



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2024 – 11:15 AM EDT

PDB ID : 4XRC
Title : Antibody hemagglutinin Complexes
Authors : Spiller, B.W.; Winarski, K.L.
Deposited on : 2015-01-20
Resolution : 2.74 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
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) : 2.39

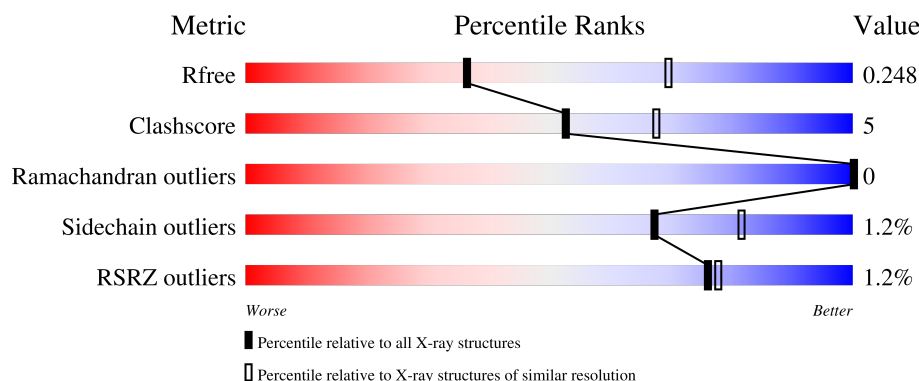
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.74 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	1649 (2.76-2.72)
Clashscore	180529	1744 (2.76-2.72)
Ramachandran outliers	177936	1710 (2.76-2.72)
Sidechain outliers	177891	1711 (2.76-2.72)
RSRZ outliers	164620	1649 (2.76-2.72)

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	208	<div> <div>88%</div> <div>11%</div> <div>.</div> </div>
1	L	208	<div> <div>88%</div> <div>12%</div> </div>
2	B	227	<div> <div>82%</div> <div>12%</div> <div>5%</div> </div>
2	H	227	<div> <div>82%</div> <div>13%</div> <div>.</div> </div>
3	C	212	<div> <div>2%</div> <div>80%</div> <div>17%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	D	212	<div><div>%</div><div><div></div><div>84%</div><div>15%</div><div></div></div><div></div></div>
4	E	3	<div><div></div><div><div>33%</div><div>67%</div></div><div></div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9883 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 H5.3 Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1569	984	257	322	6			
1	L	208	Total	C	N	O	S	0	0	0
			1569	984	257	322	6			

- Molecule 2 is a protein called H5.3 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	215	Total	C	N	O	S	0	0	0
			1610	1029	266	311	4			
2	H	217	Total	C	N	O	S	0	0	0
			1621	1035	268	314	4			

- Molecule 3 is a protein called Hemagglutinin.

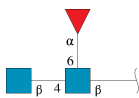
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1706	1095	290	315	6			
3	C	206	Total	C	N	O	S	0	0	0
			1665	1066	284	309	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	160	ALA	THR	engineered mutation	UNP Q6Q9G9
D	226	LEU	GLN	engineered mutation	UNP Q6Q9G9
D	228	SER	GLY	engineered mutation	UNP Q6Q9G9
C	160	ALA	THR	engineered mutation	UNP Q6Q9G9
C	226	LEU	GLN	engineered mutation	UNP Q6Q9G9
C	228	SER	GLY	engineered mutation	UNP Q6Q9G9

- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-[al

pha-L-fucopyranose-(1-6)]2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	3	Total	C	N	O	0	0	0
			38	22	2	14			

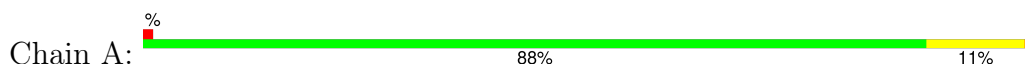
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	12	Total	O	0	0
			12	12		
5	B	17	Total	O	0	0
			17	17		
5	D	17	Total	O	0	0
			17	17		
5	L	20	Total	O	0	0
			20	20		
5	H	24	Total	O	0	0
			24	24		
5	C	15	Total	O	0	0
			15	15		

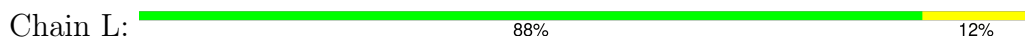
3 Residue-property plots [i](#)

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.

