



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:06 AM UTC

PDB ID : 8W50 / pdb_00008w50
Title : Crystal structure of DNA binding and cleavage core of human topoisomerase 2-alpha in a DNA binding-competent conformation
Authors : Chan, N.L.; Liu, K.T.; Chen, S.F.
Deposited on : 2023-08-25
Resolution : 2.67 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)
Xtriage (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

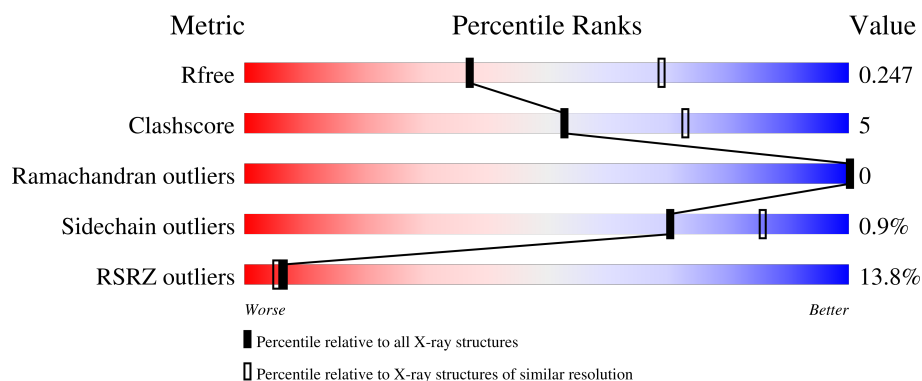
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.67 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	806	 6% 78% 12% 10%
1	B	806	 7% 77% 12% 11%
1	C	806	 14% 70% 10% 20%
1	D	806	 21% 72% 9% 19%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20918 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 DNA topoisomerase 2-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	729	Total	C	N	O	S	0	1	0
			5689	3662	932	1068	27			
1	B	716	Total	C	N	O	S	0	0	0
			5457	3500	906	1028	23			
1	C	644	Total	C	N	O	S	0	0	0
			4702	3006	788	888	20			
1	D	656	Total	C	N	O	S	0	0	0
			4673	2995	786	870	22			

There are 184 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	403	MET	-	expression tag	UNP P11388
A	404	ALA	-	expression tag	UNP P11388
A	405	SER	-	expression tag	UNP P11388
A	406	TRP	-	expression tag	UNP P11388
A	407	SER	-	expression tag	UNP P11388
A	408	HIS	-	expression tag	UNP P11388
A	409	PRO	-	expression tag	UNP P11388
A	410	GLN	-	expression tag	UNP P11388
A	411	PHE	-	expression tag	UNP P11388
A	412	GLU	-	expression tag	UNP P11388
A	413	LYS	-	expression tag	UNP P11388
A	414	GLY	-	expression tag	UNP P11388
A	415	ALA	-	expression tag	UNP P11388
A	416	ASP	-	expression tag	UNP P11388
A	417	ASP	-	expression tag	UNP P11388
A	418	ASP	-	expression tag	UNP P11388
A	419	ASP	-	expression tag	UNP P11388
A	420	LYS	-	expression tag	UNP P11388
A	421	VAL	-	expression tag	UNP P11388
A	422	PRO	-	expression tag	UNP P11388
A	423	ASP	-	expression tag	UNP P11388

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Chain	Residue	Modelled	Actual	Comment	Reference
A	424	PRO	-	expression tag	UNP P11388
A	425	THR	-	expression tag	UNP P11388
A	426	SER	-	expression tag	UNP P11388
A	427	VAL	-	expression tag	UNP P11388
A	428	ASP	-	expression tag	UNP P11388
A	1189	GLY	-	expression tag	UNP P11388
A	1190	ALA	-	expression tag	UNP P11388
A	1191	PRO	-	expression tag	UNP P11388
A	1192	GLY	-	expression tag	UNP P11388
A	1193	PHE	-	expression tag	UNP P11388
A	1194	SER	-	expression tag	UNP P11388
A	1195	SER	-	expression tag	UNP P11388
A	1196	ILE	-	expression tag	UNP P11388
A	1197	SER	-	expression tag	UNP P11388
A	1198	ALA	-	expression tag	UNP P11388
A	1199	HIS	-	expression tag	UNP P11388
A	1200	HIS	-	expression tag	UNP P11388
A	1201	HIS	-	expression tag	UNP P11388
A	1202	HIS	-	expression tag	UNP P11388
A	1203	HIS	-	expression tag	UNP P11388
A	1204	HIS	-	expression tag	UNP P11388
A	1205	HIS	-	expression tag	UNP P11388
A	1206	HIS	-	expression tag	UNP P11388
A	1207	HIS	-	expression tag	UNP P11388
A	1208	HIS	-	expression tag	UNP P11388
B	403	MET	-	expression tag	UNP P11388
B	404	ALA	-	expression tag	UNP P11388
B	405	SER	-	expression tag	UNP P11388
B	406	TRP	-	expression tag	UNP P11388
B	407	SER	-	expression tag	UNP P11388
B	408	HIS	-	expression tag	UNP P11388
B	409	PRO	-	expression tag	UNP P11388
B	410	GLN	-	expression tag	UNP P11388
B	411	PHE	-	expression tag	UNP P11388
B	412	GLU	-	expression tag	UNP P11388
B	413	LYS	-	expression tag	UNP P11388
B	414	GLY	-	expression tag	UNP P11388
B	415	ALA	-	expression tag	UNP P11388
B	416	ASP	-	expression tag	UNP P11388
B	417	ASP	-	expression tag	UNP P11388
B	418	ASP	-	expression tag	UNP P11388
B	419	ASP	-	expression tag	UNP P11388

