



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2024 – 03:19 PM EST

PDB ID : 4KV8
Title : Crystal structure of HIV RT in complex with BILR0355BS
Authors : Coulombe, R.
Deposited on : 2013-05-22
Resolution : 2.30 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
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

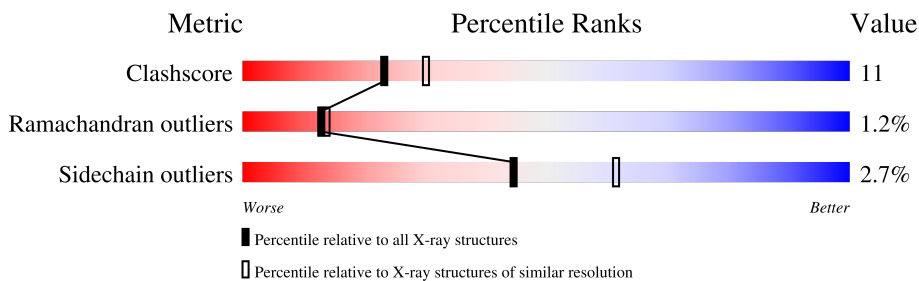
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	564	
2	B	442	
3	C	2	

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	MLA	A	601	-	X	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7964 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 HIV Reverse transcriptase P66.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	554	4513	2917	753	835	8	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP P04585
A	561	VAL	-	expression tag	UNP P04585
A	562	PRO	-	expression tag	UNP P04585
A	563	ARG	-	expression tag	UNP P04585

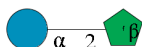
- Molecule 2 is a protein called HIV Reverse transcriptase P51.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	407	3370	2197	556	610	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

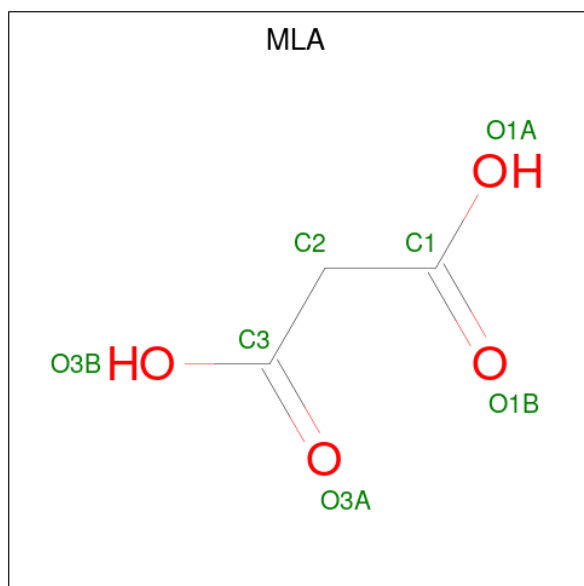
Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP P04585
B	0	SER	-	expression tag	UNP P04585

- Molecule 3 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



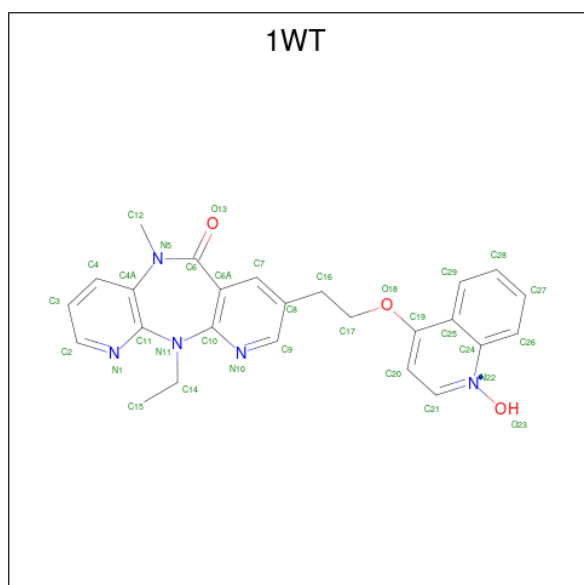
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
3	C	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 4 is MALONIC ACID (three-letter code: MLA) (formula: C₃H₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	3	4		

- Molecule 5 is 11-ethyl-5-methyl-8-[2-(1-oxidanylquinolin-4-yl)oxyethyl]dipyrido[3,2-[1,4]diazepin-6-one (three-letter code: 1WT) (formula: C₂₅H₂₄N₅O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	33	25	5	3	0	0

- Molecule 6 is water.

