/20/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1950	BES	C2-C1	3.27	1.58	1.54
7	A	1950	BES	C2-C3	-2.50	1.47	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1943	NAG	C1-O5-C5	6.98	121.65	112.19
7	A	1950	BES	O2-C2-C3	-5.96	97.78	110.63
7	A	1950	BES	O3-C3-C2	-4.51	111.86	120.00
7	A	1950	BES	O2-C2-C1	4.16	118.37	109.64
3	A	1943	NAG	C8-C7-N2	3.29	121.66	116.10
7	A	1950	BES	C7-C6-C1	3.20	120.23	113.46
7	A	1950	BES	O3-C3-N1	3.11	128.68	122.93
3	A	1943	NAG	C3-C4-C5	2.95	115.51	110.24
3	A	1943	NAG	O5-C1-C2	2.75	115.64	111.29
3	A	1943	NAG	O5-C5-C4	2.46	116.81	110.83
7	A	1950	BES	C2-C3-N1	2.32	119.46	116.25
3	A	1943	NAG	O7-C7-C8	-2.13	118.11	122.06

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1950	BES	C2-C1-C6-C7
7	A	1950	BES	N2-C1-C2-C3
7	A	1950	BES	C6-C1-C2-C3
7	A	1950	BES	O2-C2-C3-N1
7	A	1950	BES	O2-C2-C3-O3
7	A	1950	BES	C14-C13-C4-N1
7	A	1950	BES	C4-C13-C14-C16

Continued on next page...

Continued from previous page...

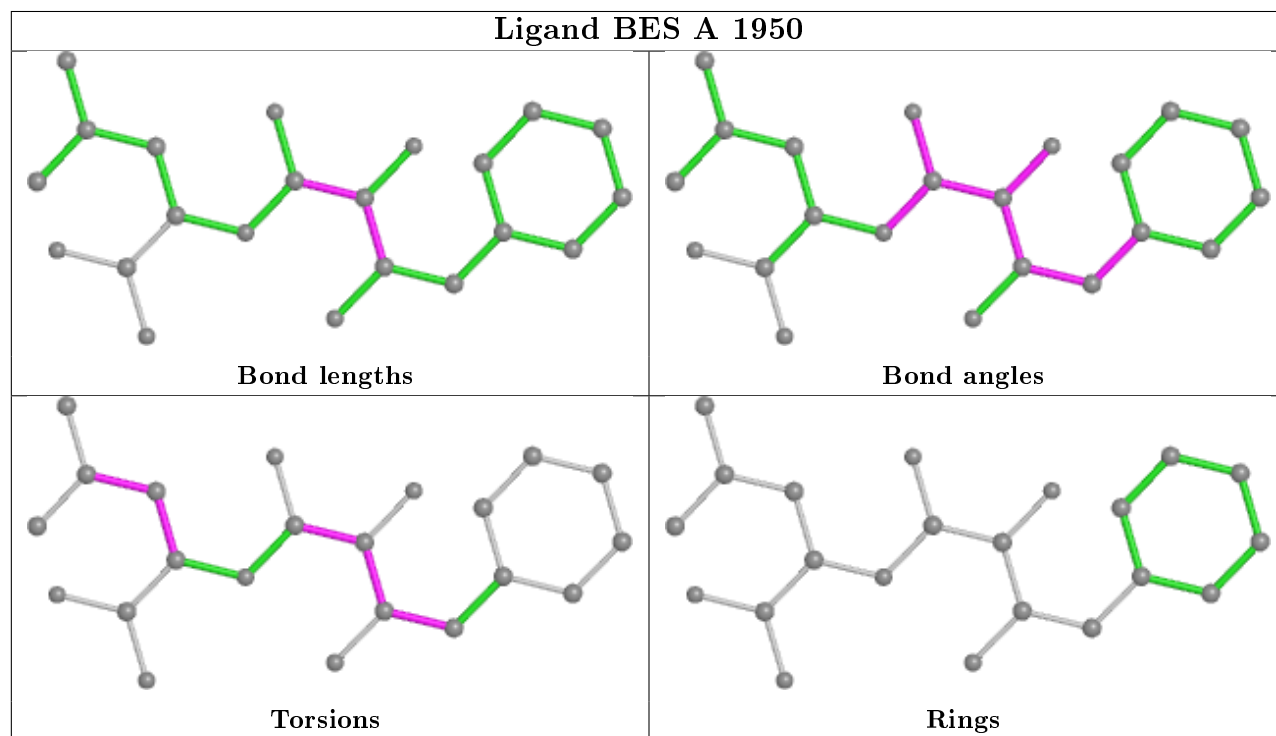
Mol	Chain	Res	Type	Atoms
7	A	1950	BES	N2-C1-C6-C7
7	A	1950	BES	C14-C13-C4-C5

