



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2021 – 01:26 PM EDT

PDB ID : 3FHQ
Title : Structure of endo-beta-N-acetylglucosaminidase A
Authors : Jie, Y.; Li, L.; Shaw, N.; Li, Y.; Song, J.; Zhang, W.; Xia, C.; Zhang, R.;
Joachimiak, A.; Zhang, H.-C.; Wang, L.-X.; Wang, P.; Liu, Z.-J.
Deposited on : 2008-12-10
Resolution : 2.45 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

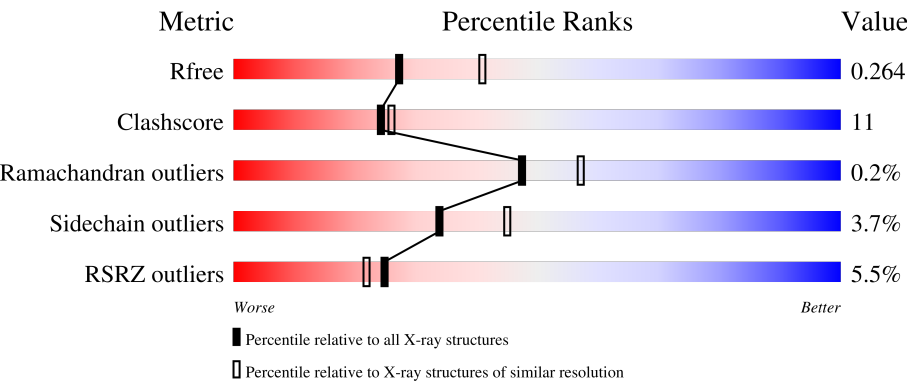
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	621	<div><div>4%</div><div>77%</div><div>18%</div><div>• •</div></div>
1	B	621	<div><div>6%</div><div>77%</div><div>18%</div><div>• •</div></div>
1	D	621	<div><div>4%</div><div>76%</div><div>18%</div><div>• •</div></div>
1	F	621	<div><div>8%</div><div>75%</div><div>19%</div><div>• •</div></div>
2	C	3	<div><div>67%</div><div>33%</div></div>

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Mol	Chain	Length	Quality of chain
2	E	3	 33%67%
2	G	3	 33%67%
2	H	3	 67%33%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20045 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.

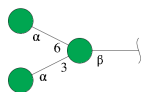
- Molecule 1 is a protein called Endo-beta-N-acetylglucosaminidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	601	Total	C	N	O	S	0	0	0
			4781	3031	801	938	11			
1	B	599	Total	C	N	O	S	0	0	0
			4757	3017	797	932	11			
1	D	597	Total	C	N	O	S	0	0	0
			4746	3011	793	931	11			
1	F	596	Total	C	N	O	S	0	0	0
			4736	3003	793	929	11			

There are 16 discrepancies between the modelled and reference sequences:

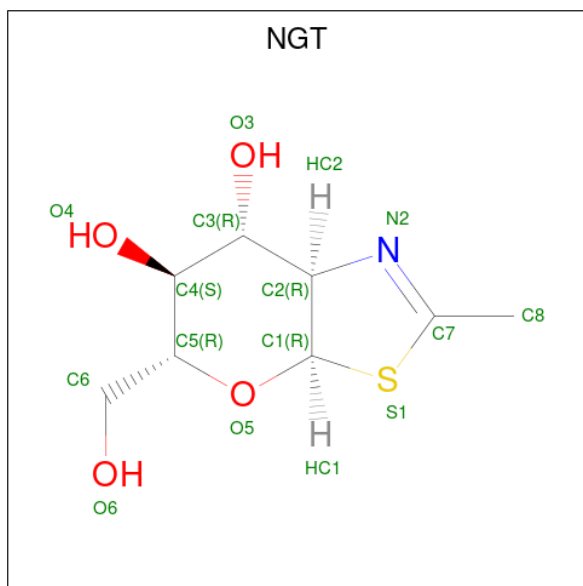
Chain	Residue	Modelled	Actual	Comment	Reference
A	43	ASP	ASN	engineered mutation	UNP Q9ZB22
A	455	ASP	GLY	engineered mutation	UNP Q9ZB22
A	518	THR	ILE	engineered mutation	UNP Q9ZB22
A	583	ILE	LEU	engineered mutation	UNP Q9ZB22
B	43	ASP	ASN	engineered mutation	UNP Q9ZB22
B	455	ASP	GLY	engineered mutation	UNP Q9ZB22
B	518	THR	ILE	engineered mutation	UNP Q9ZB22
B	583	ILE	LEU	engineered mutation	UNP Q9ZB22
D	43	ASP	ASN	engineered mutation	UNP Q9ZB22
D	455	ASP	GLY	engineered mutation	UNP Q9ZB22
D	518	THR	ILE	engineered mutation	UNP Q9ZB22
D	583	ILE	LEU	engineered mutation	UNP Q9ZB22
F	43	ASP	ASN	engineered mutation	UNP Q9ZB22
F	455	ASP	GLY	engineered mutation	UNP Q9ZB22
F	518	THR	ILE	engineered mutation	UNP Q9ZB22
F	583	ILE	LEU	engineered mutation	UNP Q9ZB22

- Molecule 2 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	3	Total	C	O	0	0	0
			33	18	15			
2	E	3	Total	C	O	0	0	0
			33	18	15			
2	G	3	Total	C	O	0	0	0
			33	18	15			
2	H	3	Total	C	O	0	0	0
			33	18	15			

- Molecule 3 is 3AR,5R,6S,7R,7AR-5-HYDROXYMETHYL-2-METHYL-5,6,7,7A-TETRAHYDRO-3AH-PYRANO[3,2-D]THIAZOLE-6,7-DIOL (three-letter code: NGT) (formula: C₈H₁₃NO₄S).



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

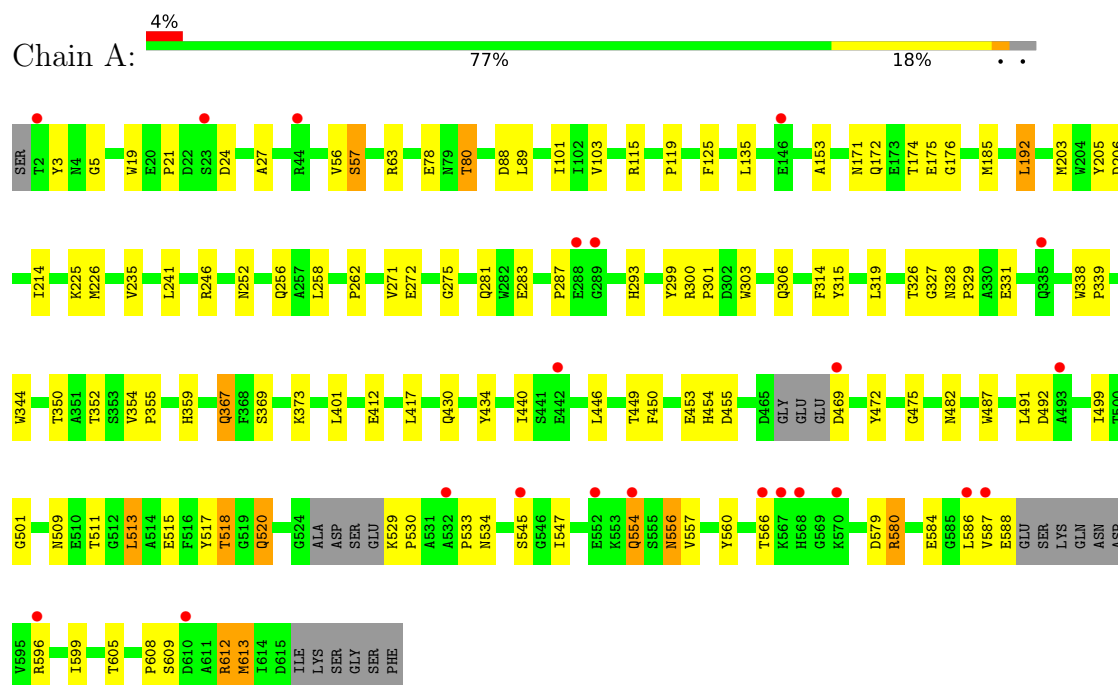
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	244	Total 244	O 244	0	0
4	B	182	Total 182	O 182	0	0
4	D	236	Total 236	O 236	0	0
4	F	175	Total 175	O 175	0	0

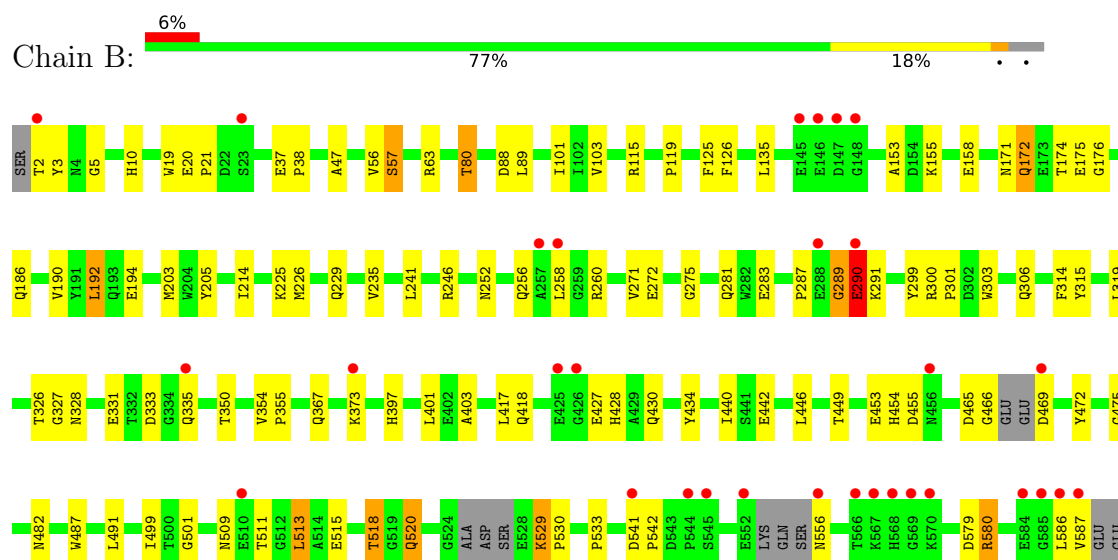
3 Residue-property plots

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: Endo-beta-N-acetylglucosaminidase