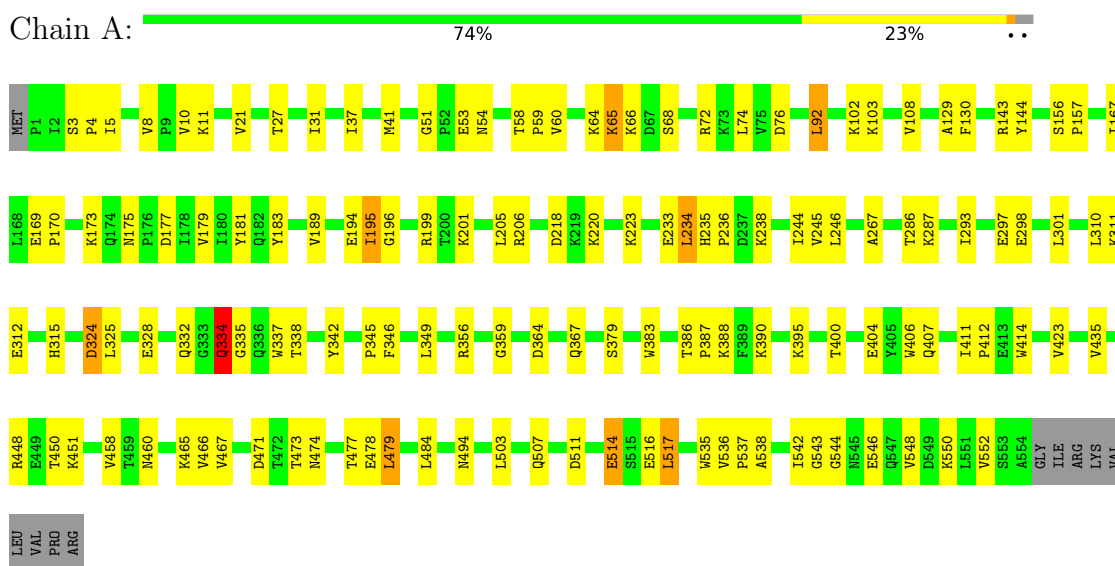
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	9	Total	O	0	0
			9	9		
6	B	9	Total	O	0	0
			9	9		

3 Residue-property plots [i](#)

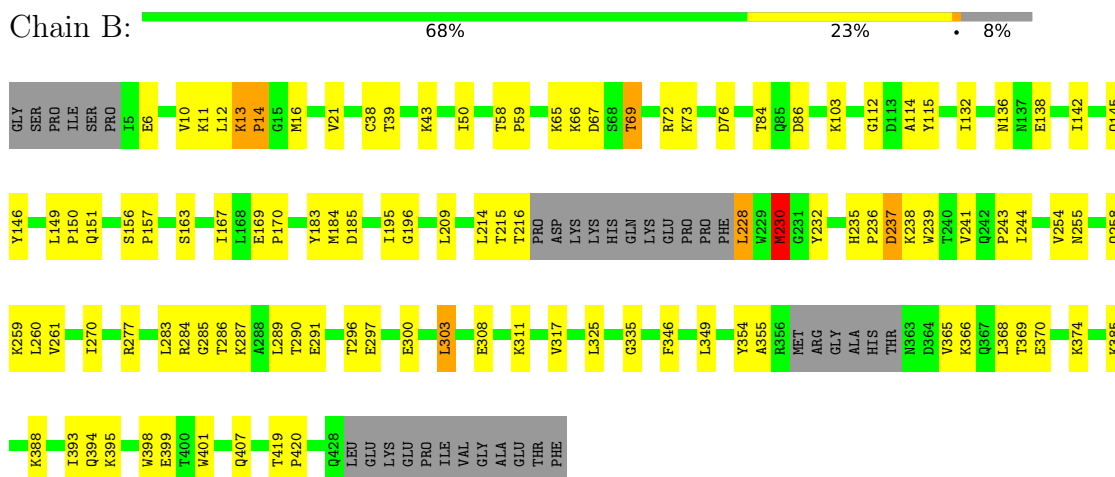
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: HIV Reverse transcriptase P66



- Molecule 2: HIV Reverse transcriptase P51



- Molecule 3: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain C:  100%

6L61
FRU2

4 Data and refinement statistics

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

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	117.21Å 154.89Å 154.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNX 2002	Depositor
R, R_{free}	0.229 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	7964	wwPDB-VP
Average B, all atoms (Å ²)	69.0	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: 1WT, GLC, FRU, MLA

