



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2026 – 11:44 PM UTC

PDB ID : 7P7P / pdb_00007p7p
Title : Crystal structure of ERAP2 aminopeptidase in complex with phosphinic pseudotriptide((1R)-1-Amino-3-phenylpropyl){(2S)-3-(((2S)-1-amino-1-oxo-3-phenylpropan-2-yl)amino)-2-{[3-(2-hydroxyphenyl)-isoxazol-5-yl]methyl}-3-oxopropyl}phosphinic acid
Authors : Giastas, P.; Stratikos, E.; Mpakali, A.
Deposited on : 2021-07-20
Resolution : 3.00 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 types of validation reports are described at

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

The following versions of software and data (see [references](#) ①) 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

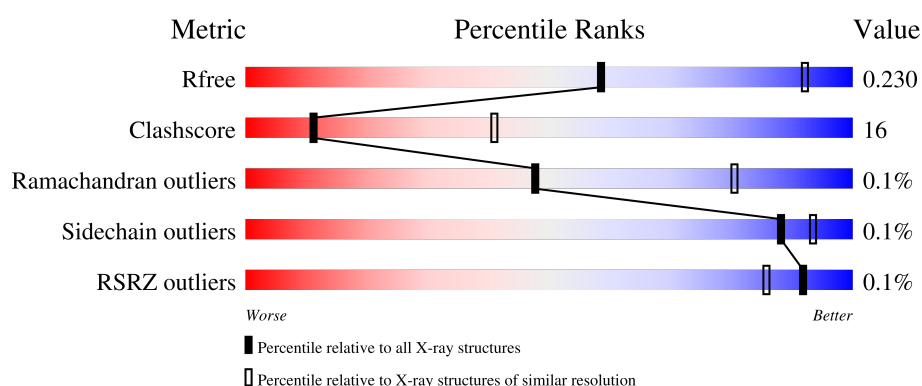
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

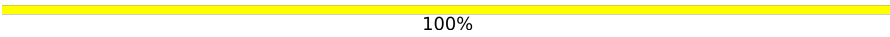
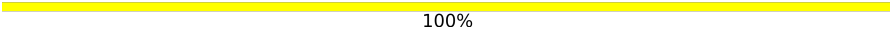
The reported resolution of this entry is 3.00 Å.

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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	962	 66% 28% 5%
1	B	962	 58% 33% 9%
2	C	4	 100%
3	D	4	 50% 50%
4	E	2	 100%

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Mol	Chain	Length	Quality of chain
4	H	2	 100%
4	I	2	 50% 50%
5	F	3	 100%
6	G	5	 20% 80%

2 Entry composition [i](#)

There are 16 unique types of molecules in this entry. The entry contains 14990 atoms, of which 76 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 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	911	Total	C	N	O	S	0	1	0
			7330	4719	1219	1359	33			
1	B	871	Total	C	N	O	S	0	0	0
			6839	4407	1134	1274	24			

There are 6 discrepancies between the modelled and reference sequences:

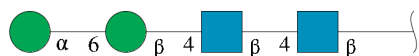
Chain	Residue	Modelled	Actual	Comment	Reference
A	392	ASN	LYS	variant	UNP Q6P179
A	961	ARG	-	expression tag	UNP Q6P179
A	962	HIS	-	expression tag	UNP Q6P179
B	392	ASN	LYS	variant	UNP Q6P179
B	961	ARG	-	expression tag	UNP Q6P179
B	962	HIS	-	expression tag	UNP Q6P179

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-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
2	C	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 3 is an oligosaccharide called 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.



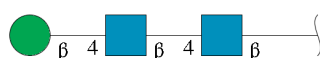
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



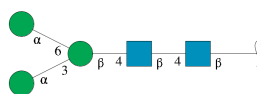
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
4	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



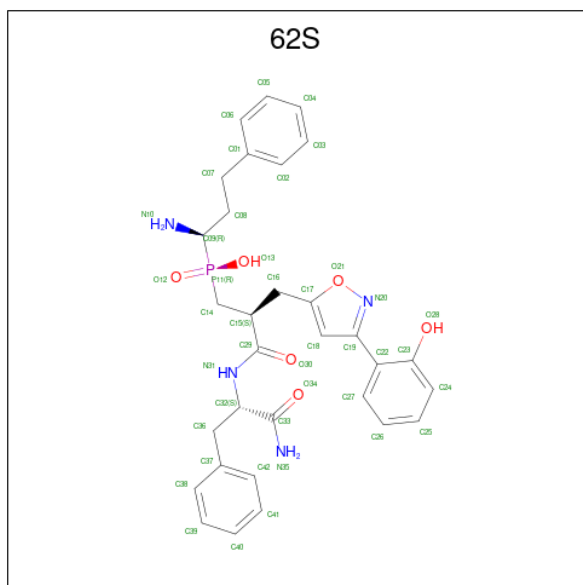
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	F	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 6 is an oligosaccharide called 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.



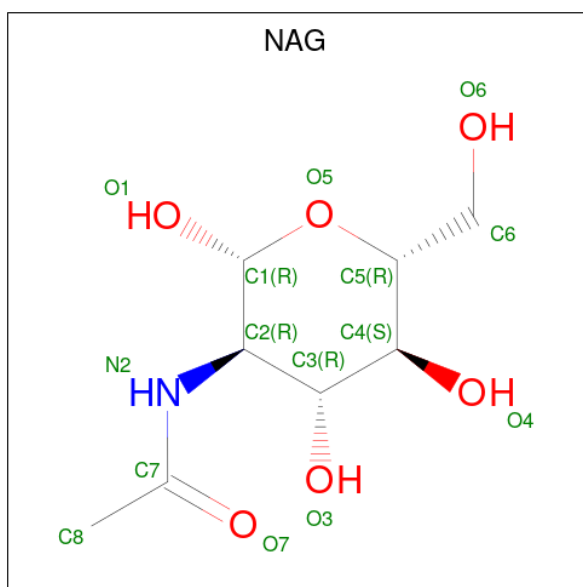
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 7 is [(2 {S})-3-[[[(2 {S})-1-azanyl-1-oxidanylidene-3-phenyl-propan-2-yl]amino]-2-[[3-(2-hydroxyphenyl)-1,2-oxazol-5-yl]methyl]-3-oxidanylidene-propyl]-[(1 {R})-1-azanyl-3-phenyl-propyl]phosphinic acid (CCD ID: 62S) (formula: C₃₁H₃₅N₄O₆P).



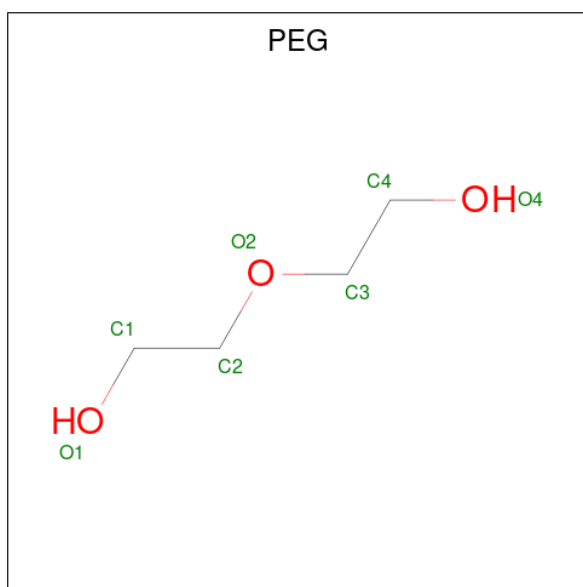
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
7	A	1	Total	C	H	N	O	P	0	0
			77	31	35	4	6	1		
7	B	1	Total	C	H	N	O	P	0	0
			77	31	35	4	6	1		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



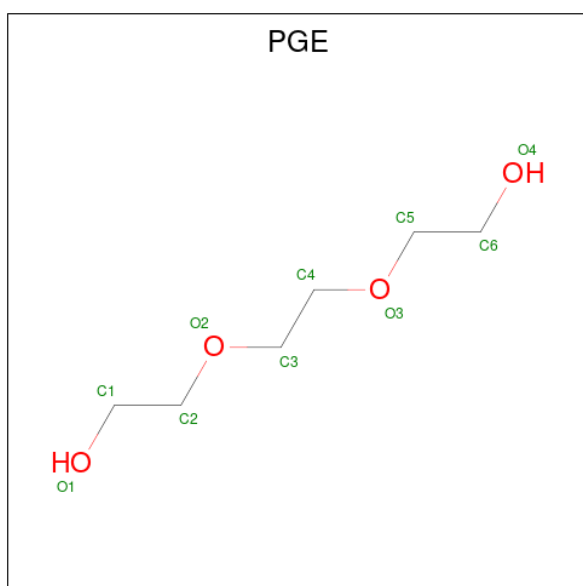
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1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

- Molecule 9 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			7	4	3		
9	A	1	Total	C	O	0	0
			7	4	3		

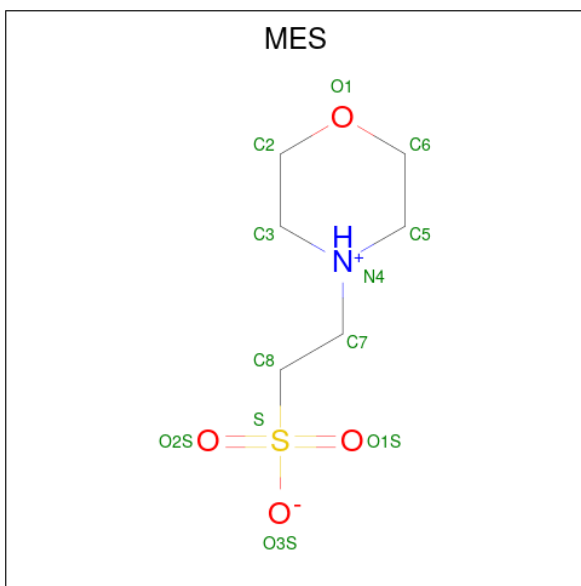
- Molecule 10 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			10	6	4		

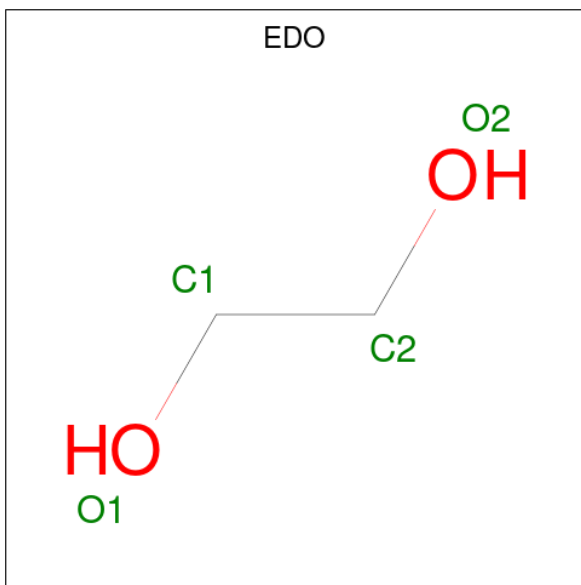
- Molecule 11 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES)

(formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 12 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



