



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 3, 2023 – 04:08 PM EDT

PDB ID : 3RSJ
Title : Structure of HCRF in complex with Ganglioside GD1a
Authors : Fu, Z.; Benson, M.A.; Barbieri, J.T.; Kim, J.-J.P.; Baldwin, M.R.
Deposited on : 2011-05-02
Resolution : 2.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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

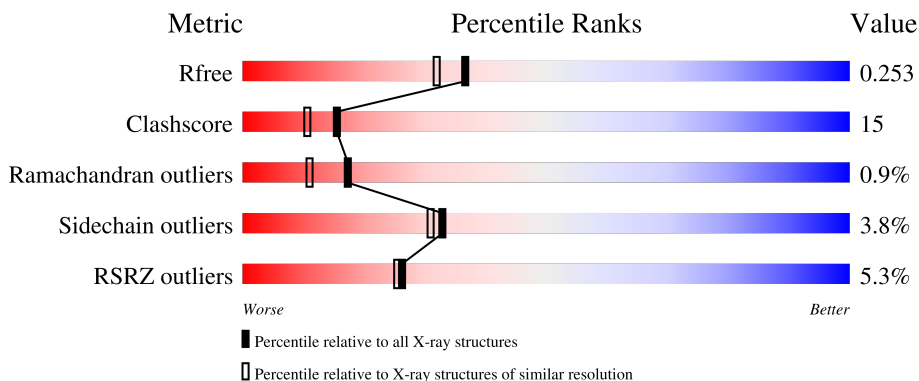
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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






Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	413	<div style="display: flex; align-items: center;"> <div style="width: 6%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 67%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 29%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">6% 67% 29% ..</p>
1	B	413	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 69%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 25%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">4% 69% 25% ..</p>
1	C	413	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 69%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 26%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">5% 69% 26% ..</p>
1	D	413	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 74%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 21%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center;">5% 74% 21% ..</p>
2	E	3	<div style="display: flex; align-items: center;"> <div style="width: 67%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 33%; height: 10px; background-color: orange;"></div> </div> <p style="text-align: center;">67% 33%</p>

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Mol	Chain	Length	Quality of chain
2	H	3	 33% 67%
3	F	5	 40% 60%
4	G	4	 75% 25%

2 Entry composition [i](#)

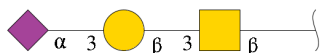
There are 5 unique types of molecules in this entry. The entry contains 13922 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BoNT/F.

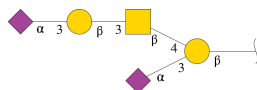
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	406	Total 3334	C 2114	N 577	O 635	S 8	0	0	0
1	B	402	Total 3307	C 2097	N 572	O 630	S 8	0	0	0
1	C	402	Total 3307	C 2097	N 572	O 630	S 8	0	0	0
1	D	404	Total 3324	C 2109	N 575	O 632	S 8	0	0	0

- Molecule 2 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	3	Total 46	C 25	N 2	O 19	0	0	0
2	H	3	Total 46	C 25	N 2	O 19	0	0	0

- Molecule 3 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	F	5	77	42	3	32	0	0	0

- Molecule 4 is an oligosaccharide called N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	G	4	57	31	2	24	0	0	0

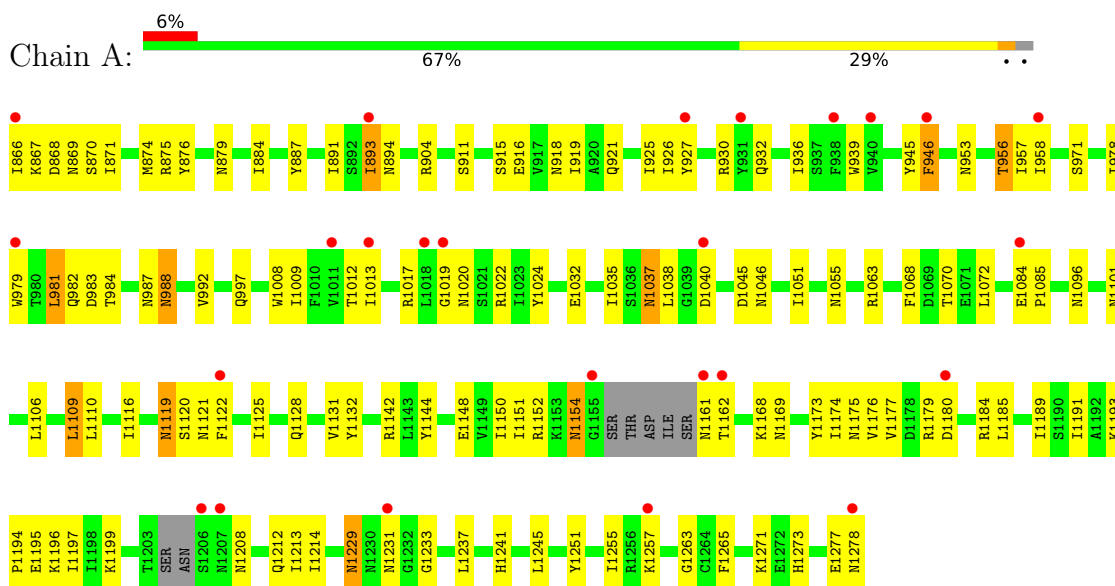
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	117	Total	O	0	0
			117	117		
5	B	98	Total	O	0	0
			98	98		
5	C	96	Total	O	0	0
			96	96		
5	D	113	Total	O	0	0
			113	113		

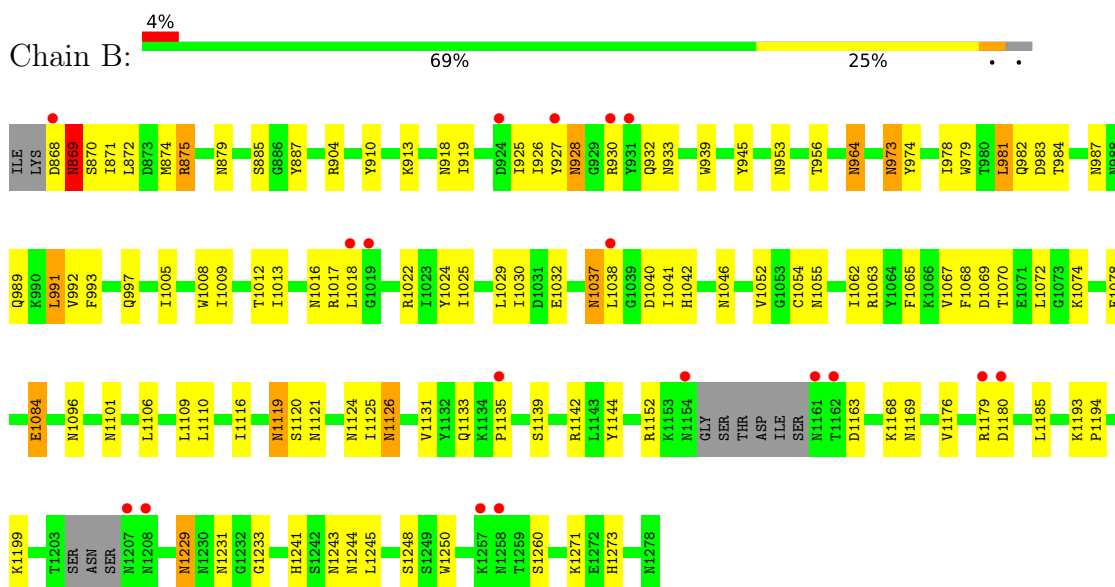
3 Residue-property plots i

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.

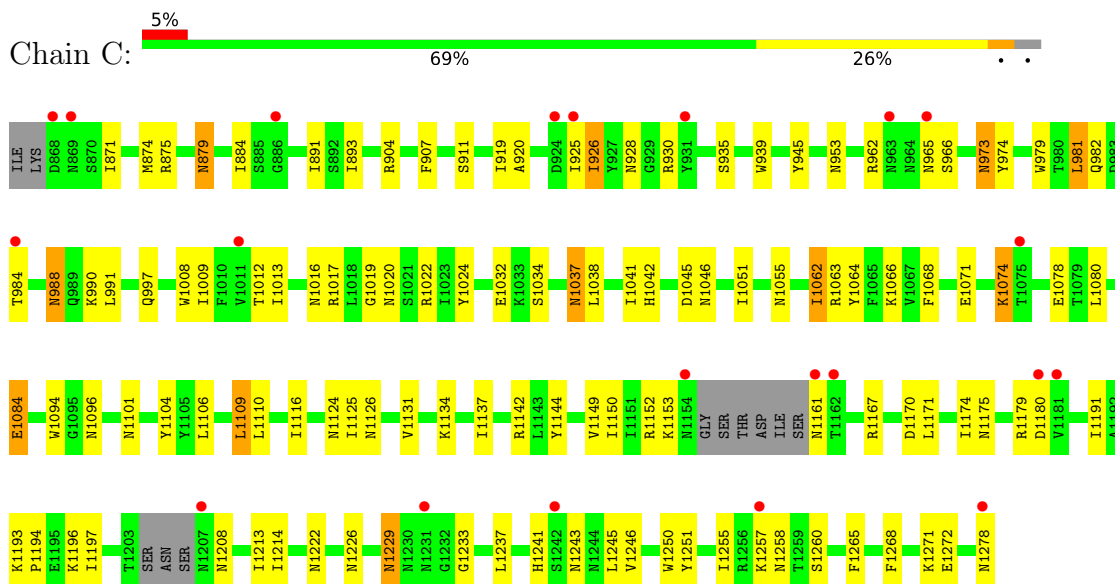
- Molecule 1: BoNT/F



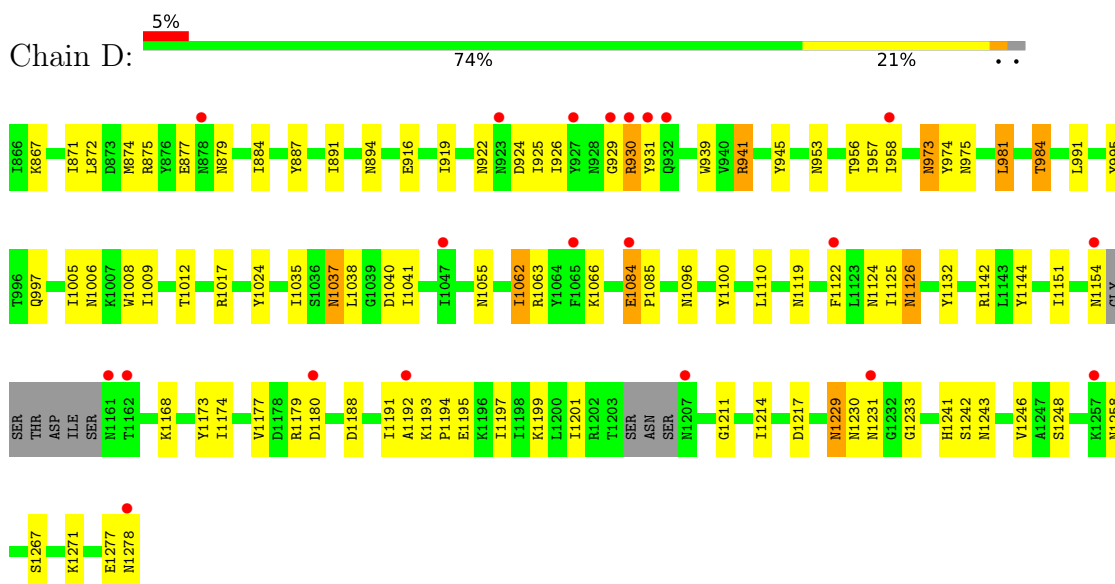
- Molecule 1: BoNT/F



- Molecule 1: BoNT/F



- Molecule 1: BoNT/F



- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose



NGA1
GAL2
STA3

- Molecule 2: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose



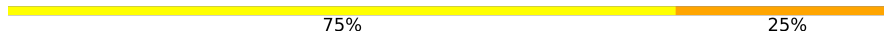
NGA1
GAL2
STA3

- Molecule 3: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-[N-acetyl-alpha-neuraminic acid-(2-3)]beta-D-galactopyranose

