wwPDB X-ray Structure Validation Summary Report (i)

Dec 15, 2024 – 06:52 AM EST

PDB ID	:	1R1A
Title	:	CRYSTAL STRUCTURE OF HUMAN RHINOVIRUS SEROTYPE 1A (HRV1A)
Authors	:	Kim, S.; Rossmann, M.G.
Deposited on	:	1989-03-15
Resolution	:	3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

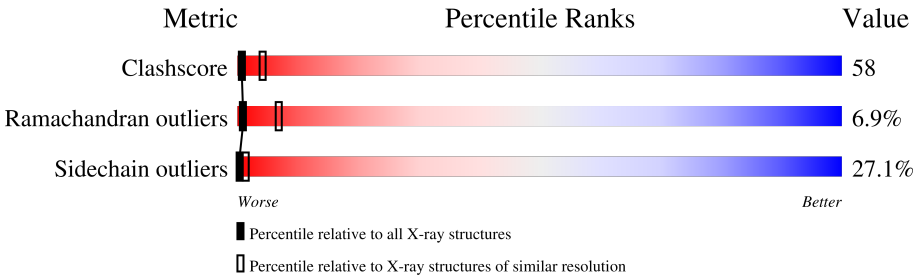
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 3.20 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	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)

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	1	287	18% 43% 25% 13% •
2	2	263	19% 36% 31% 10% •
3	3	238	19% 47% 26% 8%
4	4	44	9% 16% 9% 9% 57%
5	A	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
5	GLC	A	1	X	-	X	-
5	FRU	A	2	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6246 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 HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	1	283	2262	1431	389	430	12	0	0	0

- Molecule 2 is a protein called HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	2	253	1979	1249	349	371	10	0	0	0

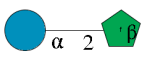
- Molecule 3 is a protein called HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	3	238	1831	1169	297	348	17	0	0	0

- Molecule 4 is a protein called HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP4).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	4	19	151	96	25	30	0	0	0

- Molecule 5 is an oligosaccharide called beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose.



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

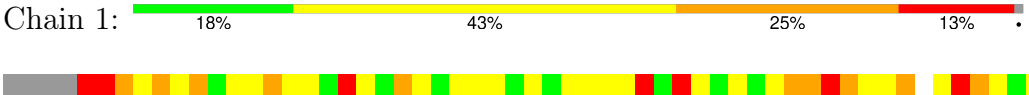
3 Residue-property plots (i)

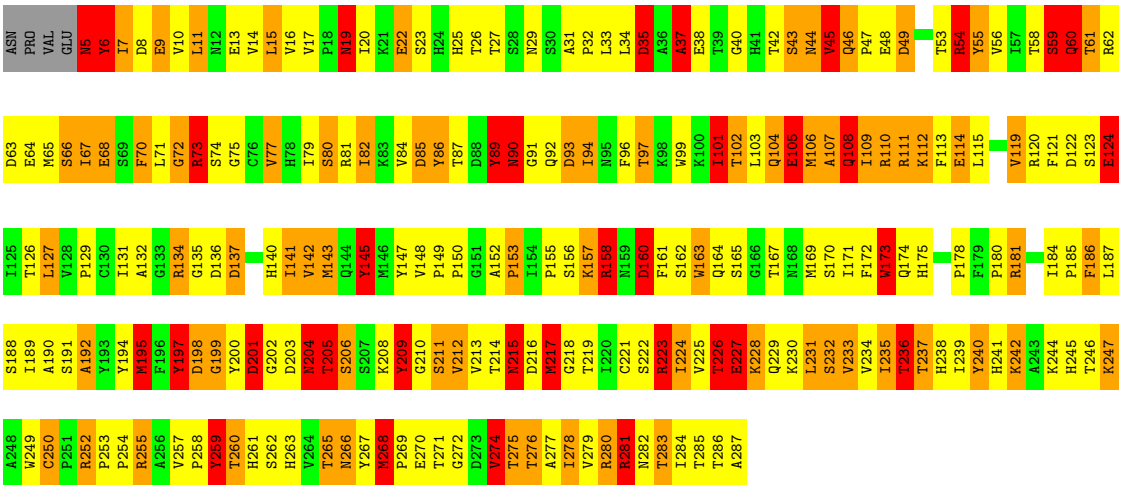
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP1)

