



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 03:40 PM EDT

PDB ID : 6P3I / pdb_00006p3i
Title : The structure of condensation and adenylation domains of teixobactin-producing nonribosomal peptide synthetase Txo1 serine module in complex with Mg
Authors : Tan, K.; Zhou, M.; Jedrzejczak, R.; Babnigg, G.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2019-05-23
Resolution : 2.15 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

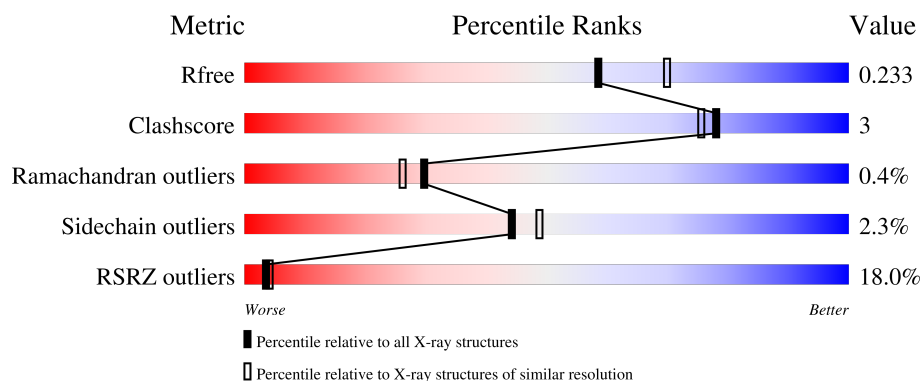
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	873	17% 86% 8% 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6563 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 Txo1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	830	Total	C	N	O	S	Se	0	4	0
			6329	3995	1160	1152	7	15			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2137	SER	-	expression tag	UNP A0A0B5GUD2
A	2138	ASN	-	expression tag	UNP A0A0B5GUD2
A	2139	ALA	-	expression tag	UNP A0A0B5GUD2

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

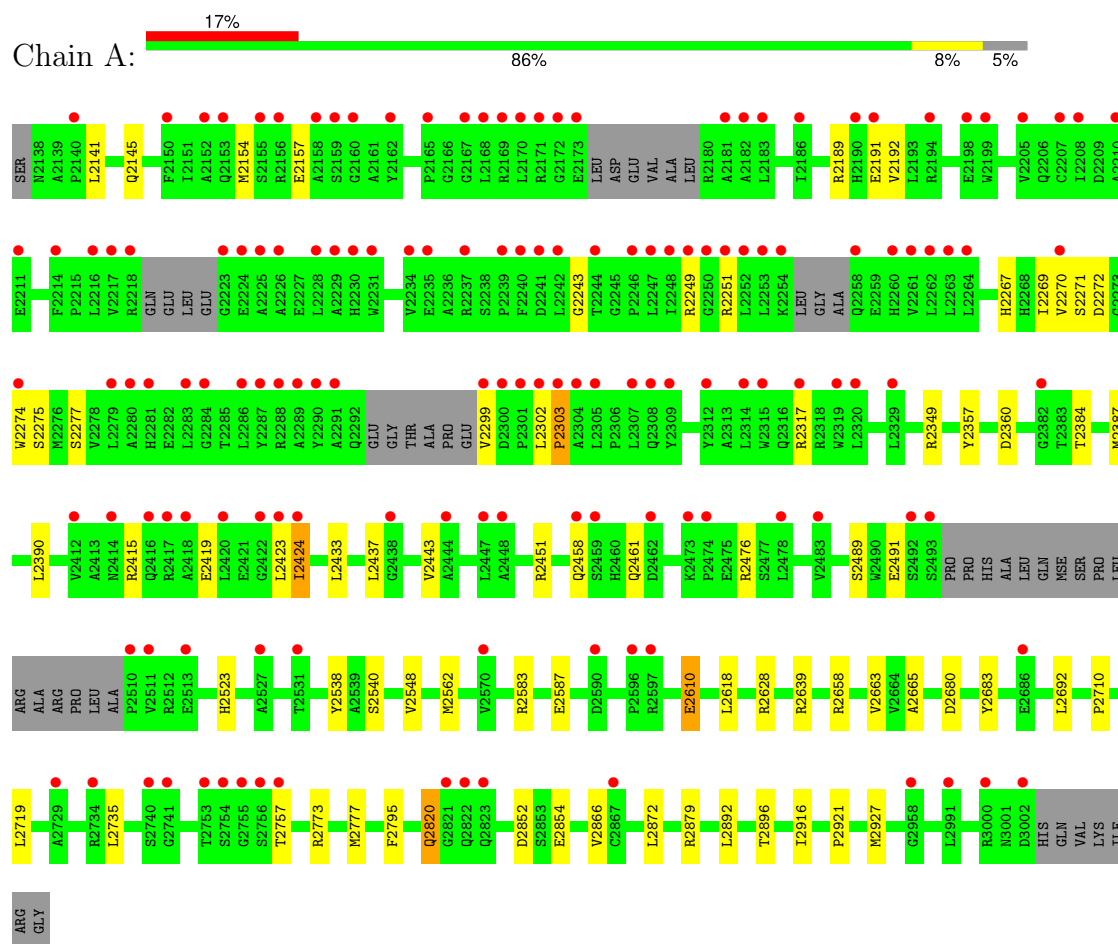
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	117	Total	O	0	0
			117	117		

