Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 03:58 PM EDT

PDB ID	:	1E8T
Title	:	Structure of the multifunctional paramyxovirus hemagglutinin-neuraminidase
Authors	:	Crennell, S.; Takimoto, T.; Portner, A.; Taylor, G.
Deposited on	:	2000-10-01
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

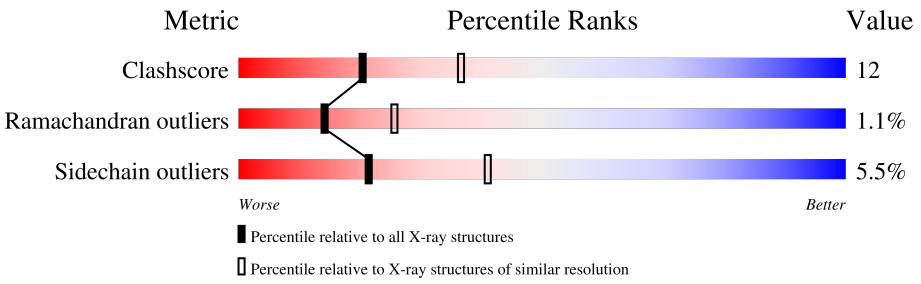
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	454	69% 27% • •
1	B	454	71% 26% • •
2	C	2	100%
2	D	2	100%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	A	1003	-	-	X	-

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7214 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 HEMAGGLUTININ-NEURAMINIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	447	3446	2172	588	667	19	0	0	1
1	B	450	3468	2185	594	670	19	0	0	1

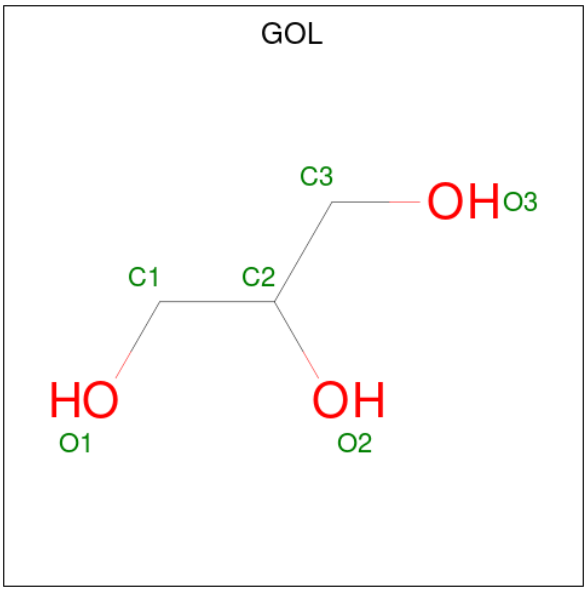
- Molecule 2 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0
2	D	2	28	16	2	10	0	0	0

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

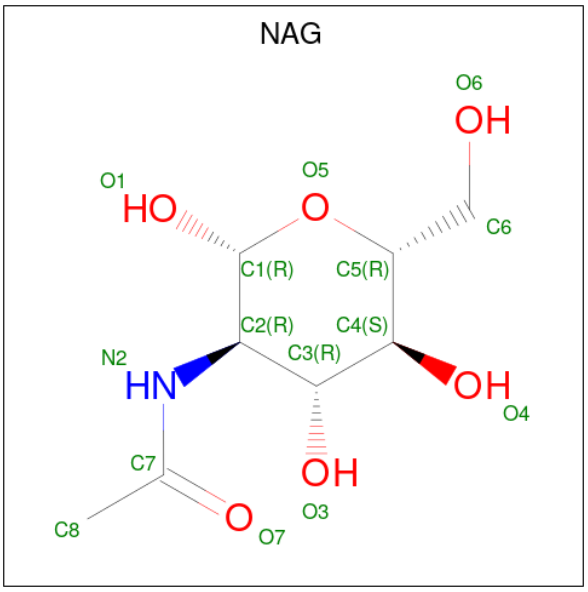
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
3	A	1	1	1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	A	1	6	3	3	0	0
			Total	C	O		
4	B	1	6	3	3	0	0

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	140	140	140	0	0
6	B	71	71	71	0	0

