



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:43 PM UTC

PDB ID : 2IBX / pdb_00002ibx
Title : Influenza virus (VN1194) H5 HA
Authors : Yamada, S.; Russell, R.J.; Gamblin, S.J.; Skehel, J.J.; Kawaoka, Y.
Deposited on : 2006-09-12
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

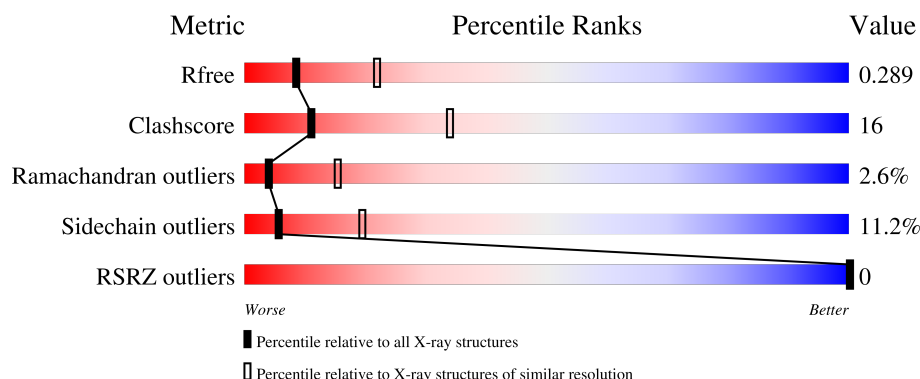
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	340	54% 34% 6% 6%
1	C	340	61% 28% 6%
1	E	340	61% 29% 6%
2	B	160	64% 30%
2	D	160	59% 35%

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Mol	Chain	Length	Quality of chain
2	F	160	 63%34%..
3	G	2	 100%
3	H	2	 100%
3	I	2	 100%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 11682 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.

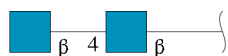
- Molecule 1 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2547	1609	439	484	15			
1	C	321	Total	C	N	O	S	0	0	0
			2547	1609	439	484	15			
1	E	321	Total	C	N	O	S	0	0	0
			2547	1609	439	484	15			

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	160	Total	C	N	O	S	0	0	0
			1291	805	223	255	8			
2	D	160	Total	C	N	O	S	0	0	0
			1291	805	223	255	8			
2	F	160	Total	C	N	O	S	0	0	0
			1291	805	223	255	8			

- 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	G	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	H	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	I	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

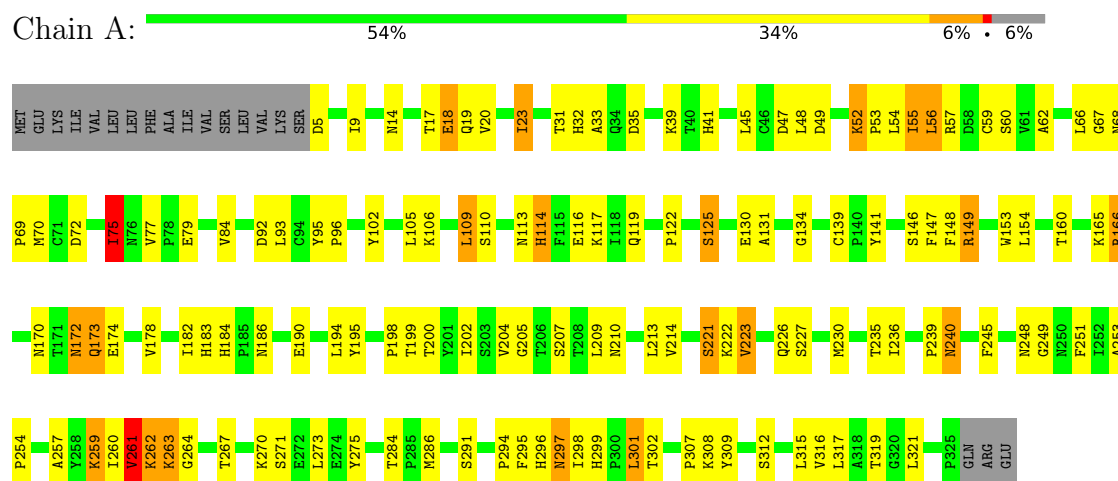


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	E	1	Total	C	N	O	0	0
			14	8	1	5		
4	F	1	Total	C	N	O	0	0
			14	8	1	5		

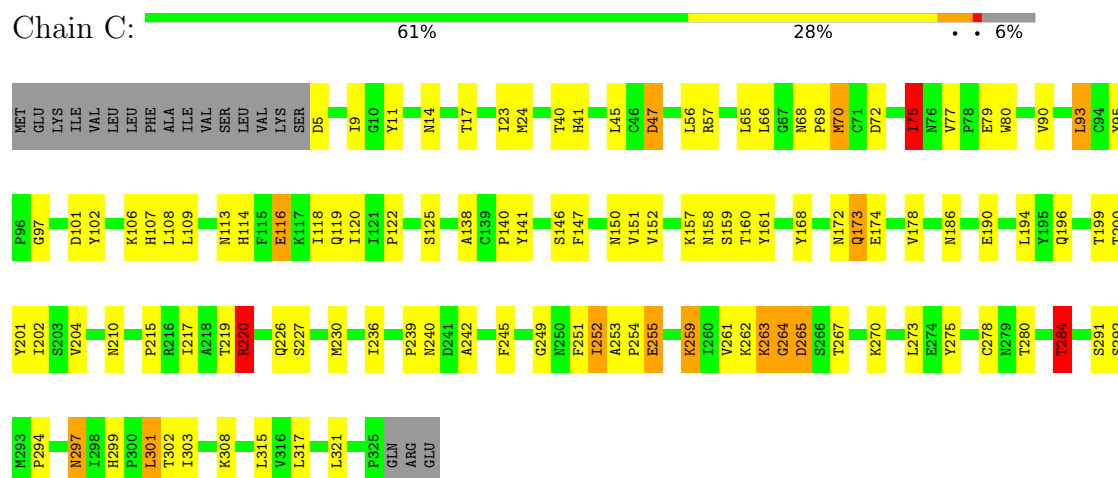
3 Residue-property plots

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: Hemagglutinin

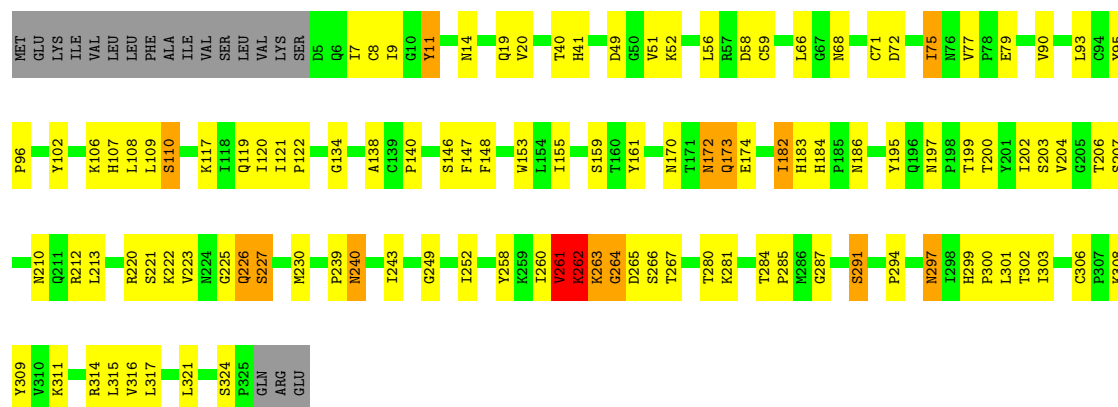


• Molecule 1: Hemagglutinin



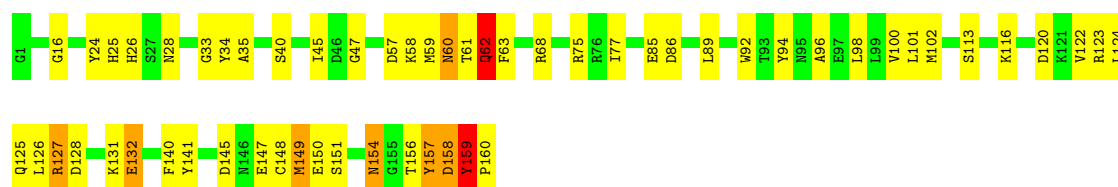
• Molecule 1: Hemagglutinin





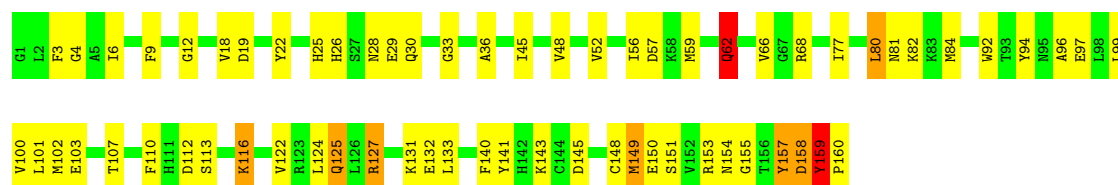
• Molecule 2: Hemagglutinin

Chain B: 64% 30% ..



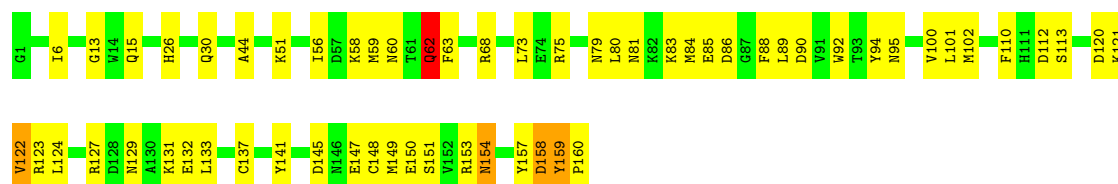
• Molecule 2: Hemagglutinin

Chain D: 59% 35% ..



• Molecule 2: Hemagglutinin

Chain F: 63% 34% ..



