



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:22 PM UTC

PDB ID : 1GHG / pdb_00001ghg
Title : CRYSTAL STRUCTURE OF VANCOMYCIN AGLYCON
Authors : Kaplan, J.; Korty, B.D.; Axelsen, P.H.; Loll, P.J.
Deposited on : 2000-12-13
Resolution : 0.98 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

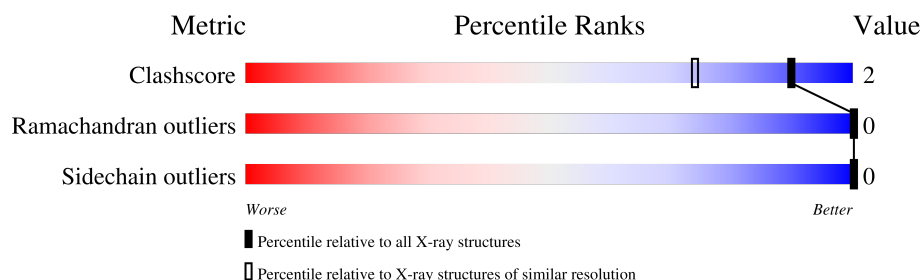
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 0.98 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	190562	1197 (1.02-0.94)
Ramachandran outliers	187476	1136 (1.02-0.94)
Sidechain outliers	187428	1137 (1.02-0.94)

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	7	
1	B	7	
1	C	7	
1	D	7	

2 Entry composition [i](#)

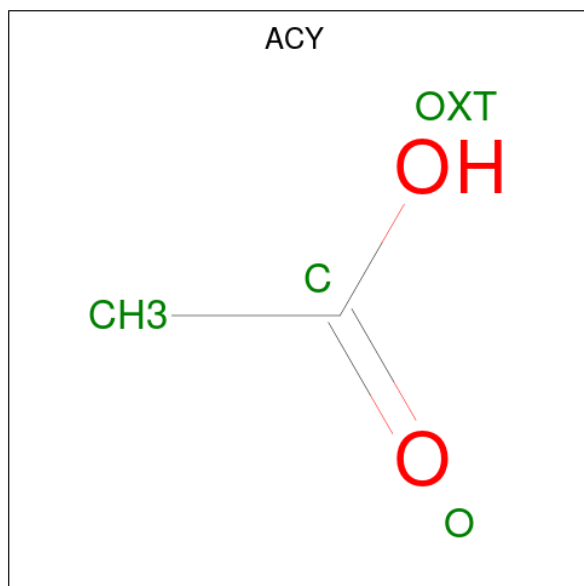
There are 4 unique types of molecules in this entry. The entry contains 411 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 VANCOMYCIN AGLYCON.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	7	Total	C	Cl	N	O	0	0	0
			80	53	2	8	17			
1	B	7	Total	C	Cl	N	O	0	0	0
			80	53	2	8	17			
1	C	7	Total	C	Cl	N	O	0	0	0
			80	53	2	8	17			
1	D	7	Total	C	Cl	N	O	0	0	0
			80	53	2	8	17			

- Molecule 2 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



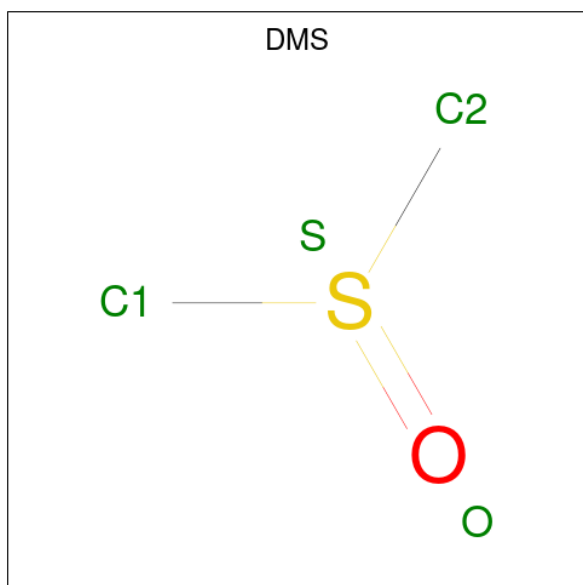
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			4	2	2		
2	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	O	S	0	0
			4	2	1	1		
3	D	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is water.