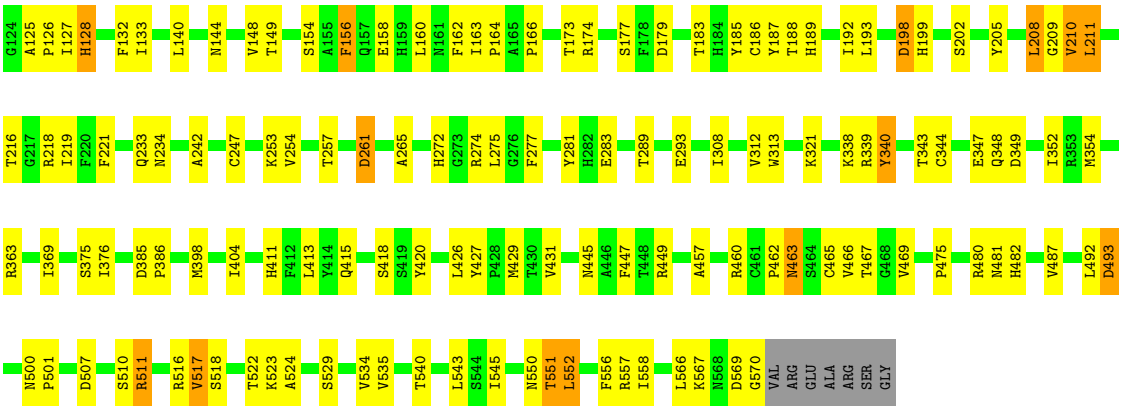
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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.

Note EDS was not executed.

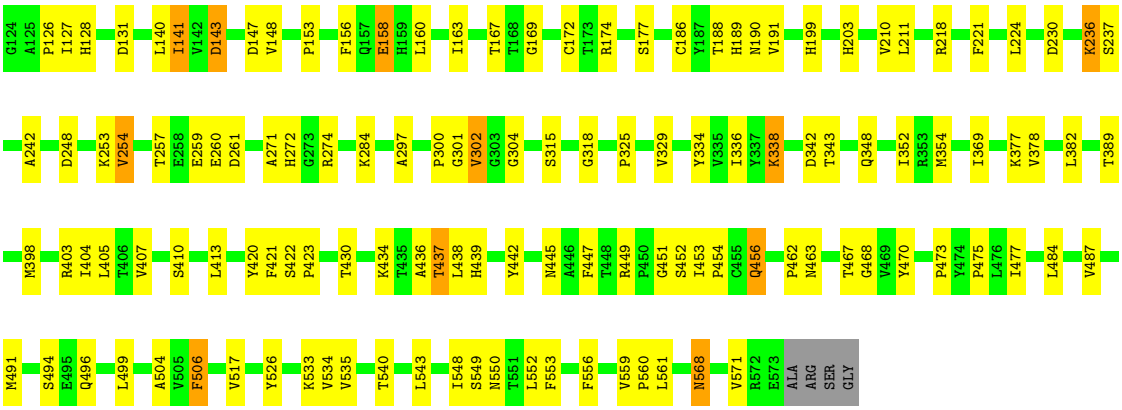
• Molecule 1: HEMAGGLUTININ-NEURAMINIDASE

Chain A:



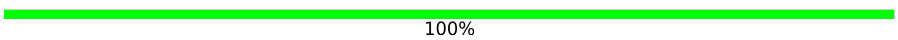
• Molecule 1: HEMAGGLUTININ-NEURAMINIDASE

Chain B:

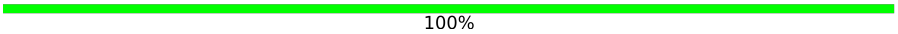


• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C:



• Molecule 2: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.71Å 77.91Å 198.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.50	Depositor
% Data completeness (in resolution range)	97.0 (6.00-2.50)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	0.03	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.276	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7214	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

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: CA, NAG, GOL

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	0.40	0/3531	0.70	0/4804
1	B	0.35	0/3553	0.62	0/4833
All	All	0.38	0/7084	0.66	0/9637

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	3446	0	3340	92	0
1	B	3468	0	3366	80	0
2	C	28	0	25	0	0
2	D	28	0	25	0	0
3	A	1	0	0	0	0
4	A	12	0	16	5	0
4	B	6	0	8	1	0
5	A	14	0	13	2	0
6	A	140	0	0	3	0
6	B	71	0	0	4	0
All	All	7214	0	6793	171	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 12.

