



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2025 – 03:08 pm BST

PDB ID : 3ZPB / pdb_00003zpb
Title : INFLUENZA VIRUS (VN1194) H5 E190D mutant HA with LSTa
Authors : Liu, J.; Stevens, D.J.; Gamblin, S.J.; Skehel, J.J.
Deposited on : 2013-02-27
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

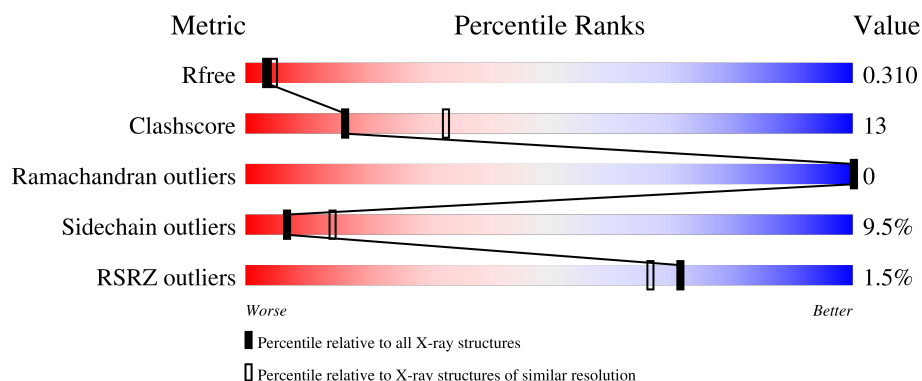
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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	E	340	<div> <div>%</div> <div> <div></div> <div>69%</div> <div>23%</div> <div>• 6%</div> </div> </div>
2	F	160	<div> <div>2%</div> <div> <div></div> <div>70%</div> <div>24%</div> <div>• •</div> </div> </div>
3	A	3	<div> <div></div> <div> <div>67%</div> <div>33%</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3857 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 HAEMAGGLUTININ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	321	Total	C	N	O	S	4	0	0
			2548	1610	440	483	15			

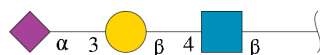
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	40	LYS	THR	conflict	UNP Q6DQ34
E	190	ASP	GLU	engineered mutation	UNP Q6DQ34

- Molecule 2 is a protein called HAEMAGGLUTININ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	157	Total	C	N	O	S	0	0	0
			1263	786	220	249	8			

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



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	A	3	Total	C	N	O	0	0	1
			32	17	1	14			

