Full wwPDB X-ray Structure Validation Report

Sep 7, 2020 – 02:24 PM BST

PDB ID	:	2ADW
Title	:	Crystal structure of Echinomycin-(ACGTACGT)2 solved by SAD
Authors	:	Cuesta-Seijo, J.A.; Sheldrick, G.M.
Deposited on	:	2005-07-21
Resolution	:	1.60 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 following versions of software and data (see references (1)) were used in the production of this report:

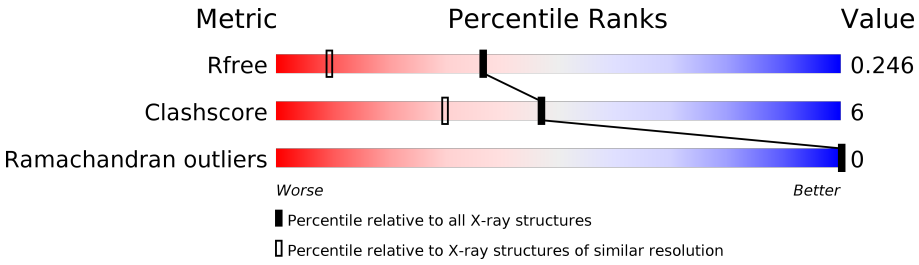
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.14.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.14.2

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 1.60 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))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)

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 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%

Mol	Chain	Length	Quality of chain
1	A	8	38% 50% 13%
1	C	8	38% 50% 13%
1	E	8	13% 88%
1	G	8	13% 75% 13%
2	H	10	30% 50% 20%
2	I	10	30% 60% 10%
2	J	10	40% 30% 30%
2	K	10	50% 50%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 1826 atoms, of which 673 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 DNA chain called 5'-D(*AP*CP*GP*TP*AP*CP*GP*T)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	8	Total	C	H	N	O	P	0	2	0
			275	85	100	30	52	8			
1	C	8	Total	C	H	N	O	P	0	5	0
			335	103	125	30	67	10			
1	E	8	Total	C	H	N	O	P	0	0	0
			251	78	90	30	46	7			
1	G	8	Total	C	H	N	O	P	0	0	0
			251	78	90	30	46	7			

- Molecule 2 is a protein called ECHINOMYCIN.

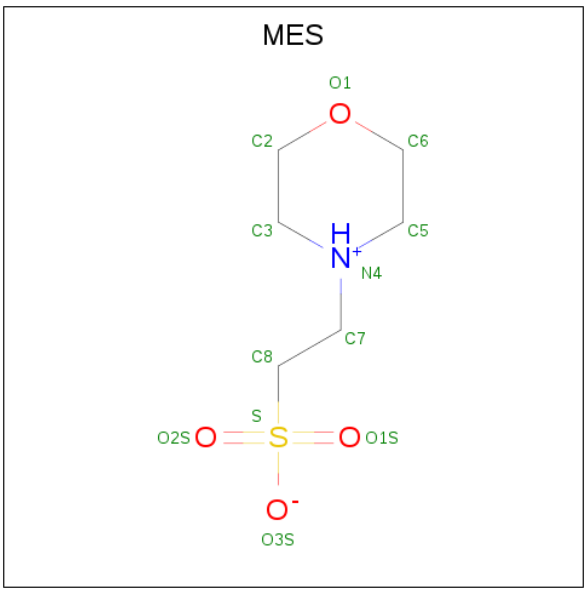
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	H	8	Total	C	H	N	O	S	0	2	0
			122	40	56	10	12	4			
2	I	8	Total	C	H	N	O	S	0	2	0
			122	40	56	10	12	4			
2	J	8	Total	C	H	N	O	S	0	2	0
			122	40	56	10	12	4			
2	K	8	Total	C	H	N	O	S	0	0	0
			100	32	48	8	10	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	3	N2C	NCY	microheterogeneity	NOR NOR01126
H	7	NCY	N2C	microheterogeneity	NOR NOR01126
I	3	N2C	NCY	microheterogeneity	NOR NOR01126
I	7	NCY	N2C	microheterogeneity	NOR NOR01126
J	3	N2C	NCY	microheterogeneity	NOR NOR01126
J	7	NCY	N2C	microheterogeneity	NOR NOR01126