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

Chain G: 100%



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

Chain H:  100%

MAG1
MAG2

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

Chain I:  100%

MAG1
MAG2

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	174.68Å 100.56Å 160.13Å 90.00° 111.39° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 30.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	76.8 (30.00-2.80) 76.2 (30.00-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.241 , 0.302 0.234 , 0.289	Depositor DCC
R_{free} test set	2498 reflections (3.93%)	wwPDB-VP
Wilson B-factor (Å ²)	60.5	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 13.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.467 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-l$ 0.467 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-l$	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11682	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.45% 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: NAG

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	0.77	1/2609 (0.0%)	1.05	8/3545 (0.2%)
1	C	0.77	0/2609	1.01	8/3545 (0.2%)
1	E	0.77	0/2609	1.03	6/3545 (0.2%)
2	B	0.80	0/1317	1.09	2/1772 (0.1%)
2	D	0.82	0/1317	1.11	3/1772 (0.2%)
2	F	0.81	0/1317	1.09	1/1772 (0.1%)
All	All	0.78	1/11778 (0.0%)	1.05	28/15951 (0.2%)

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	E	0	1
2	B	0	1
2	D	0	1
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	261	VAL	CA-C	5.02	1.59	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	291	SER	N-CA-C	7.15	118.03	108.38
2	D	12	GLY	N-CA-C	7.09	124.58	110.97
1	E	291	SER	N-CA-C	7.06	119.59	108.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	52	LYS	N-CA-C	6.88	117.51	109.60
1	A	139	CYS	CA-C-N	-6.28	113.51	119.85
1	A	139	CYS	C-N-CA	-6.28	113.51	119.85
1	E	287	GLY	N-CA-C	-6.22	103.56	110.96
1	C	114	HIS	N-CA-C	6.19	118.78	108.13
2	B	62	GLN	N-CA-C	5.95	123.47	110.80
1	C	255	GLU	N-CA-C	-5.91	105.73	113.12
1	E	303	ILE	N-CA-C	-5.87	99.30	108.81
1	C	284	THR	CA-C-N	5.84	125.54	119.82
1	C	284	THR	C-N-CA	5.84	125.54	119.82
1	A	291	SER	N-CA-C	5.76	117.54	108.96
1	A	75	ILE	CB-CA-C	-5.73	104.64	111.97
2	B	157	TYR	N-CA-C	-5.67	102.51	110.50
1	C	220	ARG	N-CA-C	5.61	117.71	109.24
1	A	114	HIS	N-CA-C	5.55	118.51	108.69
2	D	62	GLN	N-CA-C	5.52	122.56	110.80
2	F	62	GLN	N-CA-C	5.52	122.55	110.80
1	E	306	CYS	N-CA-C	5.50	119.10	109.48
1	A	18	GLU	N-CA-C	5.43	118.35	110.42
2	D	157	TYR	N-CA-C	-5.42	102.87	110.35
1	A	319	THR	N-CA-C	-5.32	106.85	113.55
1	C	17	THR	N-CA-C	-5.15	106.92	114.39
1	C	75	ILE	CB-CA-C	-5.05	104.08	112.26
1	E	11	TYR	N-CA-C	5.03	116.45	108.96
1	E	51	VAL	N-CA-C	5.02	113.98	106.85

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	159	TYR	Peptide
2	D	159	TYR	Peptide
1	E	261	VAL	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	2547	0	2487	107	1
1	C	2547	0	2487	74	1
1	E	2547	0	2487	85	2
2	B	1291	0	1202	49	0
2	D	1291	0	1202	53	0
2	F	1291	0	1202	56	0
3	G	28	0	25	0	0
3	H	28	0	25	0	0
3	I	28	0	25	0	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
4	C	14	0	13	0	0
4	D	14	0	13	0	0
4	E	14	0	13	0	0
4	F	14	0	13	1	0
All	All	11682	0	11220	375	3

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.