All (171) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:ARG:HG2	1:A:511:ARG:HH11	1.30	0.96
1:B:156:PHE:HE2	1:B:517:VAL:HA	1.35	0.91
1:A:128:HIS:HA	1:A:210:VAL:HG13	1.54	0.87
1:A:128:HIS:CD2	1:A:211:LEU:H	1.96	0.83
1:B:156:PHE:CE2	1:B:517:VAL:HA	2.18	0.78
1:A:156:PHE:CE2	1:A:517:VAL:HA	2.23	0.73
1:A:404:ILE:HD13	1:A:413:LEU:HD23	1.71	0.73
1:B:284:LYS:HD3	1:B:382:LEU:O	1.90	0.72
1:B:128:HIS:CD2	1:B:211:LEU:H	2.08	0.71
1:B:128:HIS:HD2	1:B:211:LEU:H	1.40	0.70
1:B:549:SER:HB3	1:B:556:PHE:HA	1.74	0.69
1:A:511:ARG:HH11	1:A:511:ARG:CG	2.05	0.68
1:A:149:THR:HG21	1:A:510:SER:HB2	1.76	0.67
1:B:421:PHE:CE2	1:B:423:PRO:HG2	2.29	0.66
1:B:177:SER:HB3	1:B:188:THR:HG22	1.80	0.64
1:A:469:VAL:HG11	1:A:492:LEU:HD22	1.80	0.64
1:A:466:VAL:H	4:A:1003:GOL:H11	1.62	0.64
1:A:192:ILE:HD13	1:A:202:SER:HB3	1.80	0.62
1:A:462:PRO:HD2	6:A:2052:HOH:O	1.99	0.62
1:A:154:SER:HB3	1:A:566:LEU:HD11	1.82	0.60
1:A:501:PRO:HG3	1:A:524:ALA:HB2	1.84	0.60
1:A:218:ARG:NE	1:A:218:ARG:HA	2.16	0.59
1:A:339:ARG:NH2	1:A:457:ALA:O	2.35	0.59
1:B:257:THR:HB	1:B:260:GLU:HB3	1.83	0.59
1:B:221:PHE:CE2	1:B:543:LEU:HD22	2.38	0.59
1:B:430:THR:OG1	1:B:437:THR:HG23	2.03	0.58
1:A:338:LYS:HZ1	1:A:344:CYS:HB3	1.67	0.58
1:A:369:ILE:HB	1:A:398:MET:HG3	1.86	0.57
1:A:340:TYR:HE2	5:A:1570:NAG:H82	1.70	0.57
1:A:177:SER:HB3	1:A:188:THR:HG22	1.86	0.56
1:A:179:ASP:HA	6:A:2013:HOH:O	2.04	0.56
1:A:156:PHE:HE2	1:A:517:VAL:HA	1.69	0.55
1:B:297:ALA:O	1:B:318:GLY:HA3	2.07	0.54
1:A:156:PHE:CZ	1:A:517:VAL:HA	2.44	0.53
1:A:465:CYS:HA	4:A:1003:GOL:H32	1.91	0.53
1:B:421:PHE:CZ	1:B:423:PRO:HG2	2.43	0.53
1:B:237:SER:O	1:B:300:PRO:HB2	2.09	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:500:ASN:HD21	1:A:516:ARG:NH1	2.06	0.52
1:B:334:TYR:OH	1:B:352:ILE:HD12	2.10	0.52
1:B:420:TYR:CG	1:B:462:PRO:HA	2.45	0.52
1:A:265:ALA:O	1:A:321:LYS:HE2	2.09	0.52
1:B:302:VAL:HG11	1:B:526:TYR:CE2	2.45	0.52
1:A:218:ARG:HE	1:A:219:ILE:N	2.09	0.51
1:A:308:ILE:HG21	1:A:431:VAL:HG21	1.91	0.51
1:A:218:ARG:HE	1:A:219:ILE:H	1.58	0.51
1:A:511:ARG:HG2	1:A:511:ARG:NH1	2.08	0.51
1:A:339:ARG:HD2	1:A:445:ASN:OD1	2.11	0.50
1:B:451:GLY:O	1:B:456:GLN:HA	2.11	0.50
1:B:405:LEU:HD23	1:B:405:LEU:H	1.77	0.50
1:B:533:LYS:HG2	1:B:534:VAL:N	2.28	0.49
1:B:534:VAL:HG23	1:B:534:VAL:O	2.13	0.49
1:A:340:TYR:CE2	5:A:1570:NAG:H82	2.48	0.49
1:B:491:MET:CE	1:B:506:PHE:HE2	2.25	0.49
1:A:234:ASN:HB2	1:A:254:VAL:O	2.13	0.48
1:A:466:VAL:N	4:A:1003:GOL:H11	2.28	0.48
1:A:140:LEU:HG	1:A:540:THR:HG23	1.96	0.48
1:B:191:VAL:HG13	1:B:203:HIS:HB2	1.96	0.48
1:B:494:SER:HB2	1:B:499:LEU:HD12	1.94	0.48