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES)

(formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	C	1	Total	C	H	N	O	S	0	0
			24	6	12	1	4	1		

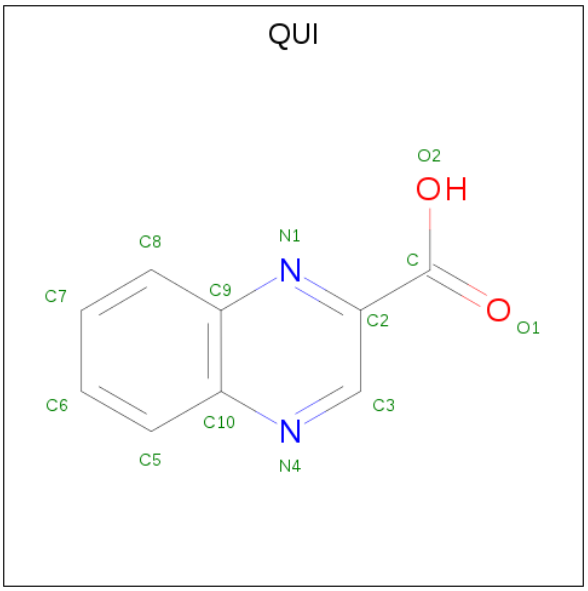
- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total	Ni	0	1
			1	1		

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

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

- Molecule 6 is 2-CARBOXYQUINOXALINE (three-letter code: QUI) (formula: $C_9H_6N_2O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	1	Total C H N O 17 9 5 2 1	0	0
6	H	1	Total C H N O 17 9 5 2 1	0	0
6	I	1	Total C H N O 17 9 5 2 1	0	0
6	I	1	Total C H N O 17 9 5 2 1	0	0
6	J	1	Total C H N O 17 9 5 2 1	0	0
6	J	1	Total C H N O 17 9 5 2 1	0	0
6	K	1	Total C H N O 17 9 5 2 1	0	0
6	K	1	Total C H N O 17 9 5 2 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	15	Total O 15 15	0	0
7	C	10	Total O 10 10	0	0
7	E	35	Total O 35 35	0	0
7	G	9	Total O 9 9	0	0

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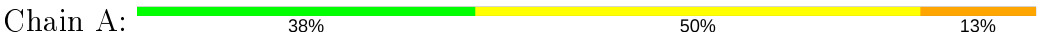
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	H	4	Total O 4 4	0	0
7	I	2	Total O 2 2	0	0
7	J	5	Total O 5 5	0	0
7	K	6	Total O 6 6	0	0

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.

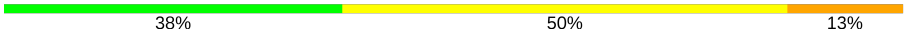
- Molecule 1: 5'-D(*AP*CP*GP*TP*AP*CP*GP*T)-3'

Chain A:



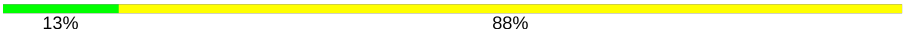
- Molecule 1: 5'-D(*AP*CP*GP*TP*AP*CP*GP*T)-3'

Chain C:



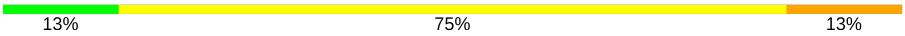
- Molecule 1: 5'-D(*AP*CP*GP*TP*AP*CP*GP*T)-3'

Chain E:



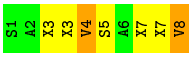
- Molecule 1: 5'-D(*AP*CP*GP*TP*AP*CP*GP*T)-3'

Chain G:



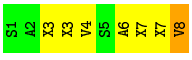
- Molecule 2: ECHINOMYCIN

Chain H:



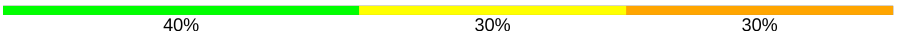
- Molecule 2: ECHINOMYCIN

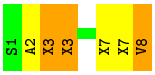
Chain I:



