W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

May 1, 2024 – 12:12 am BST

PDB ID	:	5AB7
Title	:	Crystal structure of Trypanosoma brucei SCP2-thiolase like protein (TbSLP) in complex with malonyl-CoA.
Authors	:	Harijan, R.K.; Kiema, T.R.; Wierenga, R.K.
Deposited on	:	2015-08-02
Resolution	:	2.30 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 types of validation reports are described at
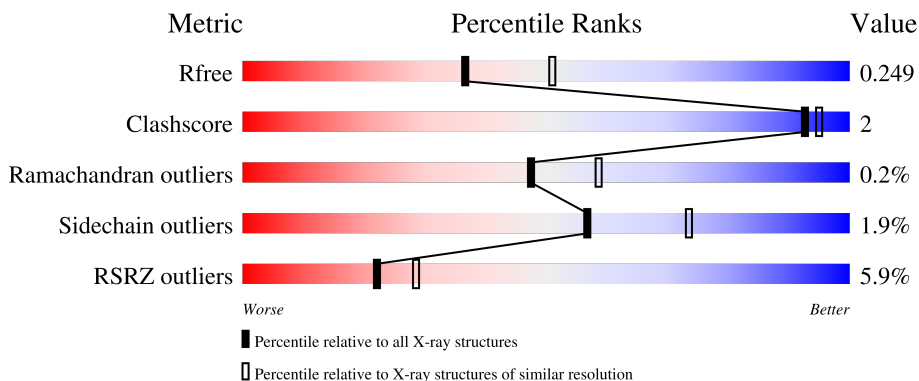http://www.wwpdb.org/validation/2017/FAQs#types.

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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 2.30 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.
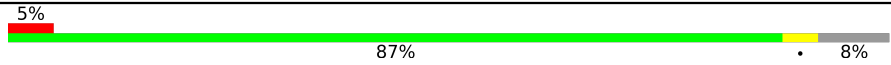
Metric	Percentile Ranks	Value
Rfree		0.249
Clashscore		2
Ramachandran outliers		0.2%
Sidechain outliers		1.9%
RSRZ outliers		5.9%

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	425	3% / 86% 6% 8%
1	B	425	6% / 88% · 8%
1	C	425	6% / 86% 6% 8%
1	D	425	2% / 90% · 7%
1	E	425	10% / 87% 5% 8%

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Mol	Chain	Length	Quality of chain
1	F	425	

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
3	SO4	C	1412	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 18248 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 SCP2-THIOLASE LIKE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total 2921	C 1850	N 509	O 537	S 25	0	1	0
1	B	392	Total 2922	C 1850	N 511	O 537	S 24	0	1	0
1	C	393	Total 2926	C 1853	N 510	O 538	S 25	0	1	0
1	D	396	Total 2948	C 1864	N 513	O 546	S 25	0	1	0
1	E	392	Total 2925	C 1853	N 511	O 537	S 24	0	1	0
1	F	391	Total 2918	C 1847	N 510	O 536	S 25	0	2	0

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	HIS	-	expression tag	UNP C9ZUV7
A	-14	HIS	-	expression tag	UNP C9ZUV7
A	-13	HIS	-	expression tag	UNP C9ZUV7
A	-12	HIS	-	expression tag	UNP C9ZUV7
A	-11	HIS	-	expression tag	UNP C9ZUV7
A	-10	HIS	-	expression tag	UNP C9ZUV7
A	-9	SER	-	expression tag	UNP C9ZUV7
A	-8	SER	-	expression tag	UNP C9ZUV7
A	-7	GLY	-	expression tag	UNP C9ZUV7
A	-6	LEU	-	expression tag	UNP C9ZUV7
A	-5	VAL	-	expression tag	UNP C9ZUV7
A	-4	PRO	-	expression tag	UNP C9ZUV7
A	-3	ARG	-	expression tag	UNP C9ZUV7
A	-2	GLY	-	expression tag	UNP C9ZUV7
A	-1	SER	-	expression tag	UNP C9ZUV7
A	0	HIS	-	expression tag	UNP C9ZUV7
B	-15	HIS	-	expression tag	UNP C9ZUV7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP C9ZUV7
B	-13	HIS	-	expression tag	UNP C9ZUV7
B	-12	HIS	-	expression tag	UNP C9ZUV7
B	-11	HIS	-	expression tag	UNP C9ZUV7
B	-10	HIS	-	expression tag	UNP C9ZUV7
B	-9	SER	-	expression tag	UNP C9ZUV7
B	-8	SER	-	expression tag	UNP C9ZUV7
B	-7	GLY	-	expression tag	UNP C9ZUV7
B	-6	LEU	-	expression tag	UNP C9ZUV7
B	-5	VAL	-	expression tag	UNP C9ZUV7
B	-4	PRO	-	expression tag	UNP C9ZUV7
B	-3	ARG	-	expression tag	UNP C9ZUV7
B	-2	GLY	-	expression tag	UNP C9ZUV7
B	-1	SER	-	expression tag	UNP C9ZUV7
B	0	HIS	-	expression tag	UNP C9ZUV7
C	-15	HIS	-	expression tag	UNP C9ZUV7
C	-14	HIS	-	expression tag	UNP C9ZUV7
C	-13	HIS	-	expression tag	UNP C9ZUV7
C	-12	HIS	-	expression tag	UNP C9ZUV7
C	-11	HIS	-	expression tag	UNP C9ZUV7
C	-10	HIS	-	expression tag	UNP C9ZUV7
C	-9	SER	-	expression tag	UNP C9ZUV7
C	-8	SER	-	expression tag	UNP C9ZUV7
C	-7	GLY	-	expression tag	UNP C9ZUV7
C	-6	LEU	-	expression tag	UNP C9ZUV7
C	-5	VAL	-	expression tag	UNP C9ZUV7
C	-4	PRO	-	expression tag	UNP C9ZUV7
C	-3	ARG	-	expression tag	UNP C9ZUV7
C	-2	GLY	-	expression tag	UNP C9ZUV7
C	-1	SER	-	expression tag	UNP C9ZUV7
C	0	HIS	-	expression tag	UNP C9ZUV7
D	-15	HIS	-	expression tag	UNP C9ZUV7
D	-14	HIS	-	expression tag	UNP C9ZUV7
D	-13	HIS	-	expression tag	UNP C9ZUV7
D	-12	HIS	-	expression tag	UNP C9ZUV7
D	-11	HIS	-	expression tag	UNP C9ZUV7
D	-10	HIS	-	expression tag	UNP C9ZUV7
D	-9	SER	-	expression tag	UNP C9ZUV7
D	-8	SER	-	expression tag	UNP C9ZUV7
D	-7	GLY	-	expression tag	UNP C9ZUV7
D	-6	LEU	-	expression tag	UNP C9ZUV7
D	-5	VAL	-	expression tag	UNP C9ZUV7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	PRO	-	expression tag	UNP C9ZUV7
D	-3	ARG	-	expression tag	UNP C9ZUV7
D	-2	GLY	-	expression tag	UNP C9ZUV7
D	-1	SER	-	expression tag	UNP C9ZUV7
D	0	HIS	-	expression tag	UNP C9ZUV7
E	-15	HIS	-	expression tag	UNP C9ZUV7
E	-14	HIS	-	expression tag	UNP C9ZUV7
E	-13	HIS	-	expression tag	UNP C9ZUV7
E	-12	HIS	-	expression tag	UNP C9ZUV7
E	-11	HIS	-	expression tag	UNP C9ZUV7
E	-10	HIS	-	expression tag	UNP C9ZUV7
E	-9	SER	-	expression tag	UNP C9ZUV7
E	-8	SER	-	expression tag	UNP C9ZUV7
E	-7	GLY	-	expression tag	UNP C9ZUV7
E	-6	LEU	-	expression tag	UNP C9ZUV7
E	-5	VAL	-	expression tag	UNP C9ZUV7
E	-4	PRO	-	expression tag	UNP C9ZUV7
E	-3	ARG	-	expression tag	UNP C9ZUV7
E	-2	GLY	-	expression tag	UNP C9ZUV7
E	-1	SER	-	expression tag	UNP C9ZUV7
E	0	HIS	-	expression tag	UNP C9ZUV7
F	-15	HIS	-	expression tag	UNP C9ZUV7
F	-14	HIS	-	expression tag	UNP C9ZUV7
F	-13	HIS	-	expression tag	UNP C9ZUV7
F	-12	HIS	-	expression tag	UNP C9ZUV7
F	-11	HIS	-	expression tag	UNP C9ZUV7
F	-10	HIS	-	expression tag	UNP C9ZUV7
F	-9	SER	-	expression tag	UNP C9ZUV7
F	-8	SER	-	expression tag	UNP C9ZUV7
F	-7	GLY	-	expression tag	UNP C9ZUV7
F	-6	LEU	-	expression tag	UNP C9ZUV7
F	-5	VAL	-	expression tag	UNP C9ZUV7
F	-4	PRO	-	expression tag	UNP C9ZUV7
F	-3	ARG	-	expression tag	UNP C9ZUV7
F	-2	GLY	-	expression tag	UNP C9ZUV7
F	-1	SER	-	expression tag	UNP C9ZUV7
F	0	HIS	-	expression tag	UNP C9ZUV7