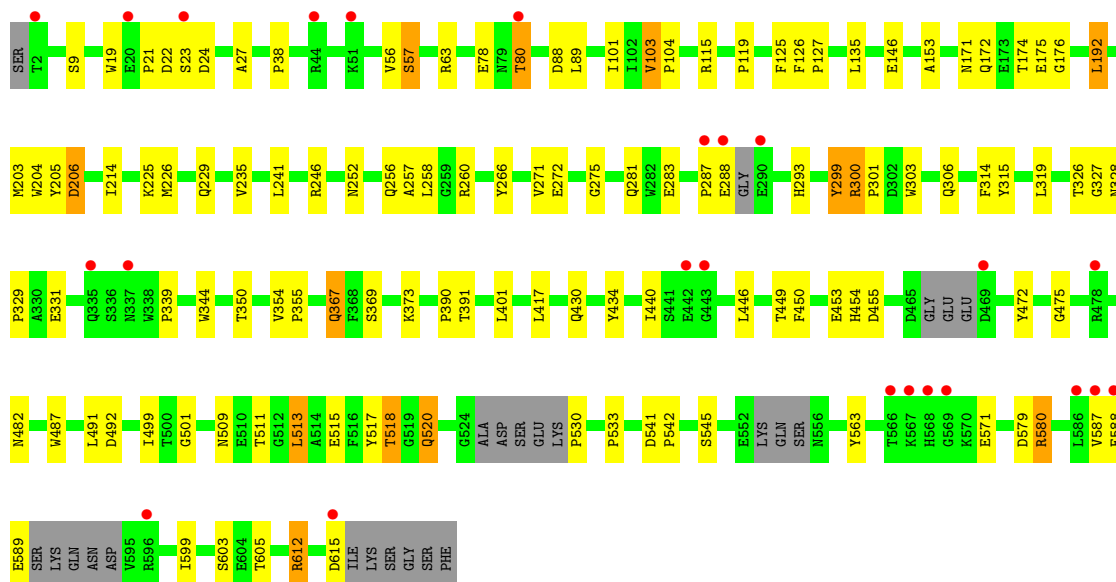
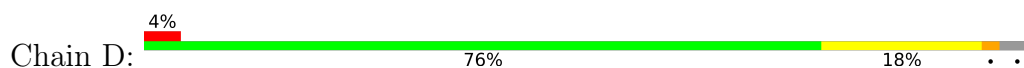


• Molecule 1: Endo-beta-N-acetylglucosaminidase

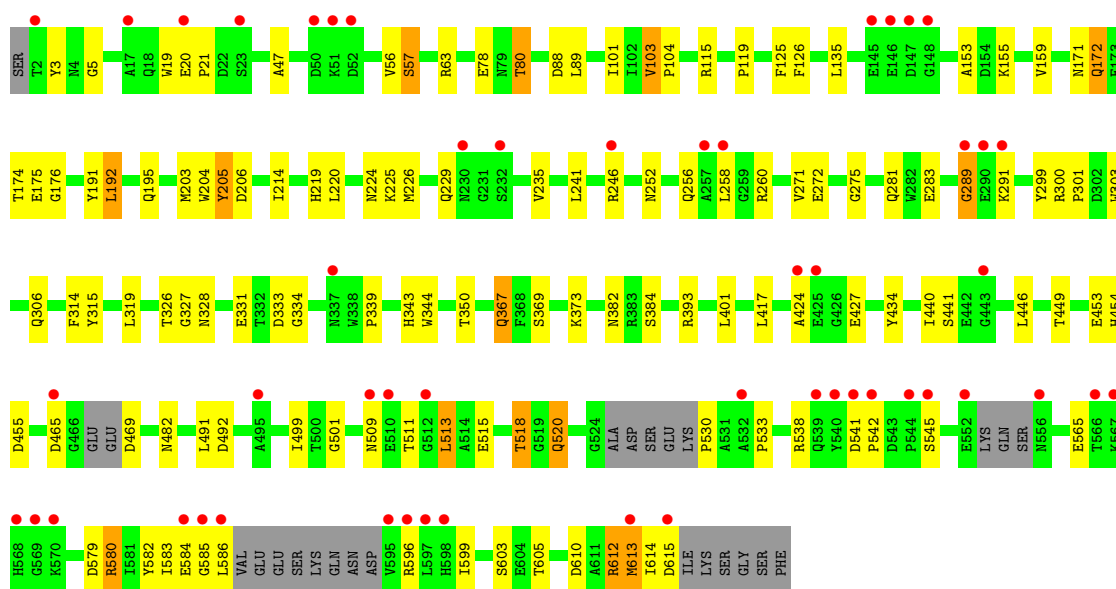
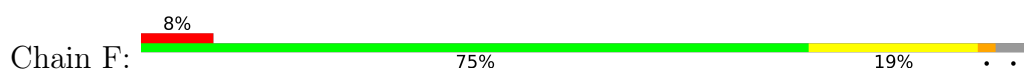





• Molecule 1: Endo-beta-N-acetylglucosaminidase



• Molecule 1: Endo-beta-N-acetylglucosaminidase



• Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose

Chain C:  67% 33%

BM11
MAN2
MAN3

- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose

Chain E:  33% 67%

BM11
MAN2
MAN3

- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose

Chain G:  33% 67%

BM11
MAN2
MAN3

- Molecule 2: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose

Chain H:  67% 33%

BM11
MAN2
MAN3

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	78.33Å 79.27Å 117.04Å 80.51° 83.84° 64.33°	Depositor
Resolution (Å)	35.41 – 2.45 35.41 – 2.45	Depositor EDS
% Data completeness (in resolution range)	94.2 (35.41-2.45) 94.2 (35.41-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.45Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.221 , 0.264 0.230 , 0.264	Depositor DCC
R_{free} test set	4331 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	36.4	Xtriage
Anisotropy	0.216	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	20045	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.43% 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: NGT, MAN, BMA

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	0.55	0/4927	0.61	0/6718
1	B	0.54	0/4902	0.60	2/6684 (0.0%)
1	D	0.56	2/4890 (0.0%)	0.61	1/6667 (0.0%)
1	F	0.51	0/4881	0.60	2/6655 (0.0%)
All	All	0.54	2/19600 (0.0%)	0.61	5/26724 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	299	TYR	CD2-CE2	-5.54	1.31	1.39
1	D	299	TYR	CD1-CE1	-5.26	1.31	1.39

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	300	ARG	N-CA-C	5.42	125.64	111.00
1	F	610	ASP	CB-CG-OD2	5.20	122.98	118.30
1	B	469	ASP	CB-CG-OD2	5.13	122.92	118.30
1	F	205	TYR	CB-CA-C	5.11	120.63	110.40
1	B	289	GLY	N-CA-C	-5.07	100.43	113.10

There are no chirality outliers.

There are no planarity outliers.

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	4781	0	4392	102	0
1	B	4757	0	4363	105	0
1	D	4746	0	4347	99	0
1	F	4736	0	4341	110	0
2	C	33	0	27	1	0
2	E	33	0	27	2	0
2	G	33	0	27	2	0
2	H	33	0	27	1	0
3	A	14	0	12	1	0
3	B	14	0	12	1	0
3	D	14	0	12	1	0
3	F	14	0	12	1	0
4	A	244	0	0	9	0
4	B	182	0	0	7	0
4	D	236	0	0	12	0
4	F	175	0	0	5	0
All	All	20045	0	17599	404	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 11.