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	0.35	0/4630	0.58	0/6291
2	B	0.36	0/3465	0.61	1/4708 (0.0%)
All	All	0.36	0/8095	0.59	1/10999 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	244	ILE	N-CA-C	-5.86	95.17	111.00

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	4513	0	4563	107	0
2	B	3370	0	3398	83	0
3	C	23	0	21	0	0
4	A	7	0	2	2	0
5	A	33	0	24	0	0
6	A	9	0	0	0	0
6	B	9	0	0	0	0
All	All	7964	0	8008	180	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (180) 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:337:TRP:HE1	1:A:367:GLN:NE2	1.59	0.99
1:A:337:TRP:HE1	1:A:367:GLN:HE21	1.00	0.94
1:A:195:ILE:HD11	1:A:199:ARG:HE	1.37	0.86
1:A:92:LEU:HD12	1:A:92:LEU:H	1.40	0.85
1:A:342:TYR:HA	1:A:349:LEU:HD23	1.61	0.82
1:A:514:GLU:H	1:A:514:GLU:CD	1.83	0.80
2:B:209:LEU:HD22	2:B:214:LEU:HD12	1.66	0.78
1:A:169:GLU:HB3	1:A:170:PRO:HD3	1.68	0.75
2:B:241:VAL:O	2:B:243:PRO:HD3	1.86	0.75
1:A:479:LEU:HB3	1:A:517:LEU:HD13	1.68	0.74
2:B:260:LEU:HD21	2:B:303:LEU:HD21	1.72	0.71
2:B:395:LYS:O	2:B:399:GLU:HG3	1.91	0.70
1:A:536:VAL:HG13	1:A:542:ILE:HD12	1.73	0.70
1:A:206:ARG:NH1	1:A:218:ASP:HA	2.06	0.70
2:B:114:ALA:HB2	2:B:214:LEU:HD21	1.76	0.67
2:B:12:LEU:HD23	2:B:84:THR:HG22	1.76	0.67
1:A:287:LYS:HD3	1:A:293:ILE:HD11	1.76	0.66
2:B:228:LEU:HD12	2:B:228:LEU:N	2.10	0.66
1:A:195:ILE:HD11	1:A:199:ARG:NE	2.10	0.66
2:B:112:GLY:HA3	2:B:151:GLN:HE21	1.62	0.65
2:B:354:TYR:HD2	2:B:374:LYS:HD3	1.63	0.64
1:A:400:THR:O	1:A:404:GLU:HG2	1.98	0.63
1:A:514:GLU:CD	1:A:514:GLU:N	2.52	0.63
1:A:66:LYS:HE3	1:A:68:SER:HB3	1.81	0.62
2:B:236:PRO:C	2:B:238:LYS:H	2.03	0.62
1:A:108:VAL:HG11	1:A:223:LYS:HE3	1.80	0.61
2:B:115:TYR:HB3	2:B:149:LEU:HB2	1.83	0.60
1:A:450:THR:O	1:A:451:LYS:HB2	2.02	0.60
1:A:325:LEU:HD21	1:A:383:TRP:CE3	2.37	0.60
2:B:58:THR:HG23	2:B:76:ASP:O	2.02	0.59
1:A:66:LYS:C	1:A:68:SER:H	2.05	0.59
1:A:324:ASP:OD2	1:A:388:LYS:HD3	2.03	0.59
1:A:332:GLN:NE2	1:A:338:THR:HB	2.17	0.59
2:B:354:TYR:CD2	2:B:374:LYS:HD3	2.38	0.59
1:A:332:GLN:HE21	1:A:338:THR:HB	1.68	0.59
1:A:474:ASN:O	1:A:478:GLU:HG2	2.03	0.59
1:A:335:GLY:HA2	1:A:367:GLN:HE22	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:ILE:CD1	1:A:267:ALA:HB2	2.36	0.56
1:A:548:VAL:O	1:A:552:VAL:HG23	2.05	0.56
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.87	0.56
2:B:10:VAL:C	2:B:11:LYS:HD3	2.26	0.55
1:A:298:GLU:CD	1:A:298:GLU:H	2.10	0.55
2:B:39:THR:HG22	2:B:43:LYS:HE3	1.87	0.55
2:B:209:LEU:HB3	2:B:214:LEU:HB2	1.89	0.55
1:A:218:ASP:OD1	1:A:220:LYS:HB2	2.07	0.54
1:A:244:ILE:HD12	1:A:267:ALA:HB2	1.89	0.54
2:B:103:LYS:O	2:B:236:PRO:HG2	2.07	0.54
2:B:308:GLU:HA	2:B:311:LYS:HE2	1.88	0.54
2:B:230:MET:HE1	2:B:232:TYR:HB3	1.89	0.54
2:B:156:SER:HB2	2:B:157:PRO:HD3	1.91	0.53
1:A:65:LYS:O	1:A:65:LYS:HD3	2.09	0.53
1:A:458:VAL:HG12	2:B:286:THR:HG21	1.89	0.53
1:A:412:PRO:HG3	2:B:401:TRP:CZ2	2.43	0.53