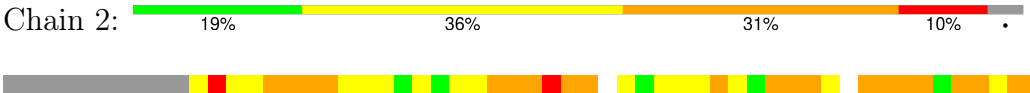
Chain 1:

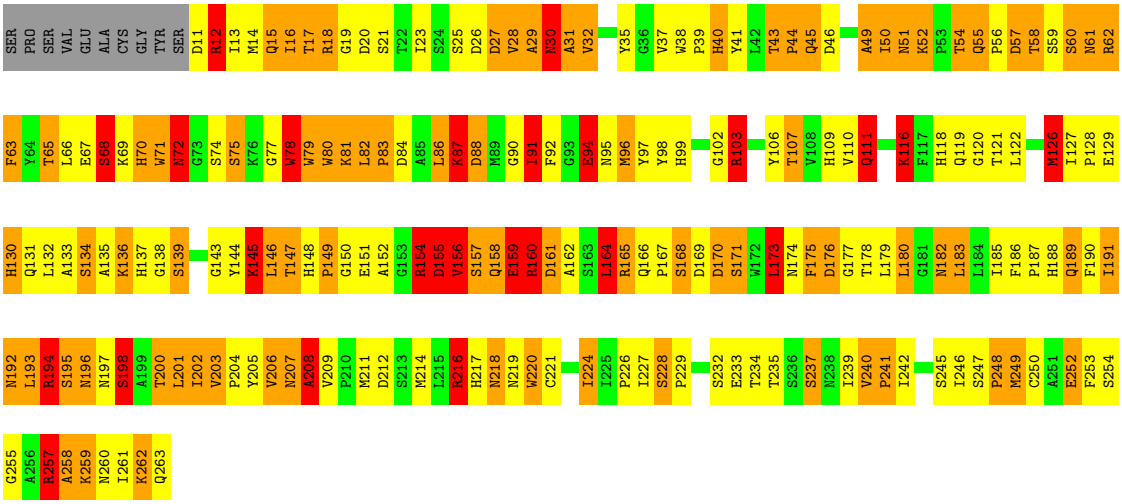




• Molecule 2: HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP2)

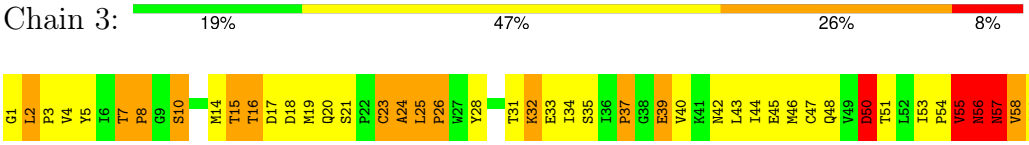
Chain 2:

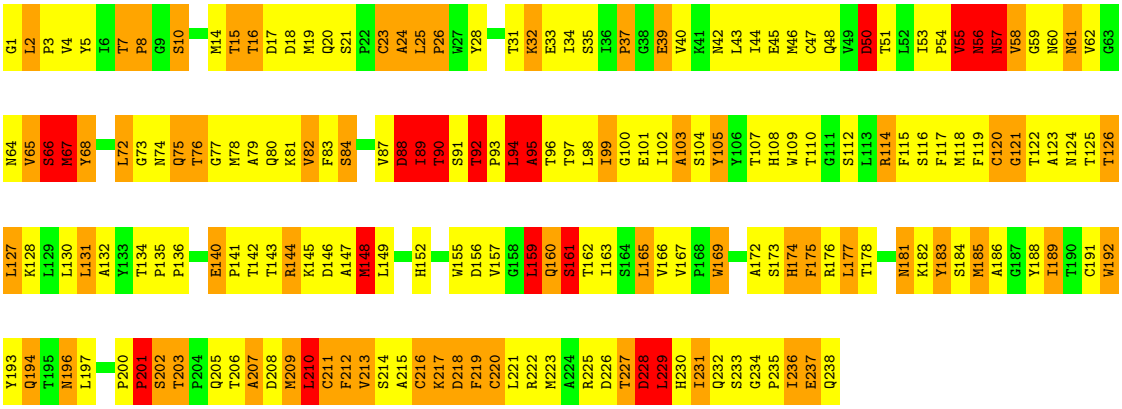




• Molecule 3: HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP3)