All (404) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:547:ILE:CD1	1:A:586:LEU:HD13	1.55	1.36
1:D:588:GLU:O	1:D:589:GLU:HB2	1.45	1.16
1:D:545:SER:HA	1:D:587:VAL:HB	1.28	1.13
1:A:547:ILE:HD13	1:A:586:LEU:HD13	1.23	1.10
1:A:547:ILE:HD11	1:A:586:LEU:HD13	1.30	1.05
1:F:56:VAL:HG12	1:F:89:LEU:HB3	1.39	1.01
1:A:56:VAL:HG12	1:A:89:LEU:HB3	1.45	0.99
1:B:56:VAL:HG12	1:B:89:LEU:HB3	1.41	0.99
1:A:554:GLN:HG3	1:A:557:VAL:HG21	1.43	0.98
1:F:596:ARG:HD2	1:F:613:MET:CE	1.93	0.98
1:B:511:THR:HG22	1:B:513:LEU:H	1.26	0.98
1:F:511:THR:HG22	1:F:513:LEU:H	1.23	0.97
1:A:511:THR:HG22	1:A:513:LEU:H	1.29	0.96
1:A:587:VAL:O	1:A:588:GLU:HG3	1.64	0.96
1:D:56:VAL:HG12	1:D:89:LEU:HB3	1.48	0.95
1:D:511:THR:HG22	1:D:513:LEU:H	1.30	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:586:LEU:O	1:B:587:VAL:HG23	1.68	0.94
1:B:335:GLN:NE2	1:F:326:THR:OG1	2.02	0.93
1:F:596:ARG:HG2	1:F:615:ASP:OD1	1.75	0.87
1:A:545:SER:HA	1:A:587:VAL:HB	1.56	0.87
1:A:115:ARG:O	1:A:350:THR:HG21	1.77	0.83
1:A:547:ILE:HD13	1:A:586:LEU:CD1	2.07	0.83
1:F:115:ARG:O	1:F:350:THR:HG21	1.80	0.82
1:D:115:ARG:O	1:D:350:THR:HG21	1.79	0.82
1:A:554:GLN:HG3	1:A:557:VAL:CG2	2.11	0.81
1:A:587:VAL:O	1:A:588:GLU:CB	2.30	0.80
1:A:587:VAL:O	1:A:588:GLU:CG	2.29	0.79
1:B:586:LEU:O	1:B:587:VAL:CG2	2.30	0.79
1:D:390:PRO:HB3	4:D:832:HOH:O	1.84	0.78
1:B:19:TRP:CH2	1:B:21:PRO:HG3	2.19	0.77
1:B:397:HIS:CE1	1:F:289:GLY:HA2	2.19	0.77
1:D:272:GLU:OE1	2:G:1:BMA:O2	2.01	0.76
1:B:20:GLU:HA	1:B:20:GLU:OE1	1.85	0.76
1:F:579:ASP:OD1	1:F:580:ARG:HG2	1.86	0.75
1:A:547:ILE:CD1	1:A:586:LEU:CD1	2.51	0.75
1:F:57:SER:OG	1:F:301:PRO:HG2	1.87	0.74
1:F:596:ARG:HD2	1:F:613:MET:HE2	1.70	0.73
1:A:587:VAL:O	1:A:588:GLU:HB2	1.89	0.72
1:B:115:ARG:O	1:B:350:THR:HG21	1.90	0.72
1:F:271:VAL:HG22	1:F:299:TYR:O	1.90	0.72
1:A:579:ASP:OD1	1:A:580:ARG:HG2	1.90	0.71
1:B:579:ASP:OD1	1:B:580:ARG:HG2	1.90	0.70
1:F:533:PRO:O	1:F:612:ARG:HD2	1.90	0.70
1:F:565:GLU:OE1	1:F:596:ARG:NE	2.23	0.70
1:D:272:GLU:HG2	2:G:2:MAN:O4	1.90	0.70
1:A:547:ILE:HD11	1:A:586:LEU:CD1	2.14	0.70
1:D:545:SER:CA	1:D:587:VAL:HB	2.17	0.70
1:B:586:LEU:O	1:B:587:VAL:CB	2.38	0.70
1:D:579:ASP:OD1	1:D:580:ARG:HG2	1.91	0.70
1:F:509:ASN:OD1	1:F:511:THR:HB	1.91	0.70
1:B:417:LEU:HB3	1:B:518:THR:HG23	1.74	0.70
1:B:57:SER:OG	1:B:301:PRO:HG2	1.91	0.69
1:D:80:THR:HG21	4:D:838:HOH:O	1.92	0.69
1:B:511:THR:HG22	1:B:513:LEU:N	2.05	0.69
1:B:533:PRO:O	1:B:612:ARG:HD2	1.92	0.69
1:F:596:ARG:CD	1:F:613:MET:CE	2.71	0.69
1:F:63:ARG:NH1	1:F:306:GLN:HG2	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:PRO:O	1:A:612:ARG:HD2	1.93	0.68
1:B:63:ARG:NH1	1:B:306:GLN:HG2	2.07	0.68
1:D:9:SER:OG	4:D:692:HOH:O	1.97	0.68
1:B:190:VAL:O	1:B:194:GLU:HG3	1.94	0.68
1:A:63:ARG:NH1	1:A:306:GLN:HG2	2.09	0.68
1:F:538:ARG:HG3	4:F:798:HOH:O	1.93	0.68
4:B:676:HOH:O	2:E:2:MAN:O6	1.76	0.67
1:B:509:ASN:OD1	1:B:511:THR:HB	1.95	0.67
1:F:511:THR:HG22	1:F:513:LEU:N	2.03	0.67
1:D:509:ASN:OD1	1:D:511:THR:HB	1.95	0.67
1:D:533:PRO:O	1:D:612:ARG:HD2	1.93	0.67
1:F:291:LYS:HB2	4:F:668:HOH:O	1.95	0.67
1:D:511:THR:HG22	1:D:513:LEU:N	2.07	0.66
1:B:449:THR:OG1	1:B:520:GLN:HG2	1.96	0.66
1:A:556:ASN:OD1	1:A:556:ASN:N	2.29	0.65
1:F:417:LEU:HB3	1:F:518:THR:HG23	1.79	0.65
1:F:449:THR:OG1	1:F:520:GLN:HG2	1.96	0.65
1:A:57:SER:OG	1:A:301:PRO:HG2	1.97	0.64
1:D:63:ARG:NH1	1:D:306:GLN:HG2	2.12	0.64
1:A:511:THR:HG22	1:A:513:LEU:N	2.07	0.64
1:A:509:ASN:OD1	1:A:511:THR:HB	1.97	0.64
1:D:57:SER:OG	1:D:301:PRO:HG2	1.96	0.64
1:B:586:LEU:C	1:B:587:VAL:HG23	2.19	0.63
1:F:596:ARG:CG	1:F:613:MET:HE1	2.28	0.63
1:A:326:THR:HB	4:A:679:HOH:O	1.98	0.63
1:B:175:GLU:HG3	1:B:214:ILE:HD12	1.81	0.63
1:D:326:THR:HG21	1:D:331:GLU:O	1.99	0.63
1:B:56:VAL:HG11	1:B:203:MET:HE1	1.82	0.62
1:F:175:GLU:HG3	1:F:214:ILE:HD12	1.82	0.62
1:F:582:TYR:CE2	1:F:584:GLU:HG3	2.35	0.62
1:D:417:LEU:HB3	1:D:518:THR:HG23	1.80	0.62
1:B:511:THR:CG2	1:B:513:LEU:HB2	2.30	0.62
1:D:588:GLU:O	1:D:589:GLU:CB	2.29	0.62
1:A:326:THR:HG21	1:A:331:GLU:O	2.00	0.61
4:A:829:HOH:O	1:B:556:ASN:HB2	1.99	0.61
1:D:146:GLU:HG3	4:D:820:HOH:O	1.98	0.61
1:A:271:VAL:HG22	1:A:299:TYR:O	2.00	0.61
1:F:326:THR:HG21	1:F:331:GLU:O	1.99	0.61
1:A:326:THR:CG2	1:A:328:ASN:HB3	2.31	0.61
1:F:511:THR:CG2	1:F:513:LEU:HB2	2.31	0.61
1:B:586:LEU:O	1:B:587:VAL:HB	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:56:VAL:HG11	1:F:203:MET:HE1	1.83	0.60
1:D:326:THR:CG2	1:D:328:ASN:HB3	2.31	0.60
1:A:256:GLN:HG2	1:B:442:GLU:OE1	2.01	0.60
1:B:287:PRO:HG2	1:B:291:LYS:O	2.01	0.60
1:D:449:THR:OG1	1:D:520:GLN:HG2	2.01	0.60
1:D:326:THR:HB	4:D:661:HOH:O	2.02	0.60
1:D:19:TRP:CH2	1:D:21:PRO:HG3	2.37	0.59
1:A:175:GLU:HG3	1:A:214:ILE:HD12	1.84	0.59
1:F:465:ASP:HB3	4:F:633:HOH:O	2.02	0.59
1:A:449:THR:OG1	1:A:520:GLN:HG2	2.03	0.59
1:D:326:THR:HG22	1:D:328:ASN:N	2.18	0.59
1:D:440:ILE:HD11	1:D:499:ILE:HG13	1.85	0.59
1:F:596:ARG:HG2	1:F:613:MET:HE1	1.85	0.59
1:F:174:THR:C	1:F:214:ILE:HD11	2.23	0.59
1:D:487:TRP:CE2	4:D:792:HOH:O	2.56	0.58
1:D:175:GLU:HG3	1:D:214:ILE:HD12	1.86	0.58
1:B:326:THR:CG2	1:B:328:ASN:HB3	2.33	0.58
1:A:417:LEU:HB3	1:A:518:THR:HG23	1.84	0.58
1:A:566:THR:HG22	4:A:877:HOH:O	2.04	0.58
1:B:80:THR:HG21	4:B:629:HOH:O	2.02	0.58
1:B:271:VAL:HG22	1:B:299:TYR:O	2.03	0.58
1:B:287:PRO:O	1:B:289:GLY:O	2.21	0.58
1:A:262:PRO:HD3	1:B:442:GLU:OE1	2.04	0.57
1:B:326:THR:HG22	1:B:328:ASN:N	2.18	0.57
1:A:554:GLN:HG2	1:A:560:TYR:OH	2.04	0.57
1:A:319:LEU:HD21	1:A:327:GLY:HA2	1.86	0.57
1:A:511:THR:CG2	1:A:513:LEU:HB2	2.34	0.57
1:B:326:THR:HG21	1:B:331:GLU:O	2.05	0.57
1:F:205:TYR:OH	3:F:625:NGT:HC1	2.05	0.57
1:B:3:TYR:CZ	1:B:5:GLY:HA3	2.40	0.56
1:D:511:THR:CG2	1:D:513:LEU:HB2	2.35	0.56
1:A:19:TRP:CH2	1:A:21:PRO:HG3	2.40	0.56
1:F:565:GLU:OE1	1:F:596:ARG:NH2	2.38	0.56
1:B:319:LEU:HD21	1:B:327:GLY:HA2	1.87	0.56
1:D:56:VAL:HG11	1:D:203:MET:HE1	1.86	0.56
1:D:319:LEU:HD21	1:D:327:GLY:HA2	1.88	0.56
1:F:326:THR:CG2	1:F:328:ASN:HB3	2.35	0.56
1:A:80:THR:HG21	4:A:626:HOH:O	2.05	0.56
1:F:219:HIS:HE1	4:F:710:HOH:O	1.88	0.56
1:A:352:THR:HB	4:A:781:HOH:O	2.06	0.56
1:B:427:GLU:CG	1:B:428:HIS:N	2.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:THR:C	1:B:214:ILE:HD11	2.27	0.56
1:D:174:THR:C	1:D:214:ILE:HD11	2.25	0.56
1:B:135:LEU:HD11	1:B:176:GLY:O	2.06	0.56
1:F:135:LEU:HD11	1:F:176:GLY:O	2.06	0.56
1:F:272:GLU:OE1	2:H:1:BMA:O2	2.16	0.55
1:D:24:ASP:HB3	1:D:27:ALA:HB2	1.88	0.55
1:D:205:TYR:OH	3:D:625:NGT:HC1	2.06	0.55
1:F:326:THR:HG22	1:F:328:ASN:N	2.22	0.55
1:B:272:GLU:OE1	2:E:1:BMA:O2	2.20	0.55
1:D:204:TRP:CD1	1:D:205:TYR:O	2.60	0.55
1:D:283:GLU:CD	1:D:283:GLU:H	2.10	0.55
1:A:326:THR:HG22	1:A:328:ASN:N	2.21	0.55
1:A:174:THR:C	1:A:214:ILE:HD11	2.26	0.55
1:A:440:ILE:HD11	1:A:499:ILE:HG13	1.89	0.55
1:D:612:ARG:HD3	4:D:836:HOH:O	2.07	0.55
1:D:293:HIS:HE1	4:D:708:HOH:O	1.90	0.54
1:F:319:LEU:HD21	1:F:327:GLY:HA2	1.89	0.54
1:A:56:VAL:HG11	1:A:203:MET:HE1	1.88	0.54
1:B:440:ILE:HD11	1:B:499:ILE:HG13	1.88	0.54
1:A:326:THR:HG22	1:A:328:ASN:HB3	1.89	0.54
1:D:22:ASP:HB2	4:D:856:HOH:O	2.07	0.54
1:B:333:ASP:OD1	1:F:333:ASP:CG	2.46	0.54
1:B:283:GLU:CD	1:B:283:GLU:H	2.11	0.54
1:D:271:VAL:HG22	1:D:299:TYR:O	2.07	0.54
1:B:101:ILE:HB	1:B:125:PHE:O	2.08	0.53
1:F:204:TRP:CD1	1:F:205:TYR:O	2.62	0.53
1:F:605:THR:HG22	1:F:605:THR:O	2.09	0.53
1:F:204:TRP:NE1	1:F:205:TYR:O	2.41	0.53
1:A:63:ARG:NH1	4:A:788:HOH:O	2.41	0.53
1:A:283:GLU:H	1:A:283:GLU:CD	2.11	0.53
1:F:283:GLU:H	1:F:283:GLU:CD	2.11	0.53
1:A:272:GLU:OE1	2:C:1:BMA:O2	2.18	0.53
1:F:153:ALA:HB1	1:F:192:LEU:HD13	1.91	0.53
1:B:613:MET:HG3	4:B:695:HOH:O	2.09	0.52
1:D:204:TRP:NE1	1:D:205:TYR:O	2.42	0.52
1:F:440:ILE:HD11	1:F:499:ILE:HG13	1.90	0.52
1:F:56:VAL:HG12	1:F:89:LEU:CB	2.26	0.52
1:F:545:SER:O	1:F:585:GLY:HA2	2.10	0.52
1:D:326:THR:HG22	1:D:328:ASN:HB3	1.90	0.52
1:A:605:THR:O	1:A:605:THR:HG22	2.09	0.52
1:F:613:MET:O	1:F:614:ILE:HD13	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:GLY:O	1:B:290:GLU:O	2.28	0.52
1:A:533:PRO:HG2	1:A:599:ILE:HG22	1.92	0.52
1:D:367:GLN:OE1	1:D:369:SER:OG	2.20	0.52
1:A:153:ALA:HB1	1:A:192:LEU:HD13	1.92	0.52
1:B:205:TYR:OH	3:B:625:NGT:HC1	2.09	0.52
1:D:38:PRO:HD2	4:D:758:HOH:O	2.10	0.52
1:F:424:ALA:O	1:F:427:GLU:HB3	2.10	0.52
1:B:434:TYR:O	1:B:501:GLY:HA2	2.10	0.52
1:F:101:ILE:HB	1:F:125:PHE:O	2.10	0.52
1:B:80:THR:O	1:B:80:THR:OG1	2.28	0.51
1:A:534:ASN:ND2	4:A:907:HOH:O	2.42	0.51
1:D:153:ALA:HB1	1:D:192:LEU:HD13	1.91	0.51
1:F:3:TYR:CZ	1:F:5:GLY:HA3	2.44	0.51
1:F:326:THR:HG22	1:F:328:ASN:HB3	1.93	0.51
1:B:225:LYS:HB2	1:B:258:LEU:HD11	1.93	0.51
1:A:80:THR:OG1	1:A:80:THR:O	2.29	0.51
1:D:605:THR:HG22	1:D:605:THR:O	2.11	0.51
1:F:174:THR:O	1:F:214:ILE:HD11	2.11	0.51
1:F:334:GLY:HA3	1:F:343:HIS:CE1	2.45	0.51
1:A:300:ARG:N	1:A:301:PRO:HD3	2.25	0.51
1:A:275:GLY:HA3	1:A:303:TRP:CD2	2.46	0.51
1:B:599:ILE:N	1:B:599:ILE:HD12	2.25	0.51
1:D:80:THR:O	1:D:80:THR:OG1	2.29	0.51
1:A:367:GLN:OE1	1:A:369:SER:OG	2.19	0.51
1:D:135:LEU:HD11	1:D:176:GLY:O	2.11	0.51
