W O R L D W I D E

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PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

May 16, 2020 – 11:18 am BST

PDB ID	:	5XN7
Title	:	Crystal structure of the effector domain RID of Vibrio vulnificus MARTX toxin
Authors	:	Yin, L.; Zhu, Y.
Deposited on	:	2017-05-18
Resolution	:	2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i)) 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	:	2.11
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)	:	2.11

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 2.70 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.
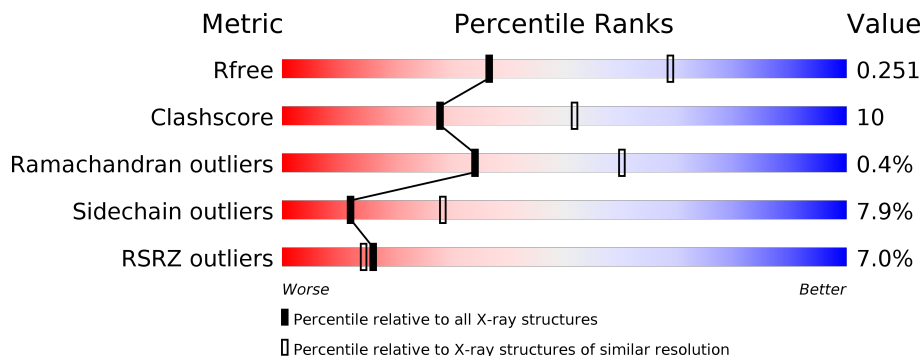
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 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% 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	616	7% ... 66% 20% • 12%
1	B	616	5% ... 69% 19% • 11%

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
6	CL	A	2906	-	-	X	-

2 Entry composition ⓘ

There are 7 unique types of molecules in this entry. The entry contains 8384 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 Putative RTX-toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total 4105	C 2576	N 726	O 794	Se 9	0	0	0
1	B	551	Total 4143	C 2597	N 731	O 807	Se 8	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2361	ARG	GLN	conflict	UNP F1CLG1
A	2541	ASP	GLY	conflict	UNP F1CLG1
A	2835	ALA	CYS	engineered mutation	UNP F1CLG1
B	2361	ARG	GLN	conflict	UNP F1CLG1
B	2541	ASP	GLY	conflict	UNP F1CLG1
B	2835	ALA	CYS	engineered mutation	UNP F1CLG1

- Molecule 2 is 1,4-DIETHYLENE DIOXIDE (three-letter code: DIO) (formula: $C_4H_8O_2$).
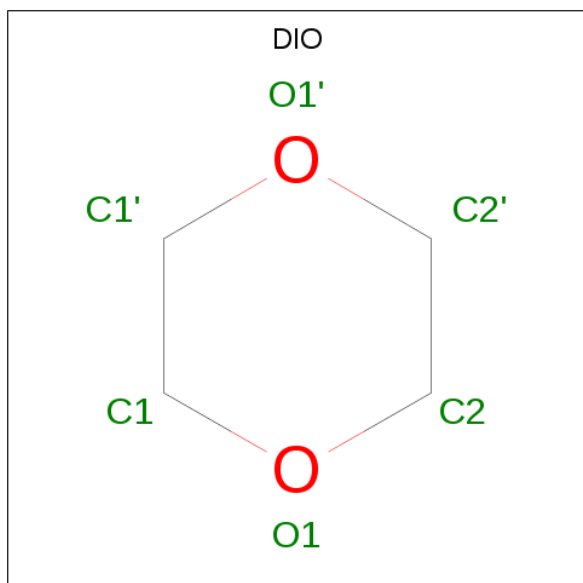
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total C O 6 4 2			0	0
2	A	1	Total C O 6 4 2			0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
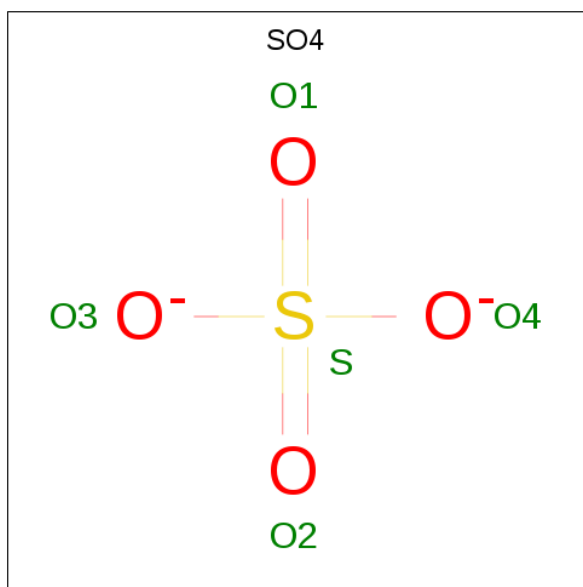
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total O S 5 4 1			0	0