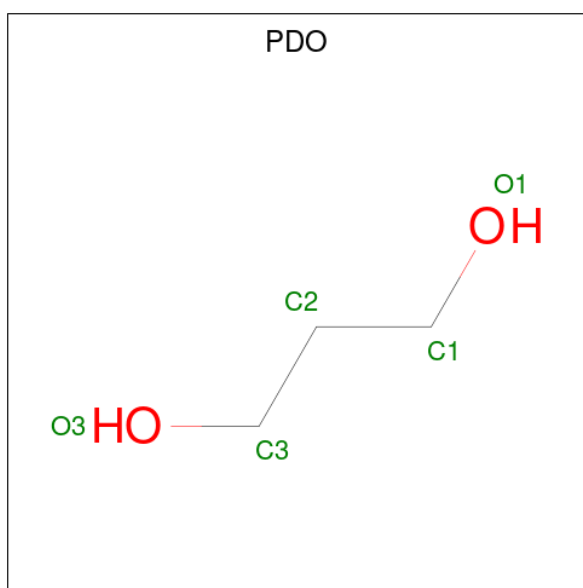
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	0	0
			4	2	2		
12	A	1	Total	C	O	0	0
			4	2	2		

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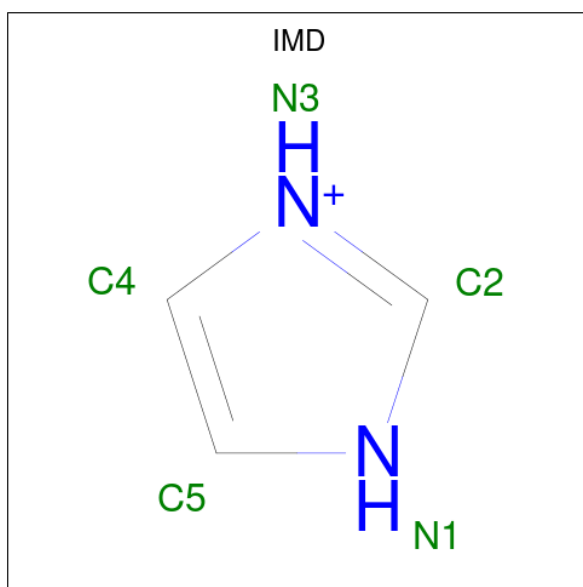
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	1	Total C O 4 2 2	0	0
12	A	1	Total C O 4 2 2	0	0
12	A	1	Total C H O 10 2 6 2	0	0
12	A	1	Total C O 4 2 2	0	0
12	A	1	Total C O 4 2 2	0	0

- Molecule 13 is 1,3-PROPANDIOL (CCD ID: PDO) (formula: $C_3H_8O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total C O 5 3 2	0	0
13	B	1	Total C O 5 3 2	0	0

- Molecule 14 is IMIDAZOLE (CCD ID: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
14	A	1	Total	C	N	0	0
			5	3	2		

- Molecule 15 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
15	A	1	Total	Zn	0	0
			1	1		
15	B	1	Total	Zn	0	0
			1	1		

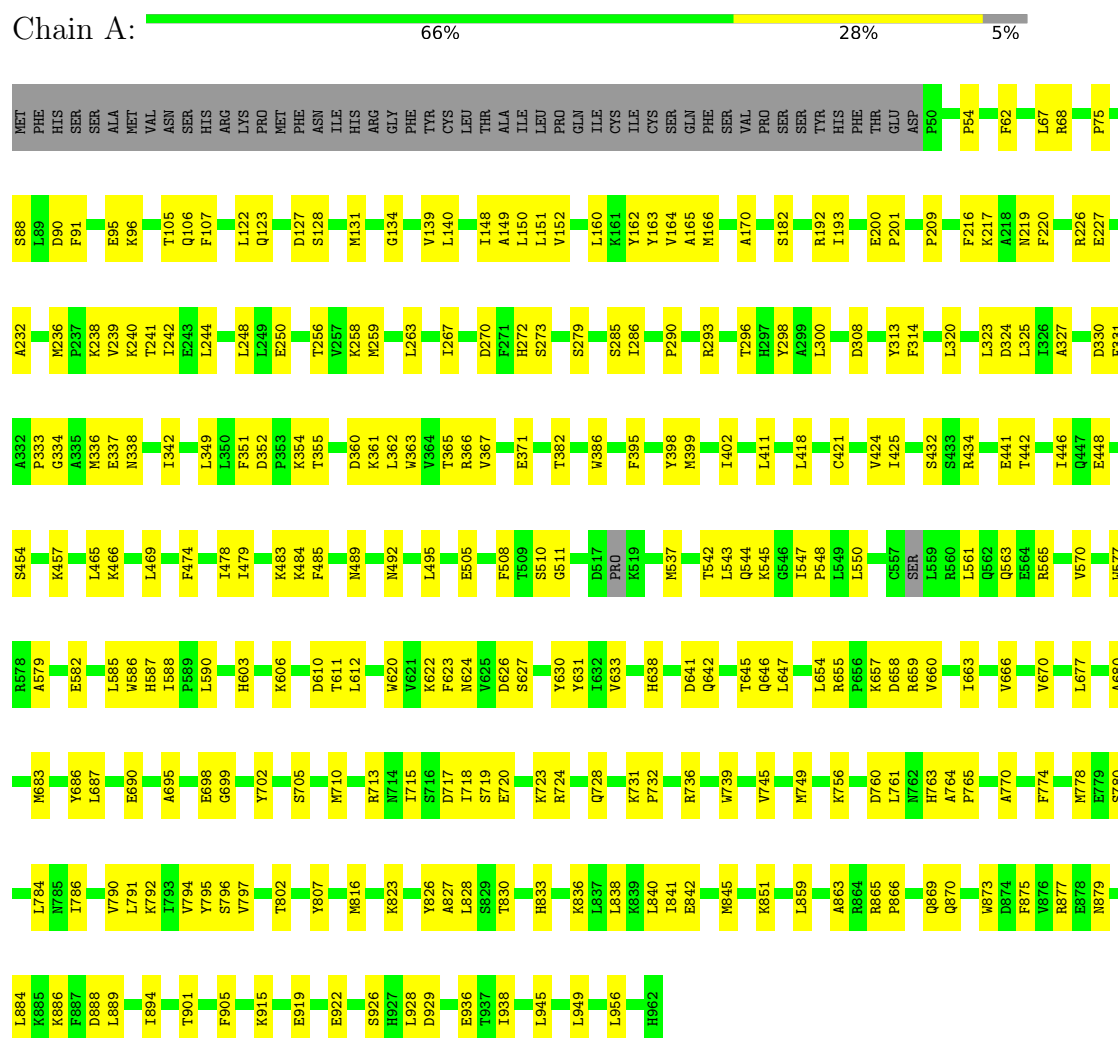
- Molecule 16 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	A	121	Total	O	0	0
			121	121		
16	B	35	Total	O	0	0
			35	35		

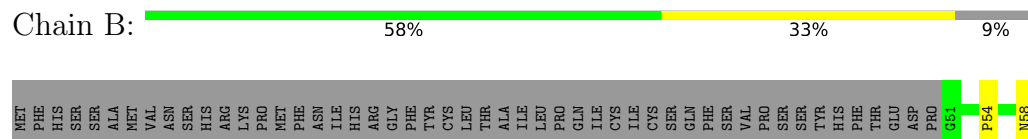
3 Residue-property plots

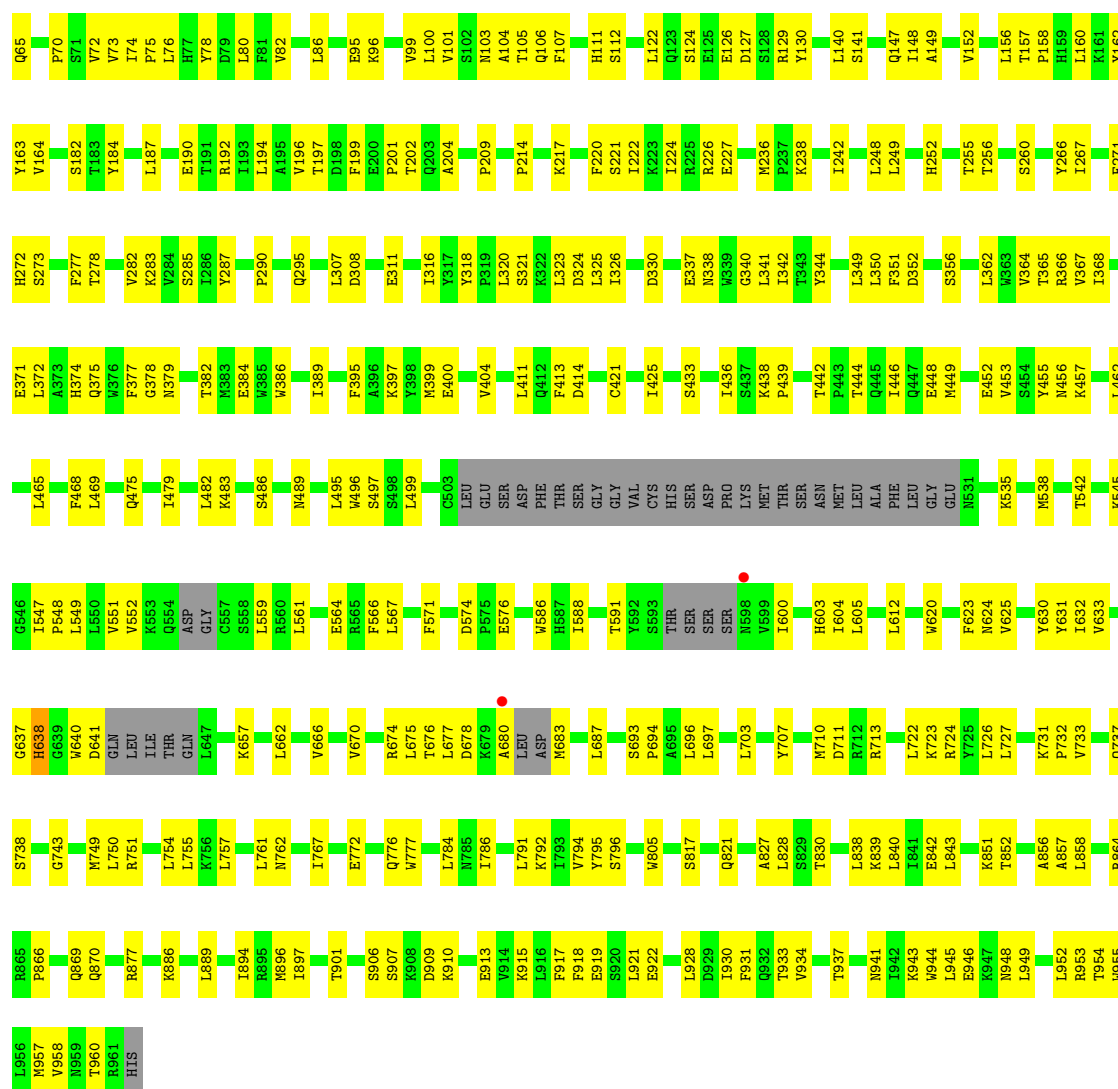
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Endoplasmic reticulum aminopeptidase 2



• Molecule 1: Endoplasmic reticulum aminopeptidase 2





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

Chain C: 100%

NA61
NA62
NA63
NA64

- Molecule 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

Chain D: 50% 50%

NA61
NA62
NA63
NA64

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

Chain E:  100%

MAG1
MAG2

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

Chain H:  100%

MAG1
MAG2

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

Chain I:  50%  50%

MAG1
MAG2

- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain F:  100%

MAG1
MAG2
BMA3

- Molecule 6: 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

Chain G:  20%  80%

MAG1
MAG2
BMA3
MAN4
MAN5

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.34Å 134.62Å 129.14Å 90.00° 90.48° 90.00°	Depositor
Resolution (Å)	50.19 – 3.00 50.19 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.19-3.00) 94.5 (50.19-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660, PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.180 , 0.231 0.182 , 0.230	Depositor DCC
R_{free} test set	2266 reflections (4.39%)	wwPDB-VP
Wilson B-factor (Å ²)	79.5	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 84.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.010 for -h,-l,-k 0.000 for -h,l,k 0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14990	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: PDO, PGE, MAN, NAG, EDO, 62S, BMA, MES, PEG, ZN, IMD

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	0.50	0/7514	0.78	4/10190 (0.0%)
1	B	0.45	0/7009	0.73	1/9536 (0.0%)
All	All	0.47	0/14523	0.76	5/19726 (0.0%)

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
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	720	GLU	N-CA-C	-8.35	105.10	114.62
1	A	717	ASP	N-CA-C	-7.58	103.09	113.18
1	A	336	MET	CA-C-N	5.81	132.29	122.65
1	A	336	MET	C-N-CA	5.81	132.29	122.65
1	B	620	TRP	CA-CB-CG	5.12	123.33	113.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	270	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	B	637	GLY	Peptide
1	B	638	HIS	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	7330	0	7172	186	0
1	B	6839	0	6480	279	0
2	C	50	0	43	2	0
3	D	50	0	43	0	0
4	E	28	0	25	0	0
4	H	28	0	25	0	0
4	I	28	0	25	0	0
5	F	39	0	34	4	0
6	G	61	0	52	4	0
7	A	42	35	0	3	0
7	B	42	35	0	1	0
8	A	56	0	52	4	0
8	B	84	0	78	0	0
9	A	14	0	20	0	0
10	A	10	0	14	1	0
11	A	12	0	12	1	0
12	A	28	6	42	3	0
13	A	5	0	8	0	0
13	B	5	0	8	0	0
14	A	5	0	5	0	0
15	A	1	0	0	0	0
15	B	1	0	0	0	0
16	A	121	0	0	1	0
16	B	35	0	0	1	0
All	All	14914	76	14138	472	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 16.