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1949	EDO	3	0
7	A	1950	BES	8	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	858/897 (95%)	-0.45	15 (1%) 70 72	5, 15, 28, 58	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	514	GLY	3.9
1	A	558	ASP	3.4
1	A	576	MET	3.1
1	A	575	ASP	3.1
1	A	559	THR	3.0
1	A	110	GLY	2.9
1	A	760	ASN	2.5
1	A	691	ASP	2.4
1	A	759	GLY	2.4
1	A	758	ASN	2.2
1	A	171	GLU	2.2
1	A	594	GLU	2.2
1	A	614	ASP	2.1
1	A	406	ASP	2.0
1	A	650	GLY	2.0

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

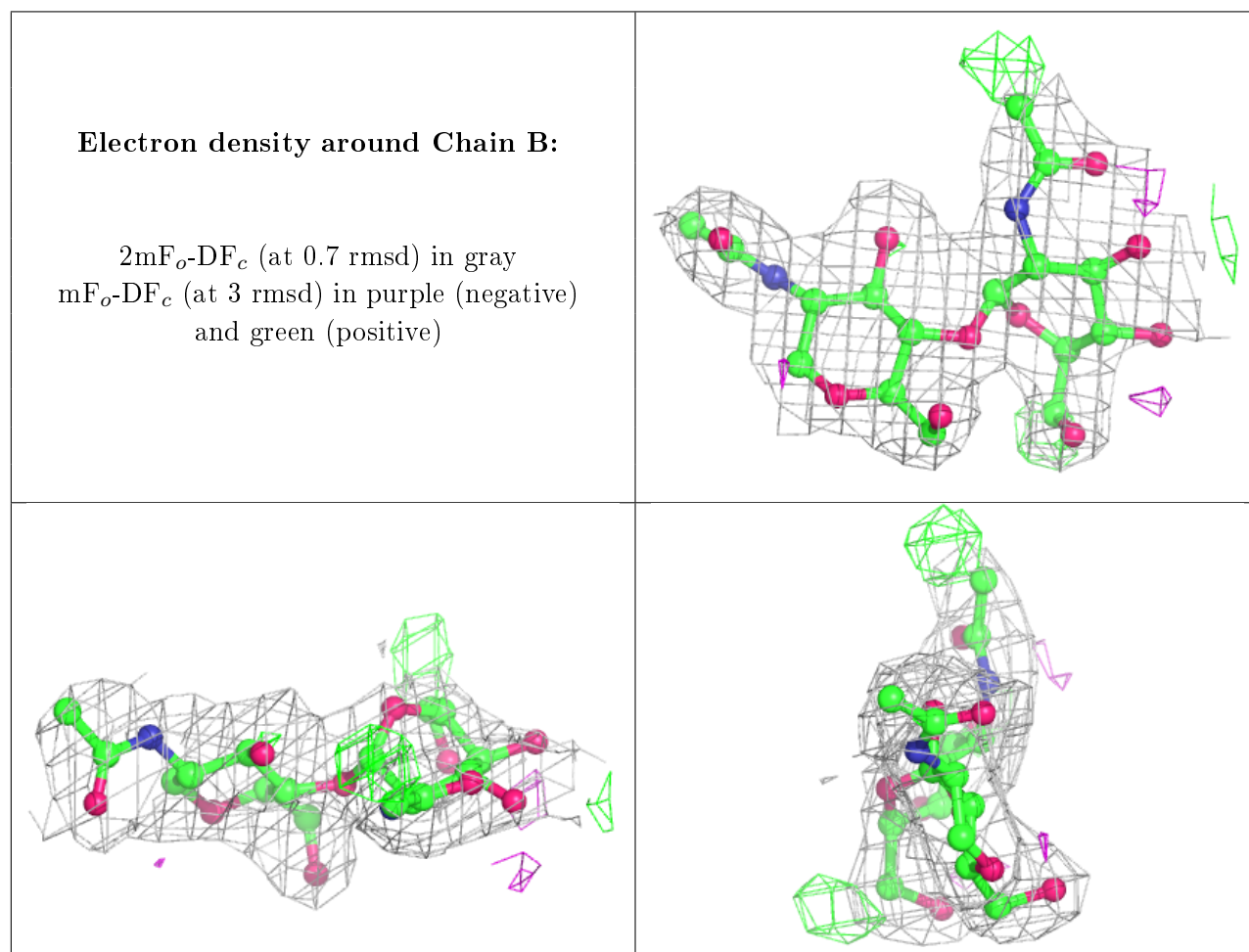
There are no non-standard protein/DNA/RNA residues in this entry.

