



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 08:03 PM UTC

PDB ID : 6CCE / pdb_00006cce
Title : Crystal structure of a Mycobacterium smegmatis RNA polymerase transcription initiation complex with inhibitor Kanglemycin A
Authors : Lilic, M.; Darst, S.A.; Campbell, E.A.
Deposited on : 2018-02-07
Resolution : 3.05 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 ⓘ 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)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

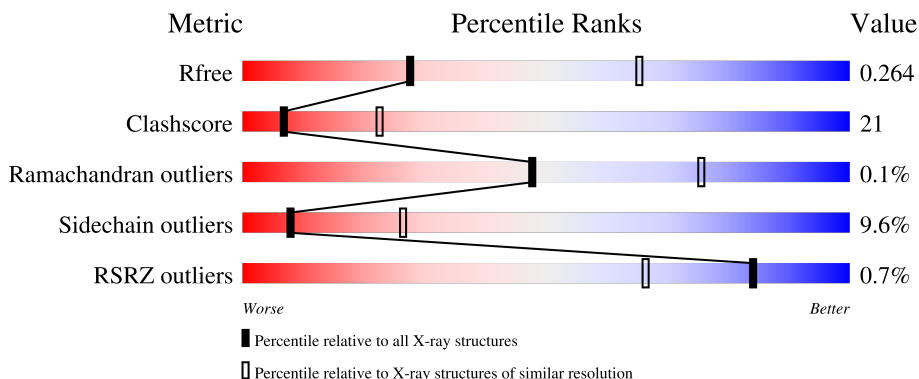
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	J	114	
2	A	350	
2	B	350	
3	C	1169	
4	D	1317	

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Mol	Chain	Length	Quality of chain
5	E	107	
6	F	466	
7	O	57	
8	G	19	

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
10	SO4	C	1202	-	-	X	-
10	SO4	C	1203	-	-	X	-
10	SO4	D	2004	-	-	X	-
10	SO4	D	2006	-	-	X	-
10	SO4	D	2007	-	-	X	-
13	GLU	D	2003	-	-	X	-

2 Entry composition [i](#)

There are 14 unique types of molecules in this entry. The entry contains 25375 atoms, of which 18 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 RNA polymerase-binding protein RbpA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	J	36	293	183	55	54	1	0	0	0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	A	221	1615	1019	273	320	3	0	0	0
2	B	226	1619	1015	278	324	2	0	0	0

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	1095	8269	5178	1448	1609	34	0	0	0

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	1195	9167	5746	1651	1734	36	0	0	0

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
5	E	77	593	379	100	114	0	0	0

- Molecule 6 is a protein called RNA polymerase sigma factor SigA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
6	F	302	2412	1511	434	460	7	0	0	0

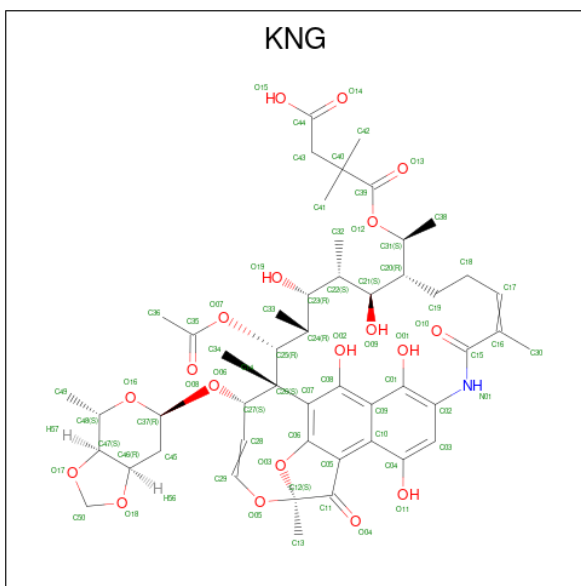
- Molecule 7 is a DNA chain called DNA (57-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
7	O	57	1161	560	208	338	55	0	0	0

- Molecule 8 is a protein called poly(UNK).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
8	G	19	95	57	19	19	0	0	0

