WORLDWIDE PDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Jan 24, 2023 – 05:53 AM EST

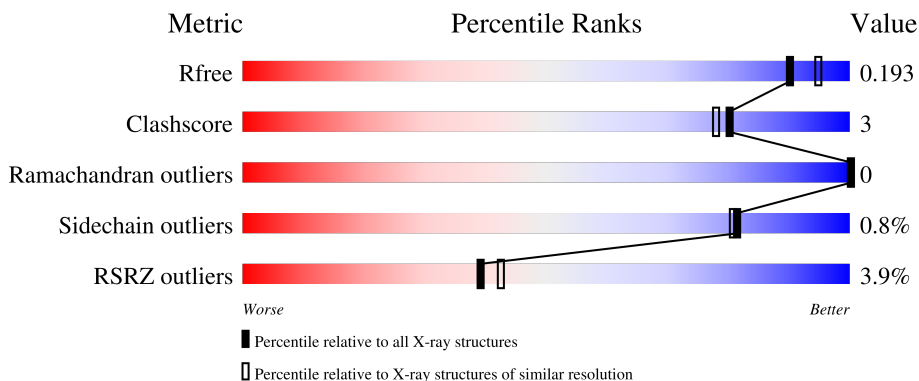|		
PDB ID	:	3JTX
Title	:	Crystal structure of Aminotransferase (NP_283882.1) from NEISSERIA MENINGITIDIS Z2491 at 1.91 A resolution
Authors	:	Joint Center for Structural Genomics (JCSG)
Deposited on	:	2009-09-14
Resolution	:	1.91 Å(reported)

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 1.91 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	Percentile Ranks	Value
Rfree		0.193
Clashscore		3
Ramachandran outliers		0
Sidechain outliers		0.8%
RSRZ outliers		3.9%

Worse   *Better*

▌Percentile relative to all X-ray structures

▯Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	396	5% / 92% / 7% ·
1	B	396	3% / 94% / 5% ·

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MES	B	400[A]	-	-	-	X

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 7062 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 aminotransferase.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	P	S	Se	0	11	0
			3137	2021	530	573	1	7	5			
1	B	393	Total	C	N	O	P	S	Se	0	11	0
			3151	2031	527	580	1	7	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP A1IRD6
B	0	GLY	-	expression tag	UNP A1IRD6

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).
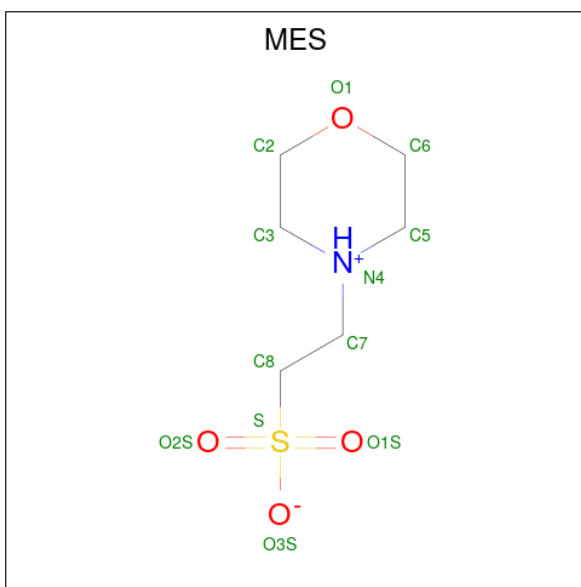
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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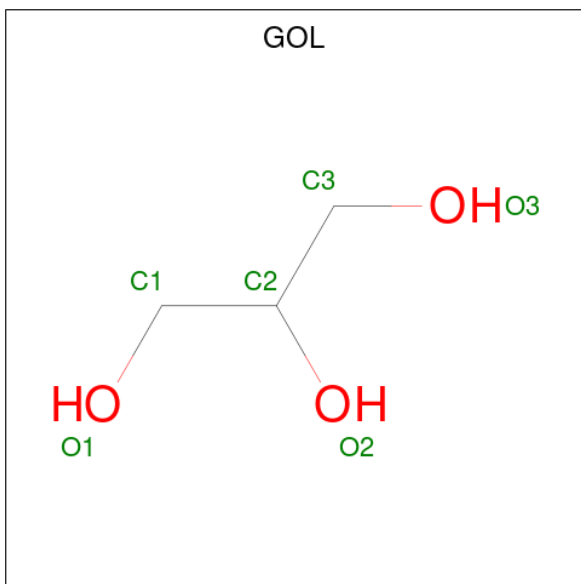*Continued from previous page...*