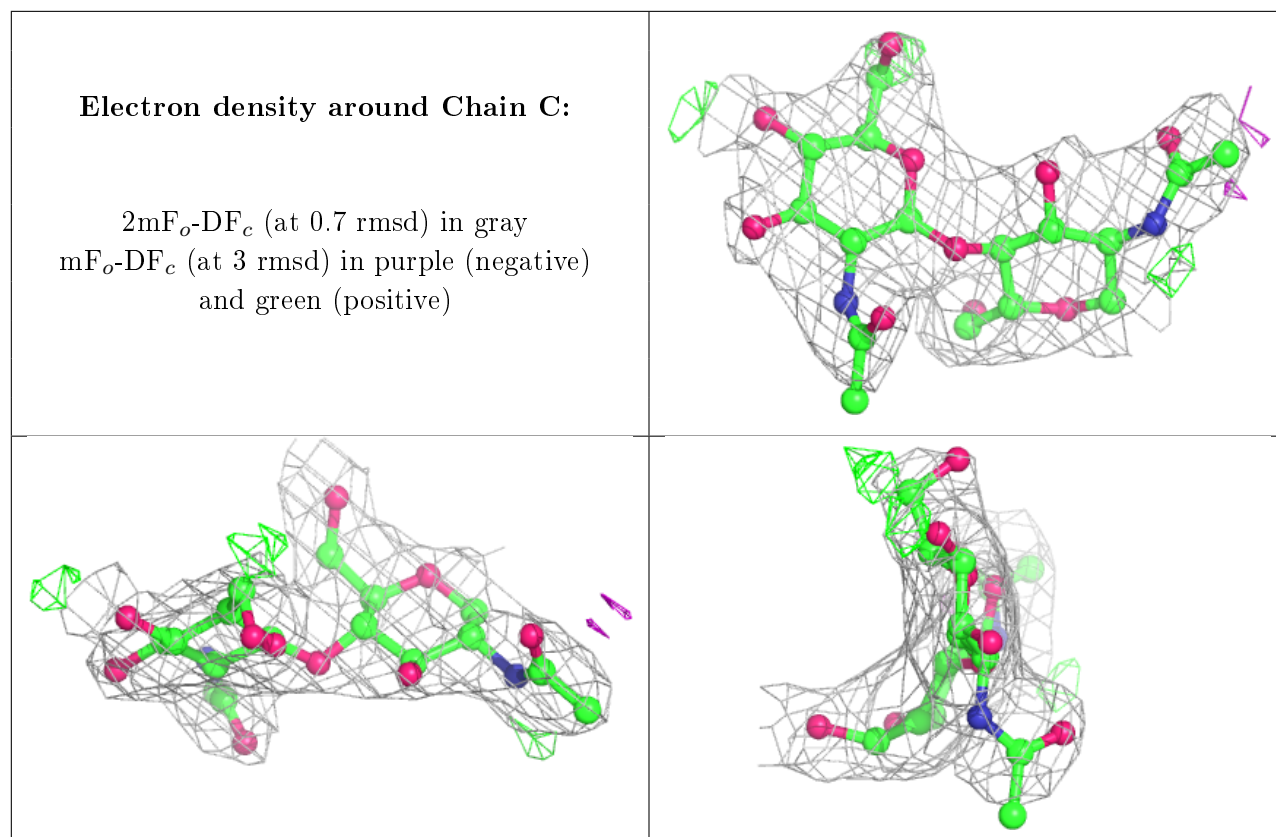
6.3 Carbohydrates [i](#)

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(\AA^2)	Q<0.9
2	NAG	B	2	14/15	0.83	0.22	33,46,57,61	0
2	NAG	C	2	14/15	0.89	0.36	36,57,64,70	0
2	NAG	B	1	14/15	0.90	0.15	19,29,40,41	0
2	NAG	C	1	14/15	0.91	0.24	27,47,60,63	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.