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Chain	Residue	Modelled	Actual	Comment	Reference
B	420	LYS	-	expression tag	UNP P11388
B	421	VAL	-	expression tag	UNP P11388
B	422	PRO	-	expression tag	UNP P11388
B	423	ASP	-	expression tag	UNP P11388
B	424	PRO	-	expression tag	UNP P11388
B	425	THR	-	expression tag	UNP P11388
B	426	SER	-	expression tag	UNP P11388
B	427	VAL	-	expression tag	UNP P11388
B	428	ASP	-	expression tag	UNP P11388
B	1189	GLY	-	expression tag	UNP P11388
B	1190	ALA	-	expression tag	UNP P11388
B	1191	PRO	-	expression tag	UNP P11388
B	1192	GLY	-	expression tag	UNP P11388
B	1193	PHE	-	expression tag	UNP P11388
B	1194	SER	-	expression tag	UNP P11388
B	1195	SER	-	expression tag	UNP P11388
B	1196	ILE	-	expression tag	UNP P11388
B	1197	SER	-	expression tag	UNP P11388
B	1198	ALA	-	expression tag	UNP P11388
B	1199	HIS	-	expression tag	UNP P11388
B	1200	HIS	-	expression tag	UNP P11388
B	1201	HIS	-	expression tag	UNP P11388
B	1202	HIS	-	expression tag	UNP P11388
B	1203	HIS	-	expression tag	UNP P11388
B	1204	HIS	-	expression tag	UNP P11388
B	1205	HIS	-	expression tag	UNP P11388
B	1206	HIS	-	expression tag	UNP P11388
B	1207	HIS	-	expression tag	UNP P11388
B	1208	HIS	-	expression tag	UNP P11388
C	403	MET	-	expression tag	UNP P11388
C	404	ALA	-	expression tag	UNP P11388
C	405	SER	-	expression tag	UNP P11388
C	406	TRP	-	expression tag	UNP P11388
C	407	SER	-	expression tag	UNP P11388
C	408	HIS	-	expression tag	UNP P11388
C	409	PRO	-	expression tag	UNP P11388
C	410	GLN	-	expression tag	UNP P11388
C	411	PHE	-	expression tag	UNP P11388
C	412	GLU	-	expression tag	UNP P11388
C	413	LYS	-	expression tag	UNP P11388
C	414	GLY	-	expression tag	UNP P11388
C	415	ALA	-	expression tag	UNP P11388

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Chain	Residue	Modelled	Actual	Comment	Reference
C	416	ASP	-	expression tag	UNP P11388
C	417	ASP	-	expression tag	UNP P11388
C	418	ASP	-	expression tag	UNP P11388
C	419	ASP	-	expression tag	UNP P11388
C	420	LYS	-	expression tag	UNP P11388
C	421	VAL	-	expression tag	UNP P11388
C	422	PRO	-	expression tag	UNP P11388
C	423	ASP	-	expression tag	UNP P11388
C	424	PRO	-	expression tag	UNP P11388
C	425	THR	-	expression tag	UNP P11388
C	426	SER	-	expression tag	UNP P11388
C	427	VAL	-	expression tag	UNP P11388
C	428	ASP	-	expression tag	UNP P11388
C	1189	GLY	-	expression tag	UNP P11388
C	1190	ALA	-	expression tag	UNP P11388
C	1191	PRO	-	expression tag	UNP P11388
C	1192	GLY	-	expression tag	UNP P11388
C	1193	PHE	-	expression tag	UNP P11388
C	1194	SER	-	expression tag	UNP P11388
C	1195	SER	-	expression tag	UNP P11388
C	1196	ILE	-	expression tag	UNP P11388
C	1197	SER	-	expression tag	UNP P11388
C	1198	ALA	-	expression tag	UNP P11388
C	1199	HIS	-	expression tag	UNP P11388
C	1200	HIS	-	expression tag	UNP P11388
C	1201	HIS	-	expression tag	UNP P11388
C	1202	HIS	-	expression tag	UNP P11388
C	1203	HIS	-	expression tag	UNP P11388
C	1204	HIS	-	expression tag	UNP P11388
C	1205	HIS	-	expression tag	UNP P11388
C	1206	HIS	-	expression tag	UNP P11388
C	1207	HIS	-	expression tag	UNP P11388
C	1208	HIS	-	expression tag	UNP P11388
D	403	MET	-	expression tag	UNP P11388
D	404	ALA	-	expression tag	UNP P11388
D	405	SER	-	expression tag	UNP P11388
D	406	TRP	-	expression tag	UNP P11388
D	407	SER	-	expression tag	UNP P11388
D	408	HIS	-	expression tag	UNP P11388
D	409	PRO	-	expression tag	UNP P11388
D	410	GLN	-	expression tag	UNP P11388
D	411	PHE	-	expression tag	UNP P11388

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Chain	Residue	Modelled	Actual	Comment	Reference
D	412	GLU	-	expression tag	UNP P11388
D	413	LYS	-	expression tag	UNP P11388
D	414	GLY	-	expression tag	UNP P11388
D	415	ALA	-	expression tag	UNP P11388
D	416	ASP	-	expression tag	UNP P11388
D	417	ASP	-	expression tag	UNP P11388
D	418	ASP	-	expression tag	UNP P11388
D	419	ASP	-	expression tag	UNP P11388
D	420	LYS	-	expression tag	UNP P11388
D	421	VAL	-	expression tag	UNP P11388
D	422	PRO	-	expression tag	UNP P11388
D	423	ASP	-	expression tag	UNP P11388
D	424	PRO	-	expression tag	UNP P11388
D	425	THR	-	expression tag	UNP P11388
D	426	SER	-	expression tag	UNP P11388
D	427	VAL	-	expression tag	UNP P11388
D	428	ASP	-	expression tag	UNP P11388
D	1189	GLY	-	expression tag	UNP P11388
D	1190	ALA	-	expression tag	UNP P11388
D	1191	PRO	-	expression tag	UNP P11388
D	1192	GLY	-	expression tag	UNP P11388
D	1193	PHE	-	expression tag	UNP P11388
D	1194	SER	-	expression tag	UNP P11388
D	1195	SER	-	expression tag	UNP P11388
D	1196	ILE	-	expression tag	UNP P11388
D	1197	SER	-	expression tag	UNP P11388
D	1198	ALA	-	expression tag	UNP P11388
D	1199	HIS	-	expression tag	UNP P11388
D	1200	HIS	-	expression tag	UNP P11388
D	1201	HIS	-	expression tag	UNP P11388
D	1202	HIS	-	expression tag	UNP P11388
D	1203	HIS	-	expression tag	UNP P11388
D	1204	HIS	-	expression tag	UNP P11388
D	1205	HIS	-	expression tag	UNP P11388
D	1206	HIS	-	expression tag	UNP P11388
D	1207	HIS	-	expression tag	UNP P11388
D	1208	HIS	-	expression tag	UNP P11388