Chain F:  40% 60%

GAL1
NGA2
GAL3
SIA4
SIA5

- Molecule 4: N-acetyl-alpha-neuraminic acid-(2-3)-beta-D-galactopyranose-(1-3)-2-acetamido-2-deoxy-beta-D-galactopyranose-(1-4)-beta-D-galactopyranose

Chain G:  75% 25%

GAL1
NGA2
GAL3
SIA4

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	65.47Å 84.27Å 117.60Å 72.55° 87.01° 67.13°	Depositor
Resolution (Å)	29.86 – 2.00 29.85 – 2.00	Depositor EDS
% Data completeness (in resolution range)	87.0 (29.86-2.00) 87.0 (29.85-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.00Å)	Xtrriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.232 , 0.263 0.223 , 0.253	Depositor DCC
R_{free} test set	12918 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtrriage
Anisotropy	0.592	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13922	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.34% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SIA, NGA, GAL

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	0.38	0/3401	0.65	0/4603
1	B	0.37	0/3374	0.64	0/4568
1	C	0.37	0/3374	0.64	0/4568
1	D	0.38	0/3391	0.66	0/4590
All	All	0.37	0/13540	0.65	0/18329

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	3334	0	3249	104	0
1	B	3307	0	3217	108	0
1	C	3307	0	3217	102	0
1	D	3324	0	3241	84	0
2	E	46	0	40	2	0
2	H	46	0	40	2	0
3	F	77	0	65	4	0
4	G	57	0	49	3	0
5	A	117	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	98	0	0	1	0
5	C	96	0	0	3	0
5	D	113	0	0	0	0
All	All	13922	0	13118	395	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 15.