The worst 5 of 472 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:945:LEU:HB3	1:B:949:LEU:CD2	1.61	1.29
1:B:945:LEU:HB3	1:B:949:LEU:HD22	1.13	1.09
1:B:945:LEU:HA	1:B:949:LEU:HD13	1.10	1.08
1:B:945:LEU:CB	1:B:949:LEU:HD22	1.94	0.98
1:B:945:LEU:CA	1:B:949:LEU:HD13	1.95	0.95

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	906/962 (94%)	858 (95%)	48 (5%)	0	100	100
1	B	859/962 (89%)	801 (93%)	56 (6%)	2 (0%)	43	76
All	All	1765/1924 (92%)	1659 (94%)	104 (6%)	2 (0%)	48	80

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	638	HIS
1	B	723	LYS

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	796/865 (92%)	796 (100%)	0	100	100
1	B	707/865 (82%)	706 (100%)	1 (0%)	88	93
All	All	1503/1730 (87%)	1502 (100%)	1 (0%)	88	93

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	384	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	375	GLN
1	B	581	GLN
1	B	904	HIS
1	B	869	GLN
1	B	230	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

22 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	C	1	1,2	14,14,15	0.63	0	17,19,21	0.61	0
2	NAG	C	2	2	14,14,15	0.53	0	17,19,21	0.69	0
2	BMA	C	3	2	11,11,12	1.18	2 (18%)	15,15,17	1.14	2 (13%)
2	MAN	C	4	2	11,11,12	2.71	3 (27%)	15,15,17	1.71	3 (20%)
3	NAG	D	1	1,3	14,14,15	0.13	0	17,19,21	0.73	0
3	NAG	D	2	3	14,14,15	0.35	0	17,19,21	0.62	0
3	BMA	D	3	3	11,11,12	0.85	0	15,15,17	1.59	2 (13%)
3	MAN	D	4	3	11,11,12	1.24	2 (18%)	15,15,17	1.10	2 (13%)
4	NAG	E	1	4,1	14,14,15	0.44	0	17,19,21	1.14	1 (5%)
4	NAG	E	2	4	14,14,15	0.95	1 (7%)	17,19,21	0.72	0
5	NAG	F	1	5,1	14,14,15	0.75	1 (7%)	17,19,21	1.18	1 (5%)
5	NAG	F	2	5	14,14,15	1.13	1 (7%)	17,19,21	1.23	2 (11%)
5	BMA	F	3	5	11,11,12	2.00	2 (18%)	15,15,17	1.15	1 (6%)
6	NAG	G	1	1,6	14,14,15	0.62	1 (7%)	17,19,21	0.60	0
6	NAG	G	2	6	14,14,15	1.16	1 (7%)	17,19,21	1.00	1 (5%)
6	BMA	G	3	6	11,11,12	1.01	1 (9%)	15,15,17	1.58	3 (20%)
6	MAN	G	4	6	11,11,12	1.99	5 (45%)	15,15,17	1.04	0
6	MAN	G	5	6	11,11,12	2.98	6 (54%)	15,15,17	2.70	4 (26%)
4	NAG	H	1	4,1	14,14,15	0.49	0	17,19,21	0.50	0
4	NAG	H	2	4	14,14,15	0.45	0	17,19,21	0.54	0
4	NAG	I	1	4,1	14,14,15	0.59	0	17,19,21	0.57	0
4	NAG	I	2	4	14,14,15	1.05	1 (7%)	17,19,21	1.71	3 (17%)

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	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	BMA	C	3	2	-	0/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
3	NAG	D	1	1,3	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	0/2/19/22	0/1/1/1
3	MAN	D	4	3	-	2/2/19/22	0/1/1/1
4	NAG	E	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	F	1	5,1	-	3/6/23/26	0/1/1/1
5	NAG	F	2	5	-	0/6/23/26	0/1/1/1
5	BMA	F	3	5	-	2/2/19/22	0/1/1/1
6	NAG	G	1	1,6	-	1/6/23/26	0/1/1/1
6	NAG	G	2	6	-	2/6/23/26	0/1/1/1
6	BMA	G	3	6	-	0/2/19/22	0/1/1/1
6	MAN	G	4	6	-	0/2/19/22	0/1/1/1
6	MAN	G	5	6	-	2/2/19/22	0/1/1/1
4	NAG	H	1	4,1	-	0/6/23/26	0/1/1/1
4	NAG	H	2	4	-	0/6/23/26	0/1/1/1
4	NAG	I	1	4,1	-	1/6/23/26	0/1/1/1
4	NAG	I	2	4	-	1/6/23/26	0/1/1/1

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4	MAN	O5-C1	6.44	1.54	1.43
6	G	5	MAN	C4-C3	5.43	1.66	1.52
5	F	3	BMA	O5-C1	4.46	1.51	1.43
2	C	4	MAN	O5-C5	4.35	1.51	1.43
6	G	5	MAN	C2-C3	4.15	1.58	1.52

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	G	5	MAN	C1-O5-C5	7.06	121.64	112.19
2	C	4	MAN	C1-O5-C5	4.83	118.66	112.19
4	I	2	NAG	C1-O5-C5	4.58	118.32	112.19
3	D	3	BMA	C1-O5-C5	4.51	118.23	112.19
6	G	5	MAN	C2-C3-C4	4.25	118.33	110.86

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

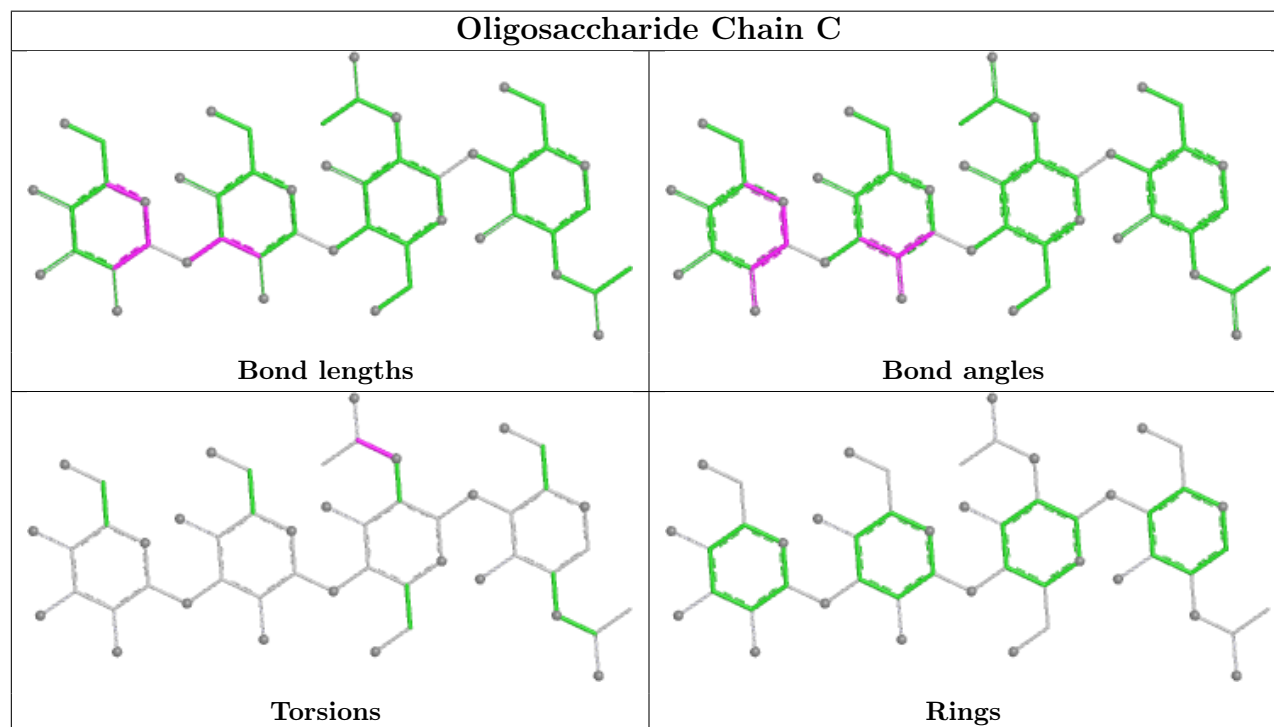
Mol	Chain	Res	Type	Atoms
5	F	3	BMA	C4-C5-C6-O6
5	F	3	BMA	O5-C5-C6-O6
5	F	1	NAG	O5-C5-C6-O6
5	F	1	NAG	C4-C5-C6-O6
3	D	4	MAN	C4-C5-C6-O6

