



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2023 – 10:00 PM EDT

PDB ID : 7KCZ  
Title : CRYSTAL STRUCTURE OF RHESUS MACAQUE (MACACA MULATTA)  
IGG1 FC FRAGMENT- FC-GAMMA RECEPTOR III COMPLEX V158  
MUTANT  
Authors : Tolbert, W.D.; Pazgier, M.  
Deposited on : 2020-10-07  
Resolution : 3.15 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

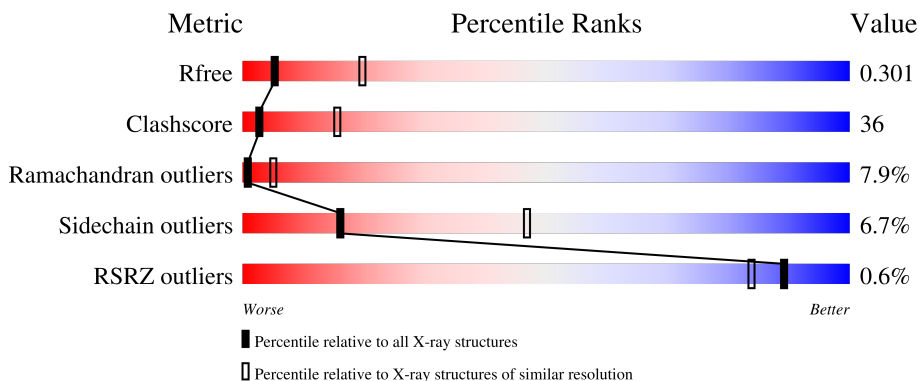
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.15 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)

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  $\geq 3$ , 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	224	
1	B	224	
1	D	224	
1	E	224	
2	C	192	

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Mol	Chain	Length	Quality of chain
2	F	192	<p>%</p> <p>38% 42% 8% 12%</p>
3	G	8	<p>50% 50%</p>
3	H	8	<p>25% 62% 12%</p>
3	J	8	<p>12% 75% 12%</p>
3	K	8	<p>38% 50% 12%</p>
4	I	4	<p>25% 50% 25%</p>
5	L	4	<p>25% 50% 25%</p>

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10027 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 IgG1 Fc.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	209	Total 1666	C 1058	N 280	O 322	S 6	0	0	0
1	B	212	Total 1690	C 1074	N 283	O 327	S 6	0	0	0
1	D	209	Total 1683	C 1067	N 284	O 326	S 6	0	2	0
1	E	212	Total 1690	C 1074	N 283	O 327	S 6	0	0	0

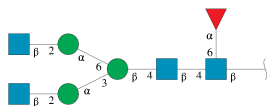
- Molecule 2 is a protein called Low affinity immunoglobulin gamma Fc region receptor III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	168	Total 1365	C 869	N 237	O 255	S 4	0	0	0
2	F	169	Total 1374	C 874	N 238	O 258	S 4	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	38	GLN	ASN	engineered mutation	UNP A3RFZ7
C	158	VAL	ILE	engineered mutation	UNP A3RFZ7
C	169	GLN	ASN	engineered mutation	UNP A3RFZ7
F	38	GLN	ASN	engineered mutation	UNP A3RFZ7
F	158	VAL	ILE	engineered mutation	UNP A3RFZ7
F	169	GLN	ASN	engineered mutation	UNP A3RFZ7

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



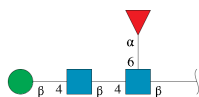
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	G	8	99	56	4	39	0	0	0
3	H	8	99	56	4	39	0	0	0
3	J	8	99	56	4	39	0	0	0
3	K	8	99	56	4	39	0	0	0

- Molecule 4 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
			Total	C	N	O			
4	I	4	50	28	2	20	0	0	0

- Molecule 5 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	L	4	49	28	2	19	0	0	0

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
6	C	1	14	8	1	5	0	0
6	C	1	14	8	1	5	0	0
6	F	1	14	8	1	5	0	0
6	F	1	14	8	1	5	0	0

- Molecule 7 is water.

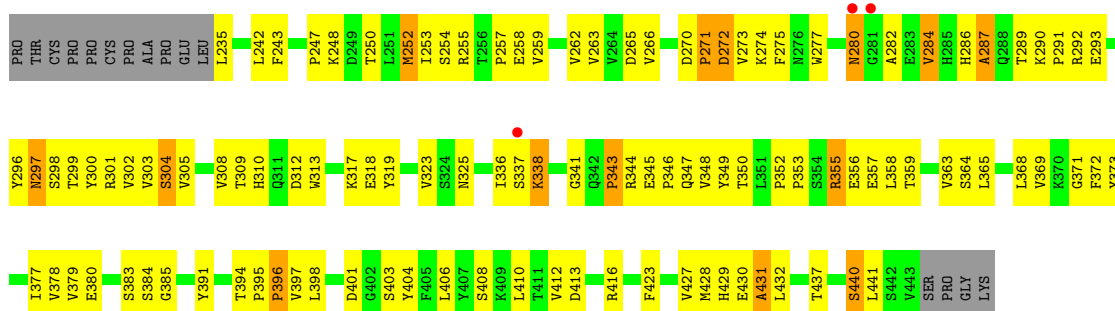
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	3	3	3	0	0
7	B	1	1	1	0	0
7	C	1	1	1	0	0
7	D	1	1	1	0	0
7	E	1	1	1	0	0
7	F	1	1	1	0	0

### 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.

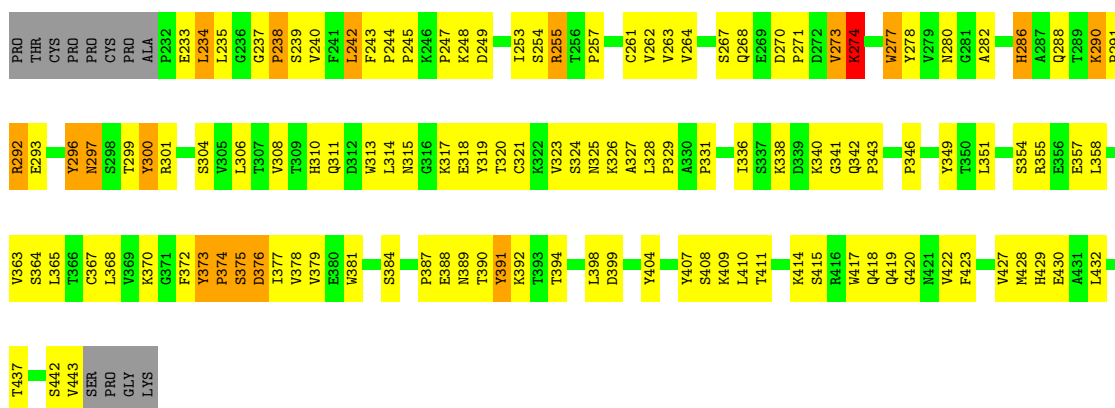
- Molecule 1: IgG1 Fc

Chain A: 



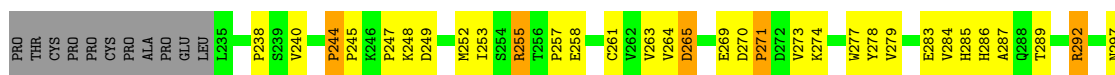
- Molecule 1: IgG1 Fc

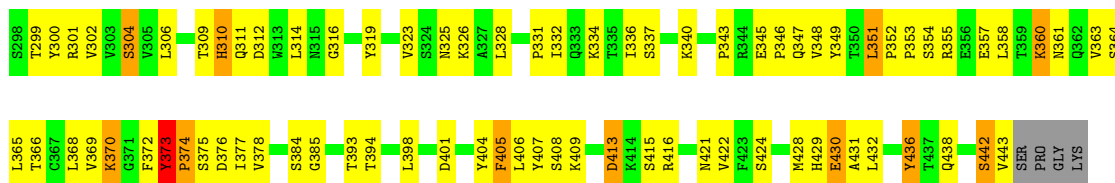
Chain B: 



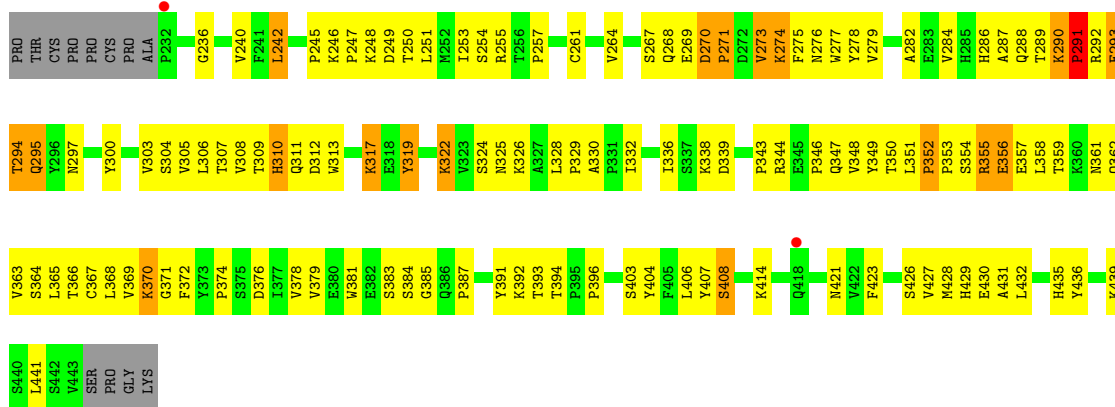
- Molecule 1: IgG1 Fc

Chain D: 

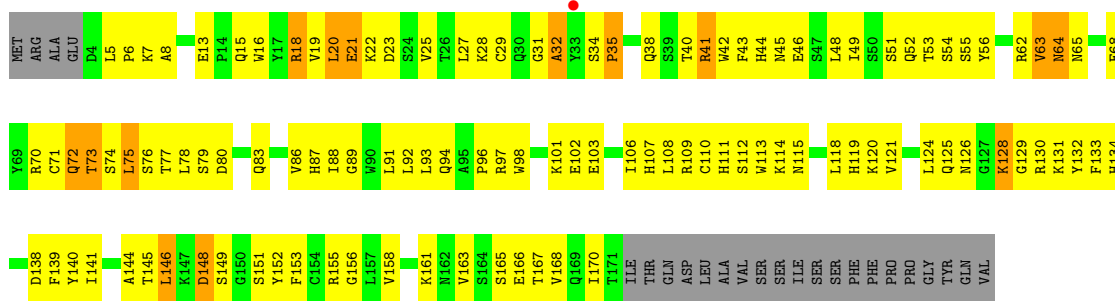




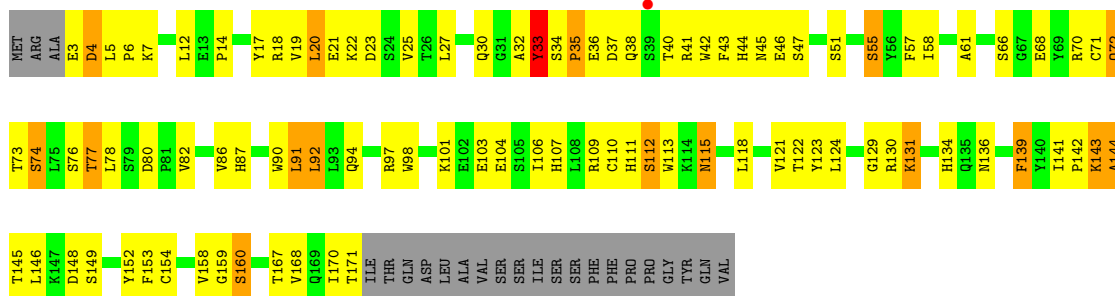
• Molecule 1: IgG1 Fc



• Molecule 2: Low affinity immunoglobulin gamma Fc region receptor III



• Molecule 2: Low affinity immunoglobulin gamma Fc region receptor III





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



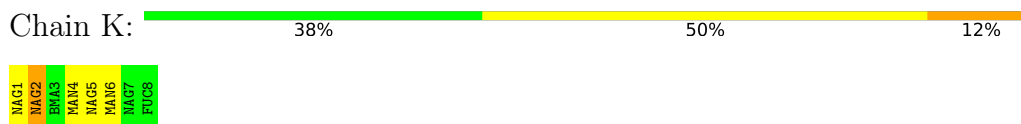
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



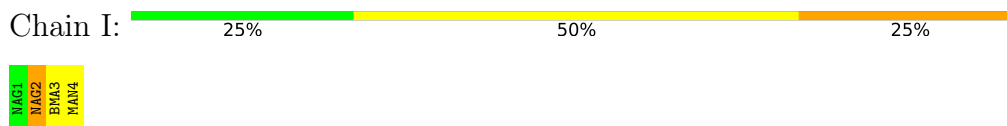
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



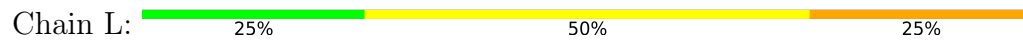
- Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-3)-[2-acetamido-2-deoxy-beta-D-glucopyranose-(1-2)-alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 4: 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



- Molecule 5: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[alpha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	215.69Å 70.11Å 135.41Å 90.00° 119.77° 90.00°	Depositor
Resolution (Å)	60.11 – 3.15 66.94 – 3.15	Depositor EDS
% Data completeness (in resolution range)	93.6 (60.11-3.15) 95.9 (66.94-3.15)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.47 (at 3.13Å)	Xtrriage
Refinement program	PHENIX (1.17.1_3660: ???), REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.269 , 0.303 0.267 , 0.301	Depositor DCC
$R_{free}$ test set	1435 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	72.7	Xtrriage
Anisotropy	0.832	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 55.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	10027	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, MAN, BMA, FUC

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	0.47	0/1712	0.71	0/2337
1	B	0.49	0/1737	0.80	0/2371
1	D	0.45	0/1729	0.70	0/2360
1	E	0.45	0/1737	0.82	1/2371 (0.0%)
2	C	0.52	0/1401	0.82	0/1900
2	F	0.43	0/1410	0.78	0/1912
All	All	0.47	0/9726	0.77	1/13251 (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	D	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	E	291	PRO	N-CA-CB	-9.67	91.70	103.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	373	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	1666	0	1628	125	0
1	B	1690	0	1653	126	0
1	D	1683	0	1640	117	0
1	E	1690	0	1653	145	0
2	C	1365	0	1324	126	0
2	F	1374	0	1330	92	0
3	G	99	0	85	0	0
3	H	99	0	85	2	0
3	J	99	0	85	3	0
3	K	99	0	85	2	0
4	I	50	0	43	3	0
5	L	49	0	43	1	0
6	C	28	0	26	1	0
6	F	28	0	26	0	0
7	A	3	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
7	E	1	0	0	0	0
7	F	1	0	0	0	0
All	All	10027	0	9706	703	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 36.