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

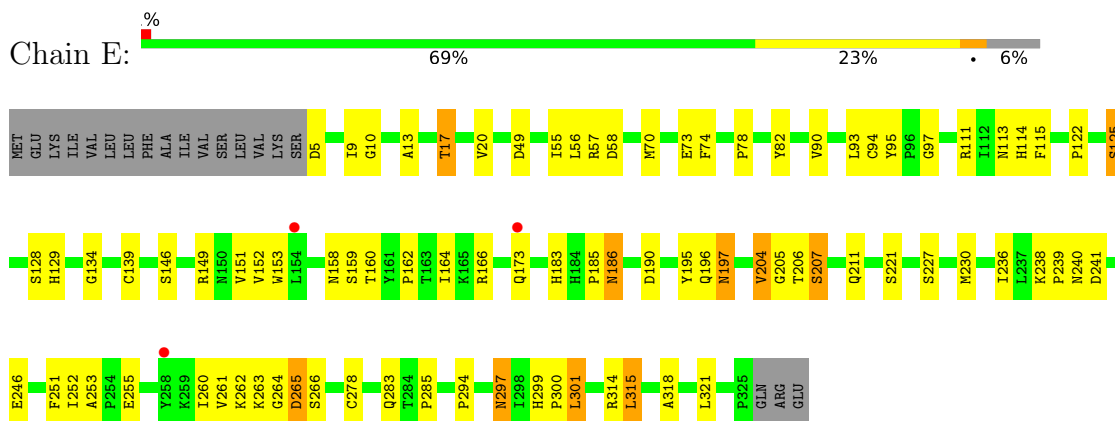


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	F	1	14	8	1	5	0	0

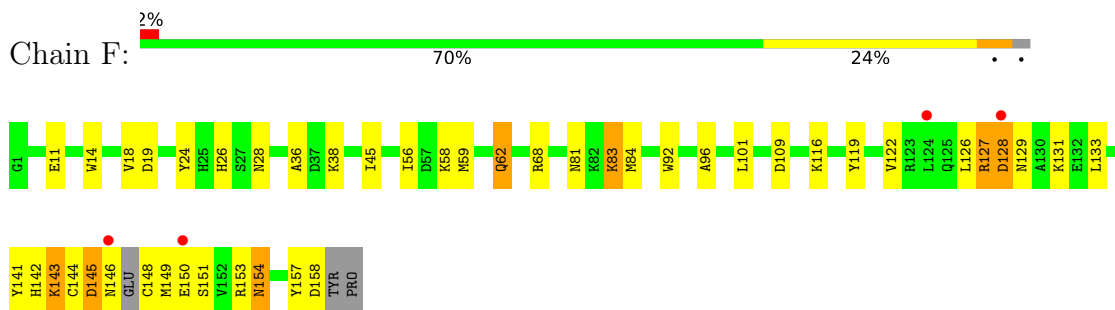
3 Residue-property plots

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.

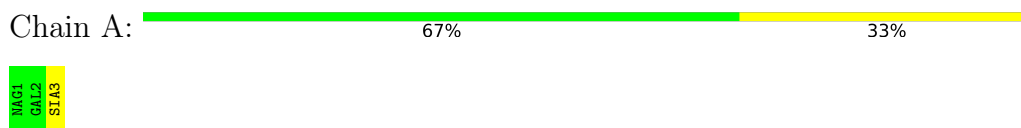
• Molecule 1: HAEMAGGLUTININ



• Molecule 2: HAEMAGGLUTININ



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



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	101.11Å 101.11Å 448.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 2.60 30.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-2.60) 99.5 (30.00-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.242 , 0.290 0.272 , 0.310	Depositor DCC
R_{free} test set	1395 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	65.4	Xtriage
Anisotropy	0.648	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3857	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.31% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	E	0.74	1/2610 (0.0%)	0.96	2/3545 (0.1%)
2	F	0.88	0/1286	1.05	3/1727 (0.2%)
All	All	0.79	1/3896 (0.0%)	0.99	5/5272 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	F	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	78	PRO	N-CD	7.01	1.57	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	18	VAL	N-CA-C	-7.25	104.46	112.80
1	E	17	THR	N-CA-C	-6.52	106.28	114.56
2	F	11	GLU	N-CA-C	6.00	117.82	111.28
2	F	109	ASP	N-CA-C	5.47	117.24	111.28
1	E	13	ALA	N-CA-C	-5.22	101.43	109.52

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	126	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2548	0	2490	63	0
2	F	1263	0	1181	40	0
3	A	32	0	26	0	0
4	F	14	0	13	0	0
All	All	3857	0	3710	97	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 13.

