



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 2, 2021 – 11:42 AM EDT

PDB ID : 3D4G
Title : ZP-N domain of mammalian sperm receptor ZP3 (crystal form II)
Authors : Jovine, L.; Monne, M.
Deposited on : 2008-05-14
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 2.23.2
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) : 2.23.2

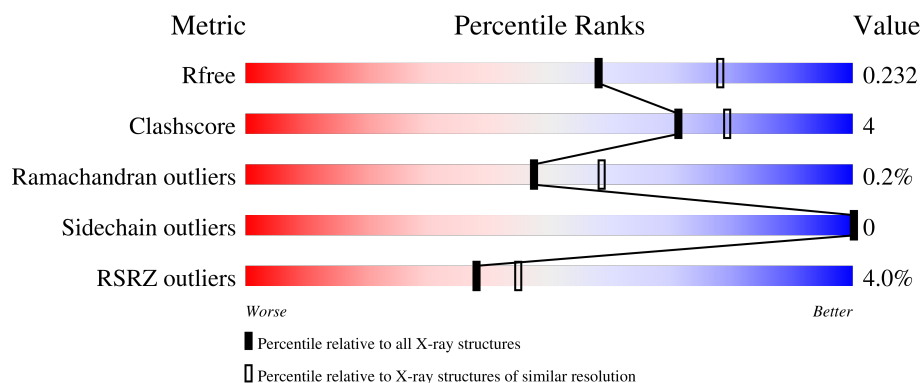
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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.



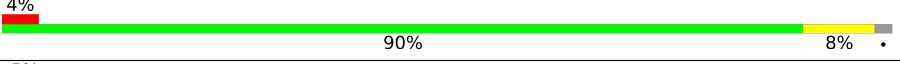


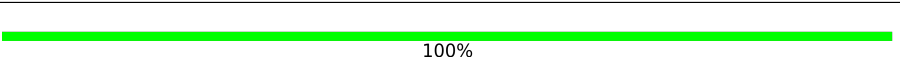







Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	481	<div> <div>2%</div> <div>90%</div> <div>7%</div> <div>..</div> </div>
1	B	481	<div> <div>4%</div> <div>88%</div> <div>10%</div> <div>.</div> </div>
1	C	481	<div> <div>3%</div> <div>89%</div> <div>9%</div> <div>.</div> </div>
1	D	481	<div> <div>5%</div> <div>91%</div> <div>7%</div> <div>.</div> </div>
1	E	481	<div> <div>3%</div> <div>91%</div> <div>7%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	481	
1	G	481	
1	H	481	
2	I	2	
2	J	2	
2	K	2	
2	L	2	
2	M	2	
2	N	2	
2	O	2	
2	P	2	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 31230 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 Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	471	Total	C	N	O	S	0	0	0
			3637	2325	605	696	11			
1	B	471	Total	C	N	O	S	0	0	0
			3637	2325	605	696	11			
1	C	471	Total	C	N	O	S	0	0	0
			3637	2325	605	696	11			
1	D	469	Total	C	N	O	S	0	0	0
			3621	2316	603	691	11			
1	E	472	Total	C	N	O	S	0	0	0
			3645	2331	606	697	11			
1	F	472	Total	C	N	O	S	0	0	0
			3645	2331	606	697	11			
1	G	472	Total	C	N	O	S	0	0	0
			3645	2331	606	697	11			
1	H	469	Total	C	N	O	S	0	0	0
			3621	2316	603	691	11			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0AEX9
A	3	THR	ILE	engineered mutation	UNP P0AEX9
A	360	ALA	GLU	engineered mutation	UNP P0AEX9
A	363	ALA	LYS	engineered mutation	UNP P0AEX9
A	364	ALA	ASP	engineered mutation	UNP P0AEX9
A	368	ASN	ARG	engineered mutation	UNP P0AEX9
A	474	LEU	-	expression tag	UNP P10761
A	475	GLU	-	expression tag	UNP P10761
A	476	HIS	-	expression tag	UNP P10761
A	477	HIS	-	expression tag	UNP P10761
A	478	HIS	-	expression tag	UNP P10761
A	479	HIS	-	expression tag	UNP P10761

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Chain	Residue	Modelled	Actual	Comment	Reference
A	480	HIS	-	expression tag	UNP P10761
A	481	HIS	-	expression tag	UNP P10761
B	1	MET	-	initiating methionine	UNP P0AEX9
B	3	THR	ILE	engineered mutation	UNP P0AEX9
B	360	ALA	GLU	engineered mutation	UNP P0AEX9
B	363	ALA	LYS	engineered mutation	UNP P0AEX9
B	364	ALA	ASP	engineered mutation	UNP P0AEX9
B	368	ASN	ARG	engineered mutation	UNP P0AEX9
B	474	LEU	-	expression tag	UNP P10761
B	475	GLU	-	expression tag	UNP P10761
B	476	HIS	-	expression tag	UNP P10761
B	477	HIS	-	expression tag	UNP P10761
B	478	HIS	-	expression tag	UNP P10761
B	479	HIS	-	expression tag	UNP P10761
B	480	HIS	-	expression tag	UNP P10761
B	481	HIS	-	expression tag	UNP P10761
C	1	MET	-	initiating methionine	UNP P0AEX9
C	3	THR	ILE	engineered mutation	UNP P0AEX9
C	360	ALA	GLU	engineered mutation	UNP P0AEX9
C	363	ALA	LYS	engineered mutation	UNP P0AEX9
C	364	ALA	ASP	engineered mutation	UNP P0AEX9
C	368	ASN	ARG	engineered mutation	UNP P0AEX9
C	474	LEU	-	expression tag	UNP P10761
C	475	GLU	-	expression tag	UNP P10761
C	476	HIS	-	expression tag	UNP P10761
C	477	HIS	-	expression tag	UNP P10761
C	478	HIS	-	expression tag	UNP P10761
C	479	HIS	-	expression tag	UNP P10761
C	480	HIS	-	expression tag	UNP P10761
C	481	HIS	-	expression tag	UNP P10761
D	1	MET	-	initiating methionine	UNP P0AEX9
D	3	THR	ILE	engineered mutation	UNP P0AEX9
D	360	ALA	GLU	engineered mutation	UNP P0AEX9
D	363	ALA	LYS	engineered mutation	UNP P0AEX9
D	364	ALA	ASP	engineered mutation	UNP P0AEX9
D	368	ASN	ARG	engineered mutation	UNP P0AEX9
D	474	LEU	-	expression tag	UNP P10761
D	475	GLU	-	expression tag	UNP P10761
D	476	HIS	-	expression tag	UNP P10761
D	477	HIS	-	expression tag	UNP P10761
D	478	HIS	-	expression tag	UNP P10761
D	479	HIS	-	expression tag	UNP P10761

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Chain	Residue	Modelled	Actual	Comment	Reference
D	480	HIS	-	expression tag	UNP P10761
D	481	HIS	-	expression tag	UNP P10761
E	1	MET	-	initiating methionine	UNP P0AEX9
E	3	THR	ILE	engineered mutation	UNP P0AEX9
E	360	ALA	GLU	engineered mutation	UNP P0AEX9
E	363	ALA	LYS	engineered mutation	UNP P0AEX9
E	364	ALA	ASP	engineered mutation	UNP P0AEX9
E	368	ASN	ARG	engineered mutation	UNP P0AEX9
E	474	LEU	-	expression tag	UNP P10761
E	475	GLU	-	expression tag	UNP P10761
E	476	HIS	-	expression tag	UNP P10761
E	477	HIS	-	expression tag	UNP P10761
E	478	HIS	-	expression tag	UNP P10761
E	479	HIS	-	expression tag	UNP P10761
E	480	HIS	-	expression tag	UNP P10761
E	481	HIS	-	expression tag	UNP P10761
F	1	MET	-	initiating methionine	UNP P0AEX9
F	3	THR	ILE	engineered mutation	UNP P0AEX9
F	360	ALA	GLU	engineered mutation	UNP P0AEX9
F	363	ALA	LYS	engineered mutation	UNP P0AEX9
F	364	ALA	ASP	engineered mutation	UNP P0AEX9
F	368	ASN	ARG	engineered mutation	UNP P0AEX9
F	474	LEU	-	expression tag	UNP P10761
F	475	GLU	-	expression tag	UNP P10761
F	476	HIS	-	expression tag	UNP P10761
F	477	HIS	-	expression tag	UNP P10761
F	478	HIS	-	expression tag	UNP P10761
F	479	HIS	-	expression tag	UNP P10761
F	480	HIS	-	expression tag	UNP P10761
F	481	HIS	-	expression tag	UNP P10761
G	1	MET	-	initiating methionine	UNP P0AEX9
G	3	THR	ILE	engineered mutation	UNP P0AEX9
G	360	ALA	GLU	engineered mutation	UNP P0AEX9
G	363	ALA	LYS	engineered mutation	UNP P0AEX9
G	364	ALA	ASP	engineered mutation	UNP P0AEX9
G	368	ASN	ARG	engineered mutation	UNP P0AEX9
G	474	LEU	-	expression tag	UNP P10761
G	475	GLU	-	expression tag	UNP P10761
G	476	HIS	-	expression tag	UNP P10761
G	477	HIS	-	expression tag	UNP P10761
G	478	HIS	-	expression tag	UNP P10761
G	479	HIS	-	expression tag	UNP P10761

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Chain	Residue	Modelled	Actual	Comment	Reference
G	480	HIS	-	expression tag	UNP P10761
G	481	HIS	-	expression tag	UNP P10761
H	1	MET	-	initiating methionine	UNP P0AEX9
H	3	THR	ILE	engineered mutation	UNP P0AEX9
H	360	ALA	GLU	engineered mutation	UNP P0AEX9
H	363	ALA	LYS	engineered mutation	UNP P0AEX9
H	364	ALA	ASP	engineered mutation	UNP P0AEX9
H	368	ASN	ARG	engineered mutation	UNP P0AEX9
H	474	LEU	-	expression tag	UNP P10761
H	475	GLU	-	expression tag	UNP P10761
H	476	HIS	-	expression tag	UNP P10761
H	477	HIS	-	expression tag	UNP P10761
H	478	HIS	-	expression tag	UNP P10761
H	479	HIS	-	expression tag	UNP P10761
H	480	HIS	-	expression tag	UNP P10761
H	481	HIS	-	expression tag	UNP P10761