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



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

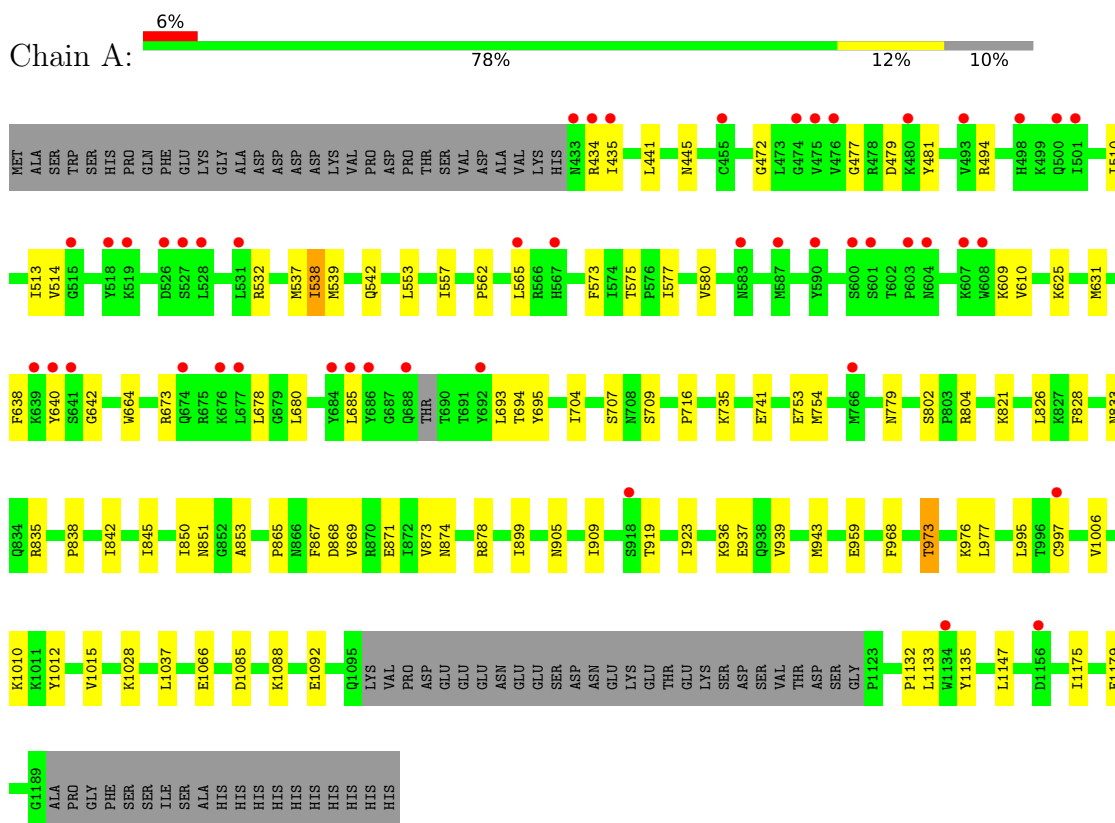
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	201	Total	O	0	0
			201	201		
3	B	120	Total	O	0	0
			120	120		
3	C	54	Total	O	0	0
			54	54		
3	D	7	Total	O	0	0
			7	7		

