



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 01:38 PM UTC

PDB ID : 8GJ4 / pdb_00008gj4
Title : A1 Tei: Adenylation domain 1 core construct from teicoplanin biosynthesis
Authors : Hansen, M.H.; Cryle, M.J.
Deposited on : 2023-03-14
Resolution : 1.81 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

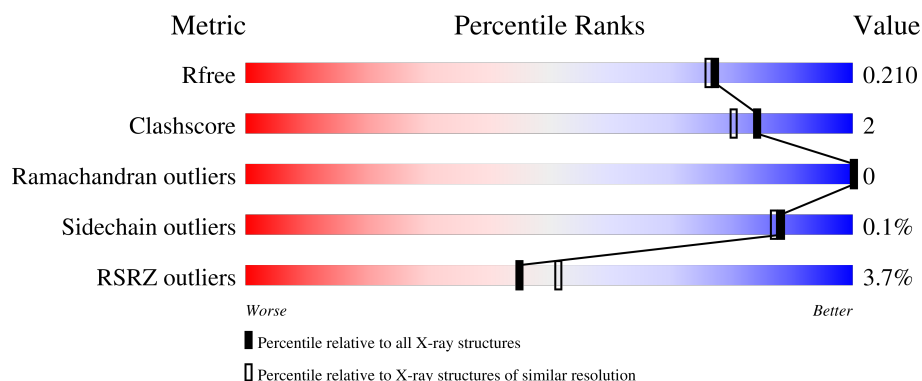
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.81 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}	180053	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	399	5% 88% 7% 5%
1	B	399	2% 94% • •
2	C	69	4% 96% • •
2	D	69	9% 81% 7% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13882 atoms, of which 6745 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 Non-ribosomal peptide synthetase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	380	Total	C	H	N	O	S	0	6	0
			5693	1780	2859	526	520	8			
1	B	387	Total	C	H	N	O	S	0	8	0
			5825	1820	2927	537	533	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	MET	-	initiating methionine	UNP Q70AZ9
A	399	GLY	-	expression tag	UNP Q70AZ9
A	400	SER	-	expression tag	UNP Q70AZ9
A	401	HIS	-	expression tag	UNP Q70AZ9
A	402	HIS	-	expression tag	UNP Q70AZ9
A	403	HIS	-	expression tag	UNP Q70AZ9
A	404	HIS	-	expression tag	UNP Q70AZ9
A	405	HIS	-	expression tag	UNP Q70AZ9
A	406	HIS	-	expression tag	UNP Q70AZ9
B	8	MET	-	initiating methionine	UNP Q70AZ9
B	399	GLY	-	expression tag	UNP Q70AZ9
B	400	SER	-	expression tag	UNP Q70AZ9
B	401	HIS	-	expression tag	UNP Q70AZ9
B	402	HIS	-	expression tag	UNP Q70AZ9
B	403	HIS	-	expression tag	UNP Q70AZ9
B	404	HIS	-	expression tag	UNP Q70AZ9
B	405	HIS	-	expression tag	UNP Q70AZ9
B	406	HIS	-	expression tag	UNP Q70AZ9

- Molecule 2 is a protein called MbtH-like short polypeptide.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	68	Total	C	H	N	O	S	0	3	0
			1039	341	497	91	109	1			

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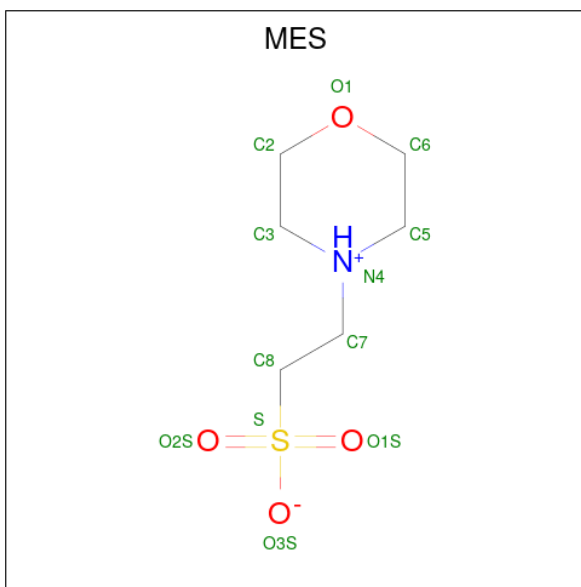
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	D	61	Total	C	H	N	O	S	0	1	0
			917	304	436	82	94	1			