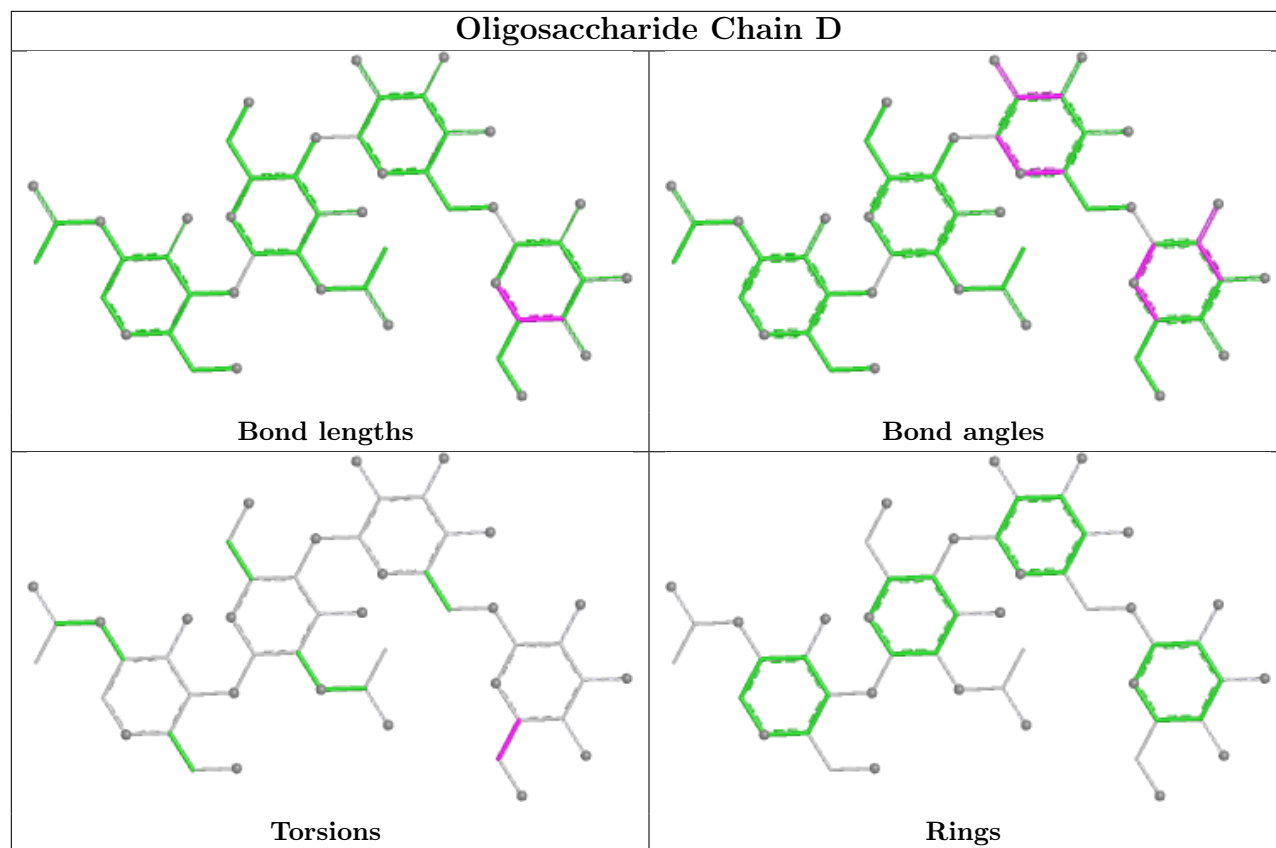
There are no ring outliers.

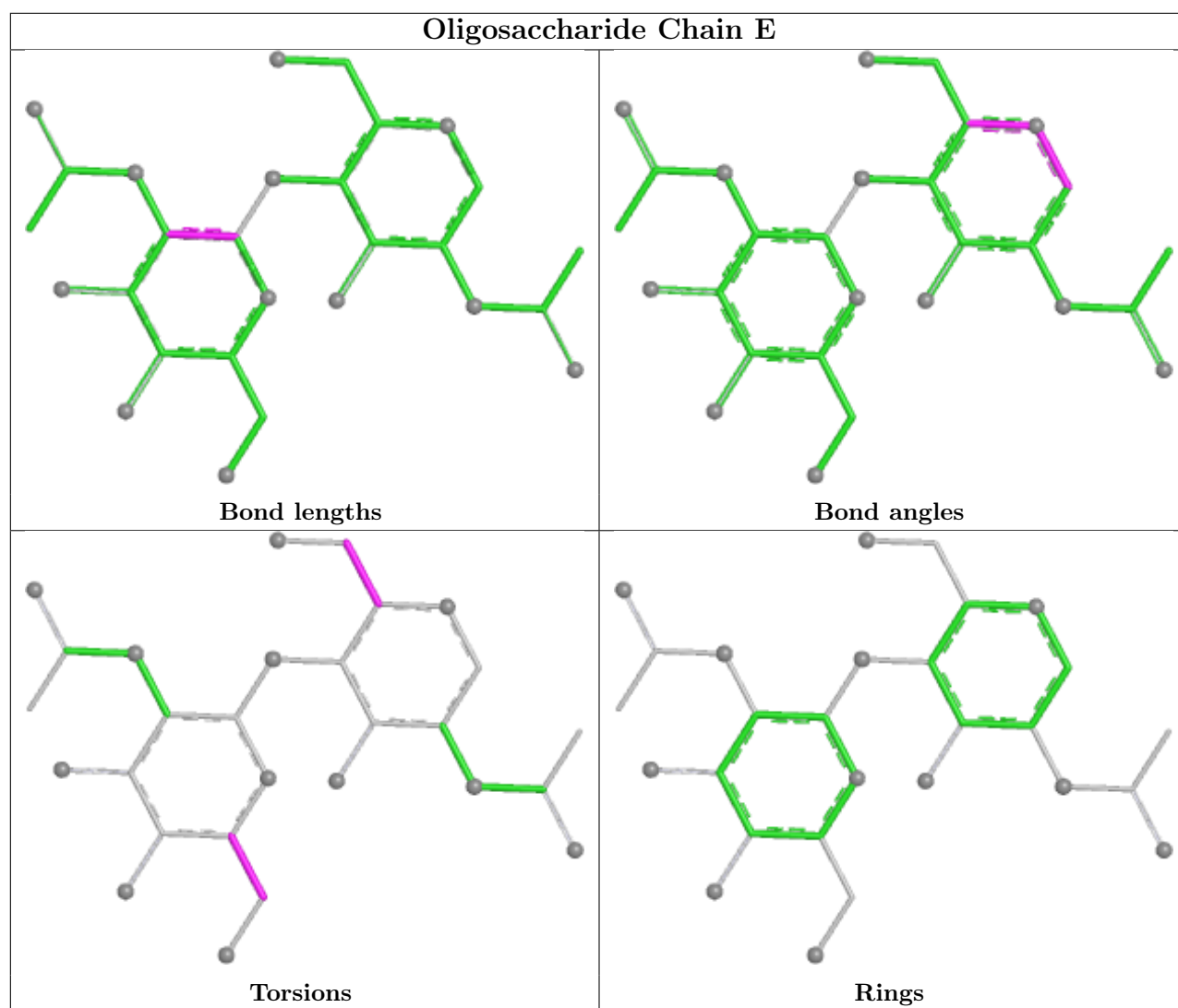
9 monomers are involved in 10 short contacts:

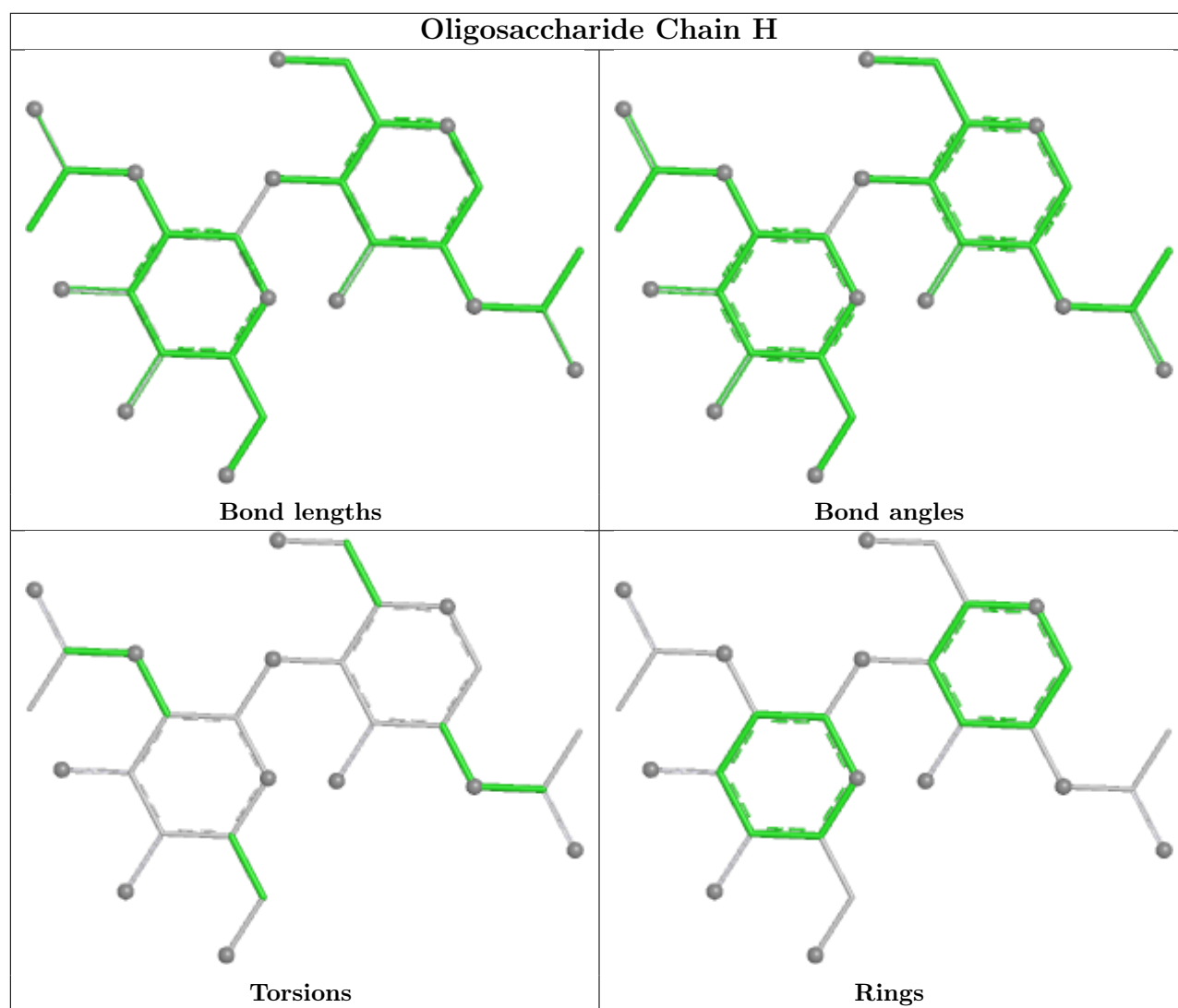
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	G	1	NAG	1	0
5	F	2	NAG	3	0
5	F	3	BMA	2	0
5	F	1	NAG	2	0
2	C	1	NAG	1	0
2	C	2	NAG	1	0
6	G	2	NAG	1	0
6	G	3	BMA	1	0
6	G	5	MAN	2	0

