



Full wwPDB X-ray Structure Validation Report i

Mar 1, 2014 – 01:29 AM GMT

PDB ID : 1C8M
Title : REFINED CRYSTAL STRUCTURE OF HUMAN RHINOVIRUS 16 COM-
PLEXED WITH VP63843 (PLECONARIL), AN ANTI-PICORNAVIRAL
DRUG CURRENTLY IN CLINICAL TRIALS
Authors : Chakravarty, S.; Bator, C.M.; Pevear, D.C.; Diana, G.D.; Rossmann, M.G.
Deposited on : 2000-05-26
Resolution : 2.80 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

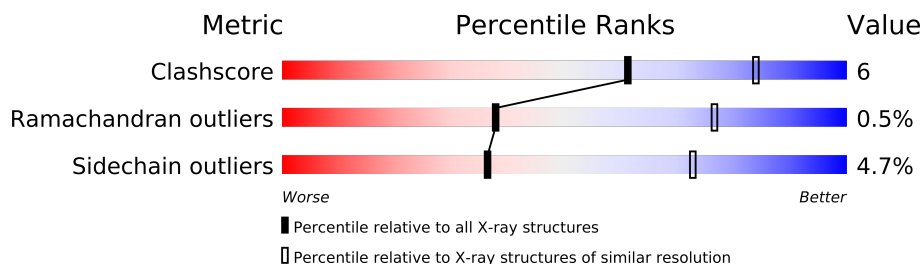
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	21963
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.80 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	79885	2295 (2.80-2.80)
Ramachandran outliers	78287	2252 (2.80-2.80)
Sidechain outliers	78261	2254 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	285	
2	2	252	
3	3	238	
4	4	77	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6820 atoms, of which 0 are hydrogen and 0 are deuterium.

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 16 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	285	Total	C	N	O	S	0	0	0
			2275	1436	393	435	11			

- Molecule 2 is a protein called HUMAN RHINOVIRUS 16 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	252	Total	C	N	O	S	0	0	0
			1965	1245	341	369	10			

- Molecule 3 is a protein called HUMAN RHINOVIRUS 16 COAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	238	Total	C	N	O	S	0	0	0
			1846	1186	298	347	15			

- Molecule 4 is a protein called HUMAN RHINOVIRUS 16 COAT PROTEIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	4	29	Total	C	N	O	0	0	0
			224	138	41	45			

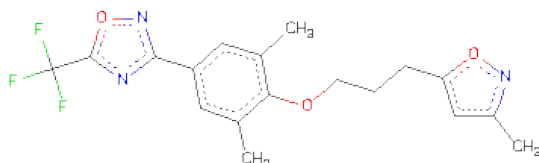
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
4	24	ILE	LEU	CONFLICT	UNP Q82122

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	1	1	Total	Zn	0	0
			1	1		

- Molecule 6 is 3-{3,5-DIMETHYL-4-[3-(3-METHYL-ISOXAZOL-5-YL)-PROPOXY]-PHE
NYL}-5-TRIFLUOROMETHYL-[1,2,4]OXADIAZOLE (three-letter code: W11) (formula:
 $C_{18}H_{18}F_3N_3O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	1	1	Total	C	F	N	O	0	0
			27	18	3	3	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	1	155	Total	O	0	0
			155	155		
7	2	170	Total	O	0	0
			170	170		
7	3	139	Total	O	0	0
			139	139		
7	4	18	Total	O	0	0
			18	18		

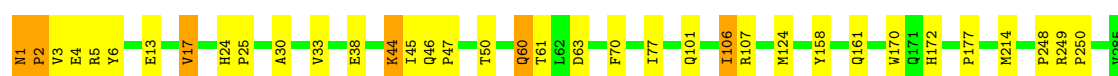
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

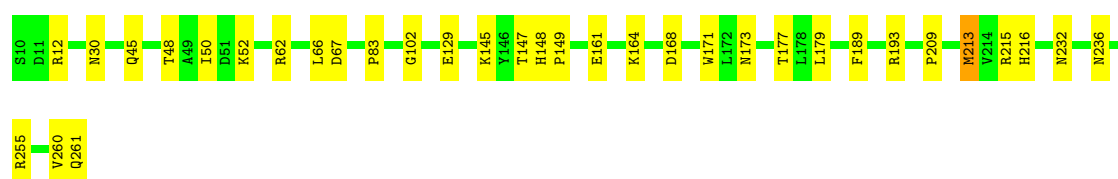
• Molecule 1: HUMAN RHINOVIRUS 16 COAT PROTEIN

Chain 1: 