All (375) 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:E:119:GLN:NE2	1:E:122:PRO:HA	1.46	1.27
1:A:119:GLN:NE2	1:A:122:PRO:HA	1.59	1.17
2:F:150:GLU:O	2:F:154:ASN:HB2	1.52	1.09
1:A:261:VAL:O	1:A:263:LYS:HG2	1.55	1.06
1:A:119:GLN:HE21	1:A:122:PRO:HA	1.10	1.05
1:A:149:ARG:HG2	1:A:149:ARG:HH11	1.23	1.03
2:D:148:CYS:O	2:D:151:SER:HB3	1.60	1.02
1:E:95:TYR:CD2	1:E:230:MET:HG2	1.96	0.99
1:E:284:THR:HG22	1:E:302:THR:HG22	1.45	0.96
2:B:158:ASP:C	2:B:160:PRO:HD2	1.92	0.94
1:A:119:GLN:HE21	1:A:122:PRO:CA	1.80	0.94
1:C:299:HIS:HD2	1:C:301:LEU:H	1.12	0.93
1:A:210:ASN:OD1	1:C:220:ARG:NH1	2.02	0.92
1:E:239:PRO:O	1:E:240:ASN:HB2	1.72	0.89
2:F:145:ASP:OD1	2:F:147:GLU:HG2	1.71	0.89
1:C:9:ILE:HD11	2:D:122:VAL:HG21	1.54	0.88
1:A:119:GLN:NE2	1:A:122:PRO:CA	2.37	0.88
1:C:261:VAL:O	1:C:263:LYS:HG2	1.73	0.87
1:C:299:HIS:CD2	1:C:301:LEU:H	1.92	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:THR:HG22	1:A:302:THR:HG22	1.56	0.87
1:C:308:LYS:HD2	2:D:62:GLN:HB2	1.57	0.86
1:E:119:GLN:NE2	1:E:122:PRO:CA	2.38	0.85
1:E:120:ILE:O	1:E:121:ILE:HG13	1.76	0.85
1:E:186:ASN:HD22	1:E:227:SER:HB3	1.40	0.85
1:E:119:GLN:HE22	1:E:122:PRO:HA	1.36	0.84
2:B:123:ARG:HD3	2:B:132:GLU:OE1	1.78	0.82
2:B:59:MET:HE2	2:D:94:TYR:OH	1.80	0.81
1:C:261:VAL:HG12	1:C:263:LYS:HE2	1.63	0.80
2:F:26:HIS:HB2	2:F:149:MET:HE3	1.63	0.79
1:A:125:SER:OG	1:A:166:ARG:NH2	2.15	0.79
1:A:239:PRO:O	1:A:240:ASN:HB2	1.81	0.79
2:B:124:LEU:HD22	2:D:132:GLU:OE2	1.81	0.78
2:D:26:HIS:HD2	2:D:153:ARG:HH22	1.31	0.78
1:A:95:TYR:CD2	1:A:230:MET:HG2	2.18	0.78
1:A:113:ASN:HB2	1:A:263:LYS:HB2	1.65	0.78
1:E:299:HIS:HD2	1:E:301:LEU:H	1.30	0.78
1:A:149:ARG:HH11	1:A:149:ARG:CG	1.95	0.77
1:E:95:TYR:HD2	1:E:230:MET:HG2	1.50	0.77
2:B:98:LEU:HG	2:B:102:MET:HE2	1.66	0.76
1:A:186:ASN:HD22	1:A:227:SER:CB	1.97	0.76
2:D:26:HIS:HD2	2:D:153:ARG:NH2	1.83	0.76
1:A:9:ILE:HD11	2:B:122:VAL:HG21	1.67	0.76
1:A:170:ASN:OD1	1:A:172:ASN:ND2	2.18	0.76
2:B:68:ARG:HH12	2:D:80:LEU:HA	1.50	0.76
1:C:146:SER:OG	1:C:147:PHE:N	2.16	0.76
1:E:262:LYS:O	1:E:264:GLY:N	2.19	0.76
1:C:45:LEU:HD11	1:C:273:LEU:HB2	1.67	0.76
1:A:72:ASP:O	1:A:75:ILE:CD1	2.33	0.75
1:E:119:GLN:HE21	1:E:122:PRO:HA	1.50	0.74
1:A:116:GLU:O	1:A:259:LYS:HB2	1.87	0.74
1:C:45:LEU:CD1	1:C:273:LEU:HB2	2.18	0.74
1:C:210:ASN:OD1	1:E:220:ARG:NH1	2.22	0.73
1:A:251:PHE:CE2	1:A:253:ALA:HA	2.24	0.72
1:E:182:ILE:HG13	1:E:202:ILE:HD12	1.71	0.72
2:B:68:ARG:NH1	2:D:80:LEU:HA	2.03	0.72
1:A:45:LEU:HD11	1:A:273:LEU:HB3	1.71	0.72
1:C:72:ASP:O	1:C:75:ILE:HG12	1.89	0.72
1:C:317:LEU:HD21	2:D:100:VAL:HG22	1.71	0.71
1:A:261:VAL:O	1:A:263:LYS:N	2.23	0.71
1:A:172:ASN:ND2	1:A:172:ASN:H	1.86	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:LYS:O	1:A:264:GLY:N	2.25	0.70
2:B:63:PHE:HZ	2:B:85:GLU:HG2	1.56	0.70
2:B:59:MET:HE3	2:B:96:ALA:HA	1.74	0.69
1:A:45:LEU:HD11	1:A:273:LEU:CB	2.22	0.69
2:D:26:HIS:HB2	2:D:149:MET:HE3	1.74	0.69
2:F:148:CYS:O	2:F:151:SER:HB3	1.92	0.69
1:C:95:TYR:CD2	1:C:230:MET:HG2	2.27	0.69
2:B:148:CYS:O	2:B:151:SER:HB3	1.92	0.69
1:C:119:GLN:NE2	1:C:122:PRO:HA	2.07	0.69
2:D:68:ARG:NH1	2:D:81:ASN:OD1	2.26	0.69
1:C:261:VAL:CG1	1:C:263:LYS:HE2	2.23	0.68
1:A:72:ASP:O	1:A:75:ILE:HD13	1.94	0.68
1:C:151:VAL:HB	1:C:252:ILE:HG22	1.73	0.68
1:E:297:ASN:C	1:E:297:ASN:HD22	2.02	0.68
2:F:129:ASN:ND2	2:F:159:TYR:HE1	1.91	0.68
1:C:299:HIS:HD2	1:C:301:LEU:N	1.89	0.68
1:E:172:ASN:H	1:E:172:ASN:HD22	1.42	0.67
1:A:186:ASN:HD22	1:A:227:SER:HB2	1.59	0.67
2:D:59:MET:O	2:D:62:GLN:HG3	1.94	0.67
2:F:131:LYS:HG2	2:F:141:TYR:CE2	2.30	0.67
1:C:113:ASN:HB2	1:C:263:LYS:HB2	1.77	0.67
1:C:245:PHE:CE1	1:C:254:PRO:HG2	2.31	0.66
1:E:40:THR:HG22	1:E:41:HIS:N	2.11	0.66
1:E:186:ASN:HD22	1:E:227:SER:CB	2.09	0.66
1:A:261:VAL:C	1:A:263:LYS:H	1.96	0.66
1:A:186:ASN:HD22	1:A:227:SER:HB3	1.60	0.66
1:E:186:ASN:ND2	1:E:227:SER:HB3	2.10	0.65
2:D:148:CYS:O	2:D:151:SER:CB	2.42	0.65
1:A:117:LYS:HG3	1:A:257:ALA:O	1.96	0.65
2:D:99:LEU:HD12	2:D:103:GLU:HG2	1.79	0.64
1:E:174:GLU:N	1:E:174:GLU:OE1	2.30	0.64
1:A:184:HIS:CD2	1:E:210:ASN:HD21	2.15	0.64
1:C:186:ASN:HD22	1:C:227:SER:CB	2.10	0.64
1:A:55:ILE:HD12	1:A:275:TYR:HB2	1.80	0.64
2:D:26:HIS:CD2	2:D:153:ARG:NH2	2.66	0.64
2:F:129:ASN:HD21	2:F:159:TYR:HE1	1.46	0.64
2:F:151:SER:OG	2:F:157:TYR:HA	1.98	0.63
1:A:296:HIS:HD2	1:A:307:PRO:HB2	1.64	0.63
1:E:172:ASN:H	1:E:172:ASN:ND2	1.96	0.63
1:A:317:LEU:HD21	2:B:100:VAL:HG22	1.81	0.63
1:C:47:ASP:OD1	1:C:275:TYR:OH	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:LEU:CD1	1:A:273:LEU:HB3	2.28	0.63
2:D:62:GLN:HG2	2:D:92:TRP:CD2	2.34	0.63
1:C:5:ASP:O	2:D:140:PHE:HD1	1.82	0.62
2:F:131:LYS:HE2	2:F:141:TYR:HE2	1.63	0.62
2:F:6:ILE:HD12	2:F:112:ASP:HA	1.82	0.62
1:A:182:ILE:HG13	1:A:202:ILE:HD12	1.81	0.62
2:F:150:GLU:HG3	2:F:153:ARG:HH11	1.63	0.62
1:A:72:ASP:O	1:A:75:ILE:HD11	1.98	0.62
1:A:35:ASP:HA	1:A:316:VAL:HG22	1.82	0.62
1:A:239:PRO:O	1:A:240:ASN:CB	2.48	0.61
1:E:170:ASN:OD1	1:E:172:ASN:ND2	2.30	0.61
2:B:47:GLY:O	1:C:24:MET:HG2	1.99	0.60
2:D:59:MET:HE2	2:F:94:TYR:CE1	2.36	0.60
1:C:284:THR:HG22	1:C:302:THR:HG22	1.82	0.60
1:C:186:ASN:HD22	1:C:227:SER:HB3	1.67	0.60
1:E:284:THR:HG22	1:E:302:THR:CG2	2.27	0.59
1:A:41:HIS:HD2	1:A:298:ILE:HD12	1.67	0.59
2:B:63:PHE:CZ	2:B:85:GLU:HG2	2.37	0.59
1:C:174:GLU:N	1:C:174:GLU:OE1	2.36	0.59
1:E:173:GLN:H	1:E:173:GLN:CD	2.11	0.59
2:F:79:ASN:HD21	2:F:83:LYS:NZ	2.00	0.59
2:D:3:PHE:O	2:D:116:LYS:HD2	2.03	0.59
1:C:317:LEU:CD2	2:D:100:VAL:HG22	2.33	0.59
2:F:147:GLU:OE2	4:F:521:NAG:H81	2.03	0.58
2:D:107:THR:O	2:D:110:PHE:HB3	2.03	0.58
2:B:120:ASP:CG	2:B:123:ARG:HH21	2.11	0.58
2:D:158:ASP:C	2:D:160:PRO:HD2	2.29	0.58
2:D:158:ASP:HB3	2:D:160:PRO:HD2	1.85	0.58
2:D:62:GLN:HG2	2:D:92:TRP:CE3	2.38	0.58
1:E:314:ARG:NH1	1:E:316:VAL:HG21	2.19	0.58
1:C:186:ASN:ND2	1:C:227:SER:HB2	2.19	0.58
1:A:170:ASN:ND2	1:A:239:PRO:HA	2.19	0.57
1:C:119:GLN:HE21	1:C:122:PRO:HA	1.67	0.57
2:B:145:ASP:OD1	2:B:147:GLU:HG3	2.04	0.57
2:D:124:LEU:O	2:D:127:ARG:N	2.27	0.57
2:D:19:ASP:HB3	2:D:36:ALA:HB2	1.87	0.57
1:C:107:HIS:CD2	2:F:75:ARG:HB3	2.40	0.57
2:B:25:HIS:HA	2:B:33:GLY:O	2.04	0.57
2:B:156:THR:HG22	2:B:156:THR:O	2.03	0.57
1:E:308:LYS:HB3	2:F:62:GLN:NE2	2.20	0.57
1:A:113:ASN:OD1	1:A:264:GLY:O	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:LYS:HD2	2:B:62:GLN:HB2	1.86	0.56
2:B:157:TYR:O	2:B:158:ASP:CG	2.49	0.56
1:C:97:GLY:HA3	1:C:230:MET:O	2.05	0.56
1:A:60:SER:OG	1:A:92:ASP:HA	2.05	0.56
1:A:173:GLN:CD	1:A:173:GLN:H	2.14	0.56
1:E:68:ASN:O	1:E:71:CYS:HB2	2.06	0.56
1:E:309:TYR:HD2	2:F:89:LEU:HD22	1.70	0.56
1:A:56:LEU:HB3	1:A:59:CYS:O	2.06	0.55
1:A:18:GLU:OE2	1:A:33:ALA:HB3	2.06	0.55
1:C:80:TRP:O	1:C:113:ASN:ND2	2.36	0.55
1:A:131:ALA:HB2	1:A:154:LEU:HD23	1.89	0.55
2:B:131:LYS:HE3	2:B:141:TYR:HE2	1.72	0.55
1:E:226:GLN:HE21	1:E:226:GLN:CA	2.19	0.55
1:C:261:VAL:O	1:C:263:LYS:N	2.40	0.55
1:E:110:SER:O	1:E:266:SER:HB3	2.08	0.54
1:E:11:TYR:CZ	2:F:6:ILE:HG23	2.42	0.54
1:A:261:VAL:O	1:A:263:LYS:CG	2.45	0.54
2:B:59:MET:CE	2:B:96:ALA:HA	2.37	0.54
1:C:11:TYR:CZ	2:D:6:ILE:HG23	2.42	0.54
2:D:125:GLN:HE22	2:D:155:GLY:C	2.16	0.54
1:E:40:THR:CG2	1:E:41:HIS:N	2.71	0.54
1:A:200:THR:HG21	1:A:249:GLY:HA3	1.89	0.54
1:C:116:GLU:O	1:C:259:LYS:HB2	2.07	0.54
1:A:119:GLN:HE22	1:A:122:PRO:HA	1.66	0.53
1:A:182:ILE:HG13	1:A:202:ILE:CD1	2.38	0.53
2:D:157:TYR:O	2:D:158:ASP:HB2	2.08	0.53
1:E:14:ASN:C	1:E:14:ASN:OD1	2.51	0.53
1:E:299:HIS:CD2	1:E:301:LEU:H	2.18	0.53
2:F:62:GLN:HG2	2:F:92:TRP:CD2	2.43	0.53
1:A:149:ARG:CG	1:A:149:ARG:NH1	2.61	0.53
1:A:296:HIS:CD2	1:A:307:PRO:HB2	2.43	0.53
2:B:158:ASP:C	2:B:160:PRO:CD	2.74	0.53
1:C:297:ASN:C	1:C:297:ASN:HD22	2.16	0.53
1:E:297:ASN:C	1:E:297:ASN:ND2	2.66	0.53
2:B:94:TYR:CE1	2:F:59:MET:HE2	2.42	0.53
1:A:52:LYS:HG3	1:A:53:PRO:HD2	1.91	0.53
1:A:186:ASN:ND2	1:A:227:SER:HB2	2.22	0.53
2:B:94:TYR:CZ	2:F:59:MET:HE2	2.44	0.52
1:E:182:ILE:HG13	1:E:202:ILE:CD1	2.39	0.52
2:B:159:TYR:N	2:B:160:PRO:HD2	2.23	0.52
2:D:29:GLU:OE2	2:D:143:LYS:HD3	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:120:ASP:CB	2:F:123:ARG:HH21	2.22	0.52
2:F:131:LYS:HG2	2:F:141:TYR:HE2	1.73	0.52
2:B:75:ARG:HB3	1:E:107:HIS:CD2	2.45	0.52
1:E:147:PHE:CZ	1:E:230:MET:HE3	2.45	0.52
1:E:324:SER:OG	2:F:13:GLY:N	2.41	0.51