All (703) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:351:LEU:HD12	1:D:352:PRO:CD	1.45	1.46
2:C:20:LEU:HD23	2:C:113:TRP:CD1	1.65	1.30
2:C:20:LEU:CD2	2:C:113:TRP:HD1	1.52	1.22
1:E:242:LEU:CD2	1:E:336:ILE:HB	1.68	1.22
1:B:271:PRO:HB3	1:B:325:ASN:OD1	1.40	1.21
1:A:258:GLU:OE1	1:A:305:VAL:HG21	1.38	1.21
2:C:20:LEU:CD2	2:C:113:TRP:CD1	2.22	1.20

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:290:LYS:HB2	1:E:291:PRO:HD3	1.24	1.19
1:D:374:PRO:HD2	1:D:429:HIS:HE1	1.08	1.19
1:E:242:LEU:HD21	1:E:336:ILE:HB	1.16	1.15
1:A:432:LEU:HD21	1:A:437:THR:HB	1.21	1.13
2:C:18:ARG:HH22	2:C:168:VAL:HG21	1.07	1.13
1:A:350:THR:CB	1:A:441:LEU:HD11	1.79	1.12
2:F:91:LEU:HD21	2:F:110:CYS:SG	1.88	1.12
1:D:351:LEU:HD21	1:E:352:PRO:HD2	1.26	1.12
1:D:351:LEU:HD12	1:D:352:PRO:HD2	1.12	1.10
1:A:257:PRO:O	1:A:308:VAL:HG12	1.51	1.09
1:E:429:HIS:HB3	1:E:432:LEU:HD13	1.28	1.08
1:D:351:LEU:CD1	1:D:352:PRO:HD2	1.83	1.07
1:E:429:HIS:HB3	1:E:432:LEU:CD1	1.83	1.07
1:A:350:THR:HB	1:A:441:LEU:HD11	1.32	1.06
1:E:294:THR:HA	1:E:300:TYR:HA	1.38	1.05
2:C:44:HIS:HB2	2:C:49:ILE:HD11	1.33	1.04
1:D:351:LEU:CD1	1:D:352:PRO:CD	2.39	1.01
1:D:351:LEU:HD12	1:D:352:PRO:HD3	1.43	1.00
1:B:271:PRO:HB3	1:B:325:ASN:CG	1.81	1.00
1:E:350:THR:C	1:E:351:LEU:HD23	1.82	1.00
1:E:346:PRO:HG3	1:E:432:LEU:HD11	1.42	0.99
1:B:240:VAL:HG21	1:B:323:VAL:HG11	1.43	0.97
1:D:374:PRO:HD2	1:D:429:HIS:CE1	2.00	0.97
1:A:257:PRO:HG2	1:A:308:VAL:HG13	1.47	0.97
1:A:257:PRO:HG2	1:A:308:VAL:CG1	1.94	0.96
1:B:234:LEU:O	1:B:235:LEU:HG	1.66	0.95
2:C:20:LEU:HD21	2:C:113:TRP:HD1	1.30	0.95
2:F:91:LEU:CD2	2:F:110:CYS:SG	2.55	0.95
1:E:242:LEU:HD21	1:E:336:ILE:CB	1.98	0.94
1:B:390:THR:HB	1:B:410:LEU:HD11	1.48	0.93
1:B:346:PRO:HD3	1:B:429:HIS:HD2	1.32	0.93
1:A:432:LEU:HD21	1:A:437:THR:CB	1.97	0.93
1:B:390:THR:HB	1:B:410:LEU:CD1	1.98	0.93
1:E:350:THR:O	1:E:351:LEU:HD23	1.70	0.91
1:A:432:LEU:CD2	1:A:437:THR:HB	1.98	0.91
2:C:34:SER:HB3	2:C:38:GLN:HA	1.52	0.90
1:D:249:ASP:HA	1:D:255:ARG:HG3	1.53	0.90
1:B:346:PRO:HB3	1:B:372:PHE:HB3	1.52	0.90
1:A:275:PHE:HE2	1:A:304:SER:HB3	1.35	0.90
1:B:273:VAL:HG13	1:B:274:LYS:H	1.37	0.89
2:C:18:ARG:NH2	2:C:168:VAL:HG21	1.87	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:338:LYS:HG2	1:E:339:ASP:H	1.37	0.87
1:A:275:PHE:CE2	1:A:304:SER:HB3	2.09	0.87
1:D:240:VAL:HG11	1:D:323:VAL:HG11	1.56	0.86
1:E:346:PRO:CG	1:E:432:LEU:HD11	2.04	0.86
1:D:351:LEU:HD21	1:E:352:PRO:CD	2.06	0.86
1:B:415:SER:O	1:B:419:GLN:HB3	1.75	0.85
1:A:379:VAL:HG21	1:A:406:LEU:HD11	1.59	0.84
2:C:5:LEU:HG	2:C:6:PRO:HD2	1.61	0.83
2:C:20:LEU:HD21	2:C:113:TRP:CD1	2.05	0.83
1:E:242:LEU:HD23	1:E:336:ILE:HB	1.60	0.83
1:B:271:PRO:HB3	1:B:325:ASN:ND2	1.94	0.82
1:B:375:SER:HB3	1:B:404:TYR:HE2	1.44	0.82
2:C:124:LEU:HA	2:C:129:GLY:HA2	1.62	0.82
1:D:353:PRO:HD3	1:D:365:LEU:HD23	1.62	0.81
2:C:19:VAL:HG11	2:C:25:VAL:HG21	1.63	0.81
2:F:72:GLN:HB2	2:F:78:LEU:HD12	1.61	0.81
2:C:32:ALA:HB3	2:C:73:THR:OG1	1.81	0.80
1:A:273:VAL:HG21	1:A:302:VAL:HG21	1.63	0.80
2:C:118:LEU:HD21	2:C:156:GLY:HA3	1.64	0.80
1:E:290:LYS:HB2	1:E:291:PRO:CD	2.10	0.79
1:E:393:THR:HG22	1:E:408:SER:HB2	1.65	0.79
1:D:351:LEU:CD2	1:E:352:PRO:O	2.31	0.78
1:D:284:VAL:HG23	1:D:286:HIS:H	1.47	0.78
2:F:34:SER:O	2:F:36:GLU:N	2.17	0.78
1:D:284:VAL:HG21	1:D:306:LEU:HD11	1.66	0.78
1:A:350:THR:OG1	1:A:441:LEU:HD11	1.85	0.77
2:C:16:TRP:HH2	2:C:107:HIS:CE1	2.03	0.77
2:F:98:TRP:CE2	2:F:168:VAL:HG11	2.19	0.76
1:D:370:LYS:HA	1:D:405:PHE:HB2	1.68	0.76
1:B:375:SER:HB3	1:B:404:TYR:CE2	2.22	0.75
1:A:348:VAL:HG22	1:A:369:VAL:HG22	1.67	0.75
1:D:277:TRP:HE1	1:D:304:SER:HG	1.34	0.75
2:C:21:GLU:HB2	2:C:88:ILE:HD13	1.67	0.75
1:A:258:GLU:HB3	1:A:305:VAL:HG23	1.69	0.74
1:E:277:TRP:CE3	1:E:306:LEU:HD22	2.22	0.74
1:B:373:TYR:HB3	1:B:374:PRO:HD3	1.70	0.74
2:C:146:LEU:HG	2:C:146:LEU:O	1.87	0.74
1:E:381:TRP:HE1	1:E:408:SER:HG	1.32	0.74
1:D:238:PRO:HG2	1:D:325:ASN:HD22	1.52	0.73
1:E:253:ILE:HA	1:E:310:HIS:CE1	2.23	0.73
2:F:20:LEU:O	2:F:22:LYS:N	2.20	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:123:TYR:CE2	2:F:139:PHE:HB2	2.22	0.73
1:B:271:PRO:CB	1:B:325:ASN:HD21	2.02	0.73
1:E:379:VAL:HG23	1:E:427:VAL:HG12	1.70	0.73
1:D:238:PRO:HD3	2:F:134:HIS:CE1	2.23	0.73
1:E:354:SER:O	1:E:356:GLU:N	2.21	0.73
1:A:440:SER:O	1:A:441:LEU:HD12	1.89	0.72
1:A:257:PRO:HG2	1:A:308:VAL:HG12	1.71	0.72
1:A:350:THR:HB	1:A:441:LEU:CD1	2.17	0.72
2:F:17:TYR:HH	2:F:98:TRP:HD1	1.36	0.72
2:F:142:PRO:O	2:F:144:ALA:N	2.23	0.72
1:D:357:GLU:OE2	1:D:364:SER:N	2.23	0.71
1:B:378:VAL:HB	1:B:428:MET:HB2	1.72	0.71
2:F:77:THR:OG1	2:F:78:LEU:N	2.24	0.71
1:B:255:ARG:O	1:B:310:HIS:NE2	2.24	0.71
1:B:240:VAL:HG21	1:B:323:VAL:CG1	2.20	0.70
1:D:238:PRO:CG	1:D:325:ASN:HD22	2.04	0.70
2:C:63:VAL:C	2:C:65:ASN:H	1.94	0.70
1:E:372:PHE:CE1	1:E:404:TYR:HB2	2.27	0.69
2:F:40:THR:HA	2:F:73:THR:HG22	1.73	0.69
1:A:357:GLU:HB2	1:B:349:TYR:CE2	2.26	0.69
1:E:363:VAL:HG22	1:E:364:SER:H	1.57	0.69
2:F:72:GLN:HG3	2:F:77:THR:O	1.92	0.69
1:A:258:GLU:HB3	1:A:305:VAL:CG2	2.22	0.69
1:A:440:SER:C	1:A:441:LEU:HD12	2.13	0.69
1:A:258:GLU:OE1	1:A:305:VAL:CG2	2.31	0.69
1:E:378:VAL:CG1	1:E:428:MET:HB2	2.23	0.69
1:E:371:GLY:HA2	1:E:403:SER:HB3	1.73	0.69
2:C:18:ARG:HG2	2:C:92:LEU:HD11	1.74	0.69
1:B:390:THR:CG2	1:B:410:LEU:HD12	2.22	0.69
1:D:314:LEU:HD22	1:D:430:GLU:OE1	1.92	0.69
1:E:432:LEU:O	1:E:435:HIS:N	2.24	0.68
1:D:360:LYS:NZ	1:E:349:TYR:OH	2.25	0.68
1:B:277:TRP:CG	1:B:306:LEU:HD13	2.29	0.68
1:B:271:PRO:CB	1:B:325:ASN:ND2	2.55	0.68
1:A:290:LYS:HB3	1:A:291:PRO:HD2	1.74	0.68
2:F:112:SER:OG	2:F:115:ASN:HA	1.93	0.68
2:C:16:TRP:CH2	2:C:107:HIS:CE1	2.82	0.68
1:A:308:VAL:HG22	1:A:309:THR:H	1.58	0.68
1:D:398:LEU:O	1:E:392:LYS:NZ	2.24	0.67
1:E:328:LEU:HD22	1:E:332:ILE:HD13	1.74	0.67
1:E:368:LEU:HB2	1:E:407:TYR:CE1	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:248:LYS:HE3	1:D:255:ARG:NH1	2.09	0.67
1:B:415:SER:O	1:B:419:GLN:CB	2.43	0.67
2:C:63:VAL:H	2:C:86:VAL:HG11	1.59	0.67
1:D:354:SER:HB2	1:E:351:LEU:CD2	2.25	0.67
1:A:308:VAL:HG22	1:A:309:THR:N	2.10	0.67
1:D:245:PRO:HB3	1:D:258:GLU:H	1.59	0.67
2:F:27:LEU:O	2:F:55:SER:HA	1.96	0.66
1:D:360:LYS:O	1:D:361[B]:ASN:ND2	2.28	0.66
2:C:42:TRP:HD1	2:C:51:SER:HG	1.42	0.66
1:D:351:LEU:CD2	1:E:352:PRO:HD2	2.15	0.66
2:F:45:ASN:HA	2:F:68:GLU:HB2	1.77	0.66
2:F:145:THR:N	2:F:148:ASP:OD2	2.29	0.66
1:B:346:PRO:HD3	1:B:429:HIS:CD2	2.23	0.66
2:C:19:VAL:CG2	2:C:86:VAL:HG22	2.26	0.65
1:E:247:PRO:HG3	1:E:376:ASP:HB2	1.78	0.65
1:E:271:PRO:O	1:E:292:ARG:NH1	2.28	0.65
1:E:429:HIS:CB	1:E:432:LEU:HD13	2.17	0.65
1:B:238:PRO:HG2	1:B:325:ASN:HD22	1.60	0.65
1:B:271:PRO:CG	1:B:325:ASN:HD21	2.08	0.65
1:E:261:CYS:HB2	1:E:277:TRP:CZ2	2.32	0.65
1:A:373:TYR:O	1:A:429:HIS:NE2	2.28	0.65
1:B:390:THR:HG22	1:B:410:LEU:HD12	1.78	0.65
2:F:7:LYS:HA	2:F:77:THR:OG1	1.97	0.65
2:C:63:VAL:O	2:C:65:ASN:N	2.30	0.65
1:D:248:LYS:HE3	1:D:255:ARG:HH12	1.61	0.64
2:F:17:TYR:OH	2:F:98:TRP:HD1	1.81	0.64
1:B:247:PRO:HG3	1:B:376:ASP:HB2	1.80	0.64
1:B:391:TYR:HA	1:B:409:LYS:O	1.96	0.64
1:B:374:PRO:HG2	1:B:430:GLU:OE2	1.98	0.64
1:E:240:VAL:HG12	1:E:332:ILE:HG21	1.79	0.64
2:C:107:HIS:CD2	2:C:140:TYR:CZ	2.86	0.64
1:E:365:LEU:HD23	1:E:441:LEU:HD11	1.79	0.64
1:E:277:TRP:H	1:E:284:VAL:HG22	1.62	0.64
2:C:103:GLU:HA	2:C:144:ALA:HB3	1.79	0.63
2:C:32:ALA:HB1	2:C:75:LEU:HD23	1.80	0.63
1:B:286:HIS:O	1:B:306:LEU:HD12	1.97	0.63
2:C:40:THR:OG1	2:C:54:SER:HA	1.98	0.63
2:F:18:ARG:HB3	2:F:92:LEU:HD21	1.80	0.63
1:A:378:VAL:HB	1:A:428:MET:HB2	1.79	0.63
2:C:72:GLN:O	2:C:72:GLN:HG2	1.96	0.63
1:E:343:PRO:O	1:E:374:PRO:HD3	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:107:HIS:HD2	2:C:140:TYR:CZ	2.17	0.62
1:E:429:HIS:HB3	1:E:432:LEU:HD11	1.80	0.62
1:D:343:PRO:HA	1:D:373:TYR:O	1.98	0.62
1:A:347:GLN:HG2	1:A:349:TYR:CE1	2.35	0.62
2:C:34:SER:HA	2:C:74:SER:HB3	1.81	0.62
2:C:148:ASP:OD1	2:C:148:ASP:N	2.31	0.62
2:F:91:LEU:CD2	2:F:154:CYS:SG	2.87	0.62
2:C:62:ARG:O	2:C:64:ASN:N	2.32	0.62
1:B:234:LEU:C	1:B:235:LEU:HG	2.20	0.62
2:C:125:GLN:OE1	2:C:130:ARG:HD2	2.00	0.62
1:E:421:ASN:HB2	1:E:423:PHE:HE2	1.64	0.62
2:F:91:LEU:HD23	2:F:154:CYS:SG	2.39	0.62
1:A:257:PRO:C	1:A:308:VAL:HG12	2.20	0.62
1:E:308:VAL:HG21	1:E:319:TYR:OH	2.00	0.62
1:E:240:VAL:HG11	1:E:332:ILE:CG2	2.30	0.61
1:B:293:GLU:O	1:B:301:ARG:N	2.33	0.61
2:F:152:TYR:O	2:F:167:THR:HA	2.00	0.61
1:E:290:LYS:CB	1:E:291:PRO:HD3	2.15	0.61
1:E:291:PRO:O	1:E:292:ARG:HG3	2.00	0.61
1:B:271:PRO:CB	1:B:325:ASN:OD1	2.34	0.61
2:F:18:ARG:HH11	2:F:18:ARG:HG2	1.64	0.61
2:F:19:VAL:CG2	2:F:86:VAL:HG22	2.30	0.61
1:E:350:THR:OG1	1:E:441:LEU:HD23	2.01	0.61
1:A:312:ASP:HB3	1:A:317:LYS:HD2	1.81	0.61
1:E:312:ASP:O	1:E:317:LYS:HD2	1.99	0.61
1:E:355:ARG:O	1:E:357:GLU:N	2.34	0.61
1:B:270:ASP:N	1:B:271:PRO:HD3	2.15	0.61
1:D:373:TYR:CD2	1:D:374:PRO:HA	2.36	0.61
1:A:289:THR:HA	1:A:304:SER:HB2	1.83	0.61
1:A:356:GLU:N	1:A:356:GLU:OE1	2.32	0.61
2:F:92:LEU:HD23	2:F:94:GLN:HG3	1.83	0.61
2:C:43:PHE:CE1	2:C:48:LEU:HD12	2.36	0.60
1:B:300:TYR:H	1:B:300:TYR:HD2	1.48	0.60
1:E:270:ASP:HB2	1:E:326:LYS:HD2	1.81	0.60
1:B:242:LEU:HD23	1:B:336:ILE:HB	1.83	0.60
2:C:45:ASN:O	2:C:46:GLU:HB2	2.01	0.60
1:A:293:GLU:HB2	1:A:301:ARG:O	2.02	0.60
1:D:309:THR:O	1:D:311[A]:GLN:N	2.34	0.60
1:E:242:LEU:HD21	1:E:336:ILE:CG2	2.31	0.60
2:C:94:GLN:OE1	2:C:109:ARG:HD3	2.00	0.60
1:E:381:TRP:NE1	1:E:408:SER:OG	2.23	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:LEU:HD23	1:A:363:VAL:HG11	1.84	0.59
1:E:276:ASN:HB2	1:E:322:LYS:HB3	1.82	0.59
2:F:42:TRP:CD1	2:F:51:SER:HB3	2.37	0.59
1:A:292:ARG:HB3	1:A:300:TYR:CD2	2.36	0.59
1:A:383:SER:O	1:A:385:GLY:N	2.35	0.59
1:B:273:VAL:CG1	1:B:274:LYS:H	2.14	0.59
1:D:297:ASN:OD1	1:D:299:THR:HG22	2.02	0.59
1:E:278:TYR:HD1	1:E:282:ALA:H	1.50	0.59
1:E:396:PRO:HG3	1:E:406:LEU:HD12	1.84	0.59
1:B:390:THR:HB	1:B:410:LEU:HD12	1.83	0.59
2:C:19:VAL:HG11	2:C:25:VAL:CG2	2.32	0.59
1:E:240:VAL:CG1	1:E:332:ILE:CG2	2.81	0.59
2:F:6:PRO:O	2:F:77:THR:N	2.32	0.59
1:B:242:LEU:HD12	1:B:321:CYS:SG	2.42	0.59
1:B:414:LYS:NZ	1:B:418:GLN:OE1	2.35	0.59
1:B:278:TYR:HA	1:B:282:ALA:HB3	1.84	0.59
1:B:398:LEU:HD23	1:B:399:ASP:O	2.03	0.59
1:E:246:LYS:HZ3	1:E:248:LYS:H	1.49	0.59
1:A:432:LEU:HD21	1:A:437:THR:CG2	2.33	0.59
1:D:360:LYS:C	1:D:361[B]:ASN:HD22	2.07	0.59
1:E:275:PHE:CE2	1:E:304:SER:HB2	2.37	0.58
1:B:311:GLN:O	1:B:315:ASN:ND2	2.37	0.58
1:B:346:PRO:CB	1:B:372:PHE:HB3	2.31	0.58
2:C:106:ILE:HB	2:C:141:ILE:HG23	1.84	0.58
1:E:268:GLN:HG2	1:E:269:GLU:OE2	2.03	0.58
2:C:20:LEU:HB2	2:C:23:ASP:OD2	2.02	0.58
1:D:248:LYS:O	1:D:255:ARG:HD3	2.02	0.58
1:D:346:PRO:HD3	1:D:429:HIS:HD2	1.67	0.58
1:A:344:ARG:HH11	1:A:345:GLU:H	1.50	0.58
2:C:32:ALA:HB1	2:C:75:LEU:CD2	2.33	0.58
2:C:149:SER:HA	2:C:170:ILE:O	2.03	0.58
1:E:351:LEU:HD23	1:E:351:LEU:N	2.09	0.58
1:E:369:VAL:HG23	1:E:372:PHE:HE2	1.69	0.58
2:F:124:LEU:HG	2:F:129:GLY:HA2	1.85	0.58
1:D:378:VAL:CG1	1:D:428:MET:HB2	2.34	0.58
1:B:243:PHE:HE2	1:B:262:VAL:HG21	1.68	0.57
1:B:390:THR:CB	1:B:410:LEU:HD12	2.34	0.57
1:A:277:TRP:HD1	1:A:287:ALA:CB	2.17	0.57
1:A:346:PRO:HB3	1:A:372:PHE:HB3	1.85	0.57
2:C:23:ASP:OD2	2:C:111:HIS:NE2	2.37	0.57
1:D:351:LEU:HD12	1:D:352:PRO:N	2.17	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:373:TYR:C	1:A:429:HIS:HE2	2.08	0.57
1:E:275:PHE:CD2	1:E:304:SER:HB2	2.40	0.57
2:F:72:GLN:O	2:F:73:THR:HG23	2.05	0.57
2:C:34:SER:OG	2:C:74:SER:HB2	2.04	0.57
1:A:257:PRO:CG	1:A:308:VAL:CG1	2.77	0.57
1:D:309:THR:O	1:D:311[B]:GLN:N	2.37	0.57
1:A:242:LEU:HG	1:A:336:ILE:HG12	1.87	0.56
2:C:141:ILE:HD11	2:C:145:THR:CG2	2.35	0.56
1:D:253:ILE:HA	1:D:310:HIS:CD2	2.40	0.56
1:E:346:PRO:CD	1:E:432:LEU:HD11	2.35	0.56
1:A:432:LEU:HD23	1:A:437:THR:N	2.21	0.56
1:A:248:LYS:NZ	1:A:380:GLU:OE2	2.31	0.56
2:C:93:LEU:HD12	2:C:109:ARG:O	2.06	0.56
2:F:121:VAL:HG21	2:F:136:ASN:HA	1.87	0.56
1:E:332:ILE:HG22	1:E:332:ILE:O	2.04	0.56
1:E:277:TRP:H	1:E:284:VAL:CG2	2.18	0.56
1:A:427:VAL:HG22	1:A:437:THR:HG22	1.87	0.56
2:C:72:GLN:NE2	2:C:77:THR:O	2.35	0.56
1:B:374:PRO:O	1:B:429:HIS:HE1	1.89	0.56
1:E:343:PRO:O	1:E:344:ARG:HB2	2.06	0.56
1:A:235:LEU:HA	2:C:119:HIS:CD2	2.41	0.56
1:A:355:ARG:HA	1:A:358:LEU:HD12	1.88	0.55
1:B:237:GLY:O	2:C:161:LYS:HD2	2.06	0.55
1:B:388:GLU:OE1	1:B:388:GLU:N	2.30	0.55
2:F:40:THR:O	2:F:72:GLN:O	2.24	0.55
1:A:282:ALA:O	1:A:284:VAL:HG13	2.06	0.55
2:C:27:LEU:O	2:C:55:SER:HA	2.06	0.55
1:E:240:VAL:HG11	1:E:332:ILE:HG22	1.88	0.55
2:C:42:TRP:HD1	2:C:51:SER:OG	1.88	0.55
1:E:338:LYS:HG2	1:E:339:ASP:N	2.15	0.55
1:D:297:ASN:OD1	1:D:297:ASN:N	2.38	0.55
1:D:424:SER:HB3	1:D:438:GLN:HE21	1.72	0.55
1:A:391:TYR:HB3	1:A:410:LEU:HB2	1.89	0.55
2:C:148:ASP:HB2	2:C:170:ILE:HD11	1.88	0.55
1:A:347:GLN:HG2	1:A:349:TYR:CZ	2.43	0.54
2:C:88:ILE:HD12	2:C:89:GLY:H	1.70	0.54
1:E:374:PRO:HB2	1:E:429:HIS:CE1	2.42	0.54
4:I:2:NAG:H3	4:I:2:NAG:H83	1.89	0.54
2:C:71:CYS:N	2:C:79:SER:OG	2.31	0.54
2:C:108:LEU:O	2:C:138:ASP:HB3	2.07	0.54
1:B:264:VAL:HG12	1:B:301:ARG:HG3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:ASN:HB3	1:B:328:LEU:HD12	1.88	0.54
1:B:367:CYS:HB2	1:B:381:TRP:CZ2	2.42	0.54
1:D:422:VAL:HG12	1:D:442:SER:HB2	1.89	0.54
1:E:353:PRO:HB3	1:E:363:VAL:CG2	2.38	0.54
2:F:103:GLU:HG3	2:F:143:LYS:HE3	1.90	0.54
2:C:51:SER:OG	2:C:52:GLN:N	2.40	0.54
2:C:130:ARG:NH1	2:C:152:TYR:OH	2.40	0.54
1:D:240:VAL:HG11	1:D:323:VAL:CG1	2.33	0.54
1:B:390:THR:CB	1:B:410:LEU:CD1	2.79	0.54
2:C:125:GLN:HG3	2:C:152:TYR:HE1	1.72	0.54
1:D:264:VAL:HG21	3:J:1:NAG:O4	2.07	0.54
2:C:128:LYS:NZ	2:C:129:GLY:O	2.40	0.54
1:E:310:HIS:O	1:E:312:ASP:N	2.37	0.54
1:B:363:VAL:O	1:B:411:THR:HA	2.07	0.54
1:D:244:PRO:HB2	1:D:245:PRO:HD2	1.90	0.54
1:E:240:VAL:CG1	1:E:332:ILE:HG21	2.38	0.53
1:B:271:PRO:HB3	1:B:325:ASN:HD21	1.66	0.53
2:C:101:LYS:HG3	2:C:102:GLU:H	1.73	0.53
1:A:345:GLU:HG3	1:A:431:ALA:O	2.08	0.53
2:F:20:LEU:C	2:F:22:LYS:H	2.10	0.53
2:F:98:TRP:CD2	2:F:168:VAL:HG11	2.43	0.53
1:A:280:ASN:ND2	1:A:318:GLU:H	2.07	0.53
1:B:299:THR:O	1:B:299:THR:OG1	2.24	0.53
6:C:202:NAG:O7	6:C:202:NAG:O3	2.18	0.53
1:B:248:LYS:HB3	1:B:255:ARG:NH1	2.24	0.53
1:A:398:LEU:O	1:B:392:LYS:HE2	2.08	0.53
2:C:141:ILE:HD11	2:C:145:THR:HG23	1.89	0.53
1:E:273:VAL:HG12	1:E:274:LYS:N	2.24	0.53
1:A:383:SER:HG	1:A:423:PHE:HE1	1.55	0.53
1:E:393:THR:HG22	1:E:408:SER:CB	2.38	0.53
2:C:6:PRO:O	2:C:76:SER:HA	2.09	0.53
2:C:107:HIS:CD2	2:C:140:TYR:CE1	2.97	0.53
2:C:126:ASN:O	2:C:126:ASN:ND2	2.41	0.53
2:F:42:TRP:HD1	2:F:51:SER:HB3	1.74	0.53
3:H:2:NAG:H3	3:H:2:NAG:H83	1.91	0.53
1:B:301:ARG:NE	3:H:2:NAG:O7	2.41	0.53
2:F:20:LEU:HA	2:F:87:HIS:O	2.09	0.52
1:A:378:VAL:O	1:A:427:VAL:HA	2.10	0.52
2:F:18:ARG:HG2	2:F:18:ARG:NH1	2.24	0.52
2:C:72:GLN:HB2	2:C:78:LEU:HA	1.91	0.52
1:E:294:THR:O	1:E:295:GLN:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:18:ARG:HH12	2:F:87:HIS:HE1	1.57	0.52
1:E:245:PRO:HD2	1:E:313:TRP:CZ2	2.44	0.52
2:C:125:GLN:HA	2:C:152:TYR:CE1	2.45	0.52
1:E:429:HIS:O	1:E:431:ALA:N	2.43	0.52
2:C:7:LYS:HA	2:C:77:THR:OG1	2.10	0.52
2:C:53:THR:HG23	2:C:55:SER:H	1.73	0.52
1:B:375:SER:OG	1:B:376:ASP:N	2.43	0.52
1:E:253:ILE:HA	1:E:310:HIS:HE1	1.74	0.52
1:A:313:TRP:CZ2	1:A:338:LYS:HB2	2.45	0.52
1:A:413:ASP:HB2	1:A:416:ARG:HB2	1.90	0.52
1:D:249:ASP:HA	1:D:255:ARG:CG	2.34	0.52
2:F:14:PRO:HG3	2:F:25:VAL:HA	1.91	0.52
2:C:43:PHE:HB2	2:C:70:ARG:HB2	1.91	0.52
2:C:113:TRP:CE3	2:C:114:LYS:HB2	2.45	0.52
1:D:334:LYS:NZ	3:J:5:NAG:O7	2.37	0.52
1:B:429:HIS:O	1:B:432:LEU:HB2	2.10	0.51
2:C:20:LEU:HD22	2:C:113:TRP:HA	1.91	0.51
1:A:284:VAL:HG23	1:A:284:VAL:O	2.10	0.51
2:C:101:LYS:HG3	2:C:102:GLU:OE1	2.10	0.51