- Molecule 9 is Kanglemycin A (CCD ID: KNG) (formula: C₅₀H₆₇NO₁₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
9	C	1	70	50	1	19	0	0

- Molecule 10 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



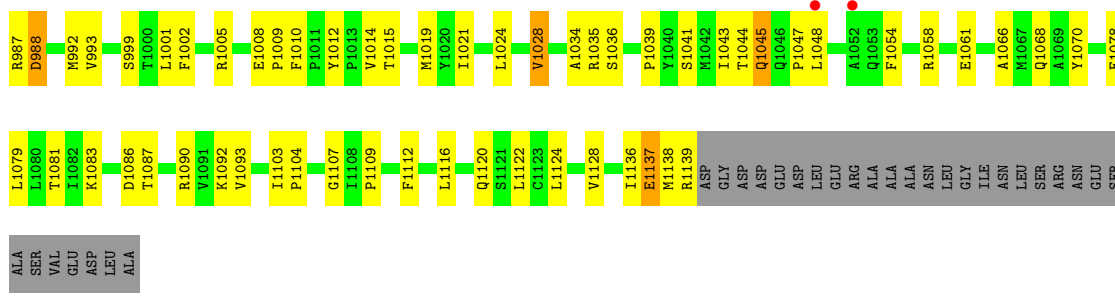
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	C	1	Total O S 5 4 1	0	0
10	C	1	Total O S 5 4 1	0	0
10	D	1	Total O S 5 4 1	0	0
10	D	1	Total O S 5 4 1	0	0
10	D	1	Total O S 5 4 1	0	0
10	D	1	Total O S 5 4 1	0	0
10	F	1	Total O S 5 4 1	0	0
10	F	1	Total O S 5 4 1	0	0

- Molecule 11 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	D	1	Total Zn 1 1	0	0

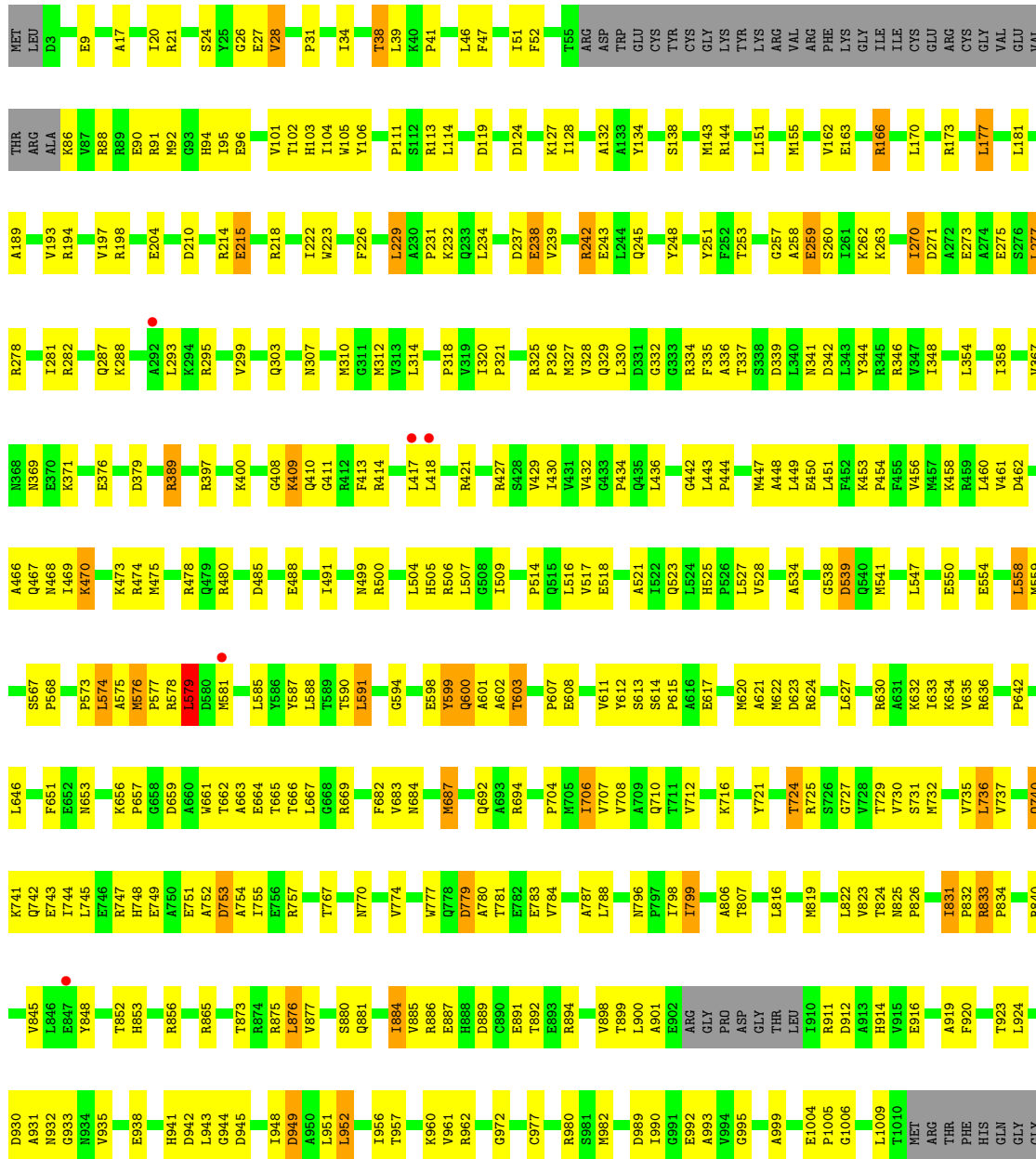
- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