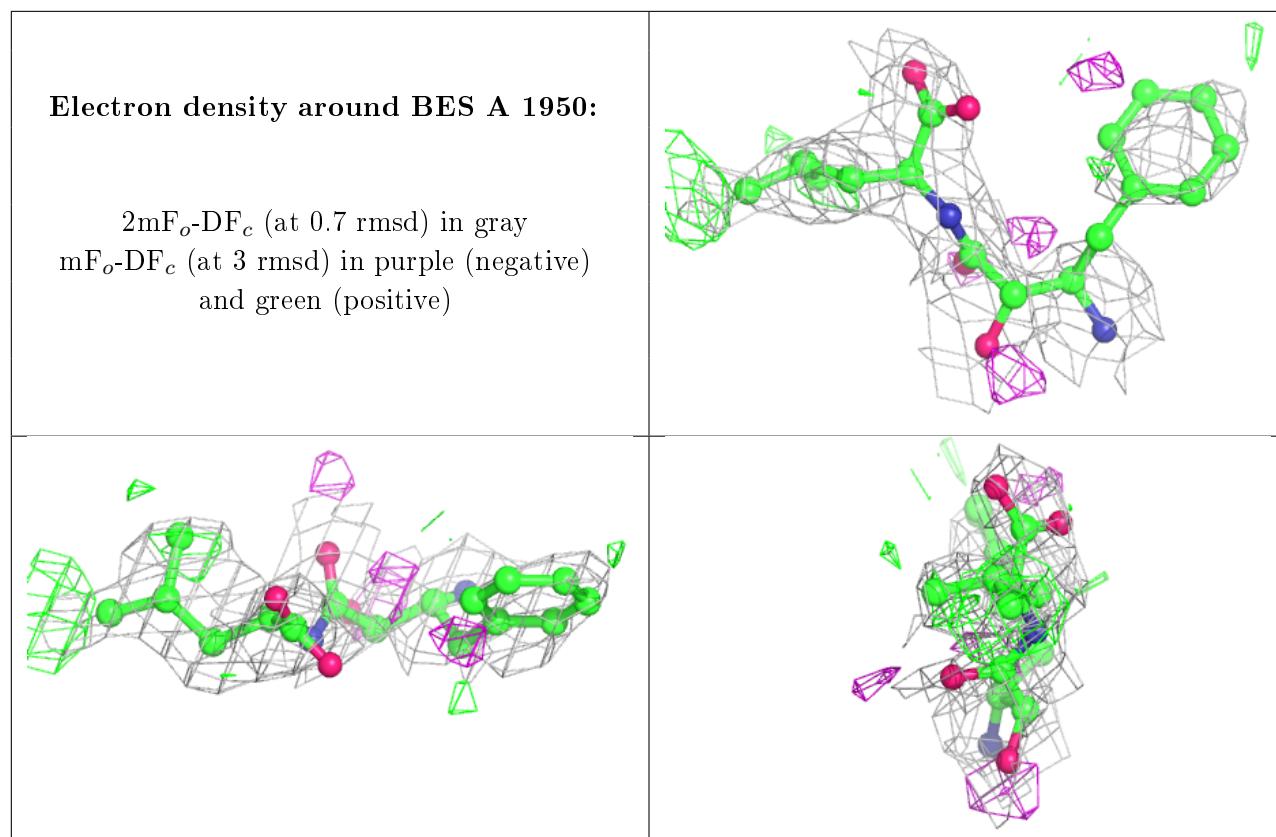


6.4 Ligands [\(i\)](#)

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(\AA^2)	Q<0.9
3	NAG	A	1943	14/15	0.81	0.31	37,68,94,98	0
6	EDO	A	1949	4/4	0.84	0.16	37,43,53,64	0
7	BES	A	1950	22/22	0.93	0.27	8,58,80,91	0
5	K	A	1948	1/1	0.98	0.09	27,27,27,27	0
5	K	A	1947	1/1	0.98	0.18	52,52,52,52	0
4	ZN	A	1946	1/1	1.00	0.09	25,25,25,25	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.