wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 3, 2023 – 01:18 pm BST

PDB ID	:	8A1I
Title	:	Crystal structure of murine Armc8 isoform beta
Authors	:	van gen Hassend, P.M.; Schindelin, H.
Deposited on	:	2022-06-01
Resolution	:	2.69 Å(reported)

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

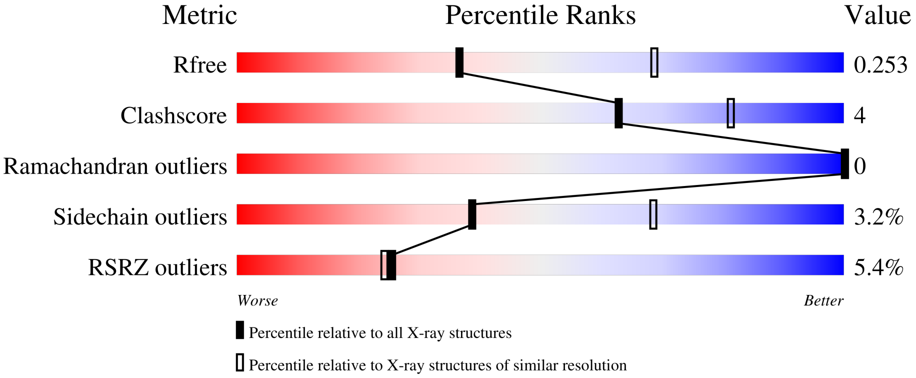
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.32.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

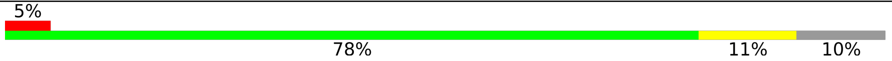
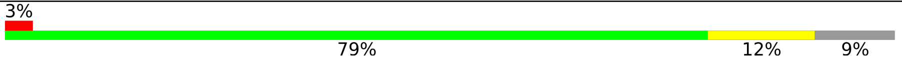
The reported resolution of this entry is 2.69 Å.

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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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% 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	401	
1	I	401	
1	P	401	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17596 atoms, of which 8912 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.

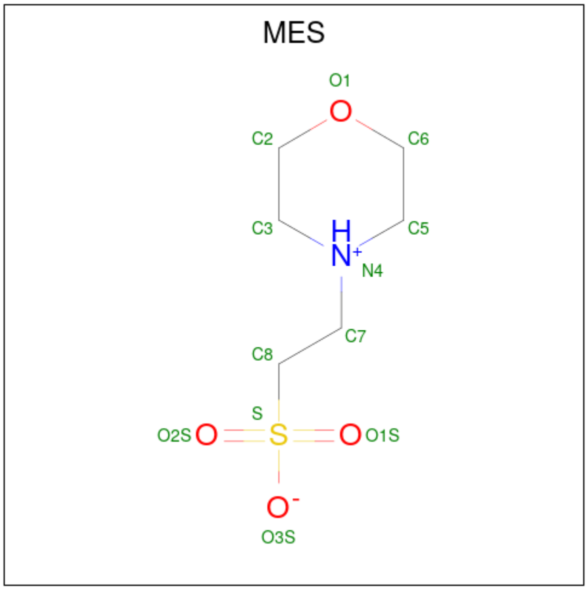
- Molecule 1 is a protein called Isoform 2 of Armadillo repeat-containing protein 8.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	370	Total	C	H	N	O	S	Se	76	0	0
			5896	1844	2995	498	536	13	10			
1	I	360	Total	C	H	N	O	S	Se	75	0	0
			5708	1788	2896	480	521	13	10			
1	P	366	Total	C	H	N	O	S	Se	75	0	0
			5836	1826	2965	491	531	13	10			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	379	ILE	-	insertion	UNP Q9DBR3-2
A	380	ILE	-	insertion	UNP Q9DBR3-2
I	379	ILE	-	insertion	UNP Q9DBR3-2
I	380	ILE	-	insertion	UNP Q9DBR3-2
P	379	ILE	-	insertion	UNP Q9DBR3-2
P	380	ILE	-	insertion	UNP Q9DBR3-2

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).