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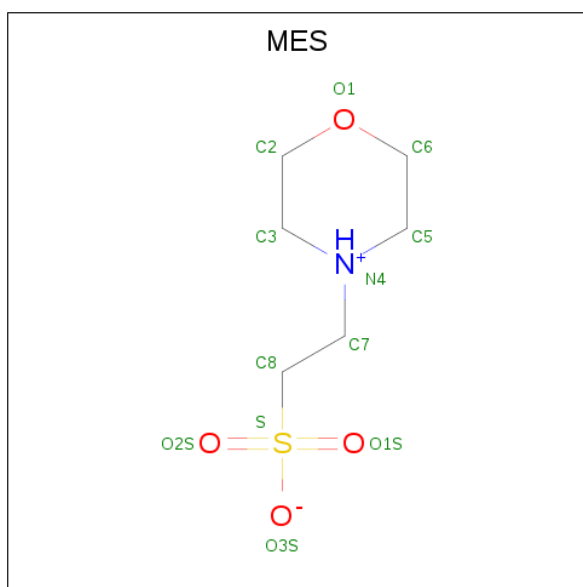
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 5 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).
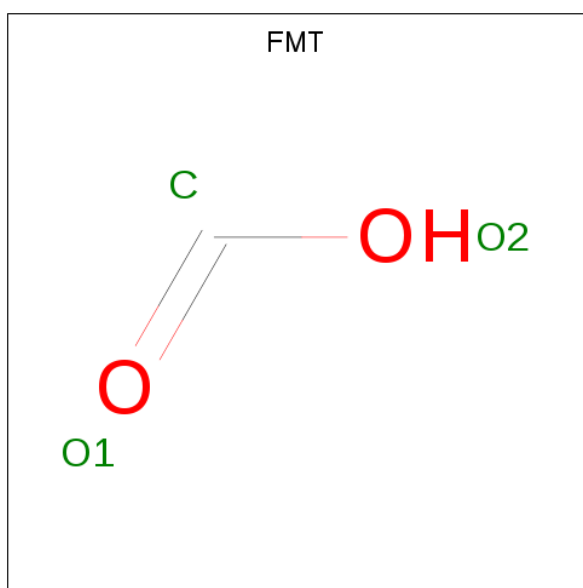
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			3	1	2		