- Molecule 2: ECHINOMYCIN

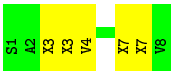
Chain J:





- Molecule 2: ECHINOMYCIN

Chain K:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α, β, γ	80.90Å 80.90Å 48.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.60 28.93 – 1.60	Depositor EDS
% Data completeness (in resolution range)	97.6 (30.00-1.60) 97.7 (28.93-1.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.75 (at 1.60Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.180 , 0.221 0.214 , 0.246	Depositor DCC
R_{free} test set	26858 reflections (9.98%)	wwPDB-VP
Wilson B-factor (Å^2)	16.0	Xtriage
Anisotropy	0.991	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 59.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	1826	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.75% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NI, ZN, NCY, N2C, DSN, MVA, MES, QUI

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	0.85	0/222	2.38	16/341 (4.7%)
1	C	0.81	0/292	2.09	9/449 (2.0%)
1	E	0.96	0/180	2.38	11/276 (4.0%)
1	G	0.90	0/180	2.54	11/276 (4.0%)
2	H	0.27	0/8	0.97	0/8
2	I	0.38	0/8	0.79	0/8
2	J	0.34	0/8	1.81	0/8
2	K	0.50	0/8	0.89	0/8
All	All	0.86	0/906	2.30	47/1374 (3.4%)

There are no bond length outliers.

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	204	DT	O4'-C1'-N1	-13.70	98.41	108.00
1	A	4	DT	O4'-C1'-N1	-12.87	98.99	108.00
1	G	304	DT	O4'-C1'-N1	-12.44	99.29	108.00
1	A	2[A]	DC	O4'-C1'-N1	-9.74	101.18	108.00
1	A	2[B]	DC	O4'-C1'-N1	-9.74	101.18	108.00
1	G	306	DC	O4'-C1'-N1	-9.69	101.21	108.00
1	G	301	DA	O4'-C1'-N9	-9.64	101.25	108.00
1	E	206	DC	O4'-C1'-N1	-9.63	101.26	108.00
1	G	303	DG	O4'-C1'-N9	9.32	114.53	108.00
1	E	205	DA	N1-C6-N6	7.86	123.31	118.60
1	E	202	DC	P-O3'-C3'	7.45	128.64	119.70
1	C	101[A]	DA	O4'-C1'-N9	-7.17	102.98	108.00
1	C	101[B]	DA	O4'-C1'-N9	-7.17	102.98	108.00
1	C	108	DT	O4'-C1'-N1	-6.80	103.24	108.00
1	C	106[A]	DC	O4'-C1'-N1	-6.77	103.26	108.00
1	C	106[B]	DC	O4'-C1'-N1	-6.77	103.26	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	5	DA	C2-N3-C4	-6.52	107.34	110.60
1	A	1[A]	DA	C2-N3-C4	-6.50	107.35	110.60
1	A	1[B]	DA	C2-N3-C4	-6.50	107.35	110.60
1	G	308	DT	N3-C4-O4	6.46	123.78	119.90
1	A	5	DA	O4'-C4'-C3'	-6.27	101.99	104.50
1	G	305	DA	C2-N3-C4	-6.24	107.48	110.60
1	G	305	DA	N1-C6-N6	6.20	122.32	118.60
1	A	5	DA	N3-C4-C5	6.09	131.06	126.80
1	C	107	DG	N1-C6-O6	6.08	123.55	119.90
1	A	6	DC	O4'-C4'-C3'	-5.97	102.11	104.50
1	C	107	DG	C2-N3-C4	-5.89	108.95	111.90
1	C	106[A]	DC	N3-C4-C5	5.75	124.20	121.90
1	C	106[B]	DC	N3-C4-C5	5.75	124.20	121.90
1	E	205	DA	O4'-C1'-N9	-5.71	104.01	108.00
1	G	305	DA	C5-C6-N1	-5.62	114.89	117.70
1	A	6	DC	C4-C5-C6	-5.52	114.64	117.40
1	G	308	DT	C4-C5-C7	-5.45	115.73	119.00
1	E	203	DG	C5-C6-O6	5.45	131.87	128.60
1	G	307	DG	N3-C4-C5	5.44	131.32	128.60
1	G	307	DG	O4'-C1'-N9	5.39	111.78	108.00
1	E	204	DT	C2-N3-C4	-5.33	124.00	127.20
1	E	208	DT	C6-C5-C7	5.32	126.09	122.90
1	A	4	DT	N3-C4-O4	5.30	123.08	119.90
1	A	1[A]	DA	N1-C6-N6	5.27	121.76	118.60
1	A	1[B]	DA	N1-C6-N6	5.27	121.76	118.60
1	E	201	DA	C1'-O4'-C4'	-5.26	104.84	110.10
1	A	2[A]	DC	C6-N1-C2	5.16	122.36	120.30
1	A	2[B]	DC	C6-N1-C2	5.16	122.36	120.30
1	A	5	DA	C8-N9-C4	5.15	107.86	105.80
1	E	204	DT	C5-C4-O4	-5.07	121.35	124.90
1	E	202	DC	O4'-C1'-N1	-5.02	104.49	108.00