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: Txo1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	154.49Å 90.66Å 98.80Å 90.00° 106.00° 90.00°	Depositor
Resolution (Å)	45.33 – 2.15 45.33 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.5 (45.33-2.15) 91.0 (45.33-2.15)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.36 (at 2.14Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.201 , 0.231 0.204 , 0.233	Depositor DCC
R_{free} test set	3391 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	46.3	Xtriage
Anisotropy	0.404	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6563	wwPDB-VP
Average B, all atoms (Å ²)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, MES, SO4

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	0.10	0/6458	0.29	0/8779

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	6329	0	6112	35	0
2	A	1	0	0	0	0
3	A	36	0	36	1	0
4	A	80	0	0	1	0
5	A	117	0	0	0	0
All	All	6563	0	6148	35	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.

All (35) 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:2390:LEU:HD11	1:A:2433:LEU:HD13	1.78	0.63
1:A:2249:ARG:HH21	1:A:2251:ARG:HE	1.47	0.61
1:A:2658:ARG:NH1	4:A:3118:SO4:O3	2.34	0.60
1:A:2773:ARG:HH12	1:A:2777:MSE:SE	2.36	0.58
1:A:2189:ARG:NH1	1:A:2303:PRO:O	2.36	0.57
1:A:2618:LEU:HD21	1:A:2663:VAL:HB	1.88	0.54
1:A:2665:ALA:HB2	1:A:2719:LEU:HD11	1.89	0.54
1:A:2189:ARG:NH1	1:A:2299:VAL:O	2.41	0.53
1:A:2384:THR:H	1:A:2387:MSE:SE	2.41	0.53
1:A:2896:THR:H	3:A:3103:MES:H72	1.75	0.51
1:A:2272:ASP:H	1:A:2275:SER:HB2	1.74	0.51
1:A:2415:ARG:NH2	1:A:2423:LEU:O	2.42	0.51
1:A:2458:GLN:O	1:A:2461:GLN:NE2	2.37	0.50
1:A:2269:ILE:HG23	1:A:2270:VAL:HG13	1.93	0.50
1:A:2489:SER:OG	1:A:2523:HIS:ND1	2.43	0.50
1:A:2639:ARG:HG2	1:A:2735:LEU:HD21	1.94	0.49
1:A:2387:MSE:HE1	1:A:2451:ARG:HG3	1.93	0.49
1:A:2538:TYR:CG	1:A:2548:VAL:HG21	2.47	0.49
1:A:2157:GLU:HG3	1:A:2357:TYR:CG	2.49	0.47
1:A:2852:ASP:OD1	1:A:2879:ARG:NH1	2.42	0.47
1:A:2610:GLU:OE1	1:A:2628[A]:ARG:NH2	2.46	0.47
1:A:2866:VAL:HG13	1:A:2892:LEU:HD13	1.97	0.47
1:A:2443:VAL:HG13	1:A:2562:MSE:HE2	1.96	0.46
1:A:2360:ASP:HB3	1:A:2538:TYR:CZ	2.51	0.46
1:A:2921:PRO:HB3	1:A:2927:MSE:HG2	1.97	0.46
1:A:2274:TRP:O	1:A:2277:SER:OG	2.24	0.45
1:A:2141:LEU:HD23	1:A:2145:GLN:HB3	1.98	0.44
1:A:2692:LEU:HD21	1:A:2710:PRO:HB3	2.00	0.43
1:A:2349:ARG:NH2	1:A:2540:SER:O	2.51	0.43
1:A:2267:HIS:O	1:A:2271:SER:OG	2.37	0.41
1:A:2872:LEU:HD23	1:A:2916:ILE:HG21	2.01	0.41
1:A:2583:ARG:HA	1:A:2587:GLU:HB2	2.03	0.41
1:A:2154:MSE:HA	1:A:2157:GLU:HB3	2.03	0.40
1:A:2275:SER:HB3	1:A:2424:ILE:HB	2.03	0.40
1:A:2680:ASP:HB3	1:A:2683:TYR:CD2	2.56	0.40