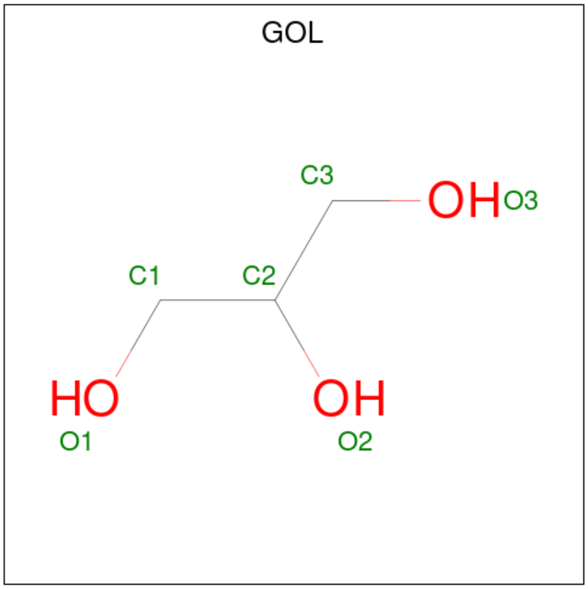


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C H N O S 25 6 13 1 4 1	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

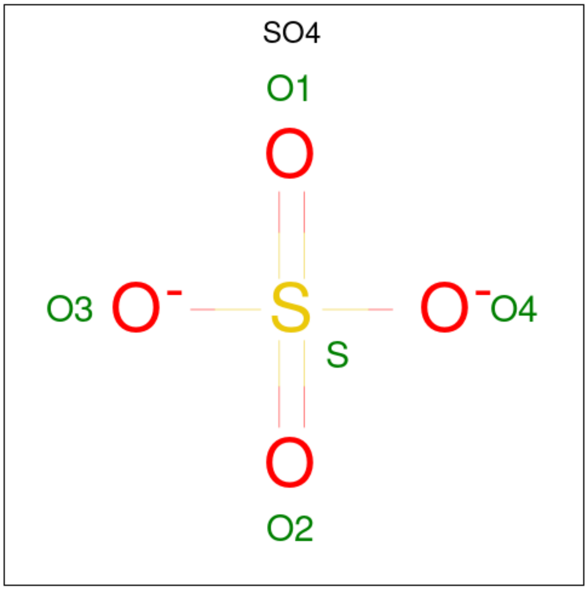
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	I	2	Total Cl 2 2	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C H O 14 3 8 3	2	0
4	A	1	Total C H O 12 3 6 3	0	0
4	A	1	Total C H O 12 3 6 3	0	0
4	I	1	Total C H O 12 3 6 3	1	0
4	I	1	Total C H O 13 3 7 3	1	0
4	P	1	Total C H O 11 3 5 3	0	0
4	P	1	Total C H O 11 3 5 3	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	I	1	Total O S 5 4 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	10	Total O 10 10	0	0
6	I	12	Total O 12 12	0	0

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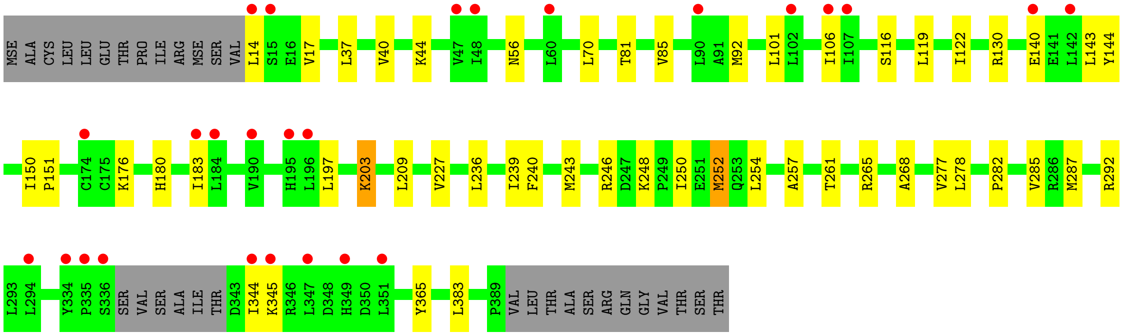
Mol	**Chain**	**Residues**	**Atoms**		**ZeroOcc**	**AltConf**
6	P	16	Total	O	0	0
			16	16		

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 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.