All (395) 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:953:ASN:HD21	1:D:1055:ASN:H	1.05	1.00
1:B:1229:ASN:HD21	1:B:1233:GLY:H	1.15	0.93
1:A:953:ASN:HD21	1:A:1055:ASN:H	1.17	0.91
1:D:945:TYR:H	1:D:997:GLN:HE22	1.18	0.90
1:C:1229:ASN:HD21	1:C:1233:GLY:H	1.22	0.88
1:D:1126:ASN:HD22	1:D:1126:ASN:H	1.17	0.88
1:A:866:ILE:HG13	1:A:868:ASP:H	1.40	0.87
1:A:945:TYR:H	1:A:997:GLN:HE22	1.24	0.85
1:D:953:ASN:ND2	1:D:1055:ASN:H	1.75	0.84
1:D:1037:ASN:H	1:D:1037:ASN:HD22	1.26	0.83
1:A:918:ASN:HD21	1:A:1046:ASN:HD22	1.25	0.82
1:A:1035:ILE:HB	1:A:1038:LEU:HD12	1.60	0.82
1:C:920:ALA:HA	1:C:1046:ASN:ND2	1.95	0.81
1:B:973:ASN:HD22	1:B:974:TYR:H	1.25	0.80
1:C:1229:ASN:ND2	1:C:1233:GLY:H	1.79	0.80
1:A:1101:ASN:HD22	1:A:1152:ARG:HH11	1.27	0.79
1:B:1229:ASN:C	1:B:1229:ASN:HD22	1.85	0.79
1:A:1229:ASN:C	1:A:1229:ASN:HD22	1.86	0.78
1:B:1229:ASN:ND2	1:B:1233:GLY:H	1.80	0.78
1:B:945:TYR:H	1:B:997:GLN:HE22	1.32	0.77
1:A:1037:ASN:H	1:A:1037:ASN:HD22	1.34	0.76
1:B:933:ASN:ND2	1:B:1017:ARG:H	1.84	0.75
1:D:1229:ASN:C	1:D:1229:ASN:HD22	1.90	0.75
1:D:973:ASN:HD22	1:D:974:TYR:H	1.34	0.75
1:A:988:ASN:C	1:A:988:ASN:HD22	1.91	0.75
1:C:1012:THR:HB	1:C:1024:TYR:HB2	1.66	0.75
1:C:973:ASN:HD22	1:C:974:TYR:H	1.31	0.74
1:B:933:ASN:HD21	1:B:1017:ARG:H	1.36	0.73
1:C:871:ILE:HB	1:C:925:ILE:HD12	1.70	0.73
1:C:953:ASN:HD21	1:C:1055:ASN:H	1.34	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1116:ILE:HD12	1:A:1245:LEU:HD11	1.70	0.73
1:A:1229:ASN:HD21	1:A:1233:GLY:H	1.35	0.72
1:A:1101:ASN:ND2	1:A:1152:ARG:HH11	1.87	0.72
1:A:1273:HIS:CD2	1:B:1273:HIS:HD2	2.08	0.71
1:C:1064:TYR:HB3	1:C:1084:GLU:OE2	1.90	0.70
1:A:1037:ASN:HD22	1:A:1037:ASN:N	1.88	0.70
1:B:973:ASN:ND2	1:B:974:TYR:H	1.89	0.70
1:B:875:ARG:HH21	1:B:875:ARG:HG3	1.55	0.70
1:A:953:ASN:ND2	1:A:1055:ASN:H	1.87	0.70
1:C:1101:ASN:ND2	1:C:1152:ARG:HH11	1.89	0.70
1:B:874:MET:HE3	1:B:1065:PHE:HB3	1.74	0.69
1:C:1229:ASN:C	1:C:1229:ASN:HD22	1.96	0.69
1:A:871:ILE:HD12	1:A:925:ILE:HG23	1.74	0.69
1:C:1022:ARG:HD3	1:C:1032:GLU:OE2	1.92	0.69
1:C:871:ILE:HD12	1:C:925:ILE:HG23	1.76	0.68
1:D:953:ASN:HD21	1:D:1055:ASN:N	1.86	0.68
1:D:1008:TRP:HE1	1:D:1096:ASN:HD21	1.40	0.68
1:D:1126:ASN:HD22	1:D:1126:ASN:N	1.91	0.68
1:D:953:ASN:H	1:D:973:ASN:HD21	1.40	0.68
1:C:1037:ASN:N	1:C:1037:ASN:HD22	1.92	0.68
1:A:939:TRP:HB2	1:A:1063:ARG:HG2	1.76	0.67
1:B:874:MET:CE	1:B:1065:PHE:HB3	2.25	0.67
1:B:984:THR:HG22	1:B:1040:ASP:HB3	1.76	0.67
1:C:920:ALA:HA	1:C:1046:ASN:HD22	1.59	0.67
1:C:1142:ARG:HH11	1:C:1278:ASN:HB2	1.60	0.67
1:C:973:ASN:ND2	1:C:974:TYR:H	1.93	0.67
1:D:1242:SER:OG	1:D:1243:ASN:N	2.27	0.66
1:A:1229:ASN:ND2	1:A:1233:GLY:H	1.94	0.66
1:C:1150:ILE:HD12	1:C:1150:ILE:O	1.95	0.66
1:C:875:ARG:HG3	1:C:884:ILE:HD13	1.76	0.65
1:D:941:ARG:HD3	1:D:1006:ASN:O	1.96	0.65
1:D:887:TYR:HB3	1:D:925:ILE:HD11	1.79	0.65
1:B:953:ASN:HD21	1:B:1055:ASN:H	1.43	0.65
1:B:1022:ARG:HD3	1:B:1032:GLU:OE2	1.96	0.65
1:C:945:TYR:H	1:C:997:GLN:HE22	1.43	0.65
1:A:953:ASN:HD21	1:A:1055:ASN:N	1.93	0.64
1:B:973:ASN:HD22	1:B:974:TYR:N	1.95	0.64
1:C:1062:ILE:HD12	1:C:1063:ARG:N	2.13	0.64
1:D:874:MET:HE3	1:D:891:ILE:HD13	1.80	0.63
1:B:983:ASP:OD2	1:B:987:ASN:HB2	1.99	0.63
1:D:1066:LYS:NZ	1:D:1084:GLU:OE2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1272:GLU:HB3	5:C:184:HOH:O	1.99	0.62
1:D:1197:ILE:HA	1:D:1246:VAL:HG12	1.82	0.62
1:D:922:ASN:HD22	1:D:924:ASP:H	1.46	0.62
1:C:1037:ASN:HD22	1:C:1037:ASN:H	1.46	0.62
1:B:1074:LYS:O	1:B:1078:GLU:HG2	1.99	0.62
1:B:1012:THR:HB	1:B:1024:TYR:HB2	1.81	0.61
1:D:1008:TRP:HE1	1:D:1096:ASN:ND2	1.97	0.61
1:A:1142:ARG:HH11	1:A:1278:ASN:HB2	1.64	0.61
1:C:1084:GLU:HA	1:C:1084:GLU:OE1	2.01	0.61
1:B:1068:PHE:CD2	1:B:1072:LEU:HD11	2.36	0.61
1:C:1101:ASN:HD22	1:C:1152:ARG:HH11	1.48	0.61
1:C:953:ASN:H	1:C:973:ASN:HD21	1.48	0.61
1:A:1116:ILE:HD11	1:A:1125:ILE:HD12	1.82	0.60
1:B:1241:HIS:HA	3:F:3:GAL:O4	2.01	0.60
1:C:1094:TRP:NE1	1:C:1272:GLU:HG3	2.16	0.60
1:A:982:GLN:HG3	1:A:987:ASN:O	2.02	0.60
1:D:973:ASN:ND2	1:D:974:TYR:H	1.99	0.60
1:A:1022:ARG:HD3	1:A:1032:GLU:OE2	2.01	0.60
1:D:1194:PRO:HG2	1:D:1195:GLU:OE2	2.02	0.60
1:B:964:ASN:N	1:B:964:ASN:HD22	2.00	0.60
1:B:930:ARG:HA	1:B:1017:ARG:HH22	1.68	0.59
1:C:1241:HIS:HA	4:G:3:GAL:O4	2.01	0.59
3:F:1:GAL:H5	3:F:5:SIA:H92	1.84	0.59
1:C:1016:ASN:HD22	1:C:1019:GLY:HA3	1.66	0.59
1:A:879:ASN:ND2	1:B:879:ASN:ND2	2.50	0.59
1:C:953:ASN:ND2	1:C:1055:ASN:H	2.00	0.59
1:B:1116:ILE:HD11	1:B:1125:ILE:HD12	1.85	0.58
1:C:1193:LYS:HG3	1:C:1194:PRO:HD2	1.85	0.58
1:D:1142:ARG:HH12	1:D:1278:ASN:HB2	1.68	0.58
1:B:1101:ASN:ND2	1:B:1152:ARG:HH11	2.02	0.58
1:D:891:ILE:HG12	1:D:919:ILE:HG12	1.86	0.58
1:C:879:ASN:N	1:C:879:ASN:HD22	1.99	0.58
1:D:984:THR:CG2	1:D:1040:ASP:HB3	2.33	0.58
1:C:871:ILE:HB	1:C:925:ILE:CD1	2.32	0.57
1:D:871:ILE:HA	1:D:887:TYR:CE2	2.39	0.57
1:D:1229:ASN:HD21	1:D:1233:GLY:H	1.52	0.57
1:B:1131:VAL:O	1:B:1142:ARG:NH2	2.37	0.57
1:C:879:ASN:N	1:C:879:ASN:ND2	2.48	0.57
1:D:887:TYR:CB	1:D:925:ILE:HD11	2.34	0.57
1:B:1008:TRP:HE1	1:B:1096:ASN:HD21	1.51	0.57
1:A:879:ASN:ND2	1:B:879:ASN:HD22	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:927:TYR:CE1	1:A:932:GLN:HG2	2.40	0.57
1:B:871:ILE:HD11	1:B:1067:VAL:HG12	1.86	0.57
1:A:1273:HIS:CD2	1:B:1273:HIS:CD2	2.93	0.56
1:A:1161:ASN:ND2	1:A:1162:THR:H	2.04	0.56
1:A:1241:HIS:HA	2:E:2:GAL:O4	2.05	0.56
1:B:1022:ARG:NH2	1:B:1032:GLU:OE2	2.39	0.56
1:B:930:ARG:HA	1:B:1017:ARG:NH2	2.20	0.56
1:B:939:TRP:HB2	1:B:1063:ARG:HG2	1.86	0.56
1:A:875:ARG:HG3	1:A:884:ILE:HD13	1.88	0.56
1:D:1062:ILE:HD12	1:D:1063:ARG:H	1.71	0.56
1:C:973:ASN:HD22	1:C:974:TYR:N	2.02	0.56
1:B:1037:ASN:ND2	1:B:1038:LEU:HG	2.21	0.55
1:B:1231:ASN:N	1:B:1231:ASN:HD22	2.04	0.55
1:B:1069:ASP:OD1	1:B:1070:THR:HG23	2.07	0.55
1:A:1208:ASN:N	1:A:1208:ASN:HD22	2.05	0.55
1:D:1229:ASN:ND2	1:D:1231:ASN:N	2.54	0.55
1:A:918:ASN:HD21	1:A:1046:ASN:ND2	1.98	0.55
1:A:946:PHE:HD1	1:A:946:PHE:H	1.55	0.55
1:B:904:ARG:HG2	1:B:904:ARG:HH21	1.72	0.54
1:D:957:ILE:HG13	1:D:958:ILE:HG13	1.89	0.54
1:B:1241:HIS:HA	3:F:3:GAL:HO4	1.72	0.54
1:D:1179:ARG:O	1:D:1180:ASP:HB2	2.06	0.54
1:C:930:ARG:HA	1:C:1017:ARG:HH22	1.72	0.54
1:C:1179:ARG:O	1:C:1180:ASP:HB2	2.08	0.54
1:A:1101:ASN:HA	1:A:1150:ILE:HD11	1.90	0.54
1:B:869:ASN:N	1:B:869:ASN:HD22	2.05	0.54
1:B:1109:LEU:HB3	1:B:1260:SER:O	2.08	0.54
1:B:1121:ASN:ND2	1:B:1199:LYS:HE2	2.23	0.54
1:D:1191:ILE:CD1	1:D:1193:LYS:HB3	2.37	0.54
1:A:946:PHE:N	1:A:946:PHE:CD1	2.76	0.54
1:A:1229:ASN:C	1:A:1229:ASN:ND2	2.60	0.53
1:A:1101:ASN:HD22	1:A:1152:ARG:NH1	2.03	0.53
1:B:1037:ASN:HD22	1:B:1037:ASN:N	2.05	0.53
1:B:1229:ASN:C	1:B:1229:ASN:ND2	2.59	0.53
1:B:918:ASN:HD21	1:B:1046:ASN:ND2	2.06	0.53
1:B:953:ASN:ND2	1:B:1055:ASN:H	2.06	0.53
1:B:1194:PRO:O	1:B:1248:SER:HA	2.07	0.53
1:C:1066:LYS:NZ	1:C:1084:GLU:OE2	2.41	0.53
1:C:1131:VAL:O	1:C:1142:ARG:NH2	2.41	0.53
1:C:1134:LYS:HE2	1:C:1137:ILE:HD12	1.91	0.53
1:B:925:ILE:O	1:B:927:TYR:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:953:ASN:H	1:B:973:ASN:HD21	1.57	0.53
1:A:1251:TYR:O	1:A:1255:ILE:HG13	2.09	0.53
1:B:1176:VAL:HG23	1:B:1185:LEU:HD11	1.91	0.53
1:C:1116:ILE:HD12	1:C:1245:LEU:HD11	1.91	0.52
1:D:1037:ASN:HD22	1:D:1037:ASN:N	1.97	0.52
1:A:1144:TYR:CE1	1:A:1271:LYS:HA	2.43	0.52
1:A:1175:ASN:OD1	1:A:1184:ARG:HA	2.09	0.52
1:B:964:ASN:HD22	1:B:964:ASN:H	1.57	0.52
1:B:1008:TRP:HE1	1:B:1096:ASN:ND2	2.08	0.52
1:B:1084:GLU:OE1	1:B:1084:GLU:HA	2.10	0.52
1:D:1229:ASN:C	1:D:1229:ASN:ND2	2.62	0.52
1:B:1168:LYS:O	1:B:1169:ASN:HB2	2.10	0.52
1:C:1109:LEU:HD23	1:C:1265:PHE:HB3	1.92	0.52
1:D:1035:ILE:HB	1:D:1038:LEU:HD12	1.90	0.52
1:D:939:TRP:HB2	1:D:1063:ARG:HG2	1.91	0.52
1:D:1154:ASN:HA	1:D:1173:TYR:CE2	2.45	0.52
1:A:1019:GLY:C	1:A:1020:ASN:HD22	2.13	0.52
1:C:1150:ILE:HD11	1:C:1175:ASN:HB2	1.91	0.52
1:D:973:ASN:HD22	1:D:974:TYR:N	2.05	0.52
1:B:1229:ASN:ND2	1:B:1233:GLY:N	2.55	0.51
1:D:1122:PHE:CE1	1:D:1199:LYS:HE2	2.44	0.51
1:A:1179:ARG:O	1:A:1180:ASP:HB2	2.09	0.51
1:D:922:ASN:ND2	1:D:924:ASP:H	2.08	0.51
1:D:1191:ILE:HD11	1:D:1195:GLU:O	2.10	0.51
1:D:1229:ASN:ND2	1:D:1233:GLY:H	2.08	0.51
1:A:1119:ASN:C	1:A:1119:ASN:HD22	2.12	0.51
1:A:1173:TYR:HB3	1:A:1184:ARG:NE	2.25	0.51
1:C:1142:ARG:NH1	1:C:1278:ASN:HB2	2.25	0.51
1:A:988:ASN:C	1:A:988:ASN:ND2	2.61	0.51
1:C:979:TRP:CE2	1:C:1013:ILE:HG21	2.45	0.51
1:B:933:ASN:HD21	1:B:1017:ARG:N	2.07	0.51
1:B:956:THR:CG2	1:B:1052:VAL:HB	2.41	0.51
1:A:946:PHE:HD1	1:A:946:PHE:N	2.08	0.50
1:C:911:SER:HB3	1:C:1051:ILE:HG21	1.91	0.50
1:D:875:ARG:HG3	1:D:884:ILE:HD13	1.93	0.50
1:A:1132:TYR:CE2	1:A:1277:GLU:HA	2.47	0.50
1:C:891:ILE:HG12	1:C:919:ILE:HG12	1.92	0.50
1:C:1008:TRP:HE1	1:C:1096:ASN:HD21	1.60	0.50
1:D:1124:ASN:HB3	1:D:1126:ASN:ND2	2.25	0.50
1:A:1037:ASN:H	1:A:1037:ASN:ND2	2.06	0.50
5:C:424:HOH:O	4:G:1:GAL:C3	2.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:894:ASN:HB2	1:A:916:GLU:HG2	1.92	0.50
1:B:979:TRP:CE2	1:B:1013:ILE:HG21	2.47	0.50
1:A:874:MET:HE3	1:A:891:ILE:HD13	1.94	0.50
1:B:927:TYR:CD1	1:B:932:GLN:HG2	2.47	0.49
1:C:1008:TRP:HE1	1:C:1096:ASN:ND2	2.09	0.49
1:D:1177:VAL:HG13	1:D:1177:VAL:O	2.11	0.49