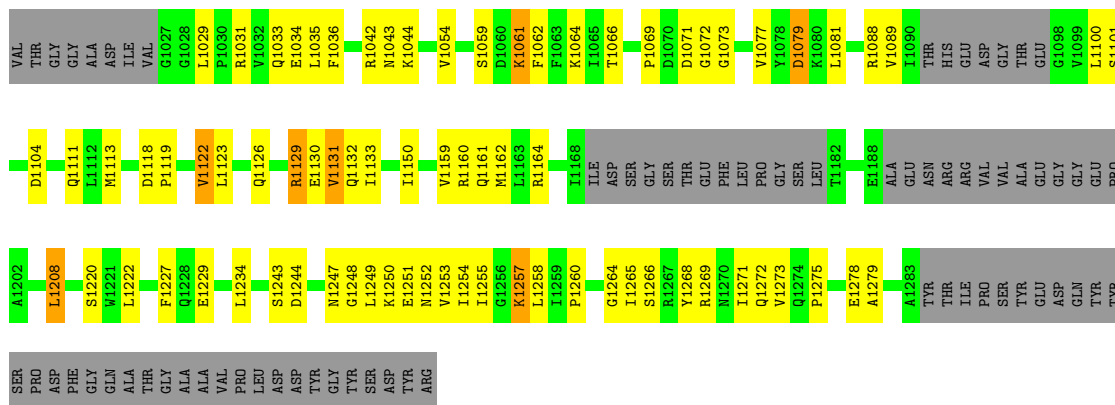
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
14	F	1	Total	C	H	O	0	0
			10	2	6	2		
14	F	1	Total	C	H	O	0	0
			10	2	6	2		
14	F	1	Total	C	H	O	0	0
			10	2	6	2		



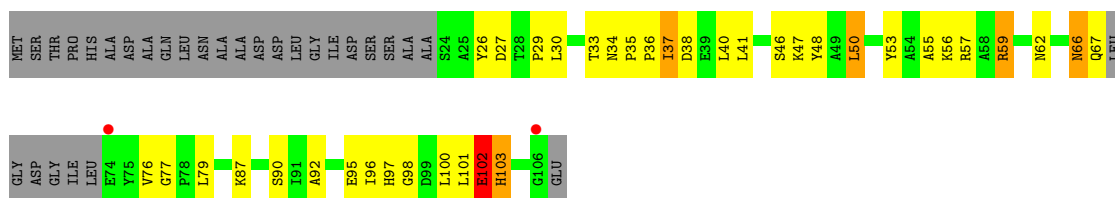
• Molecule 4: DNA-directed RNA polymerase subunit beta'