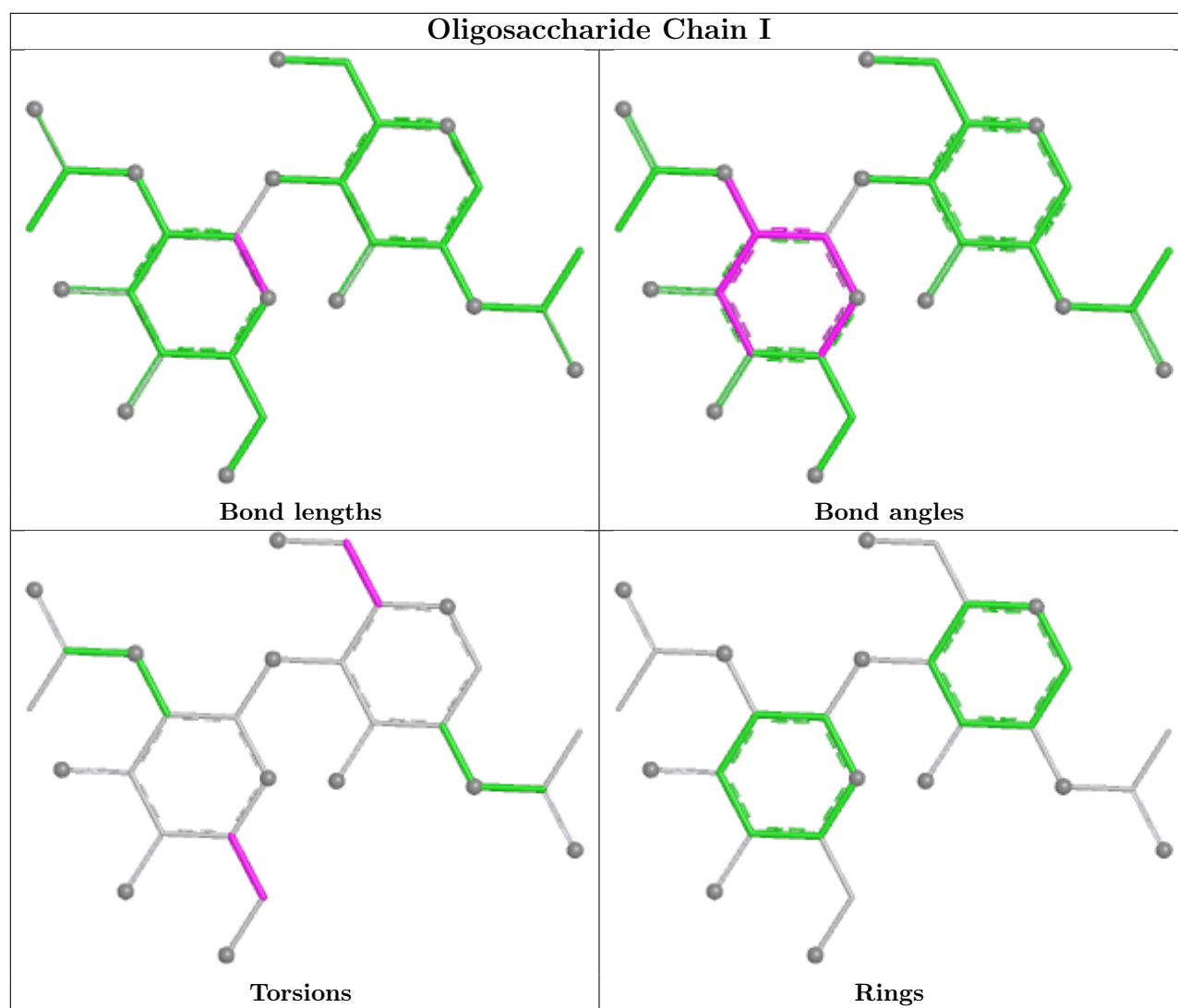
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

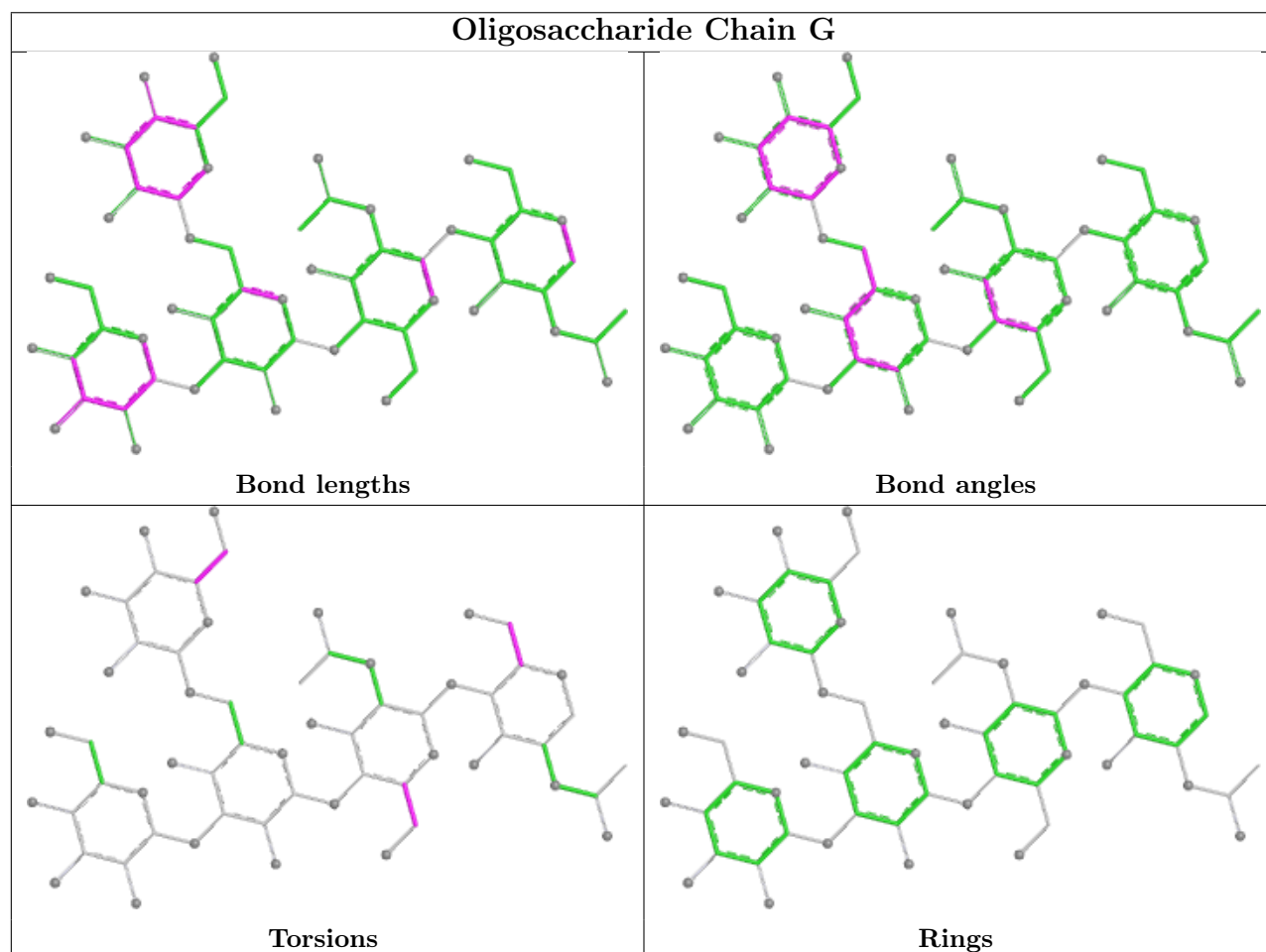
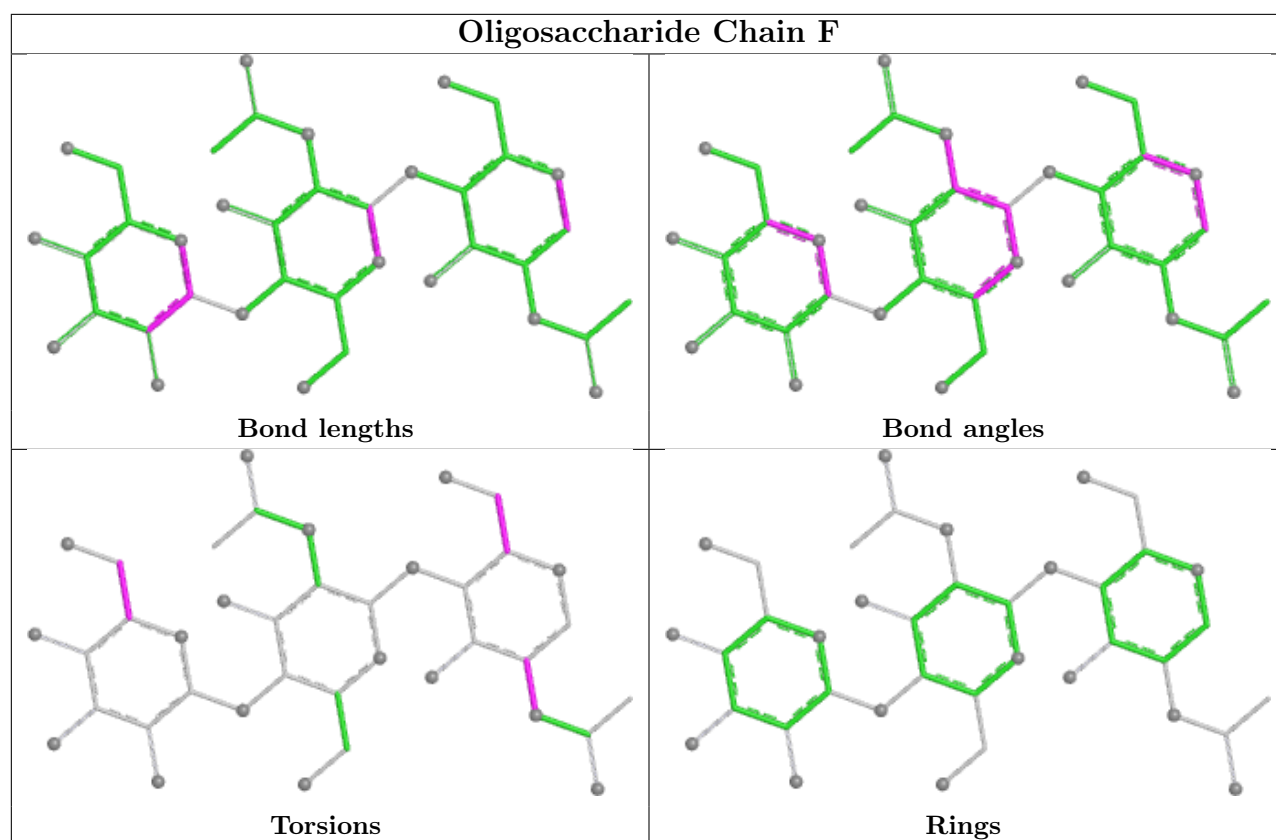












5.6 Ligand geometry

Of 28 ligands modelled in this entry, 2 are monoatomic - leaving 26 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$
12	EDO	A	1117	-	3,3,3	0.69	0	2,2,2	0.08	0
11	MES	A	1109	-	12,12,12	2.33	1 (8%)	15,16,16	1.75	2 (13%)
12	EDO	A	1113	-	3,3,3	0.80	0	2,2,2	0.21	0
12	EDO	A	1118	-	3,3,3	0.60	0	2,2,2	0.15	0
8	NAG	A	1105	1	14,14,15	0.56	0	17,19,21	2.45	3 (17%)
7	62S	B	1501	15	41,45,45	3.53	15 (36%)	51,62,62	2.56	21 (41%)
8	NAG	B	1505	1	14,14,15	0.34	0	17,19,21	0.66	0
8	NAG	B	1502	1	14,14,15	0.97	1 (7%)	17,19,21	1.17	1 (5%)
9	PEG	A	1107	-	6,6,6	0.52	0	5,5,5	0.30	0
9	PEG	A	1106	-	6,6,6	0.53	0	5,5,5	0.37	0
8	NAG	A	1102	1	14,14,15	0.59	0	17,19,21	0.67	0
7	62S	A	1101	15	41,45,45	3.44	14 (34%)	51,62,62	2.18	15 (29%)
8	NAG	A	1103	1	14,14,15	2.18	4 (28%)	17,19,21	1.86	4 (23%)
8	NAG	B	1503	1	14,14,15	0.85	1 (7%)	17,19,21	0.50	0
10	PGE	A	1108	-	9,9,9	0.54	0	8,8,8	0.38	0
12	EDO	A	1116	-	3,3,3	0.49	0	2,2,2	0.33	0
12	EDO	A	1115	-	3,3,3	0.64	0	2,2,2	0.05	0
12	EDO	A	1111	-	3,3,3	0.52	0	2,2,2	0.20	0
14	IMD	A	1114	-	5,5,5	0.61	0	5,5,5	0.49	0
8	NAG	B	1507	1	14,14,15	1.02	1 (7%)	17,19,21	1.22	2 (11%)
13	PDO	B	1508	-	4,4,4	0.35	0	3,3,3	0.39	0
8	NAG	B	1506	1	14,14,15	1.21	2 (14%)	17,19,21	0.47	0
8	NAG	B	1504	1	14,14,15	1.07	1 (7%)	17,19,21	0.90	1 (5%)
8	NAG	A	1104	1	14,14,15	0.28	0	17,19,21	0.59	0
13	PDO	A	1112	-	4,4,4	0.42	0	3,3,3	0.26	0
12	EDO	A	1110	-	3,3,3	0.53	0	2,2,2	0.31	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
12	EDO	A	1117	-	-	0/1/1/1	-
11	MES	A	1109	-	-	4/6/14/14	0/1/1/1
12	EDO	A	1113	-	-	0/1/1/1	-
12	EDO	A	1118	-	-	0/1/1/1	-
8	NAG	A	1105	1	-	3/6/23/26	0/1/1/1
7	62S	B	1501	15	-	14/34/40/40	0/4/4/4
8	NAG	B	1505	1	-	2/6/23/26	0/1/1/1
8	NAG	B	1502	1	-	2/6/23/26	0/1/1/1
9	PEG	A	1107	-	-	3/4/4/4	-
9	PEG	A	1106	-	-	1/4/4/4	-
8	NAG	A	1102	1	-	0/6/23/26	0/1/1/1
7	62S	A	1101	15	-	7/34/40/40	0/4/4/4
8	NAG	A	1103	1	-	1/6/23/26	0/1/1/1
8	NAG	B	1503	1	-	2/6/23/26	0/1/1/1
10	PGE	A	1108	-	-	3/7/7/7	-
12	EDO	A	1116	-	-	1/1/1/1	-
12	EDO	A	1115	-	-	1/1/1/1	-
12	EDO	A	1111	-	-	0/1/1/1	-
14	IMD	A	1114	-	-	-	0/1/1/1
8	NAG	B	1507	1	-	1/6/23/26	0/1/1/1
13	PDO	B	1508	-	-	1/2/2/2	-
8	NAG	B	1506	1	-	1/6/23/26	0/1/1/1
8	NAG	B	1504	1	-	2/6/23/26	0/1/1/1
8	NAG	A	1104	1	-	3/6/23/26	0/1/1/1
13	PDO	A	1112	-	-	1/2/2/2	-
12	EDO	A	1110	-	-	0/1/1/1	-