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	Cl 1	0	0
6	A	2	Total 2	Cl 2	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	60	Total 60	O 60	0	0
7	B	29	Total 29	O 29	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA 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: Putative RTX-toxin
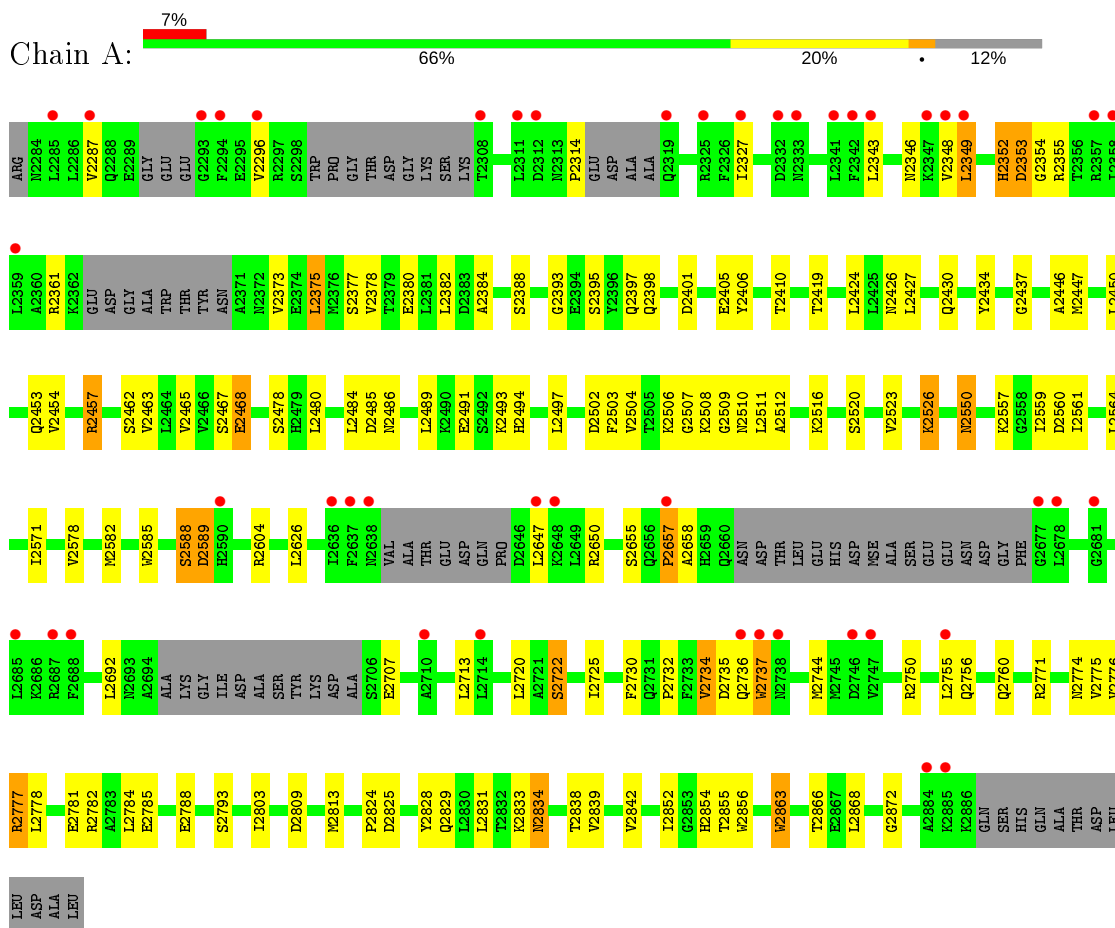
- Molecule 1: Putative RTX-toxin
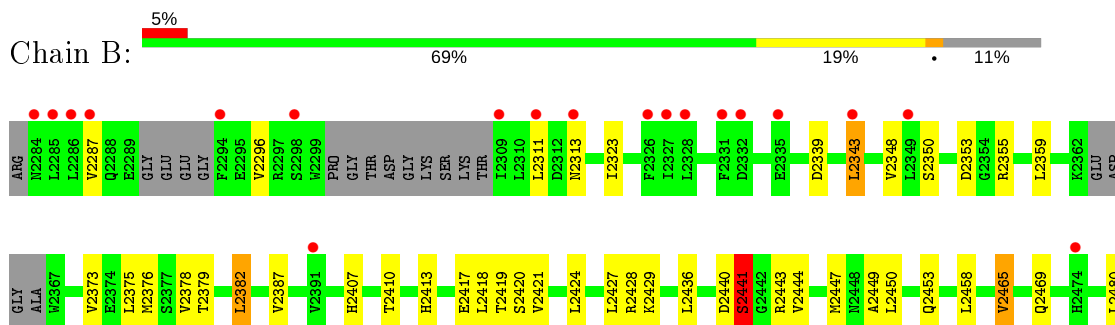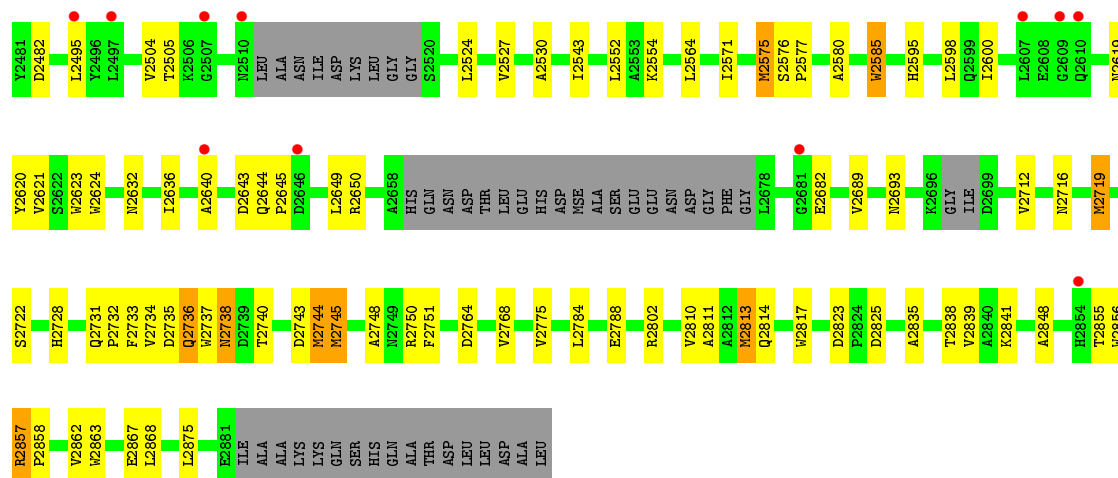
4   Data and refinement statistics   (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	124.74Å 185.19Å 81.36Å 90.00° 95.60° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 46.30 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-2.70) 99.5 (46.30-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.82 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.203 , 0.244 0.207 , 0.251	Depositor DCC
R_{free} test set	2554 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	55.5	Xtriage
Anisotropy	0.803	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 62.1	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	0.94	EDS
Total number of atoms	8384	wwPDB-VP
Average B, all atoms (Å^2)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.38% 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: FMT, DIO, SO4, MES, CL