1:A:132:PHE:CZ	1:A:211:LEU:HD22	2.49	0.48
1:A:173:THR:HB	1:A:558:ILE:HD12	1.96	0.48
1:A:518:SER:HB3	1:A:522:THR:OG1	2.13	0.48
1:B:405:LEU:HD23	1:B:405:LEU:N	2.29	0.48
1:A:133:ILE:O	1:A:535:VAL:HG21	2.14	0.48
1:A:160:LEU:HD13	1:A:221:PHE:CD1	2.49	0.48
1:B:548:ILE:HD11	1:B:559:VAL:HG21	1.95	0.47
1:B:148:VAL:HG13	1:B:477:ILE:HD12	1.96	0.47
1:A:411:HIS:HB2	1:A:429:MET:O	2.15	0.47
1:B:491:MET:HE2	1:B:506:PHE:CE2	2.49	0.47
1:A:185:TYR:CZ	1:A:209:GLY:HA3	2.50	0.47
1:A:148:VAL:HG11	1:A:507:ASP:HB3	1.97	0.46
1:A:385:ASP:N	1:A:386:PRO:HD3	2.31	0.46
1:A:551:THR:OG1	1:A:552:LEU:HD22	2.14	0.46
1:B:140:LEU:HD13	1:B:540:THR:HG23	1.98	0.46
1:A:281:TYR:CE2	1:A:283:GLU:HB2	2.51	0.46
1:B:236:LYS:HB2	1:B:236:LYS:NZ	2.31	0.46
1:B:274:ARG:HH21	1:B:378:VAL:HG13	1.79	0.46
1:B:163:ILE:HD12	1:B:560:PRO:HB3	1.96	0.46
1:B:467:THR:HG23	1:B:468:GLY:N	2.30	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:568:ASN:HB2	1:B:571:VAL:HG13	1.96	0.46
1:A:219:ILE:HD11	1:A:534:VAL:HG21	1.98	0.46
1:A:354:MET:HE2	1:A:463:ASN:HA	1.98	0.46
1:A:363:ARG:H	4:A:1003:GOL:HO2	1.62	0.46
1:B:453:ILE:HG13	1:B:496:GLN:NE2	2.30	0.46
1:A:289:THR:O	1:A:293:GLU:HB3	2.16	0.46
1:A:493:ASP:HB3	1:A:500:ASN:ND2	2.31	0.46
1:B:517:VAL:HG13	1:B:561:LEU:HD11	1.96	0.45
1:A:481:ASN:O	1:A:482:HIS:HB2	2.16	0.45
1:B:224:LEU:HD23	6:B:2020:HOH:O	2.16	0.45
1:A:511:ARG:CG	1:A:511:ARG:NH1	2.75	0.45
1:B:158:GLU:HG2	1:B:218:ARG:HG3	1.99	0.45
1:A:308:ILE:CG2	1:A:431:VAL:HG21	2.47	0.45
1:A:415:GLN:NE2	1:A:427:TYR:OH	2.49	0.45
1:B:452:SER:HB2	6:B:2061:HOH:O	2.17	0.45
1:A:166:PRO:O	1:B:169:GLY:HA3	2.17	0.45
1:A:186:CYS:SG	1:A:242:ALA:HA	2.56	0.45
1:A:475:PRO:HA	1:A:487:VAL:HG12	1.99	0.45
1:B:550:ASN:HB3	1:B:553:PHE:HD2	1.82	0.44
1:A:543:LEU:HD21	1:A:545:ILE:HD11	2.00	0.44
1:B:423:PRO:HB3	1:B:445:ASN:HA	1.98	0.44
1:B:272:HIS:CE1	1:B:382:LEU:HD23	2.52	0.44
1:B:325:PRO:O	1:B:329:VAL:HG23	2.17	0.44
1:B:403:ARG:HB2	1:B:470:TYR:OH	2.18	0.44
1:B:413:LEU:HD13	1:B:438:LEU:HD11	1.99	0.44
1:A:257:THR:O	1:A:261:ASP:HB2	2.17	0.44
1:B:174:ARG:NH2	1:B:190:ASN:OD1	2.48	0.44
1:B:211:LEU:HD21	1:B:221:PHE:CE1	2.53	0.44
1:B:475:PRO:HA	1:B:487:VAL:HG12	1.99	0.44
1:B:127:ILE:HG12	1:B:128:HIS:N	2.33	0.44
1:B:389:THR:HG21	1:B:436:ALA:O	2.18	0.43
1:A:420:TYR:CG	1:A:462:PRO:HA	2.53	0.43
1:A:233:GLN:NE2	1:A:253:LYS:HZ3	2.17	0.43
1:B:141:ILE:HD11	1:B:143:ASP:HB2	2.00	0.43
1:B:369:ILE:HB	1:B:398:MET:HG3	1.99	0.43
1:B:439:HIS:ND1	4:B:1004:GOL:H32	2.33	0.43
1:B:422:SER:N	1:B:423:PRO:HD2	2.33	0.43
1:A:187:TYR:OH	1:A:558:ILE:HG21	2.19	0.43
1:B:407:VAL:HG21	1:B:475:PRO:HB2	1.99	0.43