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	1
			12	6	1	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

GOL

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Ca 1	0	0

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).
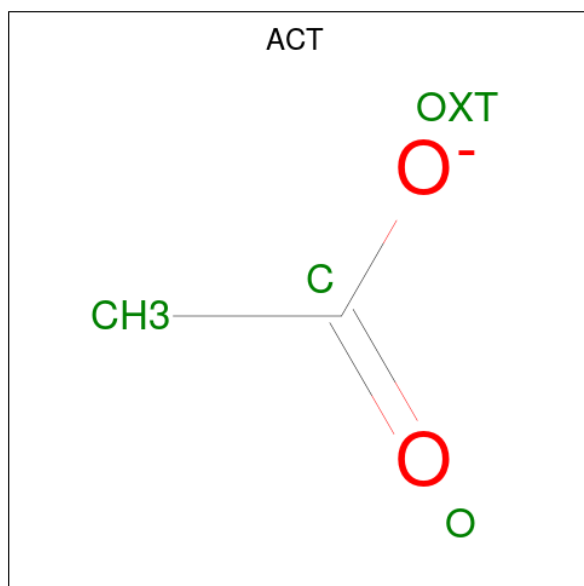
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	337	Total 339	O 339	0	2
6	B	343	Total 348	O 348	0	5

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: aminotransferase
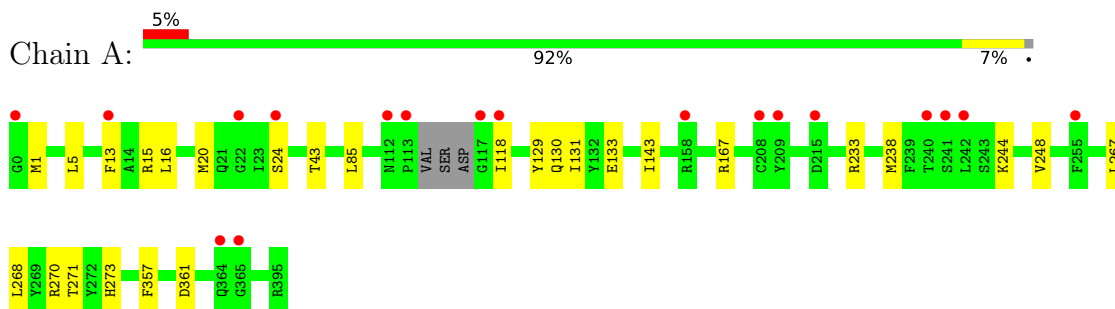
• Molecule 1: aminotransferase
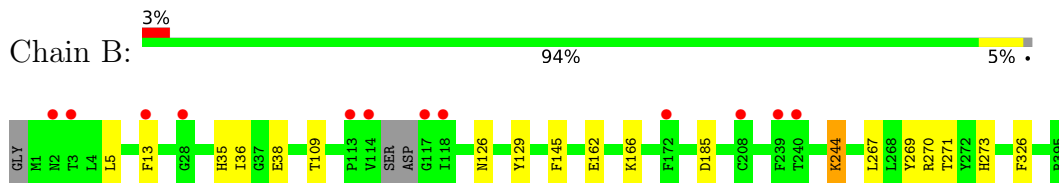
4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	112.62Å 116.89Å 145.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.31 – 1.91 29.31 – 1.91	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.31-1.91) 99.8 (29.31-1.91)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.90 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0053, PHENIX	Depositor
R, R_{free}	0.152 , 0.183 0.164 , 0.193	Depositor DCC
R_{free} test set	3737 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	22.0	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 49.2	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.026 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7062	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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 ⓘ

5.1   Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ACT, GOL, CA, MES, LLP

