



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 05:38 PM EDT

PDB ID : 3I6N / pdb_00003i6n
Title : Mode of Binding of the Tuberculosis Prodrug Isoniazid to Peroxidases: Crystal Structure of Bovine Lactoperoxidase with Isoniazid at 2.7 Resolution
Authors : Singh, A.K.; Kumar, R.P.; Pandey, N.; Singh, N.; Sinha, M.; Bhushan, A.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2009-07-07
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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

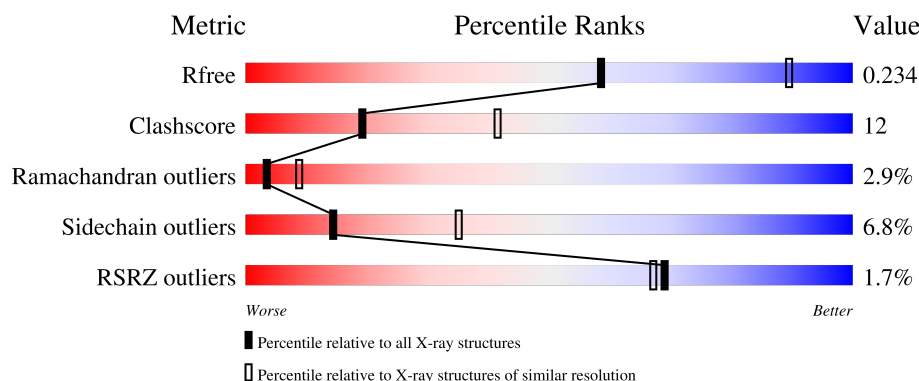
1 Overall quality at a glance

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	595	2% 65% 28% 6%
2	B	3	33% 67%
2	D	3	33% 67%
3	C	2	100%

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Mol	Chain	Length	Quality of chain
3	E	2	 100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	ISZ	A	607	-	-	X	-

2 Entry composition [i](#)

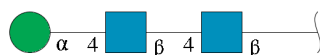
There are 9 unique types of molecules in this entry. The entry contains 5259 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lactoperoxidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	P	S	0	0	0
			4774	3037	847	863	1	26			

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



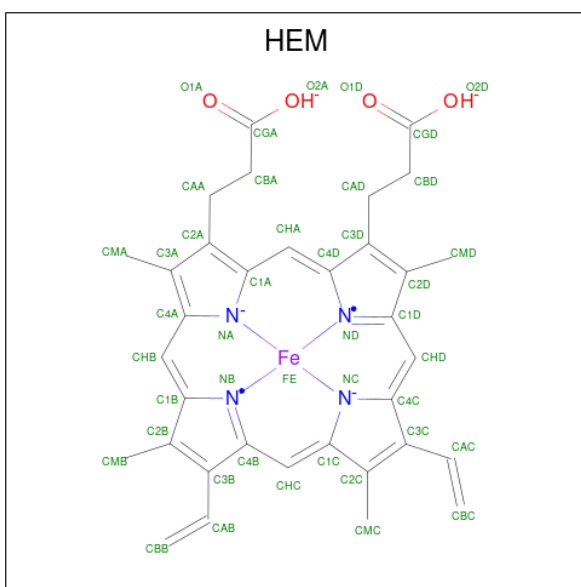
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			39	22	2	15			
2	D	3	Total	C	N	O	0	0	0
			39	22	2	15			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



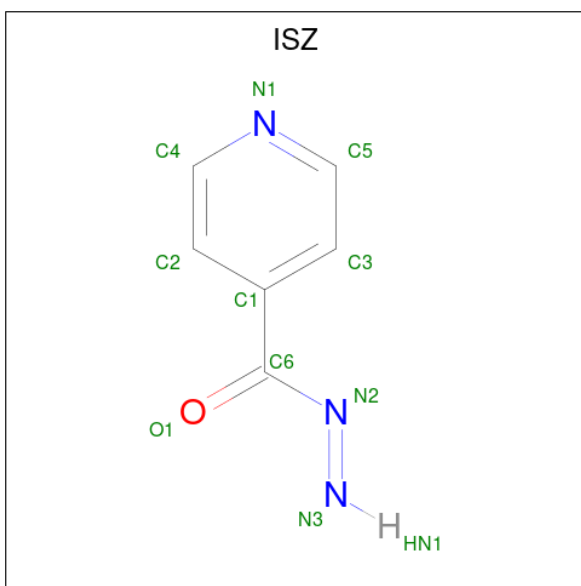
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is 4-(DIAZENYLCARBONYL)PYRIDINE (CCD ID: ISZ) (formula: $C_6H_5N_3O$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			10	6	3	1		

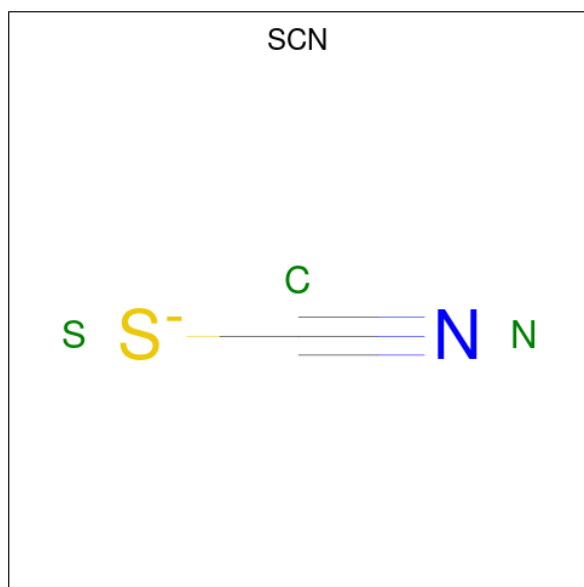
- Molecule 6 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	7	Total I 7 7	0	0

- Molecule 7 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0

- Molecule 8 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total C N S 3 1 1 1	0	0

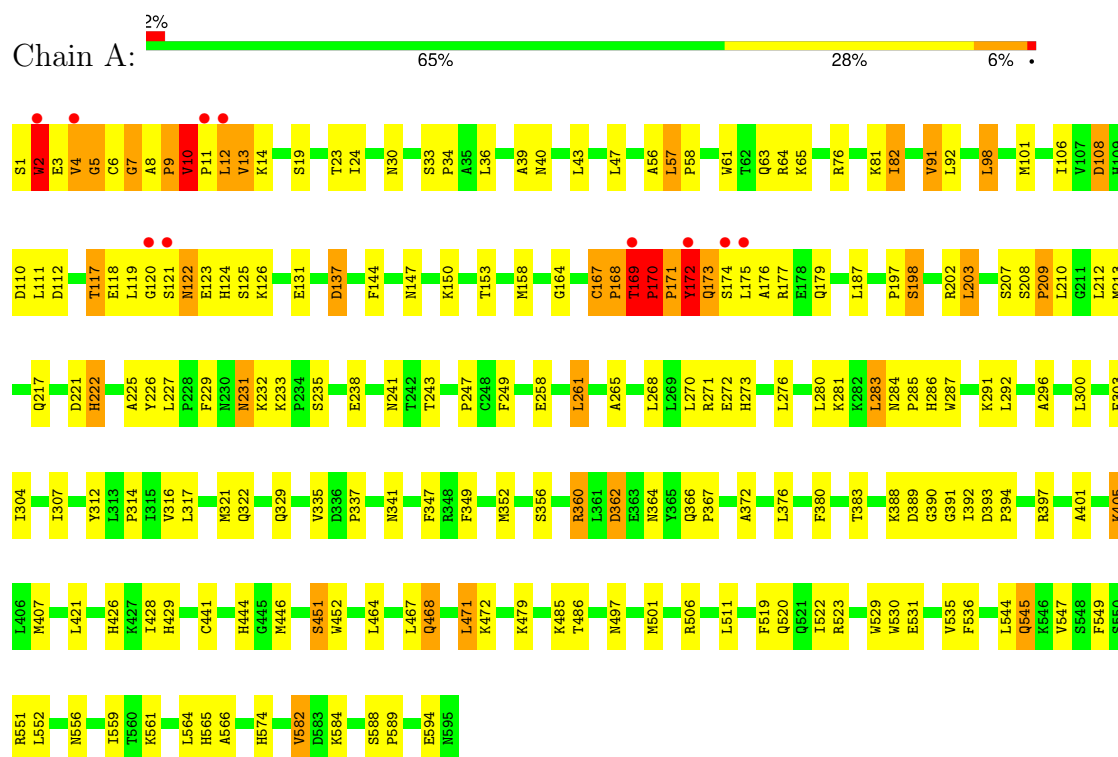
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	287	Total O 287 287	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: Lactoperoxidase