1:A:128:HIS:HD2	1:A:211:LEU:H	1.58	0.42
1:A:133:ILE:O	1:A:133:ILE:HG13	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:LEU:HD22	1:A:247:CYS:SG	2.59	0.42
1:A:274:ARG:O	1:A:281:TYR:HA	2.19	0.42
1:A:154:SER:HB3	1:A:566:LEU:CD1	2.49	0.42
1:A:529:SER:HA	1:A:543:LEU:O	2.19	0.42
1:A:144:ASN:HD21	1:A:480:ARG:H	1.67	0.42
1:A:348:GLN:O	1:A:352:ILE:HG13	2.19	0.42
1:B:172:CYS:HB2	1:B:556:PHE:O	2.19	0.42
1:A:185:TYR:CE2	1:A:221:PHE:HD2	2.37	0.42
1:B:301:GLY:O	1:B:302:VAL:HB	2.20	0.42
1:A:567:LYS:C	1:A:569:ASP:H	2.23	0.42
1:A:308:ILE:HB	1:A:313:TRP:NE1	2.35	0.42
1:A:523:LYS:HG3	6:A:2114:HOH:O	2.20	0.42
1:A:426:LEU:HD23	1:A:426:LEU:HA	1.88	0.42
1:B:126:PRO:HD3	6:B:2001:HOH:O	2.18	0.42
1:B:254:VAL:HG11	1:B:261:ASP:OD2	2.20	0.42
1:B:315:SER:HB3	1:B:404:ILE:HG13	2.02	0.42
1:B:354:MET:HE2	1:B:463:ASN:HA	2.02	0.42
1:B:160:LEU:HD13	1:B:221:PHE:CD1	2.55	0.41
1:A:125:ALA:HB1	1:A:183:THR:HG21	2.01	0.41
1:B:442:TYR:CZ	1:B:484:LEU:HB3	2.55	0.41
1:A:552:LEU:HD22	1:A:552:LEU:H	1.85	0.41
1:B:131:ASP:O	1:B:535:VAL:HG22	2.19	0.41
1:B:153:PRO:HG2	1:B:504:ALA:HA	2.02	0.41
1:B:491:MET:HE2	1:B:506:PHE:HE2	1.83	0.41
1:B:403:ARG:HA	6:B:2035:HOH:O	2.20	0.41
1:A:312:VAL:O	1:A:375:SER:HA	2.20	0.41
1:A:523:LYS:HB3	1:A:556:PHE:CE1	2.56	0.41
1:B:186:CYS:SG	1:B:242:ALA:HA	2.60	0.41
1:B:203:HIS:ND1	1:B:230:ASP:HA	2.35	0.41
1:A:418:SER:HA	1:A:467:THR:O	2.20	0.41
1:B:304:GLY:N	1:B:403:ARG:HG3	2.36	0.41
1:A:148:VAL:CG1	1:A:507:ASP:HB3	2.50	0.41
1:B:336:ILE:CD1	1:B:352:ILE:HD13	2.51	0.41
1:A:174:ARG:HH12	1:A:198:ASP:HA	1.86	0.41
1:B:210:VAL:HG13	1:B:224:LEU:HD11	2.02	0.41
1:B:253:LYS:HE3	1:B:271:ALA:HB2	2.03	0.41
1:B:348:GLN:O	1:B:352:ILE:HG12	2.21	0.41
1:B:377:LYS:HD2	1:B:377:LYS:HA	1.94	0.41
1:B:506:PHE:CD1	1:B:506:PHE:N	2.88	0.41
1:A:162:PHE:CD1	1:A:221:PHE:HB2	2.56	0.41
1:A:163:ILE:HA	1:A:164:PRO:HD3	1.91	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:404:ILE:CD1	1:A:413:LEU:HD23	2.48	0.41
1:A:164:PRO:HG2	1:A:205:TYR:CZ	2.57	0.40
1:A:166:PRO:HD3	1:A:557:ARG:HG3	2.03	0.40
1:A:126:PRO:HD3	1:A:277:PHE:CE1	2.56	0.40
1:A:344:CYS:HB2	1:A:460:ARG:O	2.21	0.40
1:A:465:CYS:HA	4:A:1003:GOL:C3	2.52	0.40
1:B:257:THR:HB	1:B:260:GLU:CB	2.49	0.40
1:A:272:HIS:ND1	1:A:376:ILE:HG21	2.36	0.40
1:B:334:TYR:CZ	1:B:352:ILE:HG23	2.56	0.40
1:A:567:LYS:HE3	1:A:570:GLY:N	2.37	0.40
1:B:338:LYS:CD	1:B:338:LYS:H	2.34	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	445/454 (98%)	406 (91%)	33 (7%)	6 (1%)	12 21
1	B	448/454 (99%)	410 (92%)	34 (8%)	4 (1%)	17 31
All	All	893/908 (98%)	816 (91%)	67 (8%)	10 (1%)	14 26