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	I	2	Total	C	O	0	0	0
			23	12	11			
2	J	2	Total	C	O	0	0	0
			23	12	11			
2	K	2	Total	C	O	0	0	0
			23	12	11			
2	L	2	Total	C	O	0	0	0
			23	12	11			
2	M	2	Total	C	O	0	0	0
			23	12	11			
2	N	2	Total	C	O	0	0	0
			23	12	11			
2	O	2	Total	C	O	0	0	0
			23	12	11			
2	P	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Ca 3 3	0	0
3	B	3	Total Ca 3 3	0	0
3	C	3	Total Ca 3 3	0	0
3	D	3	Total Ca 3 3	0	0
3	E	3	Total Ca 3 3	0	0
3	F	3	Total Ca 3 3	0	0
3	G	3	Total Ca 3 3	0	0
3	H	3	Total Ca 3 3	0	0

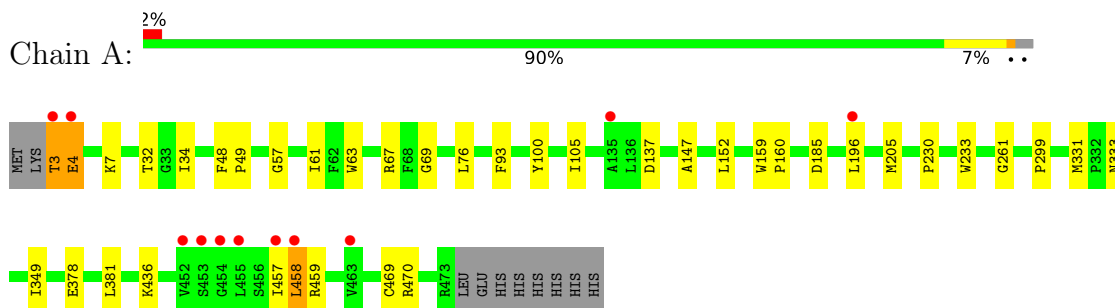
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	288	Total O 288 288	0	0
4	B	205	Total O 205 205	0	0
4	C	291	Total O 291 291	0	0
4	D	205	Total O 205 205	0	0
4	E	282	Total O 282 282	0	0
4	F	272	Total O 272 272	0	0
4	G	195	Total O 195 195	0	0
4	H	196	Total O 196 196	0	0

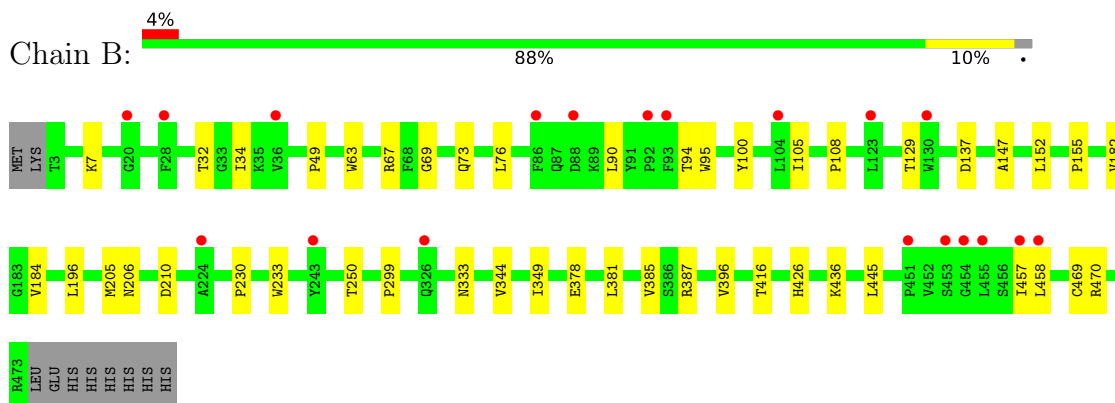
3 Residue-property plots [i](#)

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.

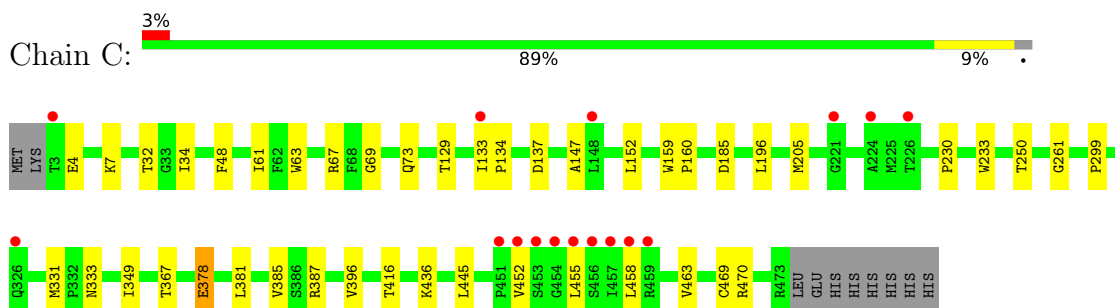
- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3



- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3

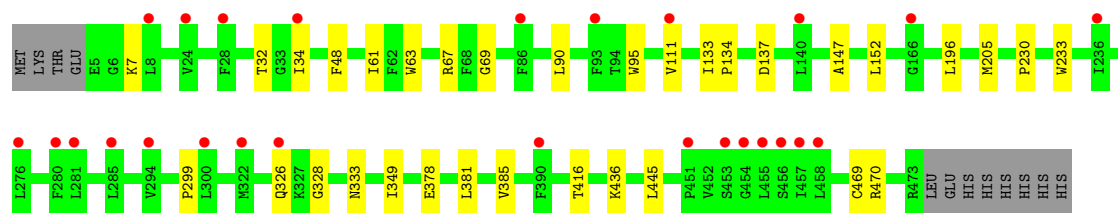


- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3

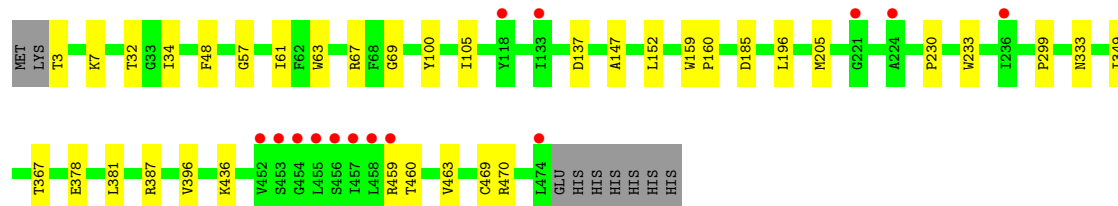
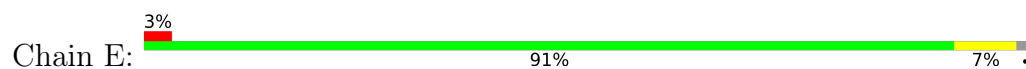


- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3

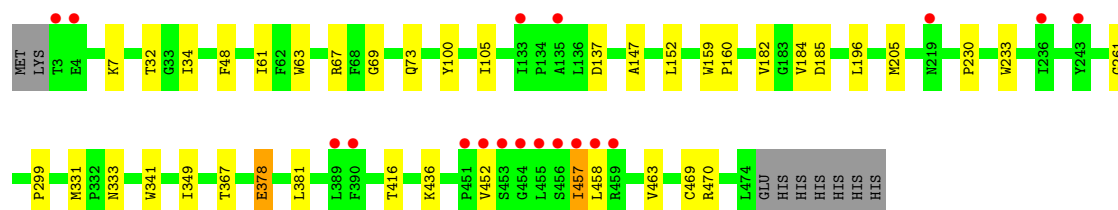
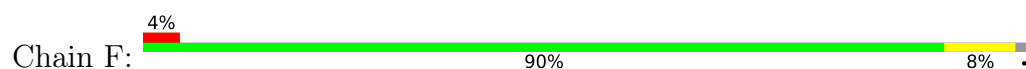




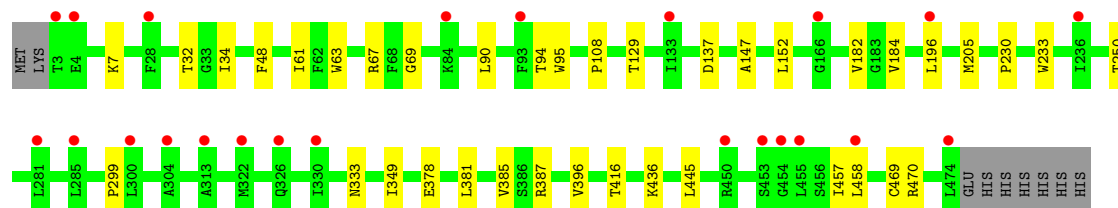
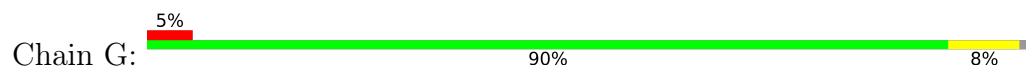
- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3



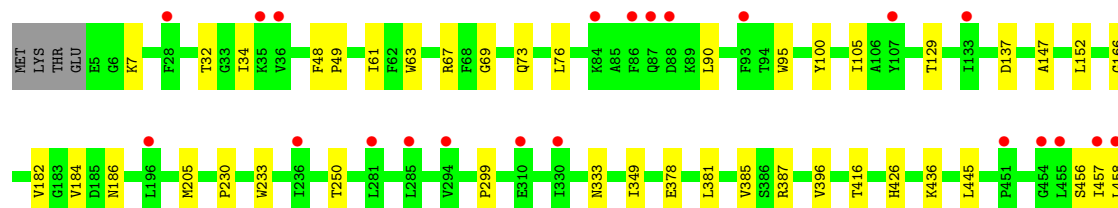
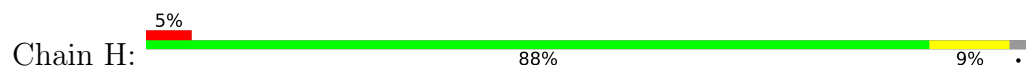
- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3



- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3



- Molecule 1: Maltose-binding periplasmic protein, LINKER, Zona pellucida protein 3





- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain I:  100%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain J:  50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain K:  50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain L:  50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain M:  50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain N:  50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain O:  50% 50%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain P: 


GLC1
GLC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	91.05Å 91.96Å 140.48Å 89.99° 90.18° 89.98°	Depositor
Resolution (Å)	50.00 – 2.30 47.64 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.5 (50.00-2.30) 94.6 (47.64-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.3.0038	Depositor
R, R_{free}	0.201 , 0.227 0.205 , 0.232	Depositor DCC
R_{free} test set	2139 reflections (1.11%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.185	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -k,h,l 0.000 for k,-h,l 0.448 for h,-k,-l 0.459 for -h,k,-l 0.447 for -h,-k,l 0.000 for -k,-h,-l 0.002 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	31230	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.90 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2121e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: GLC, CA

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.37	0/3719	0.49	0/5055
1	B	0.35	0/3719	0.49	0/5055
1	C	0.36	0/3719	0.49	0/5055
1	D	0.35	0/3703	0.48	0/5033
1	E	0.37	0/3727	0.49	0/5066
1	F	0.36	0/3727	0.49	0/5066
1	G	0.35	0/3727	0.48	0/5066
1	H	0.34	0/3703	0.48	0/5033
All	All	0.36	0/29744	0.49	0/40429

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	2
1	F	0	2
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	THR	Peptide
1	A	458	LEU	Peptide
1	F	452	VAL	Peptide

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Mol	Chain	Res	Type	Group
1	F	457	ILE	Peptide

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	3637	0	3610	26	0
1	B	3637	0	3610	35	0
1	C	3637	0	3610	30	0
1	D	3621	0	3597	21	0
1	E	3645	0	3621	23	0
1	F	3645	0	3621	26	0
1	G	3645	0	3621	25	0
1	H	3621	0	3597	29	0
2	I	23	0	21	0	0
2	J	23	0	21	0	0
2	K	23	0	21	0	0
2	L	23	0	21	0	0
2	M	23	0	21	0	0
2	N	23	0	21	1	0
2	O	23	0	21	0	0
2	P	23	0	21	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
3	G	3	0	0	0	0
3	H	3	0	0	0	0
4	A	288	0	0	2	0
4	B	205	0	0	2	0
4	C	291	0	0	2	0
4	D	205	0	0	2	0
4	E	282	0	0	2	0
4	F	272	0	0	2	0
4	G	195	0	0	2	0
4	H	196	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	31230	0	29055	204	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 4.

The worst 5 of 204 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:D:32:THR:HG22	1:D:34:ILE:HD13	1.47	0.97
1:B:32:THR:HG22	1:B:34:ILE:HD13	1.49	0.95
1:H:32:THR:HG22	1:H:34:ILE:HD13	1.48	0.94
1:E:32:THR:HG22	1:E:34:ILE:HD13	1.48	0.93
1:A:32:THR:HG22	1:A:34:ILE:HD13	1.50	0.92

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	469/481 (98%)	457 (97%)	10 (2%)	2 (0%)	34	42
1	B	469/481 (98%)	458 (98%)	10 (2%)	1 (0%)	47	58
1	C	469/481 (98%)	458 (98%)	10 (2%)	1 (0%)	47	58
1	D	467/481 (97%)	457 (98%)	9 (2%)	1 (0%)	47	58
1	E	470/481 (98%)	463 (98%)	6 (1%)	1 (0%)	47	58
1	F	470/481 (98%)	460 (98%)	9 (2%)	1 (0%)	47	58
1	G	470/481 (98%)	460 (98%)	9 (2%)	1 (0%)	47	58
1	H	467/481 (97%)	457 (98%)	9 (2%)	1 (0%)	47	58
All	All	3751/3848 (98%)	3670 (98%)	72 (2%)	9 (0%)	47	58

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	378	GLU
1	F	378	GLU
1	A	378	GLU
1	D	378	GLU
1	E	378	GLU

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	383/393 (98%)	383 (100%)	0	100	100
1	B	383/393 (98%)	383 (100%)	0	100	100
1	C	383/393 (98%)	383 (100%)	0	100	100
1	D	381/393 (97%)	381 (100%)	0	100	100
1	E	384/393 (98%)	384 (100%)	0	100	100
1	F	384/393 (98%)	384 (100%)	0	100	100
1	G	384/393 (98%)	384 (100%)	0	100	100
1	H	381/393 (97%)	381 (100%)	0	100	100
All	All	3063/3144 (97%)	3063 (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

16 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	GLC	I	1	2	12,12,12	0.99	0	17,17,17	0.76	0
2	GLC	I	2	2	11,11,12	0.46	0	15,15,17	0.97	0
2	GLC	J	1	2	12,12,12	1.01	0	16,17,17	0.88	0
2	GLC	J	2	2	11,11,12	0.76	0	15,15,17	1.15	1 (6%)
2	GLC	K	1	2	12,12,12	0.91	0	16,17,17	0.85	0
2	GLC	K	2	2	11,11,12	0.41	0	15,15,17	0.96	2 (13%)
2	GLC	L	1	2	12,12,12	1.02	0	17,17,17	0.68	0
2	GLC	L	2	2	11,11,12	0.73	0	15,15,17	1.02	1 (6%)
2	GLC	M	1	2	12,12,12	0.82	0	17,17,17	0.77	0
2	GLC	M	2	2	11,11,12	0.53	0	15,15,17	0.95	1 (6%)
2	GLC	N	1	2	12,12,12	0.90	0	17,17,17	0.68	0
2	GLC	N	2	2	11,11,12	0.46	0	15,15,17	0.86	0
2	GLC	O	1	2	12,12,12	0.96	0	16,17,17	0.75	0
2	GLC	O	2	2	11,11,12	0.80	0	15,15,17	0.98	1 (6%)
2	GLC	P	1	2	12,12,12	1.02	0	16,17,17	0.85	0
2	GLC	P	2	2	11,11,12	0.84	0	15,15,17	1.02	1 (6%)

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	GLC	I	1	2	-	0/2/22/22	0/1/1/1
2	GLC	I	2	2	-	0/2/19/22	0/1/1/1
2	GLC	J	2	2	-	0/2/19/22	0/1/1/1
2	GLC	K	2	2	-	0/2/19/22	0/1/1/1
2	GLC	L	1	2	-	1/2/22/22	0/1/1/1
2	GLC	L	2	2	-	0/2/19/22	0/1/1/1
2	GLC	M	1	2	-	1/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	M	2	2	-	0/2/19/22	0/1/1/1
2	GLC	N	1	2	-	0/2/22/22	0/1/1/1
2	GLC	N	2	2	-	0/2/19/22	0/1/1/1
2	GLC	O	2	2	-	0/2/19/22	0/1/1/1
2	GLC	P	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	2	GLC	C6-C5-C4	-2.64	106.81	113.00
2	J	2	GLC	C6-C5-C4	-2.61	106.90	113.00
2	P	2	GLC	C6-C5-C4	-2.46	107.25	113.00
2	O	2	GLC	C6-C5-C4	-2.42	107.35	113.00
2	M	2	GLC	C6-C5-C4	-2.23	107.77	113.00

There are no chirality outliers.

All (2) torsion outliers are listed below:

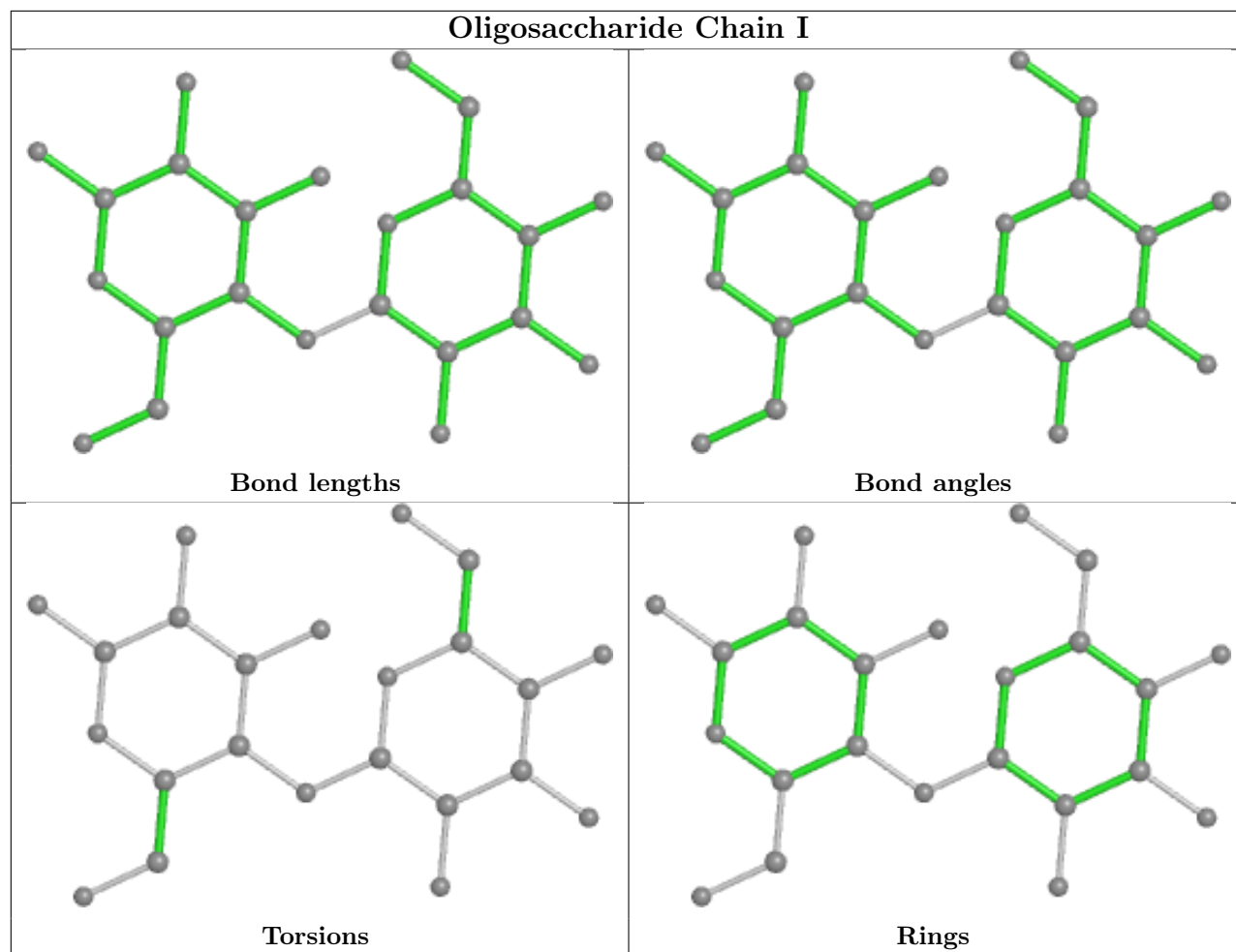
Mol	Chain	Res	Type	Atoms
2	M	1	GLC	C4-C5-C6-O6
2	L	1	GLC	C4-C5-C6-O6