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



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



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

Chain C:  100%

MAG1
MAG2

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

Chain E:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.49Å 80.55Å 77.78Å 90.00° 102.66° 90.00°	Depositor
Resolution (Å)	75.81 – 2.70 75.81 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.6 (75.81-2.70) 93.6 (75.81-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.70Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.205 , 0.232 0.196 , 0.234	Depositor DCC
R_{free} test set	865 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	42.4	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 52.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5259	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.88% 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: HEM, SCN, CA, SEP, NAG, MAN, IOD, ISZ

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	0.68	12/4891 (0.2%)	1.28	60/6634 (0.9%)

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

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	7	GLY	C-N	6.34	1.43	1.34
1	A	352	MET	CG-SD	-6.19	1.65	1.80
1	A	468	GLN	CD-OE1	5.51	1.34	1.23
1	A	322	GLN	CD-OE1	5.36	1.33	1.23
1	A	497	ASN	CG-OD1	5.35	1.33	1.23
1	A	222	HIS	ND1-CE1	5.35	1.37	1.32
1	A	64	ARG	C-N	-5.33	1.25	1.33
1	A	565	HIS	ND1-CE1	5.30	1.37	1.32
1	A	574	HIS	ND1-CE1	5.25	1.37	1.32
1	A	520	GLN	CD-OE1	5.24	1.33	1.23
1	A	364	ASN	CG-OD1	5.13	1.33	1.23
1	A	217	GLN	CD-OE1	5.07	1.33	1.23

All (60) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	108	ASP	CA-CB-CG	21.91	134.50	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	147	ASN	CA-CB-CG	14.07	126.67	112.60
1	A	316	VAL	N-CA-C	-10.33	101.86	111.67
1	A	545	GLN	OE1-CD-NE2	-10.22	112.38	122.60
1	A	169	THR	CA-C-N	10.03	130.71	120.38
1	A	169	THR	C-N-CA	10.03	130.71	120.38
1	A	63	GLN	OE1-CD-NE2	-9.73	112.87	122.60
1	A	582	VAL	N-CA-C	9.34	121.18	108.11
1	A	110	ASP	CA-CB-CG	8.92	121.52	112.60
1	A	10	VAL	CB-CA-C	8.02	125.96	111.36
1	A	312	TYR	N-CA-C	7.70	121.18	111.24
1	A	231	ASN	CA-CB-CG	7.54	120.14	112.60
1	A	43	LEU	N-CA-C	-7.51	100.61	110.53
1	A	131	GLU	N-CA-C	7.48	120.89	111.69
1	A	362	ASP	CA-CB-CG	7.15	119.75	112.60
1	A	173	GLN	N-CA-CB	7.04	121.95	110.97
1	A	349	PHE	N-CA-C	-6.88	104.15	112.54
1	A	556	ASN	N-CA-C	6.79	121.54	112.30
1	A	286	HIS	N-CA-C	6.69	120.70	112.54
1	A	112	ASP	N-CA-C	6.67	119.47	108.99
1	A	222	HIS	CB-CG-CD2	-6.67	122.53	131.20
1	A	565	HIS	CB-CG-CD2	-6.63	122.58	131.20
1	A	170	PRO	N-CA-C	6.62	118.78	110.70
1	A	23	THR	N-CA-C	-6.56	102.06	110.53
1	A	207	SER	N-CA-C	-6.55	101.54	111.56
1	A	545	GLN	CG-CD-NE2	6.52	126.19	116.40
1	A	63	GLN	CG-CD-NE2	6.43	126.04	116.40
1	A	486	THR	O-C-N	-6.34	115.59	122.06
1	A	426	HIS	CA-CB-CG	-6.28	107.52	113.80
1	A	441	CYS	N-CA-C	-6.23	104.40	111.07
1	A	428	ILE	CB-CA-C	-6.07	103.25	111.63
1	A	574	HIS	CB-CG-CD2	-6.01	123.39	131.20
1	A	153	THR	N-CA-C	5.98	121.46	114.04
1	A	111	LEU	N-CA-C	5.81	120.51	112.90
1	A	390	GLY	N-CA-C	5.67	122.51	114.85
1	A	401	ALA	N-CA-C	5.64	120.32	113.38
1	A	222	HIS	CB-CG-ND1	5.63	131.15	122.70
1	A	565	HIS	CB-CG-ND1	5.60	131.10	122.70
1	A	225	ALA	N-CA-C	5.55	118.04	110.55
1	A	232	LYS	N-CA-C	5.52	118.33	110.10
1	A	428	ILE	N-CA-C	5.51	117.15	109.55
1	A	82	ILE	CB-CA-C	-5.50	106.21	111.44
1	A	356	SER	N-CA-C	5.42	119.15	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	ASP	CB-CA-C	-5.42	110.31	116.54
1	A	33	SER	CA-C-N	5.38	125.05	119.56
1	A	33	SER	C-N-CA	5.38	125.05	119.56
1	A	92	LEU	N-CA-C	5.32	118.00	110.50
1	A	451	SER	N-CA-C	-5.32	105.48	111.28
1	A	81	LYS	N-CA-C	5.31	118.92	112.23
1	A	574	HIS	CB-CG-ND1	5.27	130.60	122.70
1	A	233	LYS	N-CA-C	-5.26	100.27	109.48
1	A	296	ALA	N-CA-C	-5.26	105.44	111.07
1	A	429	HIS	N-CA-C	-5.24	102.32	109.71
1	A	405	LYS	N-CA-C	-5.23	102.00	110.32
1	A	2	TRP	CB-CA-C	-5.14	100.20	110.42
1	A	566	ALA	N-CA-C	5.07	118.72	112.54
1	A	389	ASP	N-CA-C	5.06	116.93	110.61
1	A	19	SER	N-CA-C	-5.05	103.29	109.65
1	A	231	ASN	CA-C-N	5.04	127.92	120.82
1	A	231	ASN	C-N-CA	5.04	127.92	120.82

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	172	TYR	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4774	0	4688	111	0
2	B	39	0	34	1	0
2	D	39	0	34	1	0
3	C	28	0	25	1	0
3	E	28	0	25	1	0
4	A	43	0	30	1	0
5	A	10	0	5	5	0
6	A	7	0	0	0	0
7	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	3	0	0	0	0
9	A	287	0	0	1	0
All	All	5259	0	4841	115	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 12.