- Molecule 2 is MALONYL-COENZYME A (three-letter code: MLC) (formula: $C_{24}H_{38}N_7O_{19}P_3S$).

MLC
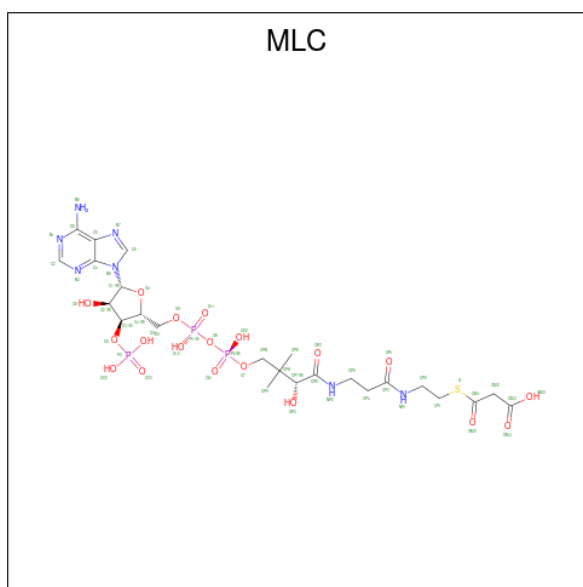
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			54	24	7	19	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			54	24	7	19	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			54	24	7	19	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			54	24	7	19	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			54	24	7	19	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			54	24	7	19	3	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

SO4

O1

O

O3 O⁻ — S — O⁻ O4

S

O

O2

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0
3	B	1	Total 5	O 4	S 1	0	0
3	C	1	Total 5	O 4	S 1	0	0
3	C	1	Total 5	O 4	S 1	0	0
3	C	1	Total 5	O 4	S 1	0	0
3	D	1	Total 5	O 4	S 1	0	0
3	D	1	Total 5	O 4	S 1	0	0
3	D	1	Total 5	O 4	S 1	0	0
3	E	1	Total 5	O 4	S 1	0	0
3	E	1	Total 5	O 4	S 1	0	0
3	F	1	Total 5	O 4	S 1	0	0
3	F	1	Total 5	O 4	S 1	0	0
3	F	1	Total 5	O 4	S 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	56	Total 56	O 56	0	0
4	B	60	Total 60	O 60	0	0
4	C	49	Total 49	O 49	0	0
4	D	49	Total 49	O 49	0	0
4	E	44	Total 44	O 44	0	0
4	F	36	Total 36	O 36	0	0

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: SCP2-THIOLASE LIKE PROTEIN
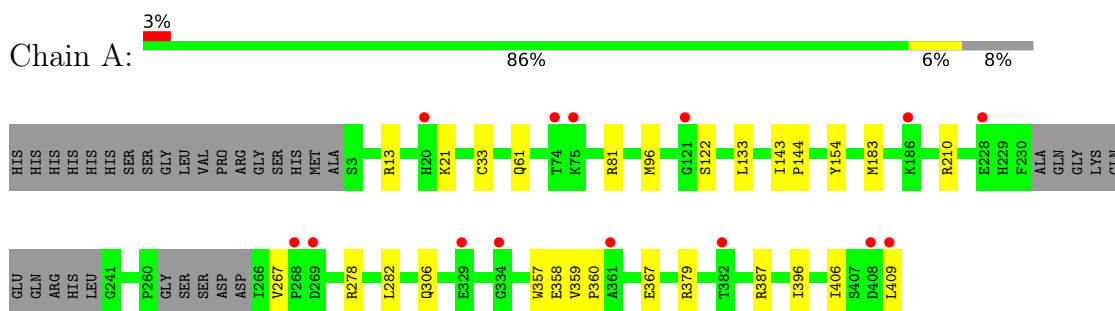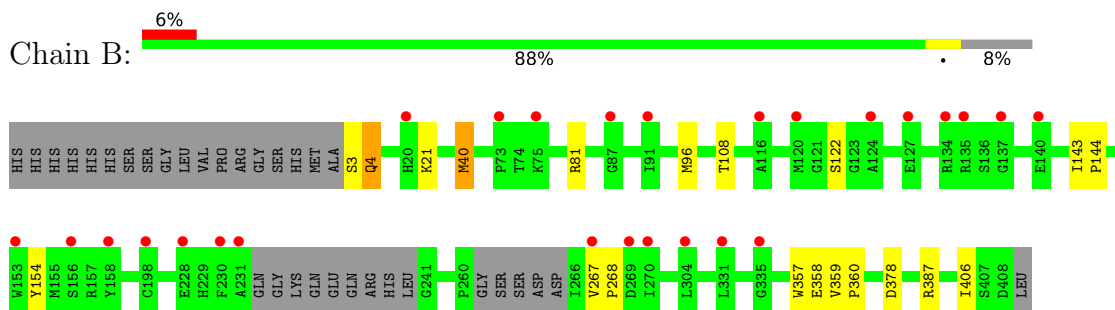
Chain A:

- Molecule 1: SCP2-THIOLASE LIKE PROTEIN

Chain B:

- Molecule 1: SCP2-THIOLASE LIKE PROTEIN

Chain C:

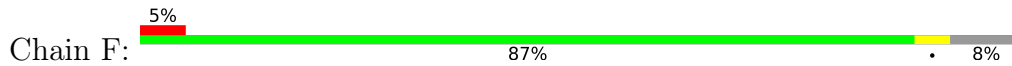- Molecule 1: SCP2-THIOLASE LIKE PROTEIN

Chain D:

• Molecule 1: SCP2-THIOLASE LIKE PROTEIN

Chain E:

• Molecule 1: SCP2-THIOLASE LIKE PROTEIN

Chain F:
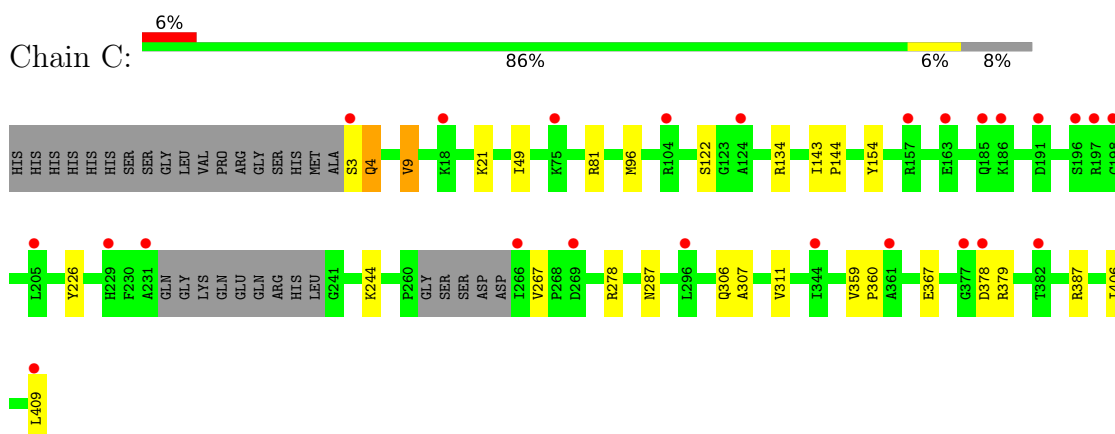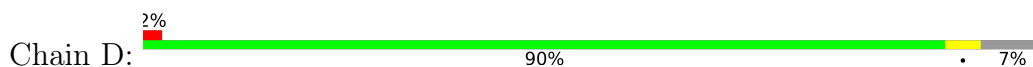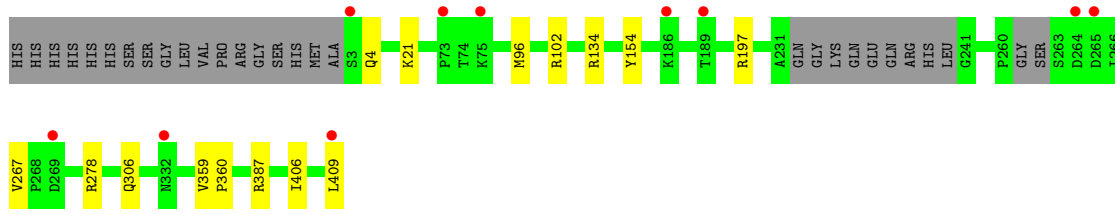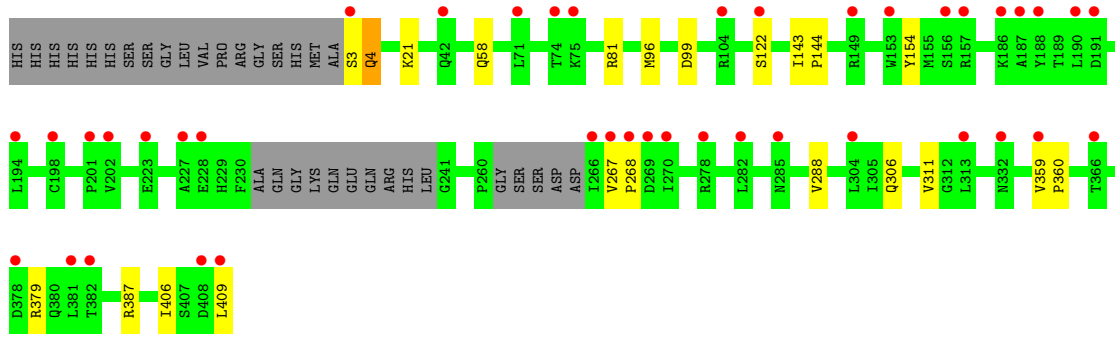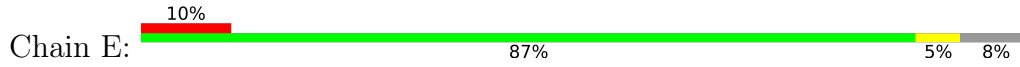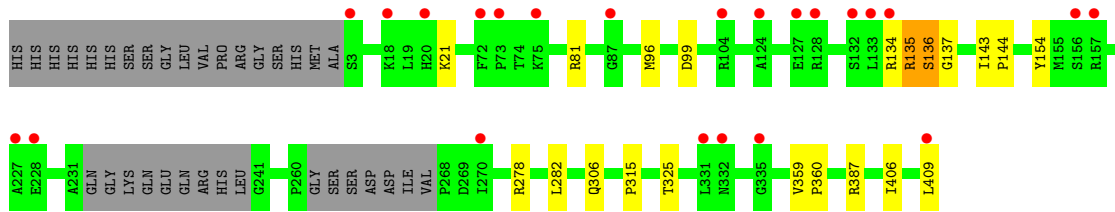
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	117.55Å 66.40Å 159.83Å 90.00° 91.18° 90.00°	Depositor
Resolution (Å)	29.40 – 2.30 29.38 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.3 (29.40-2.30) 94.4 (29.38-2.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.43 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.236 , 0.249 0.235 , 0.249	Depositor DCC
R_{free} test set	5191 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	33.4	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 28.6	EDS
L-test for twinning[2]	$< |L| > = 0.48, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	18248	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.52 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.7644e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: SO4, MLC