Chain 3:





• Molecule 4: HUMAN RHINOVIRUS 1A COAT PROTEIN (SUBUNIT VP4)

Chain 4:

• Molecule 5: beta-D-fructofuranose-(2-1)-alpha-D-glucopyranose

Chain A:

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α, β, γ	341.30Å 341.30Å 465.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	10.00 – 3.20	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-3.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.293 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6246	wwPDB-VP
Average B, all atoms (Å^2)	14.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FRU, GLC

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	1	0.98	0/2322	2.61	150/3162 (4.7%)
2	2	0.95	0/2033	2.60	151/2770 (5.5%)
3	3	0.93	0/1878	2.47	112/2570 (4.4%)
4	4	1.25	0/154	3.16	21/206 (10.2%)
All	All	0.96	0/6387	2.58	434/8708 (5.0%)

There are no bond length outliers.

The worst 5 of 434 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	2	62	ARG	CD-NE-CZ	24.85	158.39	123.60
1	1	134	ARG	NE-CZ-NH1	24.00	132.30	120.30
2	2	216	ARG	NE-CZ-NH2	-22.09	109.25	120.30
1	1	280	ARG	NE-CZ-NH2	-20.39	110.11	120.30
1	1	110	ARG	NE-CZ-NH2	-19.07	110.77	120.30

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	1	2262	0	2193	336	1
2	2	1979	0	1920	215	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	3	1831	0	1809	226	0
4	4	151	0	136	18	0
5	A	23	0	19	32	0
All	All	6246	0	6077	709	1

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 58.

The worst 5 of 709 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)
1:1:102:THR:CA	5:A:2:FRU:H61	1.09	1.55
1:1:102:THR:HA	5:A:2:FRU:C6	0.95	1.41
2:2:18:ARG:NH1	2:2:249:MET:HE2	1.54	1.21
1:1:23:SER:OG	1:1:53:THR:HG22	1.36	1.19
3:3:42:ASN:HD22	3:3:44:ILE:HG22	1.06	1.13

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:27:THR:OG1	2:2:18:ARG:NH2[2_655]	2.09	0.11

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	1	281/287 (98%)	217 (77%)	46 (16%)	18 (6%)	1 8
2	2	251/263 (95%)	201 (80%)	35 (14%)	15 (6%)	1 10
3	3	236/238 (99%)	178 (75%)	38 (16%)	20 (8%)	0 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
4	4	17/44 (39%)	9 (53%)	7 (41%)	1 (6%)	1 10
All	All	785/832 (94%)	605 (77%)	126 (16%)	54 (7%)	1 7

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	59	SER
1	1	72	GLY
1	1	107	ALA
1	1	108	GLN
1	1	114	GLU

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	1	254/258 (98%)	184 (72%)	70 (28%)	0 1
2	2	219/227 (96%)	158 (72%)	61 (28%)	0 1
3	3	209/209 (100%)	157 (75%)	52 (25%)	0 2
4	4	15/35 (43%)	9 (60%)	6 (40%)	0 0
All	All	697/729 (96%)	508 (73%)	189 (27%)	0 1

5 of 189 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	2	195	SER
3	3	60	ASN
2	2	201	LEU
2	2	262	LYS
3	3	92	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
3	3	80	GLN
3	3	124	ASN
4	4	30	ASN
2	2	51	ASN
2	2	30	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

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	$\#\|Z\| > 2$
5	GLC	A	1	5	11,11,12	2.12	2 (18%)	15,15,17	4.94	8 (53%)
5	FRU	A	2	5	11,12,12	1.09	0	10,18,18	2.26	2 (20%)

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	GLC	A	1	5	1/1/4/5	2/2/19/22	0/1/1/1
5	FRU	A	2	5	-	5/5/24/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1	GLC	O5-C1	-5.97	1.33	1.43
5	A	1	GLC	C2-C3	-2.63	1.48	1.52