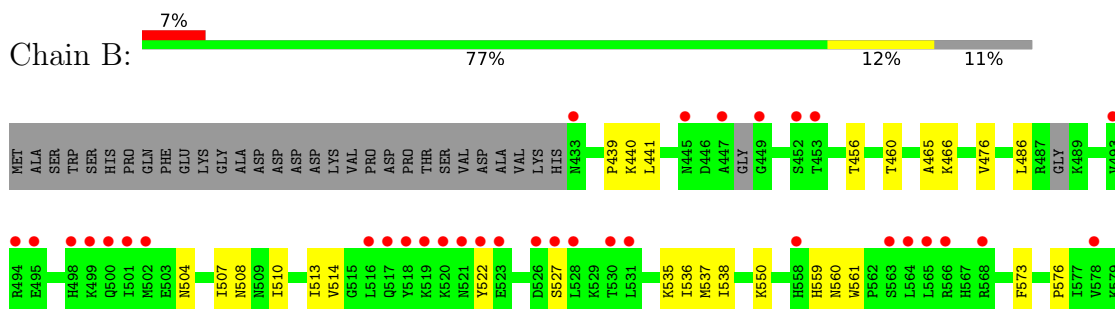
3 Residue-property plots

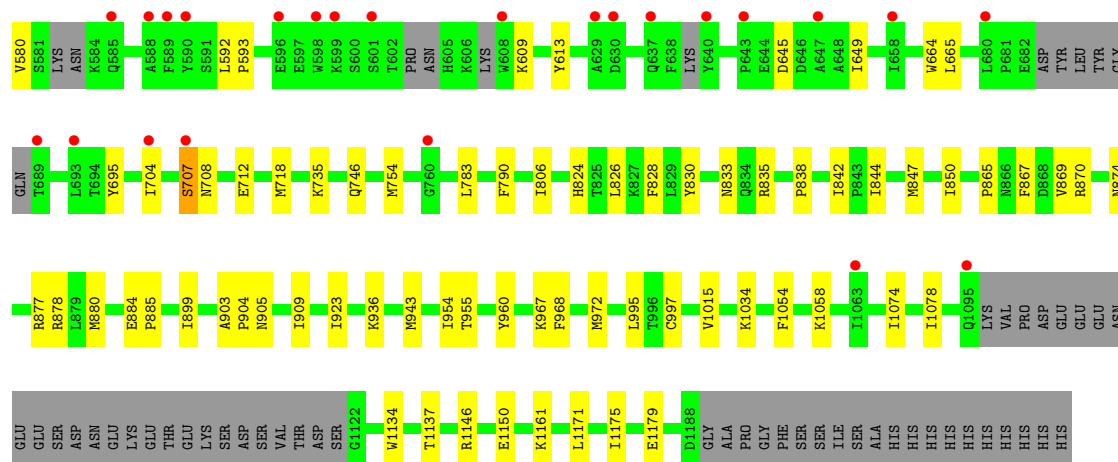
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DNA topoisomerase 2-alpha

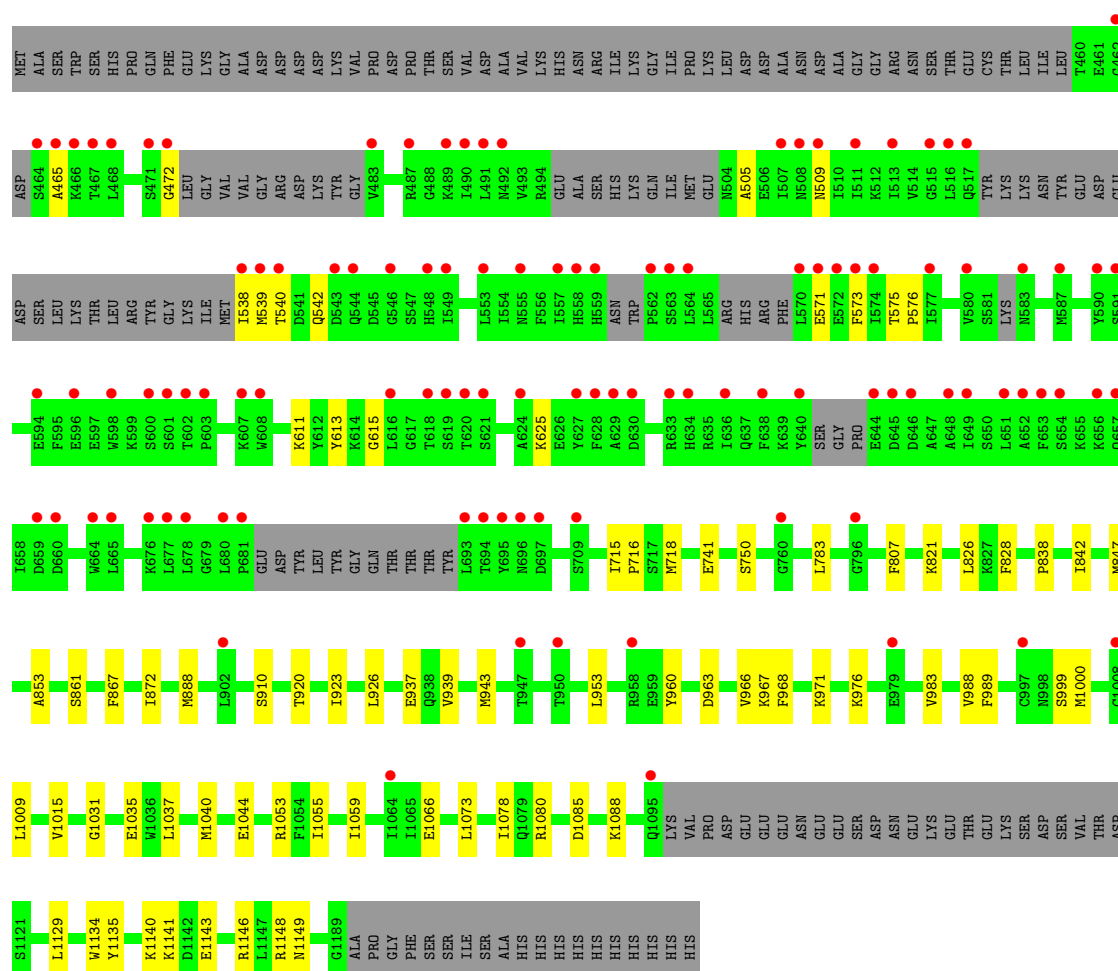


• Molecule 1: DNA topoisomerase 2-alpha





• Molecule 1: DNA topoisomerase 2-alpha



• Molecule 1: DNA topoisomerase 2-alpha





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	266.10Å 266.10Å 172.81Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	23.19 – 2.67 23.19 – 2.67	Depositor EDS
% Data completeness (in resolution range)	99.0 (23.19-2.67) 98.9 (23.19-2.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.67Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.222 , 0.248 0.222 , 0.247	Depositor DCC
R_{free} test set	2025 reflections (1.56%)	wwPDB-VP
Wilson B-factor (Å ²)	51.5	Xtriage
Anisotropy	0.329	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	20918	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.15% 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: 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	0.16	0/5810	0.34	0/7866
1	B	0.15	0/5561	0.33	0/7534
1	C	0.15	0/4786	0.30	0/6496
1	D	0.14	0/4767	0.30	0/6495
All	All	0.15	0/20924	0.32	0/28391

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	5689	0	5467	58	0
1	B	5457	0	5129	57	0
1	C	4702	0	4204	49	0
1	D	4673	0	3960	46	0
2	A	10	0	0	0	0
2	B	5	0	0	0	0
3	A	201	0	0	3	0
3	B	120	0	0	1	0
3	C	54	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	7	0	0	0	0
All	All	20918	0	18760	197	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 5.