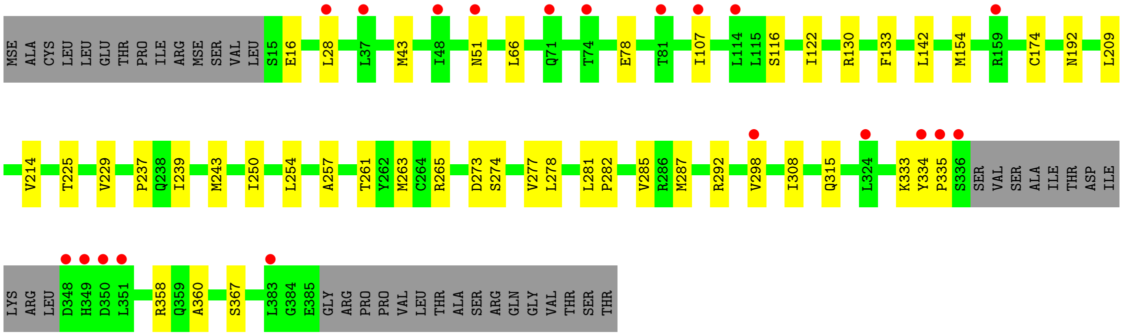
- Molecule 1: Isoform 2 of Armadillo repeat-containing protein 8

Chain A:



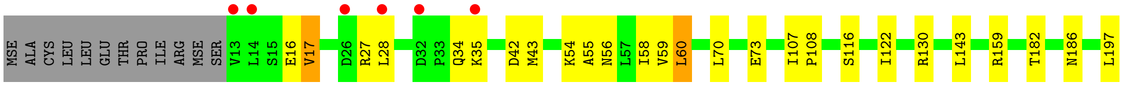
- Molecule 1: Isoform 2 of Armadillo repeat-containing protein 8

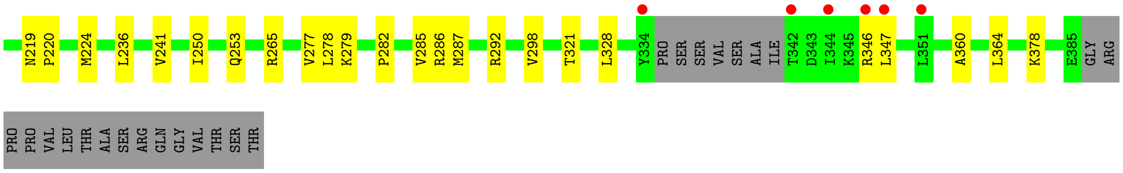
Chain I:



- Molecule 1: Isoform 2 of Armadillo repeat-containing protein 8

Chain P:




N219
P220
M224
L236
V241
I250
Q253
R265
V277
L278
K279
P282
V285
R286
M287
R292
V298
T321
L328
Y334
PRO
SER
SER
VAL
SER
ALA
ILE
T342
D343
I344
K345
R346
L347
L351
A360
L364
K378
E385
GLY
ARG
PRO
PRO
VAL
LEU
THR
ALA
SER
ARG
GLN
GLY
VAL
THR
SER
THR

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	65.64Å 148.18Å 67.14Å 90.00° 90.57° 90.00°	Depositor
Resolution (Å)	19.97 – 2.69 47.17 – 2.69	Depositor EDS
% Data completeness (in resolution range)	73.9 (19.97-2.69) 73.9 (47.17-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$[1]	1.74 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.214 , 0.248 0.222 , 0.253	Depositor DCC
R_{free} test set	1310 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	75.7	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 48.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.002 for l,k,-h 0.046 for h,-k,-l 0.027 for l,-k,h	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	17596	wwPDB-VP
Average B, all atoms (Å^2)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CL, SO4, 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	0.28	0/2939	0.46	0/3964
1	I	0.28	0/2848	0.45	0/3842
1	P	0.28	0/2906	0.46	0/3918
All	All	0.28	0/8693	0.46	0/11724

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	2901	2995	2994	28	0
1	I	2812	2896	2891	25	0
1	P	2871	2965	2963	24	1
2	A	12	13	13	0	0
3	A	1	0	0	0	0
3	I	2	0	0	0	0
4	A	18	20	24	0	0
4	I	12	13	16	1	0
4	P	12	10	16	0	0
5	I	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	10	0	0	0	0
6	I	12	0	0	0	0
6	P	16	0	0	0	0
All	All	8684	8912	8917	76	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 4.