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			9	3	3	3		
3	B	1	Total	C	H	O	0	0
			9	3	3	3		
3	B	1	Total	C	H	O	0	0
			13	3	7	3		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	S	
			25	6	13	1	4	1	

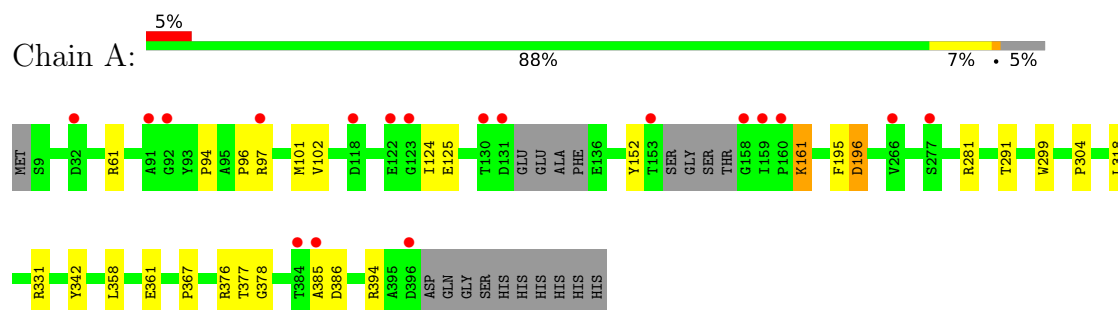
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	126	Total	O		
			126	126	0	0
5	B	178	Total	O		
			178	178	0	0
5	C	27	Total	O		
			27	27	0	0
5	D	21	Total	O		
			21	21	0	0

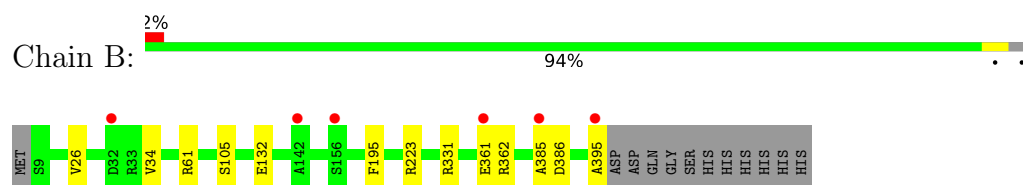
3 Residue-property plots [i](#)

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 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.

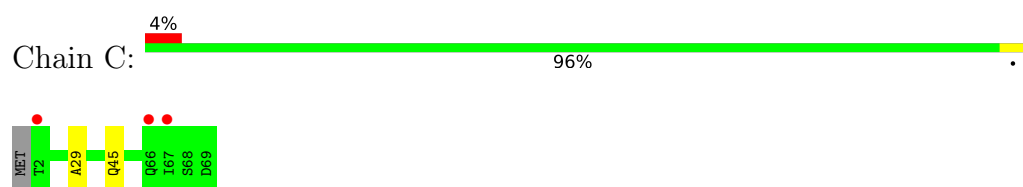
- Molecule 1: Non-ribosomal peptide synthetase



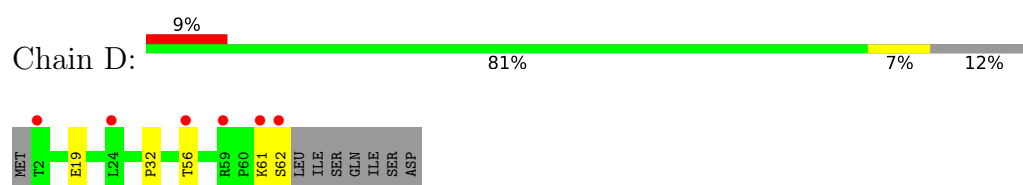
- Molecule 1: Non-ribosomal peptide synthetase



- Molecule 2: MbtH-like short polypeptide



- Molecule 2: MbtH-like short polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	42.23Å 124.00Å 176.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.05 – 1.81 44.05 – 1.81	Depositor EDS
% Data completeness (in resolution range)	98.1 (44.05-1.81) 98.7 (44.05-1.81)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 1.81Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.185 , 0.210 0.185 , 0.210	Depositor DCC
R_{free} test set	4305 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.603	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 33.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13882	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: GOL, MES