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	0.64	3/4161 (0.1%)	0.72	2/5619 (0.0%)
1	B	0.59	4/4205 (0.1%)	0.70	8/5689 (0.1%)
All	All	0.61	7/8366 (0.1%)	0.71	10/11308 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2856	TRP	CD2-CE2	5.97	1.48	1.41
1	B	2856	TRP	CD2-CE2	5.91	1.48	1.41
1	B	2817	TRP	CD2-CE2	5.58	1.48	1.41
1	B	2863	TRP	CD2-CE2	5.29	1.47	1.41
1	A	2863	TRP	CD2-CE2	5.28	1.47	1.41

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2743	ASP	N-CA-C	8.41	133.70	111.00
1	A	2834	ASN	CB-CA-C	-7.95	94.50	110.40
1	B	2744	MSE	CB-CA-C	6.32	123.04	110.40
1	A	2314	PRO	N-CA-CB	6.11	110.63	103.30
1	B	2745	MSE	N-CA-C	6.00	127.21	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2588	SER	Peptide

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	4105	0	3918	80	0
1	B	4143	0	3896	81	0
2	A	12	0	16	0	0
3	A	5	0	0	0	0
4	A	12	0	13	0	0
4	B	12	0	13	0	0
5	A	3	0	1	0	0
6	A	2	0	0	2	0
6	B	1	0	0	0	0
7	A	60	0	0	1	0
7	B	29	0	0	1	0
All	All	8384	0	7857	160	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 10.