All (115) 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:167:CYS:HB3	1:A:168:PRO:HD3	1.55	0.86
1:A:170:PRO:HB3	1:A:171:PRO:HD2	1.57	0.85
1:A:169:THR:N	1:A:170:PRO:HD2	1.95	0.82
1:A:258:GLU:HB2	5:A:607:ISZ:H3	1.63	0.79
1:A:258:GLU:HG3	5:A:607:ISZ:H3	1.66	0.76
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.23	0.73
1:A:258:GLU:CB	5:A:607:ISZ:H3	2.21	0.69
1:A:197:PRO:HD2	1:A:198:SEP:O3P	1.92	0.69
1:A:360:ARG:NH1	1:A:372:ALA:HA	2.07	0.69
1:A:175:LEU:HG	1:A:176:ALA:H	1.58	0.69
1:A:227:LEU:HD23	1:A:270:LEU:HD22	1.74	0.69
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.28	0.68
1:A:179:GLN:HG2	1:A:444:HIS:CE1	2.30	0.66
1:A:2:TRP:HE3	1:A:2:TRP:HA	1.60	0.66
1:A:258:GLU:CG	5:A:607:ISZ:H3	2.25	0.65
1:A:167:CYS:CB	1:A:168:PRO:CD	2.75	0.65
1:A:2:TRP:HA	1:A:2:TRP:CE3	2.30	0.65
1:A:588:SER:OG	1:A:589:PRO:HD3	1.97	0.64
1:A:91:VAL:HG13	1:A:405:LYS:HG3	1.80	0.64
1:A:229:PHE:CD1	1:A:247:PRO:HG2	2.32	0.64
1:A:167:CYS:HB3	1:A:168:PRO:CD	2.27	0.64
1:A:208:SER:HB3	3:C:1:NAG:H62	1.81	0.63
1:A:169:THR:HB	1:A:170:PRO:HD3	1.80	0.62
1:A:501:MET:HE1	9:A:627:HOH:O	1.98	0.62
1:A:167:CYS:CB	1:A:168:PRO:HD3	2.27	0.62
1:A:169:THR:N	1:A:170:PRO:CD	2.63	0.61
1:A:106:ILE:HD11	1:A:265:ALA:HB1	1.82	0.61
1:A:258:GLU:O	1:A:258:GLU:HG2	2.01	0.60
1:A:121:SER:O	1:A:122:ASN:CB	2.49	0.60
1:A:123:GLU:HB3	1:A:126:LYS:HE2	1.83	0.59
1:A:208:SER:HB2	1:A:210:LEU:HD12	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:ASN:HB3	1:A:446:MET:HE1	1.87	0.57
1:A:170:PRO:CB	1:A:171:PRO:HD2	2.33	0.57
1:A:221:ASP:HB2	1:A:226:TYR:CZ	2.39	0.57
1:A:8:ALA:HB3	1:A:9:PRO:HD3	1.87	0.56
1:A:202:ARG:NH2	1:A:231:ASN:HB2	2.20	0.56
1:A:535:VAL:HG12	1:A:536:PHE:CD1	2.40	0.56
1:A:123:GLU:HB3	1:A:126:LYS:HG3	1.87	0.56
1:A:281:LYS:HD2	1:A:281:LYS:O	2.06	0.56
1:A:360:ARG:HH11	1:A:372:ALA:HA	1.71	0.56
1:A:3:GLU:C	1:A:5:GLY:H	2.15	0.55
1:A:13:VAL:HG12	1:A:14:LYS:H	1.72	0.54
1:A:272:GLU:O	1:A:276:LEU:HB2	2.08	0.54
1:A:544:LEU:O	1:A:547:VAL:HG22	2.07	0.53
1:A:3:GLU:HG3	1:A:175:LEU:HD22	1.90	0.53
1:A:407:MET:HB3	1:A:501:MET:HE3	1.90	0.53
1:A:300:LEU:O	1:A:304:ILE:HG12	2.08	0.53
1:A:56:ALA:HB1	1:A:177:ARG:HD3	1.91	0.53
1:A:169:THR:HB	1:A:170:PRO:CD	2.39	0.52
1:A:519:PHE:HA	1:A:522:ILE:HG12	1.92	0.52
2:B:1:NAG:H61	2:B:2:NAG:C1	2.39	0.52
1:A:144:PHE:HE2	1:A:158:MET:HE3	1.74	0.52
1:A:118:GLU:HG3	1:A:120:GLY:H	1.74	0.51
3:E:1:NAG:H61	3:E:2:NAG:O7	2.10	0.51
1:A:117:THR:HG23	1:A:164:GLY:HA2	1.93	0.51
1:A:551:ARG:HD3	1:A:584:LYS:HA	1.94	0.50
1:A:284:ASN:O	1:A:285:PRO:C	2.54	0.50
1:A:303:PHE:O	1:A:307:ILE:HG12	2.13	0.49
1:A:335:VAL:O	1:A:337:PRO:HD3	2.13	0.49
1:A:106:ILE:HD11	1:A:265:ALA:CB	2.43	0.49
1:A:108:ASP:HB2	1:A:347:PHE:CE2	2.48	0.48
1:A:468:GLN:O	1:A:472:LYS:N	2.46	0.48
1:A:76:ARG:NH2	1:A:150:LYS:HD2	2.29	0.48
1:A:1:SER:O	1:A:2:TRP:HB2	2.13	0.48
1:A:10:VAL:HB	1:A:12:LEU:N	2.29	0.48
4:A:605:HEM:HMC2	4:A:605:HEM:HBC2	1.95	0.47
1:A:98:LEU:HD22	1:A:101:MET:HE3	1.96	0.47
1:A:108:ASP:HB2	1:A:347:PHE:CD2	2.50	0.47
1:A:258:GLU:HG3	5:A:607:ISZ:C3	2.42	0.47
1:A:280:LEU:HA	1:A:283:LEU:CD1	2.44	0.47
1:A:283:LEU:C	1:A:285:PRO:HD3	2.40	0.47
1:A:523:ARG:HG3	1:A:529:TRP:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:GLU:HG3	1:A:125:SER:H	1.80	0.46
1:A:121:SER:O	1:A:122:ASN:HB2	2.14	0.46
1:A:170:PRO:HB3	1:A:171:PRO:CD	2.39	0.45
1:A:10:VAL:HB	1:A:11:PRO:CA	2.47	0.45
1:A:366:GLN:O	1:A:367:PRO:C	2.59	0.45
1:A:397:ARG:HG2	1:A:559:ILE:HD12	1.98	0.45
1:A:47:LEU:HD12	1:A:452:TRP:CH2	2.52	0.45
1:A:82:ILE:CD1	1:A:479:LYS:HB3	2.47	0.45
1:A:588:SER:HG	1:A:589:PRO:HD3	1.80	0.45
1:A:249:PHE:CE1	1:A:383:THR:HG22	2.52	0.45
1:A:235:SER:HB3	1:A:238:GLU:HG2	2.00	0.44
1:A:168:PRO:HB2	1:A:169:THR:H	1.35	0.44
1:A:271:ARG:NH1	1:A:392:ILE:HD11	2.33	0.43
1:A:169:THR:CB	1:A:170:PRO:CD	2.96	0.43
2:D:1:NAG:H62	2:D:2:NAG:N2	2.34	0.43
1:A:221:ASP:HB2	1:A:226:TYR:CE2	2.53	0.43
1:A:362:ASP:OD2	1:A:366:GLN:HB2	2.19	0.43
1:A:393:ASP:HB2	1:A:394:PRO:HD3	2.01	0.43
1:A:61:TRP:HH2	1:A:137:ASP:O	2.02	0.43
1:A:170:PRO:CB	1:A:171:PRO:CD	2.97	0.43
1:A:39:ALA:O	1:A:40:ASN:HB2	2.19	0.42
1:A:36:LEU:HD12	1:A:36:LEU:HA	1.77	0.42
1:A:303:PHE:CE1	1:A:307:ILE:HD11	2.54	0.42
1:A:175:LEU:HG	1:A:176:ALA:N	2.31	0.42
1:A:314:PRO:HG3	1:A:321:MET:HE2	2.02	0.42
1:A:551:ARG:O	1:A:552:LEU:C	2.63	0.42
1:A:171:PRO:HB2	1:A:172:TYR:H	1.67	0.41
1:A:226:TYR:OH	1:A:391:GLY:HA2	2.19	0.41
1:A:57:LEU:HA	1:A:58:PRO:HD3	1.85	0.41
1:A:549:PHE:CE1	1:A:552:LEU:HD22	2.55	0.41
1:A:209:PRO:HD2	1:A:210:LEU:HG	2.02	0.41
1:A:303:PHE:CD2	1:A:304:ILE:HD13	2.55	0.41
1:A:241:ASN:OD1	1:A:243:THR:HB	2.21	0.41
1:A:501:MET:HE2	1:A:506:ARG:O	2.21	0.41
1:A:523:ARG:HG3	1:A:529:TRP:CD2	2.56	0.41
1:A:168:PRO:O	1:A:169:THR:OG1	2.33	0.41
1:A:287:TRP:CG	1:A:291:LYS:HG2	2.56	0.41
1:A:119:LEU:HD21	1:A:170:PRO:HA	2.01	0.40
1:A:467:LEU:HG	1:A:471:LEU:HD22	2.03	0.40
1:A:261:LEU:HD12	1:A:261:LEU:HA	1.85	0.40
1:A:380:PHE:CE2	1:A:421:LEU:HA	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:ASN:O	1:A:34:PRO:HA	2.20	0.40
1:A:203:LEU:HD12	1:A:203:LEU:HA	1.84	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	592/595 (100%)	541 (91%)	34 (6%)	17 (3%)	3 9

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	10	VAL
1	A	122	ASN
1	A	167	CYS
1	A	168	PRO
1	A	169	THR
1	A	170	PRO
1	A	171	PRO
1	A	485	LYS
1	A	174	SER
1	A	594	GLU
1	A	2	TRP
1	A	6	CYS
1	A	5	GLY
1	A	7	GLY
1	A	209	PRO
1	A	9	PRO

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	517/517 (100%)	482 (93%)	35 (7%)	14	35

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	TRP
1	A	4	VAL
1	A	10	VAL
1	A	12	LEU
1	A	13	VAL
1	A	24	ILE
1	A	57	LEU
1	A	65	LYS
1	A	91	VAL
1	A	98	LEU
1	A	117	THR
1	A	124	HIS
1	A	172	TYR
1	A	173	GLN
1	A	187	LEU
1	A	203	LEU
1	A	212	LEU
1	A	222	HIS
1	A	261	LEU
1	A	268	LEU
1	A	283	LEU
1	A	292	LEU
1	A	317	LEU
1	A	329	GLN
1	A	360	ARG
1	A	376	LEU
1	A	388	LYS
1	A	451	SER
1	A	464	LEU
1	A	471	LEU