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	0.31	0/2916	0.59	2/3975 (0.1%)
1	B	0.35	0/2988	0.57	1/4076 (0.0%)
2	C	0.59	0/569	0.71	1/779 (0.1%)
2	D	0.40	0/500	0.65	1/685 (0.1%)
All	All	0.36	0/6973	0.59	5/9515 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	195	PHE	N-CA-C	8.01	121.36	110.55
2	D	56	THR	N-CA-C	7.89	119.97	111.36
1	A	195	PHE	N-CA-C	7.45	120.61	110.55
1	A	161	LYS	CA-CB-CG	6.08	126.26	114.10
2	C	29	ALA	N-CA-C	5.51	118.43	110.28

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	A	2834	2859	2829	22	4
1	B	2898	2927	2900	8	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	542	497	489	0	2
2	D	481	436	436	3	0
3	A	6	3	8	0	0
3	B	12	10	16	1	0
4	A	12	13	12	0	0
5	A	126	0	0	6	0
5	B	178	0	0	4	0
5	C	27	0	0	0	0
5	D	21	0	0	0	0
All	All	7137	6745	6690	31	4

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 (31) 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:377:THR:O	5:A:701:HOH:O	1.80	0.99
1:A:378:GLY:HA3	5:A:701:HOH:O	1.72	0.89
1:B:331:ARG:NH2	5:B:701:HOH:O	2.06	0.87
1:A:378:GLY:CA	5:A:701:HOH:O	2.22	0.85
1:A:378:GLY:C	5:A:701:HOH:O	2.32	0.73
1:A:299:TRP:CD2	1:A:318:LEU:HD22	2.24	0.72
1:B:223[B]:ARG:NH1	5:B:703:HOH:O	2.24	0.71
1:B:361:GLU:HG2	1:B:362[B]:ARG:HG3	1.75	0.67
1:A:385:ALA:HB3	1:B:385:ALA:HB3	1.81	0.60
1:A:281:ARG:NH2	5:A:704:HOH:O	2.36	0.56
1:A:386:ASP:OD2	1:B:386:ASP:HB2	2.06	0.55
1:A:367:PRO:HA	2:D:32:PRO:HB3	1.88	0.55
1:A:61:ARG:N	1:A:61:ARG:HD3	2.22	0.54
1:A:161:LYS:HD2	1:A:358:LEU:CD2	2.40	0.51
3:B:602:GOL:H11	5:B:706:HOH:O	2.10	0.51
2:D:19:GLU:HA	2:D:19:GLU:OE1	2.12	0.50
1:A:299:TRP:CE2	1:A:318:LEU:HD22	2.47	0.49
1:A:102:VAL:HG11	1:A:124:ILE:HG13	1.96	0.48
1:B:61:ARG:HD3	1:B:105:SER:O	2.14	0.48
1:A:161:LYS:HD2	1:A:358:LEU:HD21	1.95	0.48
1:B:395:ALA:O	5:B:702:HOH:O	2.20	0.47
1:A:281:ARG:HA	1:A:304:PRO:HB3	1.98	0.45
1:A:394:ARG:NH1	5:A:701:HOH:O	2.46	0.43
1:A:196:ASP:OD2	1:A:291:THR:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:TYR:HA	1:A:161:LYS:O	2.19	0.42
1:A:97:ARG:NH1	1:A:101:MET:SD	2.93	0.42
2:D:61:LYS:O	2:D:62:SER:C	2.61	0.42
1:A:342:TYR:HE2	1:A:376:ARG:HG2	1.85	0.41
1:A:361:GLU:O	1:A:376:ARG:HD3	2.20	0.41
1:A:94:PRO:HB2	1:A:96:PRO:HD2	2.02	0.41
1:B:26:VAL:HG13	1:B:34:VAL:HG13	2.03	0.40

All (4) 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:A:125:GLU:OE2	2:C:45:GLN:HE21[4_565]	1.19	0.41
1:A:125:GLU:OE2	2:C:45:GLN:NE2[4_565]	1.79	0.41
1:A:331:ARG:HH12	1:B:132:GLU:OE2[3_555]	1.28	0.32
1:A:331:ARG:NH1	1:B:132:GLU:OE2[3_555]	2.11	0.09