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	175	100	93	1	0
1	C	210	125	108	2	0
1	E	161	90	92	0	0
1	G	161	90	92	1	0
2	H	66	56	62	3	0
2	I	66	56	60	2	0
2	J	66	56	60	2	0
2	K	52	48	49	0	0
3	C	12	12	13	0	0
4	E	1	0	0	0	0
5	E	1	0	0	0	0
6	H	24	10	10	1	0
6	I	24	10	10	0	0
6	J	24	10	10	0	0
6	K	24	10	10	0	0
7	A	15	0	0	0	0
7	C	10	0	0	0	0
7	E	35	0	0	0	0
7	G	9	0	0	0	0
7	H	4	0	0	0	0
7	I	2	0	0	0	0
7	J	5	0	0	0	0
7	K	6	0	0	0	0
All	All	1153	673	669	9	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 6.

All (9) 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:C:103[A]:DG:O4'	2:I:6:ALA:HB2	2.08	0.53
2:H:4:MVA:HG13	2:H:4:MVA:O	2.11	0.50
1:A:1[B]:DA:H2'	6:H:9:QUI:C7	2.45	0.47
2:J:8:MVA:HG13	2:J:8:MVA:O	2.15	0.46
2:J:2:ALA:HA	2:J:3[A]:N2C:HN1	1.81	0.43
2:I:8:MVA:HN2	2:I:8:MVA:HG22	2.00	0.43
1:G:305:DA:N3	1:G:305:DA:H2'	2.34	0.42
1:C:108:DT:O4'	2:H:5:DSN:HA	2.20	0.42
2:H:8:MVA:O	2:H:8:MVA:HG13	2.20	0.41

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	
2	H	2/10 (20%)	2 (100%)	0	0	100	100
2	I	2/10 (20%)	2 (100%)	0	0	100	100
2	J	2/10 (20%)	2 (100%)	0	0	100	100
2	K	2/10 (20%)	2 (100%)	0	0	100	100
All	All	8/40 (20%)	8 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

5.3.3 RNA

There are no RNA molecules in this entry.