1:B:918:ASN:HD21	1:B:1046:ASN:HD22	1.59	0.49
1:A:1191:ILE:CD1	1:A:1197:ILE:HG22	2.43	0.49
1:C:1251:TYR:O	1:C:1255:ILE:HG13	2.13	0.49
1:B:875:ARG:HG3	1:B:875:ARG:NH2	2.27	0.49
1:C:874:MET:SD	1:C:919:ILE:HD11	2.53	0.49
1:C:904:ARG:HG2	5:C:298:HOH:O	2.11	0.49
1:C:1150:ILE:HD13	1:C:1152:ARG:NE	2.28	0.49
1:C:1153:LYS:HZ3	1:C:1161:ASN:N	2.10	0.49
1:D:1192:ALA:O	1:D:1193:LYS:HB2	2.13	0.49
1:A:1008:TRP:HE1	1:A:1096:ASN:HD21	1.59	0.48
1:A:1131:VAL:O	1:A:1142:ARG:NH2	2.45	0.48
1:C:1144:TYR:CE1	1:C:1271:LYS:HA	2.48	0.48
1:D:1037:ASN:H	1:D:1037:ASN:ND2	2.04	0.48
1:B:870:SER:O	1:B:885:SER:HB2	2.12	0.48
1:B:989:GLN:OE1	1:B:989:GLN:HA	2.12	0.48
1:D:984:THR:HG21	1:D:1040:ASP:HB3	1.94	0.48
1:D:1125:ILE:HG23	1:D:1125:ILE:O	2.13	0.48
1:C:1250:TRP:CE3	4:G:3:GAL:H5	2.49	0.48
1:A:1148:GLU:O	1:A:1177:VAL:HG12	2.14	0.48
1:D:984:THR:HG22	1:D:1040:ASP:HB3	1.95	0.48
1:D:1144:TYR:CE1	1:D:1271:LYS:HA	2.49	0.48
1:A:930:ARG:HA	1:A:1017:ARG:NH2	2.29	0.48
1:B:993:PHE:CD1	1:B:1025:ILE:HG13	2.49	0.48
1:D:975:ASN:HB3	1:D:995:TYR:O	2.14	0.48
1:D:1229:ASN:ND2	1:D:1231:ASN:H	2.11	0.48
1:A:1208:ASN:N	1:A:1208:ASN:ND2	2.62	0.47
1:B:933:ASN:CG	1:B:1016:ASN:HA	2.34	0.47
1:D:1062:ILE:HD12	1:D:1063:ARG:N	2.29	0.47
1:D:1132:TYR:CE2	1:D:1277:GLU:HA	2.49	0.47
1:A:983:ASP:HB2	1:A:1040:ASP:O	2.14	0.47
1:A:1122:PHE:HE1	1:A:1199:LYS:HE2	1.80	0.47
1:B:1193:LYS:HB2	1:B:1193:LYS:NZ	2.29	0.47
1:D:874:MET:HE2	1:D:891:ILE:HG21	1.95	0.47
1:A:891:ILE:HG12	1:A:919:ILE:HG12	1.96	0.47
1:A:1068:PHE:CD2	1:A:1072:LEU:HD11	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:935:SER:HA	1:C:1013:ILE:O	2.14	0.47
1:C:1074:LYS:O	1:C:1078:GLU:HG2	2.15	0.47
1:D:981:LEU:CD2	1:D:1041:ILE:HD13	2.44	0.47
1:B:953:ASN:HD21	1:B:1054:CYS:HA	1.79	0.47
1:C:1037:ASN:H	1:C:1037:ASN:ND2	2.12	0.47
1:A:1012:THR:HB	1:A:1024:TYR:HB2	1.97	0.47
1:A:1174:ILE:HG12	1:A:1214:ILE:HD12	1.97	0.47
1:B:982:GLN:HG3	1:B:987:ASN:O	2.15	0.47
1:C:879:ASN:OD1	1:D:879:ASN:ND2	2.47	0.47
1:C:1222:ASN:ND2	1:C:1260:SER:HB2	2.29	0.47
1:B:981:LEU:HD21	1:B:1041:ILE:HD13	1.97	0.47
1:B:984:THR:CG2	1:B:1040:ASP:HB3	2.43	0.47
1:A:1237:LEU:HD12	1:A:1251:TYR:HB2	1.96	0.47
1:A:1084:GLU:HB2	1:A:1085:PRO:HD3	1.97	0.47
1:B:910:TYR:CG	1:B:913:LYS:HE2	2.49	0.47
1:B:1025:ILE:HG12	1:B:1030:ILE:HG13	1.97	0.47
1:A:866:ILE:HD12	1:A:867:LYS:H	1.79	0.46
1:A:1191:ILE:CG2	1:A:1193:LYS:HE3	2.45	0.46
1:C:966:SER:HA	1:C:982:GLN:O	2.14	0.46
1:C:1116:ILE:HD11	1:C:1125:ILE:HD12	1.97	0.46
1:A:1116:ILE:CD1	1:A:1125:ILE:HD12	2.44	0.46
1:A:1037:ASN:N	1:A:1037:ASN:ND2	2.60	0.46
1:A:930:ARG:HA	1:A:1017:ARG:HH22	1.79	0.46
1:D:1211:GLY:HA2	1:D:1230:ASN:OD1	2.16	0.46
1:B:1144:TYR:CE2	1:B:1271:LYS:HG3	2.50	0.46
1:A:979:TRP:CD2	1:A:1013:ILE:HG21	2.49	0.46
1:A:979:TRP:CZ2	1:A:981:LEU:HG	2.50	0.46
1:D:1012:THR:HB	1:D:1024:TYR:HB2	1.97	0.46
1:C:965:ASN:ND2	1:C:984:THR:HA	2.31	0.46
1:D:930:ARG:HA	1:D:1017:ARG:HH22	1.81	0.46
1:D:1174:ILE:HG12	1:D:1214:ILE:HD12	1.97	0.46
1:C:893:ILE:HG13	1:C:893:ILE:O	2.15	0.46
1:D:894:ASN:HB3	1:D:916:GLU:HG2	1.98	0.46
1:D:981:LEU:HD21	1:D:1041:ILE:HD13	1.98	0.46
1:C:979:TRP:CD2	1:C:1013:ILE:HG21	2.50	0.46
1:C:990:LYS:O	1:C:991:LEU:HD12	2.16	0.46
1:A:871:ILE:HA	1:A:887:TYR:CE2	2.51	0.45
1:C:939:TRP:HB2	1:C:1063:ARG:HG2	1.97	0.45
1:C:1191:ILE:O	1:C:1196:LYS:HE3	2.15	0.45
1:A:956:THR:HA	1:A:971:SER:HA	1.98	0.45
1:A:1109:LEU:HD23	1:A:1265:PHE:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:904:ARG:HG2	1:B:904:ARG:NH2	2.31	0.45
1:C:1104:TYR:CG	1:C:1268:PHE:HB3	2.51	0.45
1:C:1126:ASN:HB3	1:C:1243:ASN:HB3	1.97	0.45
1:B:1250:TRP:CE3	3:F:3:GAL:H5	2.51	0.45
1:C:988:ASN:HA	1:C:1038:LEU:HD21	1.98	0.45
1:D:1241:HIS:HA	2:H:2:GAL:O4	2.16	0.45
1:A:1068:PHE:CE2	1:A:1072:LEU:HD11	2.51	0.45
1:C:973:ASN:ND2	1:C:974:TYR:N	2.64	0.45
1:D:997:GLN:HA	1:D:1005:ILE:HD11	1.97	0.45
1:D:1126:ASN:N	1:D:1126:ASN:ND2	2.63	0.45
1:B:973:ASN:ND2	1:B:974:TYR:N	2.59	0.45
1:D:1142:ARG:HH22	1:D:1278:ASN:HB2	1.80	0.45
1:A:1168:LYS:O	1:A:1169:ASN:HB2	2.16	0.45
1:B:928:ASN:O	1:B:928:ASN:ND2	2.50	0.45
1:B:1037:ASN:HD22	1:B:1037:ASN:H	1.64	0.44
1:B:1144:TYR:CE1	1:B:1271:LYS:HA	2.51	0.44
1:B:1179:ARG:O	1:B:1180:ASP:HB2	2.17	0.44
1:C:871:ILE:HD12	1:C:925:ILE:HD12	2.00	0.44
1:A:1189:ILE:HA	1:A:1196:LYS:HD3	1.98	0.44
1:A:978:ILE:HG12	1:A:992:VAL:HG22	1.99	0.44
1:C:939:TRP:HA	1:C:1009:ILE:O	2.18	0.44
1:A:1110:LEU:HD12	1:A:1263:GLY:N	2.33	0.44
1:B:1124:ASN:ND2	1:B:1244:ASN:OD1	2.50	0.44
1:C:953:ASN:H	1:C:973:ASN:ND2	2.12	0.44
1:C:1020:ASN:HD22	1:C:1034:SER:N	2.16	0.44
1:B:1119:ASN:HD22	1:B:1119:ASN:HA	1.54	0.44
1:B:871:ILE:HA	1:B:887:TYR:CE2	2.53	0.44
1:B:979:TRP:CD2	1:B:1013:ILE:HG21	2.52	0.44
1:C:907:PHE:CE1	1:C:1062:ILE:HG13	2.53	0.44
1:D:1229:ASN:HD22	1:D:1231:ASN:N	2.16	0.44
1:A:921:GLN:HB2	1:A:1045:ASP:O	2.17	0.43
1:C:1149:VAL:HG21	1:C:1174:ILE:CG2	2.47	0.43
1:C:1193:LYS:CG	1:C:1194:PRO:HD2	2.47	0.43
1:B:1116:ILE:HD12	1:B:1245:LEU:HD11	2.01	0.43
1:B:1133:GLN:HB3	1:B:1139:SER:HA	2.00	0.43
1:A:984:THR:CG2	1:A:1040:ASP:HB3	2.47	0.43
1:C:928:ASN:ND2	1:C:1042:HIS:CE1	2.87	0.43
1:C:1037:ASN:N	1:C:1037:ASN:ND2	2.63	0.43
1:C:1197:ILE:HA	1:C:1246:VAL:HG12	2.00	0.43
1:D:1194:PRO:O	1:D:1248:SER:HA	2.17	0.43
1:A:1008:TRP:HE1	1:A:1096:ASN:ND2	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:868:ASP:C	1:B:870:SER:H	2.22	0.43
1:A:1191:ILE:HG23	1:A:1193:LYS:HE3	2.00	0.43
1:C:1022:ARG:HG2	1:C:1032:GLU:HG3	2.00	0.43
1:B:1179:ARG:HB3	1:B:1179:ARG:NH2	2.34	0.43
1:C:1208:ASN:HD22	1:C:1208:ASN:N	2.16	0.43
1:D:929:GLY:C	1:D:931:TYR:H	2.21	0.43
1:A:1132:TYR:CE1	1:A:1278:ASN:ND2	2.86	0.43
1:A:1194:PRO:HG2	1:A:1195:GLU:OE2	2.19	0.43
1:B:1022:ARG:HB2	1:B:1029:LEU:HD11	2.00	0.43
1:D:871:ILE:HD12	1:D:925:ILE:HG23	2.01	0.43
1:A:1128:GLN:HG3	2:H:3:SIA:H111	2.01	0.43
1:C:1171:LEU:HB3	1:C:1213:ILE:HG12	2.01	0.43
1:B:997:GLN:HA	1:B:1005:ILE:HD11	2.01	0.43
1:D:1126:ASN:H	1:D:1126:ASN:ND2	1.99	0.43
1:B:930:ARG:HG2	1:B:1040:ASP:HA	2.01	0.43
1:A:936:ILE:HG12	1:A:1013:ILE:HB	2.01	0.42
1:C:926:ILE:HD13	1:C:1045:ASP:HA	2.01	0.42
1:C:1213:ILE:HG13	1:C:1214:ILE:N	2.33	0.42
1:A:1176:VAL:HG23	1:A:1185:LEU:HD11	2.00	0.42
1:A:1241:HIS:HA	2:E:2:GAL:HO4	1.82	0.42
1:D:872:LEU:HD21	1:D:919:ILE:HD13	2.02	0.42
1:B:956:THR:HG23	1:B:1052:VAL:HB	2.01	0.42
1:B:1068:PHE:CE2	1:B:1072:LEU:HD11	2.53	0.42
1:B:871:ILE:HD12	1:B:925:ILE:HG23	2.02	0.42
1:C:1016:ASN:HB2	1:C:1071:GLU:OE2	2.19	0.42
1:A:911:SER:HB3	1:A:1051:ILE:HG21	2.02	0.42
1:A:1154:ASN:C	1:A:1154:ASN:ND2	2.72	0.42
1:B:939:TRP:HA	1:B:1009:ILE:O	2.20	0.42
1:C:930:ARG:HA	1:C:1017:ARG:NH2	2.34	0.42
1:A:957:ILE:HG13	1:A:958:ILE:HG13	2.00	0.42
1:C:962:ARG:NE	1:C:1042:HIS:CE1	2.88	0.42
1:C:1094:TRP:CD1	1:C:1272:GLU:HG3	2.54	0.42
1:D:939:TRP:HA	1:D:1009:ILE:O	2.19	0.42
1:C:1068:PHE:CZ	1:C:1080:LEU:HD11	2.55	0.42
1:D:953:ASN:H	1:D:973:ASN:ND2	2.12	0.42
1:B:1018:LEU:N	1:B:1018:LEU:HD12	2.35	0.41
1:A:939:TRP:HB2	1:A:1063:ARG:CG	2.45	0.41
1:A:1231:ASN:N	1:A:1231:ASN:HD22	2.16	0.41
1:D:874:MET:CE	1:D:891:ILE:HG21	2.49	0.41
1:A:939:TRP:HA	1:A:1009:ILE:O	2.20	0.41
1:B:1126:ASN:HB3	1:B:1243:ASN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:876:TYR:CD2	1:A:904:ARG:HB3	2.56	0.41
1:A:1151:ILE:HG12	1:A:1174:ILE:CD1	2.51	0.41
1:A:1213:ILE:HG22	1:A:1214:ILE:H	1.85	0.41
1:B:872:LEU:HD21	1:B:919:ILE:HG21	2.02	0.41
1:B:928:ASN:HA	1:B:1041:ILE:O	2.20	0.41
1:A:1120:SER:OG	1:A:1121:ASN:N	2.54	0.41
1:A:1125:ILE:HG12	1:A:1125:ILE:O	2.21	0.41
1:B:964:ASN:N	1:B:964:ASN:ND2	2.67	0.41
1:C:1062:ILE:HD12	1:C:1063:ARG:H	1.84	0.41
1:C:1116:ILE:CD1	1:C:1125:ILE:HD12	2.51	0.41
1:C:1124:ASN:HB3	1:C:1126:ASN:HD22	1.84	0.41
1:C:1125:ILE:HG12	1:C:1125:ILE:O	2.21	0.41
1:C:1208:ASN:N	1:C:1208:ASN:ND2	2.69	0.41
1:C:1226:ASN:HB2	1:C:1237:LEU:HD23	2.01	0.41
1:D:1100:TYR:CD1	1:D:1151:ILE:HG22	2.56	0.41
1:D:1231:ASN:N	1:D:1231:ASN:HD22	2.17	0.41
1:A:1084:GLU:HB2	1:A:1085:PRO:CD	2.51	0.41
1:C:1167:ARG:O	1:C:1170:ASP:HB2	2.21	0.41
1:B:983:ASP:HB2	1:B:1040:ASP:O	2.21	0.40
1:C:1150:ILE:HD12	1:C:1150:ILE:C	2.42	0.40
1:D:1177:VAL:O	1:D:1177:VAL:CG1	2.69	0.40
1:A:869:ASN:HB3	1:A:1070:THR:HG23	2.03	0.40
1:A:893:ILE:HD11	5:A:186:HOH:O	2.20	0.40
1:B:978:ILE:HG23	1:B:992:VAL:HG22	2.04	0.40
1:B:991:LEU:HD12	1:B:991:LEU:HA	1.82	0.40
1:C:928:ASN:OD1	1:C:928:ASN:O	2.38	0.40
1:D:1168:LYS:HE2	1:D:1217:ASP:OD1	2.21	0.40
1:D:1191:ILE:HD12	1:D:1191:ILE:C	2.41	0.40
1:A:979:TRP:CE2	1:A:1013:ILE:HG21	2.56	0.40
1:B:928:ASN:ND2	1:B:1042:HIS:HB2	2.37	0.40
1:B:1163:ASP:C	1:B:1163:ASP:OD2	2.60	0.40
1:C:981:LEU:HD22	1:C:1041:ILE:HD13	2.04	0.40
1:D:1037:ASN:N	1:D:1037:ASN:ND2	2.67	0.40
1:B:991:LEU:HD21	1:B:1022:ARG:HA	2.04	0.40
1:B:1025:ILE:CG1	1:B:1030:ILE:HG13	2.51	0.40
1:B:1135:PRO:HG2	5:B:146:HOH:O	2.22	0.40
1:D:1084:GLU:CB	1:D:1085:PRO:CD	2.99	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	400/413 (97%)	360 (90%)	37 (9%)	3 (1%)	19	13
1	B	396/413 (96%)	355 (90%)	37 (9%)	4 (1%)	15	9
1	C	396/413 (96%)	360 (91%)	33 (8%)	3 (1%)	19	13
1	D	398/413 (96%)	362 (91%)	32 (8%)	4 (1%)	15	9
All	All	1590/1652 (96%)	1437 (90%)	139 (9%)	14 (1%)	17	11