1:E:278:TYR:HE2	1:E:322:LYS:HD2	1.74	0.51
1:A:284:VAL:HB	1:A:286:HIS:CE1	2.46	0.51
1:B:313:TRP:O	1:B:315:ASN:N	2.42	0.51
2:C:63:VAL:HG13	4:I:2:NAG:H2	1.92	0.51
1:E:346:PRO:CD	1:E:432:LEU:CD1	2.88	0.51
1:E:369:VAL:HG22	1:E:406:LEU:HB3	1.91	0.51
2:F:66:SER:OG	2:F:86:VAL:HB	2.09	0.51
1:D:279:VAL:HG12	1:D:284:VAL:CG1	2.41	0.51
2:F:110:CYS:HB2	2:F:123:TYR:CE1	2.45	0.51
1:A:432:LEU:CD2	1:A:437:THR:CB	2.76	0.51
1:B:432:LEU:HD11	1:B:437:THR:HG22	1.92	0.51
2:C:118:LEU:CD2	2:C:156:GLY:HA3	2.40	0.51
1:A:253:ILE:HA	1:A:310:HIS:CE1	2.45	0.51
1:A:297:ASN:O	1:A:299:THR:N	2.36	0.51
1:B:255:ARG:O	1:B:257:PRO:HD3	2.11	0.51
2:C:20:LEU:CD2	2:C:113:TRP:CG	2.86	0.51
2:C:107:HIS:HD2	2:C:140:TYR:CE1	2.29	0.51
2:C:153:PHE:HB2	2:C:165:SER:OG	2.10	0.51
1:D:261:CYS:HB2	1:D:277:TRP:CZ2	2.45	0.51
1:D:263:VAL:HB	1:D:302:VAL:HG12	1.92	0.51
1:D:289:THR:HA	1:D:304:SER:HA	1.91	0.51
2:F:43:PHE:HB3	2:F:47:SER:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:LYS:HB3	1:B:291:PRO:CD	2.41	0.51
1:E:289:THR:O	1:E:289:THR:OG1	2.28	0.51
1:E:329:PRO:HB3	2:F:113:TRP:CD2	2.46	0.51
1:D:326:LYS:O	1:D:326:LYS:HG2	2.11	0.50
2:F:118:LEU:HD23	2:F:121:VAL:HG22	1.92	0.50
1:A:394:THR:HG21	1:B:394:THR:CG2	2.42	0.50
2:C:18:ARG:HD2	2:C:87:HIS:CE1	2.46	0.50
1:A:357:GLU:CD	1:B:349:TYR:HE2	2.14	0.50
1:D:257:PRO:HD3	1:D:310:HIS:CE1	2.45	0.50
1:E:368:LEU:HB2	1:E:407:TYR:CD1	2.47	0.50
1:B:358:LEU:HD23	1:B:363:VAL:HG11	1.93	0.50
1:B:368:LEU:HD13	1:B:407:TYR:CZ	2.47	0.50
1:D:249:ASP:O	1:D:257:PRO:HG3	2.11	0.50
1:A:277:TRP:HD1	1:A:287:ALA:HB1	1.75	0.50
1:A:319:TYR:N	1:A:319:TYR:HD1	2.10	0.50
1:A:308:VAL:CG2	1:A:319:TYR:HE2	2.25	0.50
1:B:308:VAL:HG13	1:B:319:TYR:OH	2.12	0.50
1:B:277:TRP:HH2	1:B:304:SER:HB3	1.76	0.50
1:E:426:SER:HB2	1:E:436:TYR:CE1	2.47	0.50
2:F:98:TRP:HE3	2:F:170:ILE:HG12	1.77	0.50
2:C:34:SER:OG	2:C:74:SER:CB	2.59	0.50
1:E:378:VAL:HG12	1:E:428:MET:HB2	1.93	0.50
2:F:42:TRP:CZ3	2:F:71:CYS:HB3	2.47	0.50
2:F:91:LEU:HD23	2:F:110:CYS:SG	2.50	0.50
1:D:368:LEU:HD13	1:D:407:TYR:CE2	2.46	0.49
1:A:257:PRO:CG	1:A:308:VAL:HG13	2.31	0.49
1:A:319:TYR:N	1:A:319:TYR:CD1	2.80	0.49
1:A:356:GLU:H	1:A:356:GLU:CD	2.15	0.49
1:A:379:VAL:HG13	1:A:427:VAL:HG12	1.94	0.49
1:D:238:PRO:HG2	1:D:325:ASN:ND2	2.23	0.49
1:E:348:VAL:HG23	1:E:439:LYS:HD2	1.93	0.49
1:B:292:ARG:HB2	1:B:300:TYR:HB3	1.94	0.49
1:D:278:TYR:CE1	1:D:283:GLU:HB3	2.48	0.49
2:C:68:GLU:HB2	2:C:83:GLN:OE1	2.13	0.49
2:F:5:LEU:O	2:F:77:THR:HG23	2.13	0.49
2:F:17:TYR:OH	2:F:98:TRP:CD1	2.59	0.49
1:A:297:ASN:OD1	1:A:299:THR:HG22	2.12	0.49
1:D:369:VAL:HG11	1:D:377:ILE:CD1	2.42	0.49
1:D:416:ARG:O	1:D:421:ASN:HB2	2.13	0.49
1:D:358:LEU:HD23	1:D:363:VAL:HG11	1.95	0.48
1:D:378:VAL:HG12	1:D:428:MET:HB2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:PRO:CG	1:A:308:VAL:HG12	2.42	0.48
1:A:401:ASP:OD1	1:A:403:SER:N	2.44	0.48
2:C:40:THR:HG22	2:C:40:THR:O	2.12	0.48
2:C:63:VAL:C	2:C:65:ASN:N	2.65	0.48
2:F:23:ASP:O	2:F:61:ALA:HB2	2.13	0.48
2:F:123:TYR:HD2	2:F:139:PHE:HD2	1.61	0.48
1:A:265:ASP:OD2	2:C:120:LYS:NZ	2.33	0.48
1:B:375:SER:O	1:B:377:ILE:N	2.46	0.48
1:A:292:ARG:HD3	1:A:302:VAL:CG1	2.43	0.48
1:B:372:PHE:HB2	1:B:429:HIS:NE2	2.29	0.48
1:E:374:PRO:O	1:E:429:HIS:HE1	1.96	0.48
1:A:263:VAL:HB	1:A:302:VAL:HG23	1.95	0.48
1:D:289:THR:HG22	1:D:304:SER:HB2	1.95	0.48
2:F:12:LEU:HD11	2:F:82:VAL:HG11	1.96	0.48
3:K:2:NAG:H3	3:K:2:NAG:H83	1.95	0.48
1:A:308:VAL:HG23	1:A:319:TYR:HE2	1.77	0.48
1:A:356:GLU:O	1:A:359:THR:OG1	2.25	0.48
1:B:324:SER:HB2	1:B:331:PRO:HG3	1.94	0.48
1:D:415:SER:OG	1:D:416:ARG:N	2.46	0.48
1:E:261:CYS:HB2	1:E:277:TRP:HZ2	1.78	0.48
2:C:158:VAL:HG23	2:C:163:VAL:HG21	1.96	0.48
2:F:32:ALA:CB	2:F:73:THR:OG1	2.62	0.48
1:A:290:LYS:HB3	1:A:291:PRO:CD	2.43	0.48
1:B:422:VAL:HG23	1:B:442:SER:HB2	1.94	0.48
2:C:16:TRP:CH2	2:C:107:HIS:HE1	2.29	0.48
1:D:394:THR:HG21	1:E:394:THR:HG22	1.96	0.48
5:L:2:NAG:H83	5:L:2:NAG:H3	1.95	0.48
1:A:262:VAL:HG22	1:A:303:VAL:HG22	1.96	0.48
1:A:308:VAL:CG2	1:A:319:TYR:CE2	2.96	0.48
2:F:57:PHE:O	2:F:58:ILE:HG13	2.14	0.48
2:F:123:TYR:CD2	2:F:139:PHE:HB2	2.48	0.48
1:B:390:THR:HG22	1:B:411:THR:H	1.79	0.47
1:D:316:GLY:CA	1:D:340:LYS:NZ	2.77	0.47
1:D:345:GLU:HG3	1:D:431:ALA:O	2.13	0.47
1:D:436:TYR:HE2	1:D:438:GLN:HB2	1.79	0.47
1:E:250:THR:O	1:E:250:THR:OG1	2.30	0.47
1:E:278:TYR:O	1:E:319:TYR:HA	2.14	0.47
1:E:372:PHE:CD1	1:E:404:TYR:HB2	2.49	0.47
2:F:106:ILE:HB	2:F:141:ILE:HB	1.96	0.47
1:A:258:GLU:CB	1:A:305:VAL:HG23	2.43	0.47
1:D:279:VAL:HG12	1:D:284:VAL:HG12	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:8:ALA:HB2	2:C:76:SER:OG	2.13	0.47
1:D:430:GLU:O	1:D:430:GLU:HG3	2.14	0.47
1:E:381:TRP:CD1	1:E:391:TYR:CD2	3.02	0.47
1:B:277:TRP:HH2	1:B:304:SER:CB	2.28	0.47
2:C:23:ASP:CG	2:C:111:HIS:HE2	2.18	0.47
1:A:272:ASP:HA	1:A:292:ARG:NH2	2.29	0.47
1:D:301:ARG:HH21	3:J:2:NAG:H81	1.79	0.47
1:B:243:PHE:CE2	1:B:262:VAL:HG21	2.49	0.47
2:C:132:TYR:CE2	2:C:134:HIS:CD2	3.03	0.47
1:D:297:ASN:C	1:D:299:THR:H	2.17	0.47
1:E:358:LEU:O	1:E:414:LYS:NZ	2.37	0.47
1:E:371:GLY:CA	1:E:403:SER:HB3	2.43	0.47
1:E:374:PRO:HD2	1:E:429:HIS:NE2	2.29	0.47
2:F:98:TRP:CZ2	2:F:168:VAL:HG11	2.50	0.47
1:A:258:GLU:CB	1:A:305:VAL:CG2	2.92	0.47
1:A:275:PHE:CD1	1:A:323:VAL:HG22	2.50	0.47
1:B:381:TRP:HD1	1:B:391:TYR:CD1	2.33	0.47
1:B:242:LEU:CD2	1:B:336:ILE:HB	2.45	0.47
1:B:248:LYS:HB3	1:B:255:ARG:HH11	1.80	0.47
2:C:72:GLN:HG3	2:C:77:THR:O	2.14	0.47
2:C:124:LEU:HD21	2:C:155:ARG:NH2	2.29	0.47
1:D:346:PRO:HD3	1:D:429:HIS:CD2	2.47	0.47
1:E:257:PRO:HG2	1:E:308:VAL:O	2.15	0.47
1:E:278:TYR:CE2	1:E:322:LYS:HD2	2.50	0.47
2:F:123:TYR:CE2	2:F:139:PHE:CB	2.94	0.47
1:A:346:PRO:HD2	1:A:432:LEU:HD13	1.97	0.47
1:A:410:LEU:CD2	1:A:412:VAL:HG13	2.44	0.47
1:B:417:TRP:CE2	1:B:443:VAL:HG22	2.50	0.46
1:D:244:PRO:HB2	1:D:245:PRO:CD	2.44	0.46
1:E:308:VAL:HG22	1:E:309:THR:N	2.29	0.46
1:D:409:LYS:HB2	1:E:407:TYR:OH	2.15	0.46
1:E:365:LEU:CD2	1:E:441:LEU:HD11	2.43	0.46
1:E:370:LYS:HE2	1:E:370:LYS:HB2	1.74	0.46
2:F:40:THR:HG23	2:F:73:THR:CG2	2.45	0.46
1:B:343:PRO:HA	1:B:373:TYR:HB3	1.97	0.46
1:B:394:THR:OG1	1:B:407:TYR:O	2.30	0.46
1:B:414:LYS:O	1:B:417:TRP:N	2.48	0.46
2:C:40:THR:O	2:C:41:ARG:O	2.33	0.46
1:D:270:ASP:N	1:D:271:PRO:HD3	2.31	0.46
1:A:341:GLY:O	1:A:343:PRO:HD3	2.15	0.46
1:E:383:SER:O	1:E:385:GLY:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:PRO:HB2	1:B:245:PRO:HD2	1.97	0.46
1:E:369:VAL:HG23	1:E:372:PHE:CE2	2.50	0.46
2:C:63:VAL:HG11	4:I:2:NAG:H4	1.97	0.46
1:D:393:THR:OG1	1:D:408:SER:OG	2.28	0.46
1:E:286:HIS:CG	1:E:307:THR:HG22	2.51	0.46
2:F:101:LYS:HB2	2:F:171:THR:C	2.36	0.46
1:A:243:PHE:O	1:A:259:VAL:HG23	2.16	0.46
2:F:94:GLN:OE1	2:F:111:HIS:HB2	2.16	0.46
1:B:270:ASP:N	1:B:270:ASP:OD1	2.48	0.46
2:C:28:LYS:HD3	2:C:55:SER:HB3	1.97	0.46
1:E:338:LYS:CG	1:E:339:ASP:H	2.12	0.46
1:E:343:PRO:HB3	1:E:431:ALA:HB2	1.98	0.46
2:F:32:ALA:HB2	2:F:76:SER:HB3	1.96	0.46
1:A:345:GLU:HG2	1:A:346:PRO:HD2	1.98	0.46
1:D:255:ARG:H	1:D:255:ARG:HG2	1.50	0.46
2:F:72:GLN:HB2	2:F:78:LEU:CD1	2.40	0.46
1:A:346:PRO:HB3	1:A:372:PHE:CB	2.46	0.45
1:B:290:LYS:HB3	1:B:291:PRO:HD2	1.98	0.45
1:E:374:PRO:HB2	1:E:429:HIS:HE1	1.81	0.45
2:F:18:ARG:NH1	2:F:87:HIS:HE1	2.14	0.45
2:C:70:ARG:HD3	2:C:78:LEU:HD21	1.98	0.45
1:A:308:VAL:HG23	1:A:319:TYR:CE2	2.50	0.45
2:C:91:LEU:HD21	2:C:118:LEU:HD11	1.99	0.45
1:B:240:VAL:CG2	1:B:323:VAL:HG11	2.31	0.45
1:B:341:GLY:O	1:B:343:PRO:HD3	2.16	0.45
1:E:264:VAL:HG11	3:K:2:NAG:H2	1.98	0.45
1:D:373:TYR:CD2	1:D:373:TYR:C	2.90	0.45
1:E:308:VAL:HG21	1:E:319:TYR:CZ	2.51	0.45
1:E:367:CYS:O	1:E:407:TYR:HA	2.17	0.45
2:F:32:ALA:O	2:F:33:TYR:HB2	2.16	0.45
2:C:18:ARG:HG3	2:C:87:HIS:CE1	2.52	0.45
1:E:284:VAL:HG12	1:E:284:VAL:O	2.17	0.45
1:A:357:GLU:CG	1:B:349:TYR:CE2	3.00	0.45
1:B:354:SER:HB3	1:B:357:GLU:HB2	1.97	0.45
1:D:238:PRO:HD3	2:F:134:HIS:ND1	2.31	0.45
2:C:98:TRP:N	2:C:98:TRP:CE3	2.85	0.45
1:D:373:TYR:HA	1:D:374:PRO:O	2.17	0.45
1:E:429:HIS:C	1:E:431:ALA:H	2.20	0.45
1:A:305:VAL:HG13	1:A:305:VAL:O	2.17	0.44
1:E:247:PRO:HA	1:E:250:THR:HG22	1.99	0.44
1:E:351:LEU:O	1:E:441:LEU:HD22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:353:PRO:HB3	1:E:363:VAL:HG21	2.00	0.44
2:F:122:THR:HG23	2:F:131:LYS:O	2.17	0.44
1:A:252:MET:CE	1:A:255:ARG:HD2	2.48	0.44
1:D:346:PRO:O	1:D:348:VAL:HG23	2.18	0.44
2:F:123:TYR:HE2	2:F:139:PHE:CB	2.31	0.44
1:A:275:PHE:HE2	1:A:304:SER:CB	2.19	0.44
1:A:349:TYR:CE1	1:B:357:GLU:HG3	2.52	0.44
1:B:373:TYR:O	1:B:375:SER:N	2.50	0.44
1:E:273:VAL:O	1:E:324:SER:O	2.36	0.44
1:A:296:TYR:C	1:A:298:SER:H	2.21	0.44
2:F:72:GLN:HG2	2:F:73:THR:N	2.33	0.44
1:A:247:PRO:HA	1:A:250:THR:HG22	2.00	0.44
1:A:349:TYR:CZ	1:B:357:GLU:HG3	2.53	0.44
1:A:349:TYR:CD1	1:B:357:GLU:HG3	2.53	0.44
2:C:106:ILE:HB	2:C:141:ILE:CG2	2.48	0.44
1:D:273:VAL:HG13	1:D:323:VAL:HG23	2.00	0.44
1:B:314:LEU:HA	1:B:338:LYS:CE	2.48	0.44
1:D:247:PRO:HB3	1:D:376:ASP:HB3	2.00	0.44
1:D:312:ASP:HB3	1:D:319:TYR:OH	2.17	0.44
2:F:149:SER:HA	2:F:170:ILE:O	2.18	0.44
1:A:353:PRO:HG3	1:A:365:LEU:HD12	2.00	0.44
1:B:355:ARG:HB3	1:B:355:ARG:CZ	2.47	0.44
2:C:5:LEU:HD12	2:C:5:LEU:HA	1.88	0.44
2:C:42:TRP:CD1	2:C:51:SER:OG	2.64	0.44
1:E:287:ALA:O	1:E:288:GLN:HB2	2.18	0.44
1:E:328:LEU:HB3	1:E:330:ALA:O	2.18	0.44
1:E:369:VAL:HG11	1:E:427:VAL:HG11	2.00	0.44
1:B:391:TYR:HB3	1:B:410:LEU:HD13	2.00	0.44
1:D:366:THR:HG22	1:E:407:TYR:OH	2.17	0.44
1:A:357:GLU:CG	1:B:349:TYR:HE2	2.31	0.43
2:C:43:PHE:CE1	2:C:48:LEU:CD1	3.01	0.43
1:D:284:VAL:O	1:D:285:HIS:HB2	2.18	0.43
1:D:372:PHE:HB2	1:D:429:HIS:NE2	2.33	0.43
1:E:369:VAL:CG2	1:E:406:LEU:HB3	2.48	0.43
1:B:271:PRO:HG2	1:B:325:ASN:HD21	1.81	0.43
1:B:351:LEU:HD23	1:B:351:LEU:HA	1.82	0.43
1:D:316:GLY:CA	1:D:340:LYS:HZ2	2.31	0.43
1:D:369:VAL:HG11	1:D:377:ILE:HD11	2.00	0.43
1:D:422:VAL:HG12	1:D:442:SER:CB	2.48	0.43
2:F:19:VAL:HG23	2:F:86:VAL:HG22	1.99	0.43
1:B:267:SER:OG	1:B:268:GLN:N	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:LEU:HD11	1:B:423:PHE:CD2	2.53	0.43
2:C:130:ARG:HH22	2:C:145:THR:HG21	1.83	0.43
1:E:251:LEU:HG	1:E:435:HIS:ND1	2.34	0.43
1:A:297:ASN:C	1:A:299:THR:H	2.20	0.43
1:A:372:PHE:CE2	1:A:377:ILE:HD13	2.53	0.43
1:B:270:ASP:N	1:B:271:PRO:CD	2.79	0.43
1:D:248:LYS:O	1:D:252:MET:HG2	2.19	0.43
1:D:314:LEU:CD2	1:D:430:GLU:OE1	2.64	0.43
1:D:351:LEU:CD1	1:D:352:PRO:HD3	2.27	0.43
2:F:106:ILE:HD12	2:F:144:ALA:HB2	2.00	0.43
1:E:289:THR:HB	1:E:303:VAL:O	2.18	0.43
2:F:33:TYR:O	2:F:34:SER:C	2.57	0.43
1:B:249:ASP:O	1:B:257:PRO:HB3	2.18	0.43
2:C:91:LEU:CD2	2:C:118:LEU:HD11	2.49	0.43
2:C:93:LEU:HD23	2:C:152:TYR:O	2.19	0.43
2:C:13:GLU:HA	2:C:13:GLU:OE1	2.18	0.43
2:C:16:TRP:CE3	2:C:94:GLN:HB3	2.53	0.43
2:C:118:LEU:HD23	2:C:121:VAL:HG22	2.00	0.43
1:D:240:VAL:HG23	1:D:334:LYS:HD2	2.01	0.43
1:D:328:LEU:HD23	1:D:328:LEU:HA	1.88	0.43
1:E:347:GLN:HA	1:E:347:GLN:OE1	2.18	0.43
1:E:348:VAL:HG12	1:E:369:VAL:HG12	2.01	0.43
2:F:19:VAL:HB	2:F:23:ASP:HB2	1.99	0.43
2:F:40:THR:HG23	2:F:73:THR:HG22	2.01	0.43
2:C:42:TRP:CZ3	2:C:71:CYS:HB3	2.53	0.43
1:A:357:GLU:CB	1:B:349:TYR:CE2	2.99	0.43
1:D:349:TYR:HB3	1:E:354:SER:CB	2.48	0.42
1:E:348:VAL:O	1:E:439:LYS:HD2	2.19	0.42
2:C:22:LYS:HD3	2:C:22:LYS:HA	1.75	0.42
2:C:88:ILE:HD12	2:C:89:GLY:N	2.32	0.42
1:D:271:PRO:O	1:D:273:VAL:HG23	2.18	0.42
1:A:357:GLU:OE2	1:A:364:SER:N	2.52	0.42
2:C:29:CYS:HB3	2:C:40:THR:HG21	2.01	0.42
1:D:249:ASP:HB3	1:D:257:PRO:HA	2.00	0.42
1:E:346:PRO:HD3	1:E:432:LEU:CD1	2.49	0.42
2:F:106:ILE:HG22	2:F:107:HIS:N	2.34	0.42
1:A:368:LEU:HD12	1:A:369:VAL:N	2.34	0.42
2:C:91:LEU:HD13	2:C:110:CYS:SG	2.59	0.42
2:C:151:SER:OG	2:C:167:THR:HB	2.19	0.42
1:E:351:LEU:HB2	1:E:366:THR:HB	2.01	0.42
1:E:371:GLY:HA2	1:E:403:SER:CB	2.45	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:TRP:HD1	1:A:287:ALA:HB2	1.83	0.42
2:C:40:THR:HA	2:C:73:THR:HA	2.02	0.42
2:C:112:SER:OG	2:C:113:TRP:N	2.52	0.42
1:B:325:ASN:C	1:B:327:ALA:H	2.23	0.42
1:D:265:ASP:HA	1:D:299:THR:OG1	2.19	0.42
1:E:329:PRO:HB3	2:F:113:TRP:CE2	2.54	0.42
2:F:14:PRO:HG2	2:F:25:VAL:HG13	2.02	0.42
1:B:296:TYR:HD2	1:B:297:ASN:N	2.17	0.42
2:C:77:THR:OG1	2:C:78:LEU:N	2.51	0.42
2:C:101:LYS:CG	2:C:102:GLU:H	2.32	0.42
1:E:312:ASP:HB2	1:E:317:LYS:CD	2.49	0.42
1:A:263:VAL:HB	1:A:302:VAL:CG2	2.49	0.41
1:B:288:GLN:OE1	1:B:288:GLN:HA	2.20	0.41
2:C:71:CYS:H	2:C:79:SER:CB	2.32	0.41
2:C:131:LYS:HE3	2:C:131:LYS:HB2	1.93	0.41
1:D:375:SER:HA	1:D:404:TYR:CD2	2.55	0.41
2:F:34:SER:HB3	2:F:74:SER:HB2	2.01	0.41
2:F:94:GLN:OE1	2:F:109:ARG:NH1	2.53	0.41
1:A:272:ASP:HA	1:A:292:ARG:HH21	1.85	0.41
1:D:328:LEU:HD21	1:D:332:ILE:HD11	2.01	0.41
1:E:361:ASN:OD1	1:E:361:ASN:N	2.47	0.41
2:F:7:LYS:HE2	2:F:80:ASP:OD1	2.20	0.41
1:B:240:VAL:HG22	1:B:263:VAL:HB	2.01	0.41
1:D:394:THR:HG21	1:E:394:THR:CG2	2.50	0.41
1:D:413:ASP:OD1	1:D:413:ASP:N	2.53	0.41
2:F:131:LYS:HD3	2:F:131:LYS:HA	1.80	0.41
2:C:118:LEU:CD2	2:C:121:VAL:HG22	2.50	0.41
1:D:292:ARG:HH11	1:D:300:TYR:HE2	1.66	0.41
2:F:14:PRO:HG3	2:F:25:VAL:HG22	2.02	0.41
1:B:278:TYR:HD2	1:B:320:THR:OG1	2.04	0.41
1:D:269:GLU:OE1	1:D:269:GLU:HA	2.20	0.41
1:D:432:LEU:HA	1:D:432:LEU:HD23	1.78	0.41
1:E:249:ASP:OD1	1:E:255:ARG:HB3	2.20	0.41
2:F:122:THR:HA	2:F:131:LYS:O	2.20	0.41
2:F:146:LEU:O	2:F:146:LEU:HD23	2.20	0.41
1:A:270:ASP:N	1:A:271:PRO:HD3	2.35	0.41
1:B:379:VAL:HG22	1:B:427:VAL:HG22	2.02	0.41
1:D:238:PRO:CG	1:D:325:ASN:ND2	2.80	0.41
1:D:336:ILE:HD12	1:D:337:SER:H	1.86	0.41
1:D:384:SER:OG	1:D:385:GLY:N	2.51	0.41
1:A:397:VAL:HG21	1:B:394:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:LYS:HB3	1:B:318:GLU:H	1.61	0.41
2:C:130:ARG:HH12	2:C:145:THR:HG21	1.86	0.41
1:D:277:TRP:CD1	1:D:287:ALA:HB2	2.56	0.41
1:D:377:ILE:HG21	1:D:406:LEU:HD21	2.03	0.41
1:A:397:VAL:O	1:A:404:TYR:HA	2.21	0.41
2:C:34:SER:CA	2:C:74:SER:HB3	2.49	0.41
1:E:372:PHE:HB2	1:E:429:HIS:NE2	2.35	0.41
1:A:266:VAL:HG23	1:A:325:ASN:ND2	2.36	0.41
1:A:310:HIS:CD2	1:A:310:HIS:N	2.88	0.41
1:B:349:TYR:N	1:B:349:TYR:CD1	2.89	0.41
2:C:34:SER:O	2:C:35:PRO:C	2.59	0.41
1:E:293:GLU:HB2	1:E:294:THR:H	1.58	0.41
1:E:374:PRO:HD2	1:E:429:HIS:CE1	2.56	0.41
1:A:395:PRO:HA	1:A:396:PRO:HD2	1.93	0.41
1:B:242:LEU:CD1	1:B:321:CYS:SG	3.09	0.41
1:B:391:TYR:H	1:B:391:TYR:HD2	1.68	0.41
2:C:101:LYS:HG3	2:C:102:GLU:N	2.35	0.41
1:E:396:PRO:CG	1:E:406:LEU:HD12	2.50	0.41
1:A:266:VAL:O	1:A:300:TYR:HB2	2.21	0.40
2:C:27:LEU:HD12	2:C:56:TYR:HB3	2.03	0.40
1:D:286:HIS:ND1	1:D:286:HIS:O	2.54	0.40
1:D:369:VAL:HG12	1:D:372:PHE:CE2	2.56	0.40
1:E:329:PRO:HD3	2:F:113:TRP:CZ3	2.57	0.40
2:F:158:VAL:O	2:F:160:SER:N	2.54	0.40
1:B:235:LEU:HD12	1:B:235:LEU:C	2.41	0.40
2:F:18:ARG:CB	2:F:92:LEU:HD21	2.49	0.40
1:B:292:ARG:CD	1:B:300:TYR:HD1	2.35	0.40
1:D:442:SER:OG	1:D:443:VAL:N	2.54	0.40
2:F:3:GLU:OE1	2:F:4:ASP:N	2.48	0.40
2:F:101:LYS:O	2:F:101:LYS:HG3	2.22	0.40
2:F:124:LEU:HA	2:F:129:GLY:HA2	2.03	0.40
1:D:284:VAL:HG23	1:D:285:HIS:N	2.37	0.40
1:A:290:LYS:HB2	1:A:303:VAL:O	2.22	0.40
1:A:349:TYR:CE2	1:B:357:GLU:HG3	2.56	0.40
1:A:383:SER:OG	1:A:423:PHE:HE1	2.03	0.40
1:A:394:THR:HG21	1:B:394:THR:HG22	2.04	0.40
1:B:253:ILE:HG22	1:B:254:SER:N	2.36	0.40
1:B:417:TRP:HA	1:B:417:TRP:CE3	2.57	0.40
2:C:133:PHE:HE2	2:C:138:ASP:O	2.04	0.40
1:E:287:ALA:HA	1:E:305:VAL:O	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	207/224 (92%)	165 (80%)	29 (14%)	13 (6%)	1	9
1	B	210/224 (94%)	154 (73%)	38 (18%)	18 (9%)	1	4
1	D	209/224 (93%)	174 (83%)	25 (12%)	10 (5%)	2	15
1	E	210/224 (94%)	147 (70%)	40 (19%)	23 (11%)	0	2
2	C	166/192 (86%)	115 (69%)	39 (24%)	12 (7%)	1	6
2	F	167/192 (87%)	122 (73%)	29 (17%)	16 (10%)	0	3
All	All	1169/1280 (91%)	877 (75%)	200 (17%)	92 (8%)	1	5