Chain D: 55% 32% 9%

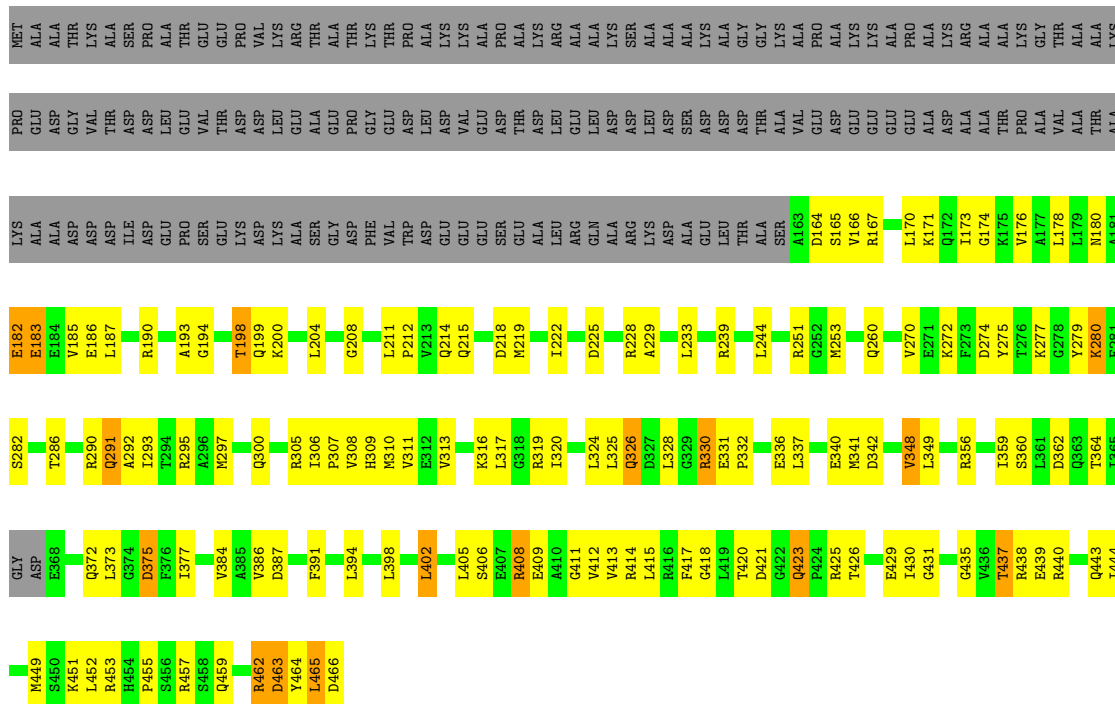
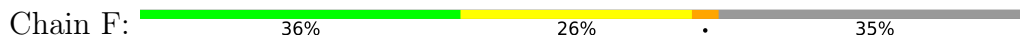




- Molecule 5: DNA-directed RNA polymerase subunit omega

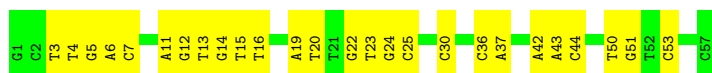


- Molecule 6: RNA polymerase sigma factor SigA



- Molecule 7: DNA (57-MER)

Chain O:  54% 46%



- Molecule 8: poly(UNK)

Chain G:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	130.56Å 161.58Å 135.14Å 90.00° 110.73° 90.00°	Depositor
Resolution (Å)	49.55 – 3.05 49.55 – 3.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.55-3.05) 99.8 (49.55-3.05)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 2.96Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.234 , 0.265 0.237 , 0.264	Depositor DCC
R_{free} test set	1951 reflections (1.76%)	wwPDB-VP
Wilson B-factor (Å ²)	105.6	Xtrriage
Anisotropy	0.103	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.020 for l,-k,h	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	25375	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.52% 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: SO4, ZN, EDO, KNG, MG