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	926	ILE
1	C	1257	LYS
1	D	1084	GLU
1	A	1257	LYS
1	D	926	ILE
1	C	1258	ASN
1	A	915	SER
1	A	926	ILE
1	B	869	ASN
1	B	1120	SER
1	C	926	ILE
1	D	930	ARG
1	D	1188	ASP
1	B	1084	GLU

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	375/382 (98%)	362 (96%)	13 (4%)	36	35
1	B	372/382 (97%)	358 (96%)	14 (4%)	33	31
1	C	372/382 (97%)	360 (97%)	12 (3%)	39	38
1	D	374/382 (98%)	357 (96%)	17 (4%)	27	24
All	All	1493/1528 (98%)	1437 (96%)	56 (4%)	33	31

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	870	SER
1	A	893	ILE
1	A	946	PHE
1	A	956	THR
1	A	981	LEU
1	A	988	ASN
1	A	1037	ASN
1	A	1106	LEU
1	A	1109	LEU
1	A	1119	ASN
1	A	1154	ASN
1	A	1212	GLN
1	A	1229	ASN
1	B	869	ASN
1	B	875	ARG
1	B	928	ASN
1	B	964	ASN
1	B	973	ASN
1	B	981	LEU
1	B	991	LEU
1	B	1037	ASN
1	B	1062	ILE
1	B	1106	LEU
1	B	1110	LEU
1	B	1119	ASN
1	B	1126	ASN
1	B	1229	ASN
1	C	879	ASN
1	C	973	ASN
1	C	981	LEU
1	C	988	ASN
1	C	1037	ASN
1	C	1062	ILE

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Mol	Chain	Res	Type
1	C	1074	LYS
1	C	1084	GLU
1	C	1106	LEU
1	C	1109	LEU
1	C	1110	LEU
1	C	1229	ASN
1	D	867	LYS
1	D	877	GLU
1	D	941	ARG
1	D	956	THR
1	D	973	ASN
1	D	981	LEU
1	D	984	THR
1	D	991	LEU
1	D	1037	ASN
1	D	1062	ILE
1	D	1110	LEU
1	D	1119	ASN
1	D	1126	ASN
1	D	1201	ILE
1	D	1229	ASN
1	D	1258	ASN
1	D	1267	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	879	ASN
1	A	928	ASN
1	A	950	ASN
1	A	953	ASN
1	A	964	ASN
1	A	988	ASN
1	A	997	GLN
1	A	1006	ASN
1	A	1020	ASN
1	A	1028	ASN
1	A	1037	ASN
1	A	1042	HIS
1	A	1046	ASN
1	A	1055	ASN
1	A	1096	ASN

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Mol	Chain	Res	Type
1	A	1101	ASN
1	A	1119	ASN
1	A	1124	ASN
1	A	1133	GLN
1	A	1154	ASN
1	A	1161	ASN
1	A	1208	ASN
1	A	1229	ASN
1	A	1231	ASN
1	A	1273	HIS
1	A	1278	ASN
1	B	869	ASN
1	B	878	ASN
1	B	928	ASN
1	B	933	ASN
1	B	950	ASN
1	B	953	ASN
1	B	964	ASN
1	B	973	ASN
1	B	997	GLN
1	B	1006	ASN
1	B	1020	ASN
1	B	1028	ASN
1	B	1037	ASN
1	B	1046	ASN
1	B	1055	ASN
1	B	1096	ASN
1	B	1101	ASN
1	B	1124	ASN
1	B	1126	ASN
1	B	1128	GLN
1	B	1222	ASN
1	B	1229	ASN
1	B	1230	ASN
1	B	1231	ASN
1	B	1244	ASN
1	B	1276	GLN
1	C	879	ASN
1	C	928	ASN
1	C	950	ASN
1	C	953	ASN
1	C	964	ASN

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Mol	Chain	Res	Type
1	C	965	ASN
1	C	973	ASN
1	C	982	GLN
1	C	988	ASN
1	C	989	GLN
1	C	997	GLN
1	C	1006	ASN
1	C	1016	ASN
1	C	1020	ASN
1	C	1037	ASN
1	C	1046	ASN
1	C	1055	ASN
1	C	1096	ASN
1	C	1101	ASN
1	C	1119	ASN
1	C	1126	ASN
1	C	1127	GLN
1	C	1133	GLN
1	C	1136	ASN
1	C	1208	ASN
1	C	1222	ASN
1	C	1229	ASN
1	C	1276	GLN
1	C	1278	ASN
1	D	869	ASN
1	D	879	ASN
1	D	921	GLN
1	D	922	ASN
1	D	928	ASN
1	D	932	GLN
1	D	953	ASN
1	D	963	ASN
1	D	964	ASN
1	D	973	ASN
1	D	997	GLN
1	D	1006	ASN
1	D	1028	ASN
1	D	1037	ASN
1	D	1046	ASN
1	D	1055	ASN
1	D	1096	ASN
1	D	1101	ASN

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Mol	Chain	Res	Type
1	D	1119	ASN
1	D	1124	ASN
1	D	1126	ASN
1	D	1229	ASN
1	D	1231	ASN
1	D	1273	HIS
1	D	1278	ASN

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](#)

15 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	NGA	E	1	2	15,15,15	0.87	0	21,21,21	1.19	2 (9%)
2	GAL	E	2	2	11,11,12	0.82	1 (9%)	15,15,17	1.20	1 (6%)
2	SIA	E	3	2	20,20,21	3.31	4 (20%)	24,28,31	1.34	2 (8%)
3	GAL	F	1	3	12,12,12	0.96	1 (8%)	17,17,17	0.99	1 (5%)
3	NGA	F	2	3	14,14,15	0.84	0	17,19,21	1.41	2 (11%)
3	GAL	F	3	3	11,11,12	0.84	1 (9%)	15,15,17	1.29	2 (13%)
3	SIA	F	4	3	20,20,21	3.24	4 (20%)	24,28,31	1.35	3 (12%)
3	SIA	F	5	3	20,20,21	1.90	4 (20%)	24,28,31	1.52	3 (12%)
4	GAL	G	1	4	12,12,12	0.65	0	17,17,17	0.81	0
4	NGA	G	2	4	14,14,15	0.88	0	17,19,21	1.43	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GAL	G	3	4	11,11,12	0.87	1 (9%)	15,15,17	1.25	2 (13%)
4	SIA	G	4	4	20,20,21	3.30	3 (15%)	24,28,31	1.35	2 (8%)
2	NGA	H	1	2	15,15,15	0.97	1 (6%)	21,21,21	1.21	2 (9%)
2	GAL	H	2	2	11,11,12	0.80	0	15,15,17	1.21	1 (6%)
2	SIA	H	3	2	20,20,21	3.28	3 (15%)	24,28,31	1.34	3 (12%)