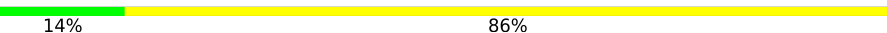
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	18	Total	O	0	0
			18	18		
4	B	15	Total	O	0	0
			15	15		
4	C	19	Total	O	0	0
			19	19		
4	D	15	Total	O	0	0
			15	15		

3 Residue-property plots

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.

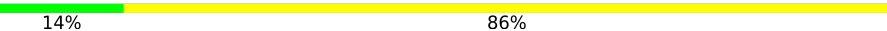
Note EDS was not executed.

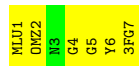
- Molecule 1: VANCOMYCIN AGLYCON

Chain A: 



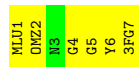
- Molecule 1: VANCOMYCIN AGLYCON

Chain B: 



- Molecule 1: VANCOMYCIN AGLYCON

Chain C: 



- Molecule 1: VANCOMYCIN AGLYCON

Chain D: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	29.48Å 29.48Å 74.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 0.98	Depositor
% Data completeness (in resolution range)	90.9 (8.00-0.98)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL	Depositor
R, R_{free}	0.150 , 0.150	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	411	wwPDB-VP
Average B, all atoms (Å ²)	11.0	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: MLU, DMS, OMZ, GHP, OMY, 3FG, ACY

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	0.60	0/7	0.74	0/8
1	B	0.78	0/7	1.99	0/8
1	C	1.31	0/7	1.56	0/8
1	D	0.92	0/7	1.86	0/8
All	All	0.94	0/28	1.61	0/32

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	80	0	45	0	0
1	B	80	0	46	0	0
1	C	80	0	43	0	0
1	D	80	0	47	1	0
2	A	4	0	3	0	0
2	B	4	0	3	0	0
2	C	4	0	3	0	0
2	D	4	0	3	0	0
3	C	4	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	4	0	6	0	0
4	A	18	0	0	0	0
4	B	15	0	0	0	0
4	C	19	0	0	0	0
4	D	15	0	0	0	0
All	All	411	0	205	1	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 2.

All (1) 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:D:4:GHP:C3	1:D:6:OMY:CL	3.02	0.44

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	1/7 (14%)	0	1 (100%)	0	100	100
1	B	1/7 (14%)	0	1 (100%)	0	100	100
1	C	1/7 (14%)	0	1 (100%)	0	100	100
1	D	1/7 (14%)	0	1 (100%)	0	100	100
All	All	4/28 (14%)	0	4 (100%)	0	100	100

There are no Ramachandran outliers to report.

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	1/1 (100%)	1 (100%)	0	100	100
1	B	1/1 (100%)	1 (100%)	0	100	100
1	C	1/1 (100%)	1 (100%)	0	100	100
1	D	1/1 (100%)	1 (100%)	0	100	100
All	All	4/4 (100%)	4 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