All (97) 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)
2:F:129:ASN:O	2:F:141:TYR:CD2	1.95	1.19
1:E:125:SER:OG	1:E:166:ARG:NH2	1.81	1.10
1:E:204:VAL:HG23	1:E:211:GLN:HB3	1.12	1.08
1:E:134:GLY:HA3	1:E:153:TRP:HB3	1.43	0.97
1:E:125:SER:HG	1:E:166:ARG:HH22	1.17	0.92
1:E:207:SER:OG	1:E:241:ASP:OD2	1.89	0.88
1:E:186:ASN:ND2	1:E:227:SER:HB2	1.89	0.87
1:E:204:VAL:HG23	1:E:211:GLN:CB	2.03	0.86
2:F:127:ARG:HH11	2:F:127:ARG:HG3	1.40	0.86
1:E:122:PRO:O	1:E:125:SER:HB3	1.77	0.84
1:E:186:ASN:HD22	1:E:227:SER:HB2	1.42	0.84
2:F:129:ASN:C	2:F:141:TYR:CD2	2.55	0.84
1:E:95:TYR:CD1	1:E:230:MET:HG2	2.13	0.82
1:E:207:SER:OG	1:E:241:ASP:CG	2.24	0.80
2:F:157:TYR:O	2:F:158:ASP:HB2	1.80	0.80
2:F:129:ASN:O	2:F:141:TYR:HD2	1.63	0.78
1:E:129:HIS:NE2	1:E:162:PRO:HD2	2.00	0.76
1:E:204:VAL:HG21	1:E:211:GLN:OE1	1.87	0.74
1:E:265:ASP:OD1	1:E:265:ASP:C	2.30	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:145:ASP:OD1	2:F:145:ASP:C	2.31	0.73
1:E:186:ASN:HD22	1:E:227:SER:CB	2.01	0.73
2:F:142:HIS:HE1	2:F:157:TYR:OH	1.72	0.72
2:F:129:ASN:O	2:F:141:TYR:CG	2.43	0.71
2:F:127:ARG:HG3	2:F:127:ARG:NH1	2.07	0.68
1:E:299:HIS:HD2	1:E:301:LEU:H	1.42	0.67
2:F:145:ASP:OD1	2:F:148:CYS:N	2.28	0.66
2:F:128:ASP:O	2:F:141:TYR:HE2	1.79	0.66
1:E:197:ASN:OD1	1:E:197:ASN:N	2.30	0.64
1:E:111:ARG:O	1:E:263:LYS:HB2	1.98	0.63
1:E:139:CYS:HB2	1:E:146:SER:O	1.99	0.63
2:F:128:ASP:O	2:F:141:TYR:CE2	2.51	0.63
2:F:129:ASN:C	2:F:141:TYR:HD2	2.05	0.62
1:E:56:LEU:HA	1:E:74:PHE:CZ	2.35	0.61
1:E:115:PHE:HE1	1:E:260:ILE:HG12	1.67	0.58
1:E:58:ASP:HB3	1:E:90:VAL:HG22	1.86	0.58
1:E:97:GLY:HA3	1:E:230:MET:O	2.03	0.58
1:E:134:GLY:CA	1:E:153:TRP:HB3	2.26	0.57
1:E:299:HIS:CD2	1:E:301:LEU:H	2.22	0.57
2:F:68:ARG:NH1	2:F:81:ASN:OD1	2.36	0.57
1:E:204:VAL:CG2	1:E:211:GLN:OE1	2.53	0.57
2:F:19:ASP:HB3	2:F:36:ALA:HB2	1.87	0.56
2:F:157:TYR:O	2:F:158:ASP:CB	2.49	0.56
1:E:183:HIS:ND1	1:E:195:TYR:OH	2.36	0.56
1:E:204:VAL:CG2	1:E:211:GLN:HB3	2.07	0.56
1:E:5:ASP:OD2	2:F:143:LYS:HB2	2.07	0.54
2:F:62:GLN:HG2	2:F:92:TRP:CD2	2.43	0.54
1:E:207:SER:OG	1:E:241:ASP:OD1	2.27	0.53
1:E:297:ASN:C	1:E:297:ASN:HD22	2.17	0.53
1:E:82:TYR:CZ	1:E:283:GLN:HG2	2.44	0.52
1:E:186:ASN:ND2	1:E:227:SER:CB	2.62	0.52
1:E:294:PRO:HG3	2:F:56:ILE:HG12	1.92	0.52
1:E:9:ILE:HG13	2:F:119:TYR:HA	1.92	0.51