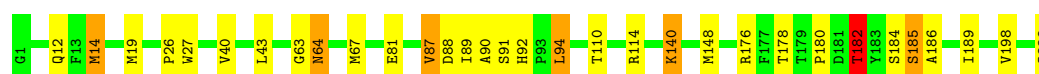
• Molecule 2: HUMAN RHINOVIRUS 16 COAT PROTEIN

Chain 2: 



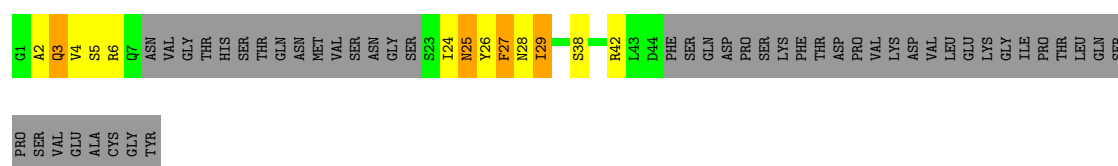
• Molecule 3: HUMAN RHINOVIRUS 16 COAT PROTEIN

Chain 3: 



• Molecule 4: HUMAN RHINOVIRUS 16 COAT PROTEIN

Chain 4: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	360.30Å 343.33Å 332.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80	Depositor
% Data completeness (in resolution range)	92.6 (20.00-2.80)	Depositor
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.219 , 0.226	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6820	wwPDB-VP
Average B, all atoms (Å ²)	18.0	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: ZN, W11

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	0.55	1/2337 (0.0%)	0.76	3/3188 (0.1%)
2	2	0.49	0/2017	0.78	1/2753 (0.0%)
3	3	0.52	0/1898	0.80	3/2596 (0.1%)
4	4	1.03	0/226	0.90	0/301
All	All	0.55	1/6478 (0.0%)	0.78	7/8838 (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
3	3	1	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1	ASN	C-N	-7.62	1.19	1.34

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	92	HIS	N-CA-C	9.36	136.26	111.00
1	1	2	PRO	CA-N-CD	7.40	122.06	111.70
1	1	1	ASN	N-CA-C	-6.81	92.62	111.00
3	3	92	HIS	C-N-CD	6.36	141.75	128.40
2	2	50	ILE	N-CA-C	5.24	125.15	111.00
1	1	30	ALA	N-CA-C	-5.14	97.12	111.00
3	3	186	ALA	N-CA-C	5.14	124.88	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	3	92	HIS	CA

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	2275	0	2182	30	0
2	2	1965	0	1899	17	0
3	3	1846	0	1826	20	0
4	4	224	0	211	12	0
5	1	1	0	0	0	0
6	1	27	0	18	3	0
7	1	155	0	0	4	0
7	2	170	0	0	2	0
7	3	139	0	0	6	0
7	4	18	0	0	0	0
All	All	6820	0	6136	72	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 6.