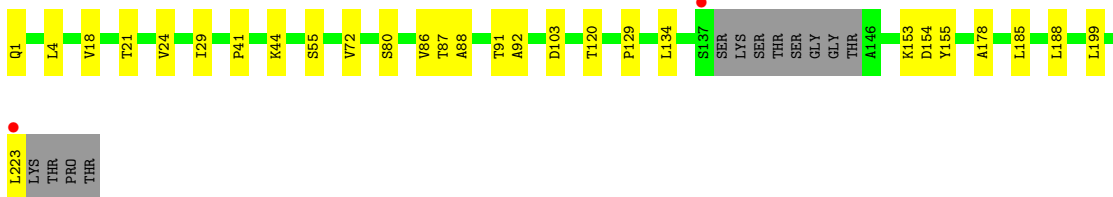
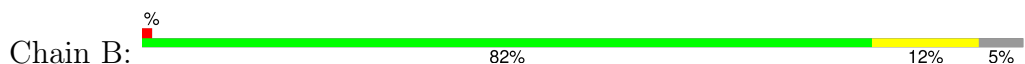
- Molecule 1: H5.3 Fab light chain



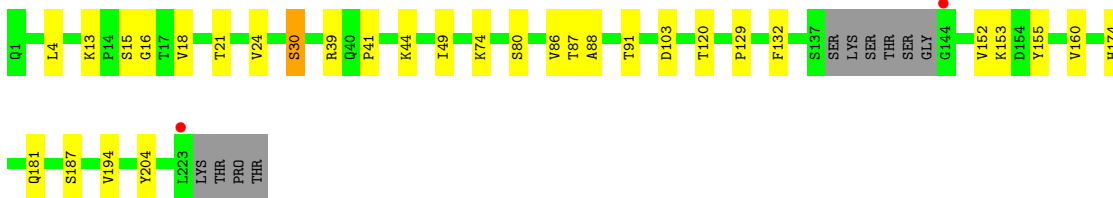
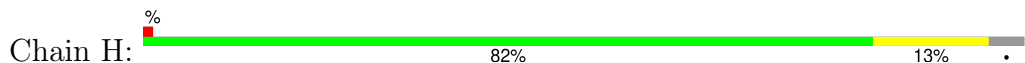
- Molecule 1: H5.3 Fab light chain