The worst 5 of 197 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:D:577:ILE:HG23	1:D:578:VAL:HG23	1.62	0.81
1:C:542:GLN:HE21	1:C:575:THR:HG22	1.55	0.72
1:D:864:ILE:HG12	1:D:1000:MET:HG2	1.72	0.71
1:C:1059:ILE:HG23	1:D:1066:GLU:HB3	1.75	0.68
1:B:850:ILE:HD12	1:B:869:VAL:HG22	1.78	0.66

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	724/806 (90%)	711 (98%)	13 (2%)	0	100	100
1	B	698/806 (87%)	683 (98%)	15 (2%)	0	100	100
1	C	622/806 (77%)	609 (98%)	13 (2%)	0	100	100
1	D	634/806 (79%)	622 (98%)	12 (2%)	0	100	100
All	All	2678/3224 (83%)	2625 (98%)	53 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	575/724 (79%)	568 (99%)	7 (1%)	63	82
1	B	535/724 (74%)	531 (99%)	4 (1%)	76	89
1	C	420/724 (58%)	416 (99%)	4 (1%)	68	84
1	D	382/724 (53%)	379 (99%)	3 (1%)	73	87
All	All	1912/2896 (66%)	1894 (99%)	18 (1%)	70	86

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	910	SER
1	D	868	ASP
1	D	753	GLU
1	B	707	SER
1	C	872	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	746	GLN
1	C	1094	GLN
1	D	789	GLN
1	C	986	HIS
1	D	445	ASN

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 [i](#)

3 ligands 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	$\# Z > 2$
2	SO4	B	1301	-	4,4,4	0.84	0	6,6,6	0.53	0
2	SO4	A	1301	-	4,4,4	0.84	0	6,6,6	0.57	0
2	SO4	A	1302	-	4,4,4	0.85	0	6,6,6	0.53	0

There are no bond length outliers.

There are no bond angle outliers.

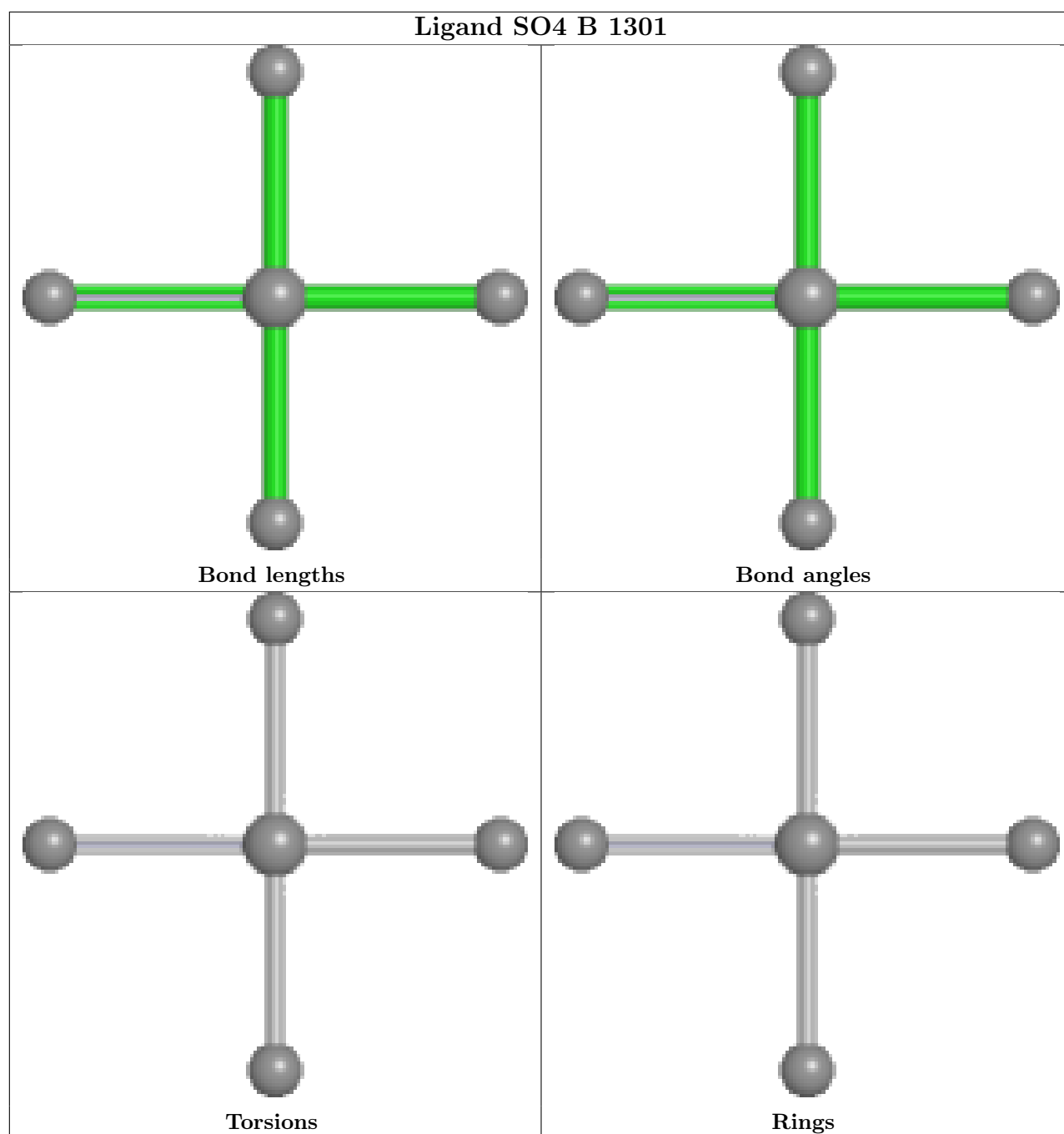
There are no chirality outliers.