All (92) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	254	SER
1	A	271	PRO
1	A	284	VAL
1	A	371	GLY
1	B	273	VAL
1	B	280	ASN
1	B	297	ASN
2	C	35	PRO
2	C	41	ARG
2	C	63	VAL
2	C	64	ASN
2	C	115	ASN
2	C	148	ASP
1	D	310	HIS
1	E	271	PRO
1	E	290	LYS
1	E	291	PRO
1	E	293	GLU
1	E	297	ASN
1	E	355	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	E	430	GLU
2	F	21	GLU
2	F	35	PRO
2	F	72	GLN
2	F	77	THR
2	F	115	ASN
1	A	337	SER
1	A	384	SER
1	A	431	ALA
1	B	233	GLU
1	B	234	LEU
1	B	274	LYS
1	B	300	TYR
1	B	376	ASP
2	C	21	GLU
2	C	72	GLN
1	D	347	GLN
1	E	254	SER
1	E	273	VAL
1	E	294	THR
1	E	295	GLN
1	E	356	GLU
1	E	384	SER
2	F	33	TYR
2	F	38	GLN
2	F	143	LYS
2	F	159	GLY
1	A	252	MET
1	A	287	ALA
1	A	297	ASN
1	A	343	PRO
1	B	238	PRO
1	B	326	LYS
1	B	373	TYR
1	B	384	SER
2	C	31	GLY
2	C	73	THR
1	D	271	PRO
1	D	360	LYS
1	D	442	SER
1	E	322	LYS
2	F	46	GLU