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	0.52	0/3219	0.64	1/4370 (0.0%)
1	B	0.54	0/3234	0.66	0/4392
All	All	0.53	0/6453	0.65	1/8762 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	233	ARG	NE-CZ-NH2	-6.45	117.08	120.30

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	3137	0	3111	16	0
1	B	3151	0	3129	20	0
2	A	12	0	12	0	0
2	B	12	0	12	1	0
3	A	18	0	24	1	0
3	B	36	0	48	0	0
4	B	1	0	0	0	0
5	B	8	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	339	0	0	4	0
6	B	348	0	0	4	0
All	All	7062	0	6342	34	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 3.

The worst 5 of 34 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:1:MSE:HE3	1:A:5:LEU:HD11	1.32	1.11
1:A:1:MSE:HE1	1:B:269:TYR:CD1	2.12	0.85
1:B:13[B]:PHE:HZ	1:B:36[B]:ILE:HA	1.48	0.77
1:A:238:MSE:CE	6:A:637:HOH:O	2.35	0.75
1:B:36[B]:ILE:HG22	1:B:38:GLU:HG2	1.69	0.74

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	A	399/396 (101%)	385 (96%)	14 (4%)	0	100	100
1	B	399/396 (101%)	389 (98%)	10 (2%)	0	100	100
All	All	798/792 (101%)	774 (97%)	24 (3%)	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	331/327 (101%)	326 (98%)	5 (2%)	65	61
1	B	336/327 (103%)	335 (100%)	1 (0%)	92	93
All	All	667/654 (102%)	661 (99%)	6 (1%)	81	78

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	361[A]	ASP
1	A	361[B]	ASP
1	B	326	PHE
1	A	24	SER
1	A	13	PHE

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 ⓘ

2 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	LLP	B	244	1	23,24,25	1.51	4 (17%)	25,32,34	1.32	2 (8%)
1	LLP	A	244	1	23,24,25	1.58	3 (13%)	25,32,34	1.62	3 (12%)

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	LLP	B	244	1	-	5/16/17/19	0/1/1/1
1	LLP	A	244	1	-	4/16/17/19	0/1/1/1

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	244	LLP	O3-C3	-4.81	1.25	1.37
1	A	244	LLP	O3-C3	-4.50	1.26	1.37
1	A	244	LLP	C4-C4'	2.59	1.51	1.46
1	B	244	LLP	C2-N1	2.43	1.38	1.33
1	B	244	LLP	C4-C4'	2.30	1.51	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	244	LLP	OP4-C5'-C5	5.46	119.75	109.35
1	B	244	LLP	C4-C4'-NZ	-3.69	107.37	124.31
1	A	244	LLP	C4-C4'-NZ	-3.32	109.07	124.31
1	B	244	LLP	OP4-C5'-C5	3.13	115.31	109.35
1	A	244	LLP	C3-C4-C5	2.44	120.13	118.26

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	244	LLP	CG-CD-CE-NZ
1	A	244	LLP	C3-C4-C4'-NZ
1	B	244	LLP	C3-C4-C4'-NZ
1	B	244	LLP	CG-CD-CE-NZ
1	A	244	LLP	C5-C4-C4'-NZ

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	244	LLP	1	0

5.5　Carbohydrates　ⓘ

There are no monosaccharides in this entry.