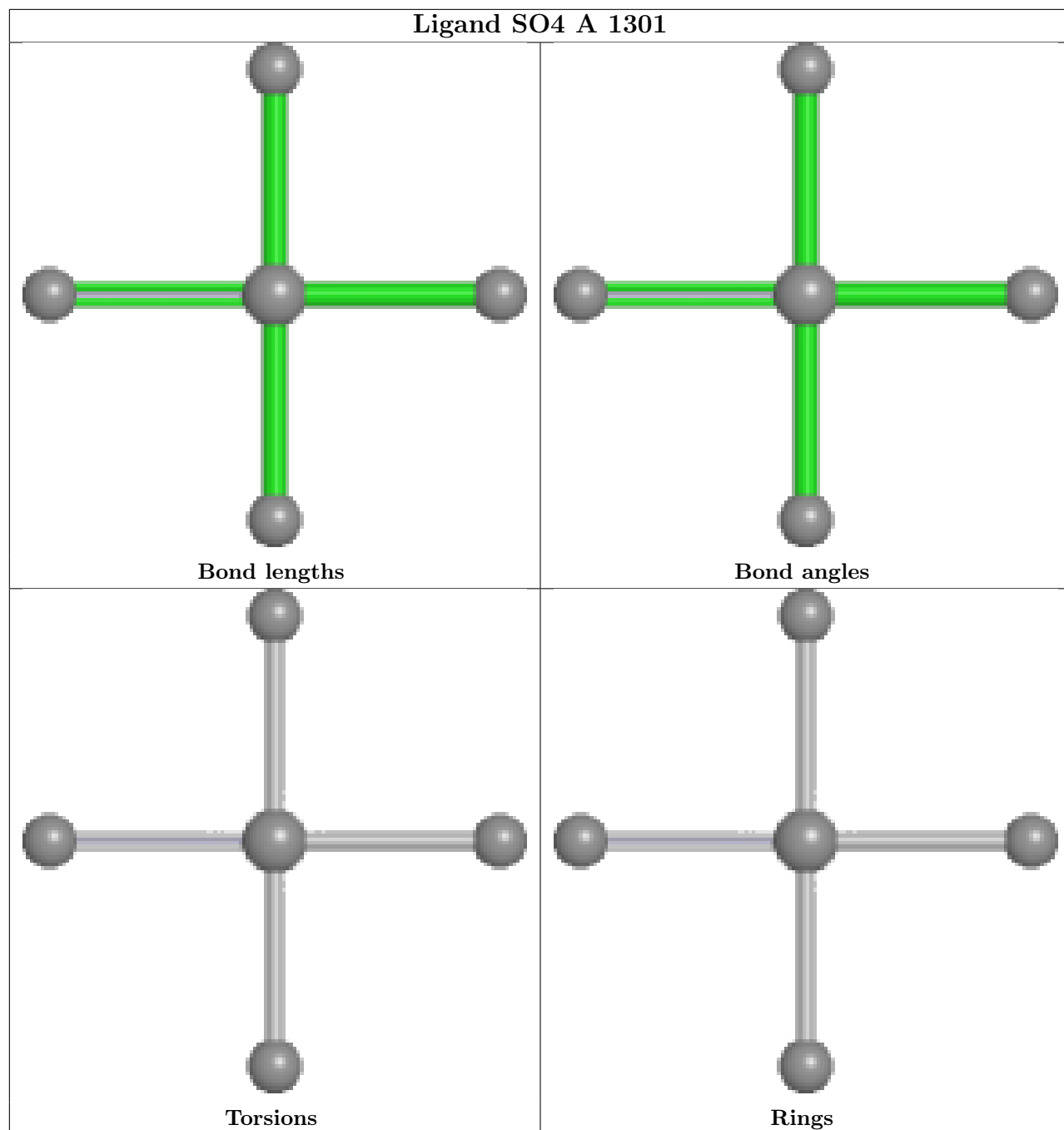
There are no torsion outliers.

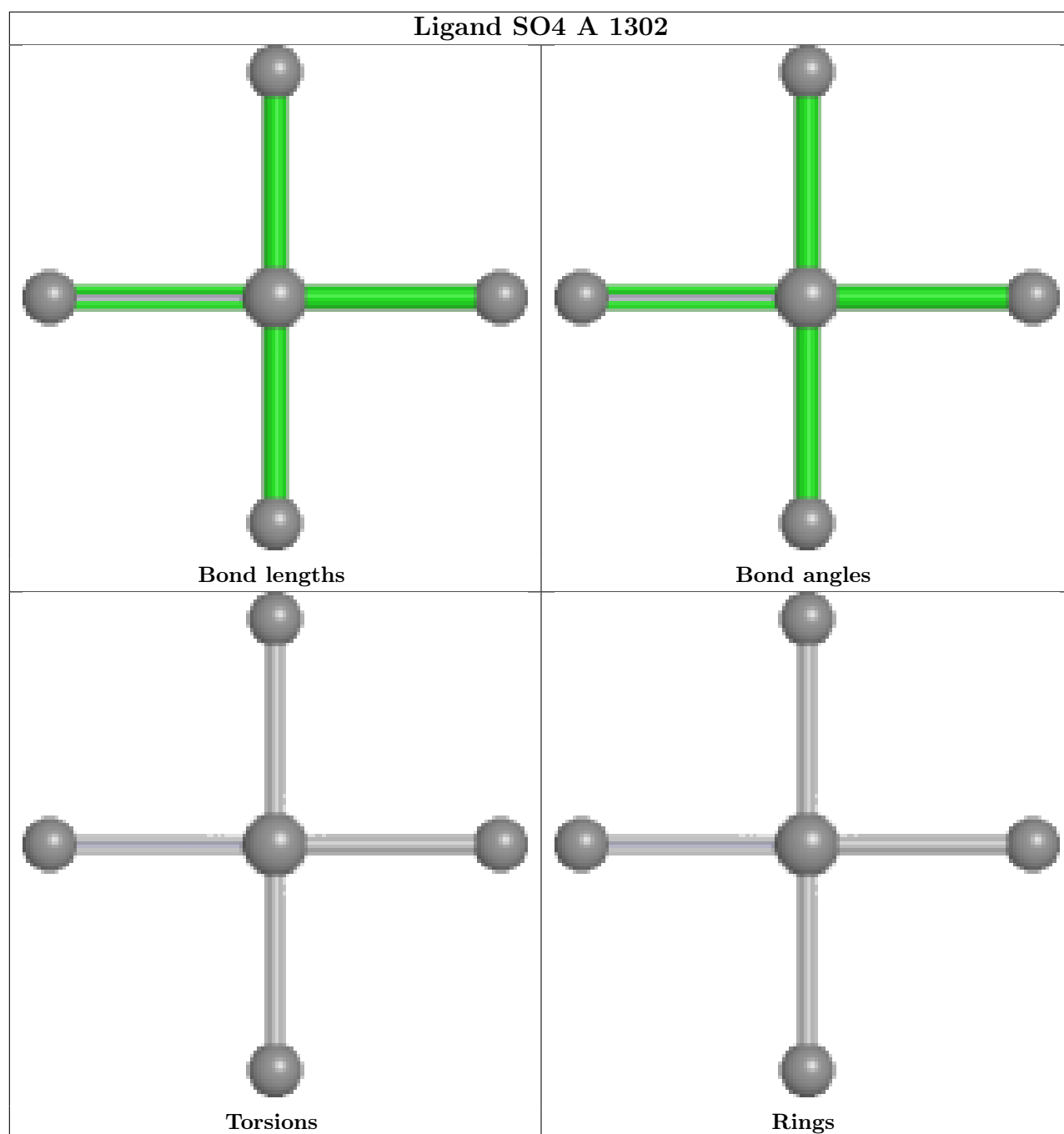
There are no ring outliers.