1:F:583:ILE:HG21	1:F:586:LEU:HD22	1.92	0.51
1:B:335:GLN:OE1	1:F:333:ASP:CB	2.60	0.50
1:B:605:THR:HG22	1:B:605:THR:O	2.11	0.50
1:F:565:GLU:OE1	1:F:596:ARG:CZ	2.59	0.50
1:A:135:LEU:HD11	1:A:176:GLY:O	2.12	0.50
1:B:229:GLN:OE1	1:B:260:ARG:HD3	2.11	0.50
1:F:541:ASP:HB2	1:F:542:PRO:HD3	1.92	0.50
1:F:300:ARG:N	1:F:301:PRO:HD3	2.26	0.50
1:D:487:TRP:NE1	4:D:792:HOH:O	2.34	0.50
1:F:596:ARG:CD	1:F:613:MET:HE1	2.41	0.50
1:D:326:THR:HG22	1:D:328:ASN:H	1.76	0.50
1:D:580:ARG:HG2	1:D:580:ARG:HH11	1.77	0.50
1:B:275:GLY:HA3	1:B:303:TRP:CD2	2.47	0.50
1:B:326:THR:HG22	1:B:328:ASN:HB3	1.93	0.50
1:A:596:ARG:HD3	1:A:613:MET:CE	2.42	0.50
1:F:191:TYR:CZ	1:F:195:GLN:HG3	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:246:ARG:HE	1:D:281:GLN:HG3	1.77	0.50
1:F:229:GLN:OE1	1:F:260:ARG:HD3	2.12	0.50
1:A:446:LEU:HG	1:A:491:LEU:HD11	1.94	0.49
1:B:246:ARG:HD3	4:B:913:HOH:O	2.12	0.49
1:A:287:PRO:HG3	1:A:293:HIS:CE1	2.47	0.49
1:F:80:THR:OG1	1:F:80:THR:O	2.28	0.49
1:F:393:ARG:HD2	4:F:695:HOH:O	2.12	0.49
1:B:153:ALA:HB1	1:B:192:LEU:HD13	1.94	0.49
1:D:275:GLY:HA3	1:D:303:TRP:CD2	2.48	0.49
1:D:446:LEU:HG	1:D:491:LEU:HD11	1.95	0.48
1:A:529:LYS:HE3	1:A:609:SER:HA	1.94	0.48
1:B:454:HIS:O	1:B:455:ASP:HB2	2.12	0.48
1:F:275:GLY:HA3	1:F:303:TRP:CD2	2.48	0.48
1:B:56:VAL:HG12	1:B:89:LEU:CB	2.29	0.48
1:B:88:ASP:O	1:B:119:PRO:HD2	2.13	0.48
1:B:446:LEU:HG	1:B:491:LEU:HD11	1.94	0.48
1:B:289:GLY:C	1:B:290:GLU:O	2.50	0.48
1:B:300:ARG:NH2	4:B:889:HOH:O	2.42	0.48
1:F:599:ILE:N	1:F:599:ILE:HD12	2.27	0.48
1:F:175:GLU:HG3	1:F:214:ILE:CD1	2.44	0.48
1:A:252:ASN:O	1:A:256:GLN:HG3	2.14	0.48
1:F:225:LYS:HB2	1:F:258:LEU:HD11	1.94	0.48
1:B:453:GLU:HB2	1:B:515:GLU:HB3	1.95	0.48
1:B:520:GLN:O	1:B:520:GLN:HG3	2.11	0.48
1:F:80:THR:HG23	1:F:315:TYR:HE1	1.78	0.48
1:A:580:ARG:HG2	1:A:580:ARG:HH11	1.78	0.47
1:B:246:ARG:HE	1:B:281:GLN:HG3	1.79	0.47
1:A:434:TYR:O	1:A:501:GLY:HA2	2.14	0.47
1:D:300:ARG:N	1:D:301:PRO:HD3	2.29	0.47
1:A:246:ARG:HE	1:A:281:GLN:HG3	1.79	0.47
1:B:511:THR:HG22	1:B:513:LEU:HB2	1.96	0.47
1:B:20:GLU:OE1	1:B:158:GLU:OE2	2.32	0.47
1:D:434:TYR:O	1:D:501:GLY:HA2	2.14	0.47
1:B:326:THR:HG22	1:B:328:ASN:H	1.78	0.47
1:D:56:VAL:HG11	1:D:203:MET:CE	2.44	0.47
1:F:19:TRP:CZ3	1:F:21:PRO:HD3	2.49	0.47
1:D:225:LYS:HB2	1:D:258:LEU:HD11	1.96	0.47
1:F:226:MET:O	1:F:235:VAL:HG21	2.14	0.47
1:B:291:LYS:HB3	4:B:767:HOH:O	2.15	0.47
1:B:397:HIS:ND1	1:F:289:GLY:CA	2.78	0.47
1:A:88:ASP:O	1:A:119:PRO:HD2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:541:ASP:HB2	1:B:542:PRO:HD3	1.96	0.46
1:F:434:TYR:O	1:F:501:GLY:HA2	2.14	0.46
1:B:335:GLN:OE1	1:F:333:ASP:HB3	2.15	0.46
1:B:300:ARG:N	1:B:301:PRO:HD3	2.29	0.46
1:D:533:PRO:HG2	1:D:599:ILE:HG22	1.97	0.46
1:D:252:ASN:O	1:D:256:GLN:HG3	2.15	0.46
1:F:246:ARG:HE	1:F:281:GLN:HG3	1.80	0.46
1:F:580:ARG:HG2	1:F:580:ARG:HH11	1.80	0.46
1:A:101:ILE:HB	1:A:125:PHE:O	2.15	0.46
1:A:225:LYS:HB2	1:A:258:LEU:HD11	1.96	0.46
1:D:257:ALA:O	1:F:441:SER:HB2	2.16	0.46
1:D:80:THR:HG23	1:D:314:PHE:HE2	1.81	0.46
1:B:63:ARG:HH12	1:B:306:GLN:HG2	1.81	0.46
1:B:80:THR:HG23	1:B:315:TYR:HE1	1.81	0.46
1:D:454:HIS:CD2	1:D:513:LEU:HB3	2.50	0.46
1:D:587:VAL:O	1:D:587:VAL:HG12	2.15	0.46
1:D:101:ILE:HB	1:D:125:PHE:O	2.16	0.46
1:A:175:GLU:HG3	1:A:214:ILE:CD1	2.45	0.45
1:D:287:PRO:HG3	1:D:293:HIS:NE2	2.31	0.45
1:A:354:VAL:HG13	1:A:355:PRO:HA	1.98	0.45
1:A:373:LYS:HE2	1:A:482:ASN:ND2	2.31	0.45
1:F:367:GLN:OE1	1:F:369:SER:OG	2.21	0.45
1:B:47:ALA:HB1	1:F:47:ALA:CB	2.46	0.45
1:A:430:GLN:HG2	1:A:472:TYR:CE2	2.52	0.45
1:A:80:THR:HG23	1:A:315:TYR:HE1	1.81	0.45
1:F:454:HIS:O	1:F:455:ASP:HB2	2.16	0.45
1:F:565:GLU:CD	1:F:596:ARG:HE	2.18	0.45
1:A:3:TYR:CZ	1:A:5:GLY:HA3	2.52	0.45
1:B:19:TRP:O	1:B:155:LYS:NZ	2.37	0.45
1:D:339:PRO:HG2	1:D:344:TRP:CH2	2.52	0.45
1:D:391:THR:HA	4:D:657:HOH:O	2.16	0.45
1:A:599:ILE:N	1:A:599:ILE:HD12	2.32	0.45
1:F:103:VAL:HA	1:F:104:PRO:HD3	1.78	0.45
1:A:175:GLU:HA	1:A:214:ILE:HD12	1.99	0.45
1:A:80:THR:HG23	1:A:314:PHE:HE2	1.82	0.44
1:D:80:THR:HG23	1:D:315:TYR:HE1	1.82	0.44
1:A:454:HIS:O	1:A:455:ASP:HB2	2.16	0.44
1:D:9:SER:O	1:D:104:PRO:HD2	2.18	0.44
1:D:56:VAL:HG13	1:D:266:TYR:CE1	2.52	0.44
1:D:175:GLU:HA	1:D:214:ILE:HD12	2.00	0.44
1:D:599:ILE:N	1:D:599:ILE:HD12	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:88:ASP:O	1:F:119:PRO:HD2	2.17	0.44
1:F:533:PRO:HG2	1:F:599:ILE:HG22	1.99	0.44
1:F:511:THR:HG22	1:F:513:LEU:HB2	1.99	0.44
1:F:20:GLU:HA	1:F:21:PRO:HD2	1.84	0.44
1:F:175:GLU:HA	1:F:214:ILE:HD12	1.98	0.44
1:F:454:HIS:CD2	1:F:513:LEU:HB3	2.52	0.44
1:B:430:GLN:HG2	1:B:472:TYR:CE2	2.53	0.44
1:F:520:GLN:HG3	1:F:520:GLN:O	2.13	0.44
1:A:56:VAL:HG11	1:A:203:MET:CE	2.47	0.44
1:A:205:TYR:OH	3:A:625:NGT:HC1	2.17	0.44
1:A:454:HIS:CD2	1:A:513:LEU:HB3	2.52	0.44
1:B:454:HIS:CD2	1:B:513:LEU:HB3	2.52	0.44
1:D:175:GLU:HG3	1:D:214:ILE:CD1	2.48	0.44
1:D:354:VAL:HG13	1:D:355:PRO:HA	1.98	0.44
1:B:47:ALA:CB	1:F:47:ALA:CB	2.96	0.44
1:D:206:ASP:O	1:D:206:ASP:CG	2.56	0.44
1:D:430:GLN:HG2	1:D:472:TYR:CE2	2.53	0.44
1:D:454:HIS:O	1:D:455:ASP:HB2	2.17	0.44
1:F:326:THR:HG22	1:F:328:ASN:H	1.82	0.44
1:F:334:GLY:CA	1:F:343:HIS:CE1	3.01	0.43
1:A:326:THR:HG22	1:A:328:ASN:CB	2.48	0.43
1:A:554:GLN:HG2	1:A:554:GLN:H	1.46	0.43
1:B:226:MET:O	1:B:235:VAL:HG21	2.17	0.43
1:D:373:LYS:HE2	1:D:482:ASN:ND2	2.33	0.43
1:F:252:ASN:O	1:F:256:GLN:HG3	2.18	0.43
1:D:78:GLU:O	1:D:80:THR:HG22	2.18	0.43
1:D:475:GLY:HA3	1:D:487:TRP:CE3	2.53	0.43
1:F:446:LEU:HG	1:F:491:LEU:HD11	1.99	0.43
1:A:326:THR:HG22	1:A:328:ASN:H	1.83	0.43
1:B:335:GLN:CD	1:F:333:ASP:HB2	2.38	0.43
1:B:465:ASP:HA	1:B:466:GLY:HA2	1.62	0.43
1:B:475:GLY:HA3	1:B:487:TRP:CE3	2.54	0.43
1:B:613:MET:CG	4:B:695:HOH:O	2.65	0.43
1:D:453:GLU:HB2	1:D:515:GLU:HB3	2.00	0.43
1:F:80:THR:HG23	1:F:314:PHE:HE2	1.84	0.43
1:A:24:ASP:HB3	1:A:27:ALA:HB2	2.00	0.43
1:B:56:VAL:HG11	1:B:203:MET:CE	2.48	0.43
1:B:126:PHE:HB2	1:B:172:GLN:HA	2.00	0.43
1:B:373:LYS:HE2	1:B:482:ASN:ND2	2.33	0.43
1:A:339:PRO:HG2	1:A:344:TRP:CH2	2.54	0.43
1:B:37:GLU:HA	1:B:38:PRO:HD3	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:GLU:HG3	1:B:214:ILE:CD1	2.46	0.43
1:F:582:TYR:OH	1:F:584:GLU:HG2	2.18	0.43
1:A:78:GLU:O	1:A:80:THR:HG22	2.19	0.43
1:A:192:LEU:HD12	1:A:192:LEU:HA	1.87	0.43
1:A:453:GLU:HB2	1:A:515:GLU:HB3	2.00	0.43
1:B:175:GLU:HA	1:B:214:ILE:HD12	2.00	0.43
1:B:354:VAL:HG13	1:B:355:PRO:HA	2.00	0.43
1:F:56:VAL:HG11	1:F:203:MET:CE	2.48	0.43
1:B:427:GLU:HG3	1:B:428:HIS:H	1.83	0.43
1:B:529:LYS:HA	1:B:530:PRO:HD3	1.80	0.43
1:D:563:TYR:HA	1:D:571:GLU:O	2.19	0.43
1:D:229:GLN:OE1	1:D:260:ARG:HD3	2.18	0.42
1:F:339:PRO:HG2	1:F:344:TRP:CH2	2.53	0.42
1:B:397:HIS:CE1	1:F:289:GLY:CA	2.98	0.42
1:D:520:GLN:O	1:D:520:GLN:HG3	2.16	0.42
1:A:469:ASP:N	4:A:652:HOH:O	2.52	0.42
1:F:582:TYR:OH	1:F:584:GLU:CG	2.68	0.42
1:D:226:MET:O	1:D:235:VAL:HG21	2.20	0.42
1:D:80:THR:CG2	1:D:314:PHE:HE2	2.32	0.42
1:D:326:THR:HG22	1:D:328:ASN:CB	2.49	0.42
1:A:596:ARG:HB3	1:A:613:MET:HE2	2.01	0.42
1:A:328:ASN:HA	1:A:329:PRO:HD2	1.89	0.42
1:D:587:VAL:O	1:D:587:VAL:CG1	2.68	0.42
1:D:88:ASP:O	1:D:119:PRO:HD2	2.20	0.42
1:F:382:ASN:OD1	1:F:384:SER:HB2	2.19	0.42
1:F:155:LYS:O	1:F:159:VAL:HG23	2.20	0.41
1:A:80:THR:CG2	1:A:314:PHE:HE2	2.33	0.41
1:B:598:HIS:CE1	1:B:613:MET:HG2	2.56	0.41
1:D:511:THR:HG22	1:D:513:LEU:HB2	2.02	0.41
1:F:220:LEU:HD12	1:F:224:ASN:OD1	2.20	0.41
1:A:450:PHE:HA	1:A:517:TYR:O	2.20	0.41
1:D:541:ASP:HB2	1:D:542:PRO:HD3	2.01	0.41
1:B:252:ASN:O	1:B:256:GLN:HG3	2.19	0.41
1:B:533:PRO:HG2	1:B:599:ILE:HG22	2.02	0.41
1:D:328:ASN:HA	1:D:329:PRO:HD2	1.90	0.41
1:F:80:THR:CG2	1:F:314:PHE:HE2	2.34	0.41
1:F:126:PHE:HB2	1:F:172:GLN:HA	2.03	0.41
1:A:511:THR:HG22	1:A:513:LEU:HB2	2.01	0.41
1:A:520:GLN:O	1:A:520:GLN:HG3	2.18	0.41
1:F:530:PRO:HG3	1:F:603:SER:HB3	2.02	0.41
1:A:475:GLY:HA3	1:A:487:TRP:CE3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:103:VAL:HA	1:D:104:PRO:HD3	1.79	0.41
1:F:78:GLU:O	1:F:80:THR:HG22	2.20	0.41
1:A:185:MET:HE2	1:A:185:MET:O	2.21	0.41
1:A:338:TRP:O	4:A:649:HOH:O	2.21	0.41
1:A:359:HIS:CD2	1:A:412:GLU:HB2	2.56	0.41
1:B:135:LEU:HD11	1:B:176:GLY:C	2.41	0.41
1:F:373:LYS:HE2	1:F:482:ASN:ND2	2.36	0.41
1:F:453:GLU:HB2	1:F:515:GLU:HB3	2.03	0.41
1:B:80:THR:HG23	1:B:314:PHE:HE2	1.86	0.40
1:B:186:GLN:O	1:B:190:VAL:HG23	2.21	0.40
1:A:530:PRO:O	1:A:609:SER:HB2	2.22	0.40
1:B:403:ALA:HA	1:B:418:GLN:O	2.21	0.40
1:B:427:GLU:HG2	1:B:428:HIS:N	2.36	0.40
1:D:63:ARG:HH12	1:D:306:GLN:HG2	1.85	0.40
1:D:126:PHE:HA	1:D:127:PRO:HD3	1.91	0.40
1:D:450:PHE:HA	1:D:517:TYR:O	2.22	0.40
1:A:63:ARG:HH12	1:A:306:GLN:HG2	1.83	0.40
1:A:226:MET:O	1:A:235:VAL:HG21	2.22	0.40
1:D:530:PRO:HG3	1:D:603:SER:HB3	2.02	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	593/621 (96%)	570 (96%)	23 (4%)	0	100	100
1	B	589/621 (95%)	566 (96%)	21 (4%)	2 (0%)	41	49
1	D	585/621 (94%)	565 (97%)	19 (3%)	1 (0%)	47	57
1	F	586/621 (94%)	562 (96%)	22 (4%)	2 (0%)	41	49
All	All	2353/2484 (95%)	2263 (96%)	85 (4%)	5 (0%)	47	57