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	NGA	E	1	2	-	2/6/26/26	0/1/1/1
2	GAL	E	2	2	-	0/2/19/22	0/1/1/1
2	SIA	E	3	2	-	2/18/34/38	0/1/1/1
3	GAL	F	1	3	-	1/2/22/22	0/1/1/1
3	NGA	F	2	3	-	2/6/23/26	0/1/1/1
3	GAL	F	3	3	-	0/2/19/22	0/1/1/1
3	SIA	F	4	3	-	0/18/34/38	0/1/1/1
3	SIA	F	5	3	-	4/18/34/38	0/1/1/1
4	GAL	G	1	4	-	1/2/22/22	0/1/1/1
4	NGA	G	2	4	-	2/6/23/26	0/1/1/1
4	GAL	G	3	4	-	2/2/19/22	0/1/1/1
4	SIA	G	4	4	-	4/18/34/38	0/1/1/1
2	NGA	H	1	2	-	2/6/26/26	0/1/1/1
2	GAL	H	2	2	-	1/2/19/22	0/1/1/1
2	SIA	H	3	2	-	1/18/34/38	0/1/1/1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	3	SIA	C2-C1	-13.60	1.40	1.52
4	G	4	SIA	C2-C1	-13.58	1.40	1.52
3	F	4	SIA	C2-C1	-13.44	1.40	1.52
2	H	3	SIA	C2-C1	-13.43	1.40	1.52
3	F	5	SIA	O6-C2	5.42	1.51	1.43
2	H	3	SIA	O6-C2	3.63	1.48	1.43
2	E	3	SIA	O6-C2	3.58	1.48	1.43
4	G	4	SIA	O6-C2	3.53	1.48	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	4	SIA	O6-C2	3.11	1.47	1.43
3	F	5	SIA	C4-C5	3.10	1.55	1.53
3	F	5	SIA	C2-C1	-2.99	1.49	1.52
3	F	1	GAL	O4-C4	-2.51	1.37	1.43
3	F	5	SIA	C3-C4	2.49	1.57	1.52
4	G	3	GAL	C2-C3	2.45	1.56	1.52
3	F	3	GAL	C2-C3	2.43	1.56	1.52
2	H	3	SIA	O6-C6	2.30	1.47	1.44
2	E	3	SIA	O6-C6	2.18	1.47	1.44
4	G	4	SIA	O6-C6	2.17	1.47	1.44
2	E	3	SIA	C7-C6	2.16	1.55	1.53
2	E	2	GAL	C2-C3	2.16	1.55	1.52
3	F	4	SIA	O6-C6	2.15	1.47	1.44
3	F	4	SIA	C7-C6	2.15	1.55	1.53
2	H	1	NGA	C1-C2	2.10	1.55	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	5	SIA	C4-C3-C2	-4.18	102.31	109.81
3	F	2	NGA	C4-C3-C2	-3.49	105.91	111.02
3	F	5	SIA	O6-C2-C1	3.48	114.52	107.70
4	G	2	NGA	C4-C3-C2	-3.12	106.45	111.02
2	H	3	SIA	O6-C2-C1	3.02	113.62	107.70
2	E	3	SIA	O6-C2-C1	2.99	113.56	107.70
4	G	4	SIA	O6-C2-C1	2.95	113.49	107.70
3	F	5	SIA	O1B-C1-C2	2.93	121.40	113.03
3	F	4	SIA	O1B-C1-C2	2.91	121.35	113.03
2	H	3	SIA	O1B-C1-C2	2.91	121.33	113.03
2	E	3	SIA	O1B-C1-C2	2.86	121.21	113.03
2	E	1	NGA	C4-C3-C2	-2.85	106.17	110.34
4	G	4	SIA	O1B-C1-C2	2.79	121.00	113.03
3	F	4	SIA	O6-C2-C1	2.76	113.11	107.70
2	H	1	NGA	C4-C3-C2	-2.49	106.69	110.34
2	H	2	GAL	O5-C5-C6	2.47	111.08	107.20
3	F	2	NGA	O7-C7-C8	-2.36	117.67	122.06
4	G	3	GAL	O5-C5-C6	2.34	110.88	107.20
3	F	3	GAL	O3-C3-C4	-2.34	104.94	110.35
4	G	2	NGA	C2-N2-C7	2.33	126.22	122.90
3	F	3	GAL	O5-C5-C6	2.31	110.83	107.20
2	H	1	NGA	O7-C7-C8	-2.31	117.76	122.06
4	G	2	NGA	O7-C7-C8	-2.30	117.78	122.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	3	GAL	O3-C3-C4	-2.22	105.21	110.35
2	E	1	NGA	O7-C7-C8	-2.20	117.97	122.06
2	E	2	GAL	O5-C5-C6	2.18	110.62	107.20
3	F	1	GAL	C3-C4-C5	-2.17	106.37	110.24
3	F	4	SIA	O6-C2-C3	2.08	113.32	110.46
2	H	3	SIA	C4-C3-C2	-2.04	106.15	109.81

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	1	NGA	C8-C7-N2-C2
2	E	1	NGA	O7-C7-N2-C2
3	F	5	SIA	C6-C7-C8-C9
3	F	5	SIA	O7-C7-C8-C9
3	F	2	NGA	O5-C5-C6-O6
2	H	1	NGA	C8-C7-N2-C2
2	H	1	NGA	O7-C7-N2-C2
4	G	2	NGA	C8-C7-N2-C2
4	G	3	GAL	O5-C5-C6-O6
3	F	5	SIA	C6-C7-C8-O8
4	G	4	SIA	O7-C7-C8-C9
3	F	2	NGA	C4-C5-C6-O6
4	G	4	SIA	C6-C7-C8-C9
4	G	2	NGA	O7-C7-N2-C2
3	F	5	SIA	O7-C7-C8-O8
4	G	4	SIA	C6-C7-C8-O8
3	F	1	GAL	O5-C5-C6-O6
4	G	1	GAL	O5-C5-C6-O6
4	G	3	GAL	C4-C5-C6-O6
4	G	4	SIA	O7-C7-C8-O8
2	E	3	SIA	C7-C8-C9-O9
2	E	3	SIA	O8-C8-C9-O9
2	H	3	SIA	O8-C8-C9-O9
2	H	2	GAL	O5-C5-C6-O6

There are no ring outliers.

8 monomers are involved in 11 short contacts:

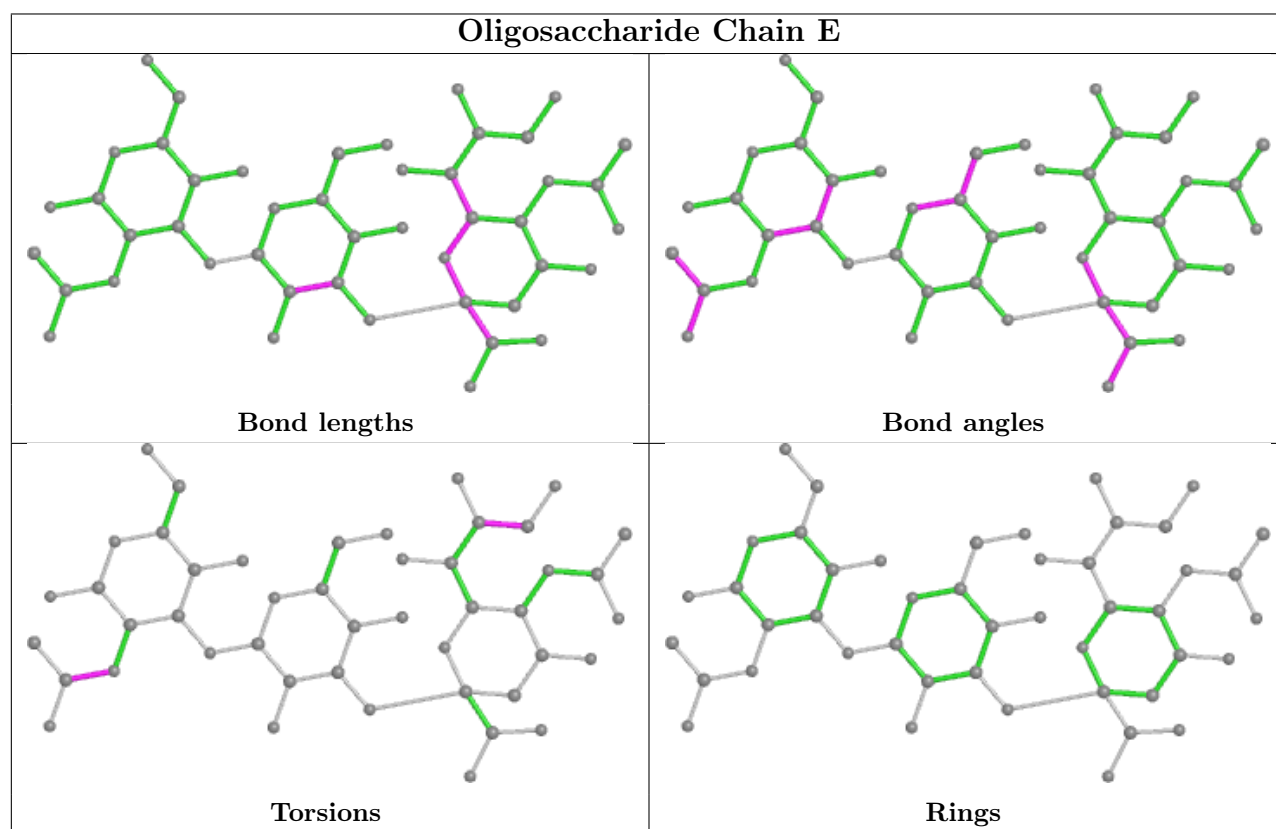
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	5	SIA	1	0