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	822/873 (94%)	801 (97%)	18 (2%)	3 (0%)	30	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2303	PRO
1	A	2820	GLN
1	A	2243	GLY

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	620/685 (90%)	606 (98%)	14 (2%)	44	49

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2191	GLU
1	A	2192	VAL
1	A	2302	LEU
1	A	2317	ARG
1	A	2419	GLU
1	A	2424	ILE
1	A	2437	LEU
1	A	2476	ARG

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Mol	Chain	Res	Type
1	A	2491	GLU
1	A	2610	GLU
1	A	2757	THR
1	A	2795	PHE
1	A	2820	GLN
1	A	2854	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2414	ASN
1	A	2449	GLN
1	A	2525	HIS
1	A	2571	GLN
1	A	2745	HIS
1	A	2791	GLN
1	A	2890	HIS
1	A	2933	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 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	MES	A	3102	-	12,12,12	2.31	1 (8%)	15,16,16	1.94	3 (20%)
4	SO4	A	3112	-	4,4,4	0.24	0	6,6,6	0.07	0
3	MES	A	3103	2	12,12,12	2.34	1 (8%)	15,16,16	1.92	4 (26%)
4	SO4	A	3106	-	4,4,4	0.23	0	6,6,6	0.10	0
4	SO4	A	3109	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	A	3105	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	3115	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	3116	-	4,4,4	0.23	0	6,6,6	0.07	0
4	SO4	A	3117	-	4,4,4	0.23	0	6,6,6	0.08	0
3	MES	A	3104	-	12,12,12	2.35	1 (8%)	15,16,16	2.43	5 (33%)
4	SO4	A	3107	-	4,4,4	0.23	0	6,6,6	0.08	0
4	SO4	A	3118	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	A	3119	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	A	3120	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	A	3114	-	4,4,4	0.23	0	6,6,6	0.07	0
4	SO4	A	3110	-	4,4,4	0.23	0	6,6,6	0.09	0
4	SO4	A	3113	-	4,4,4	0.23	0	6,6,6	0.07	0
4	SO4	A	3108	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	A	3111	-	4,4,4	0.23	0	6,6,6	0.07	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	MES	A	3103	2	-	5/6/14/14	0/1/1/1
3	MES	A	3102	-	-	5/6/14/14	0/1/1/1
3	MES	A	3104	-	-	1/6/14/14	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3104	MES	C8-S	-7.88	1.66	1.77
3	A	3103	MES	C8-S	-7.82	1.66	1.77
3	A	3102	MES	C8-S	-7.74	1.66	1.77