1:E:20:VAL:HG21	1:E:318:ALA:HB2	1.92	0.50
1:E:265:ASP:OD1	1:E:265:ASP:O	2.30	0.50
2:F:151:SER:HA	2:F:154:ASN:HB2	1.94	0.49
1:E:94:CYS:SG	1:E:95:TYR:N	2.86	0.49
2:F:142:HIS:CE1	2:F:157:TYR:OH	2.60	0.49
1:E:113:ASN:OD1	1:E:264:GLY:CA	2.61	0.48
1:E:186:ASN:OD1	1:E:186:ASN:N	2.45	0.48
1:E:9:ILE:HD11	2:F:122:VAL:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:294:PRO:CG	2:F:56:ILE:HG12	2.44	0.48
2:F:150:GLU:O	2:F:154:ASN:HB2	2.13	0.48
2:F:24:TYR:CD1	2:F:24:TYR:N	2.82	0.47
2:F:145:ASP:OD1	2:F:145:ASP:O	2.32	0.47
1:E:299:HIS:CD2	1:E:300:PRO:HD2	2.50	0.47
1:E:314:ARG:O	1:E:315:LEU:HD13	2.15	0.47
1:E:113:ASN:OD1	1:E:264:GLY:HA3	2.15	0.47
2:F:28:ASN:HD21	2:F:146:ASN:ND2	2.13	0.47
1:E:195:TYR:O	1:E:197:ASN:OD1	2.33	0.46
2:F:157:TYR:CD1	2:F:157:TYR:C	2.93	0.46
1:E:285:PRO:HG2	1:E:299:HIS:CD2	2.50	0.46
1:E:113:ASN:HB2	1:E:262:LYS:O	2.16	0.45
2:F:26:HIS:HB2	2:F:149:MET:HE3	1.98	0.45
1:E:114:HIS:HB3	1:E:261:VAL:O	2.17	0.45
1:E:297:ASN:C	1:E:297:ASN:ND2	2.74	0.45
1:E:57:ARG:HD2	1:E:73:GLU:OE1	2.17	0.44
2:F:150:GLU:HA	2:F:153:ARG:NH1	2.32	0.44
2:F:143:LYS:HB3	2:F:143:LYS:HE3	1.68	0.44
1:E:185:PRO:HB3	1:E:190:ASP:HB3	1.99	0.44
1:E:82:TYR:OH	1:E:283:GLN:HG2	2.18	0.43
1:E:205:GLY:O	1:E:206:THR:HG22	2.17	0.43
1:E:151:VAL:HB	1:E:252:ILE:HG22	2.00	0.43
1:E:158:ASN:O	1:E:159:SER:HB2	2.19	0.43
1:E:238:LYS:HB3	1:E:239:PRO:CD	2.49	0.43
2:F:59:MET:HE3	2:F:96:ALA:HA	2.01	0.42
2:F:58:LYS:HA	2:F:58:LYS:HD3	1.88	0.42
1:E:152:VAL:HG23	1:E:255:GLU:HB2	2.02	0.42
1:E:10:GLY:HA3	2:F:14:TRP:CH2	2.55	0.42
2:F:149:MET:C	2:F:151:SER:N	2.76	0.42
1:E:125:SER:O	1:E:166:ARG:NH2	2.53	0.42
1:E:164:ILE:O	1:E:246:GLU:HA	2.19	0.42
2:F:127:ARG:H	2:F:127:ARG:HG2	1.37	0.41
2:F:149:MET:O	2:F:150:GLU:C	2.63	0.41
2:F:83:LYS:HD2	2:F:83:LYS:HA	1.91	0.41
2:F:146:ASN:HD22	2:F:146:ASN:HA	1.68	0.41
1:E:205:GLY:C	1:E:206:THR:CG2	2.94	0.40
1:E:251:PHE:CE2	1:E:253:ALA:HB2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	319/340 (94%)	307 (96%)	12 (4%)	0	100	100
2	F	153/160 (96%)	145 (95%)	8 (5%)	0	100	100
All	All	472/500 (94%)	452 (96%)	20 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	E	289/307 (94%)	264 (91%)	25 (9%)	8	17
2	F	133/136 (98%)	118 (89%)	15 (11%)	4	9
All	All	422/443 (95%)	382 (90%)	40 (10%)	7	14