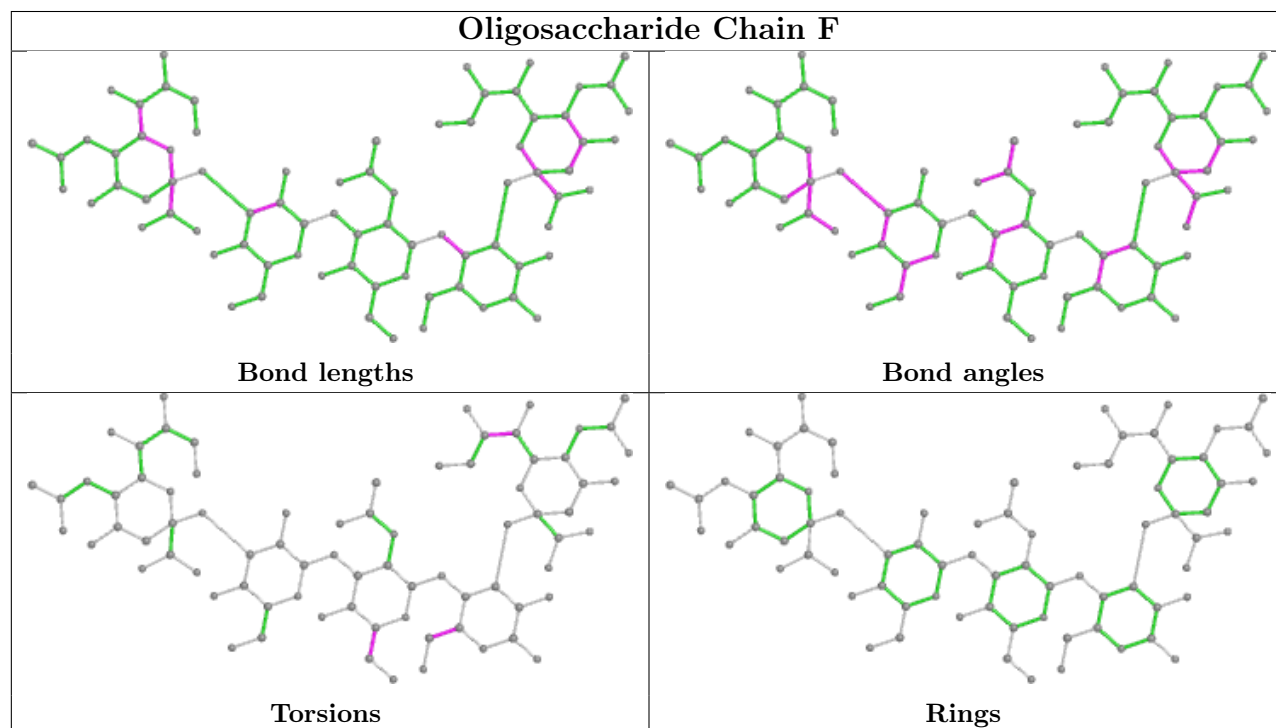
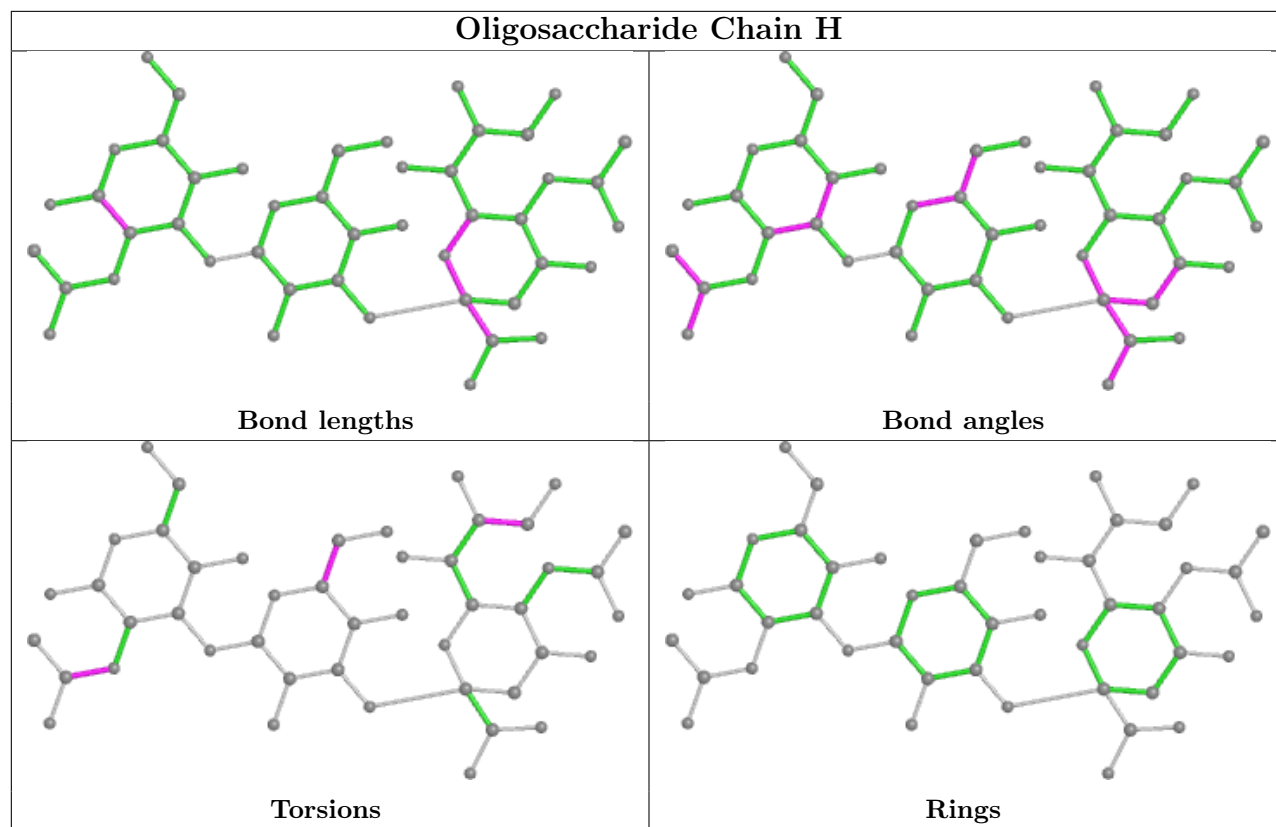
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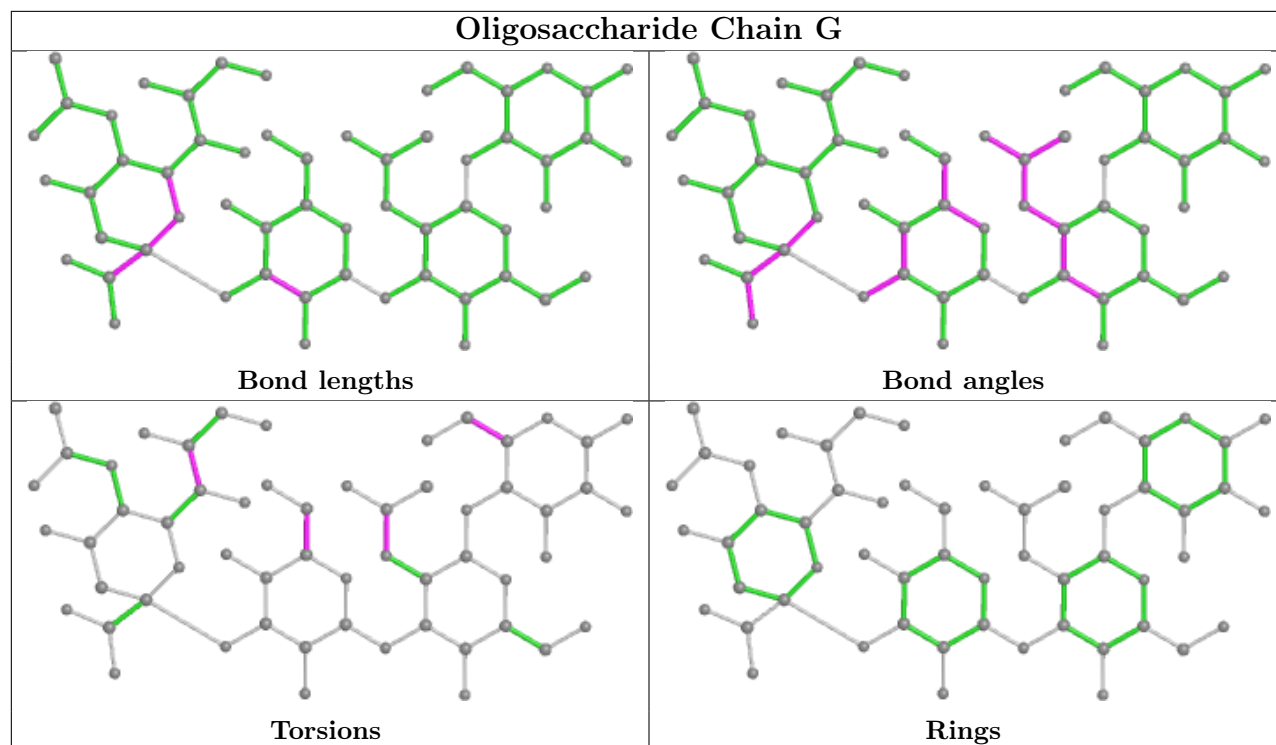
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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	3	GAL	3	0
2	H	2	GAL	1	0
2	H	3	SIA	1	0
2	E	2	GAL	2	0
3	F	1	GAL	1	0
4	G	3	GAL	2	0
4	G	1	GAL	1	0

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](#)

There are no ligands in this entry.

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	406/413 (98%)	0.23	25 (6%) 20 19	23, 39, 58, 72	0
1	B	402/413 (97%)	0.19	18 (4%) 33 32	24, 40, 62, 81	0
1	C	402/413 (97%)	0.22	21 (5%) 27 26	26, 40, 61, 76	0
1	D	404/413 (97%)	0.18	21 (5%) 27 26	24, 38, 58, 77	0
All	All	1614/1652 (97%)	0.21	85 (5%) 26 25	23, 39, 60, 81	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	929	GLY	8.8
1	D	931	TYR	6.6
1	B	931	TYR	6.0
1	B	1162	THR	5.9
1	A	1162	THR	5.9
1	A	1161	ASN	5.9
1	C	1161	ASN	5.7
1	B	868	ASP	5.6
1	D	1207	ASN	5.5
1	C	1162	THR	5.4
1	A	1278	ASN	5.2
1	B	1161	ASN	5.1
1	D	1162	THR	5.0
1	D	927	TYR	4.8
1	C	1278	ASN	4.5
1	A	931	TYR	4.3
1	A	1207	ASN	4.2
1	B	1257	LYS	4.0
1	B	1180	ASP	3.8
1	C	984	THR	3.6
1	C	925	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	C	924	ASP	3.6
1	D	1161	ASN	3.5
1	C	1180	ASP	3.4
1	C	1075	THR	3.3
1	C	1257	LYS	3.3
1	C	1154	ASN	3.3
1	D	1122	PHE	3.3
1	B	927	TYR	3.3
1	A	1206	SER	3.2
1	C	1207	ASN	3.2
1	D	1231	ASN	3.2
1	A	927	TYR	3.2
1	B	930	ARG	3.1
1	D	1257	LYS	3.1
1	A	1018	LEU	3.1
1	C	868	ASP	3.1
1	A	1122	PHE	3.1
1	D	1278	ASN	3.0
1	A	1019	GLY	3.0
1	D	878	ASN	3.0
1	B	924	ASP	3.0
1	C	1231	ASN	2.9
1	D	1084	GLU	2.9
1	C	869	ASN	2.9
1	C	886	GLY	2.8
1	A	1180	ASP	2.8
1	A	866	ILE	2.8
1	A	893	ILE	2.8
1	B	1018	LEU	2.7
1	B	1258	ASN	2.7
1	A	958	ILE	2.7
1	D	958	ILE	2.7
1	A	1155	GLY	2.7
1	D	923	ASN	2.7
1	A	1013	ILE	2.6
1	A	946	PHE	2.6
1	C	963	ASN	2.5
1	A	940	VAL	2.4
1	B	1207	ASN	2.4
1	C	931	TYR	2.4
1	D	930	ARG	2.4
1	D	1180	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	938	PHE	2.3
1	B	1154	ASN	2.3
1	B	1179	ARG	2.3
1	D	932	GLN	2.3
1	C	965	ASN	2.2
1	D	1047	ILE	2.2
1	A	1231	ASN	2.2
1	D	1192	ALA	2.2
1	A	1257	LYS	2.2
1	D	1065	PHE	2.2
1	A	1084	GLU	2.2
1	C	1011	VAL	2.1
1	A	1040	ASP	2.1
1	B	1135	PRO	2.1
1	B	1208	ASN	2.1
1	C	1242	SER	2.1
1	B	1019	GLY	2.1
1	A	1011	VAL	2.1
1	D	1154	ASN	2.1
1	A	979	TRP	2.1
1	C	1181	VAL	2.0
1	B	1038	LEU	2.0