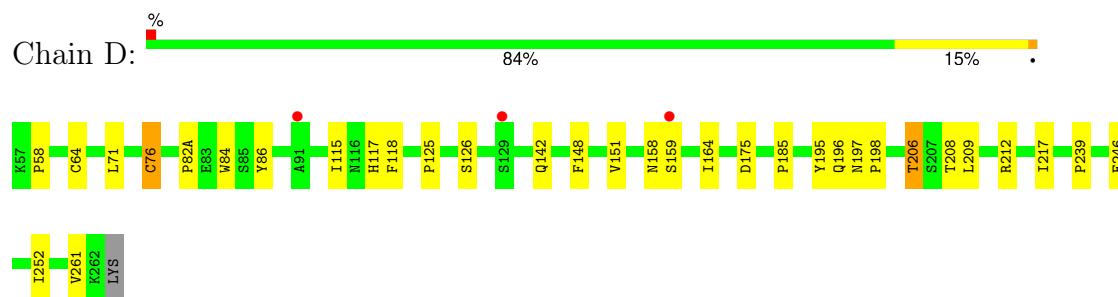
- Molecule 2: H5.3 Fab heavy chain



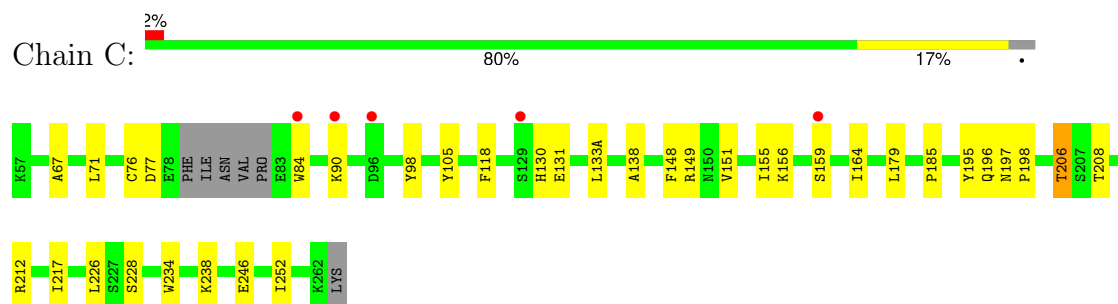
- Molecule 2: H5.3 Fab heavy chain



- Molecule 3: Hemagglutinin



• Molecule 3: Hemagglutinin



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	248.42Å 51.08Å 127.61Å 90.00° 99.94° 90.00°	Depositor
Resolution (Å)	41.92 – 2.74 41.92 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.7 (41.92-2.74) 96.5 (41.92-2.74)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 2.73Å)	Xtriage
Refinement program	PHENIX dev_1760	Depositor
R, R_{free}	0.192 , 0.248 0.194 , 0.248	Depositor DCC
R_{free} test set	2000 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	51.7	Xtriage
Anisotropy	0.525	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9883	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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, FUC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/1609	0.45	0/2201
1	L	0.26	0/1609	0.46	0/2201
2	B	0.26	0/1653	0.50	0/2262
2	H	0.26	0/1664	0.49	0/2277
3	C	0.28	0/1710	0.47	0/2324
3	D	0.26	0/1754	0.45	0/2387
All	All	0.26	0/9999	0.47	0/13652

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

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	1569	0	1513	13	0
1	L	1569	0	1512	13	0
2	B	1610	0	1593	20	0
2	H	1621	0	1603	17	0
3	C	1665	0	1626	21	0
3	D	1706	0	1669	19	0
4	E	38	0	34	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	12	0	0	0	0
5	B	17	0	0	3	0
5	C	15	0	0	1	0
5	D	17	0	0	1	0
5	H	24	0	0	0	0
5	L	20	0	0	0	0
All	All	9883	0	9550	95	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 5.