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Mol	Chain	Res	Type
2	F	55	SER
2	F	112	SER
1	B	375	SER
1	B	387	PRO
2	C	96	PRO
1	D	331	PRO
1	D	374	PRO
1	E	274	LYS
1	E	319	TYR
2	F	41	ARG
2	F	104	GLU
1	A	352	PRO
1	B	290	LYS
1	B	329	PRO
1	D	265	ASP
1	D	430	GLU
1	E	279	VAL
1	E	310	HIS
1	E	311	GLN
1	E	362	GLN
2	F	144	ALA
2	C	32	ALA
1	E	387	PRO
2	F	74	SER
1	E	352	PRO
1	B	374	PRO
1	D	244	PRO
1	A	396	PRO
1	B	420	GLY
1	E	236	GLY

### 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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	195/208 (94%)	186 (95%)	9 (5%)	27 60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	198/208 (95%)	182 (92%)	16 (8%)	11	39
1	D	197/208 (95%)	185 (94%)	12 (6%)	18	50
1	E	198/208 (95%)	189 (96%)	9 (4%)	27	61
2	C	153/174 (88%)	143 (94%)	10 (6%)	17	48
2	F	154/174 (88%)	137 (89%)	17 (11%)	6	24
All	All	1095/1180 (93%)	1022 (93%)	73 (7%)	16	47

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	272	ASP
1	A	274	LYS
1	A	280	ASN
1	A	304	SER
1	A	338	LYS
1	A	355	ARG
1	A	408	SER
1	A	430	GLU
1	A	440	SER
1	B	239	SER
1	B	242	LEU
1	B	255	ARG
1	B	261	CYS
1	B	274	LYS
1	B	277	TRP
1	B	286	HIS
1	B	292	ARG
1	B	296	TYR
1	B	340	LYS
1	B	342	GLN
1	B	364	SER
1	B	370	LYS
1	B	389	ASN
1	B	391	TYR
1	B	408	SER
2	C	15	GLN
2	C	18	ARG
2	C	20	LEU
2	C	75	LEU
2	C	80	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
2	C	97	ARG
2	C	128	LYS
2	C	139	PHE
2	C	146	LEU
2	C	166	GLU
1	D	255	ARG
1	D	274	LYS
1	D	292	ARG
1	D	304	SER
1	D	351	LEU
1	D	355	ARG
1	D	370	LYS
1	D	373	TYR
1	D	401	ASP
1	D	405	PHE
1	D	413	ASP
1	D	436	TYR
1	E	242	LEU
1	E	267	SER
1	E	270	ASP
1	E	291	PRO
1	E	317	LYS
1	E	325	ASN
1	E	359	THR
1	E	370	LYS
1	E	408	SER
2	F	4	ASP
2	F	20	LEU
2	F	30	GLN
2	F	33	TYR
2	F	35	PRO
2	F	37	ASP
2	F	44	HIS
2	F	70	ARG
2	F	90	TRP
2	F	91	LEU
2	F	92	LEU
2	F	97	ARG
2	F	130	ARG
2	F	131	LYS
2	F	139	PHE
2	F	153	PHE

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Mol	Chain	Res	Type
2	F	160	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	280	ASN
1	A	310	HIS
1	B	276	ASN
1	B	347	GLN
1	B	386	GLN
1	B	429	HIS
2	C	107	HIS
2	C	134	HIS
1	D	429	HIS
1	E	310	HIS
1	E	429	HIS
2	F	87	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

40 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	0.42	0	17,19,21	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	NAG	G	2	3	14,14,15	0.22	0	17,19,21	0.50	0
3	BMA	G	3	3	11,11,12	0.98	0	15,15,17	1.09	0
3	MAN	G	4	3	11,11,12	1.25	1 (9%)	15,15,17	1.40	1 (6%)
3	NAG	G	5	3	14,14,15	0.73	1 (7%)	17,19,21	1.24	2 (11%)
3	MAN	G	6	3	11,11,12	0.66	0	15,15,17	0.98	2 (13%)
3	NAG	G	7	3	14,14,15	0.28	0	17,19,21	0.49	0
3	FUC	G	8	3	10,10,11	0.97	0	14,14,16	1.09	2 (14%)
3	NAG	H	1	3,1	14,14,15	1.12	1 (7%)	17,19,21	1.58	1 (5%)
3	NAG	H	2	3	14,14,15	0.33	0	17,19,21	1.41	2 (11%)
3	BMA	H	3	3	11,11,12	0.54	0	15,15,17	1.17	1 (6%)
3	MAN	H	4	3	11,11,12	0.54	0	15,15,17	1.21	2 (13%)
3	NAG	H	5	3	14,14,15	0.75	1 (7%)	17,19,21	1.00	2 (11%)
3	MAN	H	6	3	11,11,12	0.73	0	15,15,17	0.89	1 (6%)
3	NAG	H	7	3	14,14,15	0.21	0	17,19,21	0.45	0
3	FUC	H	8	3	10,10,11	0.99	0	14,14,16	1.01	0
4	NAG	I	1	2,4	14,14,15	0.50	0	17,19,21	0.39	0
4	NAG	I	2	4	14,14,15	0.29	0	17,19,21	1.42	2 (11%)
4	BMA	I	3	4	11,11,12	1.16	1 (9%)	15,15,17	1.29	2 (13%)
4	MAN	I	4	4	11,11,12	1.54	3 (27%)	15,15,17	2.79	4 (26%)
3	NAG	J	1	3,1	14,14,15	0.38	0	17,19,21	0.35	0
3	NAG	J	2	3	14,14,15	0.20	0	17,19,21	0.49	0
3	BMA	J	3	3	11,11,12	0.64	0	15,15,17	1.02	1 (6%)
3	MAN	J	4	3	11,11,12	1.17	1 (9%)	15,15,17	1.19	1 (6%)
3	NAG	J	5	3	14,14,15	0.63	1 (7%)	17,19,21	1.10	2 (11%)
3	MAN	J	6	3	11,11,12	0.62	0	15,15,17	1.13	2 (13%)
3	NAG	J	7	3	14,14,15	0.25	0	17,19,21	0.51	0
3	FUC	J	8	3	10,10,11	0.90	0	14,14,16	1.10	2 (14%)
3	NAG	K	1	3,1	14,14,15	1.06	1 (7%)	17,19,21	1.64	1 (5%)
3	NAG	K	2	3	14,14,15	0.26	0	17,19,21	1.41	2 (11%)
3	BMA	K	3	3	11,11,12	0.65	0	15,15,17	0.83	0
3	MAN	K	4	3	11,11,12	0.78	0	15,15,17	1.34	3 (20%)
3	NAG	K	5	3	14,14,15	0.88	1 (7%)	17,19,21	1.04	1 (5%)
3	MAN	K	6	3	11,11,12	1.01	2 (18%)	15,15,17	1.35	2 (13%)
3	NAG	K	7	3	14,14,15	0.25	0	17,19,21	0.38	0
3	FUC	K	8	3	10,10,11	0.99	0	14,14,16	0.92	0
5	NAG	L	1	2,5	14,14,15	0.52	0	17,19,21	0.43	0
5	NAG	L	2	5	14,14,15	0.36	0	17,19,21	1.79	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	BMA	L	3	5	11,11,12	1.10	1 (9%)	15,15,17	1.18	2 (13%)
5	FUC	L	4	5	10,10,11	1.14	1 (10%)	14,14,16	1.68	4 (28%)