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	17	THR
1	E	49	ASP
1	E	55	ILE
1	E	70	MET
1	E	93	LEU
1	E	125	SER
1	E	128	SER
1	E	149	ARG

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Mol	Chain	Res	Type
1	E	160	THR
1	E	173	GLN
1	E	186	ASN
1	E	196	GLN
1	E	197	ASN
1	E	204	VAL
1	E	207	SER
1	E	221	SER
1	E	236	ILE
1	E	240	ASN
1	E	265	ASP
1	E	266	SER
1	E	278	CYS
1	E	297	ASN
1	E	301	LEU
1	E	315	LEU
1	E	321	LEU
2	F	38	LYS
2	F	45	ILE
2	F	62	GLN
2	F	83	LYS
2	F	84	MET
2	F	101	LEU
2	F	116	LYS
2	F	127	ARG
2	F	128	ASP
2	F	131	LYS
2	F	133	LEU
2	F	143	LYS
2	F	144	CYS
2	F	145	ASP
2	F	154	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	19	GLN
1	E	142	GLN
1	E	297	ASN
1	E	299	HIS
2	F	25	HIS
2	F	42	GLN

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Mol	Chain	Res	Type
2	F	142	HIS
2	F	146	ASN
2	F	154	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 ⓘ

Of 3 monosaccharides modelled in this entry, 2 were used for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GAL	A	2	3	11,11,12	0.64	0	15,15,17	0.89	0
3	SIA	A	3	3	20,20,21	0.59	0	24,28,31	1.68	4 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GAL	A	2	3	-	0/2/19/22	0/1/1/1
3	SIA	A	3	3	-	6/18/34/38	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3	SIA	C4-C5-N5	-4.76	100.95	110.38
3	A	3	SIA	C6-O6-C2	4.39	120.74	111.34
3	A	3	SIA	O6-C2-C1	2.20	112.02	107.70
3	A	3	SIA	O1B-C1-C2	2.00	118.75	113.03

There are no chirality outliers.