24 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	OMZ	D	2	1	12,14,15	1.56	5 (41%)	17,19,21	2.19	5 (29%)
1	OMZ	B	2	1	12,14,15	1.85	3 (25%)	17,19,21	1.45	3 (17%)
1	OMY	D	6	1	12,14,15	2.01	4 (33%)	17,19,21	2.56	5 (29%)
1	GHP	C	4	1	10,11,12	1.30	1 (10%)	11,14,16	2.65	7 (63%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLU	C	1	1	7,8,9	1.61	1 (14%)	7,9,11	1.62	1 (14%)
1	3FG	C	7	1	12,13,13	1.93	3 (25%)	14,18,18	2.06	3 (21%)
1	OMY	B	6	1	12,14,15	1.89	3 (25%)	17,19,21	2.06	5 (29%)
1	OMY	A	6	1	12,14,15	1.60	3 (25%)	17,19,21	1.57	4 (23%)
1	MLU	B	1	1	7,8,9	2.60	3 (42%)	7,9,11	1.01	1 (14%)
1	GHP	D	4	1	10,11,12	1.30	2 (20%)	11,14,16	2.18	4 (36%)
1	MLU	A	1	1	7,8,9	1.53	1 (14%)	7,9,11	1.09	1 (14%)
1	GHP	A	4	1	10,11,12	2.16	2 (20%)	11,14,16	1.83	5 (45%)
1	GHP	A	5	1	10,11,12	0.97	0	11,14,16	1.25	1 (9%)
1	3FG	D	7	1	12,13,13	1.81	3 (25%)	14,18,18	1.68	4 (28%)
1	OMZ	A	2	1	12,14,15	1.59	2 (16%)	17,19,21	1.77	4 (23%)
1	MLU	D	1	1	7,8,9	2.94	4 (57%)	7,9,11	1.64	2 (28%)
1	GHP	C	5	1	10,11,12	1.32	1 (10%)	11,14,16	1.82	2 (18%)
1	GHP	D	5	1	10,11,12	1.30	2 (20%)	11,14,16	1.36	1 (9%)
1	OMY	C	6	1	12,14,15	1.81	4 (33%)	17,19,21	1.86	3 (17%)
1	GHP	B	5	1	10,11,12	1.30	1 (10%)	11,14,16	1.39	2 (18%)
1	3FG	B	7	1	12,13,13	1.98	3 (25%)	14,18,18	2.08	3 (21%)
1	3FG	A	7	1	12,13,13	1.49	2 (16%)	14,18,18	1.13	0
1	OMZ	C	2	1	12,14,15	1.89	3 (25%)	17,19,21	2.34	5 (29%)
1	GHP	B	4	1	10,11,12	1.54	2 (20%)	11,14,16	1.37	2 (18%)

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
1	OMZ	D	2	1	-	0/9/10/12	0/1/1/1
1	OMZ	B	2	1	-	0/9/10/12	0/1/1/1
1	OMY	D	6	1	-	1/9/10/12	0/1/1/1
1	GHP	C	4	1	-	1/4/6/8	0/1/1/1
1	MLU	C	1	1	-	0/5/8/10	-
1	3FG	C	7	1	-	2/8/8/8	0/1/1/1
1	OMY	B	6	1	-	1/9/10/12	0/1/1/1
1	OMY	A	6	1	-	1/9/10/12	0/1/1/1
1	MLU	B	1	1	-	0/5/8/10	-
1	GHP	D	4	1	-	1/4/6/8	0/1/1/1
1	MLU	A	1	1	-	0/5/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	GHP	A	4	1	-	0/4/6/8	0/1/1/1
1	GHP	A	5	1	-	0/4/6/8	0/1/1/1
1	3FG	D	7	1	-	2/8/8/8	0/1/1/1
1	OMZ	A	2	1	-	0/9/10/12	0/1/1/1
1	MLU	D	1	1	-	0/5/8/10	-
1	GHP	C	5	1	-	0/4/6/8	0/1/1/1
1	GHP	D	5	1	-	0/4/6/8	0/1/1/1
1	OMY	C	6	1	-	1/9/10/12	0/1/1/1
1	GHP	B	5	1	-	0/4/6/8	0/1/1/1
1	3FG	B	7	1	-	2/8/8/8	0/1/1/1
1	3FG	A	7	1	-	4/8/8/8	0/1/1/1
1	OMZ	C	2	1	-	1/9/10/12	0/1/1/1
1	GHP	B	4	1	-	1/4/6/8	0/1/1/1