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	-	2/6/23/26	0/1/1/1
3	NAG	G	2	3	-	4/6/23/26	0/1/1/1
3	BMA	G	3	3	-	2/2/19/22	0/1/1/1
3	MAN	G	4	3	-	2/2/19/22	0/1/1/1
3	NAG	G	5	3	-	2/6/23/26	0/1/1/1
3	MAN	G	6	3	-	2/2/19/22	0/1/1/1
3	NAG	G	7	3	-	1/6/23/26	0/1/1/1
3	FUC	G	8	3	-	-	0/1/1/1
3	NAG	H	1	3,1	-	1/6/23/26	0/1/1/1
3	NAG	H	2	3	-	5/6/23/26	0/1/1/1
3	BMA	H	3	3	-	1/2/19/22	0/1/1/1
3	MAN	H	4	3	-	2/2/19/22	0/1/1/1
3	NAG	H	5	3	-	3/6/23/26	0/1/1/1
3	MAN	H	6	3	-	0/2/19/22	0/1/1/1
3	NAG	H	7	3	-	2/6/23/26	0/1/1/1
3	FUC	H	8	3	-	-	0/1/1/1
4	NAG	I	1	2,4	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	5/6/23/26	0/1/1/1
4	BMA	I	3	4	-	2/2/19/22	0/1/1/1
4	MAN	I	4	4	-	0/2/19/22	0/1/1/1
3	NAG	J	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	J	2	3	-	4/6/23/26	0/1/1/1
3	BMA	J	3	3	-	0/2/19/22	0/1/1/1
3	MAN	J	4	3	-	1/2/19/22	0/1/1/1
3	NAG	J	5	3	-	4/6/23/26	0/1/1/1
3	MAN	J	6	3	-	2/2/19/22	0/1/1/1
3	NAG	J	7	3	-	2/6/23/26	0/1/1/1
3	FUC	J	8	3	-	-	0/1/1/1
3	NAG	K	1	3,1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	K	2	3	-	5/6/23/26	0/1/1/1
3	BMA	K	3	3	-	0/2/19/22	0/1/1/1
3	MAN	K	4	3	-	0/2/19/22	0/1/1/1
3	NAG	K	5	3	-	1/6/23/26	0/1/1/1
3	MAN	K	6	3	-	2/2/19/22	0/1/1/1
3	NAG	K	7	3	-	2/6/23/26	0/1/1/1
3	FUC	K	8	3	-	-	0/1/1/1
5	NAG	L	1	2,5	-	4/6/23/26	0/1/1/1
5	NAG	L	2	5	-	5/6/23/26	0/1/1/1
5	BMA	L	3	5	-	2/2/19/22	0/1/1/1
5	FUC	L	4	5	-	-	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	1	NAG	O5-C1	4.08	1.50	1.43
3	K	1	NAG	O5-C1	3.86	1.49	1.43
3	J	4	MAN	O5-C1	-3.15	1.38	1.43
3	K	5	NAG	O5-C1	-3.11	1.38	1.43
3	G	4	MAN	O5-C1	-3.11	1.38	1.43
3	H	5	NAG	O5-C1	-2.62	1.39	1.43
4	I	4	MAN	C2-C3	-2.44	1.48	1.52
5	L	3	BMA	C2-C3	2.38	1.56	1.52
4	I	4	MAN	O3-C3	-2.37	1.37	1.43
5	L	4	FUC	C2-C3	-2.36	1.49	1.52
3	K	6	MAN	C1-C2	2.30	1.57	1.52
4	I	3	BMA	C4-C3	2.22	1.58	1.52
4	I	4	MAN	C1-C2	2.16	1.57	1.52
3	G	5	NAG	O5-C1	-2.16	1.40	1.43
3	K	6	MAN	C2-C3	2.15	1.55	1.52
3	J	5	NAG	O5-C1	-2.09	1.40	1.43

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	4	MAN	C1-O5-C5	8.96	124.33	112.19
3	K	1	NAG	C1-O5-C5	6.40	120.87	112.19
3	H	1	NAG	C1-O5-C5	6.15	120.53	112.19
5	L	2	NAG	C2-N2-C7	5.44	130.66	122.90
3	G	4	MAN	O2-C2-C3	-4.78	100.56	110.14
3	K	2	NAG	C2-N2-C7	4.52	129.34	122.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	2	NAG	C2-N2-C7	4.47	129.26	122.90
3	H	2	NAG	C2-N2-C7	4.35	129.10	122.90
5	L	4	FUC	C1-O5-C5	4.14	122.15	112.78
3	J	4	MAN	O2-C2-C3	-3.60	102.92	110.14
4	I	4	MAN	C1-C2-C3	3.28	113.70	109.67
3	H	4	MAN	C1-O5-C5	3.27	116.63	112.19
3	G	5	NAG	C3-C4-C5	3.10	115.77	110.24
4	I	4	MAN	O2-C2-C3	-3.08	103.96	110.14
3	G	5	NAG	C1-O5-C5	3.07	116.35	112.19
3	J	5	NAG	C1-O5-C5	3.06	116.33	112.19
3	K	6	MAN	C1-C2-C3	3.05	113.42	109.67
3	K	4	MAN	C1-C2-C3	-3.04	105.93	109.67
5	L	2	NAG	C1-C2-N2	3.02	115.64	110.49
3	H	3	BMA	C1-O5-C5	2.92	116.14	112.19
4	I	3	BMA	C2-C3-C4	2.82	115.77	110.89
3	K	4	MAN	C1-O5-C5	2.79	115.97	112.19
5	L	4	FUC	O5-C1-C2	2.77	115.05	110.77
3	J	6	MAN	C1-O5-C5	2.76	115.93	112.19
3	H	4	MAN	O2-C2-C3	-2.76	104.61	110.14
4	I	4	MAN	O5-C1-C2	2.71	114.96	110.77
3	K	5	NAG	C3-C4-C5	2.71	115.07	110.24
3	J	6	MAN	O2-C2-C3	-2.66	104.81	110.14
5	L	4	FUC	O5-C5-C4	2.65	114.27	109.52
3	G	6	MAN	O2-C2-C3	-2.58	104.97	110.14
3	H	2	NAG	C1-C2-N2	2.56	114.86	110.49
3	H	5	NAG	C3-C4-C5	2.49	114.68	110.24
3	J	3	BMA	C1-O5-C5	2.49	115.56	112.19
3	K	2	NAG	C1-C2-N2	2.48	114.73	110.49
3	K	4	MAN	O2-C2-C3	-2.46	105.21	110.14
5	L	2	NAG	C1-O5-C5	2.43	115.48	112.19
5	L	3	BMA	C1-C2-C3	2.43	112.65	109.67
3	J	5	NAG	C3-C4-C5	2.43	114.57	110.24
4	I	2	NAG	C1-C2-N2	2.43	114.63	110.49
4	I	3	BMA	C1-C2-C3	2.41	112.63	109.67
3	G	8	FUC	C1-C2-C3	2.36	112.56	109.67
3	K	6	MAN	C1-O5-C5	2.31	115.32	112.19
5	L	4	FUC	O2-C2-C1	2.26	113.77	109.15
5	L	3	BMA	C2-C3-C4	2.25	114.79	110.89
3	J	8	FUC	C1-C2-C3	2.22	112.39	109.67
3	H	6	MAN	O2-C2-C3	-2.17	105.80	110.14
3	H	5	NAG	C1-O5-C5	2.13	115.08	112.19
3	G	8	FUC	O5-C5-C4	2.13	113.33	109.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	8	FUC	O5-C5-C4	2.00	113.11	109.52
3	G	6	MAN	C1-O5-C5	2.00	114.90	112.19

There are no chirality outliers.

All (76) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	L	2	NAG	C4-C5-C6-O6
3	K	2	NAG	C4-C5-C6-O6
3	H	7	NAG	O5-C5-C6-O6
3	J	7	NAG	O5-C5-C6-O6
4	I	2	NAG	C4-C5-C6-O6
3	K	2	NAG	O5-C5-C6-O6
3	H	2	NAG	O5-C5-C6-O6
3	J	6	MAN	O5-C5-C6-O6
3	G	1	NAG	O5-C5-C6-O6
3	K	6	MAN	O5-C5-C6-O6
3	H	7	NAG	C4-C5-C6-O6
3	K	7	NAG	C4-C5-C6-O6
3	J	1	NAG	O5-C5-C6-O6
5	L	1	NAG	O5-C5-C6-O6
5	L	2	NAG	O5-C5-C6-O6
3	J	2	NAG	C4-C5-C6-O6
4	I	3	BMA	C4-C5-C6-O6
4	I	2	NAG	O5-C5-C6-O6
3	J	7	NAG	C4-C5-C6-O6
5	L	1	NAG	C1-C2-N2-C7
3	K	1	NAG	O5-C5-C6-O6
4	I	3	BMA	O5-C5-C6-O6
5	L	1	NAG	C4-C5-C6-O6
5	L	3	BMA	C4-C5-C6-O6
3	J	2	NAG	O5-C5-C6-O6
5	L	3	BMA	O5-C5-C6-O6
3	J	5	NAG	O5-C5-C6-O6
3	H	2	NAG	C4-C5-C6-O6
3	J	1	NAG	C4-C5-C6-O6
3	J	6	MAN	C4-C5-C6-O6
3	G	2	NAG	C8-C7-N2-C2
3	G	2	NAG	O7-C7-N2-C2
3	H	2	NAG	C8-C7-N2-C2
3	H	2	NAG	O7-C7-N2-C2
3	J	2	NAG	C8-C7-N2-C2

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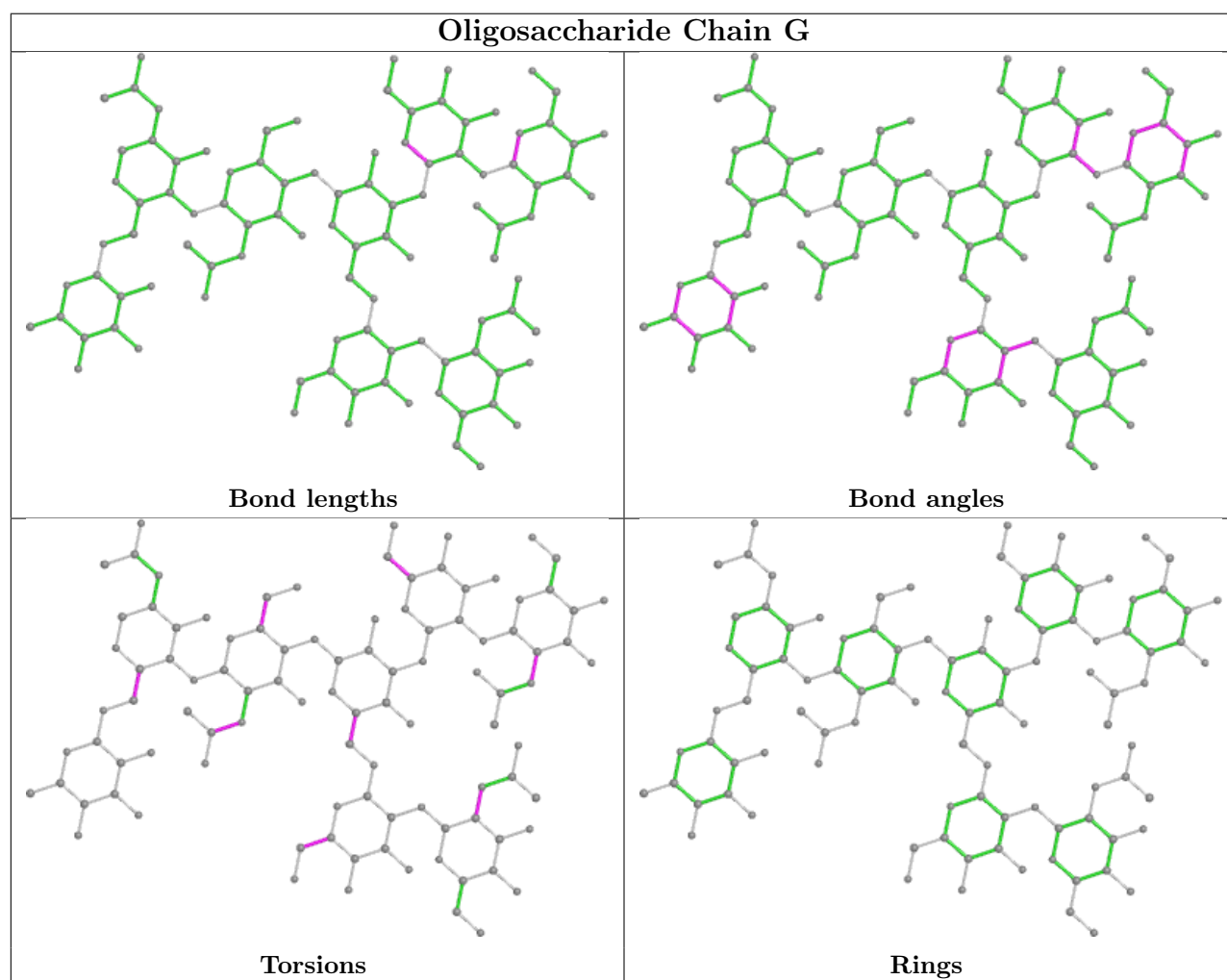
Mol	Chain	Res	Type	Atoms
3	J	2	NAG	O7-C7-N2-C2
3	K	2	NAG	C8-C7-N2-C2
3	K	2	NAG	O7-C7-N2-C2
4	I	2	NAG	C8-C7-N2-C2
4	I	2	NAG	O7-C7-N2-C2
5	L	2	NAG	C8-C7-N2-C2
5	L	2	NAG	O7-C7-N2-C2
3	G	6	MAN	O5-C5-C6-O6
3	H	5	NAG	O5-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	K	6	MAN	C4-C5-C6-O6
3	H	1	NAG	O5-C5-C6-O6
3	G	6	MAN	C4-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	K	7	NAG	O5-C5-C6-O6
3	G	3	BMA	O5-C5-C6-O6
4	I	1	NAG	C1-C2-N2-C7
3	H	4	MAN	O5-C5-C6-O6
3	G	4	MAN	C4-C5-C6-O6
3	H	4	MAN	C4-C5-C6-O6
3	J	5	NAG	C4-C5-C6-O6
3	G	4	MAN	O5-C5-C6-O6
3	G	3	BMA	C4-C5-C6-O6
3	G	2	NAG	C4-C5-C6-O6
3	H	5	NAG	C4-C5-C6-O6
3	J	4	MAN	O5-C5-C6-O6
3	G	7	NAG	C1-C2-N2-C7
3	G	5	NAG	C3-C2-N2-C7
3	H	5	NAG	C3-C2-N2-C7
3	K	2	NAG	C3-C2-N2-C7
4	I	1	NAG	C3-C2-N2-C7
4	I	2	NAG	C3-C2-N2-C7
5	L	2	NAG	C3-C2-N2-C7
3	K	1	NAG	C4-C5-C6-O6
3	G	5	NAG	C1-C2-N2-C7
3	H	3	BMA	O5-C5-C6-O6
3	H	2	NAG	C3-C2-N2-C7
3	J	5	NAG	C3-C2-N2-C7
3	K	5	NAG	C3-C2-N2-C7
5	L	1	NAG	C3-C2-N2-C7
3	J	5	NAG	C1-C2-N2-C7

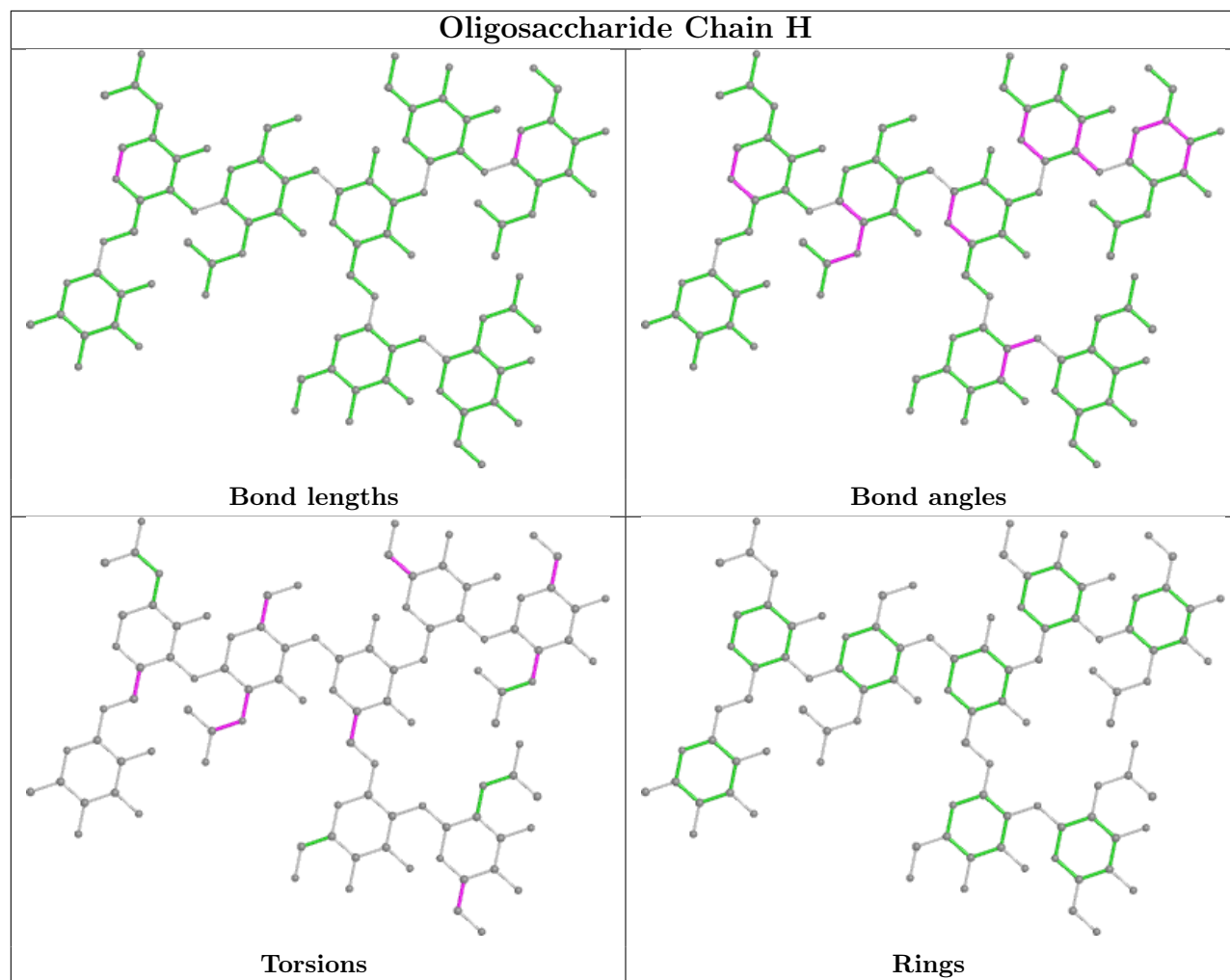
There are no ring outliers.