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	J	0.12	0/297	0.30	0/399
2	A	0.09	0/1640	0.28	0/2241
2	B	0.12	0/1644	0.34	0/2250
3	C	0.10	0/8415	0.30	0/11431
4	D	0.10	0/9306	0.30	0/12596
5	E	0.14	0/605	0.38	0/824
6	F	0.09	0/2441	0.28	0/3290
7	O	0.19	0/1301	0.37	0/2004
All	All	0.11	0/25649	0.31	0/35035

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
4	D	0	1
5	E	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	270	ILE	Peptide
5	E	102	GLU	Peptide

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	J	293	0	287	13	0
2	A	1615	0	1612	79	0
2	B	1619	0	1551	84	0
3	C	8269	0	8014	388	0
4	D	9167	0	9167	405	0
5	E	593	0	579	45	0
6	F	2412	0	2451	134	0
7	O	1161	0	650	35	0
8	G	95	0	21	0	0
9	C	70	0	0	1	0
10	C	10	0	0	4	0
10	D	20	0	0	9	0
10	F	10	0	0	0	0
11	D	1	0	0	0	0
12	D	1	0	0	0	0
13	D	9	0	5	11	0
14	F	12	18	18	5	0
All	All	25357	18	24355	1063	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 21.

The worst 5 of 1063 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)
3:C:538:PRO:HB2	3:C:546:THR:HB	1.28	1.14
5:E:102:GLU:HA	5:E:103:HIS:HB3	1.09	1.07
4:D:636:ARG:HB3	4:D:662:THR:HG22	1.40	1.04
5:E:102:GLU:HA	5:E:103:HIS:CB	1.92	0.98
6:F:290:ARG:NH1	14:F:503:EDO:O1	2.00	0.94

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	J	34/114 (30%)	34 (100%)	0	0	100	100
2	A	219/350 (63%)	216 (99%)	2 (1%)	1 (0%)	24	52
2	B	222/350 (63%)	203 (91%)	19 (9%)	0	100	100
3	C	1087/1169 (93%)	1057 (97%)	30 (3%)	0	100	100
4	D	1181/1317 (90%)	1146 (97%)	34 (3%)	1 (0%)	48	75
5	E	73/107 (68%)	67 (92%)	6 (8%)	0	100	100
6	F	298/466 (64%)	296 (99%)	2 (1%)	0	100	100
All	All	3114/3873 (80%)	3019 (97%)	93 (3%)	2 (0%)	48	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	579	LEU
2	A	183	VAL

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	J	30/98 (31%)	26 (87%)	4 (13%)	4	14
2	A	175/297 (59%)	151 (86%)	24 (14%)	3	13
2	B	168/297 (57%)	142 (84%)	26 (16%)	2	10
3	C	865/984 (88%)	779 (90%)	86 (10%)	7	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	955/1095 (87%)	881 (92%)	74 (8%)	12	35
5	E	61/86 (71%)	54 (88%)	7 (12%)	5	19
6	F	256/379 (68%)	236 (92%)	20 (8%)	11	34
All	All	2510/3236 (78%)	2269 (90%)	241 (10%)	8	26

5 of 241 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	737	VAL
6	F	182	GLU
4	D	144	ARG
5	E	102	GLU
6	F	423	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
4	D	416	ASN
4	D	649	GLN
4	D	465	HIS
4	D	540	GLN
4	D	692	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 15 ligands modelled in this entry, 2 are 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
14	EDO	F	504	-	3,3,3	0.46	0	2,2,2	0.41	0
10	SO4	D	2005	-	4,4,4	0.25	0	6,6,6	0.07	0
10	SO4	D	2006	-	4,4,4	0.24	0	6,6,6	0.08	0
10	SO4	C	1202	-	4,4,4	0.25	0	6,6,6	0.08	0
13	GLU	D	2003	-	7,8,9	0.93	0	4,9,11	1.11	0
10	SO4	D	2007	-	4,4,4	0.23	0	6,6,6	0.08	0
10	SO4	D	2004	-	4,4,4	0.22	0	6,6,6	0.11	0
9	KNG	C	1201	-	75,75,75	2.70	17 (22%)	107,114,114	1.77	19 (17%)
14	EDO	F	503	-	3,3,3	0.43	0	2,2,2	0.47	0
10	SO4	C	1203	-	4,4,4	0.24	0	6,6,6	0.05	0
14	EDO	F	505	-	3,3,3	0.45	0	2,2,2	0.39	0
10	SO4	F	501	-	4,4,4	0.24	0	6,6,6	0.06	0
10	SO4	F	502	-	4,4,4	0.23	0	6,6,6	0.10	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
14	EDO	F	504	-	-	1/1/1/1	-
13	GLU	D	2003	-	-	2/6/7/9	-
14	EDO	F	503	-	-	1/1/1/1	-
9	KNG	C	1201	-	-	17/76/113/113	0/5/6/6
14	EDO	F	505	-	-	1/1/1/1	-