2:B:11:LYS:HD3	2:B:11:LYS:N	2.24	0.53
2:B:112:GLY:HA3	2:B:151:GLN:NE2	2.24	0.53
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.91	0.52
1:A:451:LYS:HB3	1:A:471:ASP:HA	1.91	0.52
2:B:366:LYS:O	2:B:370:GLU:HG3	2.10	0.52
1:A:129:ALA:HA	1:A:144:TYR:O	2.10	0.51
1:A:206:ARG:CZ	1:A:218:ASP:HA	2.39	0.51
1:A:235:HIS:HB3	1:A:236:PRO:HD2	1.91	0.51
1:A:173:LYS:HB3	1:A:173:LYS:NZ	2.24	0.51
1:A:234:LEU:HD23	1:A:234:LEU:N	2.26	0.51
1:A:37:ILE:HG22	1:A:41:MET:CE	2.39	0.51
2:B:183:TYR:CE2	2:B:184:MET:HG3	2.46	0.51
1:A:181:TYR:CE2	1:A:183:TYR:HB2	2.46	0.51
1:A:460:ASN:HD21	4:A:601:MLA:HC22	1.75	0.51
1:A:175:ASN:OD1	1:A:201:LYS:HE3	2.11	0.51
1:A:51:GLY:HA3	1:A:53:GLU:OE2	2.11	0.50
1:A:246:LEU:HD11	1:A:310:LEU:HD12	1.93	0.50
2:B:346:PHE:CD2	2:B:346:PHE:N	2.77	0.50
1:A:335:GLY:HA3	1:A:356:ARG:HD3	1.94	0.49
1:A:411:ILE:HG22	1:A:412:PRO:O	2.12	0.49
1:A:54:ASN:O	1:A:143:ARG:NH2	2.45	0.49
1:A:233:GLU:C	1:A:234:LEU:HD23	2.32	0.49
1:A:542:ILE:HD11	2:B:261:VAL:HG11	1.94	0.49
2:B:157:PRO:HG2	2:B:184:MET:HA	1.94	0.49
1:A:473:THR:O	1:A:477:THR:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:114:ALA:CB	2:B:214:LEU:HD21	2.43	0.49
1:A:325:LEU:HD21	1:A:383:TRP:CD2	2.48	0.48
1:A:334:GLN:H	1:A:334:GLN:CD	2.17	0.48
1:A:287:LYS:HD3	1:A:293:ILE:CD1	2.44	0.48
2:B:114:ALA:HB2	2:B:214:LEU:CD2	2.42	0.48
2:B:136:ASN:HB3	2:B:138:GLU:HG3	1.96	0.48
2:B:335:GLY:O	2:B:355:ALA:HA	2.12	0.48
1:A:169:GLU:CB	1:A:170:PRO:HD3	2.43	0.48
1:A:238:LYS:HD2	1:A:315:HIS:CG	2.47	0.48
1:A:435:VAL:CG2	2:B:290:THR:HG21	2.44	0.48
1:A:3:SER:HA	1:A:4:PRO:HD3	1.68	0.47
1:A:334:GLN:H	1:A:334:GLN:NE2	2.12	0.47
1:A:544:GLY:N	2:B:285:GLY:O	2.47	0.47
1:A:467:VAL:CG2	1:A:484:LEU:HD11	2.44	0.47
1:A:435:VAL:HG22	2:B:290:THR:HG21	1.94	0.47
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.54	0.47
2:B:325:LEU:HD12	2:B:385:LYS:HG3	1.97	0.47
2:B:254:VAL:O	2:B:258:GLN:HG3	2.15	0.47
2:B:13:LYS:HE3	2:B:86:ASP:OD1	2.16	0.46
1:A:66:LYS:HE3	1:A:66:LYS:HB2	1.67	0.46
2:B:388:LYS:HB2	2:B:388:LYS:HE3	1.69	0.46
1:A:5:ILE:HD12	1:A:167:ILE:HG13	1.96	0.46
1:A:169:GLU:HB3	1:A:170:PRO:CD	2.42	0.46
2:B:236:PRO:O	2:B:238:LYS:N	2.49	0.46
1:A:503:LEU:O	1:A:507:GLN:HG3	2.15	0.46
2:B:369:THR:HG22	2:B:398:TRP:CH2	2.50	0.46
1:A:8:VAL:O	1:A:10:VAL:HG23	2.16	0.46
1:A:37:ILE:HG22	1:A:41:MET:HE2	1.98	0.46
1:A:66:LYS:CE	1:A:68:SER:HB3	2.43	0.46
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.98	0.45
1:A:494:ASN:HB3	2:B:289:LEU:HD12	1.99	0.45
1:A:406:TRP:CZ3	1:A:407:GLN:NE2	2.83	0.45
2:B:215:THR:O	2:B:216:THR:C	2.54	0.45
2:B:65:LYS:CG	2:B:66:LYS:H	2.30	0.45
1:A:379:SER:CB	1:A:387:PRO:HD3	2.47	0.45
2:B:65:LYS:HG2	2:B:66:LYS:N	2.32	0.45
1:A:74:LEU:C	1:A:74:LEU:HD23	2.37	0.45
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.52	0.45
1:A:53:GLU:H	1:A:53:GLU:CD	2.20	0.44
2:B:277:ARG:HG2	2:B:277:ARG:HH11	1.83	0.44