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	HIS
1	A	551	THR
1	B	158	GLU
1	A	127	ILE
1	A	156	PHE
1	A	340	TYR
1	A	493	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	342	ASP
1	B	302	VAL
1	B	473	PRO

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	387/392 (99%)	366 (95%)	21 (5%)	22	42
1	B	389/392 (99%)	367 (94%)	22 (6%)	20	39
All	All	776/784 (99%)	733 (94%)	43 (6%)	21	41

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	GLU
1	A	189	HIS
1	A	193	LEU
1	A	198	ASP
1	A	199	HIS
1	A	208	LEU
1	A	210	VAL
1	A	211	LEU
1	A	216	THR
1	A	261	ASP
1	A	275	LEU
1	A	343	THR
1	A	347	GLU
1	A	349	ASP
1	A	447	PHE
1	A	449	ARG
1	A	463	ASN
1	A	511	ARG
1	A	517	VAL
1	A	550	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	552	LEU
1	B	141	ILE
1	B	143	ASP
1	B	147	ASP
1	B	167	THR
1	B	189	HIS
1	B	199	HIS
1	B	236	LYS
1	B	248	ASP
1	B	254	VAL
1	B	259	GLU
1	B	338	LYS
1	B	343	THR
1	B	410	SER
1	B	434	LYS
1	B	437	THR
1	B	447	PHE
1	B	449	ARG
1	B	454	PRO
1	B	456	GLN
1	B	506	PHE
1	B	552	LEU
1	B	568	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	HIS
1	A	199	HIS
1	A	203	HIS
1	A	233	GLN
1	A	323	ASN
1	A	371	GLN
1	A	415	GLN
1	A	463	ASN
1	A	482	HIS
1	A	500	ASN
1	B	128	HIS
1	B	157	GLN
1	B	351	GLN
1	B	496	GLN

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)

4 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	NAG	C	1	2,1	14,14,15	0.44	0	17,19,21	0.68	0
2	NAG	C	2	2	14,14,15	0.44	0	17,19,21	0.57	0
2	NAG	D	1	2,1	14,14,15	0.43	0	17,19,21	0.62	0
2	NAG	D	2	2	14,14,15	0.42	0	17,19,21	0.68	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	C	2	2	-	2/6/23/26	0/1/1/1
2	NAG	D	1	2,1	-	2/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