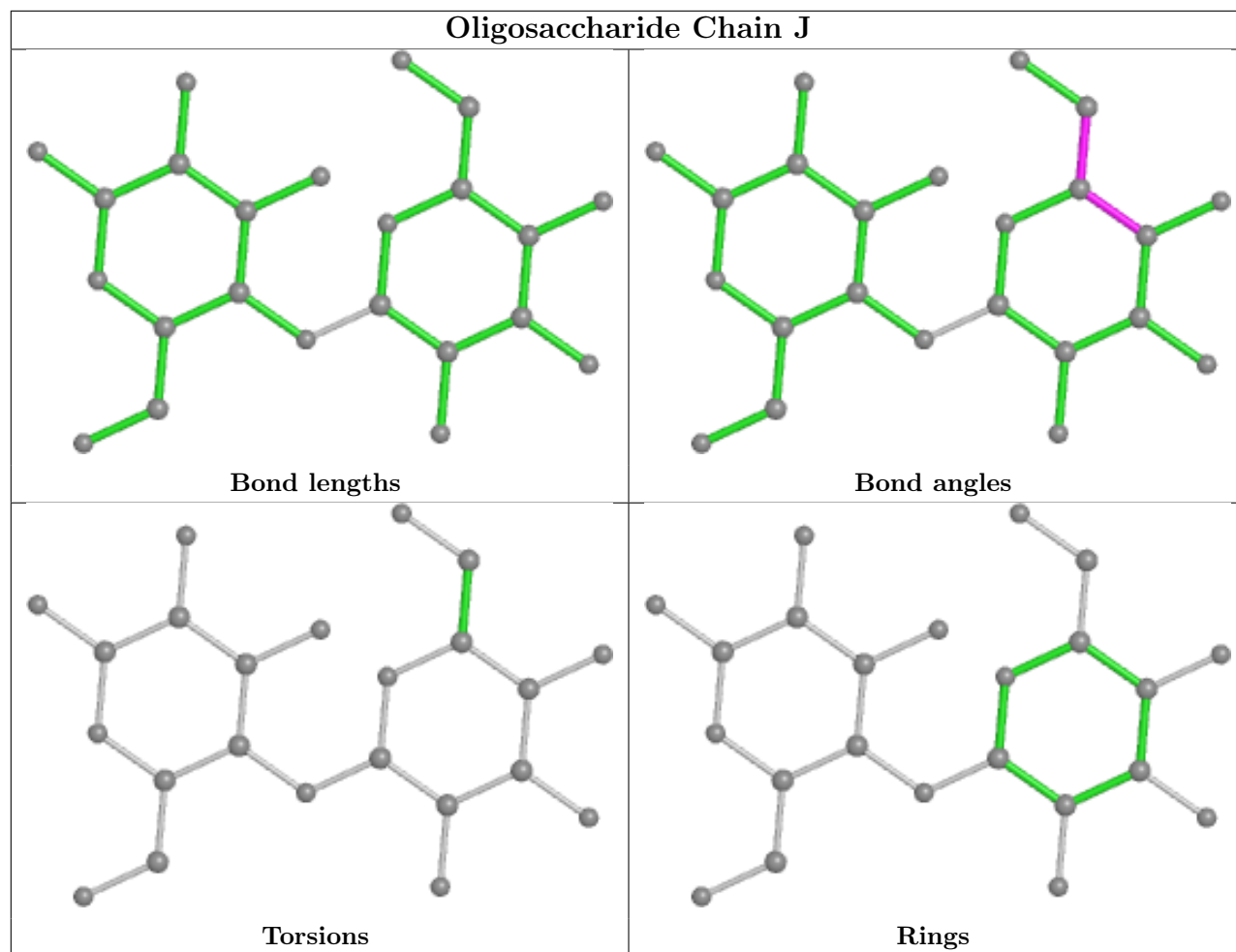
There are no ring outliers.

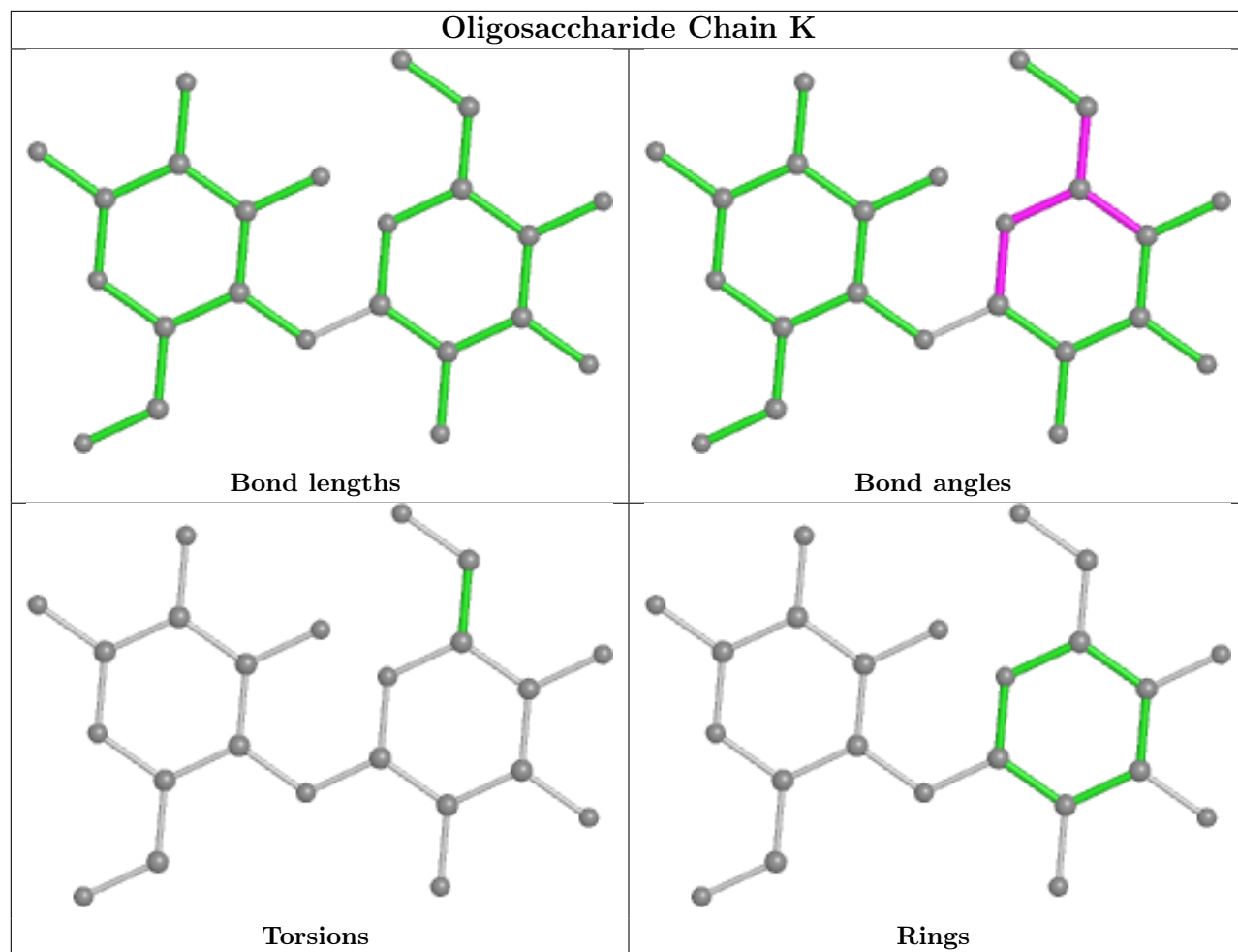
1 monomer is involved in 1 short contact:

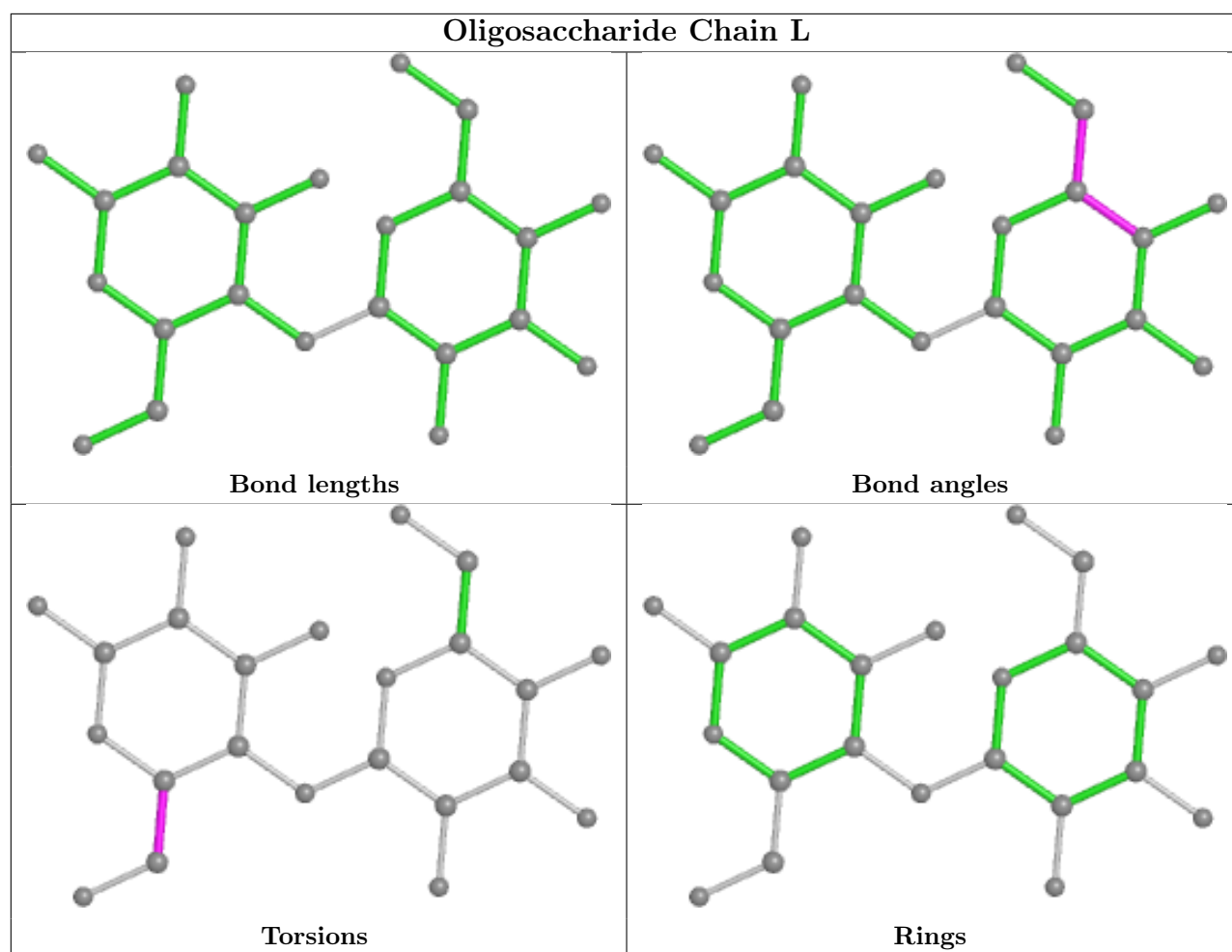
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	N	2	GLC	1	0

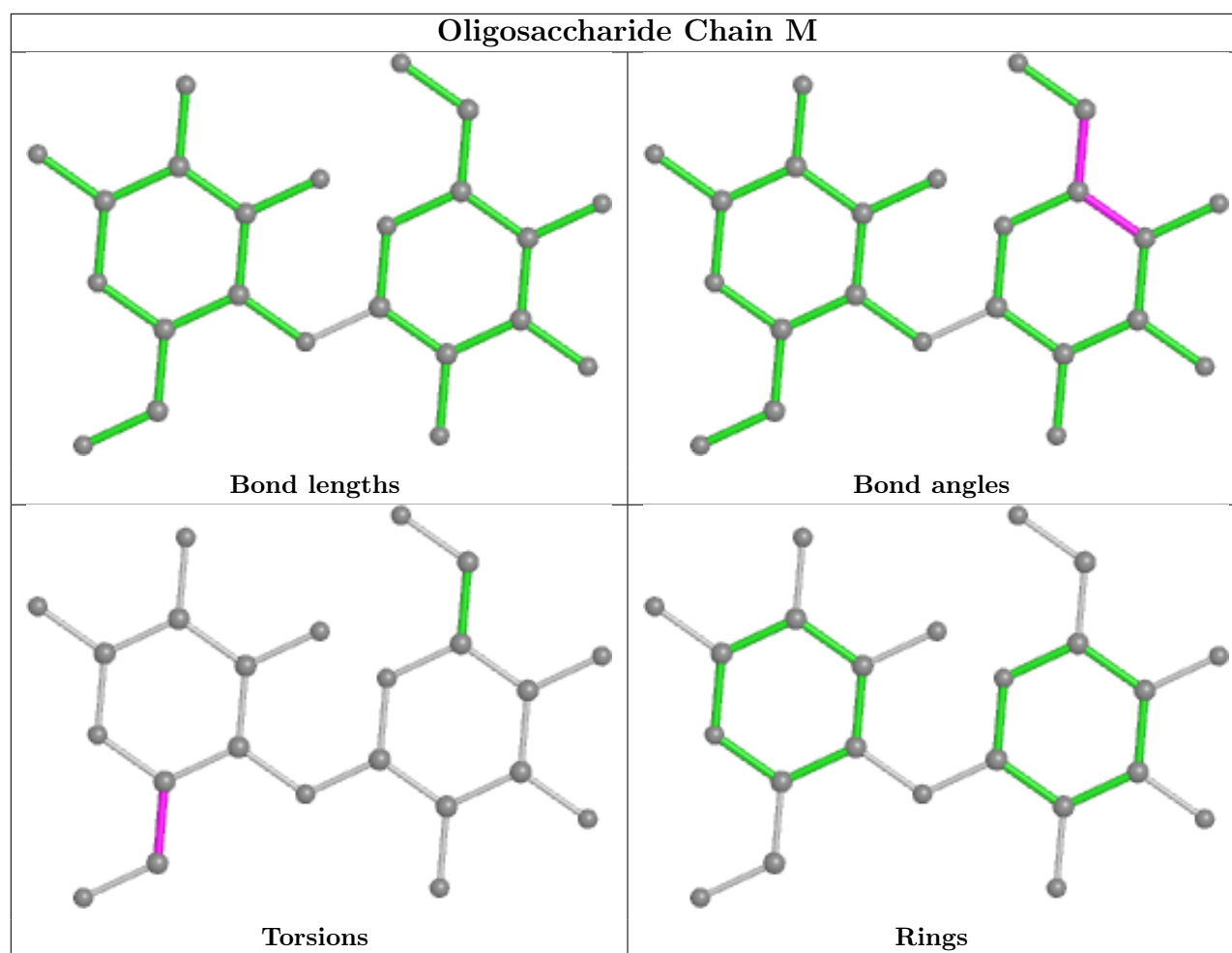
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