No monomer is involved in short contacts.

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 [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(Å ²)	Q<0.9
1	A	729/806 (90%)	0.26	46 (6%)	26 22	27, 51, 100, 151	1 (0%)
1	B	716/806 (88%)	0.36	58 (8%)	18 15	29, 56, 113, 167	0
1	C	644/806 (79%)	0.84	110 (17%)	4 3	41, 68, 127, 158	0
1	D	656/806 (81%)	1.46	166 (25%)	1 1	54, 91, 116, 142	0
All	All	2745/3224 (85%)	0.71	380 (13%)	6 5	27, 67, 118, 167	1 (0%)

The worst 5 of 380 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	562	PRO	7.6
1	D	902	LEU	6.2
1	B	433	ASN	6.1
1	C	538	ILE	6.0
1	D	559	HIS	5.3

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 [i](#)

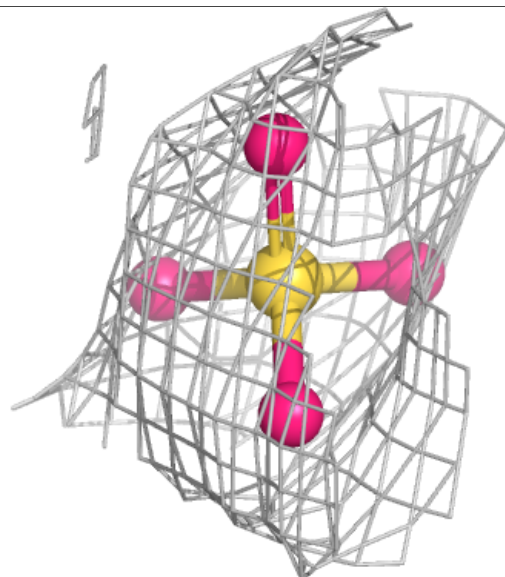
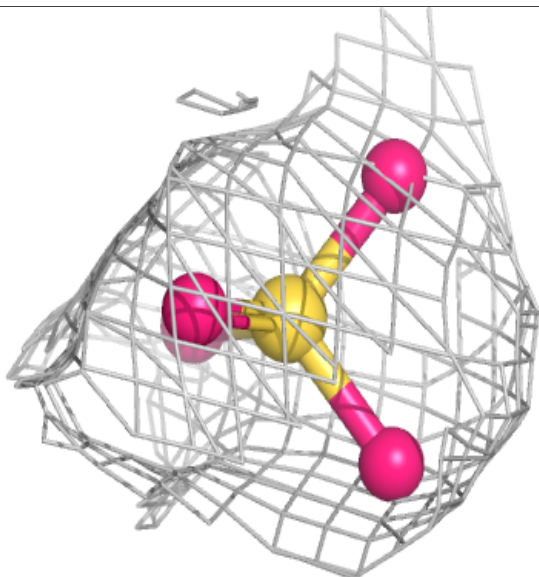
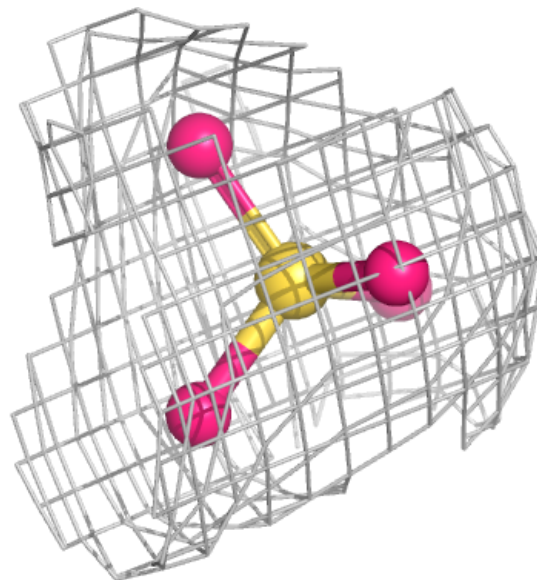
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	A	1301	5/5	0.75	0.15	139,139,140,144	0
2	SO4	A	1302	5/5	0.82	0.15	95,96,97,104	0
2	SO4	B	1301	5/5	0.91	0.17	115,115,119,124	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.