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	0.29	0/2984	0.51	0/4049
1	B	0.29	0/2986	0.51	1/4052 (0.0%)
1	C	0.29	0/2989	0.54	1/4056 (0.0%)
1	D	0.29	0/3011	0.53	1/4086 (0.0%)
1	E	0.30	0/2989	0.52	2/4056 (0.0%)
1	F	0.33	0/2985	0.53	0/4049
All	All	0.30	0/17944	0.52	5/24348 (0.0%)

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	F	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	379	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	B	40	MET	CG-SD-CE	5.58	109.12	100.20
1	D	134	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	C	134	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	E	379	ARG	NE-CZ-NH1	5.03	122.82	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	134	ARG	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	A	2921	0	2921	16	0
1	B	2922	0	2917	10	0
1	C	2926	0	2926	11	1
1	D	2948	0	2939	6	0
1	E	2925	0	2923	9	0
1	F	2918	0	2914	11	0
2	A	54	0	33	0	0
2	B	54	0	33	0	0
2	C	54	0	33	0	0
2	D	54	0	33	1	0
2	E	54	0	33	0	0
2	F	54	0	33	0	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
3	C	15	0	0	0	0
3	D	15	0	0	0	0
3	E	10	0	0	0	0
3	F	15	0	0	0	0
4	A	56	0	0	0	0
4	B	60	0	0	0	0
4	C	49	0	0	0	0
4	D	49	0	0	0	0
4	E	44	0	0	0	0
4	F	36	0	0	0	0
All	All	18248	0	17738	54	1

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 2.

The worst 5 of 54 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:4:GLN:O	1:D:102:ARG:NH1	2.10	0.85
1:E:81:ARG:HD3	1:F:96:MET:CE	2.18	0.73
1:A:183:MET:CE	1:A:210:ARG:HG3	2.19	0.71
1:E:96:MET:CE	1:F:81:ARG:HD3	2.23	0.67
1:C:367:GLU:OE2	1:C:379:ARG:NH1	2.32	0.63

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:278:ARG:NH1	1:C:378:ASP:OD2[2_454]	1.98	0.22

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	387/425 (91%)	379 (98%)	8 (2%)	0	100	100
1	B	387/425 (91%)	378 (98%)	8 (2%)	1 (0%)	41	50
1	C	388/425 (91%)	380 (98%)	7 (2%)	1 (0%)	41	50
1	D	391/425 (92%)	382 (98%)	9 (2%)	0	100	100
1	E	387/425 (91%)	378 (98%)	8 (2%)	1 (0%)	41	50
1	F	387/425 (91%)	376 (97%)	10 (3%)	1 (0%)	41	50
All	All	2327/2550 (91%)	2273 (98%)	50 (2%)	4 (0%)	47	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	4	GLN
1	C	4	GLN
1	E	4	GLN
1	F	136	SER

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	305/332 (92%)	298 (98%)	7 (2%)	50	67
1	B	304/332 (92%)	301 (99%)	3 (1%)	76	87
1	C	305/332 (92%)	297 (97%)	8 (3%)	46	63
1	D	308/332 (93%)	303 (98%)	5 (2%)	62	78
1	E	305/332 (92%)	299 (98%)	6 (2%)	55	72
1	F	304/332 (92%)	298 (98%)	6 (2%)	55	72
All	All	1831/1992 (92%)	1796 (98%)	35 (2%)	57	73

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	409	LEU
1	F	21	LYS
1	F	154	TYR
1	C	122	SER
1	C	21	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	GLN
1	B	292	HIS
1	F	64	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 monosaccharides in this entry.

5.6   Ligand geometry ⓘ

20 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	$\#|Z| > 2$
3	SO4	D	1410	-	4,4,4	0.32	0	6,6,6	0.10	0
3	SO4	E	1410	-	4,4,4	0.33	0	6,6,6	0.05	0
2	MLC	B	1410	-	47,56,56	1.00	3 (6%)	60,83,83	1.56	7 (11%)
2	MLC	E	1411	-	47,56,56	1.01	2 (4%)	60,83,83	1.23	7 (11%)
3	SO4	E	1412	-	4,4,4	0.34	0	6,6,6	0.15	0
3	SO4	A	1411	-	4,4,4	0.33	0	6,6,6	0.06	0
3	SO4	B	1409	-	4,4,4	0.30	0	6,6,6	0.12	0
3	SO4	C	1412	-	4,4,4	0.32	0	6,6,6	0.09	0
3	SO4	D	1413	-	4,4,4	0.32	0	6,6,6	0.12	0
3	SO4	F	1411	-	4,4,4	0.33	0	6,6,6	0.08	0
2	MLC	D	1411	-	47,56,56	1.04	3 (6%)	60,83,83	1.35	6 (10%)
3	SO4	F	1413	-	4,4,4	0.33	0	6,6,6	0.07	0
3	SO4	D	1412	-	4,4,4	0.34	0	6,6,6	0.09	0
2	MLC	A	1410	-	47,56,56	1.02	2 (4%)	60,83,83	1.24	5 (8%)
3	SO4	C	1411	-	4,4,4	0.34	0	6,6,6	0.11	0
3	SO4	F	1410	-	4,4,4	0.33	0	6,6,6	0.12	0
3	SO4	B	1411	-	4,4,4	0.34	0	6,6,6	0.08	0
3	SO4	C	1410	-	4,4,4	0.34	0	6,6,6	0.07	0
2	MLC	C	1413	-	47,56,56	1.01	2 (4%)	60,83,83	1.33	6 (10%)
2	MLC	F	1412	-	47,56,56	0.99	2 (4%)	60,83,83	1.30	6 (10%)

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
2	MLC	A	1410	-	-	14/50/71/71	0/3/3/3
2	MLC	D	1411	-	-	10/50/71/71	0/3/3/3
2	MLC	B	1410	-	-	11/50/71/71	0/3/3/3
2	MLC	E	1411	-	-	14/50/71/71	0/3/3/3
2	MLC	C	1413	-	-	13/50/71/71	0/3/3/3
2	MLC	F	1412	-	-	9/50/71/71	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1411	MLC	CM1-S	-3.90	1.66	1.76
2	C	1413	MLC	CM1-S	-3.63	1.67	1.76
2	A	1410	MLC	CM1-S	-3.63	1.67	1.76
2	E	1411	MLC	CM1-S	-3.51	1.67	1.76
2	B	1410	MLC	CM1-S	-3.50	1.67	1.76

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1410	MLC	CM2-CM1-S	7.42	122.94	113.69
2	F	1412	MLC	CM2-CM1-S	5.14	120.09	113.69
2	D	1411	MLC	CM2-CM1-S	4.91	119.81	113.69
2	A	1410	MLC	CM2-CM1-S	4.81	119.68	113.69
2	C	1413	MLC	CM2-CM1-S	4.77	119.64	113.69

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1410	MLC	C3'-O3'-P3-O33
2	A	1410	MLC	C5'-O5'-P1-O11
2	A	1410	MLC	CPB-O7-P2-O22
2	A	1410	MLC	CP7-CPA-CPB-O7
2	A	1410	MLC	CP8-CPA-CPB-O7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1411	MLC	1	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 then 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.