1:A:202:ILE:O	1:A:213:LEU:N	2.41	0.51
2:D:26:HIS:HB2	2:D:149:MET:CE	2.40	0.51
1:E:96:PRO:HG3	1:E:223:VAL:O	2.09	0.51
1:A:297:ASN:C	1:A:297:ASN:HD22	2.18	0.51
1:C:157:LYS:C	1:C:159:SER:H	2.19	0.51
2:D:157:TYR:O	2:D:158:ASP:CB	2.57	0.51
1:E:161:TYR:CZ	1:E:249:GLY:HA2	2.46	0.51
1:A:202:ILE:HD11	1:A:251:PHE:HA	1.93	0.51
2:B:151:SER:OG	2:B:157:TYR:HA	2.11	0.50
1:E:206:THR:HG22	1:E:243:ILE:HA	1.94	0.50
1:E:294:PRO:CG	2:F:56:ILE:HG12	2.41	0.50
1:A:172:ASN:ND2	1:A:172:ASN:N	2.58	0.50
2:B:26:HIS:HB2	2:B:149:MET:HG2	1.92	0.50
1:C:264:GLY:O	1:C:265:ASP:HB2	2.12	0.50
1:A:45:LEU:HD11	1:A:273:LEU:HB2	1.94	0.50
1:A:262:LYS:O	1:A:263:LYS:C	2.54	0.50
1:A:96:PRO:HB3	1:A:223:VAL:HG12	1.94	0.50
1:C:69:PRO:HB2	1:C:141:TYR:HB2	1.93	0.50
2:B:124:LEU:CD2	2:D:132:GLU:OE2	2.57	0.49
1:C:40:THR:HG22	1:C:41:HIS:N	2.26	0.49
1:E:75:ILE:O	1:E:117:LYS:HE2	2.12	0.49
1:E:262:LYS:O	1:E:262:LYS:HG2	2.12	0.49
1:A:41:HIS:CD2	1:A:298:ILE:HD12	2.48	0.49
1:A:172:ASN:H	1:A:172:ASN:HD22	1.58	0.49
1:A:245:PHE:CE1	1:A:254:PRO:HG2	2.48	0.49
1:A:299:HIS:CD2	1:A:301:LEU:H	2.30	0.49
1:E:172:ASN:ND2	1:E:172:ASN:N	2.60	0.49
1:A:174:GLU:N	1:A:174:GLU:OE1	2.46	0.49
2:F:158:ASP:C	2:F:160:PRO:CD	2.86	0.49
1:A:261:VAL:C	1:A:263:LYS:N	2.67	0.49
1:E:7:ILE:HD12	2:F:149:MET:HG3	1.95	0.49
1:E:226:GLN:CA	1:E:226:GLN:NE2	2.76	0.49
1:C:118:ILE:HG12	1:C:259:LYS:CD	2.43	0.49
1:C:245:PHE:HE1	1:C:254:PRO:HG2	1.75	0.49
1:C:168:TYR:O	1:C:242:ALA:HA	2.13	0.48
2:F:150:GLU:O	2:F:154:ASN:CB	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:PRO:HB2	1:A:295:PHE:CD1	2.49	0.48
2:F:30:GLN:OE1	2:F:145:ASP:HB2	2.13	0.48
1:A:20:VAL:HG12	1:A:316:VAL:HG12	1.95	0.48
1:C:239:PRO:O	1:C:240:ASN:HB2	2.12	0.48
1:A:205:GLY:HA2	1:A:209:LEU:O	2.14	0.48
2:F:158:ASP:C	2:F:160:PRO:HD2	2.39	0.47
1:A:114:HIS:HB3	1:A:261:VAL:HB	1.96	0.47
1:A:170:ASN:HD22	1:A:239:PRO:HA	1.80	0.47
1:E:202:ILE:O	1:E:213:LEU:N	2.43	0.47
1:E:226:GLN:HE21	1:E:226:GLN:N	2.11	0.47
1:C:101:ASP:OD2	2:F:73:LEU:HD13	2.14	0.47
1:A:41:HIS:NE2	1:A:286:MET:HE2	2.29	0.47
2:B:126:LEU:O	2:B:127:ARG:C	2.56	0.47
1:E:203:SER:HB3	1:E:212:ARG:HG3	1.97	0.47
1:E:285:PRO:HD3	1:E:301:LEU:O	2.15	0.47
1:E:161:TYR:CE1	1:E:249:GLY:HA2	2.49	0.47
2:D:25:HIS:ND1	2:D:33:GLY:O	2.47	0.47
2:F:123:ARG:HD3	2:F:132:GLU:OE1	2.15	0.47
1:A:183:HIS:ND1	1:A:195:TYR:OH	2.39	0.47
1:C:45:LEU:HD12	1:C:273:LEU:HB2	1.95	0.47
1:C:151:VAL:HA	1:C:253:ALA:O	2.15	0.47
2:D:150:GLU:O	2:D:154:ASN:HB2	2.15	0.47
1:E:102:TYR:CZ	1:E:106:LYS:HE3	2.50	0.47
1:E:170:ASN:ND2	1:E:239:PRO:HA	2.29	0.46
1:C:157:LYS:C	1:C:159:SER:N	2.74	0.46
1:A:261:VAL:CG1	1:A:263:LYS:HE2	2.45	0.46
2:D:28:ASN:ND2	2:D:145:ASP:HA	2.30	0.46
2:D:131:LYS:HD2	2:D:141:TYR:HE2	1.79	0.46
1:E:294:PRO:HG2	2:F:56:ILE:HG12	1.98	0.46
2:B:124:LEU:O	2:B:127:ARG:N	2.49	0.46
1:A:55:ILE:C	1:A:57:ARG:H	2.23	0.46
1:A:309:TYR:HE2	2:B:89:LEU:HD13	1.81	0.46
1:C:65:LEU:O	1:C:150:ASN:ND2	2.47	0.46
2:F:84:MET:HE3	2:F:88:PHE:HD1	1.81	0.46
1:E:9:ILE:HD11	2:F:122:VAL:HG21	1.98	0.46
1:A:48:LEU:O	1:A:49:ASP:HB2	2.15	0.46
1:E:186:ASN:ND2	1:E:227:SER:CB	2.75	0.46
1:C:118:ILE:HG12	1:C:259:LYS:HD3	1.98	0.45
1:A:67:GLY:O	1:A:68:ASN:C	2.60	0.45
1:E:72:ASP:O	1:E:75:ILE:HG12	2.16	0.45
2:F:94:TYR:O	2:F:95:ASN:C	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:158:ASP:O	2:F:160:PRO:HD2	2.17	0.45
1:C:159:SER:O	1:C:196:GLN:OE1	2.34	0.45
2:B:60:ASN:C	2:B:60:ASN:OD1	2.59	0.45
2:B:154:ASN:HB3	2:B:156:THR:H	1.82	0.45
1:E:121:ILE:HG22	1:E:121:ILE:O	2.16	0.45
1:C:14:ASN:OD1	1:C:14:ASN:C	2.59	0.45
1:E:262:LYS:C	1:E:264:GLY:H	2.23	0.45
2:F:79:ASN:HD21	2:F:83:LYS:HZ2	1.62	0.45
1:A:190:GLU:HG2	1:A:194:LEU:HD11	1.98	0.45
1:C:68:ASN:OD1	1:C:69:PRO:HD2	2.17	0.45
1:C:120:ILE:HG22	1:C:168:TYR:CZ	2.52	0.45
1:E:183:HIS:ND1	1:E:195:TYR:OH	2.36	0.45
1:C:297:ASN:C	1:C:297:ASN:ND2	2.75	0.45
1:E:56:LEU:HB3	1:E:59:CYS:O	2.17	0.45
2:B:68:ARG:NH1	2:D:80:LEU:CA	2.78	0.44
1:C:157:LYS:O	1:C:159:SER:N	2.50	0.44
1:E:161:TYR:HB3	1:E:197:ASN:ND2	2.32	0.44
1:C:138:ALA:C	1:C:140:PRO:HD3	2.42	0.44
2:D:116:LYS:HZ2	2:D:116:LYS:HG2	1.70	0.44
2:F:129:ASN:ND2	2:F:159:TYR:CE1	2.80	0.44
2:B:24:TYR:HD1	2:B:35:ALA:O	2.00	0.44
2:D:159:TYR:N	2:D:160:PRO:HD2	2.32	0.44
1:A:119:GLN:NE2	1:A:122:PRO:CB	2.80	0.44
2:F:68:ARG:NH1	2:F:81:ASN:OD1	2.49	0.44
2:F:26:HIS:CD2	2:F:153:ARG:HH22	2.35	0.44
1:A:221:SER:HB2	1:E:207:SER:HA	1.99	0.44
1:A:299:HIS:HD2	1:A:301:LEU:H	1.65	0.44
2:D:30:GLN:OE1	2:D:145:ASP:HB2	2.18	0.44
1:E:8:CYS:HA	2:F:137:CYS:HA	2.00	0.44
1:A:14:ASN:OD1	1:A:14:ASN:C	2.61	0.44
1:C:9:ILE:CD1	2:D:122:VAL:HG21	2.38	0.44
2:D:66:VAL:HG11	2:F:83:LYS:NZ	2.32	0.44
1:A:75:ILE:O	1:A:117:LYS:NZ	2.43	0.43
2:B:16:GLY:HA3	2:B:34:TYR:CE1	2.53	0.43
1:C:173:GLN:CD	1:C:173:GLN:H	2.26	0.43
1:C:201:TYR:CD1	1:C:201:TYR:C	2.95	0.43
1:E:117:LYS:HD3	1:E:258:TYR:CE2	2.53	0.43
1:E:226:GLN:NE2	1:E:226:GLN:HA	2.32	0.43
1:E:261:VAL:HG12	1:E:263:LYS:HE3	1.99	0.43
1:A:147:PHE:CE1	1:A:230:MET:HE3	2.54	0.43
2:D:6:ILE:HD12	2:D:112:ASP:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:6:ILE:HD12	2:F:112:ASP:CA	2.48	0.43
1:E:58:ASP:HB3	1:E:90:VAL:HG22	2.00	0.43
1:A:31:THR:O	1:A:32:HIS:CG	2.71	0.43
2:F:84:MET:HE3	2:F:88:PHE:CD1	2.53	0.43
1:A:134:GLY:HA3	1:A:153:TRP:HB3	2.01	0.43
1:A:172:ASN:OD1	1:A:259:LYS:HD2	2.19	0.43
1:A:5:ASP:O	2:B:140:PHE:HD1	2.02	0.43
1:C:75:ILE:HG12	1:C:75:ILE:H	1.55	0.42
2:D:59:MET:CE	2:D:96:ALA:HA	2.49	0.42
1:A:297:ASN:C	1:A:297:ASN:ND2	2.77	0.42
1:A:184:HIS:HD2	1:E:210:ASN:HD21	1.63	0.42
2:B:58:LYS:HE3	2:D:97:GLU:OE1	2.19	0.42
2:B:62:GLN:HA	2:B:92:TRP:CZ2	2.54	0.42
1:C:294:PRO:CG	2:D:56:ILE:HG12	2.49	0.42
1:A:96:PRO:HG3	1:A:223:VAL:O	2.20	0.42
2:B:150:GLU:O	2:B:154:ASN:HB2	2.20	0.42
1:E:134:GLY:HA3	1:E:153:TRP:HB3	2.01	0.42
2:F:121:LYS:O	2:F:121:LYS:HG3	2.20	0.42
1:A:23:ILE:HG22	2:F:51:LYS:HA	2.02	0.42
1:A:66:LEU:O	1:A:148:PHE:HB3	2.20	0.42
1:A:113:ASN:HB2	1:A:263:LYS:CB	2.45	0.42
1:A:309:TYR:CE2	2:B:89:LEU:HD13	2.54	0.42
1:C:161:TYR:CZ	1:C:249:GLY:HA2	2.55	0.42
1:A:45:LEU:HD22	1:A:84:VAL:HG21	2.02	0.42
1:C:202:ILE:HD13	1:C:251:PHE:HD1	1.85	0.42
2:D:48:VAL:O	2:D:52:VAL:HG23	2.19	0.42
2:F:44:ALA:HA	2:F:110:PHE:CZ	2.54	0.42
2:F:79:ASN:CG	2:F:83:LYS:HZ1	2.27	0.42
2:B:131:LYS:HE3	2:B:141:TYR:CE2	2.54	0.42
1:C:109:LEU:HD23	1:C:109:LEU:HA	1.90	0.42
1:C:152:VAL:HG23	1:C:255:GLU:HB2	2.01	0.42
2:F:157:TYR:O	2:F:158:ASP:CB	2.68	0.42
2:D:26:HIS:HB2	2:D:149:MET:HG2	2.02	0.41
2:D:59:MET:HE2	2:F:94:TYR:CZ	2.54	0.41
2:F:157:TYR:O	2:F:158:ASP:HB2	2.20	0.41
2:B:59:MET:HE2	2:D:94:TYR:CZ	2.52	0.41
2:B:75:ARG:HD3	2:B:75:ARG:HA	1.77	0.41
2:B:26:HIS:CB	2:B:149:MET:HG2	2.51	0.41
2:B:59:MET:O	2:B:62:GLN:HG3	2.21	0.41
1:C:102:TYR:O	1:C:106:LYS:HG3	2.21	0.41
1:C:204:VAL:HG22	1:C:245:PHE:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:LEU:HD23	1:A:109:LEU:HA	1.88	0.41
1:A:69:PRO:HB2	1:A:141:TYR:HB2	2.03	0.41
2:F:123:ARG:HH12	2:F:124:LEU:HD23	1.85	0.41
1:A:105:LEU:O	1:A:106:LYS:C	2.64	0.41
2:D:4:GLY:O	2:D:9:PHE:CD2	2.74	0.41
1:E:68:ASN:OD1	1:E:68:ASN:C	2.63	0.41
1:E:138:ALA:C	1:E:140:PRO:HD3	2.46	0.41
1:A:62:ALA:HB2	1:A:102:TYR:CE1	2.56	0.41
2:B:28:ASN:OD1	2:B:28:ASN:C	2.64	0.41
1:C:40:THR:CG2	1:C:41:HIS:N	2.84	0.41
1:C:70:MET:HE3	1:C:70:MET:HA	2.02	0.41
1:E:146:SER:O	1:E:147:PHE:HB2	2.20	0.41
1:E:173:GLN:OE1	1:E:173:GLN:N	2.41	0.41
1:E:203:SER:HA	1:E:212:ARG:HA	2.02	0.41
1:A:200:THR:HG22	1:A:248:ASN:OD1	2.21	0.41
1:C:190:GLU:HG2	1:C:194:LEU:HD11	2.03	0.41
1:E:317:LEU:CD2	2:F:100:VAL:HG22	2.51	0.41
1:A:146:SER:OG	1:A:147:PHE:N	2.54	0.40
1:E:49:ASP:OD1	1:E:281:LYS:HG2	2.21	0.40
1:E:225:GLY:C	1:E:226:GLN:HE21	2.29	0.40
1:E:311:LYS:HE3	2:F:90:ASP:OD1	2.21	0.40
1:A:56:LEU:O	1:A:57:ARG:C	2.64	0.40
1:A:271:SER:C	1:A:273:LEU:H	2.29	0.40
1:E:109:LEU:HD23	1:E:109:LEU:HA	1.83	0.40
1:C:200:THR:OG1	1:C:215:PRO:HG2	2.22	0.40
1:C:210:ASN:HD21	1:E:184:HIS:CD2	2.40	0.40
1:E:299:HIS:CD2	1:E:300:PRO:HD2	2.56	0.40
2:F:63:PHE:HZ	2:F:85:GLU:HG2	1.86	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:173:GLN:NE2	1:E:260:ILE:O[2_556]	1.99	0.21
1:A:260:ILE:O	1:C:173:GLN:NE2[4_456]	2.17	0.03
1:E:172:ASN:OD1	1:E:263:LYS:NZ[2_556]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone

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	319/340 (94%)	277 (87%)	36 (11%)	6 (2%)	6	22
1	C	319/340 (94%)	289 (91%)	21 (7%)	9 (3%)	4	14
1	E	319/340 (94%)	287 (90%)	27 (8%)	5 (2%)	7	27
2	B	158/160 (99%)	142 (90%)	10 (6%)	6 (4%)	2	9
2	D	158/160 (99%)	142 (90%)	11 (7%)	5 (3%)	3	11
2	F	158/160 (99%)	140 (89%)	12 (8%)	6 (4%)	2	9
All	All	1431/1500 (95%)	1277 (89%)	117 (8%)	37 (3%)	4	15

All (37) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	ASN
1	A	262	LYS
1	A	263	LYS
2	B	62	GLN
2	B	127	ARG
2	B	158	ASP
2	B	159	TYR
1	C	56	LEU
1	C	158	ASN
1	C	262	LYS
2	D	62	GLN
1	E	240	ASN
1	E	263	LYS
2	F	62	GLN
2	F	154	ASN
2	B	125	GLN
1	C	93	LEU
1	C	125	SER
1	C	264	GLY
2	D	158	ASP

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Mol	Chain	Res	Type
1	E	264	GLY
2	F	15	GLN
2	F	159	TYR
1	A	56	LEU
1	A	221	SER
2	D	127	ARG
2	D	159	TYR
1	E	148	PHE
1	E	262	LYS
2	B	132	GLU
1	C	263	LYS
1	C	265	ASP
2	F	127	ARG
2	F	158	ASP
1	A	198	PRO
1	C	57	ARG
2	D	125	GLN

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	289/307 (94%)	248 (86%)	41 (14%)	3	12
1	C	289/307 (94%)	255 (88%)	34 (12%)	5	17
1	E	289/307 (94%)	257 (89%)	32 (11%)	6	20
2	B	136/136 (100%)	123 (90%)	13 (10%)	8	26
2	D	136/136 (100%)	122 (90%)	14 (10%)	7	23
2	F	136/136 (100%)	127 (93%)	9 (7%)	15	43
All	All	1275/1329 (96%)	1132 (89%)	143 (11%)	6	19

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	THR

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Mol	Chain	Res	Type
1	A	19	GLN
1	A	23	ILE
1	A	39	LYS
1	A	47	ASP
1	A	54	LEU
1	A	55	ILE
1	A	70	MET
1	A	75	ILE
1	A	77	VAL
1	A	79	GLU
1	A	93	LEU
1	A	109	LEU
1	A	110	SER
1	A	125	SER
1	A	130	GLU
1	A	149	ARG
1	A	160	THR
1	A	165	LYS
1	A	166	ARG
1	A	172	ASN
1	A	173	GLN
1	A	178	VAL
1	A	199	THR
1	A	204	VAL
1	A	207	SER
1	A	214	VAL
1	A	222	LYS
1	A	223	VAL
1	A	226	GLN
1	A	235	THR
1	A	236	ILE
1	A	259	LYS
1	A	261	VAL
1	A	267	THR
1	A	270	LYS
1	A	297	ASN
1	A	301	LEU
1	A	312	SER
1	A	315	LEU
1	A	321	LEU
2	B	40	SER
2	B	45	ILE

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Mol	Chain	Res	Type
2	B	57	ASP
2	B	60	ASN
2	B	61	THR
2	B	77	ILE
2	B	86	ASP
2	B	101	LEU
2	B	113	SER
2	B	116	LYS
2	B	128	ASP
2	B	149	MET
2	B	154	ASN
1	C	23	ILE
1	C	47	ASP
1	C	66	LEU
1	C	70	MET
1	C	75	ILE
1	C	77	VAL
1	C	79	GLU
1	C	90	VAL
1	C	93	LEU
1	C	108	LEU
1	C	116	GLU
1	C	160	THR
1	C	172	ASN
1	C	173	GLN
1	C	178	VAL
1	C	199	THR
1	C	217	ILE
1	C	219	THR
1	C	220	ARG
1	C	226	GLN
1	C	236	ILE
1	C	252	ILE
1	C	259	LYS
1	C	267	THR
1	C	270	LYS
1	C	278	CYS
1	C	280	THR
1	C	284	THR
1	C	292	SER
1	C	297	ASN
1	C	301	LEU