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	1101	62S	P11-C14	16.41	1.95	1.79
7	B	1501	62S	P11-C14	13.92	1.93	1.79
7	B	1501	62S	C16-C17	7.82	1.57	1.49
7	B	1501	62S	C29-N31	7.81	1.50	1.34
11	A	1109	MES	C8-S	-7.44	1.67	1.77

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1105	NAG	C2-N2-C7	9.20	135.23	122.90
7	A	1101	62S	C17-O21-N20	7.12	113.65	108.30
7	B	1501	62S	C18-C19-N20	-6.82	104.90	111.17
7	B	1501	62S	O21-C17-C16	5.98	125.45	116.00
7	B	1501	62S	O21-C17-C18	-5.33	104.78	109.73

There are no chirality outliers.

5 of 53 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	1101	62S	C16-C15-C29-N31
7	A	1101	62S	C16-C15-C29-O30
7	A	1101	62S	C15-C16-C17-O21
7	A	1101	62S	C08-C09-P11-O12
7	A	1101	62S	C15-C14-P11-O12

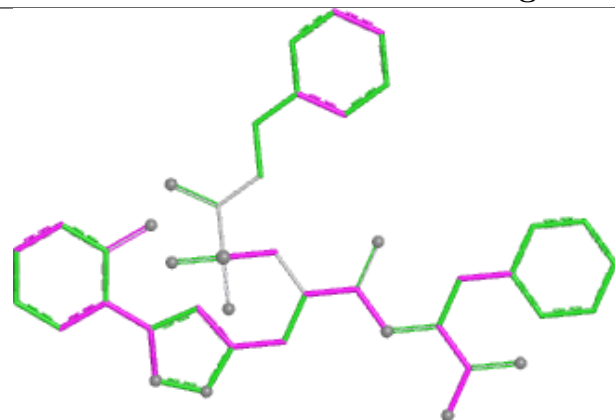
There are no ring outliers.

8 monomers are involved in 13 short contacts:

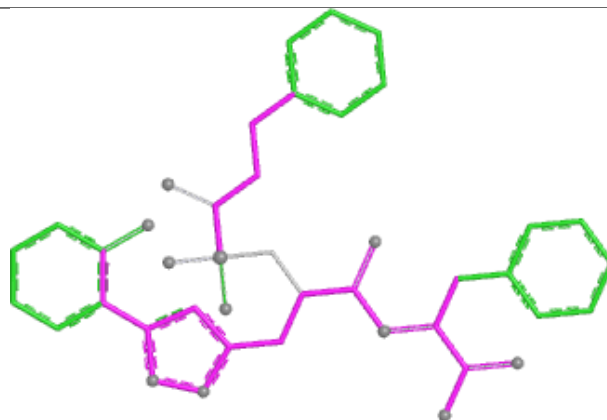
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	1109	MES	1	0
12	A	1113	EDO	1	0
8	A	1105	NAG	4	0
7	B	1501	62S	1	0
7	A	1101	62S	3	0
10	A	1108	PGE	1	0
12	A	1116	EDO	1	0
12	A	1110	EDO	1	0

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

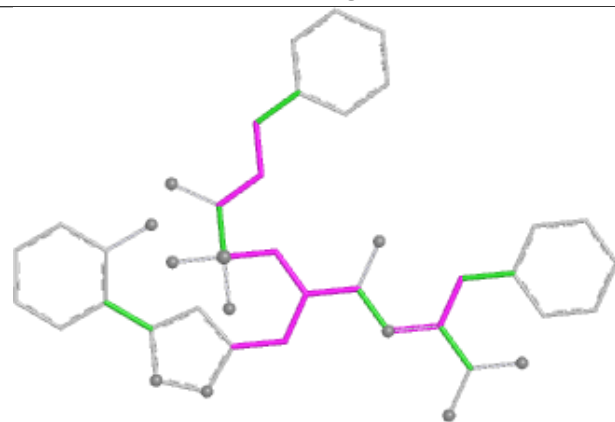
Ligand 62S B 1501



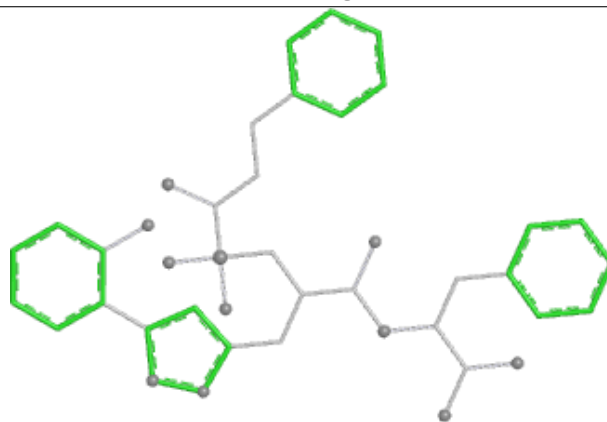
Bond lengths



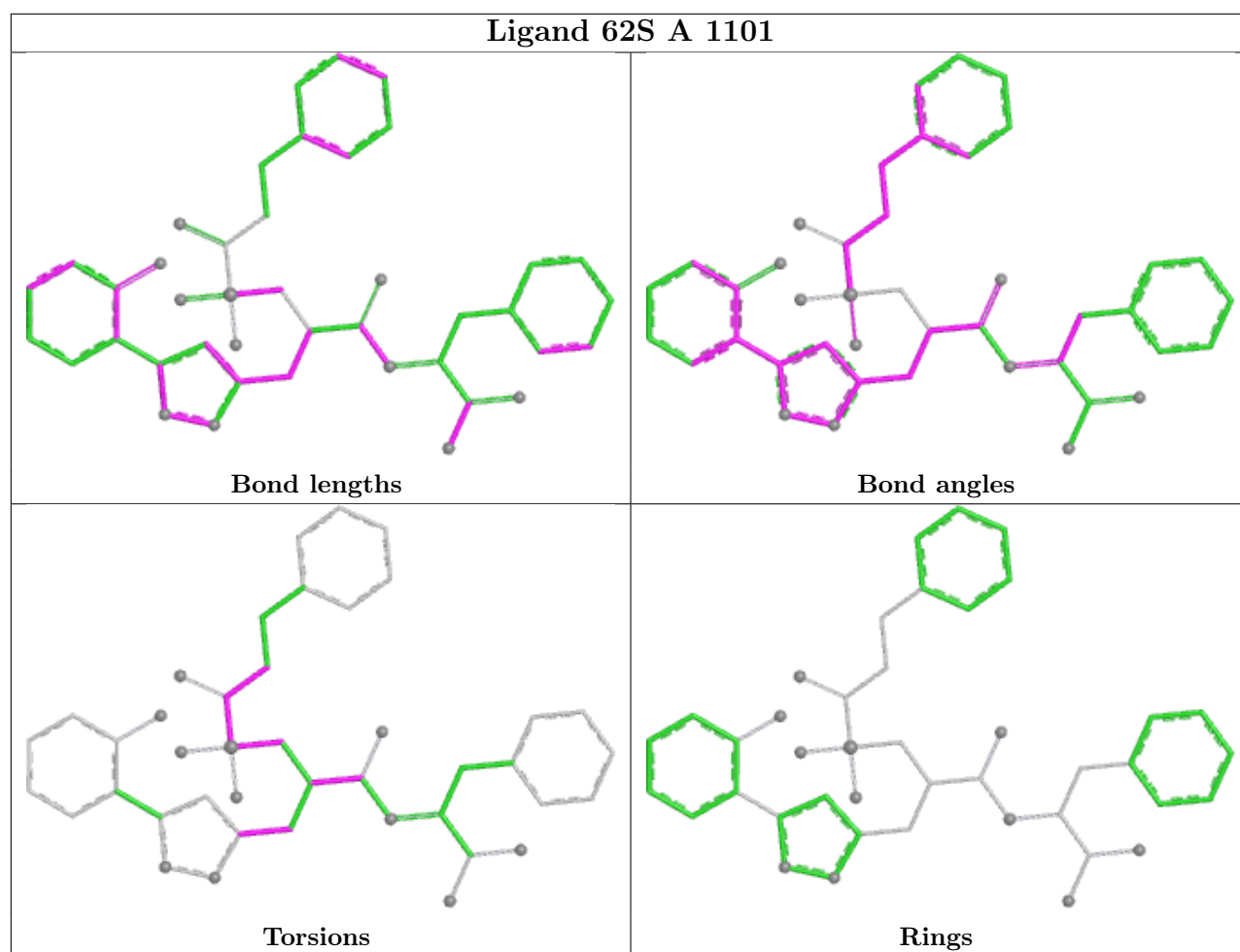
Bond angles



Torsions



Rings



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	911/962 (94%)	-0.69	0 100 100	39, 70, 124, 190	1 (0%)
1	B	871/962 (90%)	-0.28	2 (0%) 91 83	38, 108, 163, 240	0
All	All	1782/1924 (92%)	-0.49	2 (0%) 92 86	38, 85, 153, 240	1 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	680	ALA	2.3
1	B	598	ASN	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.