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	290	GLU
1	B	10	HIS
1	F	206	ASP
1	D	206	ASP
1	F	289	GLY

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	498/515 (97%)	477 (96%)	21 (4%)	30	39
1	B	494/515 (96%)	477 (97%)	17 (3%)	37	48
1	D	493/515 (96%)	475 (96%)	18 (4%)	34	45
1	F	492/515 (96%)	475 (96%)	17 (4%)	36	47
All	All	1977/2060 (96%)	1904 (96%)	73 (4%)	34	45

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

Mol	Chain	Res	Type
1	A	57	SER
1	A	80	THR
1	A	103	VAL
1	A	171	ASN
1	A	172	GLN
1	A	192	LEU
1	A	206	ASP
1	A	241	LEU
1	A	367	GLN
1	A	401	LEU
1	A	492	ASP
1	A	513	LEU
1	A	518	THR
1	A	520	GLN
1	A	554	GLN

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Mol	Chain	Res	Type
1	A	556	ASN
1	A	580	ARG
1	A	584	GLU
1	A	608	PRO
1	A	612	ARG
1	A	613	MET
1	B	2	THR
1	B	57	SER
1	B	80	THR
1	B	103	VAL
1	B	171	ASN
1	B	172	GLN
1	B	192	LEU
1	B	241	LEU
1	B	290	GLU
1	B	367	GLN
1	B	401	LEU
1	B	513	LEU
1	B	518	THR
1	B	520	GLN
1	B	529	LYS
1	B	580	ARG
1	B	612	ARG
1	D	23	SER
1	D	57	SER
1	D	80	THR
1	D	103	VAL
1	D	171	ASN
1	D	172	GLN
1	D	192	LEU
1	D	241	LEU
1	D	288	GLU
1	D	367	GLN
1	D	401	LEU
1	D	492	ASP
1	D	513	LEU
1	D	518	THR
1	D	520	GLN
1	D	580	ARG
1	D	612	ARG
1	D	615	ASP
1	F	57	SER

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Mol	Chain	Res	Type
1	F	80	THR
1	F	103	VAL
1	F	171	ASN
1	F	172	GLN
1	F	192	LEU
1	F	241	LEU
1	F	367	GLN
1	F	401	LEU
1	F	469	ASP
1	F	492	ASP
1	F	513	LEU
1	F	518	THR
1	F	520	GLN
1	F	580	ARG
1	F	612	ARG
1	F	613	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	428	HIS
1	B	335	GLN
1	D	48	ASN
1	D	250	GLN
1	D	293	HIS
1	D	539	GLN
1	F	48	ASN
1	F	171	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 ⓘ

12 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BMA	C	1	3,2	11,11,12	1.24	1 (9%)	15,15,17	1.93	5 (33%)
2	MAN	C	2	2	11,11,12	1.78	3 (27%)	15,15,17	2.31	7 (46%)
2	MAN	C	3	2	11,11,12	1.09	1 (9%)	15,15,17	2.34	7 (46%)
2	BMA	E	1	3,2	11,11,12	1.24	1 (9%)	15,15,17	1.93	5 (33%)
2	MAN	E	2	2	11,11,12	1.77	2 (18%)	15,15,17	2.31	7 (46%)
2	MAN	E	3	2	11,11,12	1.09	1 (9%)	15,15,17	2.35	7 (46%)
2	BMA	G	1	3,2	11,11,12	1.24	1 (9%)	15,15,17	1.92	5 (33%)
2	MAN	G	2	2	11,11,12	1.79	3 (27%)	15,15,17	2.31	7 (46%)
2	MAN	G	3	2	11,11,12	1.09	1 (9%)	15,15,17	2.35	7 (46%)
2	BMA	H	1	3,2	11,11,12	1.23	1 (9%)	15,15,17	1.94	5 (33%)
2	MAN	H	2	2	11,11,12	1.78	3 (27%)	15,15,17	2.30	7 (46%)
2	MAN	H	3	2	11,11,12	1.08	1 (9%)	15,15,17	2.34	7 (46%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BMA	C	1	3,2	-	0/2/19/22	0/1/1/1
2	MAN	C	2	2	-	2/2/19/22	0/1/1/1
2	MAN	C	3	2	-	0/2/19/22	0/1/1/1
2	BMA	E	1	3,2	-	0/2/19/22	0/1/1/1
2	MAN	E	2	2	-	2/2/19/22	0/1/1/1
2	MAN	E	3	2	-	0/2/19/22	0/1/1/1
2	BMA	G	1	3,2	-	0/2/19/22	0/1/1/1
2	MAN	G	2	2	-	2/2/19/22	0/1/1/1
2	MAN	G	3	2	-	0/2/19/22	0/1/1/1
2	BMA	H	1	3,2	-	0/2/19/22	0/1/1/1
2	MAN	H	2	2	-	2/2/19/22	0/1/1/1
2	MAN	H	3	2	-	0/2/19/22	0/1/1/1