All (58) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4	GHP	C1-CA	5.66	1.58	1.52
1	D	1	MLU	CN-N	5.63	1.60	1.46
1	B	1	MLU	CN-N	5.29	1.59	1.46
1	C	7	3FG	CG1-CB	4.81	1.46	1.39
1	C	2	OMZ	CE2-CZ	-4.38	1.32	1.39
1	D	6	OMY	CG-CB	4.31	1.58	1.51
1	B	7	3FG	CG1-CB	4.22	1.45	1.39
1	A	2	OMZ	CG-CB	-3.98	1.46	1.51
1	B	6	OMY	CE2-CZ	-3.96	1.32	1.39
1	D	1	MLU	CB-CA	-3.88	1.49	1.53
1	B	2	OMZ	CE2-CZ	-3.79	1.33	1.39
1	D	7	3FG	CB-CA	-3.72	1.48	1.52
1	B	7	3FG	CG2-CD2	-3.71	1.33	1.39
1	D	6	OMY	CE2-CZ	-3.68	1.33	1.39
1	A	6	OMY	CE2-CZ	-3.44	1.33	1.39
1	B	4	GHP	CA-C	3.29	1.56	1.51
1	B	2	OMZ	CZ-CE1	3.15	1.42	1.39
1	D	7	3FG	CG1-CB	3.12	1.43	1.39
1	C	1	MLU	CB-CA	3.12	1.57	1.53
1	C	2	OMZ	OC-CB	-3.10	1.36	1.42
1	A	6	OMY	CG-CB	2.99	1.56	1.51
1	A	7	3FG	CZ-CD2	-2.94	1.34	1.39
1	B	2	OMZ	CD1-CE1	-2.94	1.33	1.38
1	C	6	OMY	CG-CB	2.91	1.56	1.51
1	A	1	MLU	CN-N	2.87	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	4	GHP	C6-C5	-2.80	1.34	1.38
1	C	6	OMY	CE2-CZ	-2.78	1.34	1.39
1	C	6	OMY	CD2-CE2	2.77	1.43	1.38
1	C	6	OMY	OCZ-CZ	2.73	1.41	1.36
1	B	6	OMY	CD2-CG	-2.72	1.34	1.39
1	B	1	MLU	CB-CA	-2.71	1.50	1.53
1	D	6	OMY	ODE-CB	-2.70	1.37	1.42
1	C	7	3FG	CG2-CD2	-2.63	1.35	1.39
1	D	1	MLU	CA-N	-2.63	1.42	1.47
1	C	5	GHP	C2-C1	-2.63	1.35	1.39
1	A	4	GHP	CA-C	2.60	1.55	1.51
1	B	1	MLU	CA-N	-2.60	1.42	1.47
1	D	2	OMZ	CD1-CE1	-2.59	1.34	1.38
1	D	5	GHP	CA-C	2.56	1.55	1.51
1	B	6	OMY	CG-CB	2.50	1.55	1.51
1	B	7	3FG	CB-CA	-2.43	1.49	1.52
1	C	7	3FG	O-C	2.39	1.29	1.22
1	B	5	GHP	CA-C	2.39	1.55	1.51
1	A	7	3FG	CG1-CD1	-2.38	1.35	1.39
1	D	7	3FG	OD1-CD1	2.38	1.42	1.37
1	C	4	GHP	C1-CA	2.33	1.54	1.52
1	B	4	GHP	C3-C4	2.30	1.43	1.39
1	D	2	OMZ	CZ-CE1	2.25	1.41	1.39
1	D	2	OMZ	CE2-CD2	2.24	1.42	1.38
1	A	6	OMY	CD2-CG	-2.18	1.35	1.39
1	D	4	GHP	CA-C	2.17	1.54	1.51
1	D	5	GHP	C6-C5	-2.14	1.35	1.38
1	D	2	OMZ	CG-CB	-2.14	1.48	1.51
1	D	6	OMY	OCZ-CZ	2.12	1.40	1.36
1	D	2	OMZ	CE2-CZ	-2.08	1.35	1.39
1	C	2	OMZ	OH-CZ	2.04	1.40	1.36
1	D	1	MLU	O-C	2.03	1.27	1.20
1	A	2	OMZ	CD2-CG	2.00	1.42	1.39