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3104	MES	C5-N4-C3	5.37	120.40	108.84
3	A	3102	MES	C5-N4-C3	4.79	119.16	108.84
3	A	3104	MES	C6-C5-N4	-4.08	103.92	110.12
3	A	3103	MES	C5-N4-C3	3.68	116.76	108.84
3	A	3103	MES	C6-C5-N4	-3.64	104.59	110.12
3	A	3104	MES	C7-N4-C5	3.57	120.74	111.24
3	A	3104	MES	C7-N4-C3	2.80	118.69	111.24
3	A	3103	MES	C7-N4-C5	2.71	118.46	111.24
3	A	3102	MES	C7-N4-C5	2.23	117.18	111.24
3	A	3104	MES	O2S-S-C8	2.20	110.05	106.73
3	A	3103	MES	O2S-S-C8	2.14	109.97	106.73
3	A	3102	MES	C7-N4-C3	2.10	116.84	111.24

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3102	MES	C7-C8-S-O1S
3	A	3102	MES	C7-C8-S-O2S
3	A	3103	MES	C8-C7-N4-C5
3	A	3104	MES	C8-C7-N4-C5
3	A	3103	MES	C7-C8-S-O3S
3	A	3102	MES	C7-C8-S-O3S
3	A	3102	MES	C8-C7-N4-C5
3	A	3103	MES	C7-C8-S-O1S
3	A	3103	MES	C7-C8-S-O2S
3	A	3103	MES	N4-C7-C8-S
3	A	3102	MES	C8-C7-N4-C3

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3103	MES	1	0
4	A	3118	SO4	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(Å ²)	Q<0.9
1	A	816/873 (93%)	1.01	147 (18%) 3 4	28, 72, 170, 208	3 (0%)

All (147) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2286	LEU	8.1
1	A	2248	ILE	7.0
1	A	2307	LEU	6.8
1	A	2247	LEU	6.4
1	A	2253	LEU	5.9
1	A	2216	LEU	5.7
1	A	2290	TYR	5.6
1	A	2424	ILE	5.4
1	A	2252	LEU	5.2
1	A	2493	SER	5.1
1	A	2492	SER	4.9
1	A	2158	ALA	4.8
1	A	2152	ALA	4.8
1	A	2301	PRO	4.7
1	A	2302	LEU	4.6
1	A	2300	ASP	4.5
1	A	2153	GLN	4.5
1	A	2168	LEU	4.5
1	A	2303	PRO	4.4
1	A	2237	ARG	4.3
1	A	2217	VAL	4.3
1	A	2299	VAL	4.3
1	A	2305	LEU	4.2
1	A	2182	ALA	4.2
1	A	2181	ALA	4.2
1	A	2319	TRP	4.1
1	A	2234	VAL	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	2231	TRP	4.1
1	A	2258	GLN	4.1
1	A	2250	GLY	4.0
1	A	2284	GLY	4.0
1	A	2423	LEU	4.0
1	A	3002	ASP	4.0
1	A	2228	LEU	4.0
1	A	2262	LEU	4.0
1	A	2210	ALA	3.9
1	A	2270	VAL	3.9
1	A	2821	GLY	3.8
1	A	2308	GLN	3.7
1	A	2417	ARG	3.7
1	A	2823	GLN	3.7