5.6　Ligand geometry　ⓘ

Of 14 ligands modelled in this entry, 1 is monoatomic - leaving 13 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	$\#|Z| > 2$
3	GOL	B	405	-	5,5,5	0.42	0	5,5,5	0.13	0
3	GOL	B	401	-	5,5,5	0.23	0	5,5,5	1.19	0
3	GOL	A	396	-	5,5,5	0.38	0	5,5,5	0.31	0
3	GOL	B	404	-	5,5,5	0.44	0	5,5,5	0.63	0
5	ACT	B	397	-	3,3,3	0.87	0	3,3,3	1.72	1 (33%)
3	GOL	B	402	-	5,5,5	0.42	0	5,5,5	0.39	0
3	GOL	B	403	-	5,5,5	0.28	0	5,5,5	0.23	0
3	GOL	A	398	-	5,5,5	0.37	0	5,5,5	0.26	0
5	ACT	B	398	-	3,3,3	0.86	0	3,3,3	1.58	1 (33%)
3	GOL	A	397	-	5,5,5	0.27	0	5,5,5	0.59	0
2	MES	B	400[A]	-	12,12,12	2.10	1 (8%)	14,16,16	2.56	7 (50%)
2	MES	A	400	-	12,12,12	1.63	1 (8%)	14,16,16	2.43	4 (28%)
3	GOL	B	399	-	5,5,5	0.47	0	5,5,5	0.67	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
3	GOL	B	405	-	-	2/4/4/4	-
3	GOL	B	401	-	-	2/4/4/4	-
3	GOL	A	396	-	-	0/4/4/4	-
3	GOL	B	404	-	-	4/4/4/4	-
3	GOL	B	402	-	-	4/4/4/4	-
3	GOL	B	403	-	-	4/4/4/4	-
3	GOL	A	398	-	-	2/4/4/4	-
3	GOL	A	397	-	-	1/4/4/4	-
2	MES	B	400[A]	-	-	1/6/14/14	0/1/1/1
2	MES	A	400	-	-	2/6/14/14	0/1/1/1
3	GOL	B	399	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400[A]	MES	C8-S	-6.96	1.67	1.77
2	A	400	MES	C8-S	-4.95	1.70	1.77

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	MES	C7-N4-C5	4.97	123.93	111.23
2	A	400	MES	C5-N4-C3	4.55	119.07	108.83
2	B	400[A]	MES	O3S-S-C8	4.10	112.40	105.77
2	B	400[A]	MES	C7-N4-C3	3.99	121.43	111.23
2	B	400[A]	MES	C5-N4-C3	3.85	117.50	108.83

There are no chirality outliers.

5 of 24 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	400	MES	C8-C7-N4-C5
2	A	400	MES	N4-C7-C8-S
2	B	400[A]	MES	C8-C7-N4-C5
3	A	398	GOL	C1-C2-C3-O3
3	A	398	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	398	GOL	1	0
2	B	400[A]	MES	1	0

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 ⓘ

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(Å²)	Q<0.9
1	A	387/396 (97%)	0.14	18 (4%)	31	34	12, 17, 31, 43	0
1	B	387/396 (97%)	-0.04	12 (3%)	49	52	11, 16, 26, 47	0
All	All	774/792 (97%)	0.05	30 (3%)	39	42	11, 17, 29, 47	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	118	ILE	8.0
1	A	117	GLY	7.7
1	A	113	PRO	5.4
1	A	365	GLY	4.4
1	A	112	ASN	4.3

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

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(Å²)	Q<0.9
1	LLP	A	244	24/25	0.97	0.16	16,20,23,24	0
1	LLP	B	244	24/25	0.98	0.13	15,18,22,24	0

6.3 Carbohydrates ⓘ

There are no monosaccharides 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(Å^2)	Q<0.9
3	GOL	A	398	6/6	0.69	0.38	67,68,69,69	0
2	MES	B	400[A]	12/12	0.72	0.46	39,41,44,44	12
3	GOL	B	403	6/6	0.78	0.20	41,49,50,51	0
3	GOL	A	396	6/6	0.82	0.19	56,58,59,60	0
5	ACT	B	397	4/4	0.82	0.21	53,54,54,54	0
3	GOL	B	405	6/6	0.86	0.20	63,64,64,65	0
3	GOL	B	399	6/6	0.86	0.27	42,48,50,51	0
3	GOL	B	401	6/6	0.87	0.23	39,43,43,43	0
5	ACT	B	398	4/4	0.90	0.20	52,52,53,53	0
3	GOL	B	404	6/6	0.91	0.21	39,42,45,46	0
3	GOL	B	402	6/6	0.92	0.21	40,43,45,48	0
3	GOL	A	397	6/6	0.92	0.20	43,45,46,47	0
2	MES	A	400	12/12	0.92	0.14	37,40,41,42	0
4	CA	B	396	1/1	0.98	0.09	45,45,45,45	0

6.5 Other polymers (i)

There are no such residues in this entry.