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2	MAN	C2-C3	4.04	1.58	1.52
2	H	2	MAN	C2-C3	4.04	1.58	1.52
2	C	2	MAN	C2-C3	4.03	1.58	1.52
2	G	2	MAN	C2-C3	4.03	1.58	1.52
2	G	1	BMA	C1-C2	3.04	1.59	1.52
2	C	1	BMA	C1-C2	3.02	1.59	1.52
2	E	1	BMA	C1-C2	3.01	1.59	1.52
2	H	1	BMA	C1-C2	2.99	1.59	1.52
2	G	2	MAN	O3-C3	-2.67	1.36	1.43
2	C	2	MAN	O3-C3	-2.65	1.36	1.43
2	E	2	MAN	O3-C3	-2.64	1.36	1.43
2	H	2	MAN	O3-C3	-2.64	1.36	1.43
2	G	3	MAN	O2-C2	-2.58	1.37	1.43
2	C	3	MAN	O2-C2	-2.57	1.37	1.43
2	E	3	MAN	O2-C2	-2.56	1.37	1.43
2	H	3	MAN	O2-C2	-2.54	1.38	1.43
2	H	2	MAN	O2-C2	-2.03	1.39	1.43
2	G	2	MAN	O2-C2	-2.03	1.39	1.43
2	C	2	MAN	O2-C2	-2.02	1.39	1.43

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1	BMA	O2-C2-C1	4.49	118.34	109.15
2	C	1	BMA	O2-C2-C1	4.48	118.31	109.15
2	G	1	BMA	O2-C2-C1	4.47	118.29	109.15
2	E	1	BMA	O2-C2-C1	4.46	118.28	109.15
2	G	3	MAN	O2-C2-C3	4.34	118.83	110.14
2	E	3	MAN	O2-C2-C3	4.33	118.82	110.14
2	C	3	MAN	O2-C2-C3	4.31	118.78	110.14
2	H	3	MAN	O2-C2-C3	4.30	118.75	110.14
2	H	3	MAN	O3-C3-C2	4.04	117.73	109.99
2	E	3	MAN	O3-C3-C2	4.03	117.71	109.99
2	C	3	MAN	O3-C3-C2	4.03	117.70	109.99
2	G	3	MAN	O3-C3-C2	4.02	117.69	109.99
2	E	2	MAN	O5-C5-C6	3.75	113.09	107.20
2	C	2	MAN	O5-C5-C6	3.74	113.06	107.20
2	H	2	MAN	O3-C3-C2	3.73	117.15	109.99
2	G	2	MAN	O5-C5-C6	3.73	113.06	107.20
2	C	2	MAN	O3-C3-C2	3.72	117.11	109.99
2	G	2	MAN	O3-C3-C2	3.71	117.10	109.99
2	H	2	MAN	O5-C5-C6	3.71	113.02	107.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	2	MAN	O3-C3-C2	3.71	117.10	109.99
2	G	2	MAN	O2-C2-C3	3.53	117.21	110.14
2	H	2	MAN	O2-C2-C3	3.51	117.17	110.14
2	C	2	MAN	O2-C2-C3	3.51	117.16	110.14
2	E	2	MAN	O2-C2-C3	3.50	117.15	110.14
2	E	2	MAN	O3-C3-C4	3.15	117.63	110.35
2	G	2	MAN	O3-C3-C4	3.13	117.59	110.35
2	C	2	MAN	O3-C3-C4	3.13	117.59	110.35
2	H	2	MAN	O3-C3-C4	3.13	117.58	110.35
2	E	3	MAN	C1-O5-C5	3.00	116.25	112.19
2	C	3	MAN	C1-O5-C5	3.00	116.25	112.19
2	H	3	MAN	C1-O5-C5	3.00	116.25	112.19
2	G	3	MAN	C1-O5-C5	2.99	116.25	112.19
2	G	2	MAN	O5-C1-C2	-2.93	106.25	110.77
2	C	2	MAN	O5-C1-C2	-2.91	106.28	110.77
2	H	2	MAN	O5-C1-C2	-2.90	106.30	110.77
2	E	2	MAN	O5-C1-C2	-2.89	106.31	110.77
2	E	3	MAN	C1-C2-C3	-2.85	106.17	109.67
2	G	3	MAN	C1-C2-C3	-2.81	106.21	109.67
2	H	1	BMA	O4-C4-C5	2.81	116.27	109.30
2	C	3	MAN	C1-C2-C3	-2.81	106.22	109.67
2	E	1	BMA	O4-C4-C5	2.80	116.24	109.30
2	E	1	BMA	O2-C2-C3	2.78	115.71	110.14
2	C	1	BMA	O2-C2-C3	2.78	115.71	110.14
2	C	1	BMA	O4-C4-C5	2.78	116.20	109.30
2	H	1	BMA	O2-C2-C3	2.78	115.70	110.14
2	G	1	BMA	O2-C2-C3	2.77	115.68	110.14
2	G	1	BMA	O4-C4-C5	2.77	116.16	109.30
2	H	3	MAN	C1-C2-C3	-2.76	106.27	109.67
2	H	1	BMA	O5-C5-C6	2.75	111.52	107.20
2	H	3	MAN	O2-C2-C1	2.72	114.73	109.15
2	C	1	BMA	O5-C5-C6	2.72	111.47	107.20
2	C	3	MAN	O2-C2-C1	2.72	114.71	109.15
2	E	3	MAN	O2-C2-C1	2.71	114.70	109.15
2	E	1	BMA	O5-C5-C6	2.71	111.45	107.20
2	G	3	MAN	O2-C2-C1	2.71	114.69	109.15
2	G	1	BMA	O5-C5-C6	2.70	111.44	107.20
2	E	3	MAN	O5-C5-C6	2.65	111.36	107.20
2	H	3	MAN	O5-C5-C6	2.63	111.32	107.20
2	C	3	MAN	O5-C5-C6	2.62	111.31	107.20
2	G	3	MAN	O5-C5-C6	2.61	111.30	107.20
2	G	3	MAN	O4-C4-C5	2.37	115.19	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	3	MAN	O4-C4-C5	2.36	115.15	109.30
2	E	3	MAN	O4-C4-C5	2.35	115.14	109.30
2	C	3	MAN	O4-C4-C5	2.35	115.14	109.30
2	C	2	MAN	C2-C3-C4	2.18	114.66	110.89
2	E	2	MAN	C2-C3-C4	2.17	114.65	110.89
2	H	2	MAN	C2-C3-C4	2.17	114.65	110.89
2	G	2	MAN	C1-O5-C5	2.17	115.13	112.19
2	C	2	MAN	C1-O5-C5	2.17	115.13	112.19
2	G	2	MAN	C2-C3-C4	2.16	114.64	110.89
2	E	2	MAN	C1-O5-C5	2.15	115.10	112.19
2	H	2	MAN	C1-O5-C5	2.13	115.08	112.19
2	C	1	BMA	O5-C1-C2	-2.07	107.57	110.77
2	E	1	BMA	O5-C1-C2	-2.07	107.57	110.77
2	H	1	BMA	O5-C1-C2	-2.07	107.58	110.77
2	G	1	BMA	O5-C1-C2	-2.05	107.60	110.77

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	2	MAN	C4-C5-C6-O6
2	E	2	MAN	C4-C5-C6-O6
2	G	2	MAN	C4-C5-C6-O6
2	H	2	MAN	C4-C5-C6-O6
2	C	2	MAN	O5-C5-C6-O6
2	G	2	MAN	O5-C5-C6-O6
2	H	2	MAN	O5-C5-C6-O6
2	E	2	MAN	O5-C5-C6-O6

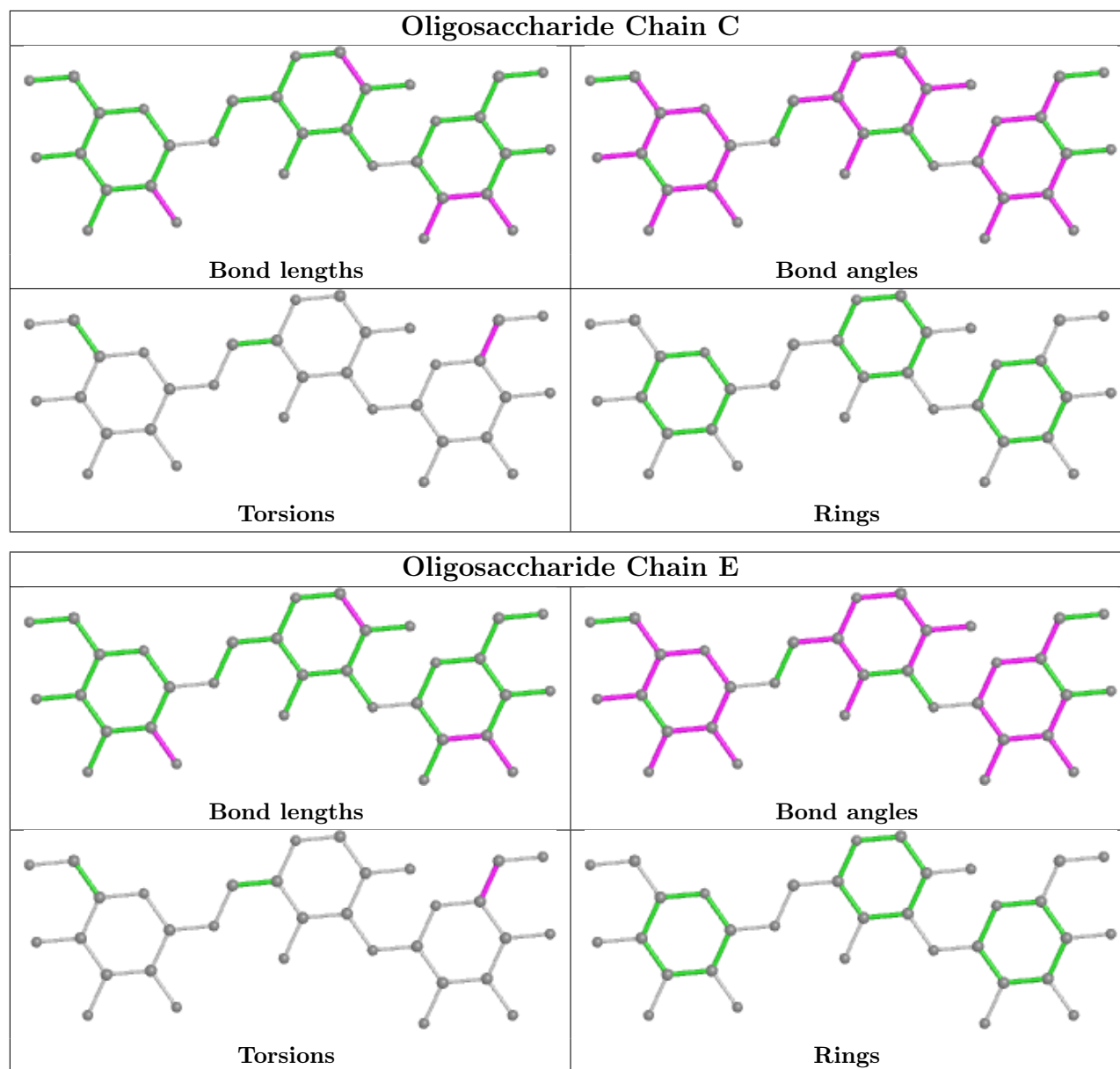
There are no ring outliers.