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

30 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	$\#\|Z\| > 2$
2	MVA	J	8	2	6,7,8	0.56	0	7,8,10	1.70	1 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	N2C	J	3[A]	2	5,6,8	1.87	1 (20%)	5,6,9	0.84	0
2	NCY	J	7[A]	2	5,6,7	2.32	1 (20%)	5,6,8	2.05	2 (40%)
2	N2C	H	3[A]	2	5,6,8	2.62	1 (20%)	5,6,9	1.84	2 (40%)
2	N2C	J	7[B]	2	5,6,8	1.75	1 (20%)	5,6,9	1.93	1 (20%)
2	MVA	H	4	2	6,7,8	0.34	0	7,8,10	1.12	1 (14%)
2	MVA	J	4	2	6,7,8	0.21	0	7,8,10	0.70	0
2	NCY	J	3[B]	2	5,6,7	2.45	1 (20%)	5,6,8	2.97	1 (20%)
2	NCY	H	7[A]	2	5,6,7	1.39	1 (20%)	5,6,8	1.89	1 (20%)
2	N2C	I	7[B]	2	5,6,8	1.80	1 (20%)	5,6,9	1.95	1 (20%)
2	MVA	K	4	2	6,7,8	0.29	0	7,8,10	1.34	2 (28%)
2	N2C	K	3	2	5,6,8	1.60	1 (20%)	5,6,9	2.15	3 (60%)
2	MVA	H	8	2	6,7,8	0.32	0	7,8,10	1.75	1 (14%)
2	NCY	I	7[A]	2	5,6,7	2.51	1 (20%)	5,6,8	1.81	2 (40%)
2	N2C	I	3[A]	2	5,6,8	2.10	1 (20%)	5,6,9	1.82	1 (20%)
2	MVA	I	4	2	6,7,8	0.67	0	7,8,10	3.12	4 (57%)
2	NCY	H	3[B]	2	5,6,7	1.50	1 (20%)	5,6,8	1.59	1 (20%)
2	MVA	I	8	2	6,7,8	0.42	0	7,8,10	1.51	3 (42%)
2	NCY	I	3[B]	2	5,6,7	2.23	1 (20%)	5,6,8	1.30	1 (20%)
2	MVA	K	8	2	6,7,8	0.48	0	7,8,10	1.04	0
2	NCY	K	7	2	5,6,7	2.38	1 (20%)	5,6,8	2.60	2 (40%)
2	N2C	H	7[B]	2	5,6,8	2.39	1 (20%)	5,6,9	1.79	1 (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
2	MVA	J	8	2	-	1/6/8/10	-
2	N2C	J	3[A]	2	-	1/3/6/9	-
2	NCY	J	7[A]	2	-	2/3/6/8	-
2	N2C	H	3[A]	2	-	0/3/6/9	-
2	N2C	J	7[B]	2	-	2/3/6/9	-
2	MVA	H	4	2	-	1/6/8/10	-
2	MVA	J	4	2	-	2/6/8/10	-
2	NCY	J	3[B]	2	-	2/3/6/8	-
2	NCY	H	7[A]	2	-	2/3/6/8	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	N2C	I	7[B]	2	-	2/3/6/9	-
2	MVA	K	4	2	-	2/6/8/10	-
2	N2C	K	3	2	-	2/3/6/9	-
2	MVA	H	8	2	-	1/6/8/10	-
2	NCY	I	7[A]	2	-	0/3/6/8	-
2	N2C	I	3[A]	2	-	2/3/6/9	-
2	MVA	I	4	2	-	2/6/8/10	-
2	NCY	H	3[B]	2	-	2/3/6/8	-
2	MVA	I	8	2	-	1/6/8/10	-
2	NCY	I	3[B]	2	-	0/3/6/8	-
2	MVA	K	8	2	-	5/6/8/10	-
2	NCY	K	7	2	-	0/3/6/8	-
2	N2C	H	7[B]	2	-	0/3/6/9	-

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	3[A]	N2C	CB-CA	-5.72	1.46	1.53
2	I	7[A]	NCY	CB-CA	-5.31	1.47	1.53
2	J	3[B]	NCY	CB-CA	-5.27	1.47	1.53
2	H	7[B]	N2C	CB-CA	-5.24	1.47	1.53
2	J	7[A]	NCY	CB-CA	-5.08	1.47	1.53
2	K	7	NCY	CB-CA	-4.99	1.47	1.53
2	I	3[B]	NCY	CB-CA	-4.75	1.47	1.53
2	I	3[A]	N2C	CB-CA	4.17	1.57	1.53
2	J	3[A]	N2C	CB-CA	3.72	1.57	1.53
2	J	7[B]	N2C	CB-CA	3.63	1.57	1.53
2	I	7[B]	N2C	CB-CA	3.40	1.56	1.53
2	K	3	N2C	CB-CA	3.36	1.56	1.53
2	H	3[B]	NCY	CB-CA	3.00	1.56	1.53
2	H	7[A]	NCY	CB-CA	2.81	1.56	1.53