2:B:228:LEU:C	2:B:230:MET:H	2.21	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:VAL:HG12	1:A:11:LYS:N	2.32	0.44
2:B:65:LYS:HG2	2:B:66:LYS:H	1.82	0.44
1:A:311:LYS:HG3	1:A:312:GLU:HG2	2.00	0.44
1:A:60:VAL:CG2	1:A:130:PHE:HB2	2.48	0.44
2:B:297:GLU:HA	2:B:300:GLU:HG3	1.99	0.44
1:A:194:GLU:OE1	1:A:194:GLU:N	2.36	0.43
2:B:365:VAL:O	2:B:369:THR:HG23	2.17	0.43
1:A:66:LYS:C	1:A:68:SER:N	2.72	0.43
1:A:479:LEU:HD12	1:A:479:LEU:HA	1.86	0.43
2:B:236:PRO:C	2:B:238:LYS:N	2.69	0.43
1:A:156:SER:HB2	1:A:157:PRO:HD3	2.00	0.43
2:B:146:TYR:CD2	2:B:150:PRO:HB3	2.54	0.43
2:B:296:THR:O	2:B:300:GLU:HG3	2.18	0.43
1:A:173:LYS:NZ	1:A:173:LYS:CB	2.81	0.43
1:A:359:GLY:HA2	1:A:514:GLU:HG3	2.00	0.42
1:A:465:LYS:HG2	1:A:466:VAL:N	2.33	0.42
2:B:11:LYS:HE2	2:B:13:LYS:NZ	2.34	0.42
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.52	0.42
2:B:12:LEU:HD23	2:B:84:THR:CG2	2.47	0.42
1:A:467:VAL:HG22	1:A:484:LEU:HD11	2.02	0.42
2:B:50:ILE:CG2	2:B:145:GLN:HG2	2.49	0.42
2:B:72:ARG:HG2	2:B:73:LYS:N	2.33	0.42
2:B:195:ILE:HG23	2:B:196:GLY:N	2.34	0.42
2:B:235:HIS:HB3	2:B:238:LYS:HD3	2.00	0.42
2:B:317:VAL:HG12	2:B:349:LEU:HD23	2.00	0.42
1:A:64:LYS:HE2	1:A:68:SER:O	2.20	0.42
2:B:69:THR:O	2:B:69:THR:HG23	2.19	0.42
2:B:270:ILE:HG12	2:B:346:PHE:O	2.20	0.42
2:B:65:LYS:CG	2:B:66:LYS:N	2.83	0.42
1:A:21:VAL:HB	1:A:59:PRO:HD3	2.02	0.42
1:A:346:PHE:CD2	1:A:346:PHE:N	2.85	0.42
2:B:277:ARG:HG2	2:B:277:ARG:NH1	2.34	0.42
2:B:230:MET:CE	2:B:232:TYR:HB3	2.50	0.42
1:A:58:THR:HG23	1:A:76:ASP:O	2.20	0.41
1:A:286:THR:C	1:A:287:LYS:HG3	2.40	0.41
1:A:297:GLU:O	1:A:301:LEU:HG	2.21	0.41
1:A:543:GLY:HA3	2:B:283:LEU:O	2.21	0.41
2:B:255:ASN:HD21	2:B:259:LYS:NZ	2.18	0.41
1:A:64:LYS:O	1:A:66:LYS:N	2.53	0.41
1:A:102:LYS:C	1:A:103:LYS:HD2	2.41	0.41
1:A:179:VAL:O	1:A:189:VAL:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:ASN:ND2	4:A:601:MLA:HC22	2.35	0.41
2:B:151:GLN:HB3	2:B:185:ASP:OD2	2.21	0.41
2:B:169:GLU:HB3	2:B:170:PRO:CD	2.51	0.41
2:B:195:ILE:HD12	2:B:195:ILE:HA	1.89	0.41
2:B:419:THR:HA	2:B:420:PRO:HD3	1.90	0.41
1:A:386:THR:HG21	2:B:401:TRP:CH2	2.56	0.41
1:A:194:GLU:O	1:A:196:GLY:N	2.54	0.40
2:B:228:LEU:HD11	2:B:407:GLN:HE22	1.85	0.40
1:A:286:THR:HG23	1:A:286:THR:O	2.21	0.40
1:A:537:PRO:HD2	1:A:542:ILE:CD1	2.52	0.40
2:B:393:ILE:HG12	2:B:394:GLN:N	2.36	0.40
1:A:460:ASN:HA	2:B:286:THR:O	2.22	0.40
1:A:546:GLU:O	1:A:550:LYS:HG3	2.21	0.40
1:A:27:THR:O	1:A:31:ILE:HG13	2.21	0.40
1:A:328:GLU:OE1	1:A:342:TYR:OH	2.28	0.40
2:B:142:ILE:H	2:B:142:ILE:HG13	1.69	0.40
2:B:163:SER:O	2:B:167:ILE:HG13	2.22	0.40
2:B:287:LYS:HD3	2:B:291:GLU:OE2	2.21	0.40
2:B:21:VAL:HB	2:B:59:PRO:HD3	2.02	0.40
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.56	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	552/564 (98%)	524 (95%)	23 (4%)	5 (1%)	17	20
2	B	401/442 (91%)	375 (94%)	20 (5%)	6 (2%)	10	10
All	All	953/1006 (95%)	899 (94%)	43 (4%)	11 (1%)	13	14