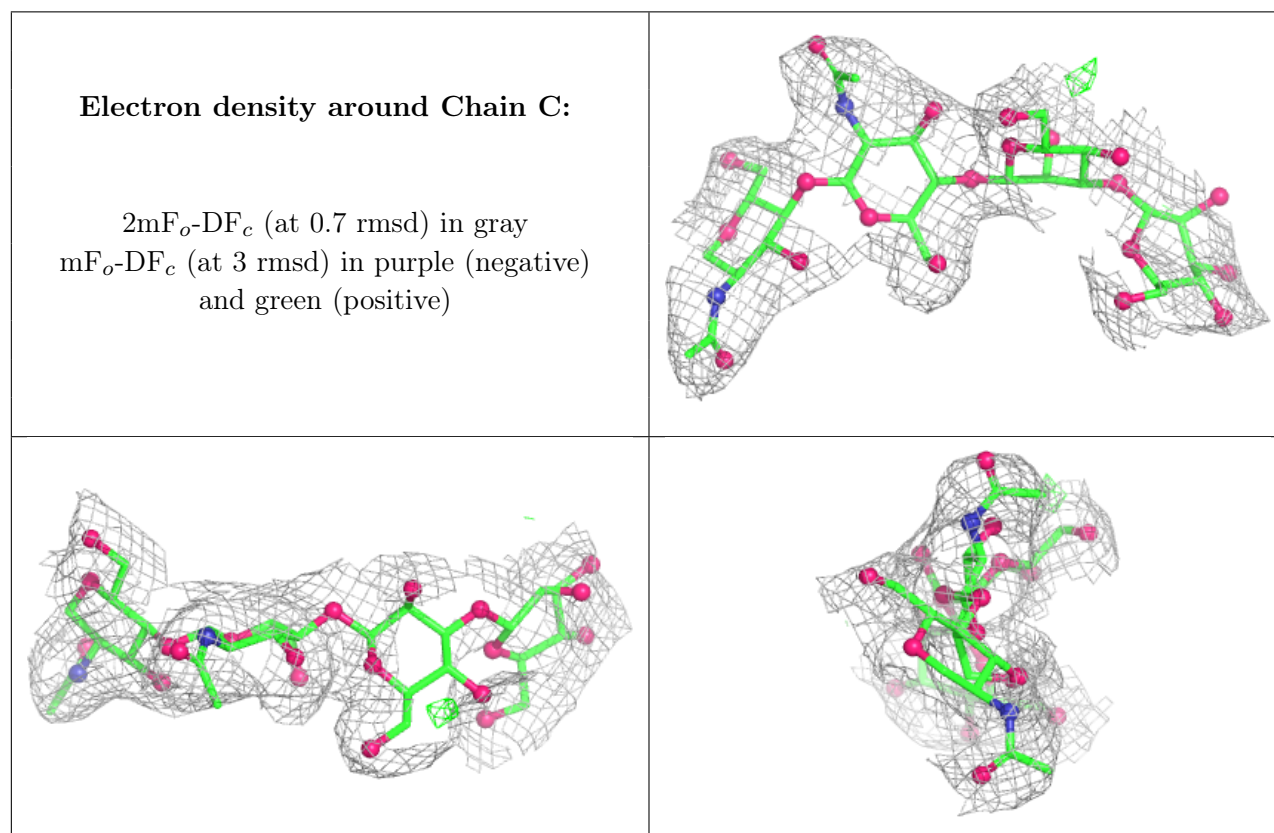
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MAN	C	4	11/12	0.20	0.11	143,171,177,180	0
3	MAN	D	4	11/12	0.26	0.10	175,183,188,195	0
4	NAG	I	2	14/15	0.45	0.12	145,161,169,171	0
3	BMA	D	3	11/12	0.46	0.09	141,161,172,181	0
2	BMA	C	3	11/12	0.49	0.10	151,159,169,175	0
5	BMA	F	3	11/12	0.56	0.09	115,153,157,163	0
4	NAG	E	2	14/15	0.67	0.10	156,170,176,177	0

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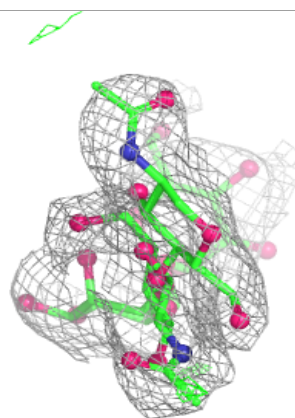
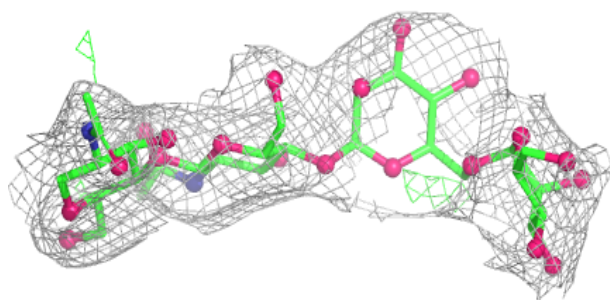
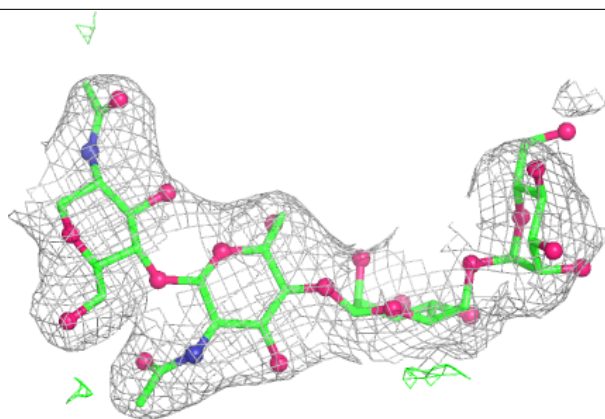
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	NAG	F	2	14/15	0.72	0.09	112,147,152,159	0
6	BMA	G	3	11/12	0.79	0.06	94,119,126,131	0
6	MAN	G	4	11/12	0.79	0.09	107,123,148,155	0
4	NAG	I	1	14/15	0.81	0.10	99,138,150,160	0
4	NAG	H	2	14/15	0.81	0.09	97,132,151,156	0
6	NAG	G	2	14/15	0.83	0.11	94,114,123,125	0
5	NAG	F	1	14/15	0.85	0.09	161,169,180,186	0
4	NAG	H	1	14/15	0.86	0.10	102,115,139,139	0
2	NAG	C	2	14/15	0.86	0.08	101,116,134,142	0
6	MAN	G	5	11/12	0.86	0.08	57,104,116,121	0
3	NAG	D	2	14/15	0.88	0.09	90,102,124,151	0
3	NAG	D	1	14/15	0.93	0.08	67,83,89,89	0
4	NAG	E	1	14/15	0.93	0.09	96,114,132,157	0
2	NAG	C	1	14/15	0.95	0.07	70,93,109,114	0
6	NAG	G	1	14/15	0.95	0.07	54,73,77,94	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.

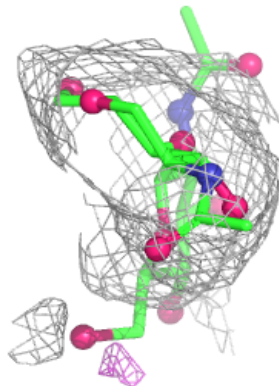
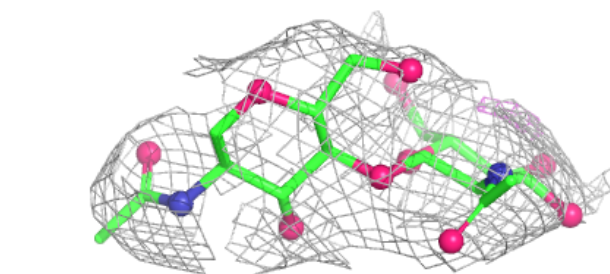
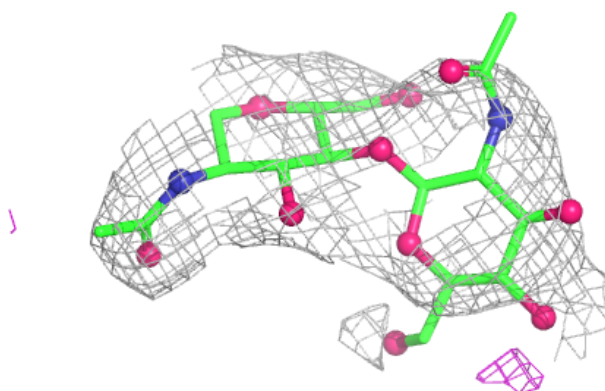


Electron density around Chain D:

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

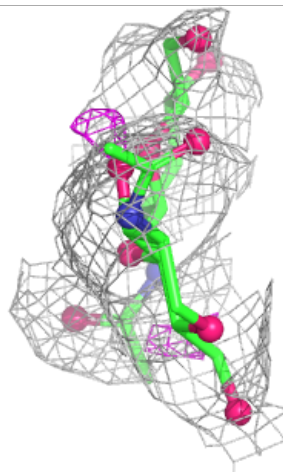
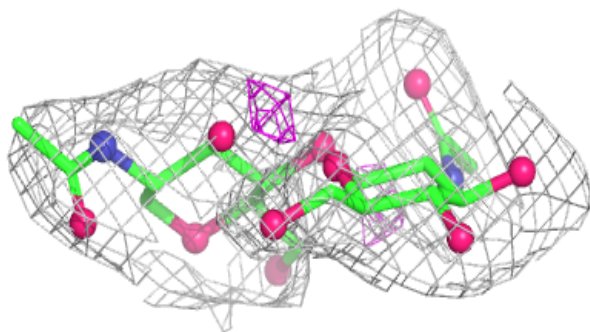
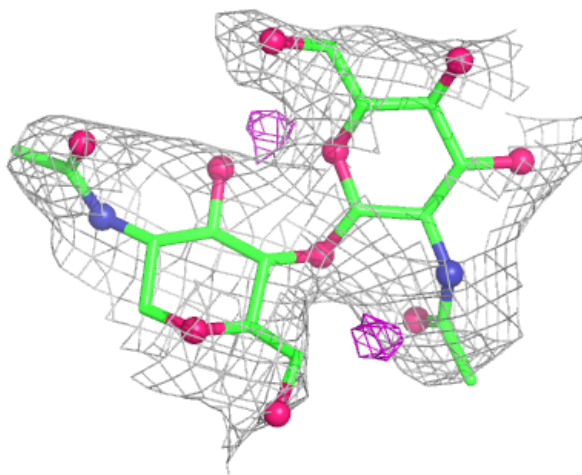
**Electron density around Chain E:**

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



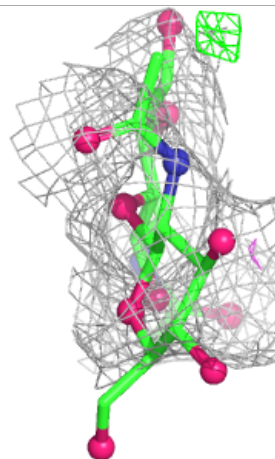
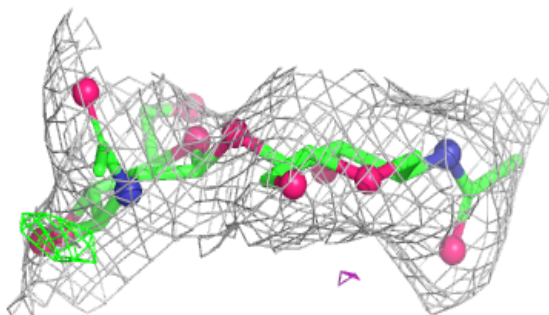
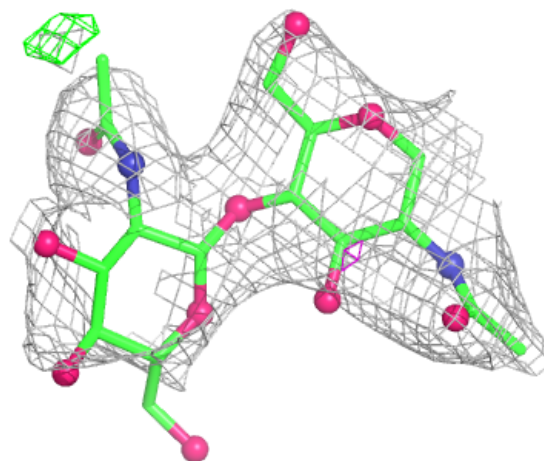
Electron density around Chain H:

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



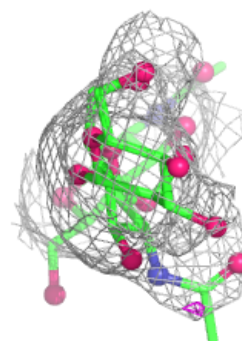
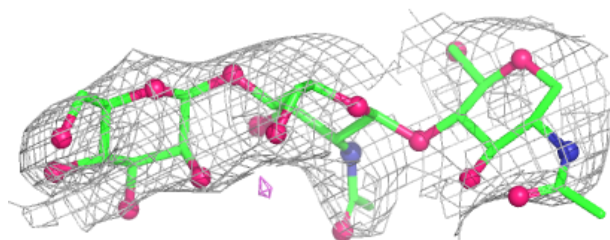
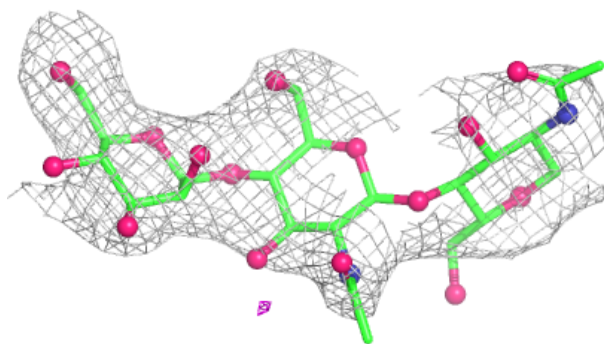
Electron density around Chain I:

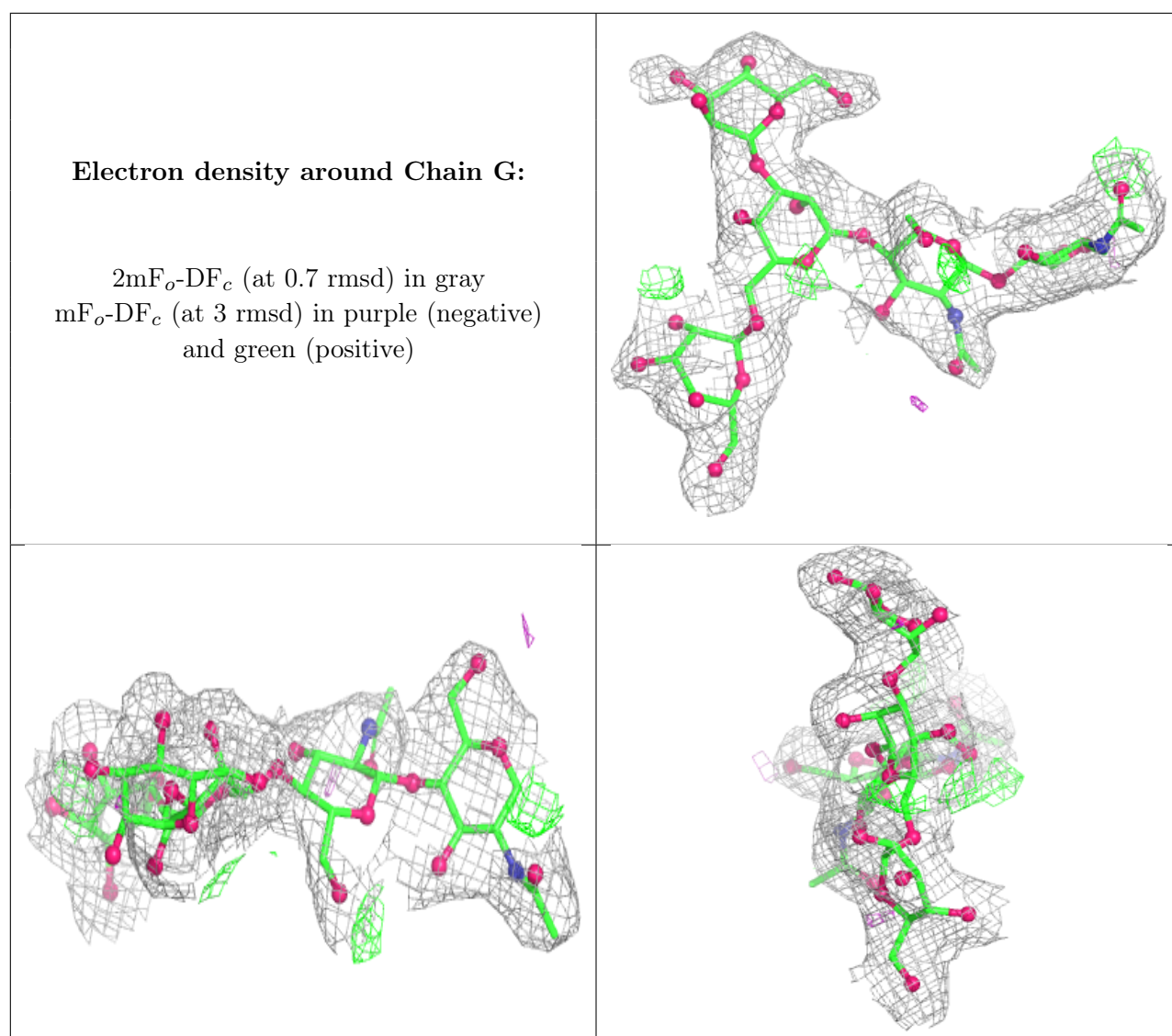
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain F:

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





6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	NAG	B	1503	14/15	0.49	0.11	175,193,205,212	0
8	NAG	B	1502	14/15	0.54	0.11	136,153,159,160	0
8	NAG	B	1507	14/15	0.60	0.11	149,171,180,180	0
8	NAG	B	1504	14/15	0.61	0.11	144,165,175,182	0
8	NAG	A	1105	14/15	0.62	0.09	136,151,166,170	0
11	MES	A	1109	12/12	0.69	0.18	106,146,352,353	0
8	NAG	A	1103	14/15	0.71	0.10	93,134,148,154	0

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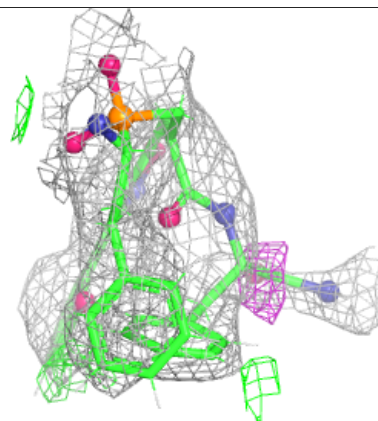
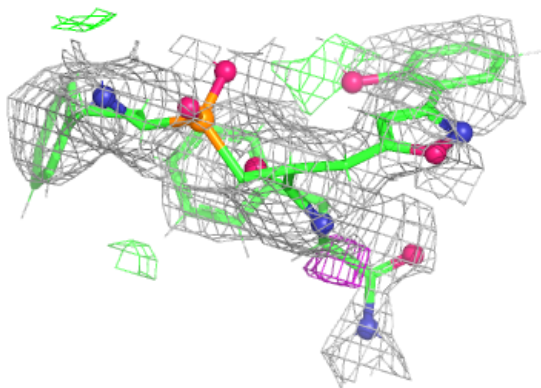
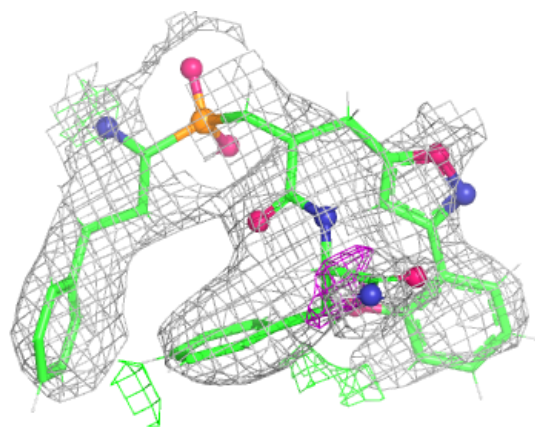
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
13	PDO	B	1508	5/5	0.71	0.17	117,122,130,133	0
8	NAG	B	1505	14/15	0.75	0.10	115,142,159,163	0
8	NAG	A	1104	14/15	0.75	0.10	153,167,181,184	0
8	NAG	A	1102	14/15	0.77	0.11	124,131,136,139	0
8	NAG	B	1506	14/15	0.78	0.08	172,179,187,187	0
9	PEG	A	1106	7/7	0.79	0.10	85,100,114,114	0
12	EDO	A	1111	4/4	0.81	0.11	116,116,117,117	0
14	IMD	A	1114	5/5	0.83	0.20	116,117,120,122	0
12	EDO	A	1110	4/4	0.84	0.13	121,123,125,127	0
9	PEG	A	1107	7/7	0.84	0.10	104,113,121,124	0
12	EDO	A	1115	4/4	0.88	0.21	87,98,100,105	0
10	PGE	A	1108	10/10	0.89	0.11	72,121,132,137	0
12	EDO	A	1117	4/4	0.90	0.19	77,77,82,83	0
12	EDO	A	1113	4/4	0.92	0.12	64,83,100,100	0
13	PDO	A	1112	5/5	0.93	0.14	87,91,97,98	0
12	EDO	A	1116	4/4	0.94	0.14	81,98,115,115	0
7	62S	B	1501	42/42	0.94	0.11	70,104,156,175	0
12	EDO	A	1118	4/4	0.94	0.21	49,72,86,87	0
7	62S	A	1101	42/42	0.96	0.11	40,89,181,207	0
15	ZN	A	1119	1/1	1.00	0.02	45,45,45,45	0
15	ZN	B	1509	1/1	1.00	0.01	66,66,66,66	0

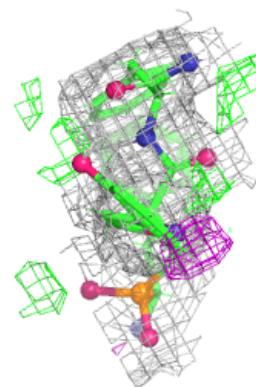
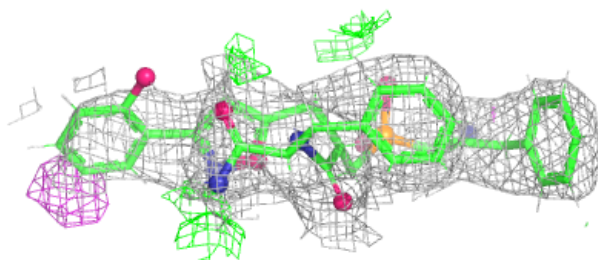
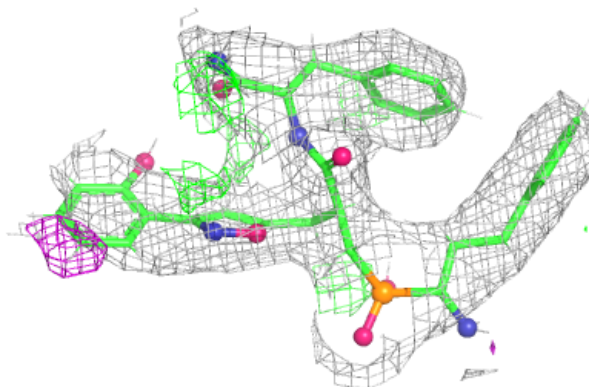
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 62S B 1501:

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

**Electron density around 62S A 1101:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.