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	2	OMZ	CD1-CE1-CZ	-7.31	116.66	120.92
1	D	6	OMY	CG-CB-CA	-6.40	103.17	111.58
1	D	6	OMY	CE2-CD2-CG	-5.56	115.64	121.18
1	D	2	OMZ	CE2-CD2-CG	-5.53	115.66	121.18
1	C	6	OMY	CG-CB-CA	-5.10	104.89	111.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	7	3FG	CD2-CG2-CB	5.07	124.46	120.09
1	B	7	3FG	CD2-CG2-CB	5.00	124.40	120.09
1	D	2	OMZ	CD1-CE1-CZ	-4.81	118.11	120.92
1	B	6	OMY	CG-CB-CA	-4.78	105.30	111.58
1	C	5	GHP	C3-C2-C1	4.12	125.29	121.18
1	A	2	OMZ	CE2-CZ-CE1	4.08	122.33	118.49
1	C	7	3FG	CD1-CG1-CB	-3.86	116.75	120.09
1	D	4	GHP	C3-C2-C1	-3.83	117.36	121.18
1	B	6	OMY	CD1-CE1-CZ	-3.83	118.69	120.92
1	D	7	3FG	CD1-CG1-CB	-3.81	116.80	120.09
1	C	4	GHP	C6-C1-C2	3.66	122.84	118.30
1	A	2	OMZ	CD2-CE2-CZ	-3.60	116.90	120.50
1	D	6	OMY	CD2-CG-CD1	3.59	122.90	118.74
1	D	4	GHP	C2-C3-C4	3.52	123.60	119.88
1	B	7	3FG	CD1-CG1-CB	-3.49	117.08	120.09
1	B	2	OMZ	CD1-CE1-CZ	-3.42	118.93	120.92
1	C	5	GHP	C2-C3-C4	-3.37	116.31	119.88
1	C	2	OMZ	CE2-CZ-CE1	3.36	121.65	118.49
1	B	6	OMY	CD2-CG-CD1	3.29	122.55	118.74
1	D	6	OMY	CD2-CE2-CZ	3.27	123.77	120.50
1	A	6	OMY	CE2-CD2-CG	-3.26	117.93	121.18
1	C	6	OMY	CE2-CD2-CG	-3.23	117.96	121.18
1	C	4	GHP	C5-C6-C1	-3.23	117.96	121.18
1	C	4	GHP	C5-C4-C3	-3.17	114.72	119.77
1	B	7	3FG	CG2-CB-CA	3.16	124.64	119.79
1	C	4	GHP	C2-C3-C4	3.16	123.22	119.88
1	D	7	3FG	CZ-CD1-CG1	3.10	124.73	120.47
1	D	4	GHP	C6-C5-C4	3.10	123.16	119.88
1	C	4	GHP	C3-C2-C1	-3.02	118.16	121.18
1	A	6	OMY	CG-CB-CA	-3.00	107.64	111.58
1	C	4	GHP	C6-C5-C4	2.95	123.00	119.88
1	C	4	GHP	C2-C1-CA	-2.94	116.06	120.64
1	D	1	MLU	O-C-CA	-2.91	117.29	124.77
1	A	4	GHP	C5-C6-C1	-2.86	118.33	121.18
1	D	6	OMY	ODE-CB-CA	2.85	113.76	107.49
1	C	7	3FG	CG2-CB-CA	2.82	124.12	119.79
1	D	4	GHP	C5-C4-C3	-2.80	115.30	119.77
1	D	2	OMZ	CD1-CE1-CL	2.78	123.00	118.45
1	A	5	GHP	C3-C2-C1	-2.78	118.41	121.18
1	D	2	OMZ	CD2-CG-CD1	2.69	121.86	118.74
1	B	6	OMY	CE2-CZ-CE1	2.67	121.00	118.49
1	A	6	OMY	CD2-CG-CD1	2.65	121.81	118.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	4	GHP	C5-C4-C3	-2.62	115.60	119.77
1	C	1	MLU	O-C-CA	-2.60	118.07	124.77
1	D	5	GHP	C2-C3-C4	-2.58	117.15	119.88
1	A	4	GHP	C6-C1-C2	2.55	121.47	118.30
1	B	2	OMZ	CE2-CD2-CG	-2.48	118.71	121.18
1	B	5	GHP	C1-CA-C	-2.42	105.30	112.09
1	C	2	OMZ	CE1-CD1-CG	2.37	123.57	120.28
1	C	2	OMZ	O-C-CA	-2.37	118.69	124.77
1	B	6	OMY	CE2-CD2-CG	-2.35	118.84	121.18
1	A	4	GHP	C6-C5-C4	2.25	122.26	119.88
1	A	4	GHP	C5-C4-C3	-2.20	116.27	119.77
1	C	6	OMY	ODE-CB-CA	2.19	112.30	107.49
1	A	4	GHP	C6-C1-CA	-2.15	117.30	120.64
1	B	4	GHP	C2-C3-C4	2.14	122.14	119.88
1	C	2	OMZ	CG-CB-CA	-2.14	108.78	111.58
1	D	7	3FG	CG2-CB-CA	2.13	123.06	119.79
1	D	7	3FG	OD1-CD1-CZ	-2.13	114.29	119.85
1	B	1	MLU	O-C-CA	-2.13	119.30	124.77
1	A	6	OMY	CD2-CE2-CZ	2.12	122.62	120.50
1	A	2	OMZ	CD1-CE1-CL	2.10	121.89	118.45
1	D	1	MLU	CB-CA-C	-2.10	107.76	110.99
1	B	5	GHP	C2-C3-C4	-2.07	117.69	119.88
1	B	2	OMZ	CE2-CZ-CE1	2.05	120.42	118.49
1	A	1	MLU	O-C-CA	-2.04	119.52	124.77
1	A	2	OMZ	CD1-CE1-CZ	-2.04	119.73	120.92
1	D	2	OMZ	OC-CB-CG	2.00	115.56	111.20