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	1201	KNG	O04-C11	12.44	1.40	1.21
9	C	1201	KNG	C17-C16	9.73	1.53	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	C	1201	KNG	O03-C06	9.55	1.55	1.37
9	C	1201	KNG	C15-N01	4.70	1.45	1.35
9	C	1201	KNG	C12-C11	-3.97	1.39	1.54

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	1201	KNG	C18-C17-C16	-6.03	114.83	128.94
9	C	1201	KNG	O04-C11-C05	-5.16	122.12	131.63
9	C	1201	KNG	O07-C35-C36	5.03	120.06	111.09
9	C	1201	KNG	O03-C06-C07	4.63	129.01	121.16
9	C	1201	KNG	C12-C11-C05	4.31	115.63	107.30

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	C	1201	KNG	O07-C25-C26-C34
9	C	1201	KNG	C40-C43-C44-O14
9	C	1201	KNG	O07-C25-C26-C27
9	C	1201	KNG	C24-C25-C26-C34
9	C	1201	KNG	O12-C39-C40-C42

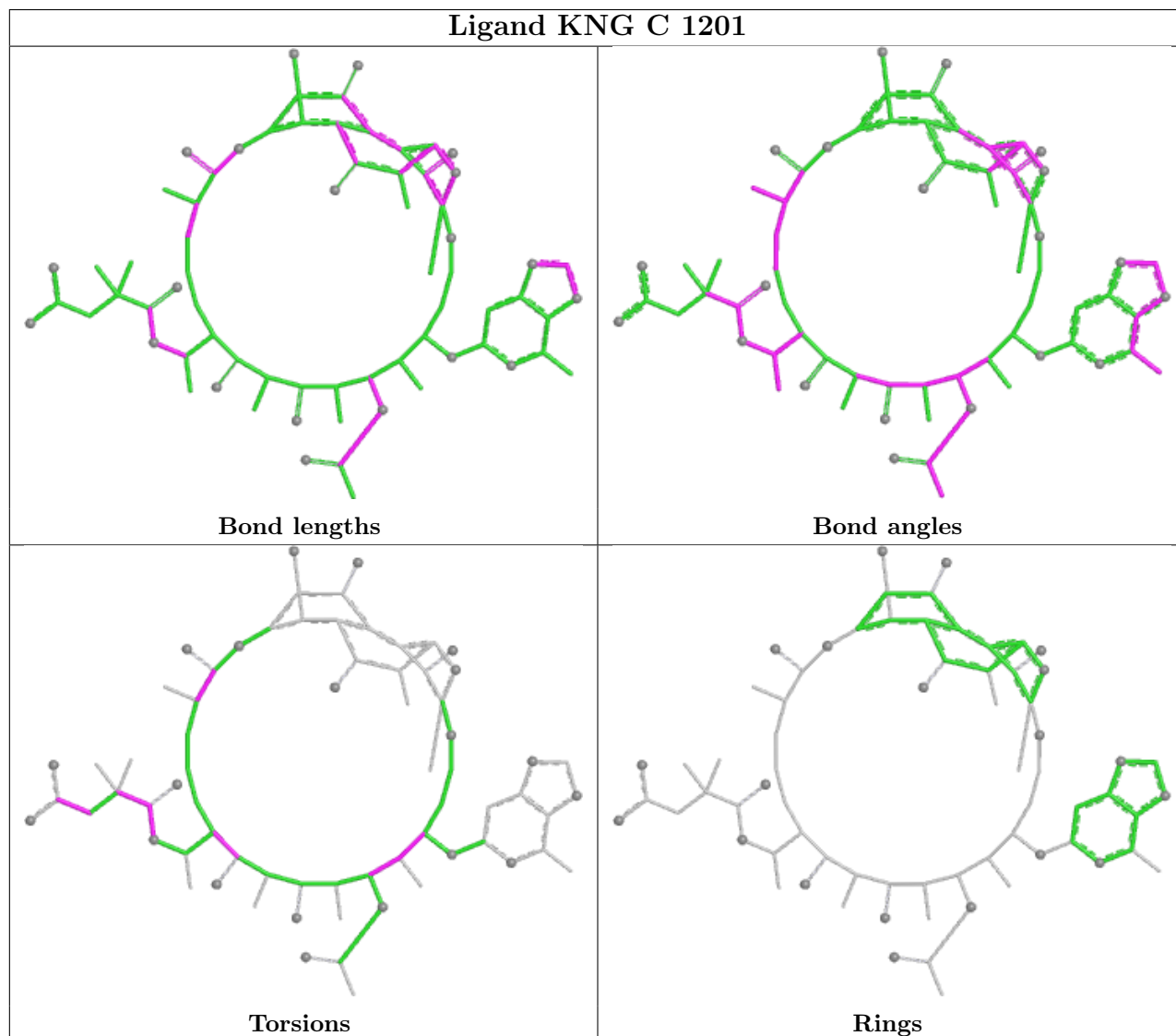
There are no ring outliers.