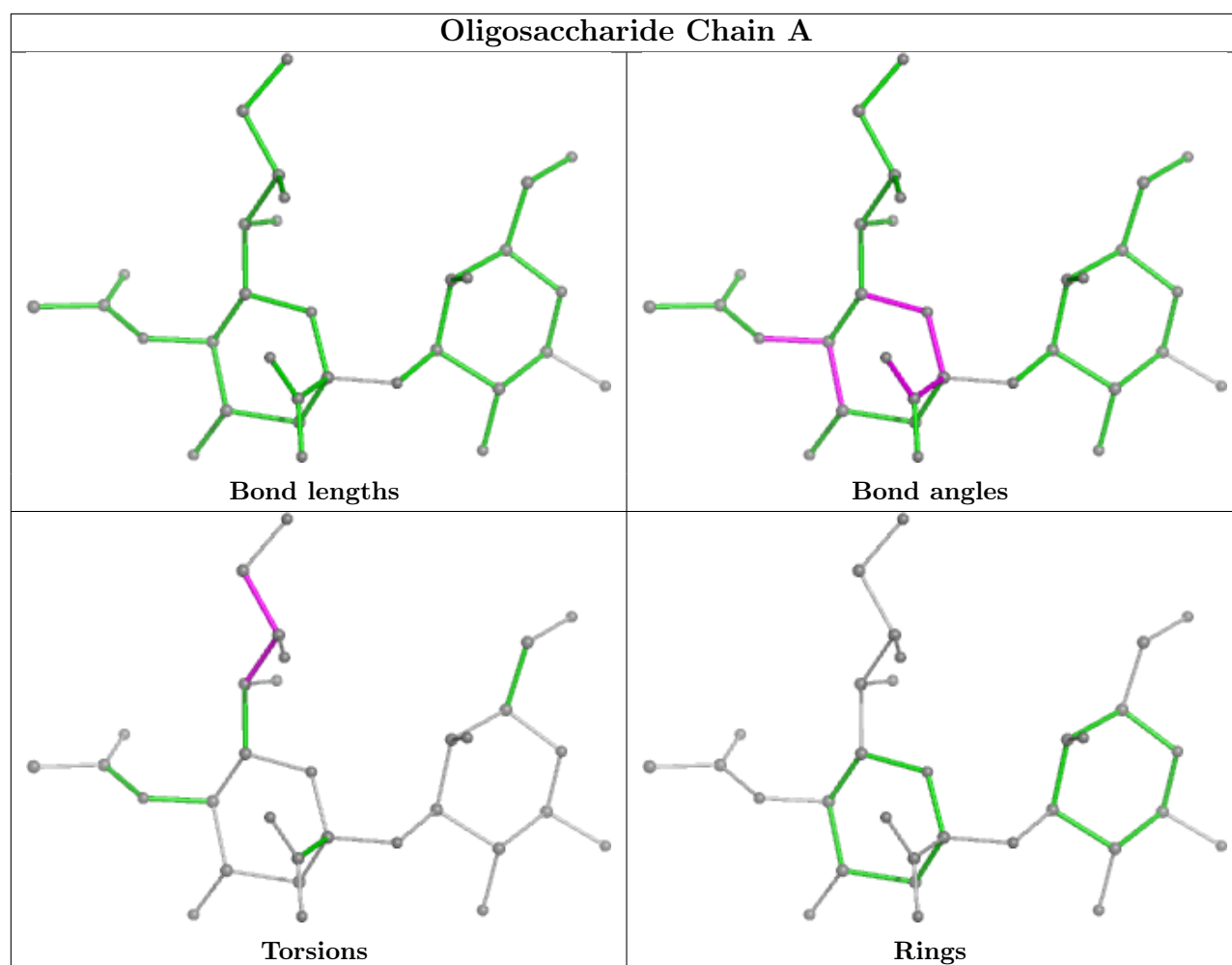
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3	SIA	C6-C7-C8-C9
3	A	3	SIA	C6-C7-C8-O8
3	A	3	SIA	O7-C7-C8-C9
3	A	3	SIA	O7-C7-C8-O8
3	A	3	SIA	C7-C8-C9-O9
3	A	3	SIA	O8-C8-C9-O9

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	F	421	1	14,14,15	0.42	0	17,19,21	1.09	2 (11%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.

'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	F	421	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	421	NAG	C4-C3-C2	-2.44	107.44	111.02
4	F	421	NAG	C2-N2-C7	-2.12	119.88	122.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	E	321/340 (94%)	0.10	3 (0%) 81 77	26, 55, 70, 76	1 (0%)
2	F	157/160 (98%)	-0.13	4 (2%) 58 53	17, 39, 69, 82	0
All	All	478/500 (95%)	0.02	7 (1%) 71 67	17, 52, 70, 82	1 (0%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	150	GLU	3.3
1	E	154	LEU	2.4
1	E	258	TYR	2.2
2	F	128	ASP	2.2
2	F	124	LEU	2.1
2	F	146	ASN	2.0
1	E	173	GLN	2.0