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	334	GLN
1	A	538	ALA
2	B	67	ASP
1	A	65	LYS
2	B	6	GLU
2	B	14	PRO
2	B	230	MET
2	B	237	ASP
1	A	345	PRO
1	A	195	ILE
2	B	13	LYS

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	495/504 (98%)	481 (97%)	14 (3%)	43 60
2	B	370/401 (92%)	361 (98%)	9 (2%)	49 66
All	All	865/905 (96%)	842 (97%)	23 (3%)	44 61

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ARG
1	A	92	LEU
1	A	177	ASP
1	A	205	LEU
1	A	234	LEU
1	A	245	VAL
1	A	324	ASP
1	A	334	GLN
1	A	448	ARG
1	A	479	LEU
1	A	511	ASP
1	A	514	GLU
1	A	516	GLU

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Mol	Chain	Res	Type
1	A	517	LEU
2	B	14	PRO
2	B	16	MET
2	B	69	THR
2	B	228	LEU
2	B	230	MET
2	B	237	ASP
2	B	284	ARG
2	B	303	LEU
2	B	368	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	174	GLN
1	A	258	GLN
1	A	332	GLN
1	A	334	GLN
1	A	336	GLN
1	A	348	ASN
1	A	367	GLN
1	A	407	GLN
1	A	475	GLN
1	A	480	GLN
1	A	500	GLN
1	A	524	GLN
2	B	151	GLN
2	B	161	GLN
2	B	208	HIS
2	B	242	GLN
2	B	255	ASN
2	B	269	GLN
2	B	348	ASN
2	B	394	GLN
2	B	407	GLN

5.3.3 RNA

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](#)

2 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
3	GLC	C	1	3	11,11,12	0.95	1 (9%)	15,15,17	0.66	1 (6%)
3	FRU	C	2	3	11,12,12	0.83	1 (9%)	10,18,18	0.46	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
3	GLC	C	1	3	-	0/2/19/22	0/1/1/1
3	FRU	C	2	3	-	2/5/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	GLC	O5-C1	2.37	1.47	1.43
3	C	2	FRU	O2-C2	2.22	1.44	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1	GLC	C2-C3-C4	-2.19	107.11	110.89

There are no chirality outliers.