1	A	2160	GLY	3.7
1	A	2422	GLY	3.7
1	A	2511	VAL	3.7
1	A	2753	THR	3.7
1	A	2183	LEU	3.6
1	A	2279	LEU	3.6
1	A	2740	SER	3.6
1	A	2312	TYR	3.6
1	A	2309	TYR	3.5
1	A	2274	TRP	3.5
1	A	2186	ILE	3.5
1	A	2755	GLY	3.5
1	A	2199	TRP	3.5
1	A	2246	PRO	3.5
1	A	2214	PHE	3.4
1	A	2229	ALA	3.4
1	A	2211	GLU	3.4
1	A	2242	LEU	3.4
1	A	2459	SER	3.4
1	A	2741	GLY	3.3
1	A	2218	ARG	3.3
1	A	2418	ALA	3.3
1	A	2171	ARG	3.3
1	A	2734[A]	ARG	3.3
1	A	2444	ALA	3.2
1	A	2462	ASP	3.2
1	A	2412	VAL	3.2
1	A	2416	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	2173	GLU	3.2
1	A	2420	LEU	3.1
1	A	2382	GLY	3.1
1	A	2263	LEU	3.1
1	A	2261	VAL	3.1
1	A	2414	ASN	3.0
1	A	2159	SER	3.0
1	A	2244	THR	3.0
1	A	2289	ALA	3.0
1	A	2510	PRO	3.0
1	A	2207	CYS	2.9
1	A	2991	LEU	2.9
1	A	2287	TYR	2.9
1	A	2224	GLU	2.9
1	A	2254	LYS	2.9
1	A	2527	ALA	2.9
1	A	2225	ALA	2.9
1	A	2729	ALA	2.9
1	A	2597	ARG	2.8
1	A	2478	LEU	2.8
1	A	2169	ARG	2.8
1	A	2447	LEU	2.8
1	A	2754	SER	2.7
1	A	2226	ALA	2.7
1	A	2291	ALA	2.7
1	A	2165	PRO	2.7
1	A	2239	PRO	2.7
1	A	2483	VAL	2.7
1	A	2260	HIS	2.7
1	A	2756	SER	2.7
1	A	2223	GLY	2.7
1	A	2280	ALA	2.7
1	A	2283	LEU	2.7
1	A	2757	THR	2.7
1	A	2241	ASP	2.7
1	A	2448	ALA	2.7
1	A	2249	ARG	2.7
1	A	2458	GLN	2.6
1	A	2150	PHE	2.6
1	A	2230	HIS	2.6
1	A	2474	PRO	2.6
1	A	2438	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	2314	LEU	2.6
1	A	2251	ARG	2.6
1	A	2590	ASP	2.6
1	A	2596	PRO	2.6
1	A	2155	SER	2.5
1	A	2190	HIS	2.5
1	A	2686	GLU	2.5
1	A	2304	ALA	2.5
1	A	2570	VAL	2.4
1	A	2235	GLU	2.4
1	A	2264	LEU	2.4
1	A	2320	LEU	2.4
1	A	2281	HIS	2.4
1	A	2208	ILE	2.4
1	A	2162	TYR	2.4
1	A	2317	ARG	2.4
1	A	2140	PRO	2.4
1	A	2315	TRP	2.4
1	A	2172	GLY	2.3
1	A	2822	GLN	2.3
1	A	2191	GLU	2.3
1	A	2240	PHE	2.2
1	A	2531	THR	2.2
1	A	2194	ARG	2.2
1	A	2473	LYS	2.2
1	A	2167	GLY	2.2
1	A	2867	CYS	2.2
1	A	3000	ARG	2.2
1	A	2198	GLU	2.1
1	A	2156	ARG	2.1
1	A	2513	GLU	2.1
1	A	2205	VAL	2.1
1	A	2329	LEU	2.1
1	A	2288	ARG	2.1
1	A	2958	GLY	2.1
1	A	2170	LEU	2.0