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	A	380/399 (95%)	373 (98%)	7 (2%)	0	100	100
1	B	393/399 (98%)	385 (98%)	8 (2%)	0	100	100
2	C	69/69 (100%)	69 (100%)	0	0	100	100
2	D	60/69 (87%)	60 (100%)	0	0	100	100
All	All	902/936 (96%)	887 (98%)	15 (2%)	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	285/295 (97%)	284 (100%)	1 (0%)	84	81
1	B	291/295 (99%)	291 (100%)	0	100	100
2	C	61/59 (103%)	61 (100%)	0	100	100
2	D	52/59 (88%)	52 (100%)	0	100	100
All	All	689/708 (97%)	688 (100%)	1 (0%)	88	87

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	54	ASN
2	D	54	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](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

4 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
4	MES	A	602	-	12,12,12	2.30	1 (8%)	15,16,16	2.00	6 (40%)
3	GOL	A	601	-	5,5,5	0.88	0	5,5,5	1.17	1 (20%)
3	GOL	B	601	-	5,5,5	0.86	0	5,5,5	1.11	1 (20%)
3	GOL	B	602	-	5,5,5	0.78	0	5,5,5	0.84	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
4	MES	A	602	-	-	1/6/14/14	0/1/1/1
3	GOL	A	601	-	-	0/4/4/4	-
3	GOL	B	601	-	-	2/4/4/4	-
3	GOL	B	602	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	MES	C8-S	-7.71	1.66	1.77

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	602	MES	C5-N4-C3	3.62	116.64	108.84
4	A	602	MES	C2-C3-N4	-3.22	105.22	110.12
4	A	602	MES	C6-C5-N4	-3.09	105.42	110.12
4	A	602	MES	C7-N4-C3	2.62	118.21	111.24
3	A	601	GOL	C3-C2-C1	-2.16	103.88	111.80
4	A	602	MES	O1S-S-C8	2.14	109.96	106.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	601	GOL	C3-C2-C1	-2.05	104.28	111.80
4	A	602	MES	O3S-S-C8	2.01	109.93	106.00

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	601	GOL	O2-C2-C3-O3
3	B	601	GOL	C1-C2-C3-O3
4	A	602	MES	N4-C7-C8-S

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	GOL	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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	380/399 (95%)	0.23	18 (4%) 36 43	13, 31, 52, 68	3 (0%)
1	B	387/399 (96%)	0.06	6 (1%) 70 77	12, 28, 46, 67	5 (1%)
2	C	68/69 (98%)	0.36	3 (4%) 39 45	15, 34, 48, 62	2 (2%)
2	D	61/69 (88%)	0.49	6 (9%) 13 15	16, 34, 51, 68	1 (1%)
All	All	896/936 (95%)	0.19	33 (3%) 45 51	12, 30, 49, 68	11 (1%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	395	ALA	4.5
1	A	131	ASP	4.0
1	A	396	ASP	3.6
2	D	59	ARG	3.5
1	A	153	THR	3.5
2	D	24	LEU	3.4
1	B	361	GLU	3.2
2	D	62	SER	3.2
1	B	142	ALA	3.1
1	A	158	GLY	3.1
1	A	92	GLY	3.1
1	A	385	ALA	3.0
1	A	130	THR	3.0
2	C	2	THR	3.0
2	D	56	THR	2.9
1	A	122	GLU	2.9
1	A	160	PRO	2.7
1	B	385	ALA	2.7
2	D	2	THR	2.6
1	B	32	ASP	2.5
2	C	67	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	32	ASP	2.4
1	A	384	THR	2.4
2	D	61	LYS	2.3
1	A	123	GLY	2.3
1	A	118	ASP	2.3
1	B	156	SER	2.2
1	A	97	ARG	2.1
1	A	91	ALA	2.1
1	A	159	ILE	2.1
1	A	266	VAL	2.1
2	C	66	GLN	2.1
1	A	277	SER	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MES	A	602	12/12	0.76	0.20	30,43,53,60	25
3	GOL	B	602	6/6	0.82	0.16	35,52,63,71	0
3	GOL	A	601	6/6	0.86	0.15	32,39,46,46	0
3	GOL	B	601	6/6	0.87	0.13	23,37,41,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.