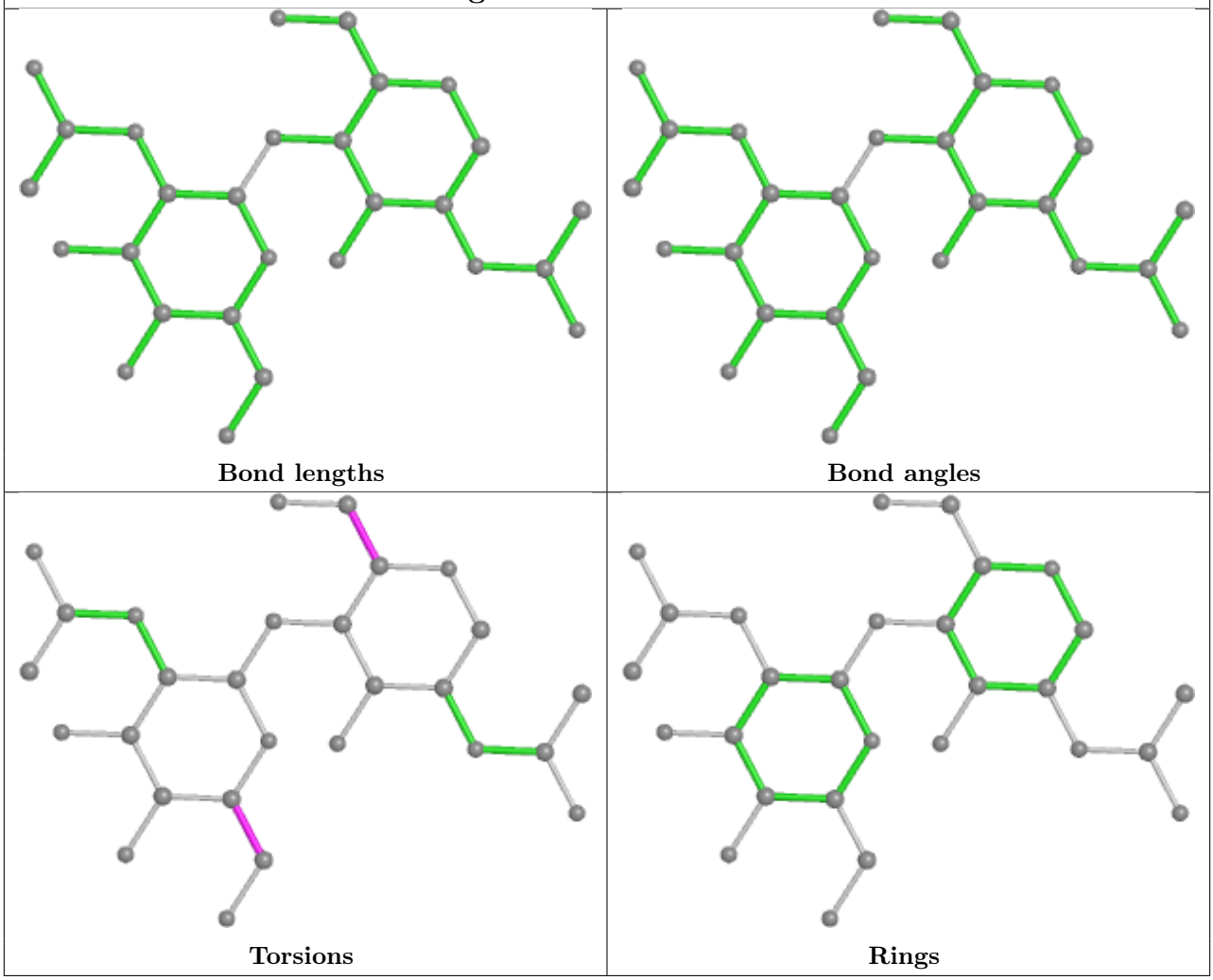
Mol	Chain	Res	Type	Atoms
2	D	2	NAG	O5-C5-C6-O6
2	C	2	NAG	O5-C5-C6-O6
2	D	1	NAG	O5-C5-C6-O6
2	C	2	NAG	C4-C5-C6-O6
2	C	1	NAG	C4-C5-C6-O6
2	D	1	NAG	C4-C5-C6-O6
2	D	2	NAG	C4-C5-C6-O6
2	C	1	NAG	O5-C5-C6-O6

There are no ring outliers.

