



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 06:29 PM UTC

PDB ID : 8BQU / pdb_00008bqu
Title : Molecular basis of ZP3/ZP1 heteropolymerization: crystal structure of a native vertebrate egg coat filament
Authors : Bokhove, M.; de Sanctis, D.; Yasumasu, S.; Jovine, L.
Deposited on : 2022-11-21
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 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

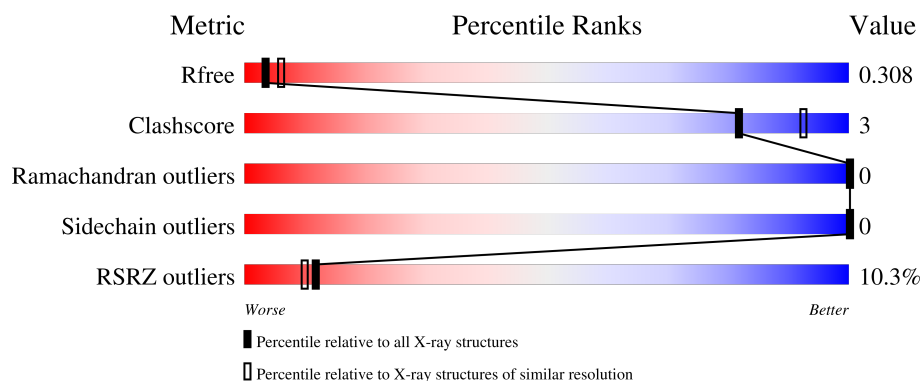
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (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 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	320	8% 87% 6% 7%
2	B	170	10% 93% . .
3	C	167	13% 90% 5% 5%
4	D	7	57% 14% 29%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9490 atoms, of which 4638 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 Zona pellucida sperm-binding protein 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	298	Total	C	H	N	O	S	0	0	0
			4503	1466	2204	377	443	13			

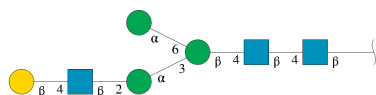
- Molecule 2 is a protein called Choriogenin H.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	165	Total	C	H	N	O	S	0	0	0
			2495	813	1222	209	241	10			

- Molecule 3 is a protein called Choriogenin H.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	159	Total	C	H	N	O	S	0	0	0
			2330	749	1136	194	239	12			

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

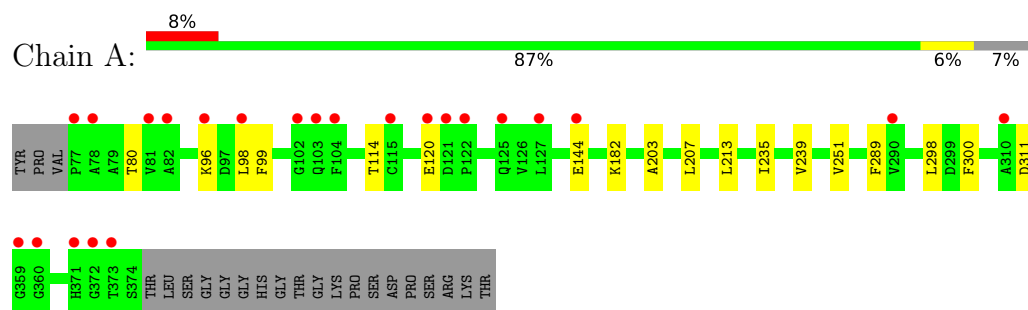


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	7	Total	C	H	N	O	0	0	0
			162	48	76	3	35			

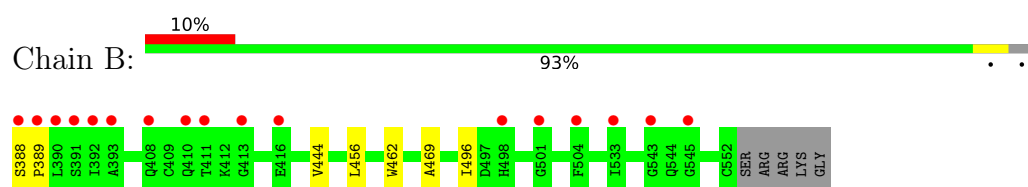
3 Residue-property plots [i](#)

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.