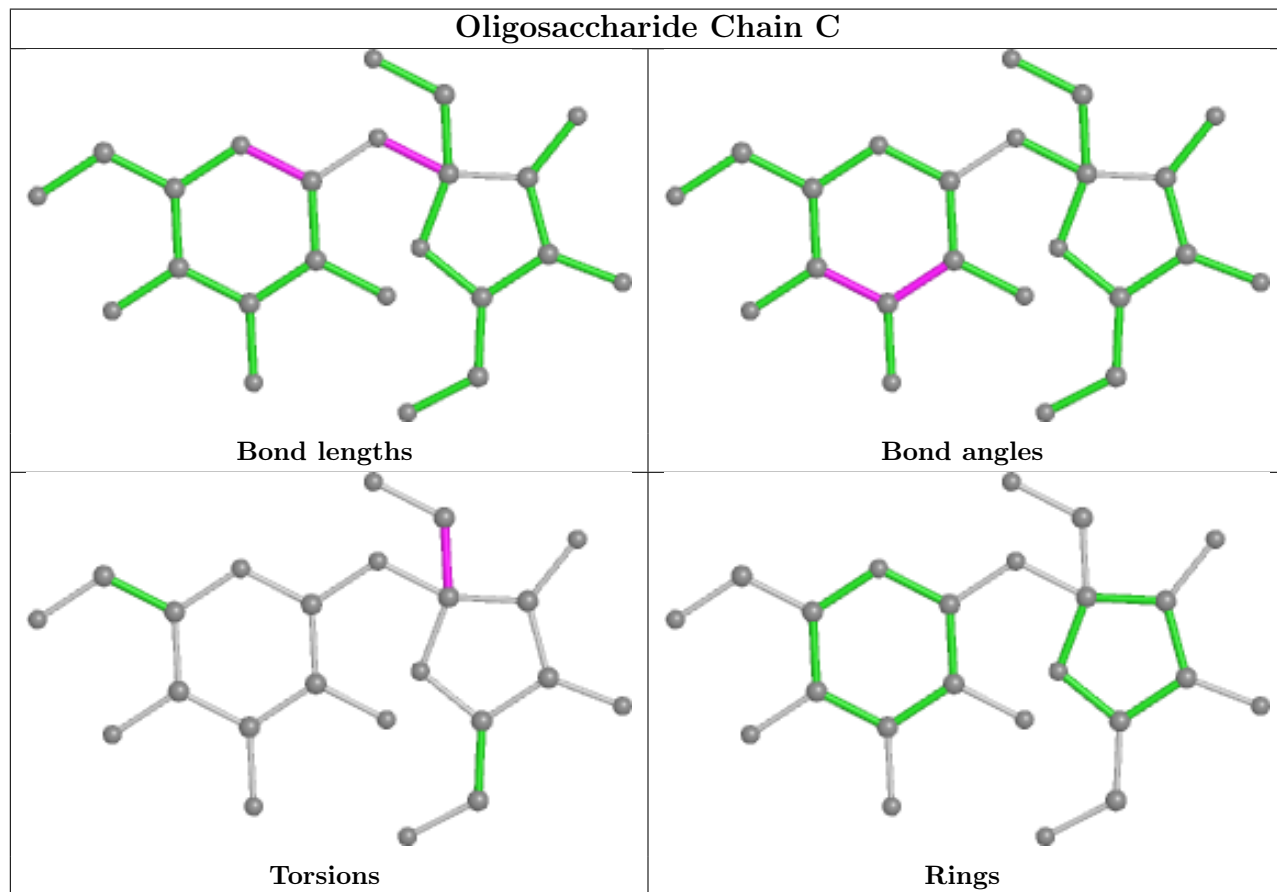
All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	FRU	O1-C1-C2-O2
3	C	2	FRU	O1-C1-C2-O5

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](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	1WT	A	602	-	32,37,37	1.73	10 (31%)	42,53,53	1.53	8 (19%)
4	MLA	A	601	-	6,6,6	2.63	4 (66%)	7,7,7	2.10	2 (28%)