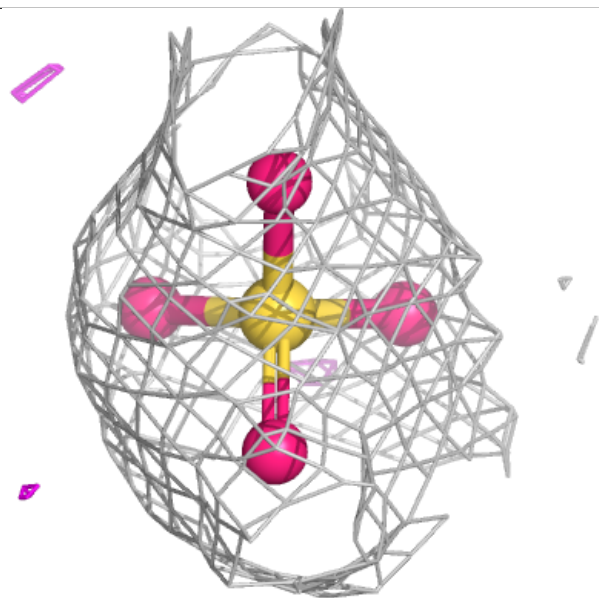
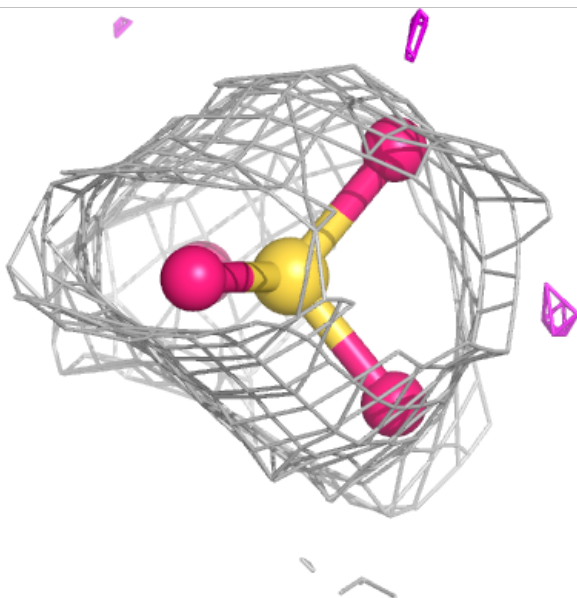
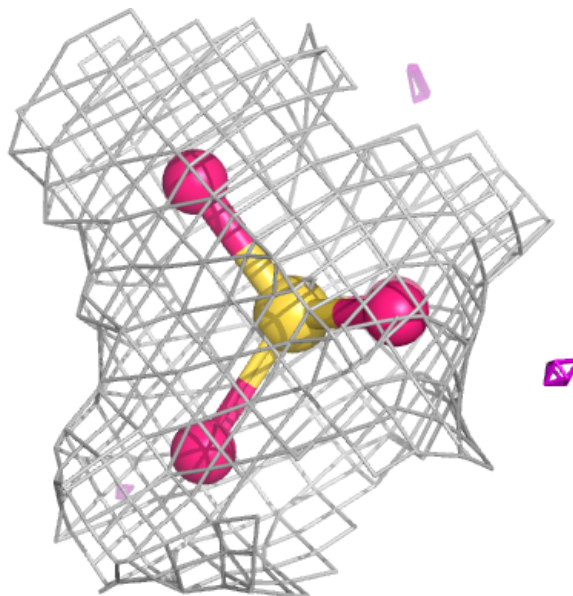
Electron density around SO4 A 1301:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



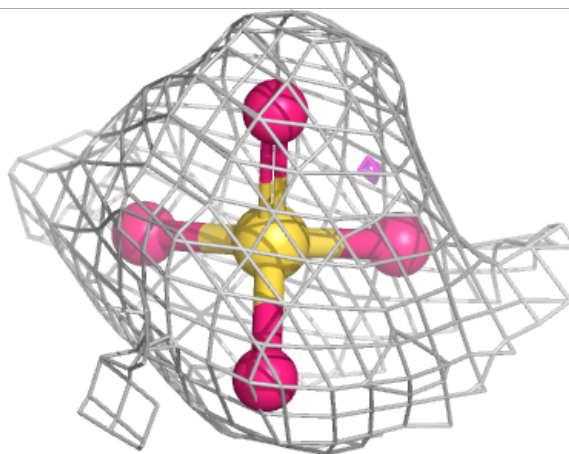
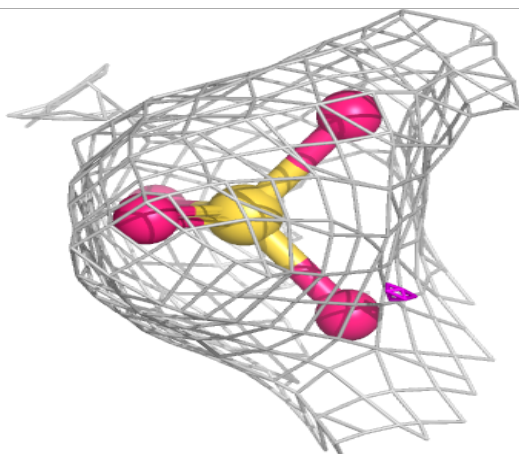
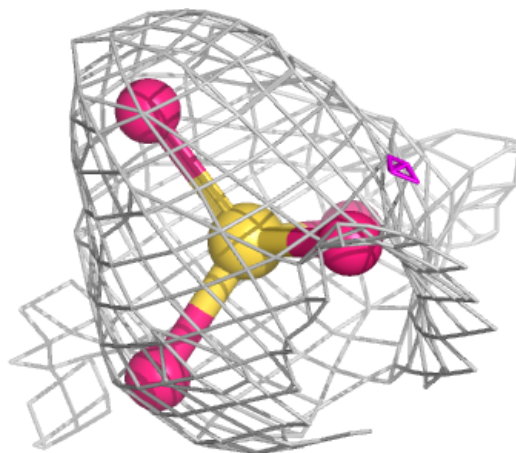
Electron density around SO4 A 1302:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around SO4 B 1301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.