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

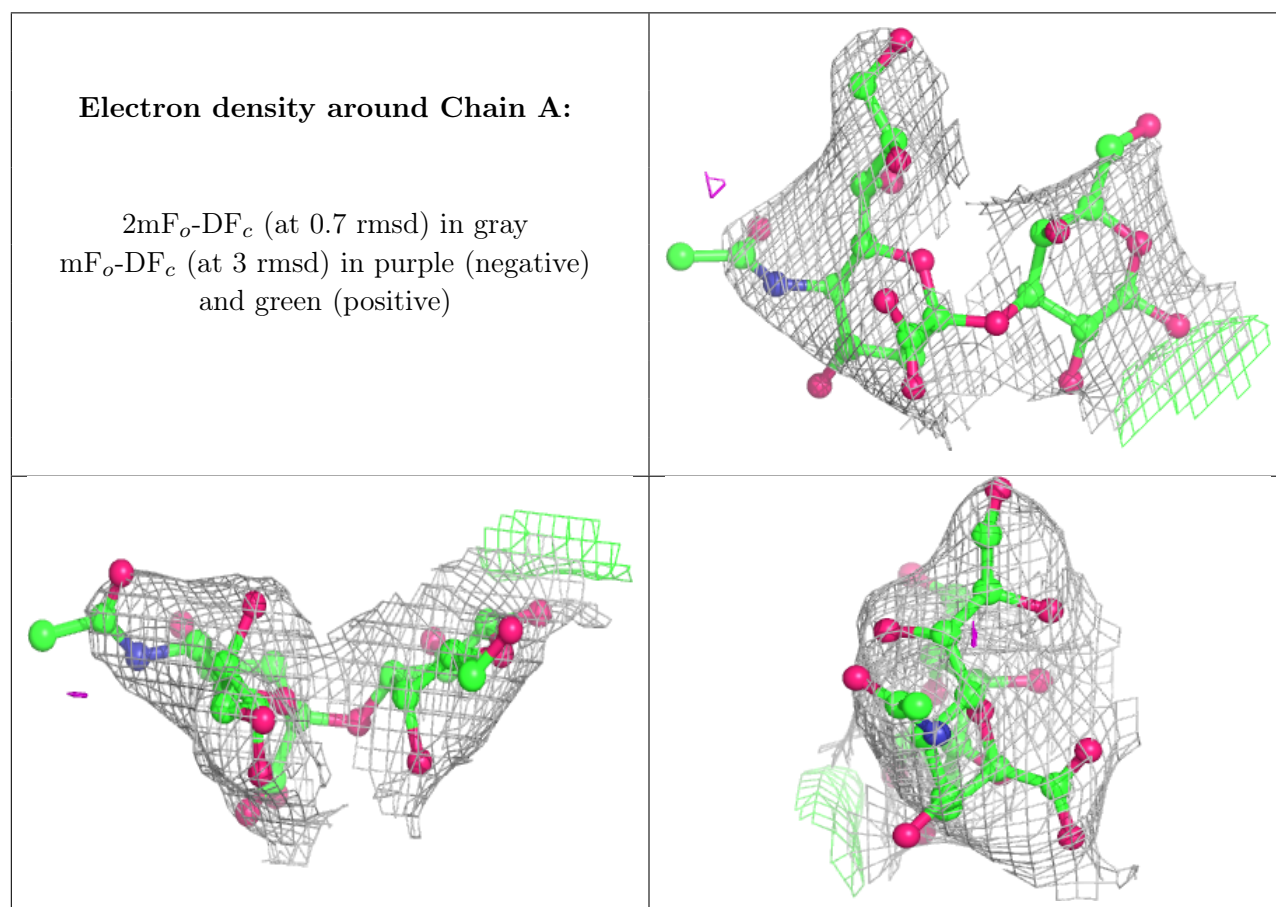
There are no non-standard protein/DNA/RNA residues in this entry.

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
3	NAG	A	1	1/15	-	-	116,116,116,116	0
3	GAL	A	2	11/12	-	-	109,114,115,115	0
3	SIA	A	3	20/21	-	-	99,104,107,107	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.



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
4	NAG	F	421	14/15	0.79	0.19	110,110,111,111	0

6.5 Other polymers [i](#)

There are no such residues in this entry.