All (95) 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:B:153:LYS:NZ	5:B:301:HOH:O	2.00	0.91
3:C:130:HIS:O	5:C:301:HOH:O	2.00	0.78
1:L:37:LYS:NZ	1:L:79:MET:O	2.17	0.77
3:C:77:ASP:OD2	3:C:149:ARG:NE	2.21	0.73
3:D:212:ARG:NH1	5:D:301:HOH:O	2.20	0.73
3:D:206:THR:HG22	3:D:209:LEU:HB3	1.72	0.70
3:C:138:ALA:HB2	3:C:226:LEU:HD13	1.74	0.69
2:B:199:LEU:HB3	2:B:223:LEU:HD21	1.77	0.66
3:D:206:THR:HG23	3:D:208:THR:H	1.61	0.64
1:L:148:LYS:HB2	1:L:191:SER:HB3	1.79	0.63
3:D:159:SER:O	3:D:196:GLN:HG3	1.99	0.63
3:C:159:SER:O	3:C:196:GLN:HG3	1.99	0.62
1:L:81:GLU:HB2	1:L:104:VAL:HG12	1.82	0.62
2:B:18:VAL:HG23	2:B:86:VAL:HG11	1.83	0.60
2:B:120:THR:OG1	5:B:302:HOH:O	2.16	0.59
2:H:129:PRO:HB3	2:H:155:TYR:HB3	1.84	0.59
3:D:151:VAL:HG12	3:D:252:ILE:HG22	1.85	0.59
2:H:87:THR:HG22	2:H:88:ALA:H	1.69	0.58
2:B:87:THR:HG22	2:B:88:ALA:H	1.67	0.58
1:A:148:LYS:HB2	1:A:191:SER:HB3	1.86	0.58
2:B:4:LEU:HD22	2:B:24:VAL:HG22	1.85	0.57
3:C:133(A):LEU:HB2	3:C:155:ILE:HD11	1.86	0.57
3:D:185:PRO:HG2	3:D:217:ILE:HG12	1.85	0.57
2:B:21:THR:HG22	2:B:80:SER:HB3	1.85	0.57
1:L:89:TRP:CZ2	1:L:92:SER:HA	2.39	0.56
1:L:103:THR:HG21	1:L:140:PRO:HB3	1.87	0.56
2:B:91:THR:HG23	2:B:120:THR:HA	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:48:GLN:NE2	2:B:103:ASP:OD1	2.36	0.55
3:C:151:VAL:HG12	3:C:252:ILE:HG22	1.87	0.55
2:H:91:THR:HG23	2:H:120:THR:HA	1.88	0.54
2:H:181:GLN:OE1	2:H:187:SER:OG	2.23	0.54
3:C:164:ILE:O	3:C:246:GLU:HA	2.08	0.54
3:C:131:GLU:HB3	3:C:155:ILE:HG13	1.88	0.54
1:L:59:ARG:HG3	1:L:74:SER:O	2.07	0.53
3:D:125:PRO:HG2	3:D:126:SER:HB3	1.91	0.53
2:H:30:SER:HB3	2:H:74:LYS:HE2	1.91	0.53
3:D:84:TRP:HB2	3:D:118:PHE:HB3	1.91	0.53
3:C:185:PRO:HG2	3:C:217:ILE:HG12	1.90	0.53
2:H:18:VAL:HG23	2:H:86:VAL:HG11	1.91	0.52
1:A:144:THR:HG23	1:A:195:THR:HB	1.91	0.52
1:A:19:ILE:HD12	1:A:71:LEU:HD23	1.92	0.51
2:B:55:SER:HB2	3:C:212:ARG:HH21	1.76	0.50
3:D:82(A):PRO:HG2	3:C:238:LYS:HE2	1.94	0.50
2:B:1:GLN:OE1	2:B:1:GLN:N	2.39	0.49
3:D:142:GLN:HG2	3:C:212:ARG:NH1	2.27	0.49
1:A:10:SER:HB2	1:A:105:LEU:HD21	1.94	0.49
3:C:98:TYR:HH	3:C:228:SER:HG	1.59	0.49
3:C:206:THR:HG22	3:C:208:THR:H	1.78	0.48
1:A:117:PHE:CD1	2:B:134:LEU:HB3	2.48	0.48
1:L:31:VAL:N	1:L:49:ASP:OD1	2.36	0.47
3:D:164:ILE:O	3:D:246:GLU:HA	2.13	0.47
3:C:179:LEU:HD23	3:C:234:TRP:HB3	1.97	0.47
2:B:129:PRO:HB3	2:B:155:TYR:HB3	1.95	0.47
3:D:71:LEU:O	3:D:148:PHE:HB3	2.15	0.47
1:L:78:ALA:HA	1:L:104:VAL:HG11	1.97	0.47