Ligand MLC B 1410

Bond lengths

Bond angles

Torsions

Rings

Ligand MLC E 1411

Bond lengths

Bond angles

Torsions

Rings

Ligand MLC D 1411

Bond lengths

Bond angles

Torsions

Rings

Ligand MLC A 1410

Bond lengths

Bond angles

Torsions

Rings

Ligand MLC C 1413

Bond lengths

Bond angles

Torsions

Rings

Ligand MLC F 1412

Bond lengths

Bond angles

Torsions

Rings
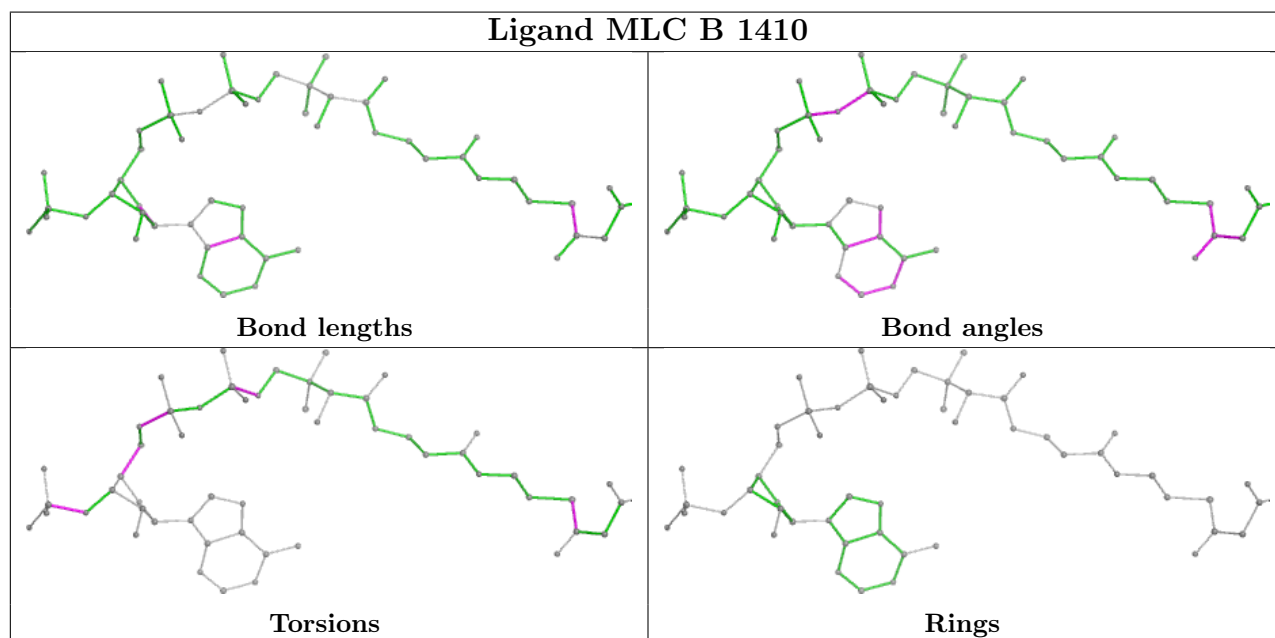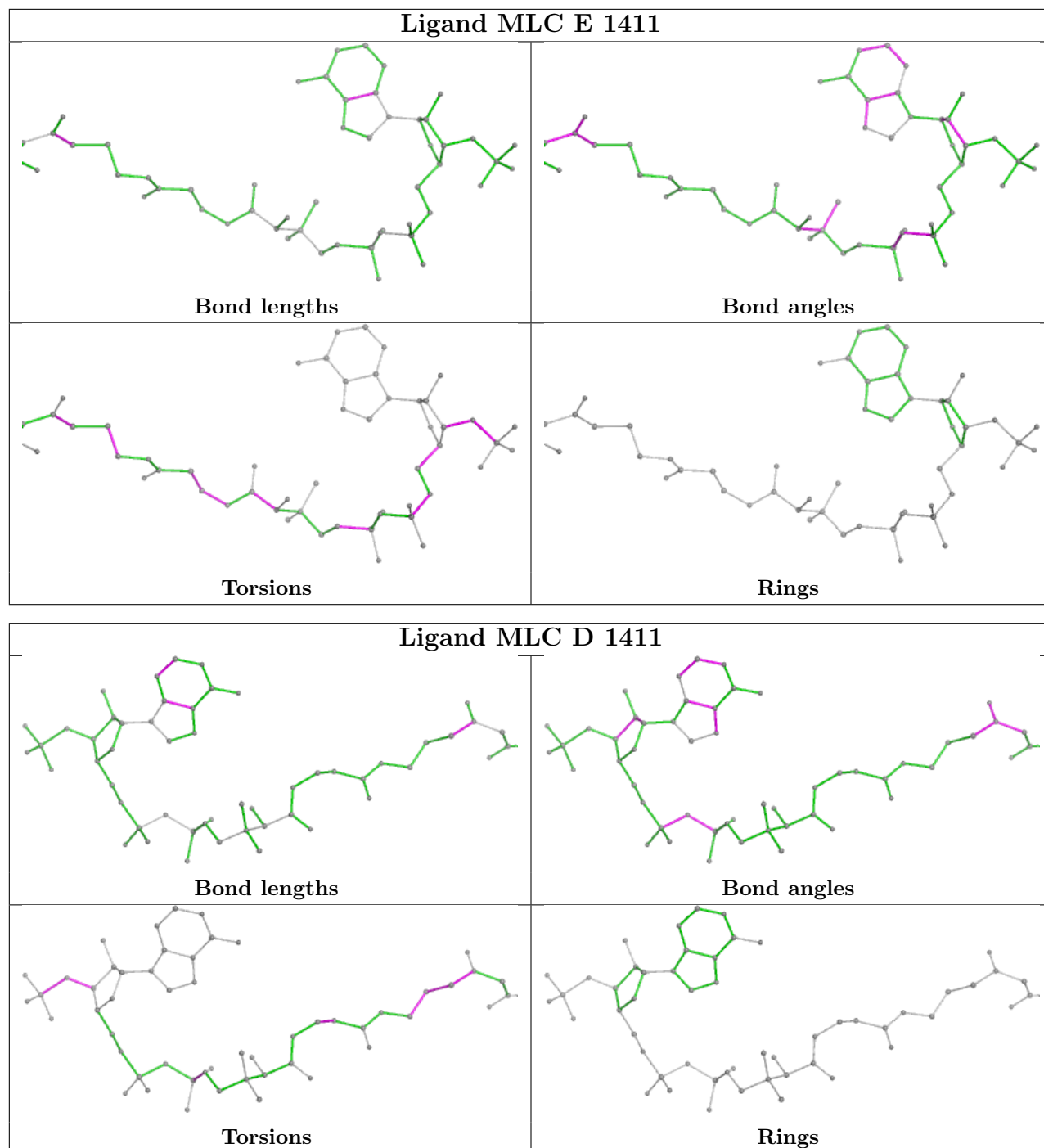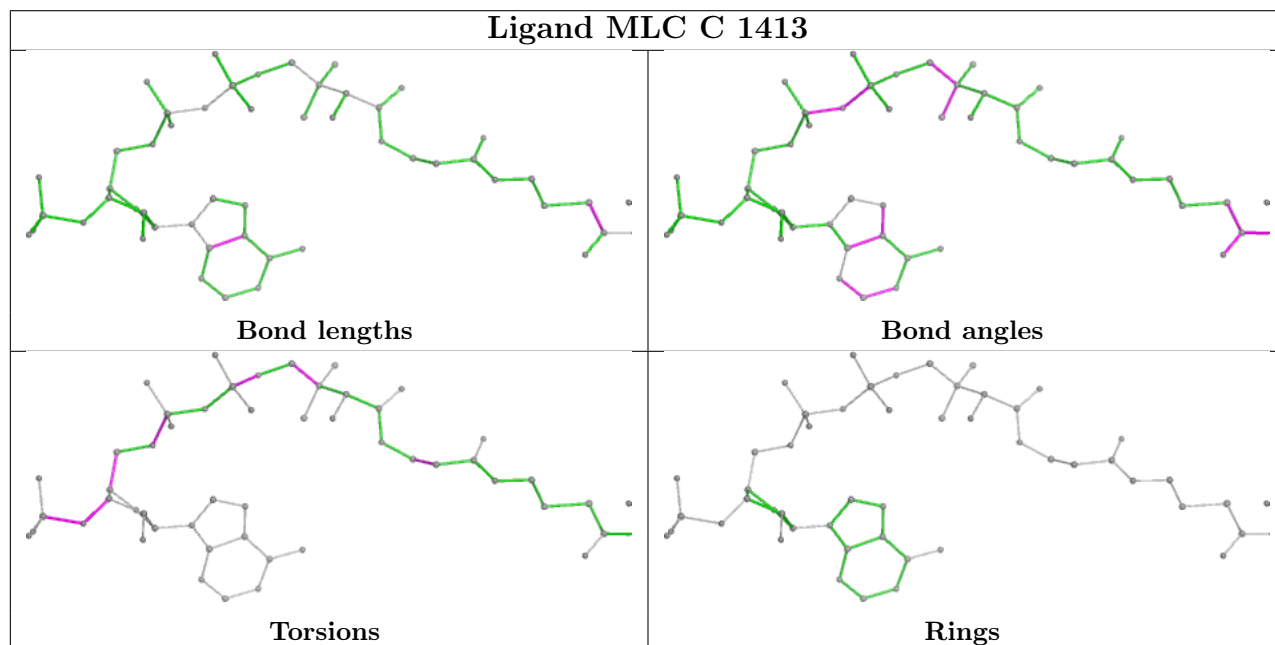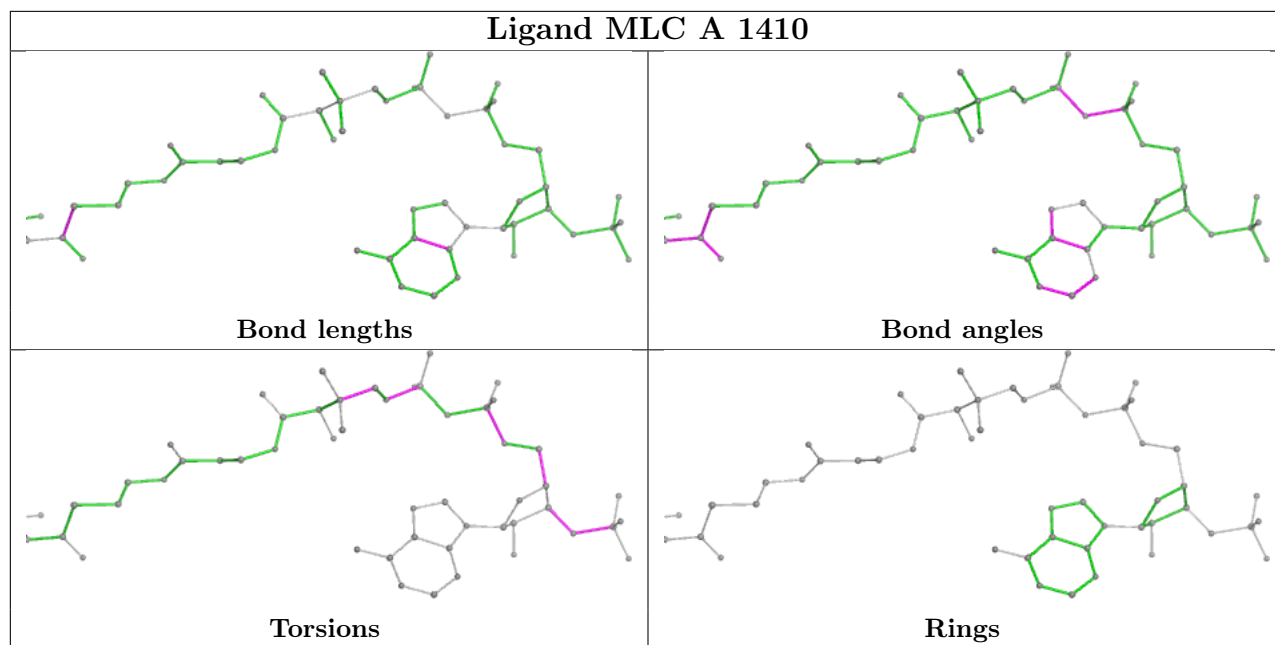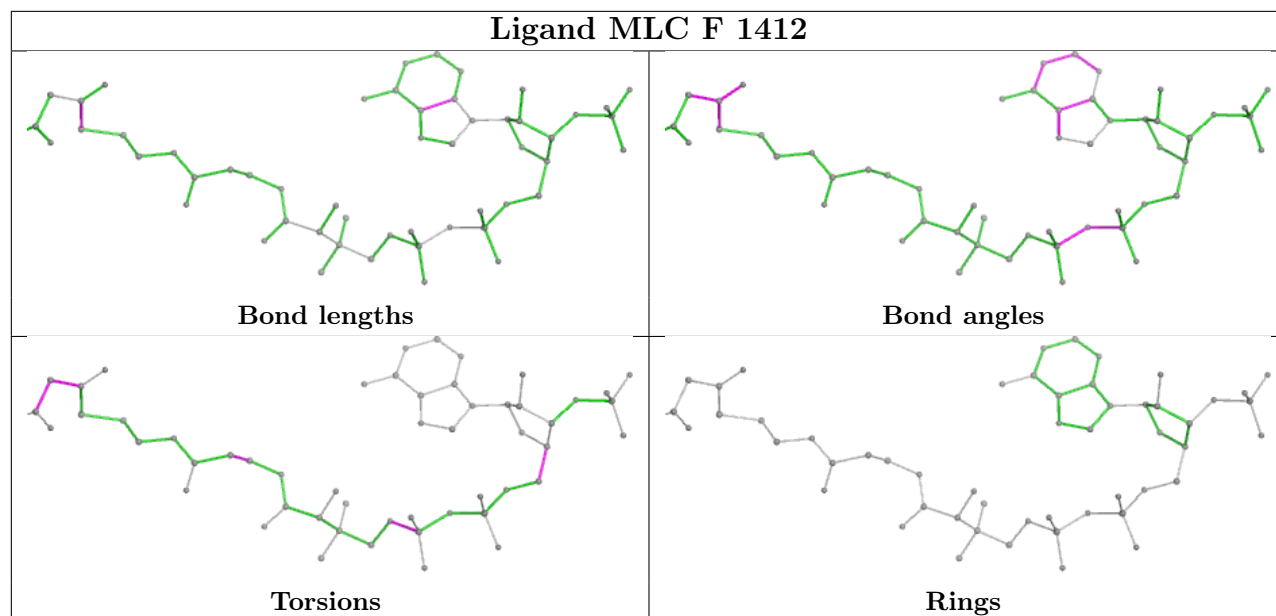
5.7 Other polymers ⓘ