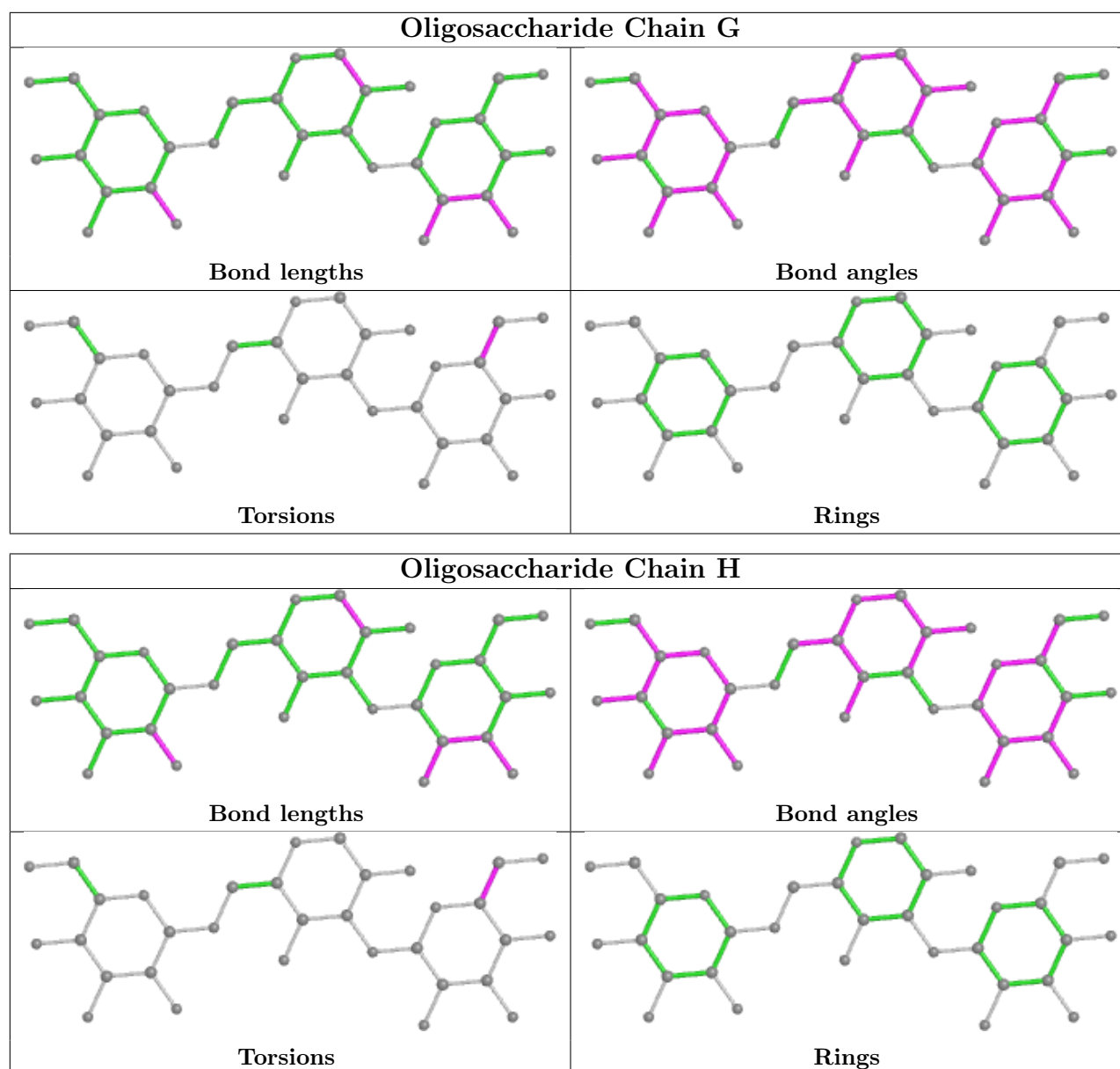
6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1	BMA	1	0
2	H	1	BMA	1	0
2	E	1	BMA	1	0
2	E	2	MAN	1	0
2	G	2	MAN	1	0
2	C	1	BMA	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

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
3	NGT	D	625	2	13,15,15	2.86	1 (7%)	12,22,22	1.46	1 (8%)
3	NGT	B	625	2	13,15,15	2.86	1 (7%)	12,22,22	1.47	1 (8%)
3	NGT	F	625	2	13,15,15	2.82	1 (7%)	12,22,22	1.45	1 (8%)
3	NGT	A	625	2	13,15,15	2.84	1 (7%)	12,22,22	1.46	1 (8%)

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	NGT	D	625	2	-	0/2/30/30	0/2/2/2
3	NGT	B	625	2	-	0/2/30/30	0/2/2/2
3	NGT	F	625	2	-	0/2/30/30	0/2/2/2
3	NGT	A	625	2	-	0/2/30/30	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	625	NGT	C7-S1	-10.21	1.68	1.77
3	D	625	NGT	C7-S1	-10.21	1.68	1.77
3	A	625	NGT	C7-S1	-10.13	1.68	1.77
3	F	625	NGT	C7-S1	-10.08	1.68	1.77

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	625	NGT	C8-C7-S1	3.91	124.84	118.96
3	A	625	NGT	C8-C7-S1	3.89	124.81	118.96
3	D	625	NGT	C8-C7-S1	3.87	124.79	118.96
3	F	625	NGT	C8-C7-S1	3.85	124.76	118.96

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	625	NGT	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	625	NGT	1	0
3	F	625	NGT	1	0
3	A	625	NGT	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

6.1 Protein, DNA and RNA chains

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	601/621 (96%)	0.23	22 (3%) 41 38	20, 31, 52, 75	0
1	B	599/621 (96%)	0.39	35 (5%) 23 20	20, 36, 57, 89	0
1	D	597/621 (96%)	0.21	24 (4%) 38 35	21, 33, 51, 74	0
1	F	596/621 (95%)	0.54	51 (8%) 10 7	20, 39, 60, 81	0
All	All	2393/2484 (96%)	0.34	132 (5%) 25 22	20, 34, 56, 89	0

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	568	HIS	6.9
1	F	510	GLU	6.7
1	F	596	ARG	6.2
1	F	257	ALA	6.1
1	A	568	HIS	5.9
1	A	567	LYS	5.8
1	A	586	LEU	5.7
1	F	568	HIS	5.5
1	B	587	VAL	5.2
1	B	335	GLN	5.2
1	F	567	LYS	5.1
1	F	569	GLY	5.1
1	A	335	GLN	5.0
1	F	148	GLY	4.9
1	A	596	ARG	4.8
1	B	596	ARG	4.8
1	B	257	ALA	4.8
1	F	585	GLY	4.7
1	D	288	GLU	4.7
1	D	567	LYS	4.7
1	D	44	ARG	4.5

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Mol	Chain	Res	Type	RSRZ
1	B	567	LYS	4.5
1	A	566	THR	4.4
1	D	335	GLN	4.3
1	B	146	GLU	4.3
1	F	556	ASN	4.3
1	F	290	GLU	4.2
1	D	596	ARG	4.2
1	F	2	THR	4.2
1	F	545	SER	4.1
1	F	552	GLU	4.1
1	A	23	SER	4.1
1	F	289	GLY	4.0
1	B	2	THR	4.0
1	B	290	GLU	4.0
1	B	510	GLU	3.9
1	F	51	LYS	3.9
1	A	288	GLU	3.8
1	B	456	ASN	3.7
1	F	544	PRO	3.7
1	B	568	HIS	3.6
1	F	425	GLU	3.6
1	B	148	GLY	3.6
1	A	587	VAL	3.5
1	F	50	ASP	3.4
1	D	566	THR	3.4
1	B	23	SER	3.4
1	B	541	ASP	3.3
1	B	552	GLU	3.3
1	B	425	GLU	3.3
1	F	246	ARG	3.3
1	D	23	SER	3.2
1	A	44	ARG	3.2
1	A	493	ALA	3.1
1	D	615	ASP	3.1
1	B	544	PRO	3.1
1	A	552	GLU	3.1
1	D	290	GLU	3.1
1	F	566	THR	3.1
1	F	509	ASN	3.1
1	F	424	ALA	3.1
1	B	569	GLY	3.0
1	F	23	SER	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	613	MET	2.9
1	D	2	THR	2.9
1	A	2	THR	2.9
1	B	586	LEU	2.9
1	F	20	GLU	2.9
1	F	539	GLN	2.9
1	A	289	GLY	2.8
1	B	545	SER	2.8
1	B	584	GLU	2.8
1	D	569	GLY	2.8
1	D	478	ARG	2.8
1	D	51	LYS	2.8
1	F	230	ASN	2.8
1	A	554	GLN	2.7
1	F	541	ASP	2.7
1	B	426	GLY	2.7
1	B	469	ASP	2.6
1	F	147	ASP	2.6
1	B	556	ASN	2.6
1	F	542	PRO	2.6
1	F	258	LEU	2.6
1	F	443	GLY	2.6
1	F	146	GLU	2.6
1	F	615	ASP	2.5
1	B	570	LYS	2.5
1	F	145	GLU	2.5
1	F	595	VAL	2.5
1	B	598	HIS	2.5
1	A	570	LYS	2.5
1	B	145	GLU	2.5
1	F	495	ALA	2.5
1	D	337	ASN	2.5
1	F	17	ALA	2.5
1	F	570	LYS	2.4
1	D	588	GLU	2.4
1	B	566	THR	2.4
1	A	469	ASP	2.4
1	F	465	ASP	2.4
1	D	442	GLU	2.4
1	A	146	GLU	2.4
1	F	598	HIS	2.4
1	B	585	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	532	ALA	2.4
1	D	587	VAL	2.3
1	A	532	ALA	2.3
1	F	232	SER	2.3
1	B	613	MET	2.3
1	A	545	SER	2.2
1	B	258	LEU	2.2
1	D	443	GLY	2.2
1	F	512	GLY	2.2
1	F	584	GLU	2.2
1	F	337	ASN	2.2
1	F	586	LEU	2.2
1	D	586	LEU	2.1
1	B	610	ASP	2.1
1	F	52	ASP	2.1
1	B	373	LYS	2.1
1	A	610	ASP	2.1
1	F	291	LYS	2.1
1	F	540	TYR	2.1
1	A	442	GLU	2.1
1	D	20	GLU	2.1
1	D	469	ASP	2.1
1	B	288	GLU	2.1
1	D	287	PRO	2.0
1	F	597	LEU	2.0
1	D	80	THR	2.0
1	B	147	ASP	2.0