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Mol	Chain	Res	Type
1	A	511	LEU
1	A	545	GLN
1	A	561	LYS
1	A	564	LEU
1	A	582	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	ASN
1	A	273	HIS
1	A	568	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	A	198	1	8,9,10	1.62	1 (12%)	7,12,14	1.84	1 (14%)

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
1	SEP	A	198	1	-	6/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	SEP	P-O1P	3.35	1.60	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	SEP	OG-CB-CA	4.13	112.16	108.14

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	198	SEP	N-CA-CB-OG
1	A	198	SEP	C-CA-CB-OG
1	A	198	SEP	CB-OG-P-O1P
1	A	198	SEP	CB-OG-P-O2P
1	A	198	SEP	CB-OG-P-O3P
1	A	198	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	198	SEP	1	0

5.5 Carbohydrates

10 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NAG	B	1	2,1	14,14,15	0.88	0	17,19,21	1.31	2 (11%)
2	NAG	B	2	2	14,14,15	1.15	2 (14%)	17,19,21	1.13	2 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAN	B	3	2	11,11,12	0.88	0	15,15,17	0.68	0
3	NAG	C	1	3,1	14,14,15	0.68	0	17,19,21	0.75	0
3	NAG	C	2	3	14,14,15	0.86	1 (7%)	17,19,21	1.30	2 (11%)
2	NAG	D	1	2,1	14,14,15	0.54	0	17,19,21	0.85	1 (5%)
2	NAG	D	2	2	14,14,15	0.56	0	17,19,21	1.04	1 (5%)
2	MAN	D	3	2	11,11,12	0.68	0	15,15,17	0.37	0
3	NAG	E	1	3,1	14,14,15	0.98	1 (7%)	17,19,21	1.43	1 (5%)
3	NAG	E	2	3	14,14,15	1.05	2 (14%)	17,19,21	1.18	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1	2,1	-	4/6/23/26	0/1/1/1
2	NAG	B	2	2	-	4/6/23/26	0/1/1/1
2	MAN	B	3	2	-	0/2/19/22	0/1/1/1
3	NAG	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	MAN	D	3	2	-	0/2/19/22	1/1/1/1
3	NAG	E	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	E	2	3	-	3/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	2	NAG	C1-C2	2.94	1.56	1.52
3	E	1	NAG	C3-C2	2.35	1.57	1.52
2	B	2	NAG	C1-C2	2.31	1.55	1.52
2	B	2	NAG	C3-C2	2.31	1.57	1.52
3	E	2	NAG	C3-C2	2.17	1.57	1.52
3	C	2	NAG	C1-C2	2.02	1.55	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	1	NAG	C4-C3-C2	4.87	118.15	111.02
3	C	2	NAG	C4-C3-C2	3.96	116.82	111.02
3	E	2	NAG	C4-C3-C2	3.89	116.72	111.02
2	B	2	NAG	C4-C3-C2	3.24	115.76	111.02
2	B	1	NAG	C1-O5-C5	2.92	116.11	112.19
2	B	2	NAG	C2-N2-C7	-2.78	119.17	122.90
2	B	1	NAG	C2-N2-C7	-2.60	119.42	122.90
2	D	2	NAG	C2-N2-C7	-2.50	119.55	122.90
3	C	2	NAG	C3-C4-C5	2.40	114.59	110.23
2	D	1	NAG	C2-N2-C7	-2.14	120.03	122.90

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NAG	C8-C7-N2-C2
2	B	2	NAG	O7-C7-N2-C2
2	B	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O7-C7-N2-C2
3	E	1	NAG	C8-C7-N2-C2
2	B	1	NAG	O5-C5-C6-O6
2	B	1	NAG	C4-C5-C6-O6
3	E	1	NAG	O7-C7-N2-C2
2	D	2	NAG	C4-C5-C6-O6
2	B	2	NAG	O5-C5-C6-O6
3	E	1	NAG	C4-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
3	C	2	NAG	C8-C7-N2-C2
3	E	1	NAG	O5-C5-C6-O6
3	C	2	NAG	O7-C7-N2-C2
2	D	2	NAG	O5-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
3	E	2	NAG	C4-C5-C6-O6
2	B	2	NAG	C4-C5-C6-O6
3	E	2	NAG	C8-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2

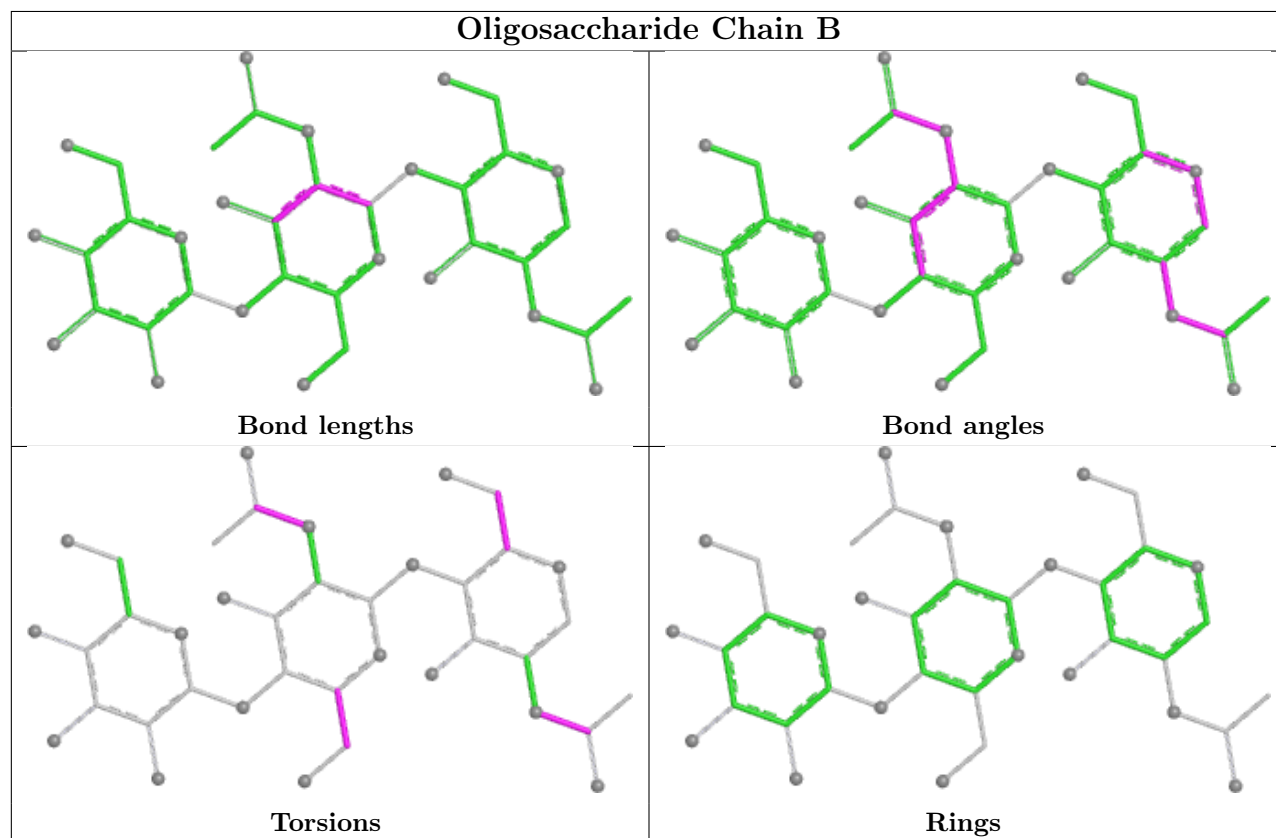
All (1) ring outliers are listed below:

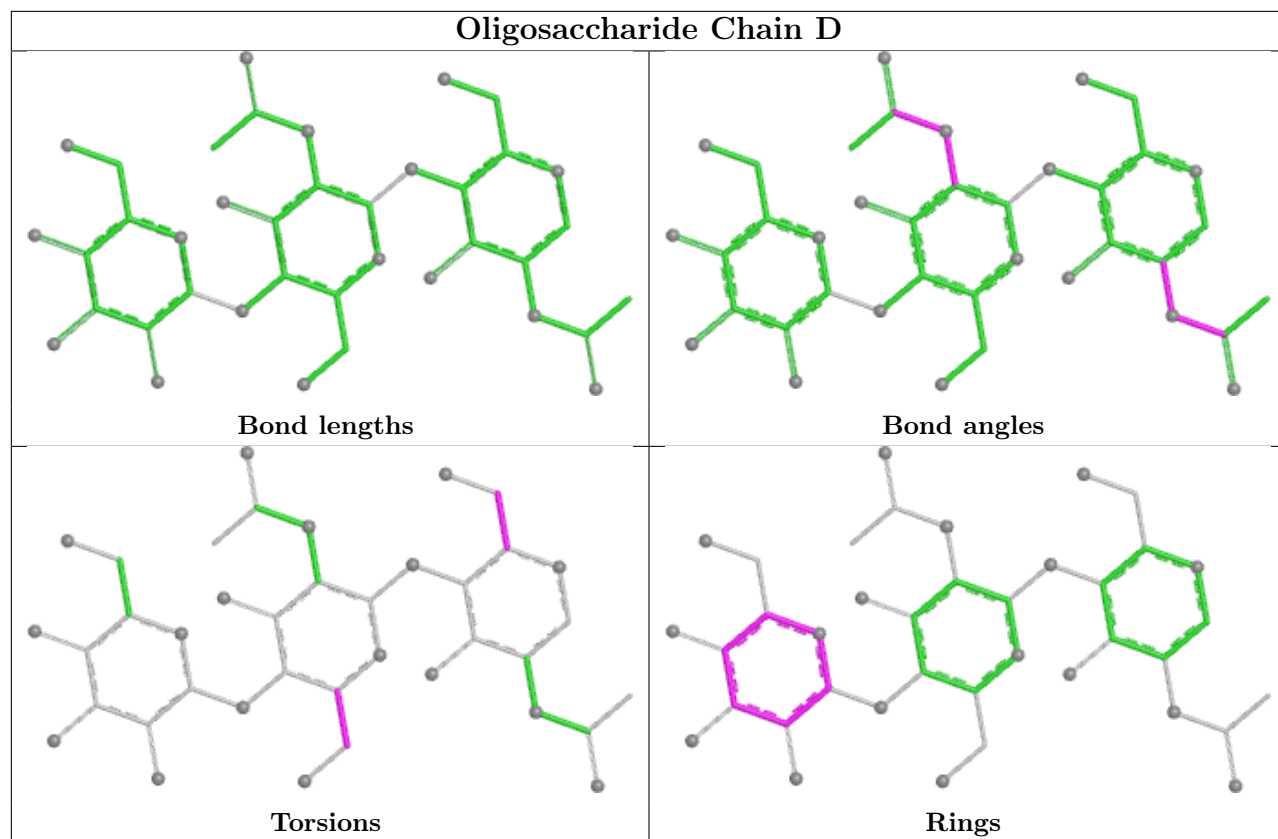
Mol	Chain	Res	Type	Atoms
2	D	3	MAN	C1-C2-C3-C4-C5-O5

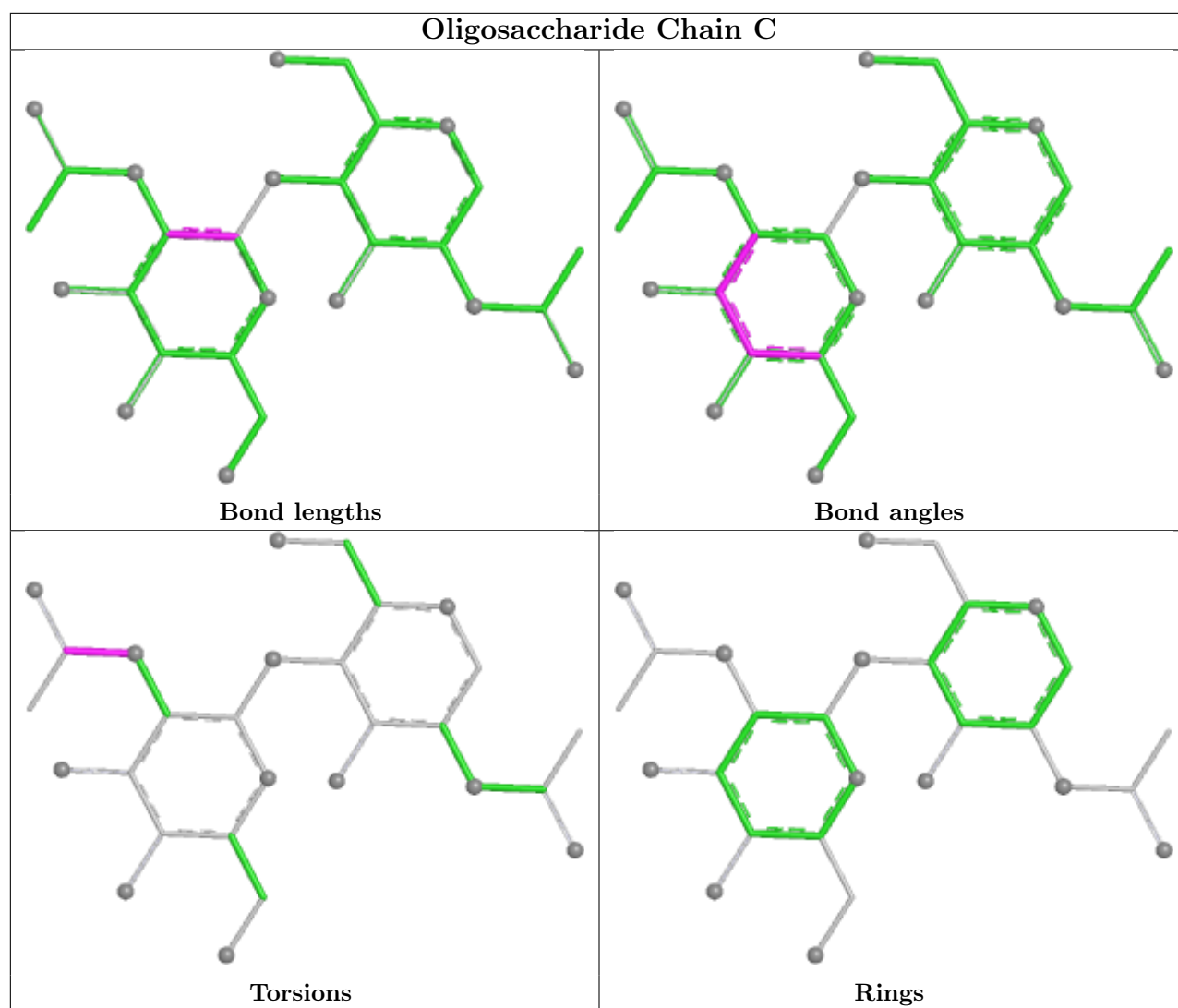
7 monomers are involved in 4 short contacts:

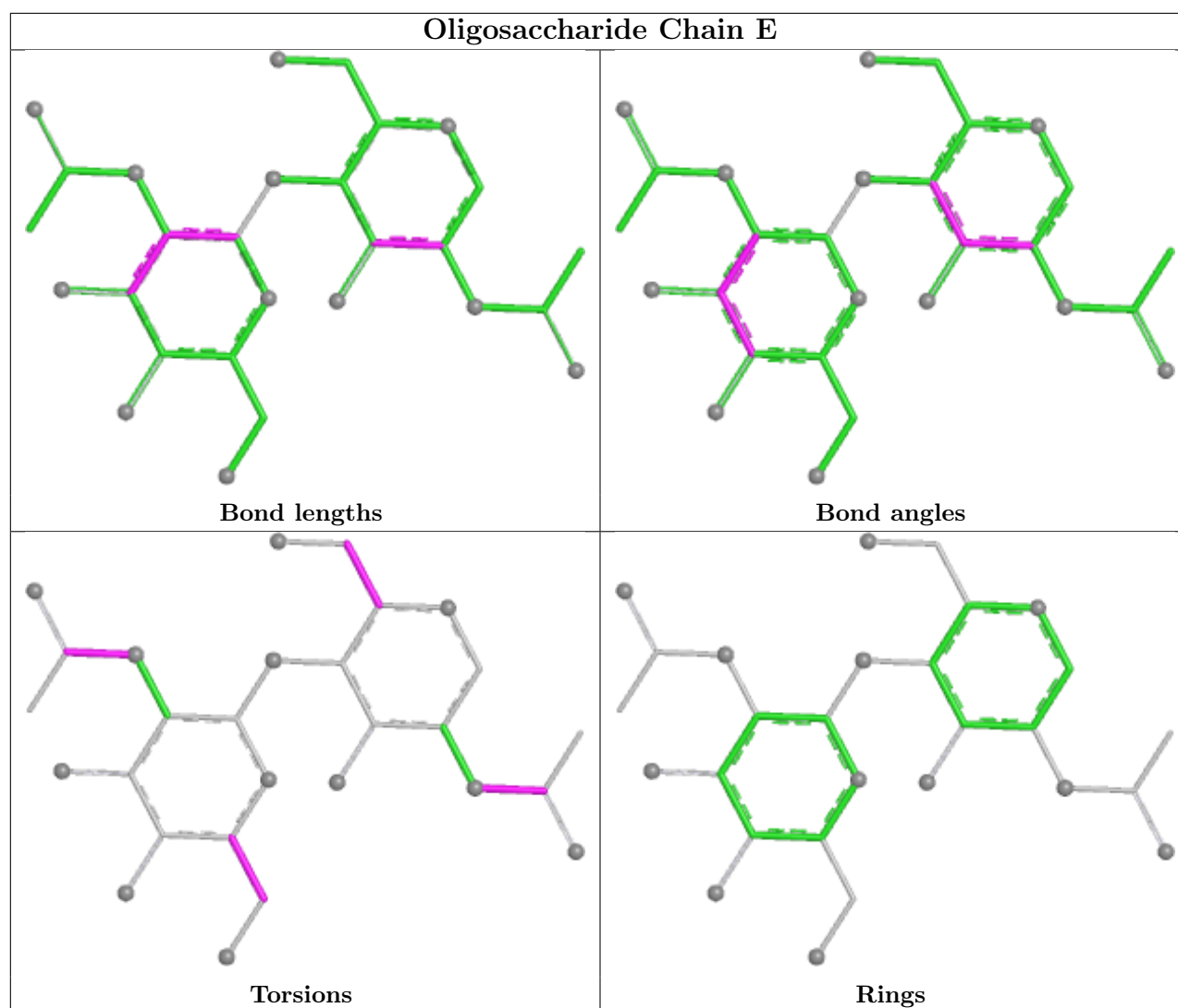
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	1	0
3	E	1	NAG	1	0
2	D	2	NAG	1	0
2	B	2	NAG	1	0
2	D	1	NAG	1	0
3	E	2	NAG	1	0
2	B	1	NAG	1	0