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	392/425 (92%)	0.24	14 (3%)	42	49	24, 35, 52, 73	0
1	B	392/425 (92%)	0.27	26 (6%)	18	23	24, 34, 53, 76	0
1	C	393/425 (92%)	0.39	25 (6%)	19	25	25, 40, 58, 73	0
1	D	396/425 (93%)	0.25	10 (2%)	57	64	24, 34, 53, 74	0
1	E	392/425 (92%)	0.61	41 (10%)	6	8	26, 41, 64, 87	0
1	F	391/425 (92%)	0.38	23 (5%)	22	28	25, 36, 60, 86	0
All	All	2356/2550 (92%)	0.36	139 (5%)	22	28	24, 36, 59, 87	0

The worst 5 of 139 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	409	LEU	9.2
1	C	409	LEU	7.7
1	F	75	LYS	6.8
1	D	409	LEU	6.1
1	E	269	ASP	5.7

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 monosaccharides in this entry.

WORLDWIDE
wwPDB
PROTEIN DATA BANK

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(Å^2)	Q<0.9
2	MLC	E	1411	54/54	0.63	0.34	53,86,101,102	0
2	MLC	A	1410	54/54	0.66	0.31	51,71,81,82	0
2	MLC	D	1411	54/54	0.71	0.24	57,73,94,96	0
2	MLC	C	1413	54/54	0.73	0.27	53,84,100,103	0
2	MLC	B	1410	54/54	0.78	0.29	59,80,99,100	0
3	SO4	C	1412	5/5	0.78	0.41	88,89,90,91	0
3	SO4	B	1411	5/5	0.83	0.32	78,78,81,81	0
2	MLC	F	1412	54/54	0.83	0.21	52,69,84,86	0
3	SO4	D	1412	5/5	0.83	0.20	74,74,77,77	0
3	SO4	E	1412	5/5	0.86	0.24	74,76,76,77	0
3	SO4	C	1410	5/5	0.87	0.23	84,84,85,86	0
3	SO4	D	1413	5/5	0.91	0.19	63,63,66,67	0
3	SO4	E	1410	5/5	0.93	0.19	79,80,80,80	0
3	SO4	B	1409	5/5	0.93	0.31	57,58,60,60	0
3	SO4	F	1410	5/5	0.93	0.19	64,65,66,66	0
3	SO4	F	1411	5/5	0.94	0.38	65,65,67,67	0