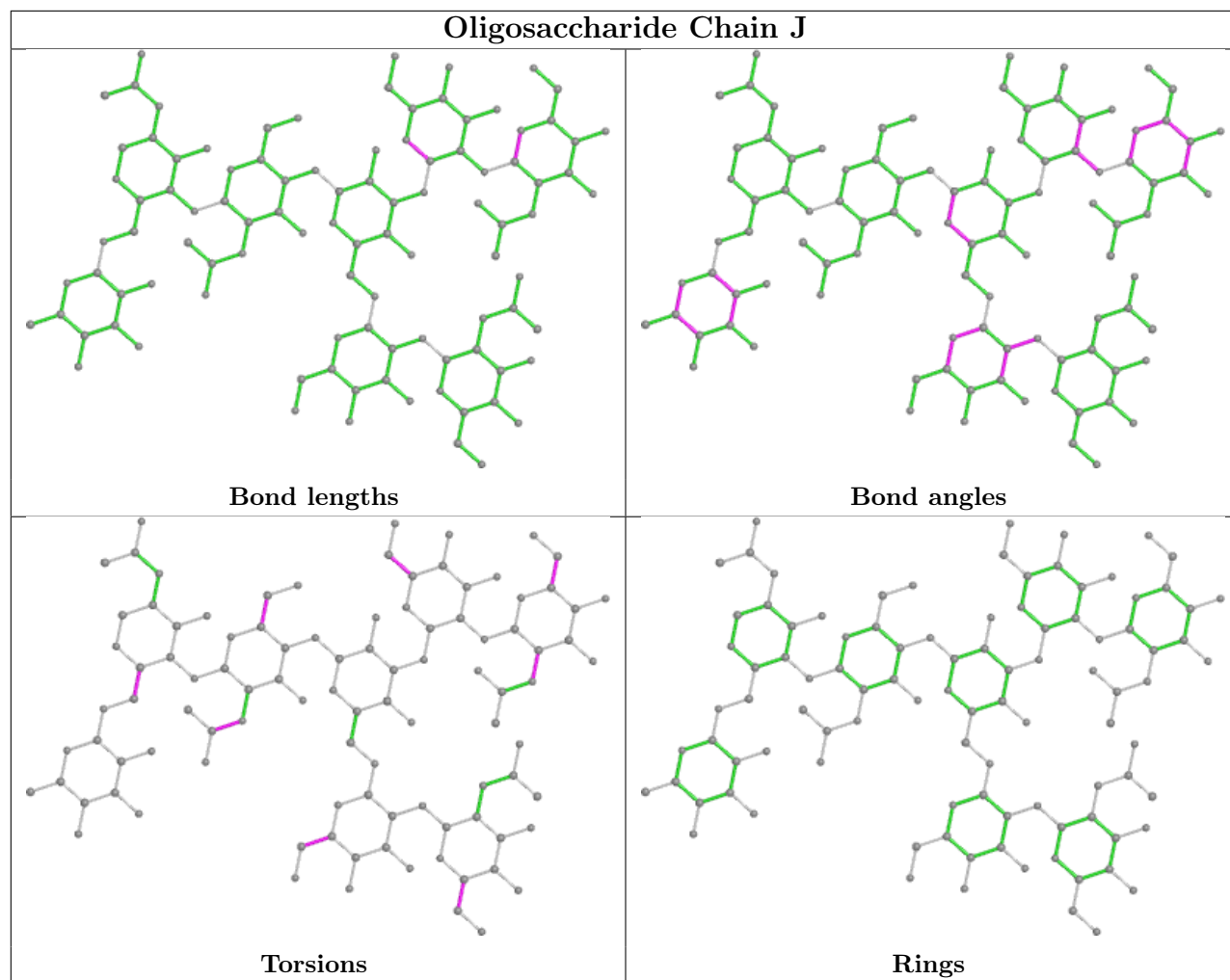
7 monomers are involved in 11 short contacts:

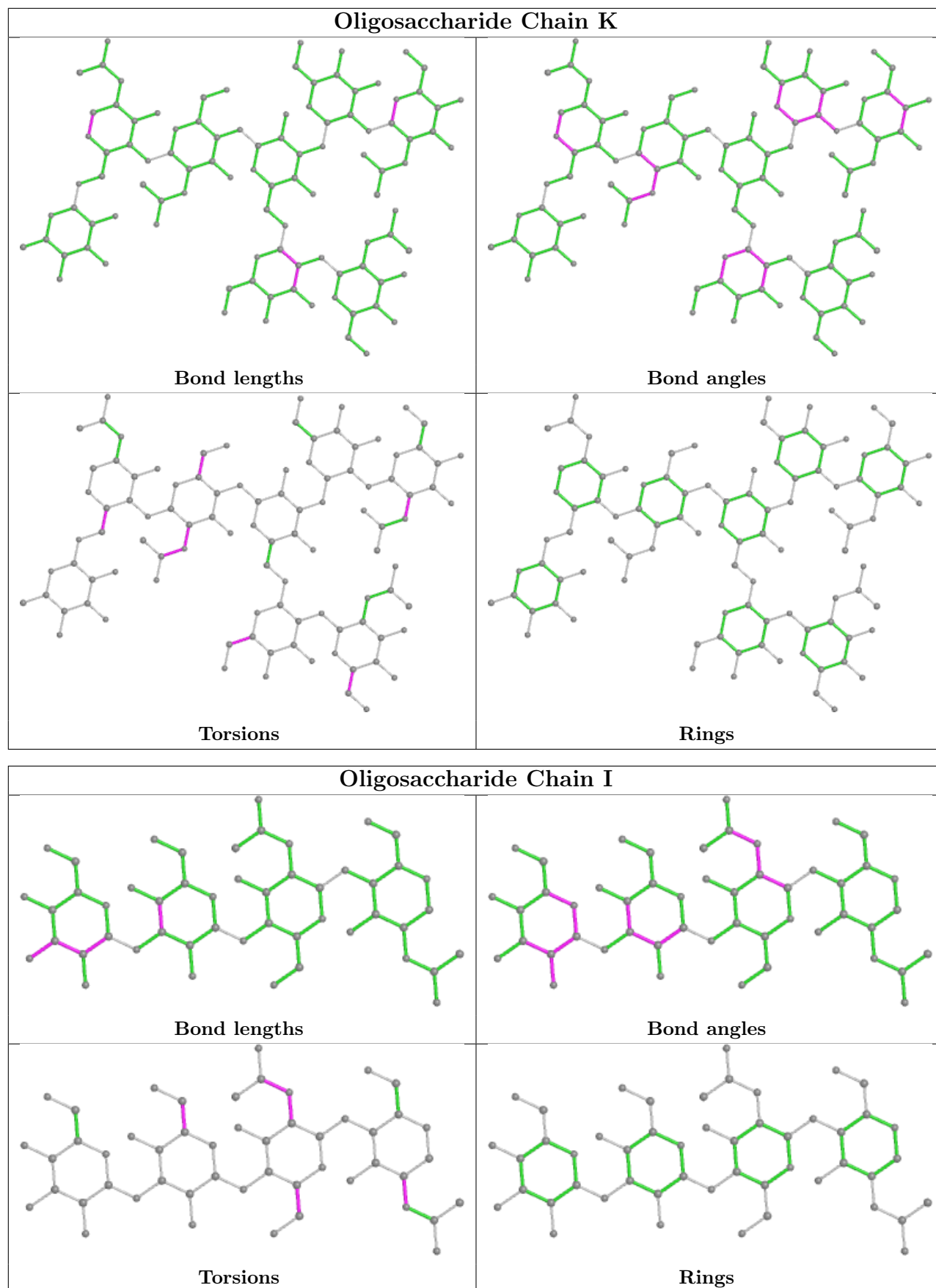
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	L	2	NAG	1	0
4	I	2	NAG	3	0
3	J	2	NAG	1	0
3	K	2	NAG	2	0
3	J	5	NAG	1	0
3	J	1	NAG	1	0
3	H	2	NAG	2	0

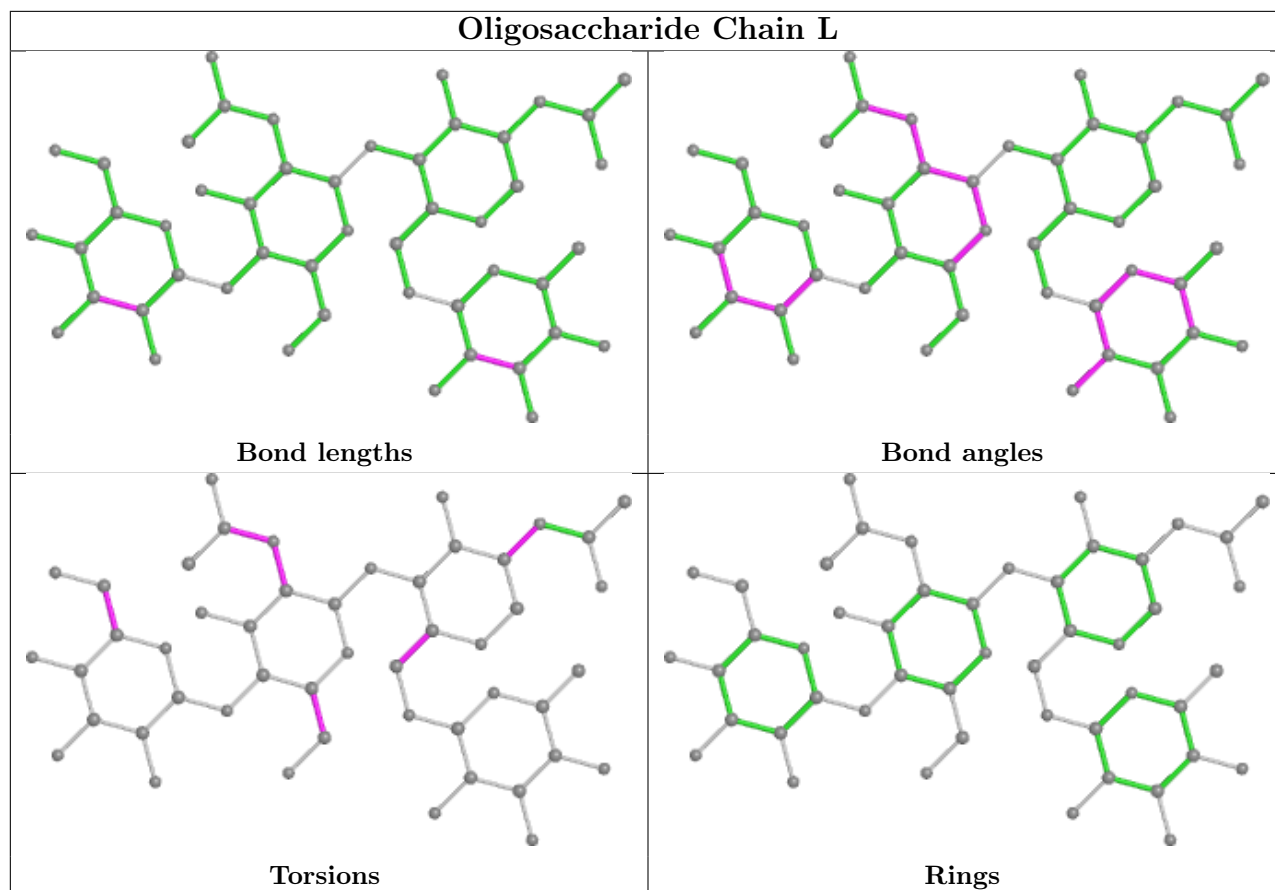
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.











## 5.6 Ligand geometry [i](#)

4 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	$\# Z  > 2$
6	NAG	F	201	2	14,14,15	0.46	0	17,19,21	1.76	3 (17%)
6	NAG	C	202	2	14,14,15	0.65	1 (7%)	17,19,21	0.78	1 (5%)
6	NAG	C	201	2	14,14,15	0.54	0	17,19,21	1.08	1 (5%)
6	NAG	F	202	2	14,14,15	0.37	0	17,19,21	0.37	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
6	NAG	F	201	2	-	3/6/23/26	0/1/1/1
6	NAG	C	202	2	-	4/6/23/26	0/1/1/1
6	NAG	C	201	2	-	2/6/23/26	0/1/1/1
6	NAG	F	202	2	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	202	NAG	C1-C2	2.03	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	201	NAG	C1-O5-C5	5.93	120.23	112.19
6	F	201	NAG	C3-C4-C5	3.01	115.61	110.24
6	C	201	NAG	C1-O5-C5	2.89	116.11	112.19
6	C	202	NAG	C2-N2-C7	2.64	126.67	122.90
6	F	201	NAG	O5-C5-C4	2.29	116.41	110.83

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	202	NAG	C3-C2-N2-C7
6	C	201	NAG	C4-C5-C6-O6
6	F	202	NAG	O5-C5-C6-O6
6	C	201	NAG	O5-C5-C6-O6
6	F	201	NAG	O5-C5-C6-O6
6	F	202	NAG	C4-C5-C6-O6
6	C	202	NAG	C4-C5-C6-O6
6	F	201	NAG	C4-C5-C6-O6
6	C	202	NAG	C1-C2-N2-C7
6	C	202	NAG	O5-C5-C6-O6
6	F	201	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	202	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	209/224 (93%)	-0.16	3 (1%) 75 63	45, 69, 103, 126	0
1	B	212/224 (94%)	-0.11	0 100 100	42, 65, 103, 118	0
1	D	209/224 (93%)	-0.24	0 100 100	53, 68, 89, 98	0
1	E	212/224 (94%)	-0.20	2 (0%) 84 75	49, 80, 120, 133	0
2	C	168/192 (87%)	-0.13	1 (0%) 89 84	67, 80, 109, 128	0
2	F	169/192 (88%)	0.05	1 (0%) 89 84	63, 80, 109, 127	0
All	All	1179/1280 (92%)	-0.14	7 (0%) 89 84	42, 74, 109, 133	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	281	GLY	3.7
2	C	33	TYR	2.6
1	E	232	PRO	2.5
1	A	337	SER	2.4
1	A	280	ASN	2.3
2	F	39	SER	2.2
1	E	418	GLN	2.1