10 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	D	2005	SO4	1	0
10	D	2006	SO4	2	0
10	C	1202	SO4	2	0
13	D	2003	GLU	11	0
10	D	2007	SO4	3	0
10	D	2004	SO4	3	0
9	C	1201	KNG	1	0
14	F	503	EDO	2	0
10	C	1203	SO4	2	0
14	F	505	EDO	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will

also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [\(i\)](#)

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 [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(Å ²)	Q<0.9
1	J	36/114 (31%)	-0.20	0 100 100	75, 99, 146, 158	0
2	A	221/350 (63%)	0.01	0 100 100	76, 106, 144, 170	0
2	B	226/350 (64%)	0.28	1 (0%) 88 75	101, 137, 164, 184	0
3	C	1095/1169 (93%)	0.00	14 (1%) 75 53	54, 110, 174, 200	0
4	D	1195/1317 (90%)	-0.18	5 (0%) 88 75	45, 96, 152, 196	0
5	E	77/107 (71%)	-0.01	2 (2%) 57 34	76, 109, 153, 172	0
6	F	302/466 (64%)	-0.15	0 100 100	57, 98, 144, 165	0
7	O	57/57 (100%)	-0.55	0 100 100	74, 103, 133, 140	0
8	G	0/19	-	-	-	-
All	All	3209/3949 (81%)	-0.07	22 (0%) 84 66	45, 106, 167, 200	0

The worst 5 of 22 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	E	106	GLY	3.2
4	D	417	LEU	2.7
3	C	397	THR	2.7
3	C	311	LEU	2.6
3	C	1052	ALA	2.6

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](#)