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

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

6.3 Carbohydrates [i](#)

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

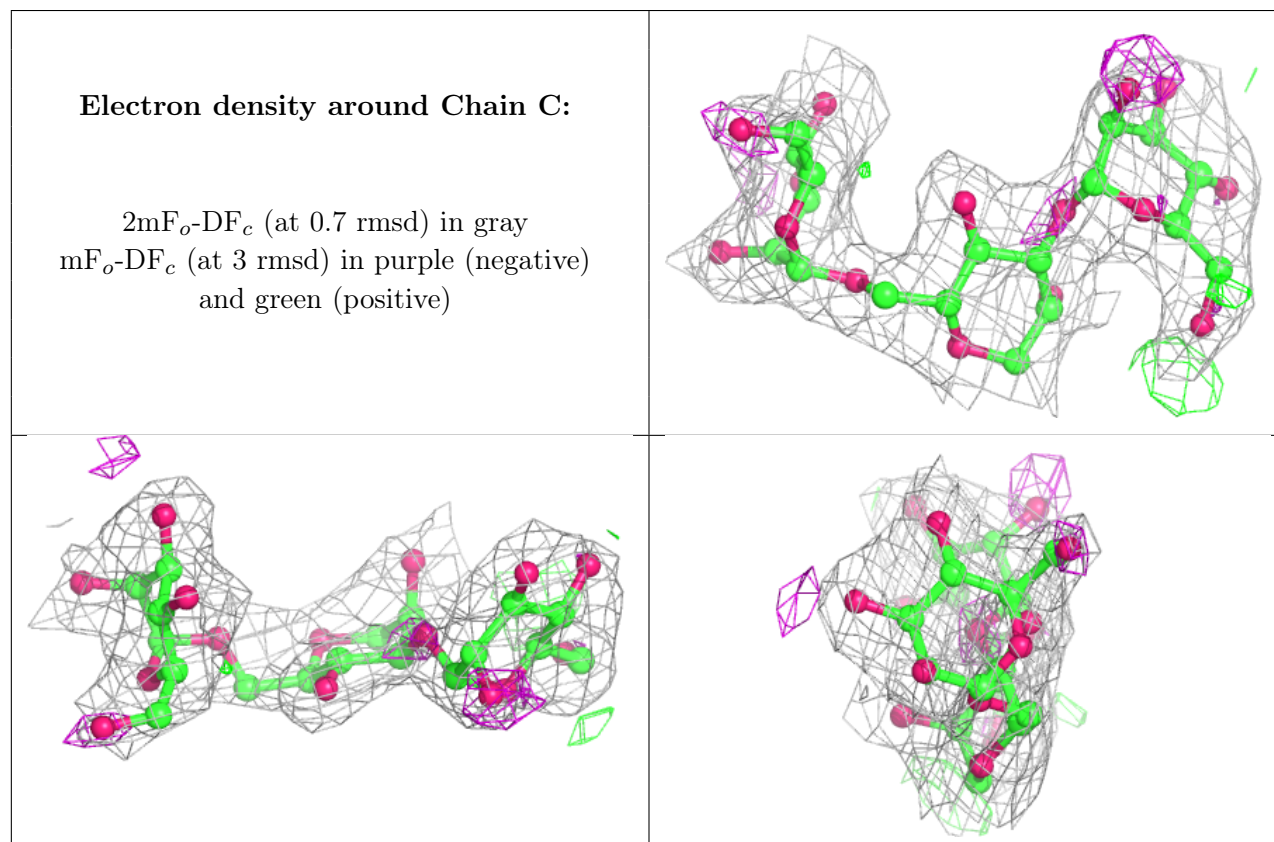
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	E	2	11/12	0.81	0.20	20,20,20,20	0

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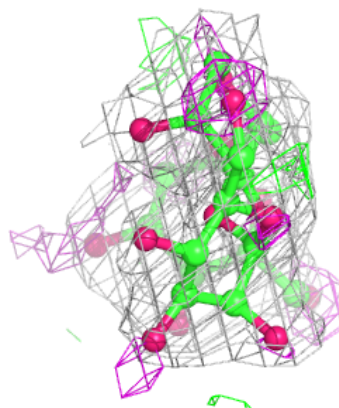
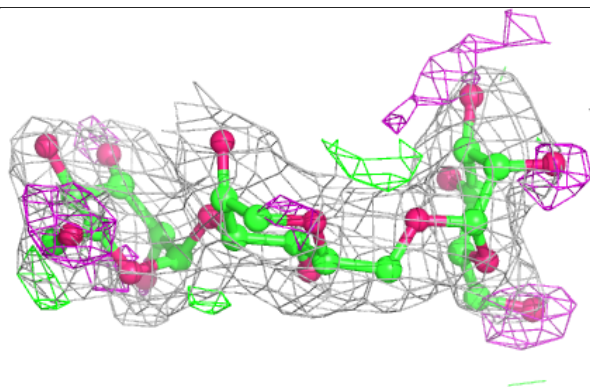
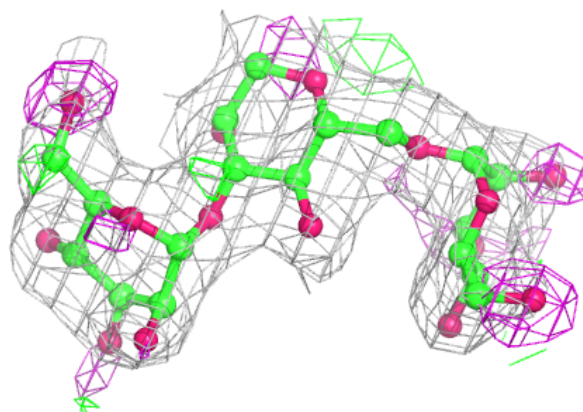
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	MAN	E	3	11/12	0.81	0.21	20,20,20,20	0
2	MAN	H	3	11/12	0.84	0.21	20,20,20,20	0
2	MAN	G	2	11/12	0.85	0.19	20,20,20,20	0
2	BMA	G	1	11/12	0.85	0.15	20,20,20,20	0
2	BMA	E	1	11/12	0.87	0.13	20,20,20,20	0
2	MAN	C	2	11/12	0.88	0.20	20,20,20,20	0
2	MAN	G	3	11/12	0.88	0.18	20,20,20,20	0
2	MAN	H	2	11/12	0.88	0.20	20,20,20,20	0
2	MAN	C	3	11/12	0.88	0.16	20,20,20,20	0
2	BMA	C	1	11/12	0.91	0.14	20,20,20,20	0
2	BMA	H	1	11/12	0.91	0.14	20,20,20,20	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.

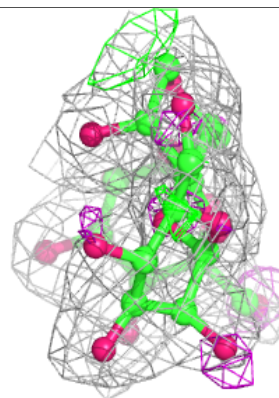
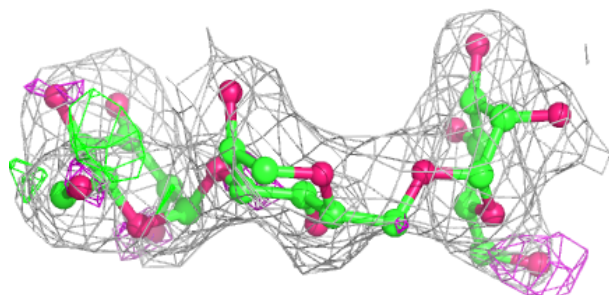
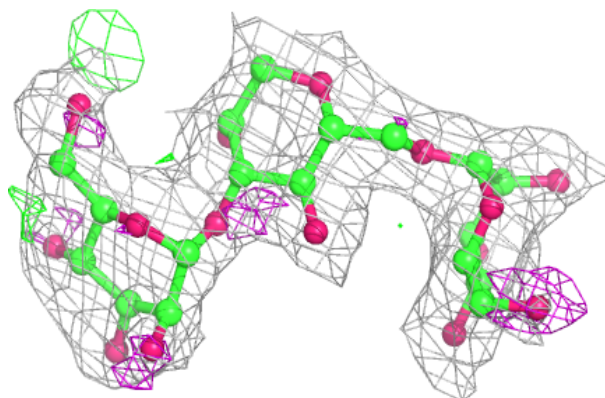


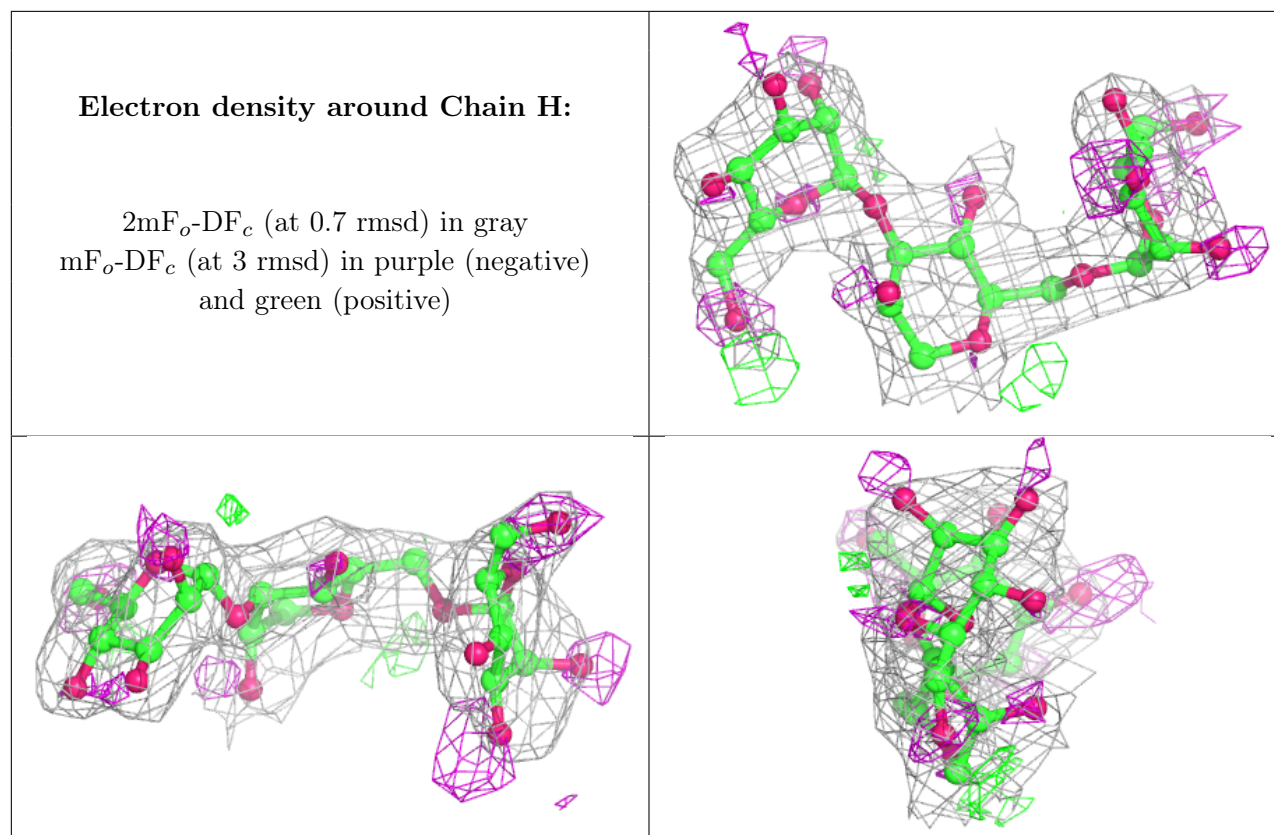
Electron density around Chain E:

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

**Electron density around Chain G:**

$2mF_o-DF_c$ (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(\AA^2)	Q<0.9
3	NGT	B	625	14/14	0.91	0.14	20,20,20,20	0
3	NGT	F	625	14/14	0.92	0.14	20,20,20,20	0
3	NGT	D	625	14/14	0.93	0.13	20,20,20,20	0
3	NGT	A	625	14/14	0.93	0.13	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.