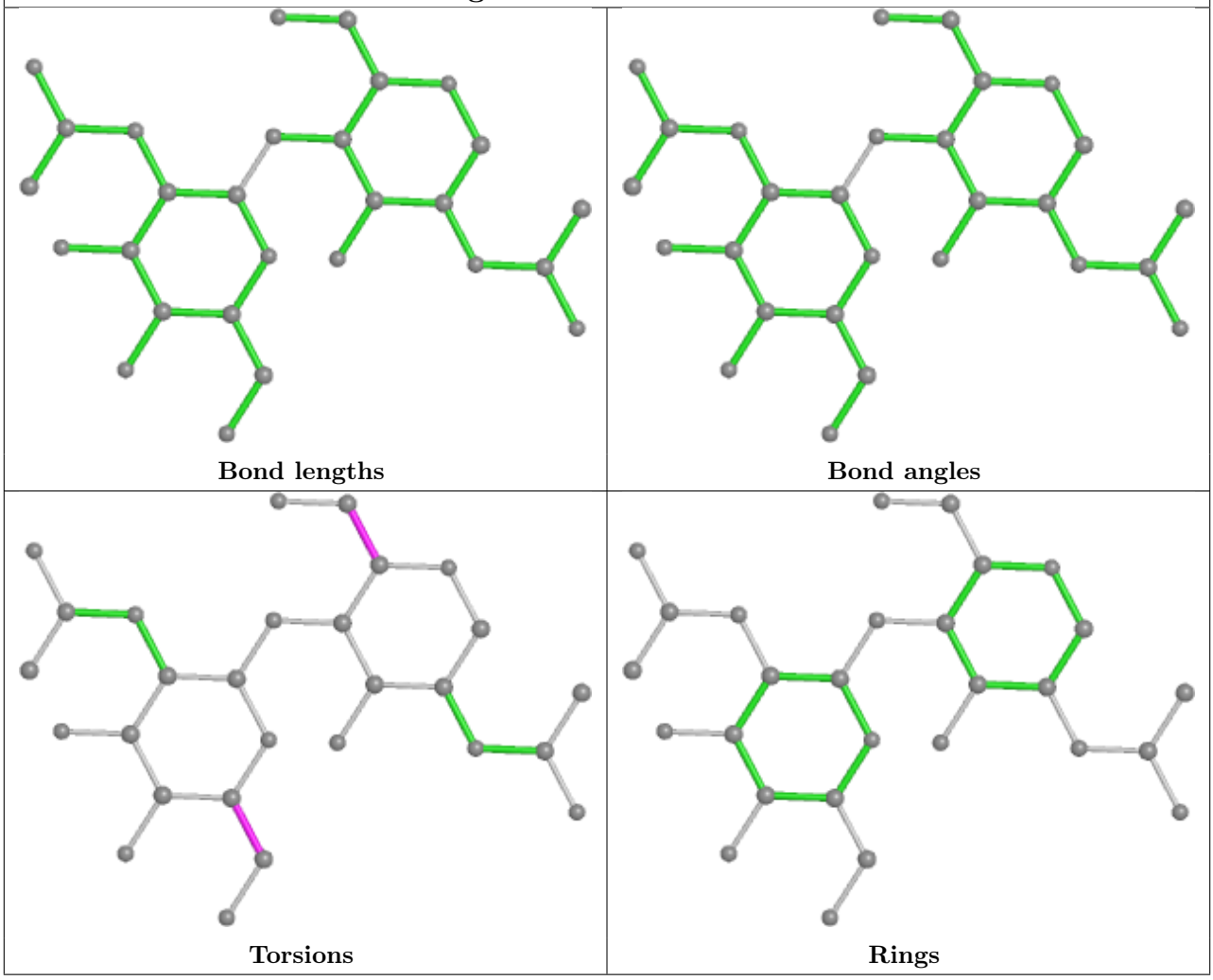
No monomer is involved in short contacts.

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

Oligosaccharide Chain C



Oligosaccharide Chain D



5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\#\|Z\| > 2$
4	GOL	A	1002	-	5,5,5	0.55	0	5,5,5	0.38	0
5	NAG	A	1570	1	14,14,15	0.43	0	17,19,21	0.68	0
4	GOL	A	1003	-	5,5,5	1.15	1 (20%)	5,5,5	0.34	0
4	GOL	B	1004	-	5,5,5	0.94	0	5,5,5	0.24	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	1002	-	-	2/4/4/4	-
5	NAG	A	1570	1	-	0/6/23/26	0/1/1/1
4	GOL	A	1003	-	-	2/4/4/4	-
4	GOL	B	1004	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1003	GOL	C1-C2	2.11	1.60	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1002	GOL	O1-C1-C2-C3
4	A	1003	GOL	O1-C1-C2-C3
4	B	1004	GOL	O1-C1-C2-C3
4	A	1002	GOL	O1-C1-C2-O2
4	B	1004	GOL	O1-C1-C2-O2
4	A	1003	GOL	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1570	NAG	2	0
4	A	1003	GOL	5	0
4	B	1004	GOL	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.