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	2	OMZ	O-C-CA-CB
1	A	6	OMY	O-C-CA-CB
1	B	6	OMY	O-C-CA-CB
1	D	6	OMY	O-C-CA-CB
1	A	7	3FG	O-C-CA-CB
1	A	7	3FG	OXT-C-CA-CB
1	B	7	3FG	C-CA-CB-CG1
1	B	7	3FG	C-CA-CB-CG2
1	D	7	3FG	C-CA-CB-CG1
1	C	7	3FG	C-CA-CB-CG2
1	D	7	3FG	C-CA-CB-CG2

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Mol	Chain	Res	Type	Atoms
1	B	4	GHP	C6-C1-CA-C
1	C	4	GHP	C6-C1-CA-C
1	D	4	GHP	C6-C1-CA-C
1	A	7	3FG	C-CA-CB-CG1
1	C	7	3FG	C-CA-CB-CG1
1	C	6	OMY	O-C-CA-CB
1	A	7	3FG	OXT-C-CA-N

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	6	OMY	1	0
1	D	4	GHP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
3	DMS	C	12	-	3,3,3	0.53	0	3,3,3	0.96	0
2	ACY	D	11	-	3,3,3	1.24	0	3,3,3	0.93	0
2	ACY	C	11	-	3,3,3	0.91	0	3,3,3	0.74	0
2	ACY	B	11	-	3,3,3	1.62	1 (33%)	3,3,3	1.93	1 (33%)
3	DMS	D	12	-	3,3,3	0.36	0	3,3,3	0.35	0
2	ACY	A	11	-	3,3,3	1.04	0	3,3,3	0.78	0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	11	ACY	O-C	2.55	1.33	1.22

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	11	ACY	OXT-C-CH3	2.60	125.96	115.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.