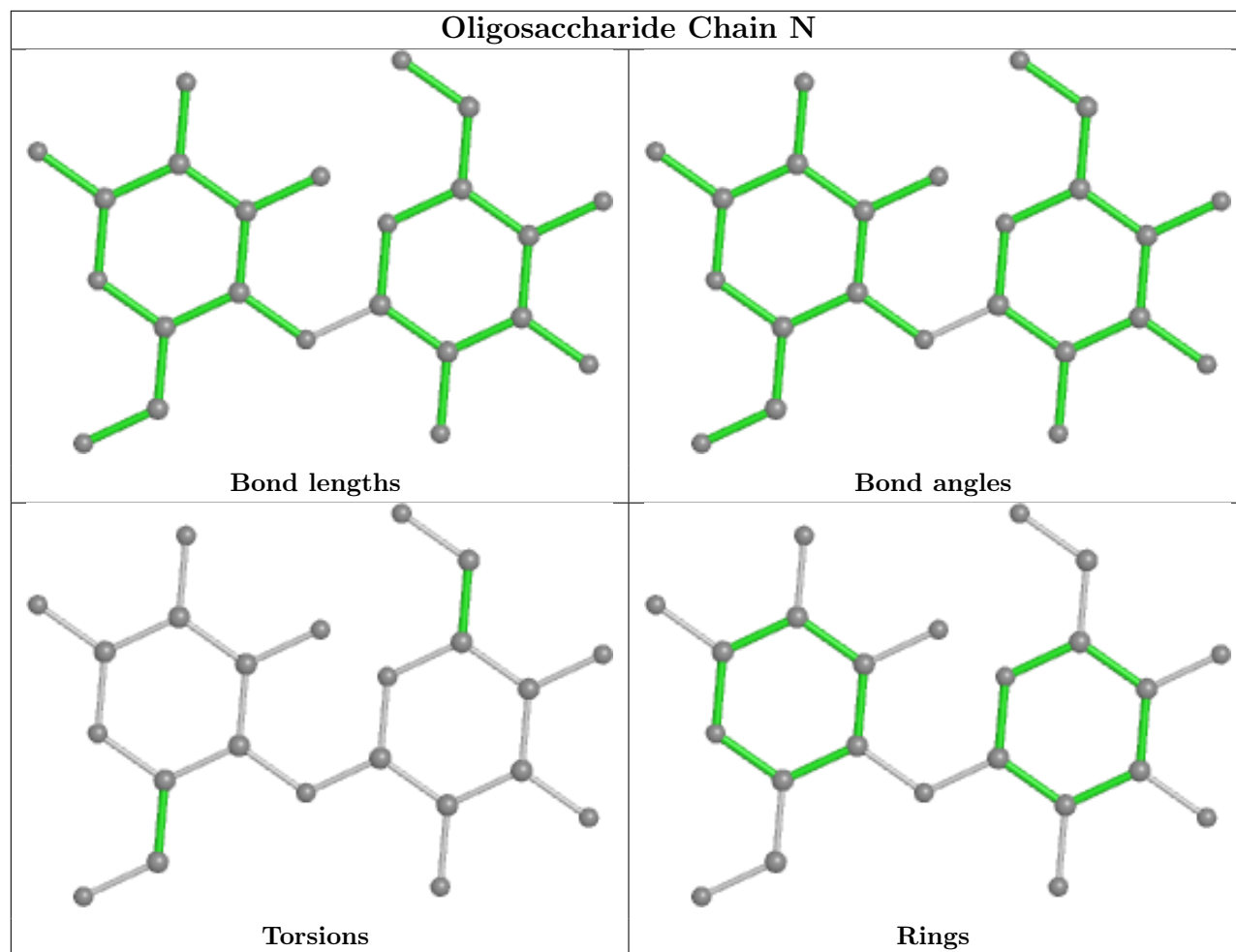


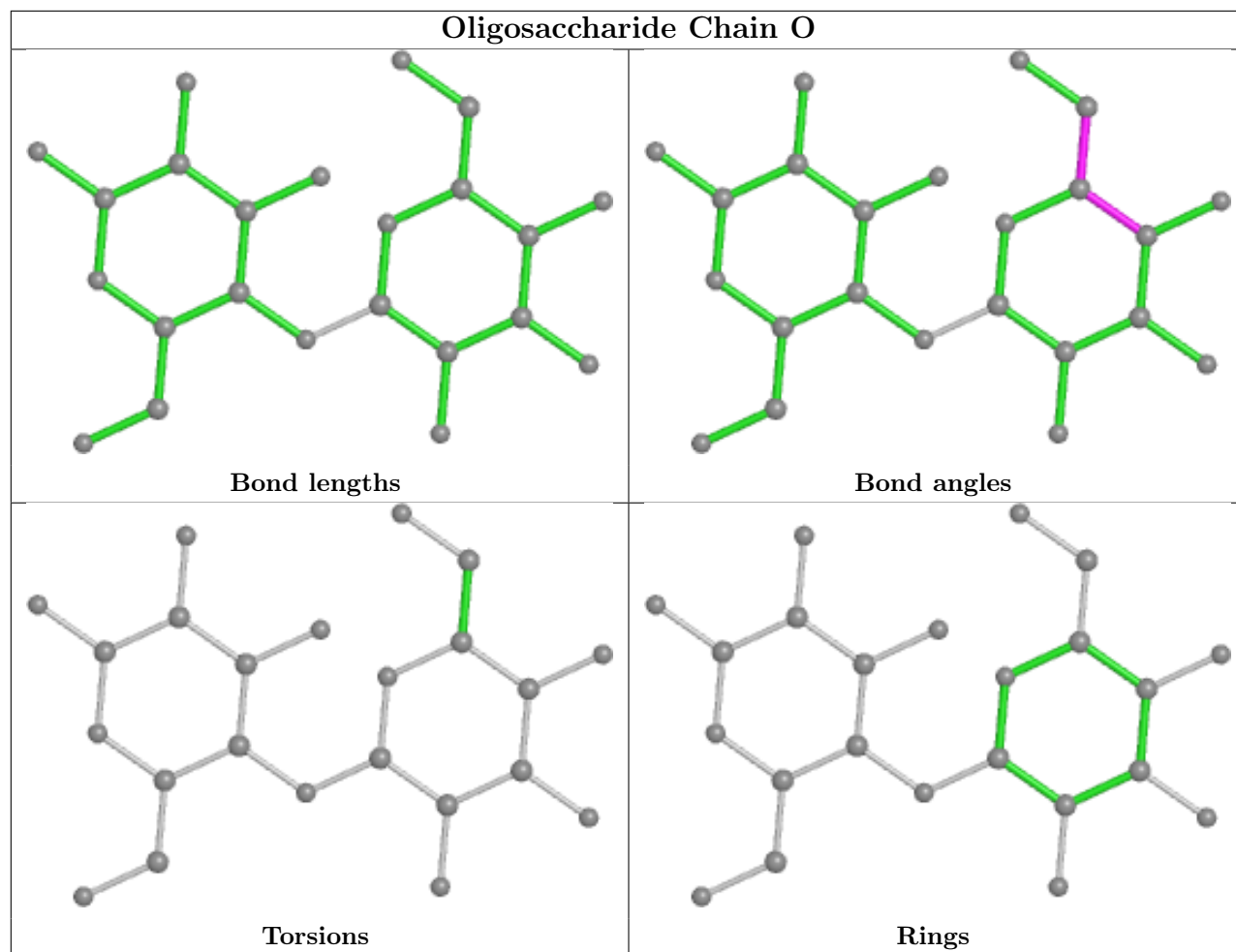


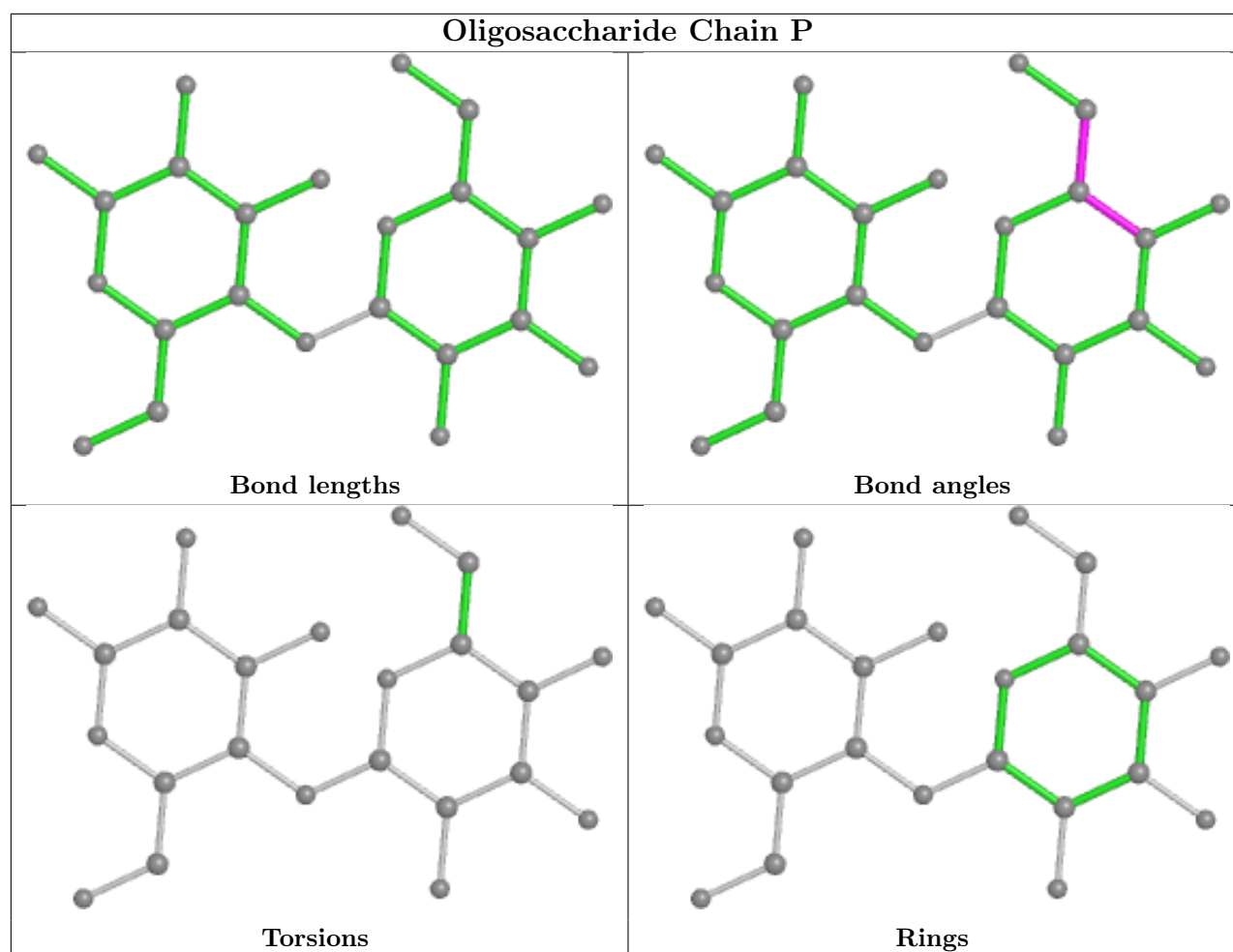












5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	471/481 (97%)	0.24	11 (2%) 60 67	28, 52, 96, 152	0
1	B	471/481 (97%)	0.42	19 (4%) 38 45	29, 64, 111, 134	0
1	C	471/481 (97%)	0.19	16 (3%) 45 52	28, 52, 98, 161	0
1	D	469/481 (97%)	0.49	26 (5%) 25 31	30, 66, 117, 143	0
1	E	472/481 (98%)	0.29	14 (2%) 50 57	28, 52, 97, 162	0
1	F	472/481 (98%)	0.25	18 (3%) 40 47	28, 53, 96, 166	0
1	G	472/481 (98%)	0.39	23 (4%) 29 36	30, 65, 114, 139	0
1	H	469/481 (97%)	0.40	22 (4%) 31 38	30, 66, 113, 133	0
All	All	3767/3848 (97%)	0.34	149 (3%) 38 45	28, 58, 109, 166	0

The worst 5 of 149 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	454	GLY	9.0
1	E	453	SER	8.4
1	F	454	GLY	7.9
1	A	454	GLY	6.5
1	B	454	GLY	6.5

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,

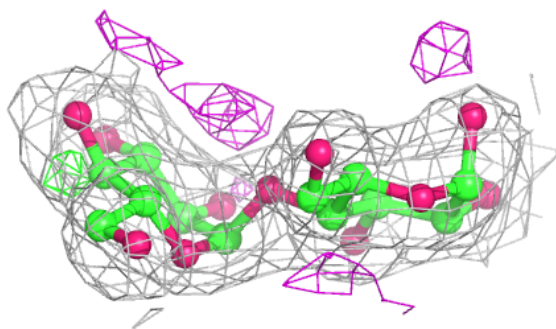
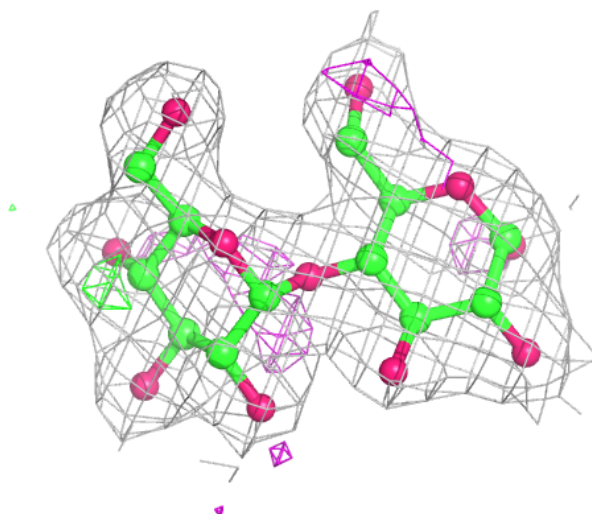
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	L	1	12/12	0.93	0.17	47,53,56,57	0
2	GLC	J	1	12/12	0.94	0.15	45,49,51,52	0
2	GLC	P	1	12/12	0.94	0.15	45,50,51,52	0
2	GLC	K	2	11/12	0.95	0.14	29,32,34,35	0
2	GLC	J	2	11/12	0.95	0.12	39,41,44,44	0
2	GLC	L	2	11/12	0.95	0.14	40,43,45,46	0
2	GLC	M	1	12/12	0.95	0.14	33,38,40,41	0
2	GLC	N	1	12/12	0.95	0.15	36,41,42,42	0
2	GLC	O	2	11/12	0.95	0.14	39,40,42,43	0
2	GLC	K	1	12/12	0.95	0.13	35,39,41,41	0
2	GLC	N	2	11/12	0.96	0.12	30,33,36,37	0
2	GLC	O	1	12/12	0.96	0.15	44,48,50,50	0
2	GLC	M	2	11/12	0.96	0.15	28,31,34,35	0
2	GLC	I	2	11/12	0.96	0.15	27,30,32,33	0
2	GLC	P	2	11/12	0.96	0.15	39,41,43,43	0
2	GLC	I	1	12/12	0.97	0.12	33,37,39,40	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.