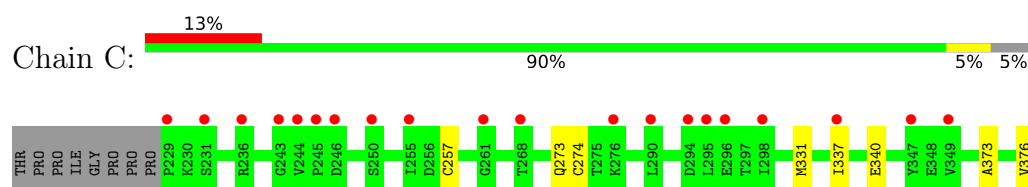
- Molecule 1: Zona pellucida sperm-binding protein 3



- Molecule 2: Choriogenin H



- Molecule 3: Choriogenin H



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	59.06Å 59.06Å 473.92Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	51.15 – 2.70 51.15 – 2.70	Depositor EDS
% Data completeness (in resolution range)	49.5 (51.15-2.70) 44.7 (51.15-2.70)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 2.42Å)	Xtriage
Refinement program	PHENIX dev_4742	Depositor
R, R_{free}	0.247 , 0.307 0.247 , 0.308	Depositor DCC
R_{free} test set	646 reflections (1.68%)	wwPDB-VP
Wilson B-factor (Å ²)	19.7	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 20.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.068 for -h,-k,l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	9490	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.26% 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: BMA, GAL, NAG, MAN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.13	0/2360	0.33	0/3218
2	B	0.13	0/1311	0.32	0/1797
3	C	0.13	0/1221	0.32	0/1668
All	All	0.13	0/4892	0.33	0/6683

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	2299	2204	2203	15	0
2	B	1273	1222	1219	5	0
3	C	1194	1136	1136	7	0
4	D	86	76	73	1	0
All	All	4852	4638	4631	24	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 3.

All (24) 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:213:LEU:HD23	1:A:235:ILE:HG12	1.83	0.58
1:A:207:LEU:HD12	3:C:373:ALA:CB	2.34	0.57
1:A:144:GLU:OE2	1:A:182:LYS:NZ	2.36	0.57
1:A:114:THR:HG22	1:A:114:THR:O	2.08	0.54
2:B:496:ILE:HG23	2:B:496:ILE:O	2.09	0.51
1:A:203:ALA:HB3	3:C:274:CYS:SG	2.51	0.51
4:D:4:MAN:O2	4:D:5:NAG:H83	2.11	0.50
2:B:462:TRP:CZ2	2:B:469:ALA:HB1	2.48	0.48
3:C:376:VAL:HG13	3:C:376:VAL:O	2.13	0.47
1:A:251:VAL:O	1:A:251:VAL:HG13	2.14	0.46
1:A:311:ASP:OD1	1:A:312:SER:N	2.48	0.45
1:A:289:PHE:CD1	1:A:300:PHE:HB3	2.52	0.45
2:B:444:VAL:HG12	2:B:456:LEU:HD21	1.98	0.44
3:C:257:CYS:SG	3:C:273:GLN:NE2	2.89	0.44
1:A:207:LEU:HD11	3:C:337:ILE:HD12	2.00	0.44
2:B:388:SER:HB3	2:B:389:PRO:HD3	2.00	0.44
1:A:80:THR:HG21	1:A:98:LEU:HG	2.00	0.44
3:C:331:MET:HE1	3:C:340:GLU:HB2	2.00	0.44
1:A:207:LEU:HD12	3:C:373:ALA:HB1	1.98	0.44
1:A:98:LEU:HD22	1:A:99:PHE:CE1	2.53	0.42
1:A:251:VAL:HG12	1:A:298:LEU:HD23	2.01	0.42
1:A:96:LYS:HE2	1:A:120:GLU:HG3	2.01	0.42
2:B:462:TRP:HZ2	2:B:469:ALA:HB1	1.86	0.41
1:A:239:VAL:O	1:A:239:VAL:HG13	2.21	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	296/320 (92%)	288 (97%)	8 (3%)	0	100	100
2	B	163/170 (96%)	157 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	157/167 (94%)	155 (99%)	2 (1%)	0	100	100
All	All	616/657 (94%)	600 (97%)	16 (3%)	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	251/268 (94%)	251 (100%)	0	100	100
2	B	143/147 (97%)	143 (100%)	0	100	100
3	C	137/144 (95%)	137 (100%)	0	100	100
All	All	531/559 (95%)	531 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