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	J	3[B]	NCY	CA-CB-SG	6.36	121.35	114.19
2	I	4	MVA	CB-CA-C	-4.97	106.81	113.04
2	K	7	NCY	CA-CB-SG	4.93	119.73	114.19
2	I	4	MVA	CG2-CB-CA	-4.71	104.00	111.21
2	J	8	MVA	CB-CA-C	-4.29	107.66	113.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	I	4	MVA	CB-CA-N	4.02	116.40	111.17
2	I	7[B]	N2C	CA-CB-SG	-3.98	109.72	114.19
2	J	7[A]	NCY	CA-CB-SG	3.87	118.55	114.19
2	H	7[A]	NCY	CA-CB-SG	-3.73	110.01	114.19
2	J	7[B]	N2C	CA-CB-SG	-3.56	110.20	114.19
2	H	7[B]	N2C	CA-CB-SG	3.50	118.14	114.19
2	I	3[A]	N2C	CA-CB-SG	-3.49	110.27	114.19
2	H	8	MVA	CB-CA-C	-3.25	108.97	113.04
2	I	7[A]	NCY	CA-CB-SG	3.16	117.75	114.19
2	K	3	N2C	O-C-CA	-3.01	116.88	124.78
2	H	3[A]	N2C	CA-CB-SG	2.99	117.56	114.19
2	H	3[B]	NCY	CA-CB-SG	-2.83	111.01	114.19
2	H	4	MVA	CB-CA-C	-2.66	109.71	113.04
2	H	3[A]	N2C	O-C-CA	-2.61	117.95	124.78
2	I	8	MVA	CB-CA-N	2.58	114.52	111.17
2	I	3[B]	NCY	O-C-CA	-2.57	118.04	124.78
2	K	3	N2C	CN-N-CA	2.47	121.32	113.64
2	I	7[A]	NCY	O-C-CA	-2.44	118.39	124.78
2	K	7	NCY	O-C-CA	-2.43	118.41	124.78
2	K	3	N2C	CB-CA-N	2.39	114.67	111.19
2	I	8	MVA	CG2-CB-CA	-2.20	107.83	111.21
2	I	4	MVA	CG2-CB-CG1	2.17	116.65	110.59
2	K	4	MVA	CB-CA-C	-2.12	110.38	113.04
2	K	4	MVA	CG2-CB-CA	-2.06	108.05	111.21
2	I	8	MVA	CB-CA-C	-2.03	110.49	113.04
2	J	7[A]	NCY	O-C-CA	-2.02	119.49	124.78

There are no chirality outliers.

All (32) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	J	3[A]	N2C	N-CA-CB-SG
2	J	7[A]	NCY	N-CA-CB-SG
2	J	7[B]	N2C	N-CA-CB-SG
2	H	4	MVA	CB-CA-N-CN
2	J	4	MVA	CB-CA-N-CN
2	J	3[B]	NCY	N-CA-CB-SG
2	H	7[A]	NCY	N-CA-CB-SG
2	I	7[B]	N2C	N-CA-CB-SG
2	K	3	N2C	N-CA-CB-SG
2	K	3	N2C	C-CA-CB-SG
2	H	8	MVA	CB-CA-N-CN

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Mol	Chain	Res	Type	Atoms
2	I	3[A]	N2C	N-CA-CB-SG
2	I	4	MVA	CB-CA-N-CN
2	H	3[B]	NCY	N-CA-CB-SG
2	I	8	MVA	CB-CA-N-CN
2	K	8	MVA	N-CA-CB-CG1
2	K	8	MVA	N-CA-CB-CG2
2	K	8	MVA	C-CA-CB-CG1
2	I	4	MVA	C-CA-CB-CG1
2	K	8	MVA	C-CA-CB-CG2
2	J	4	MVA	N-CA-CB-CG2
2	K	4	MVA	N-CA-CB-CG2
2	J	7[A]	NCY	C-CA-CB-SG
2	J	7[B]	N2C	C-CA-CB-SG
2	J	3[B]	NCY	C-CA-CB-SG
2	H	7[A]	NCY	C-CA-CB-SG
2	I	7[B]	N2C	C-CA-CB-SG
2	I	3[A]	N2C	C-CA-CB-SG
2	H	3[B]	NCY	C-CA-CB-SG
2	J	8	MVA	CB-CA-N-CN
2	K	4	MVA	CB-CA-N-CN
2	K	8	MVA	CB-CA-N-CN