### 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](#)

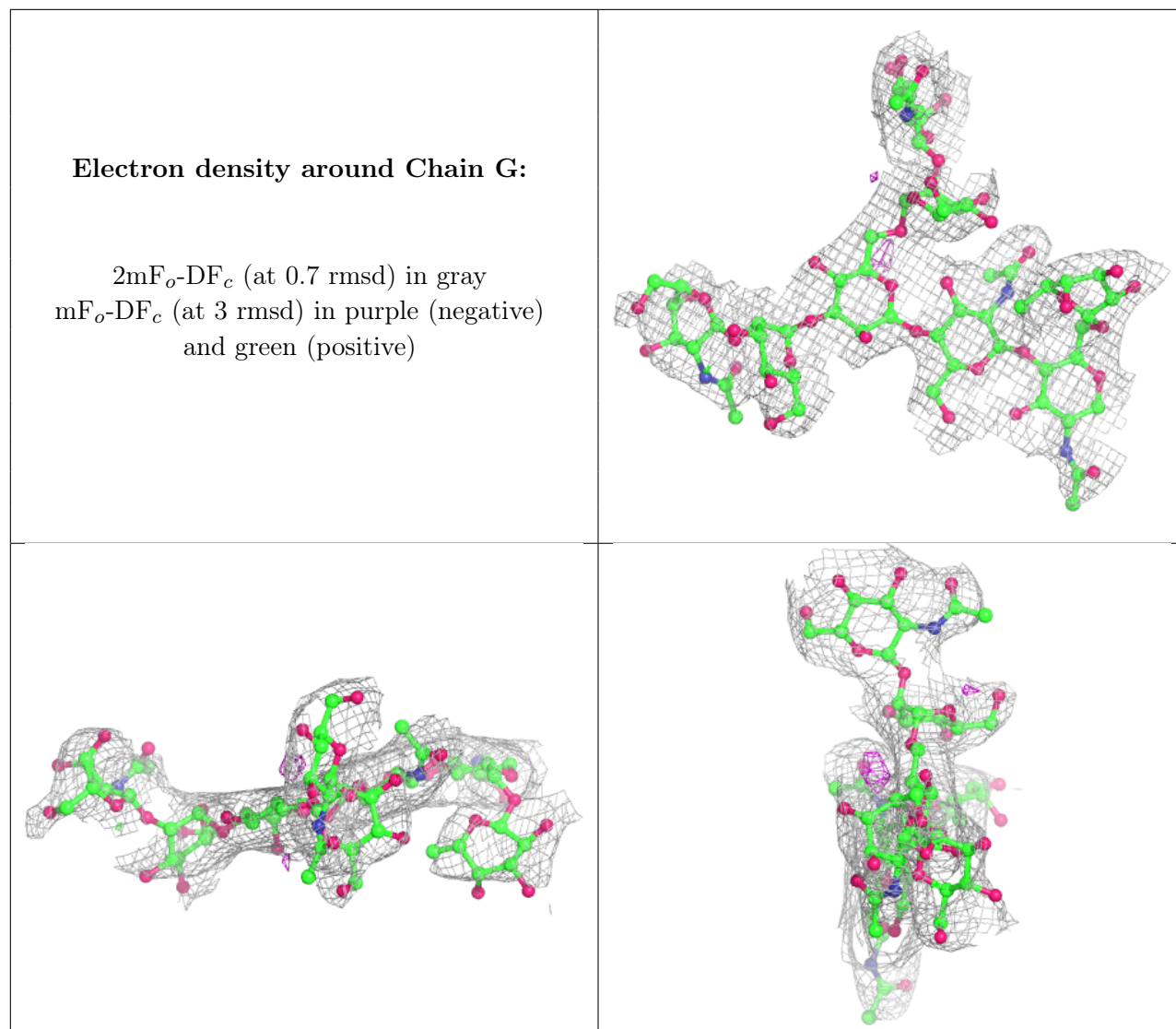
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column

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 <sup>2</sup> )	Q<0.9
4	MAN	I	4	11/12	0.65	0.21	89,105,115,118	0
3	NAG	K	5	14/15	0.74	0.26	105,112,116,121	0
3	NAG	G	5	14/15	0.75	0.29	99,103,106,109	0
5	FUC	L	4	10/11	0.78	0.34	85,99,109,112	0
3	NAG	J	5	14/15	0.79	0.34	111,116,123,124	0
3	FUC	G	8	10/11	0.79	0.30	85,92,97,99	0
3	NAG	H	5	14/15	0.79	0.31	85,101,106,106	0
3	FUC	H	8	10/11	0.79	0.27	85,91,97,99	0
3	MAN	K	4	11/12	0.82	0.30	94,100,101,108	0
5	BMA	L	3	11/12	0.83	0.17	99,101,102,103	0
4	BMA	I	3	11/12	0.84	0.13	68,79,86,98	0
3	NAG	K	7	14/15	0.85	0.21	85,88,91,92	0
3	FUC	K	8	10/11	0.85	0.30	92,96,98,103	0
5	NAG	L	1	14/15	0.86	0.16	68,83,91,94	0
3	MAN	G	4	11/12	0.86	0.20	92,98,101,102	0
3	NAG	G	7	14/15	0.86	0.18	77,85,91,91	0
3	NAG	J	7	14/15	0.87	0.26	61,62,65,65	0
3	NAG	J	1	14/15	0.87	0.20	56,70,83,85	0
3	FUC	J	8	10/11	0.88	0.24	79,88,99,101	0
3	MAN	G	6	11/12	0.88	0.21	68,81,82,87	0
3	NAG	H	1	14/15	0.89	0.18	49,61,77,81	0
3	NAG	G	1	14/15	0.89	0.19	28,50,75,77	0
4	NAG	I	2	14/15	0.90	0.16	58,70,75,78	0
5	NAG	L	2	14/15	0.90	0.16	80,88,90,93	0
3	MAN	H	4	11/12	0.90	0.15	66,76,84,84	0
3	NAG	K	1	14/15	0.90	0.18	55,63,79,88	0
3	MAN	J	4	11/12	0.91	0.18	92,94,100,107	0
3	NAG	G	2	14/15	0.91	0.16	42,49,54,67	0
3	MAN	K	6	11/12	0.91	0.18	76,83,92,93	0
3	MAN	J	6	11/12	0.91	0.32	54,57,63,69	0
3	NAG	H	2	14/15	0.92	0.16	43,46,68,69	0
3	NAG	K	2	14/15	0.92	0.20	41,50,64,65	0
3	BMA	K	3	11/12	0.93	0.15	57,64,78,83	0
3	BMA	H	3	11/12	0.93	0.13	50,58,66,69	0
4	NAG	I	1	14/15	0.93	0.18	15,23,49,56	0
3	BMA	J	3	11/12	0.93	0.16	66,74,84,92	0
3	BMA	G	3	11/12	0.93	0.16	60,68,77,80	0
3	NAG	H	7	14/15	0.94	0.19	43,51,72,75	0
3	NAG	J	2	14/15	0.94	0.20	66,72,80,82	0
3	MAN	H	6	11/12	0.94	0.14	38,43,54,58	0

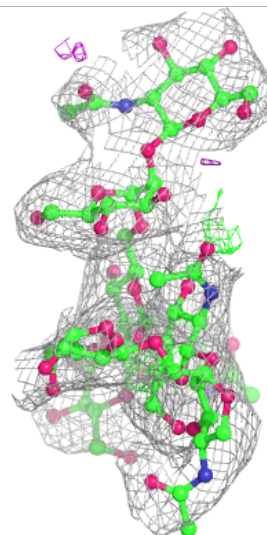
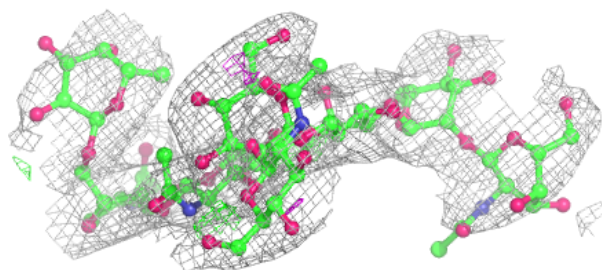
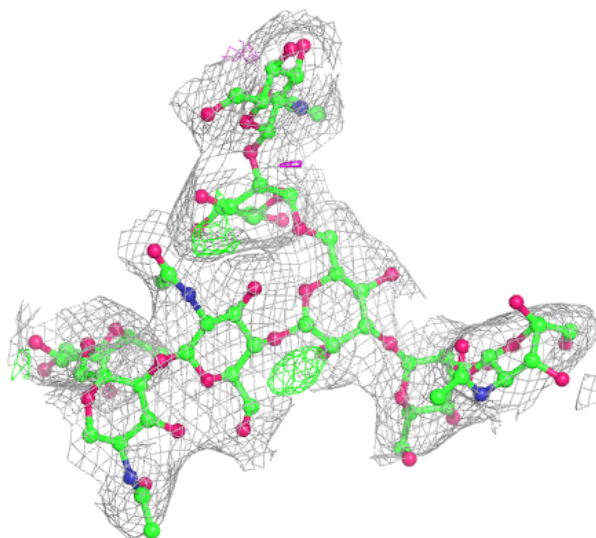
The following is a graphical depiction of the model fit to experimental electron density for oligosac-

charide. Each fit is shown from different orientation to approximate a three-dimensional view.



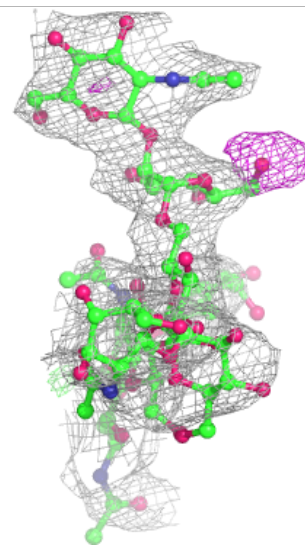
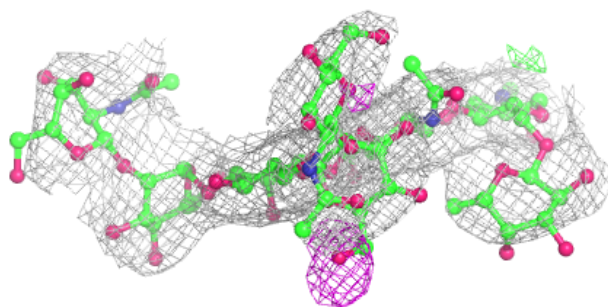
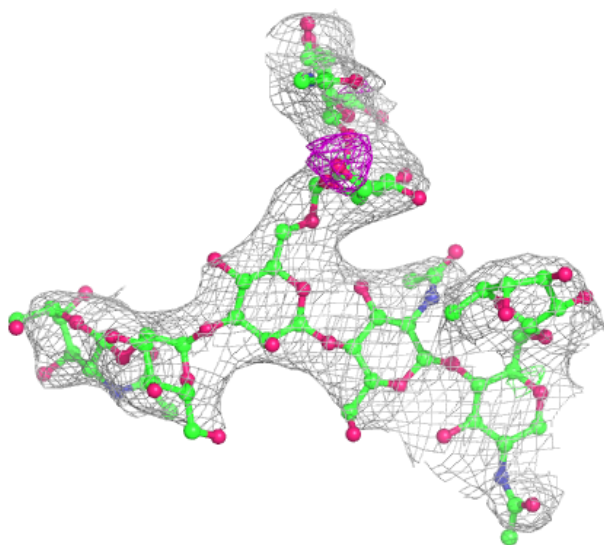
**Electron density around Chain H:**

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



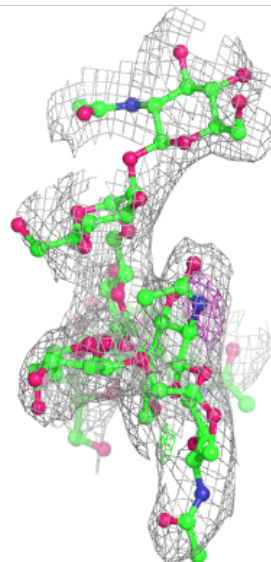
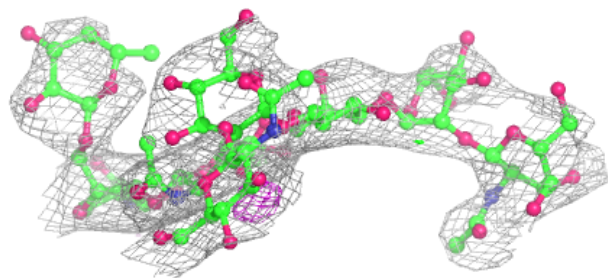
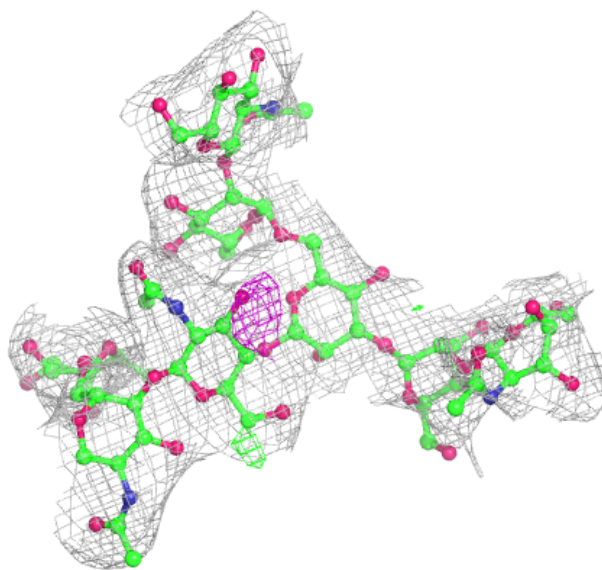
**Electron density around Chain J:**

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



**Electron density around Chain K:**

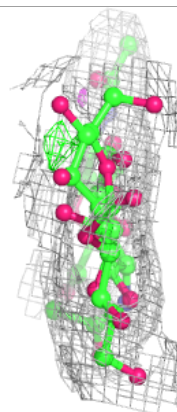
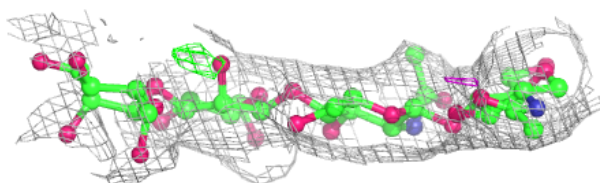
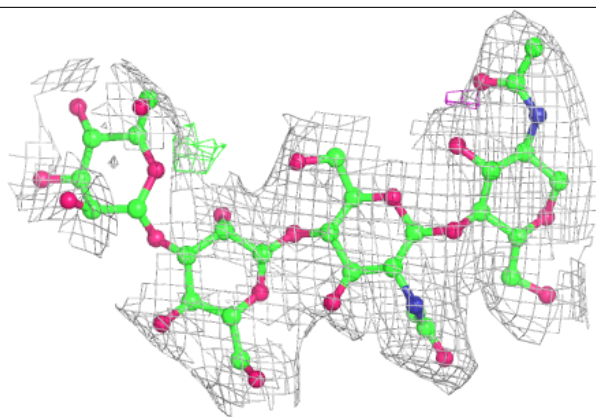
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



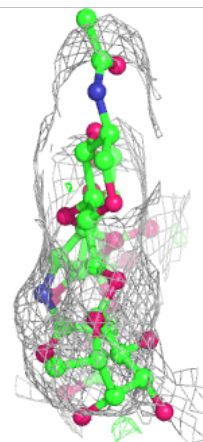
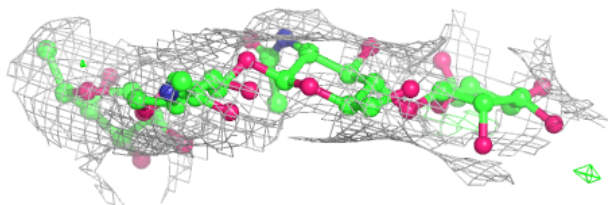
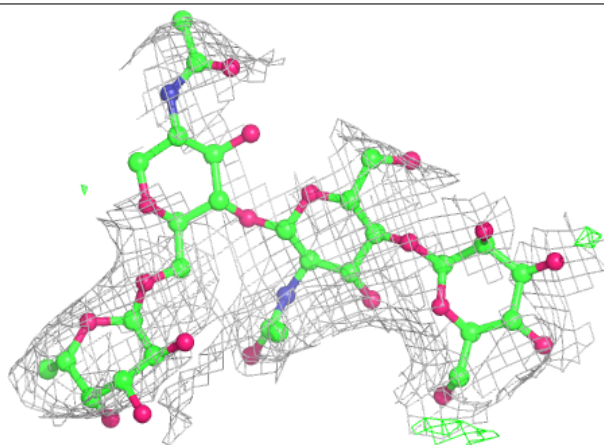


**Electron density around Chain I:**

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

**Electron density around Chain L:**

$2mF_o-DF_c$  (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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
6	NAG	C	201	14/15	0.56	0.37	86,97,114,119	0
6	NAG	F	202	14/15	0.65	0.30	73,90,106,110	0
6	NAG	C	202	14/15	0.72	0.28	69,79,90,92	0
6	NAG	F	201	14/15	0.76	0.24	91,102,117,120	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.