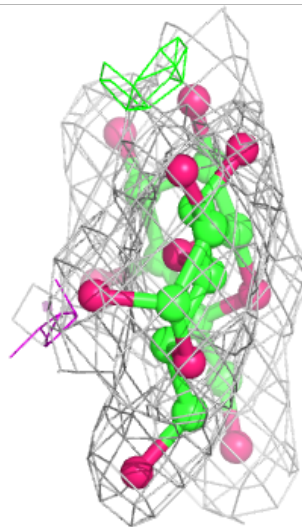
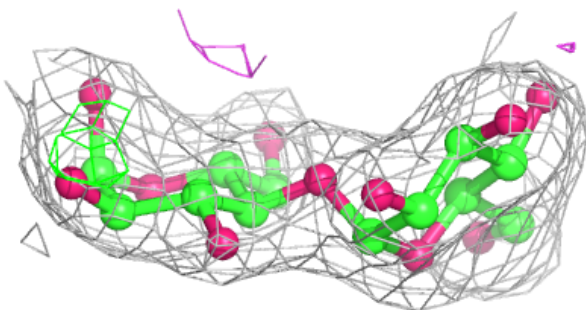
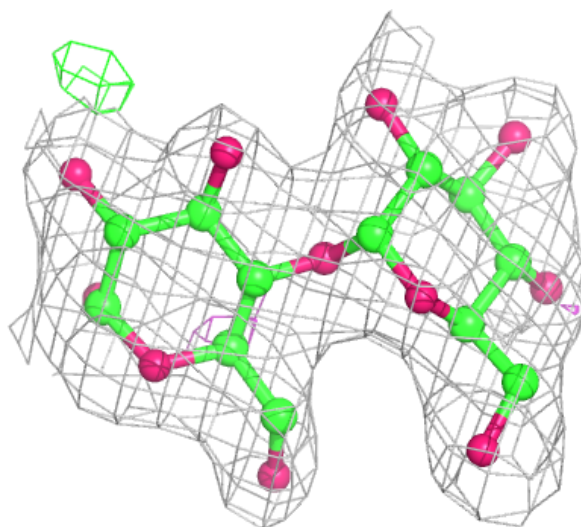
Electron density around Chain I:

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



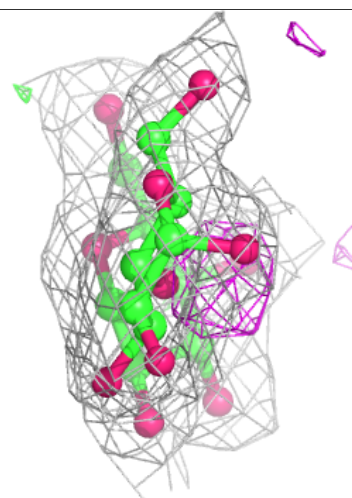
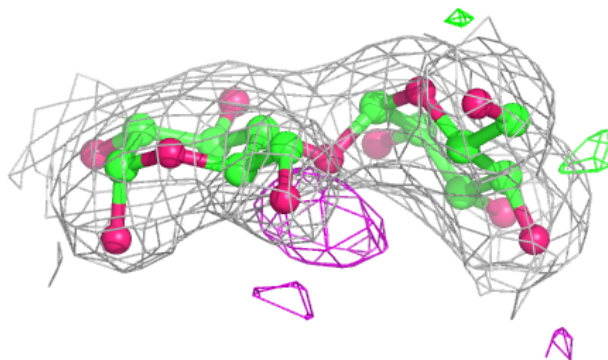
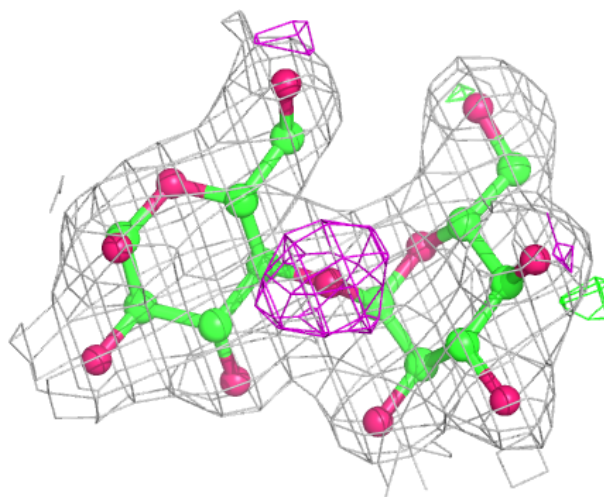
Electron density around Chain J:

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



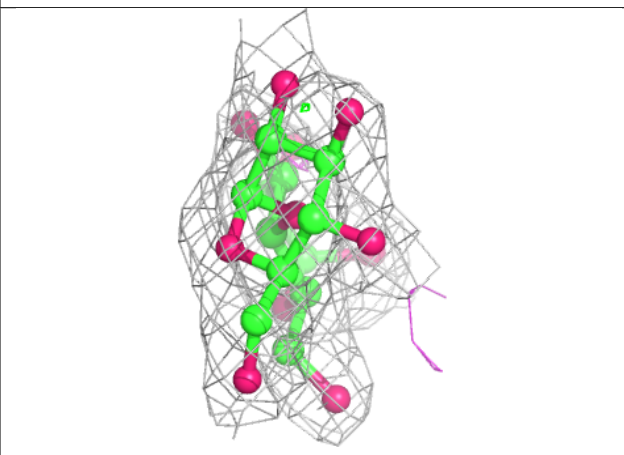
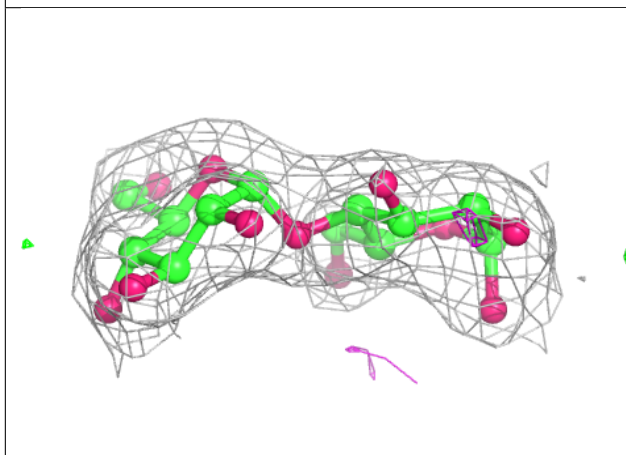
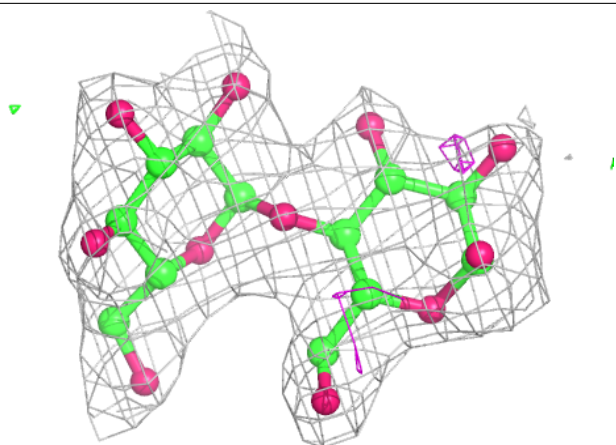
Electron density around Chain K:

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



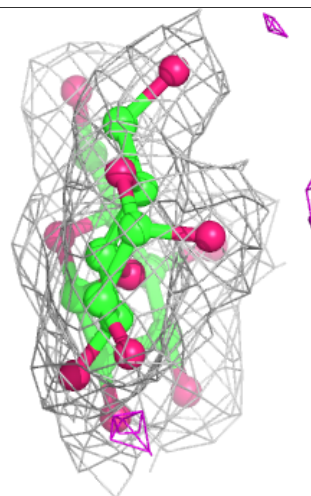
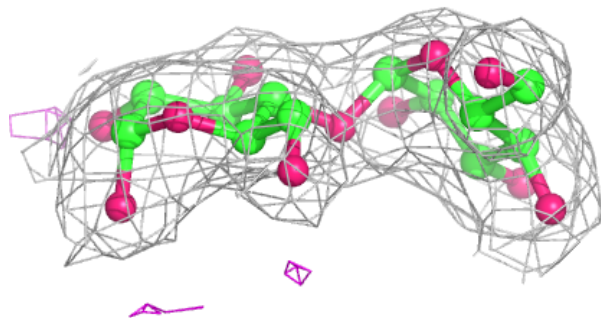
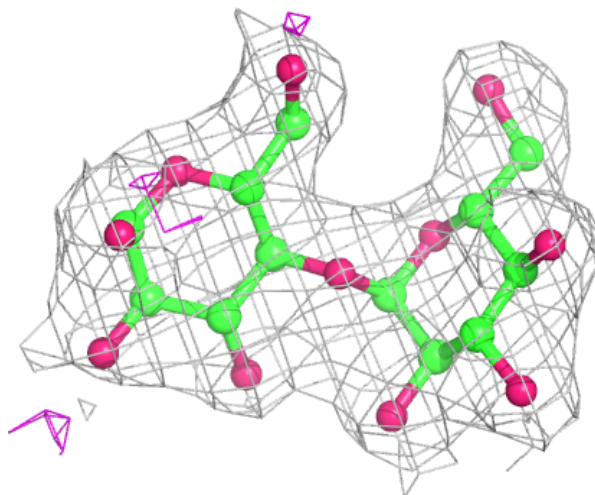
Electron density around Chain L:

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



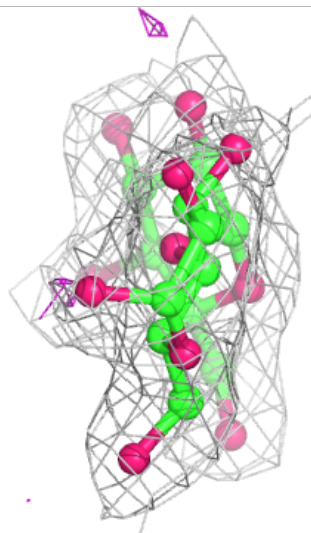
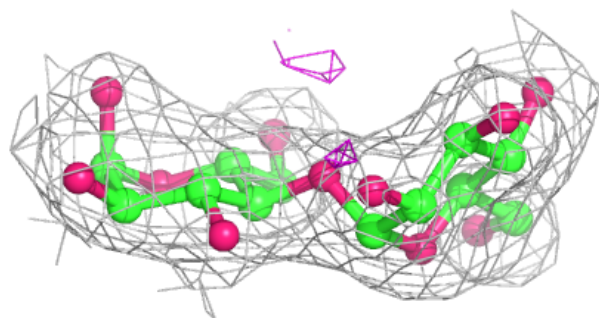
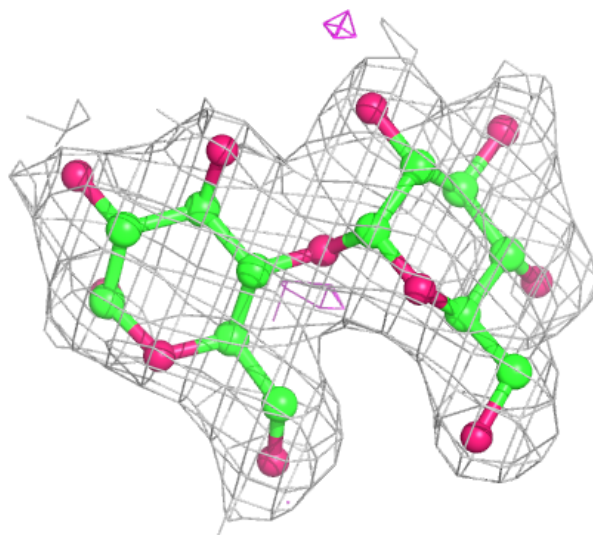
Electron density around Chain M:

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



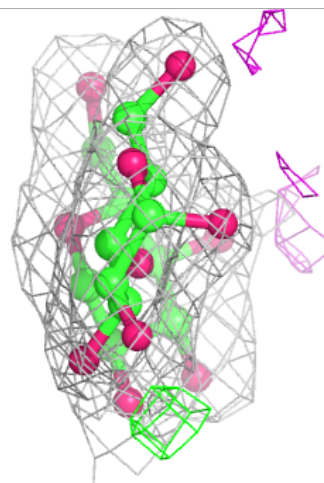
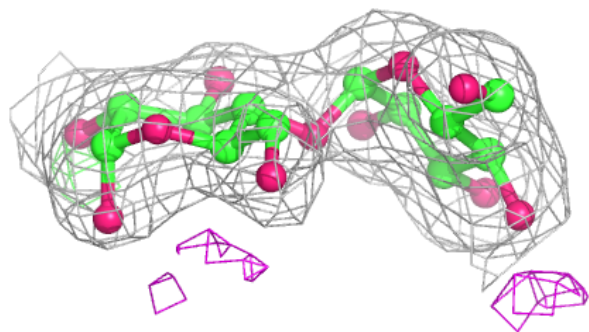
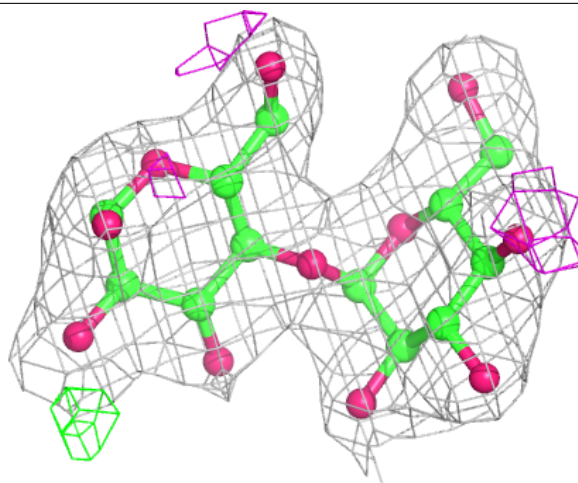
Electron density around Chain N:

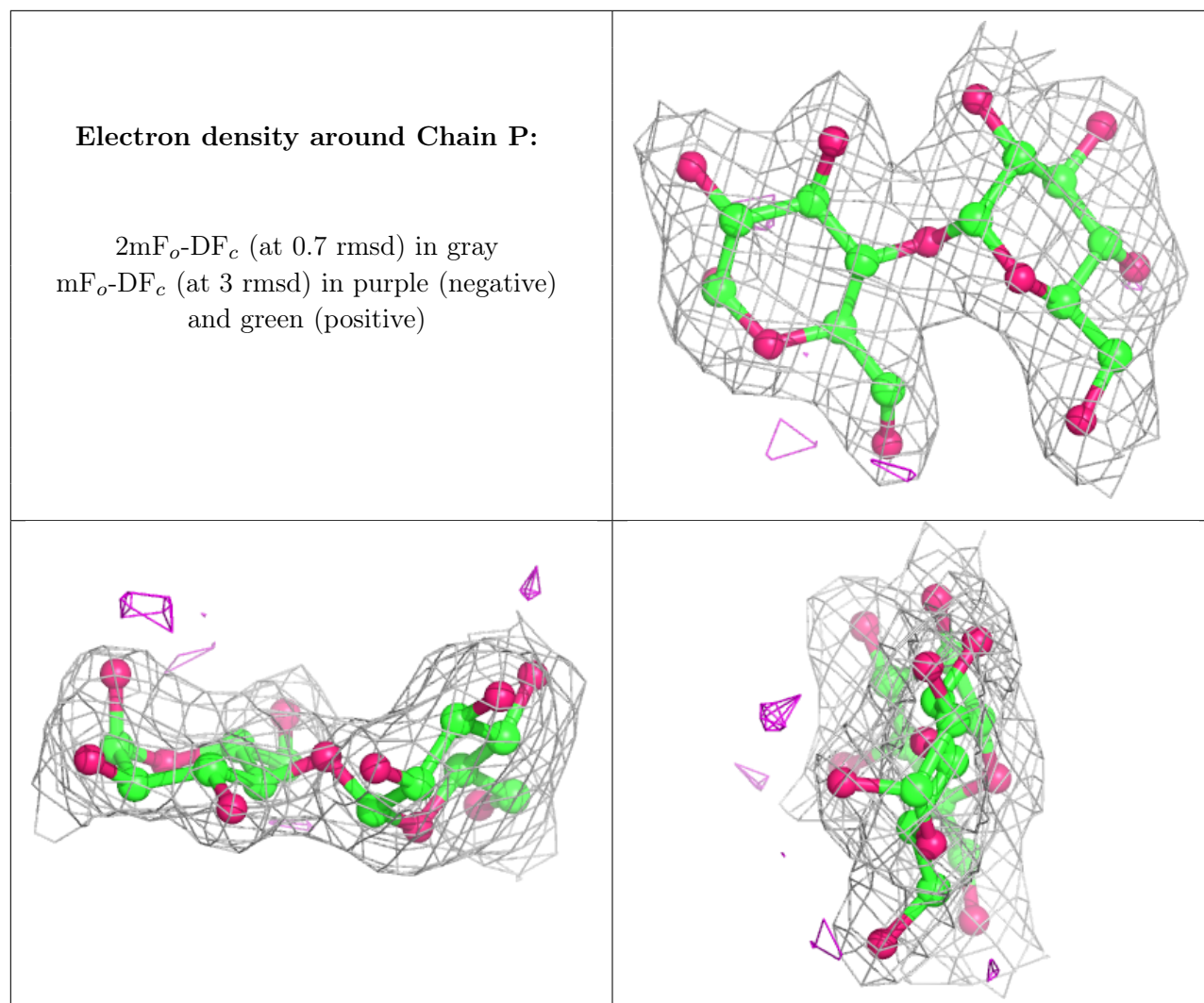
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain O:

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





6.4 Ligands ⓘ

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	CA	F	483	1/1	0.64	0.10	71,71,71,71	0
3	CA	A	485	1/1	0.77	0.08	61,61,61,61	0
3	CA	A	483	1/1	0.81	0.06	70,70,70,70	0
3	CA	D	483	1/1	0.83	0.09	95,95,95,95	0
3	CA	G	485	1/1	0.83	0.07	59,59,59,59	0
3	CA	A	484	1/1	0.85	0.19	57,57,57,57	0
3	CA	C	485	1/1	0.86	0.06	61,61,61,61	0
3	CA	B	483	1/1	0.87	0.05	93,93,93,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	CA	F	485	1/1	0.88	0.07	60,60,60,60	0
3	CA	F	484	1/1	0.88	0.24	57,57,57,57	0
3	CA	E	484	1/1	0.89	0.20	58,58,58,58	0
3	CA	D	485	1/1	0.90	0.14	58,58,58,58	0
3	CA	C	483	1/1	0.90	0.06	64,64,64,64	0
3	CA	E	485	1/1	0.91	0.06	61,61,61,61	0
3	CA	G	483	1/1	0.92	0.09	85,85,85,85	0
3	CA	C	484	1/1	0.92	0.15	57,57,57,57	0
3	CA	B	484	1/1	0.93	0.05	54,54,54,54	0
3	CA	E	483	1/1	0.94	0.05	67,67,67,67	0
3	CA	G	484	1/1	0.95	0.06	54,54,54,54	0
3	CA	H	485	1/1	0.95	0.05	59,59,59,59	0
3	CA	H	484	1/1	0.96	0.03	54,54,54,54	0
3	CA	H	483	1/1	0.97	0.08	89,89,89,89	0
3	CA	B	485	1/1	0.97	0.07	59,59,59,59	0
3	CA	D	484	1/1	0.97	0.04	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.