3:C:71:LEU:O	3:C:148:PHE:HB3	2.16	0.46
1:A:44:LEU:HD11	1:A:47:TYR:HB3	1.97	0.46
3:D:64:CYS:HB2	3:D:76:CYS:HB3	1.80	0.46
1:A:59:ARG:HG3	1:A:74:SER:O	2.15	0.46
1:A:25:THR:HG23	3:D:158:ASN:HA	1.98	0.45
2:B:154:ASP:HA	2:B:185:LEU:HB3	1.98	0.45
3:C:84:TRP:HB2	3:C:118:PHE:HB3	1.98	0.45
3:D:117:HIS:HB3	3:D:261:VAL:HB	1.99	0.45
2:H:4:LEU:HD22	2:H:24:VAL:HG22	1.98	0.45
1:A:131:LEU:HB2	1:A:177:LEU:HB3	1.99	0.44
1:L:15:GLN:O	1:L:76:THR:HG22	2.17	0.44
2:H:132:PHE:HE2	2:H:153:LYS:HE2	1.82	0.44
1:L:123:GLU:OE2	2:H:153:LYS:NZ	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:39:ARG:HB3	2:H:49:ILE:HD11	1.99	0.44
2:H:194:VAL:HG11	2:H:204:TYR:CE1	2.52	0.44
2:B:178:ALA:HA	2:B:188:LEU:HB3	1.99	0.44
3:C:67:ALA:HB2	3:C:105:TYR:CE1	2.53	0.43
1:L:19:ILE:HD12	1:L:71:LEU:HD23	2.01	0.43
2:B:91:THR:OG1	5:B:303:HOH:O	2.21	0.43
1:L:3:LEU:HB2	1:L:97:GLY:HA2	2.01	0.43
3:C:156:LYS:CD	3:C:196:GLN:HG2	2.49	0.42
2:H:15:SER:HB3	2:H:86:VAL:N	2.34	0.42
2:H:21:THR:HG22	2:H:80:SER:HB3	2.01	0.42
2:B:41:PRO:HA	2:B:92:ALA:HA	2.01	0.42
3:D:175:ASP:OD1	3:D:239:PRO:HD3	2.20	0.42
2:H:41:PRO:HG2	2:H:44:LYS:HB2	2.02	0.41
2:H:103:ASP:HB2	3:C:226:LEU:HG	2.02	0.41
2:H:13:LYS:O	2:H:16:GLY:N	2.53	0.41
1:A:6:PRO:HA	1:A:7:PRO:HD3	1.95	0.41
2:B:41:PRO:HG2	2:B:44:LYS:HB2	2.03	0.41
1:L:166:GLN:OE1	1:L:172:ALA:HB2	2.21	0.41
2:B:29:ILE:HG21	2:B:72:VAL:CG2	2.50	0.41
1:A:3:LEU:HB2	1:A:97:GLY:HA2	2.02	0.41
3:D:58:PRO:HB3	3:D:86:TYR:CZ	2.56	0.41
2:B:153:LYS:HB2	2:B:153:LYS:HE2	1.79	0.40
2:H:152:VAL:HG11	2:H:160:VAL:HG11	2.03	0.40
3:D:197:ASN:HA	3:D:198:PRO:HD3	1.94	0.40
3:C:197:ASN:HA	3:C:198:PRO:HD3	1.85	0.40
1:A:168:ASN:O	1:A:169:ASN:HB2	2.21	0.40
3:D:86:TYR:HB3	3:D:115:ILE:O	2.22	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	206/208 (99%)	205 (100%)	1 (0%)	0	100	100
1	L	206/208 (99%)	204 (99%)	2 (1%)	0	100	100
2	B	211/227 (93%)	207 (98%)	4 (2%)	0	100	100
2	H	213/227 (94%)	210 (99%)	3 (1%)	0	100	100
3	C	202/212 (95%)	199 (98%)	3 (2%)	0	100	100
3	D	209/212 (99%)	203 (97%)	6 (3%)	0	100	100
All	All	1247/1294 (96%)	1228 (98%)	19 (2%)	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	A	179/179 (100%)	176 (98%)	3 (2%)	56	73
1	L	179/179 (100%)	178 (99%)	1 (1%)	84	90
2	B	184/194 (95%)	184 (100%)	0	100	100
2	H	185/194 (95%)	183 (99%)	2 (1%)	70	83
3	C	186/192 (97%)	182 (98%)	4 (2%)	47	68
3	D	191/192 (100%)	188 (98%)	3 (2%)	58	75
All	All	1104/1130 (98%)	1091 (99%)	13 (1%)	67	82