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Mol	Chain	Res	Type
1	C	303	ILE
1	C	315	LEU
1	C	321	LEU
2	D	18	VAL
2	D	22	TYR
2	D	45	ILE
2	D	57	ASP
2	D	77	ILE
2	D	80	LEU
2	D	82	LYS
2	D	84	MET
2	D	101	LEU
2	D	102	MET
2	D	113	SER
2	D	116	LYS
2	D	133	LEU
2	D	149	MET
1	E	19	GLN
1	E	20	VAL
1	E	52	LYS
1	E	66	LEU
1	E	75	ILE
1	E	77	VAL
1	E	79	GLU
1	E	93	LEU
1	E	108	LEU
1	E	110	SER
1	E	155	ILE
1	E	159	SER
1	E	172	ASN
1	E	173	GLN
1	E	182	ILE
1	E	199	THR
1	E	200	THR
1	E	204	VAL
1	E	221	SER
1	E	222	LYS
1	E	226	GLN
1	E	227	SER
1	E	252	ILE
1	E	261	VAL
1	E	262	LYS

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Mol	Chain	Res	Type
1	E	265	ASP
1	E	267	THR
1	E	280	THR
1	E	291	SER
1	E	297	ASN
1	E	315	LEU
1	E	321	LEU
2	F	58	LYS
2	F	60	ASN
2	F	80	LEU
2	F	86	ASP
2	F	101	LEU
2	F	102	MET
2	F	113	SER
2	F	122	VAL
2	F	133	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	ASN
1	A	107	HIS
1	A	114	HIS
1	A	119	GLN
1	A	142	GLN
1	A	172	ASN
1	A	186	ASN
1	A	226	GLN
1	A	297	ASN
1	A	299	HIS
2	B	26	HIS
2	B	62	GLN
2	B	72	ASN
2	B	125	GLN
2	B	146	ASN
1	C	107	HIS
1	C	119	GLN
1	C	142	GLN
1	C	186	ASN
1	C	196	GLN
1	C	277	ASN
1	C	297	ASN

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Mol	Chain	Res	Type
1	C	299	HIS
2	D	26	HIS
2	D	62	GLN
2	D	125	GLN
2	D	146	ASN
2	D	154	ASN
1	E	6	GLN
1	E	91	ASN
1	E	107	HIS
1	E	119	GLN
1	E	184	HIS
1	E	186	ASN
1	E	197	ASN
1	E	210	ASN
1	E	226	GLN
1	E	297	ASN
1	E	299	HIS
2	F	26	HIS
2	F	42	GLN
2	F	62	GLN
2	F	125	GLN
2	F	146	ASN

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 ⓘ

6 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
3	NAG	G	1	3,1	14,14,15	0.52	0	17,19,21	1.18	1 (5%)
3	NAG	G	2	3	14,14,15	0.51	0	17,19,21	1.74	3 (17%)
3	NAG	H	1	3,1	14,14,15	0.46	0	17,19,21	1.47	4 (23%)
3	NAG	H	2	3	14,14,15	0.55	0	17,19,21	1.94	2 (11%)
3	NAG	I	1	3,1	14,14,15	0.57	0	17,19,21	1.33	2 (11%)
3	NAG	I	2	3	14,14,15	0.55	0	17,19,21	1.28	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
3	NAG	G	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	G	2	3	-	1/6/23/26	0/1/1/1
3	NAG	H	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	H	2	3	-	1/6/23/26	0/1/1/1
3	NAG	I	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	I	2	3	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	2	NAG	C1-O5-C5	6.05	120.30	112.19
3	H	2	NAG	O5-C1-C2	4.18	117.76	111.29
3	G	2	NAG	C1-O5-C5	4.15	117.75	112.19
3	G	2	NAG	O5-C1-C2	4.13	117.68	111.29
3	I	2	NAG	O5-C1-C2	3.32	116.42	111.29
3	I	1	NAG	O4-C4-C3	-3.21	102.81	110.38
3	G	1	NAG	O4-C4-C3	-2.52	104.44	110.38
3	H	1	NAG	O5-C5-C6	2.50	112.52	107.66
3	G	2	NAG	C4-C3-C2	2.44	114.59	111.02
3	H	1	NAG	O4-C4-C5	2.22	114.78	109.32
3	H	1	NAG	O5-C1-C2	-2.19	107.91	111.29
3	H	1	NAG	O3-C3-C2	2.17	113.91	109.40
3	I	2	NAG	C4-C3-C2	2.12	114.13	111.02
3	I	2	NAG	C1-O5-C5	2.10	115.01	112.19
3	I	1	NAG	O5-C5-C6	2.03	111.61	107.66

There are no chirality outliers.

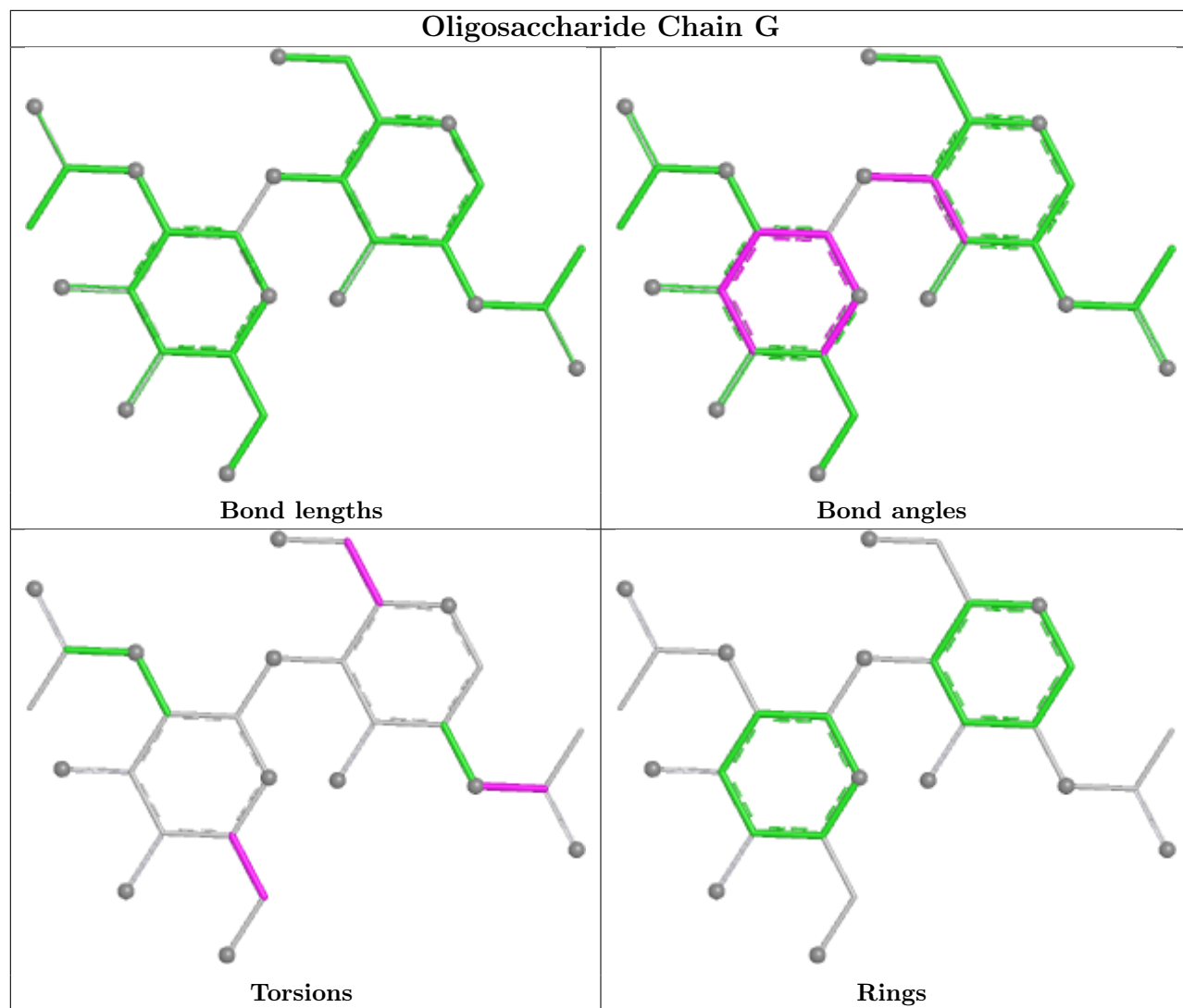
All (17) torsion outliers are listed below:

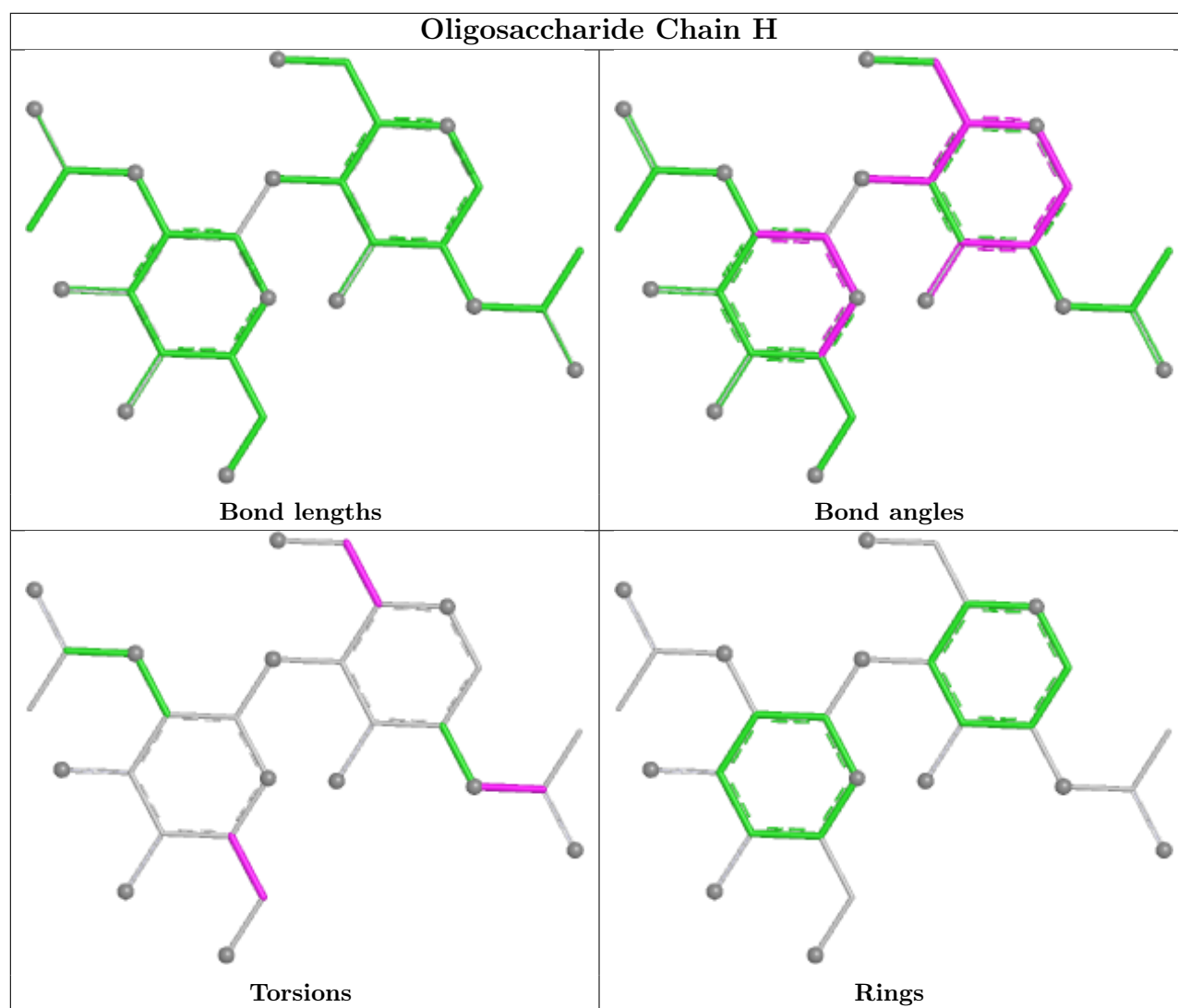
Mol	Chain	Res	Type	Atoms
3	G	1	NAG	C8-C7-N2-C2
3	G	1	NAG	O7-C7-N2-C2
3	H	1	NAG	C8-C7-N2-C2
3	H	1	NAG	O7-C7-N2-C2
3	I	2	NAG	C8-C7-N2-C2
3	I	2	NAG	O7-C7-N2-C2
3	H	1	NAG	O5-C5-C6-O6
3	I	1	NAG	C8-C7-N2-C2
3	I	1	NAG	O7-C7-N2-C2
3	I	1	NAG	O5-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6

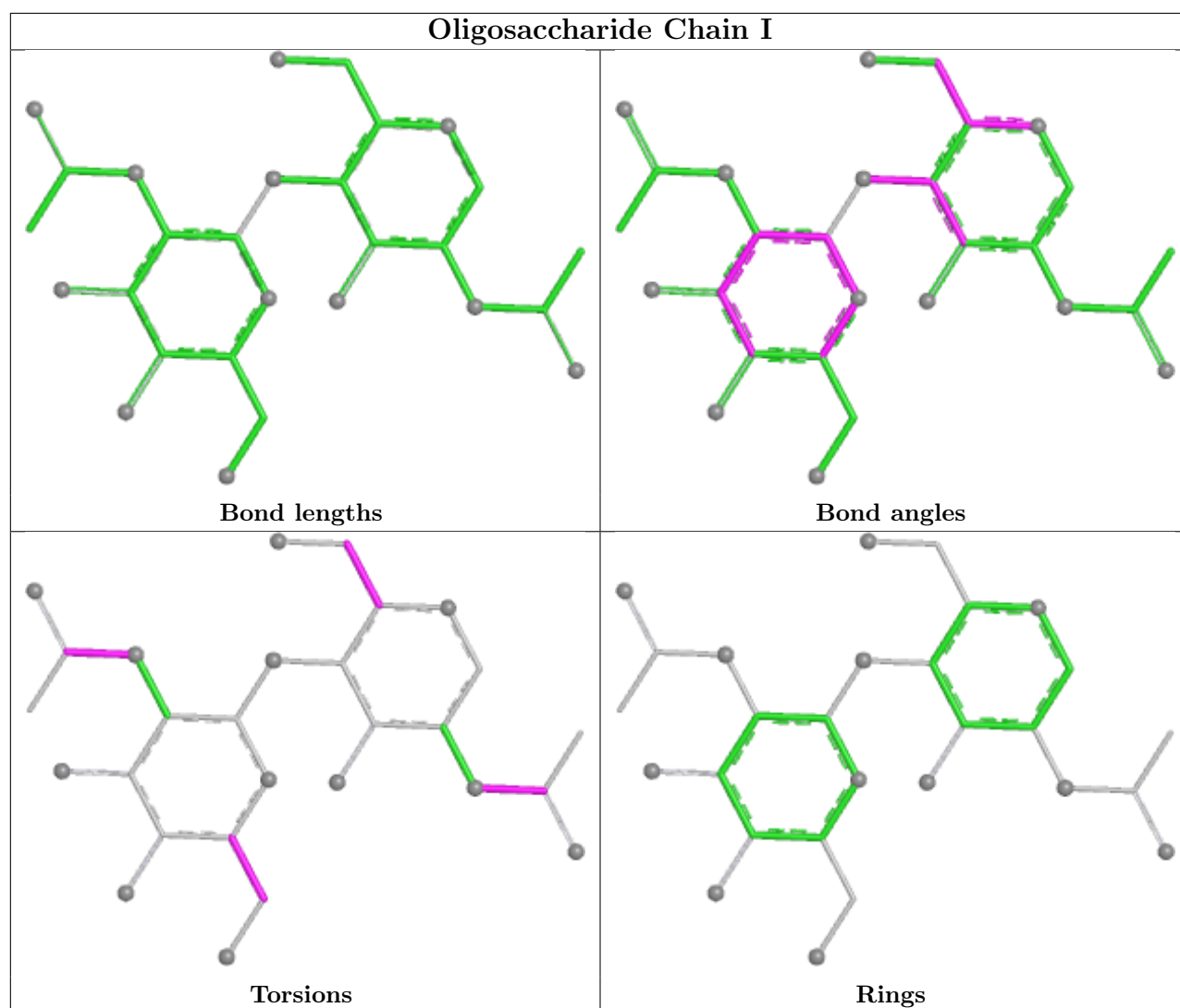
There are no ring outliers.

No monomer is involved in short contacts.

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](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	C	509	1	14,14,15	0.43	0	17,19,21	1.51	2 (11%)
4	NAG	D	514	-	14,14,15	0.67	0	17,19,21	1.16	2 (11%)
4	NAG	A	502	1	14,14,15	0.60	0	17,19,21	0.92	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	F	521	-	14,14,15	0.45	0	17,19,21	1.71	4 (23%)
4	NAG	E	516	1	14,14,15	0.55	0	17,19,21	1.30	3 (17%)
4	NAG	B	507	-	14,14,15	0.61	0	17,19,21	1.63	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
4	NAG	C	509	1	-	2/6/23/26	0/1/1/1
4	NAG	D	514	-	-	2/6/23/26	0/1/1/1
4	NAG	A	502	1	-	2/6/23/26	0/1/1/1
4	NAG	F	521	-	-	3/6/23/26	0/1/1/1
4	NAG	E	516	1	-	3/6/23/26	0/1/1/1
4	NAG	B	507	-	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	509	NAG	C1-O5-C5	4.79	118.60	112.19
4	F	521	NAG	O5-C1-C2	-4.58	104.21	111.29
4	B	507	NAG	C4-C3-C2	4.28	117.28	111.02
4	B	507	NAG	O5-C1-C2	-3.48	105.90	111.29
4	E	516	NAG	C1-O5-C5	3.38	116.72	112.19
4	F	521	NAG	C1-O5-C5	2.80	115.94	112.19
4	D	514	NAG	O5-C1-C2	-2.64	107.20	111.29
4	F	521	NAG	C4-C3-C2	-2.55	107.28	111.02
4	C	509	NAG	C2-N2-C7	-2.44	119.63	122.90
4	E	516	NAG	C2-N2-C7	-2.41	119.67	122.90
4	F	521	NAG	C2-N2-C7	2.39	126.10	122.90
4	D	514	NAG	C4-C3-C2	2.29	114.38	111.02
4	E	516	NAG	C1-C2-N2	2.13	113.78	110.43
4	B	507	NAG	C3-C4-C5	2.10	114.03	110.23

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	507	NAG	C3-C2-N2-C7
4	B	507	NAG	C8-C7-N2-C2
4	B	507	NAG	O7-C7-N2-C2
4	D	514	NAG	C8-C7-N2-C2
4	D	514	NAG	O7-C7-N2-C2
4	F	521	NAG	C3-C2-N2-C7
4	F	521	NAG	C8-C7-N2-C2
4	F	521	NAG	O7-C7-N2-C2
4	C	509	NAG	C8-C7-N2-C2
4	A	502	NAG	C8-C7-N2-C2
4	A	502	NAG	O7-C7-N2-C2
4	C	509	NAG	O7-C7-N2-C2
4	E	516	NAG	C8-C7-N2-C2
4	E	516	NAG	O7-C7-N2-C2
4	E	516	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	521	NAG	1	0

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	321/340 (94%)	-1.36	0 100 100	29, 58, 70, 74	0
1	C	321/340 (94%)	-1.39	0 100 100	31, 56, 72, 77	0
1	E	321/340 (94%)	-1.38	0 100 100	32, 55, 70, 74	0
2	B	160/160 (100%)	-1.35	0 100 100	28, 48, 71, 93	0
2	D	160/160 (100%)	-1.35	0 100 100	27, 47, 72, 99	0
2	F	160/160 (100%)	-1.36	0 100 100	25, 48, 74, 97	0
All	All	1443/1500 (96%)	-1.37	0 100 100	25, 54, 71, 99	0

There are no RSRZ outliers to report.