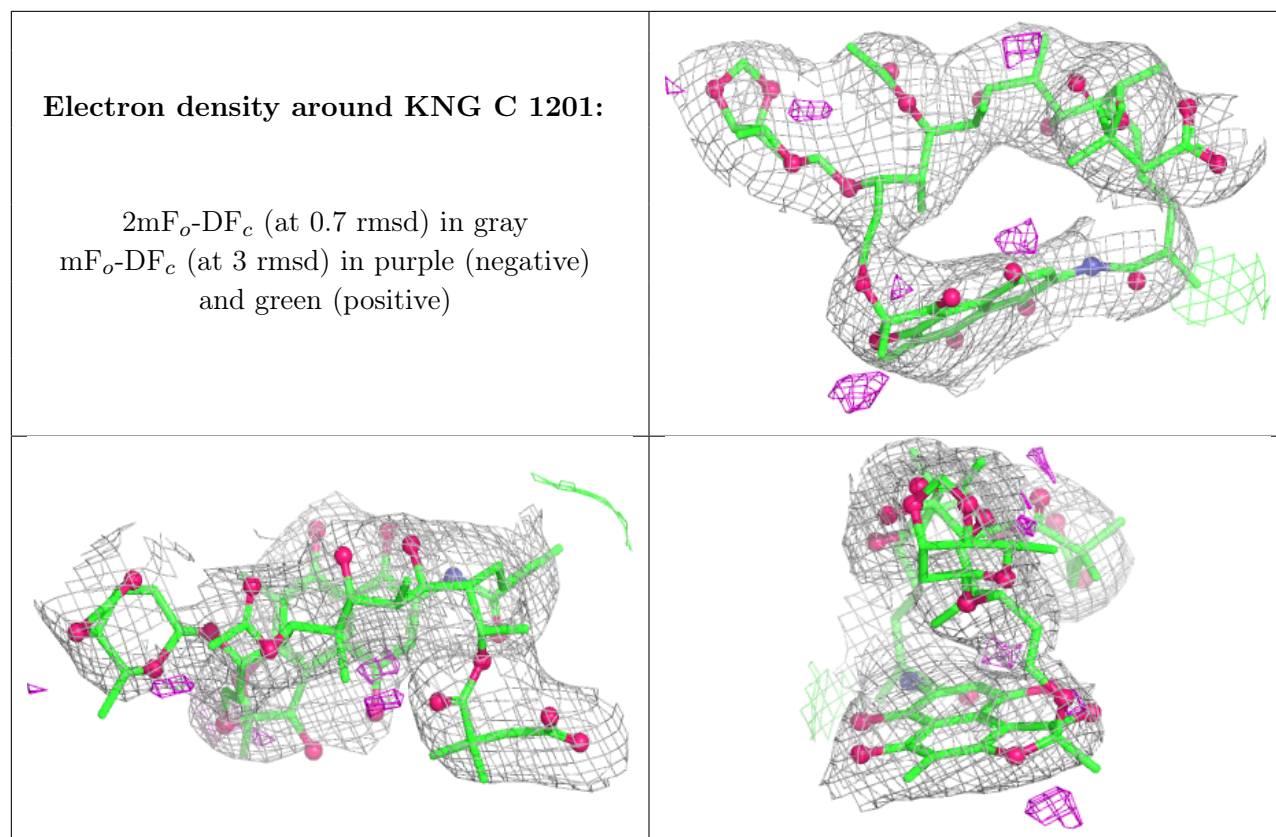
There are no oligosaccharides in this entry.

6.4 Ligands

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(\AA^2)	Q<0.9
10	SO4	D	2007	5/5	0.67	0.07	135,138,154,236	0
10	SO4	F	502	5/5	0.69	0.18	103,105,125,132	0
10	SO4	C	1202	5/5	0.75	0.07	129,134,157,157	0
10	SO4	D	2004	5/5	0.76	0.08	120,136,154,158	0
14	EDO	F	505	4/4	0.76	0.12	90,108,127,127	0
12	MG	D	2002	1/1	0.78	0.09	109,109,109,109	0
10	SO4	C	1203	5/5	0.82	0.16	122,132,137,156	0
10	SO4	D	2005	5/5	0.87	0.12	109,117,126,129	0
13	GLU	D	2003	9/10	0.89	0.08	96,108,115,117	0
10	SO4	D	2006	5/5	0.89	0.19	115,123,131,165	0
14	EDO	F	503	4/4	0.90	0.14	73,88,103,104	0
10	SO4	F	501	5/5	0.91	0.08	97,98,114,116	0
9	KNG	C	1201	70/70	0.91	0.10	75,100,119,136	0
14	EDO	F	504	4/4	0.95	0.16	95,114,127,127	0
11	ZN	D	2001	1/1	1.00	0.07	116,116,116,116	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 [i](#)

There are no such residues in this entry.