The worst 5 of 76 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:I:298:VAL:HG23	1:I:360:ALA:HB2	1.60	0.83
1:A:248:LYS:HD2	1:A:252:MSE:HE3	1.68	0.75
1:I:308:ILE:HD11	1:I:315:GLN:HA	1.72	0.71
1:P:17:VAL:HG21	1:P:60:LEU:HD11	1.75	0.69
1:I:154:MSE:HE1	1:I:192:ASN:HB2	1.76	0.68

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:P:16:GLU:OE1	1:P:378:LYS:NZ[1_556]	2.13	0.07

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	366/401 (91%)	364 (100%)	2 (0%)	0	100	100
1	I	356/401 (89%)	352 (99%)	4 (1%)	0	100	100
1	P	362/401 (90%)	359 (99%)	3 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1084/1203 (90%)	1075 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	A	329/344 (96%)	317 (96%)	12 (4%)	35	64
1	I	318/344 (92%)	310 (98%)	8 (2%)	47	76
1	P	325/344 (94%)	314 (97%)	11 (3%)	37	66
All	All	972/1032 (94%)	941 (97%)	31 (3%)	39	68

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	78	GLU
1	P	265	ARG
1	I	292	ARG
1	P	346	ARG
1	P	130	ARG

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

5.3.3 RNA ⓘ

There are no RNA molecules 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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 3 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	$\#\|Z\| > 2$
4	GOL	P	502	-	5,5,5	0.86	0	5,5,5	0.99	0
4	GOL	A	504	-	5,5,5	0.98	0	5,5,5	0.91	0
2	MES	A	501	-	12,12,12	2.13	1 (8%)	14,16,16	1.59	3 (21%)
4	GOL	I	504	-	5,5,5	0.91	0	5,5,5	0.94	0
4	GOL	P	501	-	5,5,5	0.86	0	5,5,5	0.97	0
4	GOL	I	505	-	5,5,5	0.99	0	5,5,5	0.96	0
5	SO4	I	503	-	4,4,4	0.14	0	6,6,6	0.09	0
4	GOL	A	503	-	5,5,5	0.97	0	5,5,5	0.93	0
4	GOL	A	505	-	5,5,5	0.93	0	5,5,5	0.83	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	GOL	P	502	-	-	0/4/4/4	-
4	GOL	A	504	-	-	2/4/4/4	-
2	MES	A	501	-	-	1/6/14/14	0/1/1/1
4	GOL	I	504	-	-	1/4/4/4	-
4	GOL	P	501	-	-	0/4/4/4	-
4	GOL	I	505	-	-	2/4/4/4	-
4	GOL	A	503	-	-	0/4/4/4	-
4	GOL	A	505	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	MES	C8-S	-7.09	1.67	1.77

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	MES	O1S-S-C8	2.95	110.47	106.92
2	A	501	MES	C5-N4-C3	2.44	114.31	108.83
2	A	501	MES	O3S-S-C8	2.27	109.44	105.77

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	MES	N4-C7-C8-S
4	A	505	GOL	O1-C1-C2-C3
4	A	505	GOL	O1-C1-C2-O2
4	A	504	GOL	O1-C1-C2-C3
4	I	504	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	504	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	360/401 (89%)	0.56	26 (7%)	15	13	49, 80, 132, 171	0
1	I	350/401 (87%)	0.57	20 (5%)	23	22	47, 83, 136, 207	0
1	P	356/401 (88%)	0.40	12 (3%)	45	45	49, 79, 129, 166	0
All	All	1066/1203 (88%)	0.51	58 (5%)	25	24	47, 80, 132, 207	0

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	351	LEU	9.2
1	I	349	HIS	8.2
1	I	334	TYR	7.5
1	I	348	ASP	5.8
1	P	344	ILE	5.2

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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(Å^2)	Q<0.9
4	GOL	I	505	6/6	0.79	0.26	89,93,112,112	1
4	GOL	I	504	6/6	0.81	0.31	95,98,118,118	1
4	GOL	A	503	6/6	0.82	0.26	93,112,117,117	2
4	GOL	P	501	6/6	0.82	0.24	106,108,130,130	0
2	MES	A	501	12/12	0.84	0.18	120,130,152,156	0
4	GOL	A	504	6/6	0.85	0.21	97,100,121,121	0
4	GOL	A	505	6/6	0.88	0.30	74,75,90,90	0
3	CL	A	502	1/1	0.89	0.09	89,89,89,89	0
3	CL	I	501	1/1	0.89	0.15	89,89,89,89	0
4	GOL	P	502	6/6	0.91	0.18	84,85,102,103	0
5	SO4	I	503	5/5	0.93	0.08	120,121,122,122	0
3	CL	I	502	1/1	0.97	0.16	84,84,84,84	0

6.5 Other polymers ⓘ

There are no such residues in this entry.