7 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	D	1	4,1	14,14,15	0.26	0	17,19,21	0.58	0
4	NAG	D	2	4	14,14,15	0.32	0	17,19,21	0.41	0
4	BMA	D	3	4	11,11,12	0.61	0	15,15,17	0.66	0
4	MAN	D	4	4	11,11,12	0.57	0	15,15,17	1.13	2 (13%)
4	NAG	D	5	4	14,14,15	0.63	0	17,19,21	0.70	1 (5%)
4	GAL	D	6	4	11,11,12	0.57	0	15,15,17	0.82	0
4	MAN	D	7	4	11,11,12	0.92	0	15,15,17	1.07	2 (13%)

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	4,1	-	0/6/23/26	0/1/1/1
4	NAG	D	2	4	-	0/6/23/26	0/1/1/1
4	BMA	D	3	4	-	2/2/19/22	0/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
4	NAG	D	5	4	-	2/6/23/26	0/1/1/1
4	GAL	D	6	4	-	0/2/19/22	0/1/1/1
4	MAN	D	7	4	-	2/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	4	MAN	C1-O5-C5	3.16	116.43	112.19
4	D	7	MAN	C1-O5-C5	3.03	116.24	112.19
4	D	4	MAN	O2-C2-C3	-2.24	105.50	110.15
4	D	7	MAN	O2-C2-C3	-2.17	105.65	110.15
4	D	5	NAG	C2-N2-C7	2.02	125.60	122.90

There are no chirality outliers.

All (6) torsion outliers are listed below:

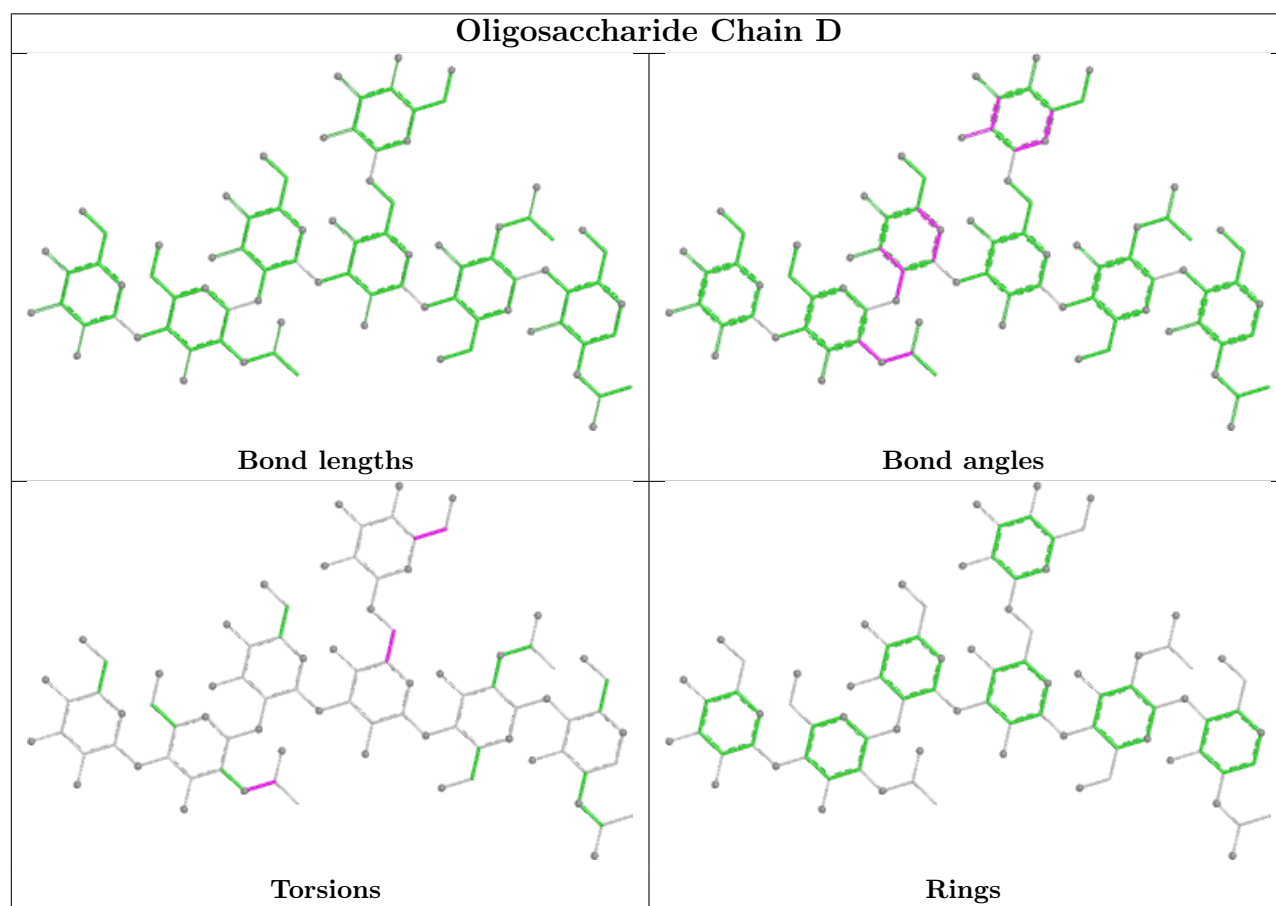
Mol	Chain	Res	Type	Atoms
4	D	5	NAG	C8-C7-N2-C2
4	D	5	NAG	O7-C7-N2-C2
4	D	7	MAN	O5-C5-C6-O6
4	D	3	BMA	O5-C5-C6-O6
4	D	3	BMA	C4-C5-C6-O6
4	D	7	MAN	C4-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	5	NAG	1	0
4	D	4	MAN	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](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	298/320 (93%)	0.75	25 (8%) 17 14	10, 24, 54, 84	0
2	B	165/170 (97%)	0.73	17 (10%) 12 10	8, 19, 62, 89	0
3	C	159/167 (95%)	0.97	22 (13%) 6 5	16, 29, 59, 89	0
All	All	622/657 (94%)	0.80	64 (10%) 12 10	8, 25, 57, 89	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	387	ASP	6.9
3	C	347	TYR	4.5
1	A	104	PHE	4.2
1	A	96	LYS	4.1
1	A	103	GLN	4.0
1	A	125	GLN	3.7
1	A	371	HIS	3.6
2	B	498	HIS	3.5
1	A	373	THR	3.4
2	B	410	GLN	3.3
3	C	337	ILE	3.3
3	C	385	PRO	3.3
1	A	359	GLY	3.3
3	C	255	ILE	3.3
3	C	296	GLU	3.3
1	A	360	GLY	3.1
3	C	229	PRO	3.1
3	C	290	LEU	2.9
2	B	413	GLY	2.9
2	B	411	THR	2.9
3	C	243	GLY	2.8
3	C	231	SER	2.8
1	A	78	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	290	VAL	2.7
2	B	389	PRO	2.7
1	A	115	CYS	2.7
1	A	372	GLY	2.7
1	A	122	PRO	2.7
2	B	543	GLY	2.7
1	A	144	GLU	2.7
3	C	246	ASP	2.7
3	C	276	LYS	2.7
1	A	127	LEU	2.7
1	A	120	GLU	2.6
1	A	77	PRO	2.6
2	B	408	GLN	2.6
2	B	501	GLY	2.6
2	B	504	PHE	2.6
3	C	245	PRO	2.6
3	C	295	LEU	2.5
1	A	81	VAL	2.4
3	C	244	VAL	2.4
2	B	533	ILE	2.4
1	A	310	ALA	2.3
3	C	268	THR	2.3
3	C	236	ARG	2.3
2	B	545	GLY	2.3
1	A	121	ASP	2.2
1	A	98	LEU	2.2
1	A	347	SER	2.1
2	B	391	SER	2.1
2	B	392	ILE	2.1
3	C	349	VAL	2.1
3	C	294	ASP	2.0
1	A	82	ALA	2.0
2	B	388	SER	2.0
2	B	393	ALA	2.0
2	B	416	GLU	2.0
3	C	250	SER	2.0
3	C	261	GLY	2.0
1	A	358	SER	2.0
2	B	390	LEU	2.0
1	A	102	GLY	2.0
3	C	298	ILE	2.0