The worst 5 of 160 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:B:2736:GLN:HE22	1:B:2750:ARG:HH22	0.95	0.93
1:B:2736:GLN:HE22	1:B:2750:ARG:NH2	1.70	0.89
1:A:2777:ARG:O	1:A:2781:GLU:HG3	1.85	0.75
1:A:2737:TRP:NE1	1:A:2744:MSE:HG2	2.04	0.72
1:A:2377:SER:OG	1:A:2380:GLU:HG3	1.89	0.72

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	529/616 (86%)	486 (92%)	41 (8%)	2 (0%)	34	60
1	B	537/616 (87%)	498 (93%)	37 (7%)	2 (0%)	34	60
All	All	1066/1232 (86%)	984 (92%)	78 (7%)	4 (0%)	34	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2589	ASP
1	A	2657	PRO
1	B	2441	SER
1	B	2737	TRP

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	412/496 (83%)	381 (92%)	31 (8%)	13	31
1	B	412/496 (83%)	378 (92%)	34 (8%)	11	25
All	All	824/992 (83%)	759 (92%)	65 (8%)	12	28

5 of 65 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2855	THR
1	B	2379	THR

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Mol	Chain	Res	Type
1	B	2813	MSE
1	A	2866	THR
1	B	2353	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2319	GLN
1	B	2834	ASN
1	B	2756	GLN
1	A	2716	ASN
1	B	2736	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	MES	B	2901	-	12,12,12	2.27	1 (8%)	14,16,16	2.06	5 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	DIO	A	2901	-	6,6,6	0.62	0	6,6,6	0.93	0
5	FMT	A	2905	-	0,2,2	0.00	-	0,1,1	0.00	-
2	DIO	A	2902	-	6,6,6	0.56	0	6,6,6	0.74	0
3	SO4	A	2903	-	4,4,4	0.38	0	6,6,6	0.13	0
4	MES	A	2904	-	12,12,12	2.13	1 (8%)	14,16,16	1.54	3 (21%)

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	2904	-	-	3/6/14/14	0/1/1/1
4	MES	B	2901	-	-	1/6/14/14	0/1/1/1
2	DIO	A	2902	-	-	-	0/1/1/1
2	DIO	A	2901	-	-	-	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2901	MES	C8-S	-7.37	1.67	1.77
4	A	2904	MES	C8-S	-6.98	1.67	1.77

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	2901	MES	O3S-S-C8	4.28	112.69	105.77
4	B	2901	MES	O1S-S-C8	4.16	111.93	106.92
4	A	2904	MES	O2S-S-C8	2.79	110.28	106.92
4	A	2904	MES	O1S-S-C8	2.42	109.83	106.92
4	B	2901	MES	O3S-S-O1S	-2.39	105.43	111.27

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2904	MES	C8-C7-N4-C5
4	A	2904	MES	C8-C7-N4-C3
4	A	2904	MES	N4-C7-C8-S
4	B	2901	MES	C8-C7-N4-C5

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	536/616 (87%)	0.41	45 (8%)	11	9	32, 69, 134, 188	0
1	B	542/616 (87%)	0.33	30 (5%)	25	24	38, 74, 127, 162	0
All	All	1078/1232 (87%)	0.37	75 (6%)	16	14	32, 71, 132, 188	0

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2687	ARG	5.4
1	B	2285	LEU	5.4
1	B	2286	LEU	5.3
1	A	2343	LEU	5.3
1	A	2678	LEU	5.2

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 carbohydrates 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(Å²)	Q<0.9
2	DIO	A	2901	6/6	0.85	0.19	104,108,115,117	0
4	MES	A	2904	12/12	0.91	0.27	106,126,136,138	0
3	SO4	A	2903	5/5	0.93	0.22	96,100,109,110	0
4	MES	B	2901	12/12	0.94	0.20	58,63,72,73	0
6	CL	A	2906	1/1	0.95	0.13	92,92,92,92	0
6	CL	A	2907	1/1	0.95	0.23	63,63,63,63	0
5	FMT	A	2905	3/3	0.95	0.15	54,54,60,62	0
2	DIO	A	2902	6/6	0.98	0.24	63,70,71,75	0
6	CL	B	2902	1/1	0.99	0.18	45,45,45,45	0

6.5　Other polymers ⓘ

There are no such residues in this entry.