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	8	MVA	1	0
2	J	3[A]	N2C	1	0
2	H	4	MVA	1	0
2	H	8	MVA	1	0
2	I	8	MVA	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	QUI	H	0	2	13,13,14	0.75	0	17,17,19	1.80	5 (29%)
6	QUI	I	9	2	13,13,14	0.76	0	17,17,19	1.82	4 (23%)
6	QUI	J	0	2	13,13,14	0.86	0	17,17,19	1.98	5 (29%)
3	MES	C	406	-	12,12,12	0.38	0	14,16,16	1.62	2 (14%)
6	QUI	K	0	2	13,13,14	0.82	0	17,17,19	0.91	0
6	QUI	K	9	2	13,13,14	0.83	0	17,17,19	0.97	0
6	QUI	I	0	2	13,13,14	0.70	0	17,17,19	1.49	2 (11%)
6	QUI	J	9	2	13,13,14	0.87	0	17,17,19	1.87	3 (17%)
6	QUI	H	9	2	13,13,14	0.77	0	17,17,19	1.34	2 (11%)

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	QUI	H	0	2	-	0/2/2/4	0/2/2/2
6	QUI	I	9	2	-	0/2/2/4	0/2/2/2
6	QUI	J	0	2	-	0/2/2/4	0/2/2/2
3	MES	C	406	-	-	0/6/14/14	0/1/1/1
6	QUI	K	0	2	-	0/2/2/4	0/2/2/2
6	QUI	K	9	2	-	0/2/2/4	0/2/2/2
6	QUI	I	0	2	-	0/2/2/4	0/2/2/2
6	QUI	J	9	2	-	0/2/2/4	0/2/2/2
6	QUI	H	9	2	-	0/2/2/4	0/2/2/2

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	J	9	QUI	C-C2-N1	5.10	119.66	114.66
3	C	406	MES	O1S-S-C8	-4.62	101.35	106.92
6	J	0	QUI	C3-C2-N1	4.62	124.33	121.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	J	0	QUI	C2-C3-N4	-4.19	120.34	123.63
6	J	9	QUI	C3-C2-C	-4.11	118.22	121.85
6	H	0	QUI	C3-C2-C	-3.80	118.50	121.85
6	H	0	QUI	C3-C2-N1	3.77	123.76	121.25
6	I	9	QUI	C3-C2-C	-3.59	118.68	121.85
6	J	0	QUI	C3-C2-C	-3.48	118.78	121.85
6	H	9	QUI	C-C2-N1	3.45	118.04	114.66
6	I	9	QUI	C-C2-N1	3.30	117.90	114.66
6	I	9	QUI	C3-C2-N1	3.25	123.41	121.25
6	H	0	QUI	C2-C3-N4	-3.12	121.18	123.63
6	H	0	QUI	C-C2-N1	3.12	117.72	114.66
6	I	0	QUI	C-C2-N1	2.83	117.43	114.66
6	I	9	QUI	C2-N1-C9	-2.72	115.36	117.83
6	J	9	QUI	C2-N1-C9	-2.67	115.41	117.83
6	I	0	QUI	C2-N1-C9	-2.61	115.46	117.83
6	H	9	QUI	C3-C2-C	-2.40	119.73	121.85
6	J	0	QUI	C-C2-N1	2.25	116.87	114.66
6	H	0	QUI	C2-N1-C9	-2.24	115.80	117.83
3	C	406	MES	O1-C2-C3	2.15	116.53	111.80
6	J	0	QUI	C2-N1-C9	-2.03	115.98	117.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	H	9	QUI	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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.