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 ⓘ

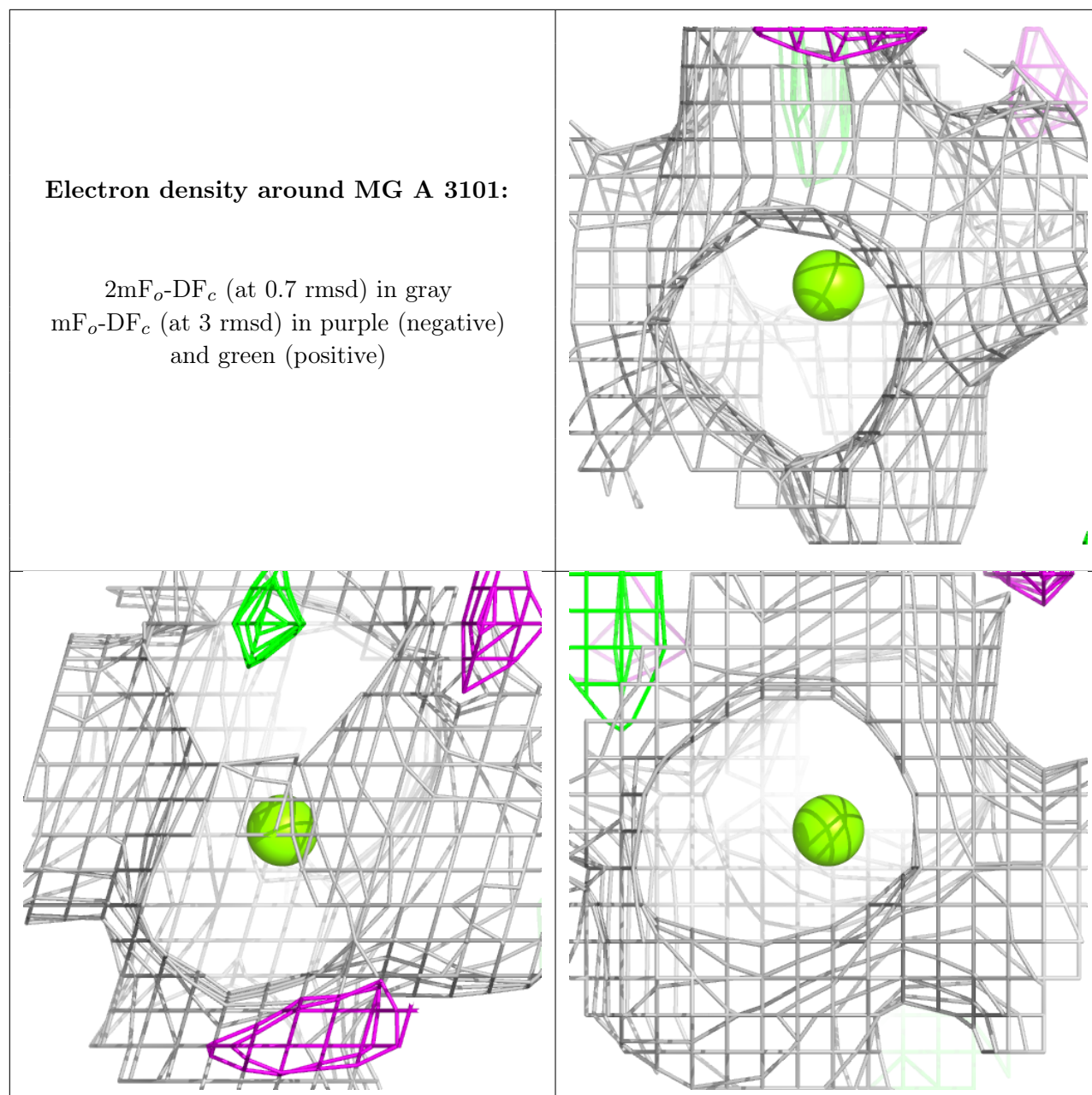
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
4	SO4	A	3116	5/5	0.54	0.15	153,156,158,159	0
4	SO4	A	3118	5/5	0.55	0.22	160,164,165,167	0
4	SO4	A	3111	5/5	0.61	0.10	120,121,122,124	5
4	SO4	A	3120	5/5	0.67	0.11	163,164,165,167	0
3	MES	A	3104	12/12	0.68	0.24	139,146,196,206	0
4	SO4	A	3119	5/5	0.69	0.16	155,158,160,161	0
3	MES	A	3103	12/12	0.70	0.26	119,130,132,144	0
4	SO4	A	3110	5/5	0.71	0.12	122,122,124,129	5
4	SO4	A	3107	5/5	0.71	0.14	130,133,134,136	0
4	SO4	A	3115	5/5	0.72	0.15	166,167,168,169	5
4	SO4	A	3108	5/5	0.75	0.12	154,154,158,159	5
4	SO4	A	3114	5/5	0.81	0.19	161,162,162,162	5
4	SO4	A	3113	5/5	0.82	0.23	151,152,152,153	5
4	SO4	A	3106	5/5	0.83	0.11	91,102,104,105	5
4	SO4	A	3112	5/5	0.83	0.10	100,104,105,110	5
4	SO4	A	3117	5/5	0.83	0.25	146,149,152,152	5
4	SO4	A	3109	5/5	0.84	0.10	149,151,152,155	0
4	SO4	A	3105	5/5	0.88	0.10	130,132,133,134	0
3	MES	A	3102	12/12	0.92	0.12	73,84,97,98	0
2	MG	A	3101	1/1	0.99	0.04	50,50,50,50	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.