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1	GLC	O3-C3-C2	14.18	139.00	110.05
5	A	1	GLC	C1-O5-C5	7.07	121.67	112.19
5	A	1	GLC	O2-C2-C3	6.27	123.13	110.15
5	A	2	FRU	O2-C2-O5	5.80	120.45	109.33
5	A	1	GLC	O5-C5-C6	5.14	117.67	107.66

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1	GLC	C1

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2	FRU	O1-C1-C2-C3
5	A	2	FRU	O1-C1-C2-O2
5	A	2	FRU	O5-C5-C6-O6
5	A	1	GLC	O5-C5-C6-O6
5	A	1	GLC	C4-C5-C6-O6

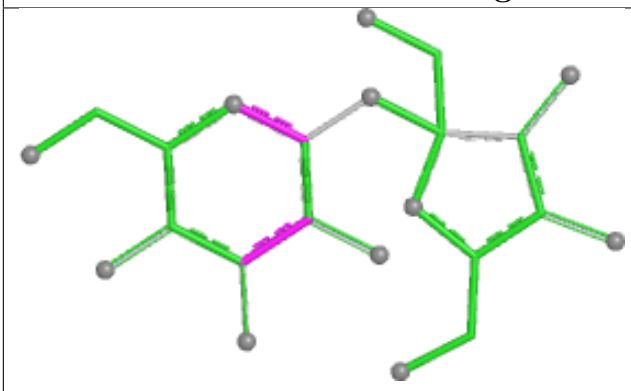
There are no ring outliers.

2 monomers are involved in 32 short contacts:

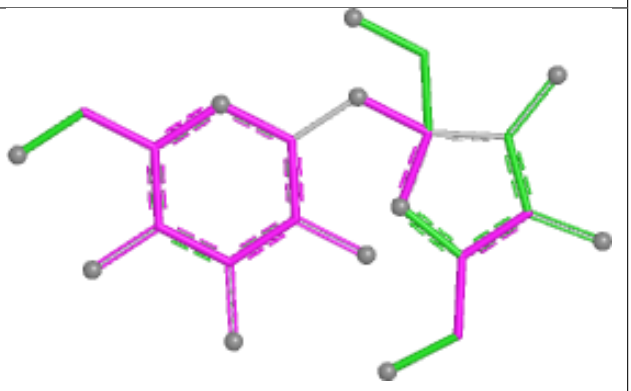
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1	GLC	6	0
5	A	2	FRU	27	0

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

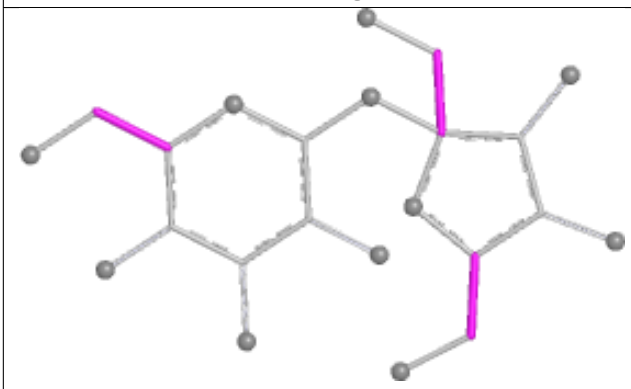
Oligosaccharide Chain A



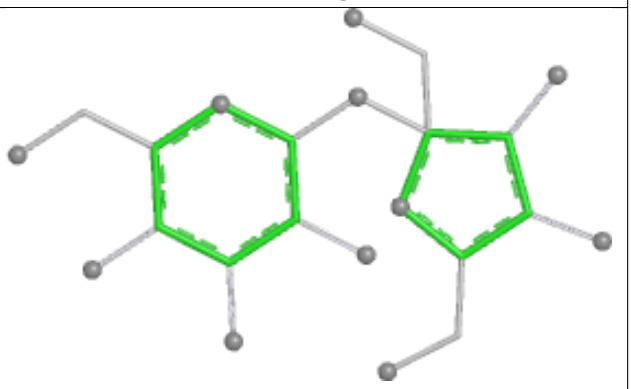
Bond lengths



Bond angles



Torsions



Rings

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

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.