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

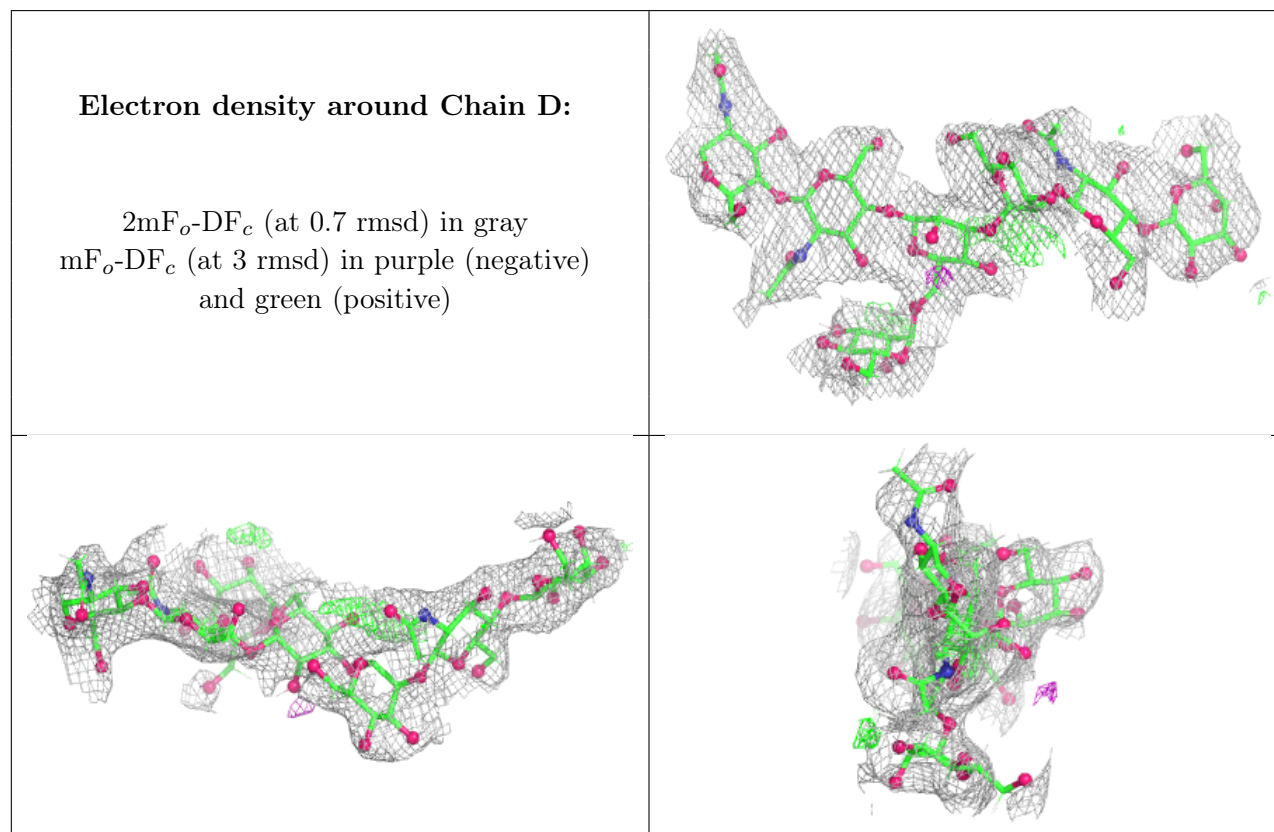
There are no non-standard protein/DNA/RNA residues in this entry.

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	GAL	D	6	11/12	0.72	0.14	41,49,60,60	0
4	MAN	D	7	11/12	0.74	0.15	22,31,37,42	0
4	BMA	D	3	11/12	0.80	0.14	30,38,47,50	0
4	NAG	D	5	14/15	0.84	0.12	32,44,53,58	0
4	MAN	D	4	11/12	0.85	0.13	43,52,63,64	0
4	NAG	D	2	14/15	0.87	0.12	18,24,30,33	0
4	NAG	D	1	14/15	0.94	0.10	8,15,19,19	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.