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









5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	SCN	A	616	-	1,2,2	1.95	0	0,1,1	-	-
5	ISZ	A	607	-	9,10,10	1.01	0	12,12,12	3.42	2 (16%)
4	HEM	A	605	9,1	50,50,50	2.29	20 (40%)	67,82,82	1.74	11 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ISZ	A	607	-	-	4/4/6/6	0/1/1/1
4	HEM	A	605	9,1	-	4/14/54/54	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	605	HEM	C3D-C2D	7.20	1.52	1.36
4	A	605	HEM	CAC-C3C	4.36	1.59	1.47
4	A	605	HEM	FE-NC	4.05	2.08	1.95
4	A	605	HEM	CAB-C3B	3.94	1.57	1.47
4	A	605	HEM	CMC-C2C	3.74	1.58	1.50
4	A	605	HEM	CAD-C3D	3.69	1.60	1.51
4	A	605	HEM	FE-NB	3.51	2.05	1.94
4	A	605	HEM	CHA-C1A	-3.14	1.32	1.39
4	A	605	HEM	CBD-CAD	3.12	1.62	1.51
4	A	605	HEM	C4D-ND	-3.08	1.34	1.40
4	A	605	HEM	C1A-NA	-3.02	1.33	1.39
4	A	605	HEM	C1D-C2D	-2.93	1.38	1.44
4	A	605	HEM	C1A-C2A	2.68	1.50	1.44
4	A	605	HEM	C1B-NB	-2.45	1.36	1.40
4	A	605	HEM	O1A-CGA	2.34	1.29	1.22
4	A	605	HEM	C1C-NC	-2.26	1.35	1.39
4	A	605	HEM	CHC-C4B	-2.26	1.34	1.39
4	A	605	HEM	C1C-C2C	2.07	1.49	1.45
4	A	605	HEM	C2A-C3A	-2.06	1.33	1.38
4	A	605	HEM	FE-ND	-2.06	1.88	1.94

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	607	ISZ	C6-N2-N3	10.90	157.72	116.52
4	A	605	HEM	CAD-C3D-C4D	6.90	136.72	124.70
4	A	605	HEM	CMD-C2D-C1D	4.48	132.04	125.03
4	A	605	HEM	CAD-C3D-C2D	-3.95	120.46	127.87
4	A	605	HEM	CHD-C1D-C2D	-3.73	119.14	125.03
5	A	607	ISZ	C1-C6-N2	3.55	120.58	114.22
4	A	605	HEM	C2D-C1D-ND	2.94	113.30	109.90
4	A	605	HEM	C4D-C3D-C2D	-2.84	102.76	106.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	605	HEM	CHD-C1D-ND	2.80	127.44	124.42
4	A	605	HEM	C4C-C3C-C2C	-2.50	104.65	106.81
4	A	605	HEM	C1D-C2D-C3D	-2.24	104.63	106.98
4	A	605	HEM	CHD-C4C-NC	-2.18	122.07	124.45
4	A	605	HEM	C1C-CHC-C4B	2.10	130.47	126.02

There are no chirality outliers.

All (8) torsion outliers are listed below:

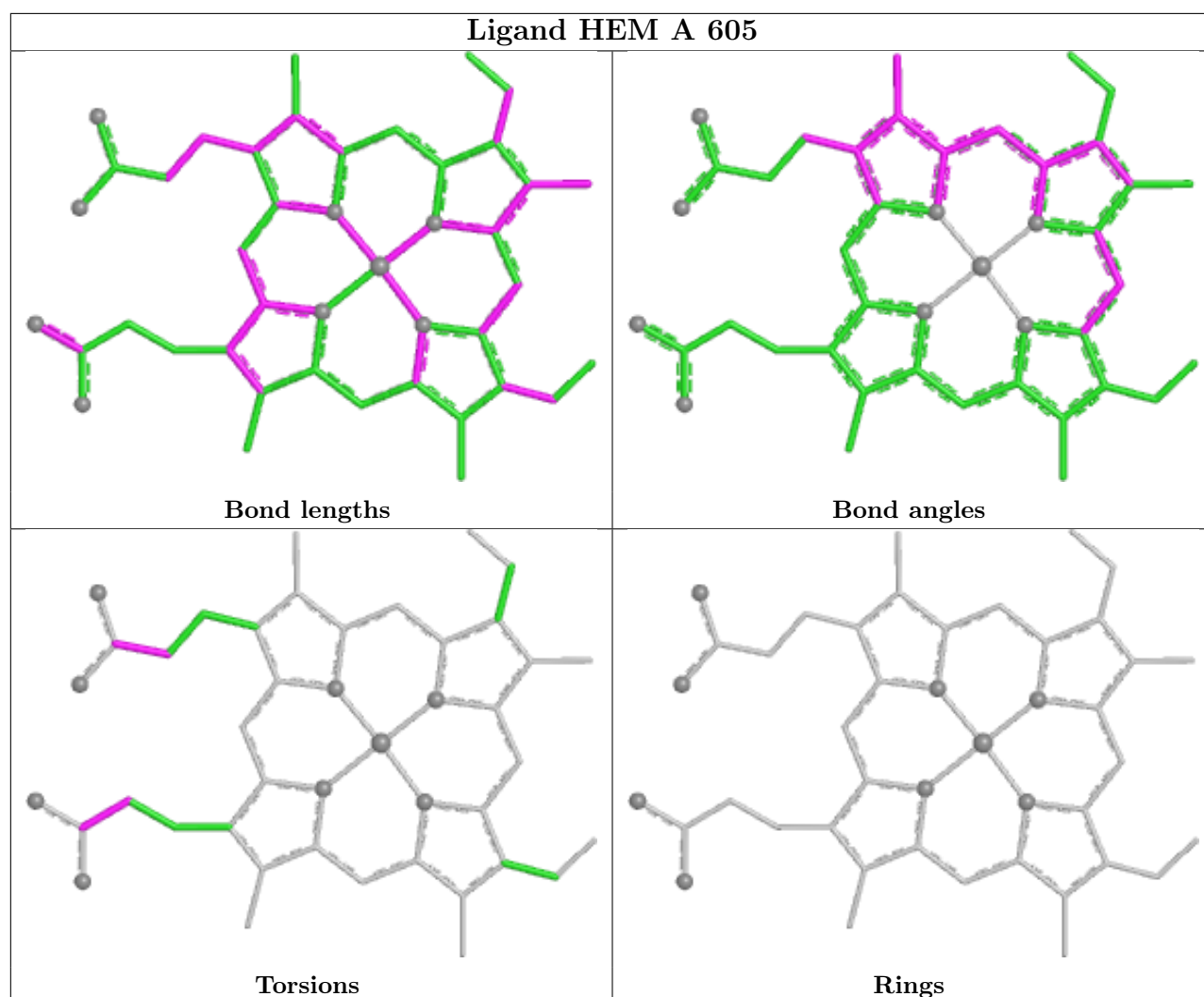
Mol	Chain	Res	Type	Atoms
5	A	607	ISZ	C2-C1-C6-O1
5	A	607	ISZ	C2-C1-C6-N2
5	A	607	ISZ	C3-C1-C6-O1
5	A	607	ISZ	C3-C1-C6-N2
4	A	605	HEM	CAD-CBD-CGD-O2D
4	A	605	HEM	CAD-CBD-CGD-O1D
4	A	605	HEM	CAA-CBA-CGA-O2A
4	A	605	HEM	CAA-CBA-CGA-O1A

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	607	ISZ	5	0
4	A	605	HEM	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.