All (72) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:1:7001:W11:O1A	6:1:7001:W11:N1A	1.58	1.11
4:4:2:ALA:HB2	4:4:29:ILE:HA	1.36	1.05
3:3:87:VAL:HG23	3:3:189:ILE:HG13	1.55	0.88
4:4:2:ALA:CB	4:4:29:ILE:HA	2.08	0.81
4:4:4:VAL:HG22	4:4:27:PHE:HD2	1.50	0.74
1:1:2:PRO:HD2	7:1:5475:HOH:O	1.87	0.74
1:1:158:TYR:O	1:1:161:GLN:HG3	1.89	0.72
4:4:4:VAL:HG22	4:4:27:PHE:CD2	2.24	0.71
1:1:124:MET:HB2	1:1:177:PRO:HG2	1.80	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:1:170:TRP:CD1	1:1:177:PRO:HD3	2.34	0.62
2:2:173:ASN:HD21	2:2:179:LEU:HA	1.66	0.60
4:4:5:SER:O	4:4:25:ASN:HA	2.02	0.59
3:3:88:ASP:HB2	3:3:91:SER:HB3	1.84	0.59
4:4:25:ASN:H	4:4:25:ASN:ND2	2.00	0.58
3:3:12:GLN:NE2	7:3:5468:HOH:O	2.37	0.58
1:1:24:HIS:HB3	1:1:25:PRO:HD2	1.88	0.56
2:2:83:PRO:CG	2:2:213:MET:HG3	2.37	0.55
2:2:83:PRO:HG3	2:2:213:MET:HG3	1.89	0.54
1:1:2:PRO:O	1:1:5:ARG:CB	2.56	0.54
4:4:26:TYR:HE2	4:4:42:ARG:HH21	1.56	0.53
3:3:176:ARG:HG2	3:3:184:SER:HB2	1.91	0.53
3:3:26:PRO:HG2	7:3:5300:HOH:O	2.08	0.52
4:4:6:ARG:HG2	4:4:25:ASN:OD1	2.10	0.52
3:3:182:THR:O	3:3:185:SER:HB3	2.10	0.51
2:2:67:ASP:HB2	7:2:5290:HOH:O	2.11	0.51
1:1:17:VAL:HG21	7:3:5425:HOH:O	2.10	0.51
1:1:33:VAL:HG12	1:1:45:ILE:CD1	2.41	0.51
1:1:13:GLU:HA	1:1:61:THR:HG21	1.93	0.51
2:2:147:THR:C	2:2:149:PRO:HD3	2.32	0.50
1:1:106:ILE:HG23	7:1:5020:HOH:O	2.12	0.50
3:3:27:TRP:HE3	7:3:5300:HOH:O	1.95	0.49
1:1:248:PRO:HD3	3:3:40:VAL:CG2	2.42	0.49
2:2:148:HIS:N	2:2:149:PRO:HD3	2.27	0.49
1:1:38:GLU:HA	2:2:189:PHE:HB2	1.94	0.49
2:2:129:GLU:OE1	2:2:216:HIS:HE1	1.96	0.48
1:1:60:GLN:H	1:1:60:GLN:CD	2.16	0.48
1:1:1:ASN:CA	7:1:5475:HOH:O	2.61	0.47
1:1:44:LYS:HD2	1:1:44:LYS:HA	1.53	0.47
2:2:255:ARG:HH11	2:2:255:ARG:HG3	1.80	0.47
2:2:62:ARG:HD3	7:2:5160:HOH:O	2.15	0.47
1:1:33:VAL:HG12	1:1:50:THR:HG22	1.97	0.47
2:2:171:TRP:CE2	3:3:63:GLY:HA2	2.50	0.47
1:1:45:ILE:O	3:3:114:ARG:NH1	2.49	0.46
1:1:6:TYR:HE2	7:1:5287:HOH:O	1.98	0.46
1:1:33:VAL:HA	1:1:45:ILE:HD12	1.99	0.45
4:4:26:TYR:CZ	4:4:28:ASN:HB2	2.51	0.45
1:1:2:PRO:O	1:1:5:ARG:N	2.50	0.45
3:3:198:VAL:HG23	7:3:5401:HOH:O	2.17	0.45
3:3:64:ASN:O	3:3:67:MET:HG2	2.16	0.45
1:1:3:VAL:HG11	4:4:24:ILE:HG23	1.99	0.44
1:1:249:ARG:HB2	1:1:250:PRO:CD	2.47	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:1:46:GLN:HB3	1:1:47:PRO:HD2	1.99	0.44
1:1:1:ASN:O	1:1:4:GLU:N	2.49	0.44
3:3:87:VAL:CG2	3:3:189:ILE:HG13	2.37	0.44
1:1:101:GLN:HA	1:1:107:ARG:HD2	2.00	0.44
4:4:25:ASN:HD22	4:4:25:ASN:H	1.63	0.44
1:1:77:ILE:HD11	6:1:7001:W11:HM21	1.99	0.44
2:2:145:LYS:HB3	2:2:261:GLN:OE1	2.18	0.44
1:1:77:ILE:HD11	6:1:7001:W11:CM2	2.48	0.43
2:2:48:THR:HG22	2:2:209:PRO:CG	2.49	0.43
3:3:90:ALA:HB3	3:3:178:THR:O	2.19	0.43
3:3:89:ILE:HD12	3:3:89:ILE:HA	1.77	0.43
3:3:88:ASP:O	3:3:94:LEU:HD11	2.19	0.42
3:3:14:MET:HG3	7:3:5468:HOH:O	2.20	0.41
1:1:60:GLN:HG2	3:3:110:THR:HG21	2.02	0.41
2:2:48:THR:HG22	2:2:209:PRO:HG3	2.02	0.41
2:2:102:GLY:HA3	2:2:213:MET:SD	2.60	0.41
2:2:260:VAL:CG1	2:2:261:GLN:N	2.84	0.41
4:4:3:GLN:O	4:4:3:GLN:HG2	2.21	0.41
3:3:81:GLU:OE2	3:3:140:LYS:HE3	2.21	0.40
1:1:70:PHE:CD1	3:3:43:LEU:HD11	2.57	0.40
1:1:250:PRO:HB2	2:2:177:THR:HB	2.03	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	1	283/285 (99%)	275 (97%)	8 (3%)	0	100	100
2	2	250/252 (99%)	230 (92%)	19 (8%)	1 (0%)	43	80
3	3	236/238 (99%)	223 (94%)	11 (5%)	2 (1%)	27	65
4	4	25/77 (32%)	22 (88%)	2 (8%)	1 (4%)	5	14
All	All	794/852 (93%)	750 (94%)	40 (5%)	4 (0%)	38	76