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](#)

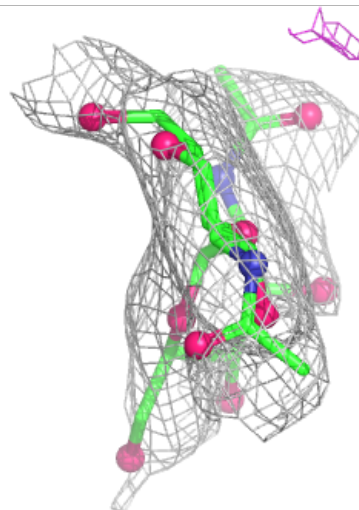
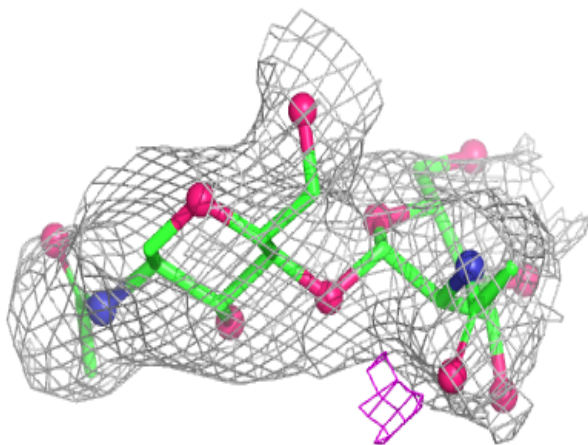
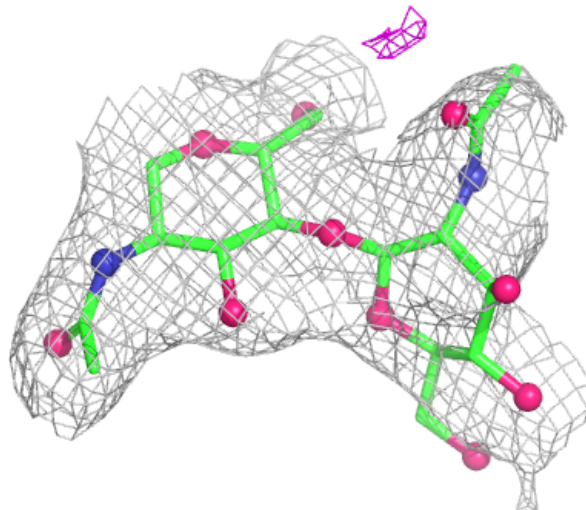
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	I	2	14/15	0.95	0.05	86,89,91,92	0
3	NAG	G	2	14/15	0.97	0.05	86,88,89,90	0
3	NAG	H	2	14/15	0.98	0.04	86,88,89,89	0
3	NAG	G	1	14/15	0.99	0.04	74,76,78,82	0
3	NAG	I	1	14/15	0.99	0.03	72,74,77,82	0
3	NAG	H	1	14/15	0.99	0.03	71,73,77,82	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.

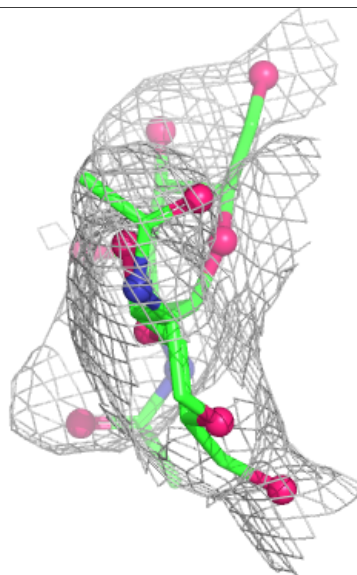
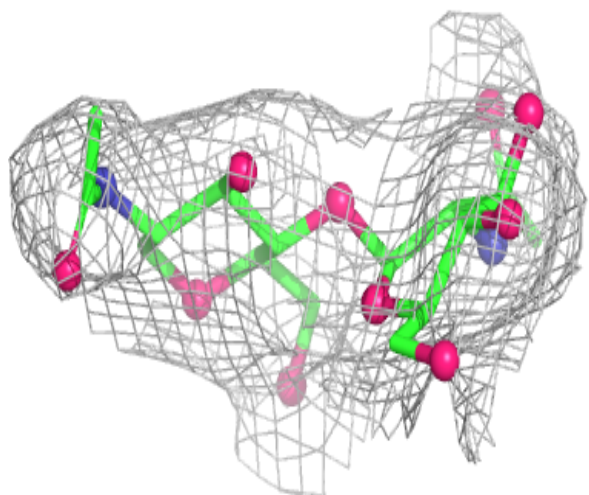
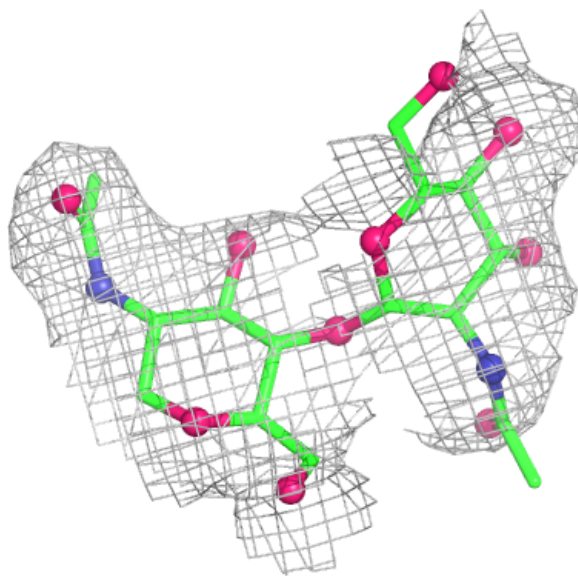
Electron density around Chain G:

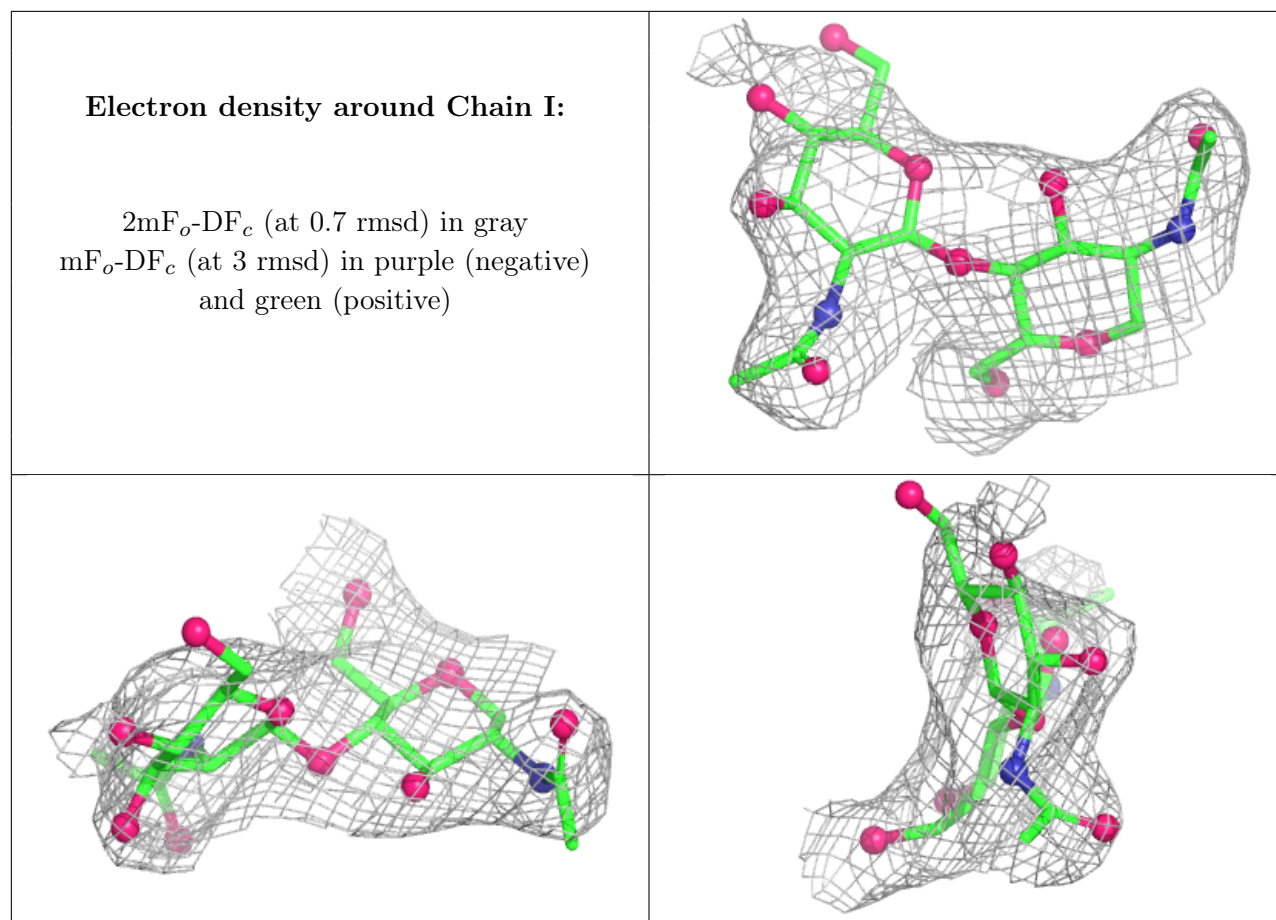
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



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)





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
4	NAG	D	514	14/15	0.94	0.09	105,106,107,107	0
4	NAG	C	509	14/15	0.96	0.05	65,70,73,74	0
4	NAG	A	502	14/15	0.96	0.05	64,70,72,73	0
4	NAG	B	507	14/15	0.97	0.06	96,98,99,99	0
4	NAG	F	521	14/15	0.97	0.06	99,100,102,102	0
4	NAG	E	516	14/15	0.98	0.04	62,65,67,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.