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	594/595 (99%)	-0.32	10 (1%) 69 67	20, 39, 81, 98	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	TRP	3.3
1	A	175	LEU	3.2
1	A	169	THR	3.1
1	A	4	VAL	3.1
1	A	12	LEU	2.7
1	A	11	PRO	2.7
1	A	121	SER	2.4
1	A	172	TYR	2.3
1	A	120	GLY	2.3
1	A	174	SER	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	198	10/11	0.91	0.14	38,39,41,43	0

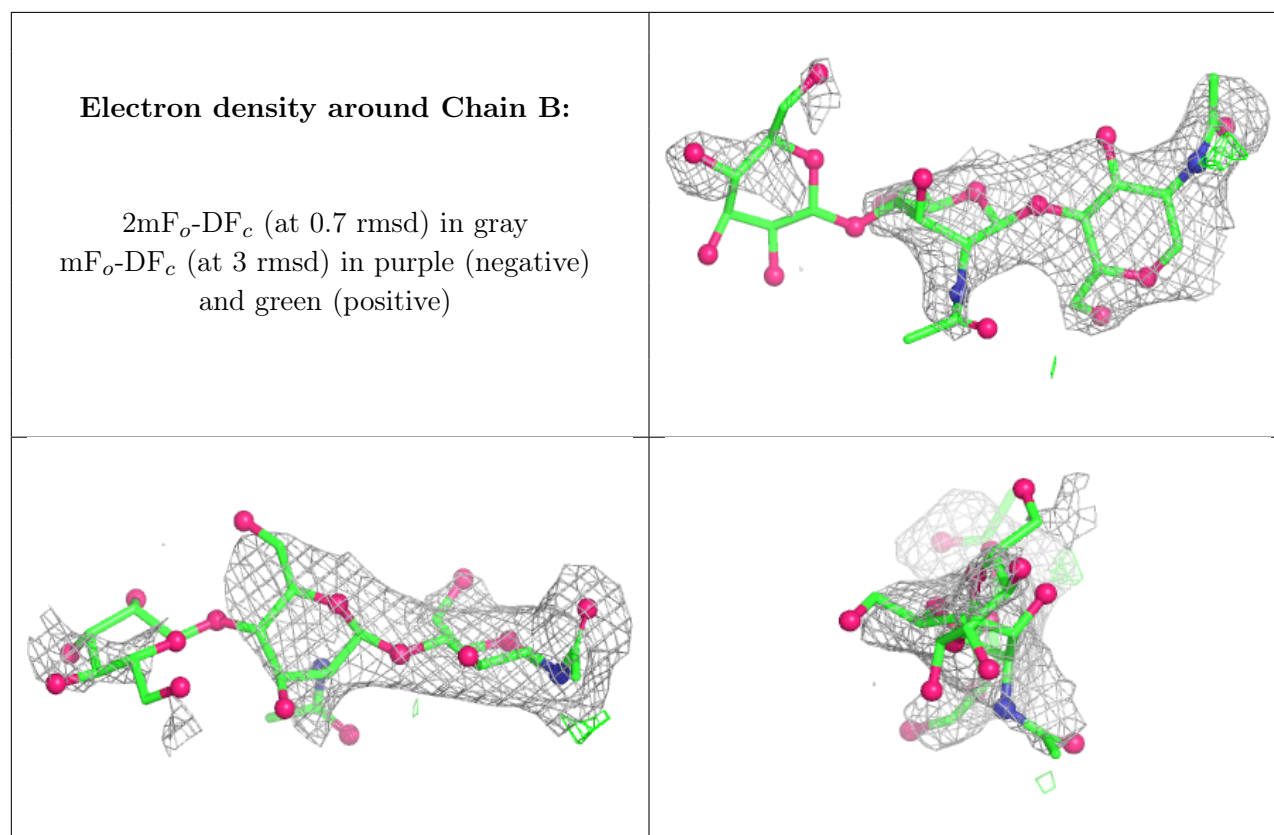
6.3 Carbohydrates [i](#)

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.

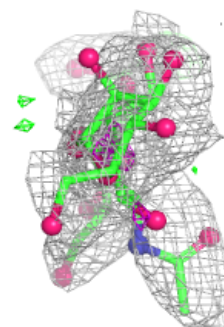
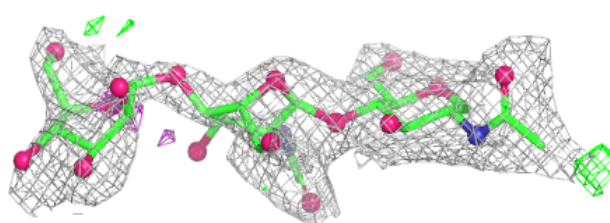
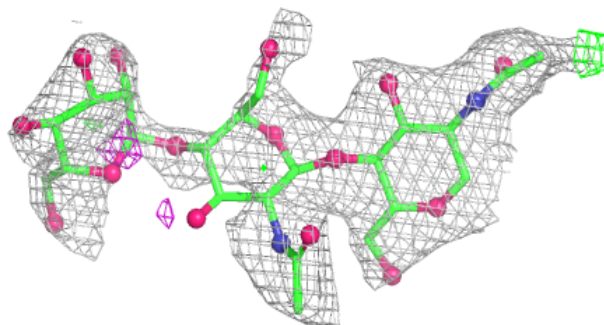
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	E	2	14/15	0.26	0.15	88,91,92,92	0
2	MAN	B	3	11/12	0.40	0.13	97,99,99,99	0
2	MAN	D	3	11/12	0.41	0.12	82,83,84,85	0
2	NAG	D	2	14/15	0.55	0.14	71,74,76,79	0
3	NAG	E	1	14/15	0.60	0.13	72,78,80,84	0
2	NAG	B	1	14/15	0.77	0.11	66,70,74,80	0
3	NAG	C	2	14/15	0.77	0.10	68,70,71,72	0
2	NAG	B	2	14/15	0.80	0.10	86,90,91,94	0
3	NAG	C	1	14/15	0.84	0.10	57,59,62,65	0
2	NAG	D	1	14/15	0.89	0.08	55,58,61,66	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.

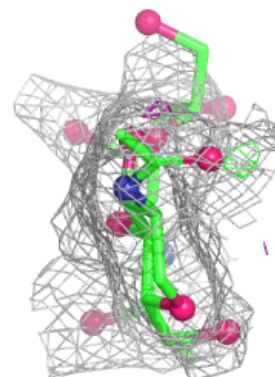
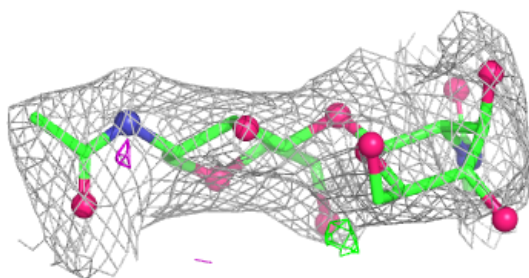
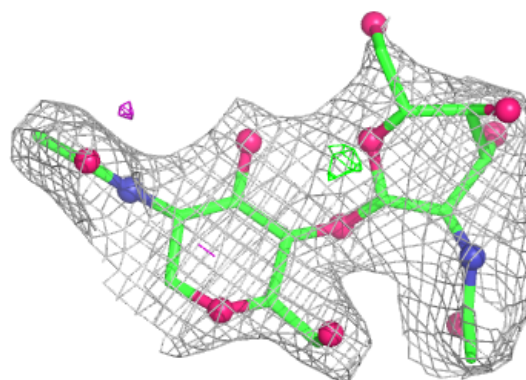