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	161	GLU
3	3	182	THR
4	4	27	PHE
3	3	180	PRO

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	1	253/256 (99%)	246 (97%)	7 (3%)	56	88
2	2	217/221 (98%)	205 (94%)	12 (6%)	30	65
3	3	210/210 (100%)	200 (95%)	10 (5%)	35	72
4	4	23/66 (35%)	19 (83%)	4 (17%)	3	8
All	All	703/753 (93%)	670 (95%)	33 (5%)	36	73

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	17	VAL
1	1	44	LYS
1	1	60	GLN
1	1	63	ASP
1	1	106	ILE
1	1	172	HIS
1	1	214	MET
2	2	12	ARG
2	2	30	ASN
2	2	45	GLN
2	2	52	LYS
2	2	66	LEU
2	2	164	LYS
2	2	168	ASP
2	2	193	ARG
2	2	213	MET
2	2	215	ARG

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Mol	Chain	Res	Type
2	2	232	ASN
2	2	236	ASN
3	3	14	MET
3	3	19	MET
3	3	64	ASN
3	3	87	VAL
3	3	94	LEU
3	3	140	LYS
3	3	148	MET
3	3	182	THR
3	3	185	SER
3	3	238	GLN
4	4	3	GLN
4	4	25	ASN
4	4	29	ILE
4	4	38	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	12	ASN
1	1	89	ASN
1	1	171	GLN
2	2	30	ASN
2	2	55	GLN
2	2	173	ASN
2	2	216	HIS
2	2	232	ASN
3	3	12	GLN
3	3	174	GLN
4	4	25	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
6	W11	1	7001	-	29,29,29	5.34	14 (48%)	38,42,42	3.38	21 (55%)

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
6	W11	1	7001	-	-	0/13/17/17	0/2/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	1	7001	W11	O1A-N1A	19.44	1.58	1.42
6	1	7001	W11	O1-N2	13.62	1.53	1.42
6	1	7001	W11	O1A-C3A	11.25	1.42	1.36
6	1	7001	W11	C2A-N3A	5.72	1.44	1.36
6	1	7001	W11	C1B-C6B	4.33	1.48	1.40
6	1	7001	W11	C2A-N1A	4.13	1.39	1.33
6	1	7001	W11	CM4-C3A	3.46	1.54	1.51
6	1	7001	W11	C3A-N3A	2.90	1.43	1.36
6	1	7001	W11	CM6-C6B	2.88	1.57	1.51
6	1	7001	W11	F1-CM4	2.17	1.41	1.32
6	1	7001	W11	C4-C3	2.16	1.44	1.39
6	1	7001	W11	C5B-C6B	2.11	1.43	1.39
6	1	7001	W11	C4B-C2A	-2.06	1.42	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	1	7001	W11	CM2-C2B	-2.00	1.46	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1	7001	W11	C5-O1-N2	-9.56	104.55	107.66
6	1	7001	W11	C4B-C3B-C2B	-5.82	114.86	122.50
6	1	7001	W11	O1-C5-C1C	-5.64	113.09	116.70
6	1	7001	W11	C3B-C2B-C1B	5.10	125.50	117.77
6	1	7001	W11	C5B-C4B-C3B	4.84	126.21	118.27
6	1	7001	W11	O1B-C1B-C6B	4.74	127.61	118.86
6	1	7001	W11	C4B-C5B-C6B	-4.45	116.66	122.50
6	1	7001	W11	C2C-C1C-C5	-4.38	103.78	113.89
6	1	7001	W11	F2-CM4-C3A	-4.33	106.60	111.29
6	1	7001	W11	CM6-C6B-C1B	4.02	127.31	120.96
6	1	7001	W11	F1-CM4-C3A	-3.93	107.04	111.29
6	1	7001	W11	C1C-C5-C4	3.89	136.98	128.51
6	1	7001	W11	CM4-C3A-N3A	3.78	126.09	122.41
6	1	7001	W11	C3B-C4B-C2A	-3.51	114.97	120.35
6	1	7001	W11	O1B-C3C-C2C	-3.30	95.46	108.42
6	1	7001	W11	CM6-C6B-C5B	-3.13	113.36	119.41
6	1	7001	W11	O1-N2-C3	2.68	107.63	105.68
6	1	7001	W11	C3C-O1B-C1B	2.60	121.81	114.10
6	1	7001	W11	CM2-C2B-C1B	-2.46	117.06	120.96
6	1	7001	W11	O1B-C1B-C2B	-2.15	114.88	118.86
6	1	7001	W11	C6B-C1B-C2B	-2.01	117.51	122.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.