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

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

6.3 Carbohydrates [\(i\)](#)

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

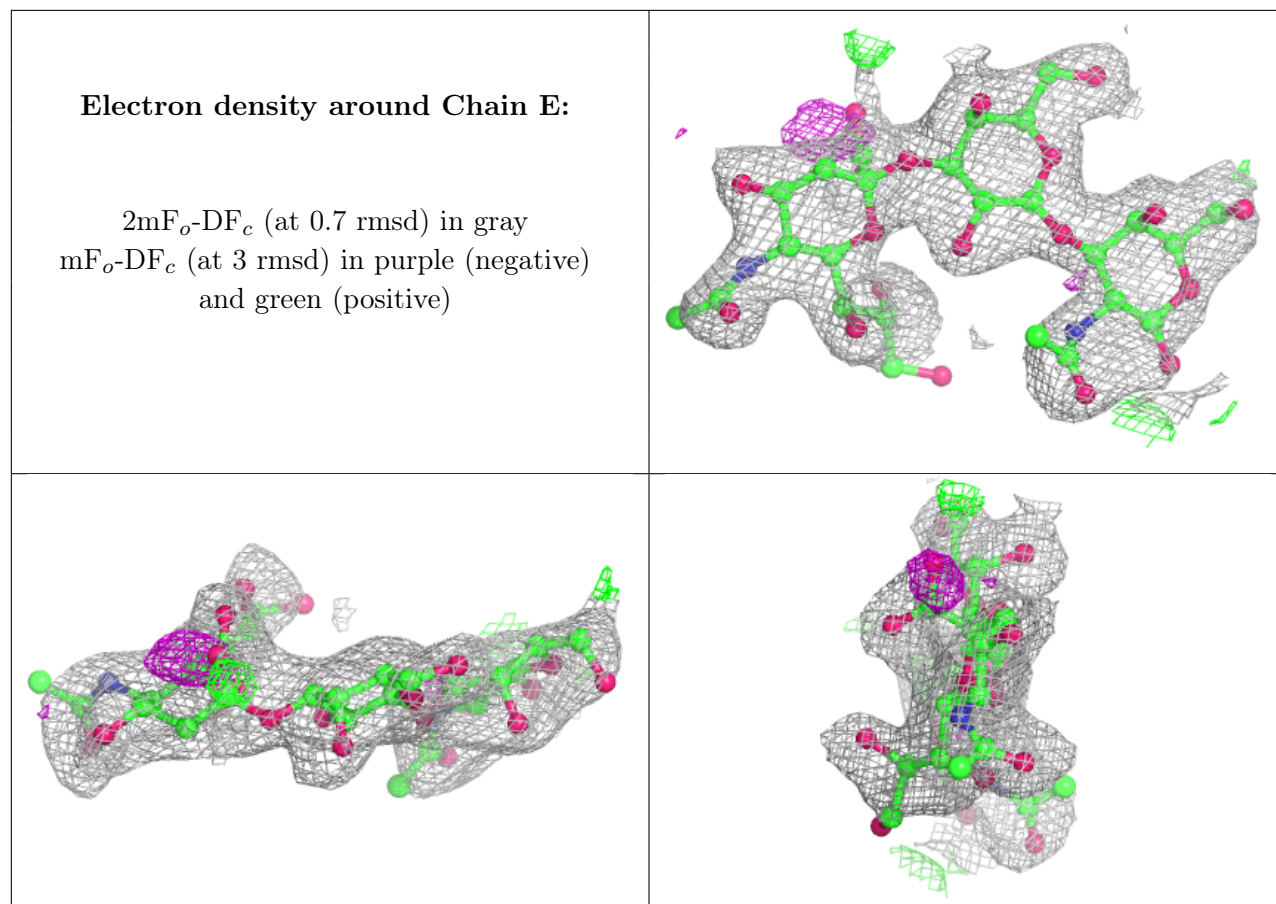
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GAL	G	1	12/12	0.64	0.27	78,83,84,86	0
3	SIA	F	5	20/21	0.71	0.38	81,83,86,86	0
2	NGA	H	1	15/15	0.73	0.32	71,75,76,77	0
2	SIA	H	3	20/21	0.75	0.24	74,76,79,79	0
2	SIA	E	3	20/21	0.77	0.27	64,66,73,74	0
4	NGA	G	2	14/15	0.78	0.24	64,69,72,73	0

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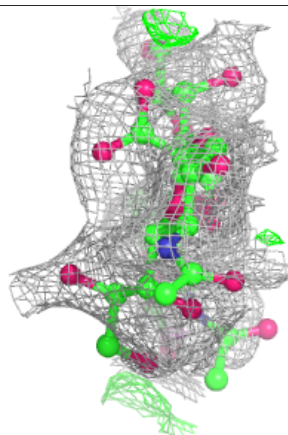
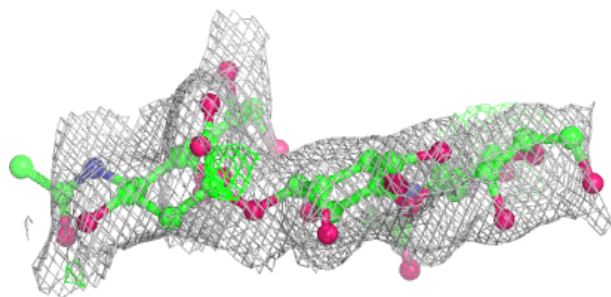
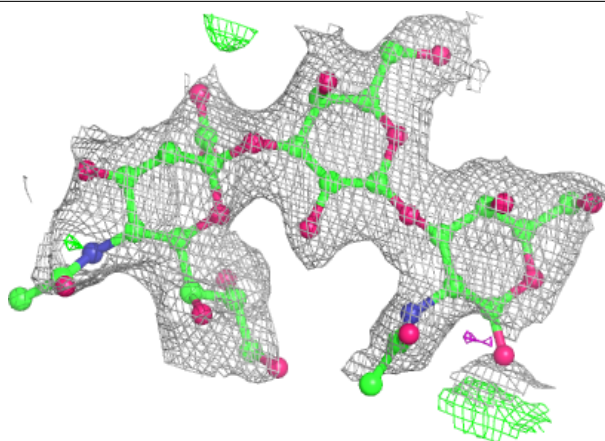
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NGA	E	1	15/15	0.80	0.25	66,68,71,72	0
4	GAL	G	3	11/12	0.82	0.14	57,60,62,63	0
2	GAL	E	2	11/12	0.84	0.15	59,63,65,65	0
3	GAL	F	1	12/12	0.84	0.22	65,74,77,81	0
2	GAL	H	2	11/12	0.86	0.17	68,71,72,73	0
3	SIA	F	4	20/21	0.88	0.16	53,57,60,61	0
4	SIA	G	4	20/21	0.88	0.21	61,63,65,67	0
3	NGA	F	2	14/15	0.91	0.14	45,55,57,58	0
3	GAL	F	3	11/12	0.92	0.11	43,46,49,49	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.

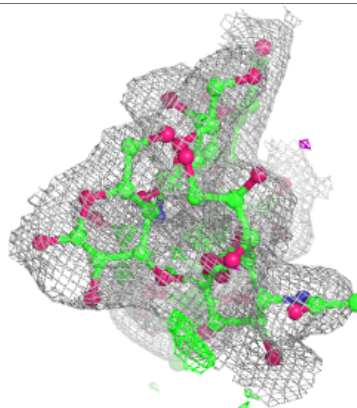
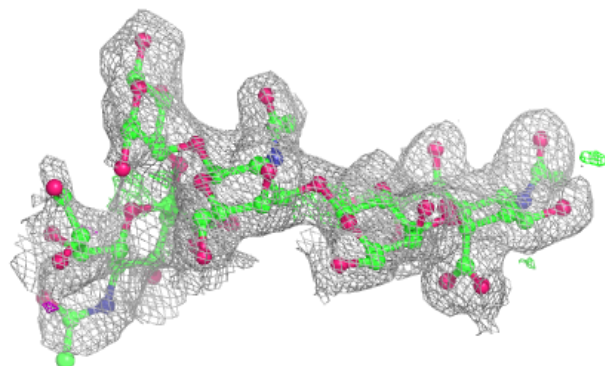
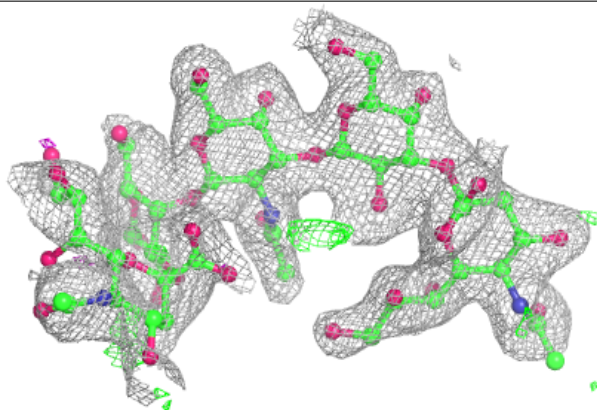


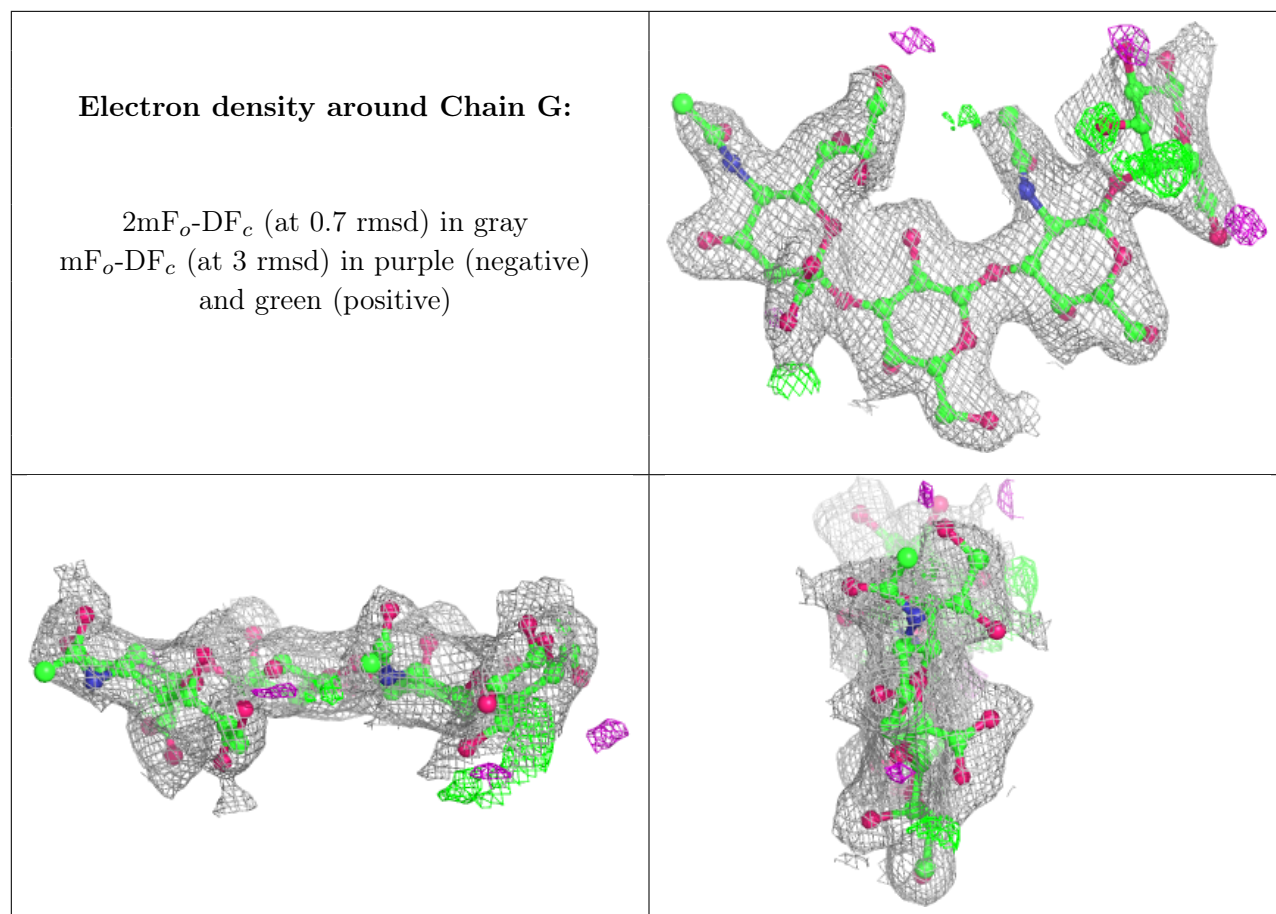
Electron density around Chain H:

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

**Electron density around Chain F:**

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





6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.