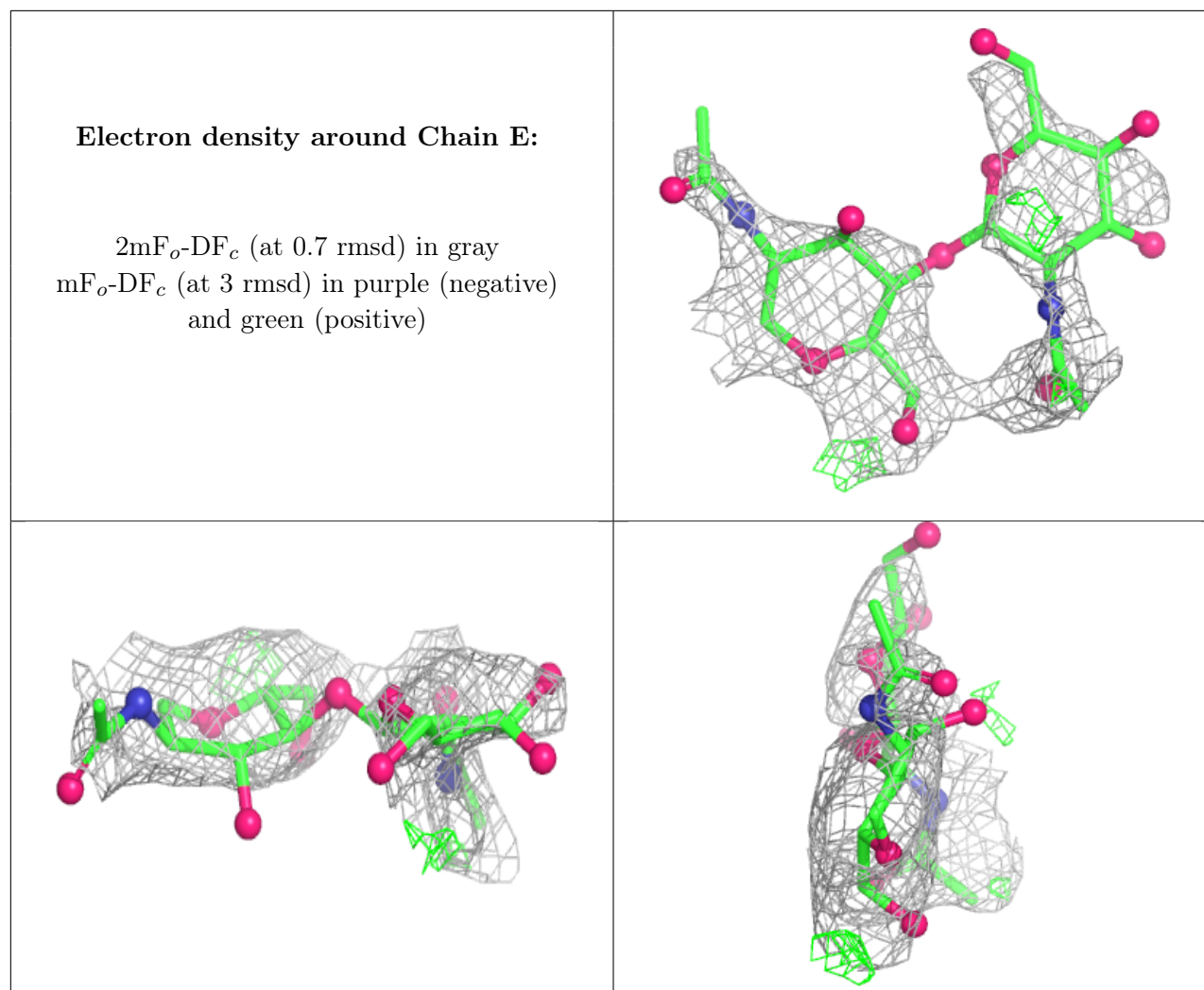
Electron density around Chain D:

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

**Electron density around Chain C:**

$2mF_o-DF_c$ (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.

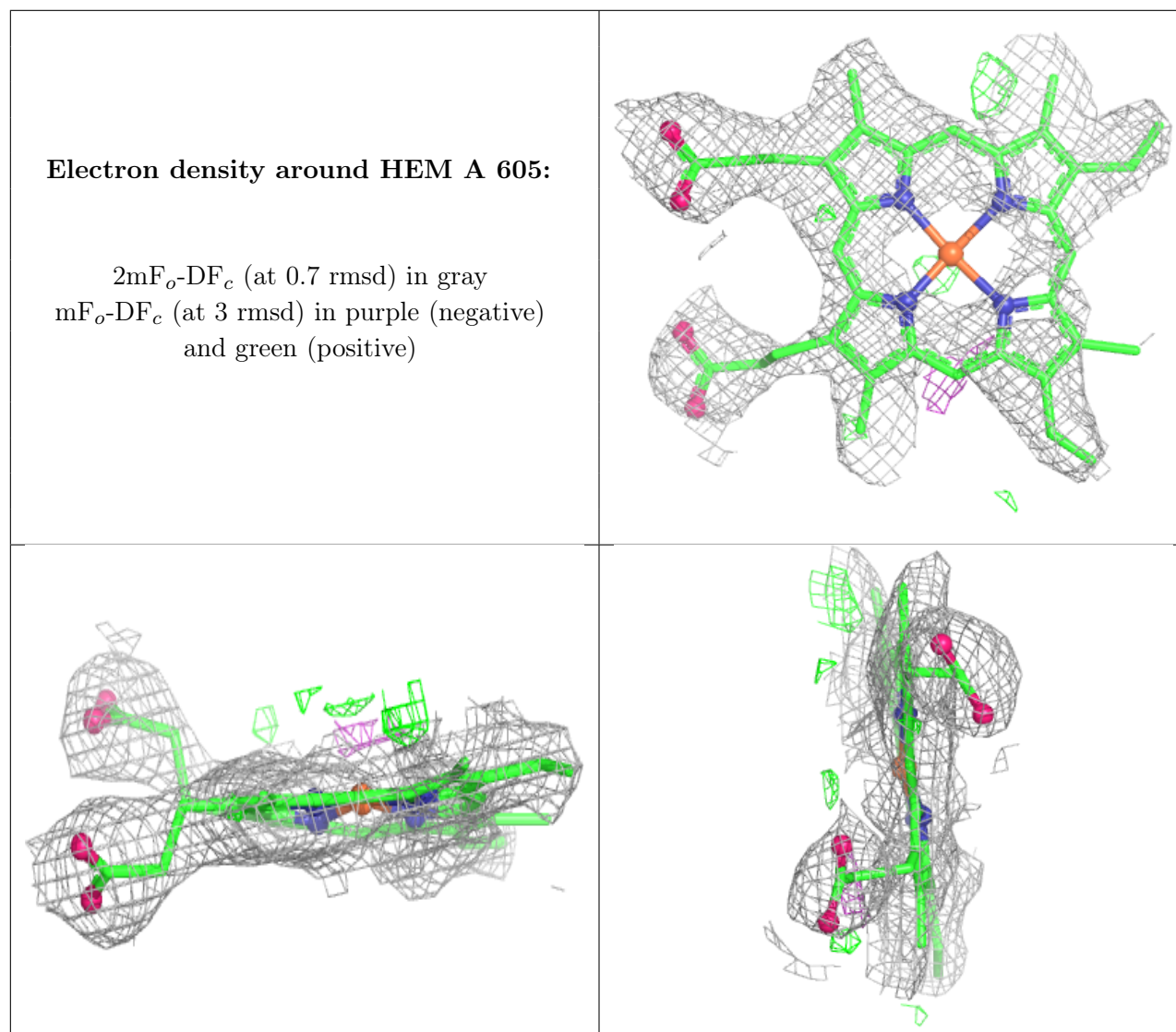
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	ISZ	A	607	10/10	0.83	0.17	27,30,34,35	0
4	HEM	A	605	43/43	0.94	0.10	28,34,38,39	0
6	IOD	A	610	1/1	0.96	0.07	57,57,57,57	1
6	IOD	A	612	1/1	0.96	0.06	54,54,54,54	1
6	IOD	A	613	1/1	0.97	0.08	45,45,45,45	1
7	CA	A	615	1/1	0.97	0.03	24,24,24,24	0
8	SCN	A	616	3/3	0.97	0.06	20,20,21,21	0
6	IOD	A	609	1/1	0.98	0.05	51,51,51,51	1
6	IOD	A	611	1/1	0.98	0.07	44,44,44,44	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	IOD	A	614	1/1	0.99	0.02	32,32,32,32	1
6	IOD	A	608	1/1	1.00	0.01	34,34,34,34	0

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



6.5 Other polymers ⓘ

There are no such residues in this entry.