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
5	1WT	A	602	-	-	1/8/32/32	0/5/5/5
4	MLA	A	601	-	-	2/4/4/4	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601	MLA	O1B-C1	3.83	1.34	1.22
5	A	602	1WT	C7-C6A	3.38	1.45	1.39
4	A	601	MLA	O1A-C1	-3.37	1.19	1.30
5	A	602	1WT	C10-N10	3.25	1.40	1.34
4	A	601	MLA	C2-C1	3.00	1.55	1.51
5	A	602	1WT	O23-N22	-2.85	1.31	1.37
5	A	602	1WT	C20-C19	2.81	1.44	1.38
5	A	602	1WT	C11-N1	2.69	1.39	1.34
5	A	602	1WT	C7-C8	2.66	1.43	1.39
5	A	602	1WT	C25-C24	2.60	1.46	1.42
5	A	602	1WT	C27-C26	2.32	1.42	1.36
5	A	602	1WT	C4-C4A	2.29	1.43	1.39
5	A	602	1WT	C28-C29	2.12	1.41	1.36
4	A	601	MLA	C2-C3	2.02	1.54	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	1WT	N1-C11-N11	4.20	120.11	114.86
5	A	602	1WT	N10-C10-N11	3.80	119.61	114.86
4	A	601	MLA	O1A-C1-C2	3.61	126.07	114.54
4	A	601	MLA	O1B-C1-C2	-3.41	112.12	122.08
5	A	602	1WT	O13-C6-C6A	-3.16	114.70	120.01
5	A	602	1WT	C10-C6A-C6	-2.29	121.81	123.77
5	A	602	1WT	C4A-C11-N11	-2.26	118.50	120.09
5	A	602	1WT	C11-N11-C10	-2.17	112.53	114.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	602	1WT	C16-C8-C7	2.01	123.84	120.54
5	A	602	1WT	C2-N1-C11	2.01	119.80	115.14

There are no chirality outliers.

All (3) torsion outliers are listed below:

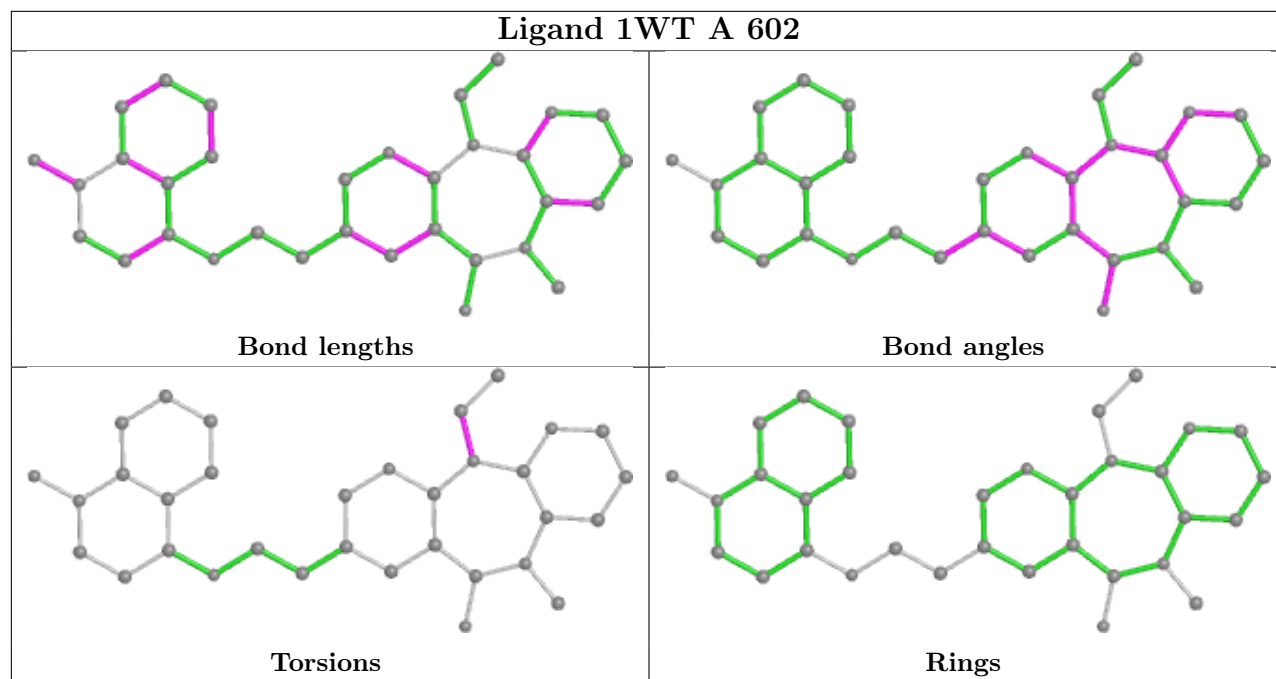
Mol	Chain	Res	Type	Atoms
5	A	602	1WT	C15-C14-N11-C11
4	A	601	MLA	O1B-C1-C2-C3
4	A	601	MLA	O1A-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	601	MLA	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.