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	59	ARG
1	A	144	THR
3	D	76	CYS
3	D	195	TYR
3	D	206	THR
1	L	162	LYS

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Mol	Chain	Res	Type
2	H	30	SER
2	H	174	HIS
3	C	76	CYS
3	C	90	LYS
3	C	195	TYR
3	C	206	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	64	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 ⓘ

3 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	$\# Z > 2$
4	NAG	E	1	4,1	14,14,15	0.23	0	17,19,21	0.49	0
4	NAG	E	2	4	14,14,15	0.58	1 (7%)	17,19,21	0.45	0
4	FUC	E	3	4	10,10,11	0.99	0	14,14,16	0.96	1 (7%)

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	E	1	4,1	-	2/6/23/26	0/1/1/1
4	NAG	E	2	4	-	2/6/23/26	0/1/1/1
4	FUC	E	3	4	-	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	2	NAG	C1-C2	2.03	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	3	FUC	O5-C5-C4	2.19	113.49	109.55

There are no chirality outliers.

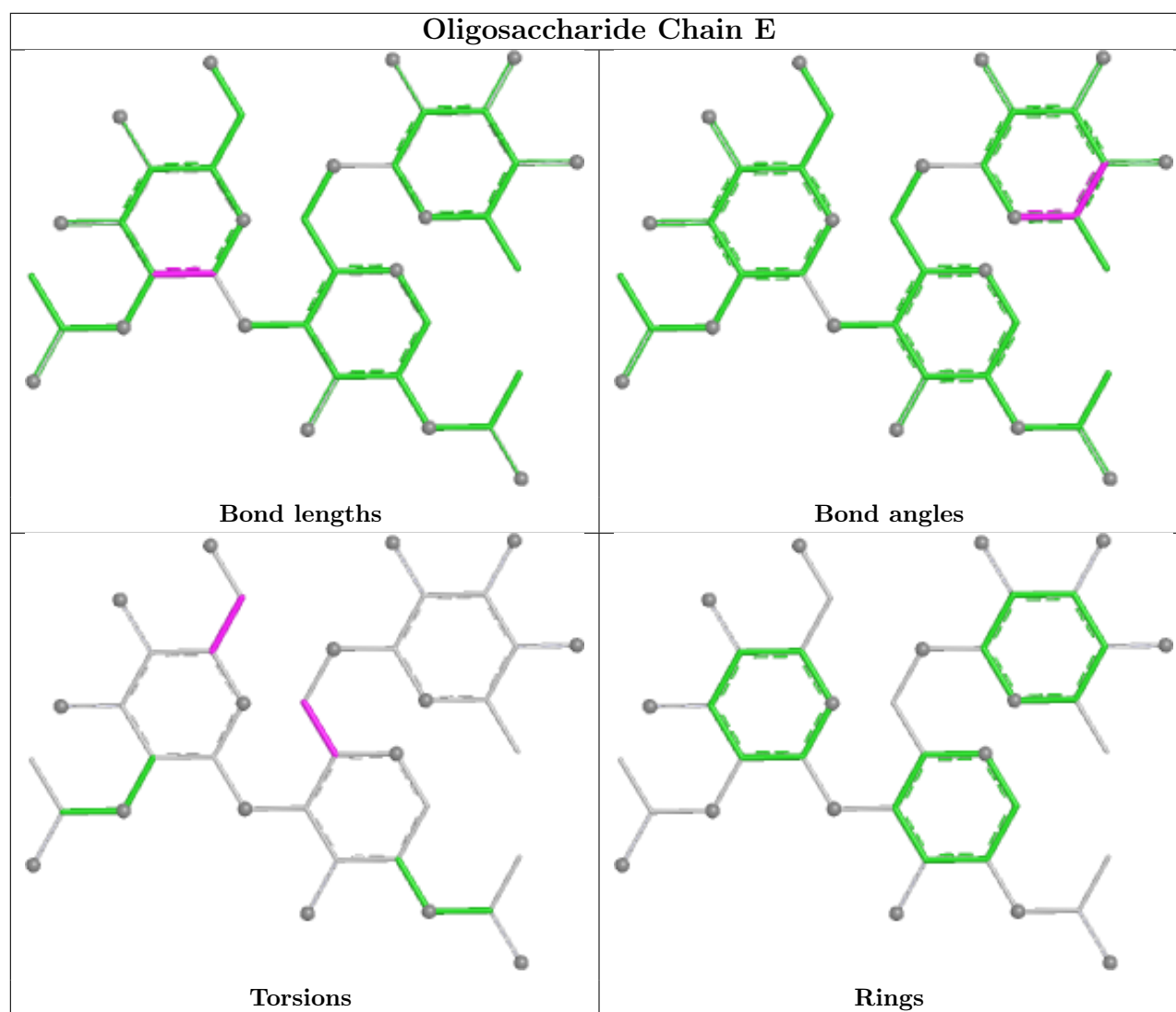
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	1	NAG	O5-C5-C6-O6
4	E	2	NAG	O5-C5-C6-O6
4	E	1	NAG	C4-C5-C6-O6
4	E	2	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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



5.6 Ligand geometry [i](#)

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	208/208 (100%)	0.03	3 (1%) 73 74	52, 84, 116, 137	0
1	L	208/208 (100%)	-0.36	0 100 100	35, 61, 94, 116	0
2	B	215/227 (94%)	-0.31	2 (0%) 81 82	38, 56, 107, 145	0
2	H	217/227 (95%)	-0.15	2 (0%) 81 82	36, 66, 99, 116	0
3	C	206/212 (97%)	-0.16	5 (2%) 59 59	31, 55, 116, 140	0
3	D	211/212 (99%)	-0.04	3 (1%) 73 74	43, 71, 104, 130	0
All	All	1265/1294 (97%)	-0.17	15 (1%) 76 78	31, 66, 108, 145	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	129	SER	3.5
2	H	223	LEU	3.3
3	C	159	SER	3.1
3	D	129	SER	3.0
2	B	137	SER	2.7
3	D	91	ALA	2.6
3	C	84	TRP	2.5
3	D	159	SER	2.4
2	B	223	LEU	2.3
1	A	106	GLY	2.2
2	H	144	GLY	2.2
1	A	105	LEU	2.1
1	A	110	ALA	2.1
3	C	90	LYS	2.1
3	C	96	ASP	2.1

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

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

6.3 Carbohydrates [i](#)

SUGAR-RSR INFOmissingINFO

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.