3	SO4	A	1411	5/5	0.95	0.28	66,67,68,68	0
3	SO4	F	1413	5/5	0.95	0.13	70,70,71,72	0
3	SO4	D	1410	5/5	0.96	0.15	61,61,62,62	0
3	SO4	C	1411	5/5	0.97	0.14	56,58,58,58	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 MLC E 1411:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
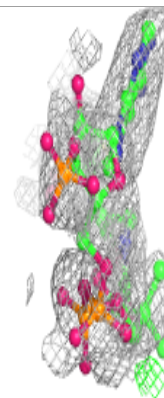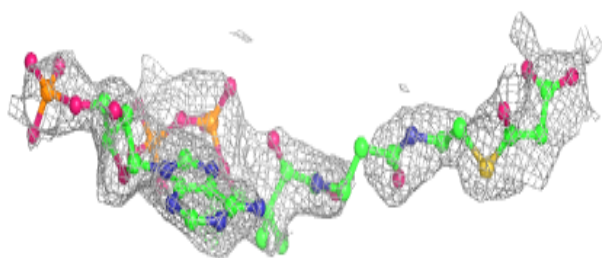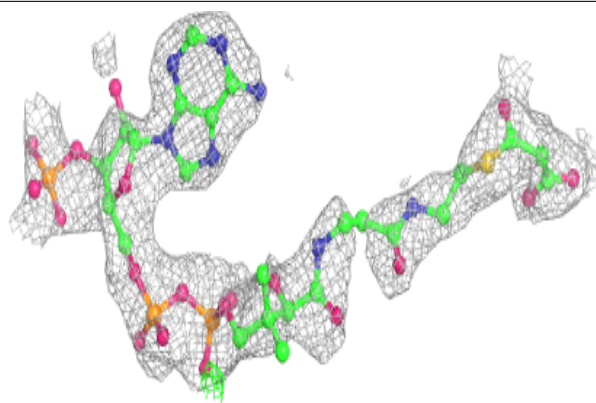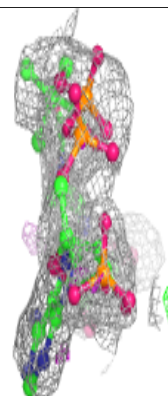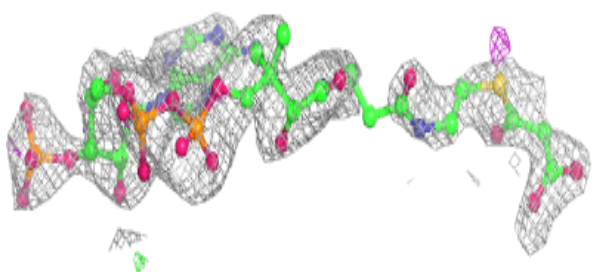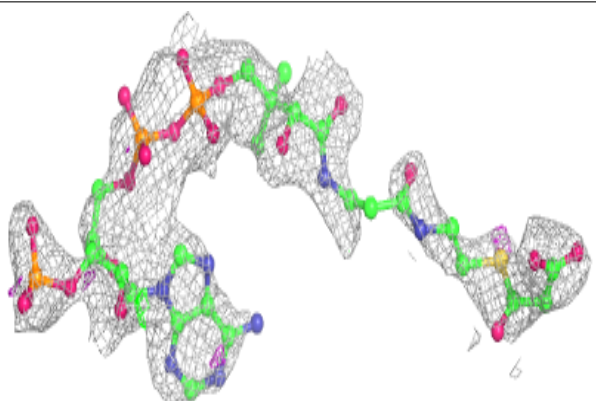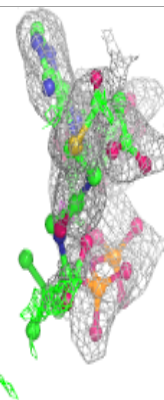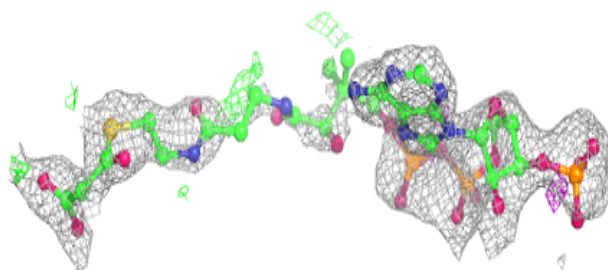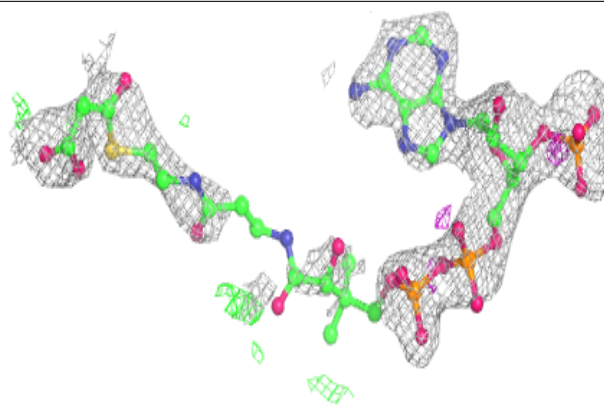and green (positive)
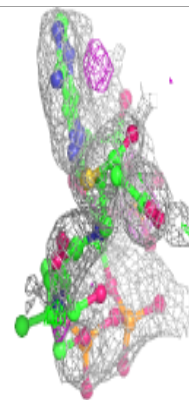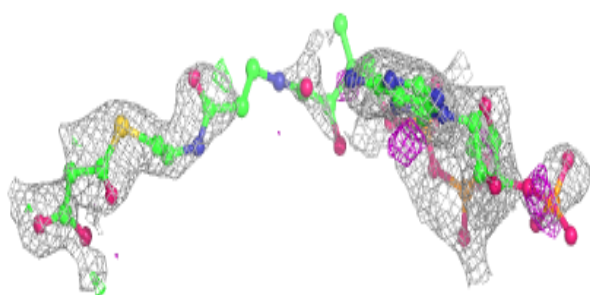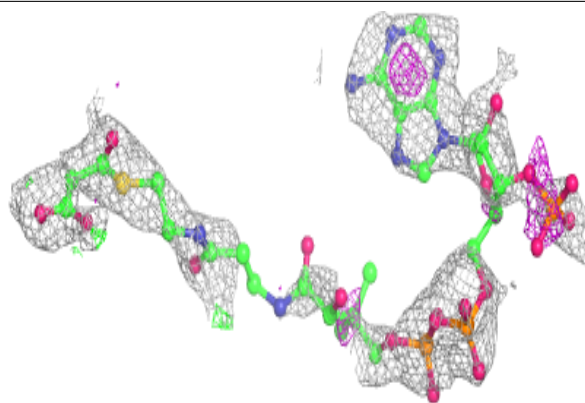
Electron density around MLC A 1410:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
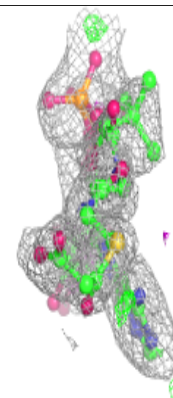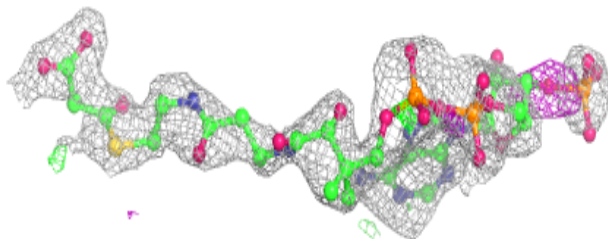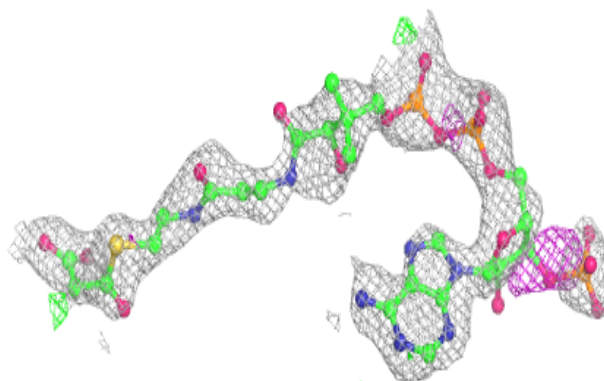
Electron density around MLC D 1411:

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

Electron density around MLC C 1413:

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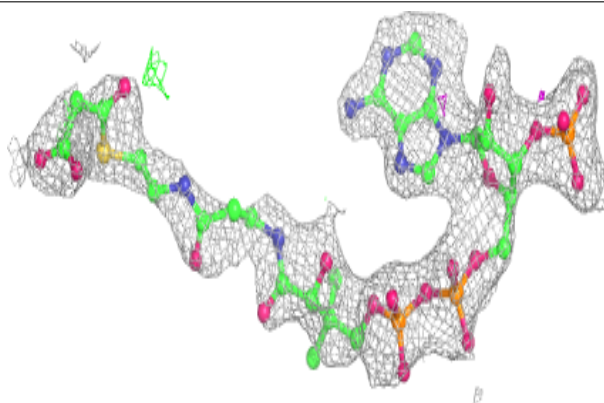and green (positive)

Electron density around MLC B 1410:

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

Electron density around MLC F 1412:

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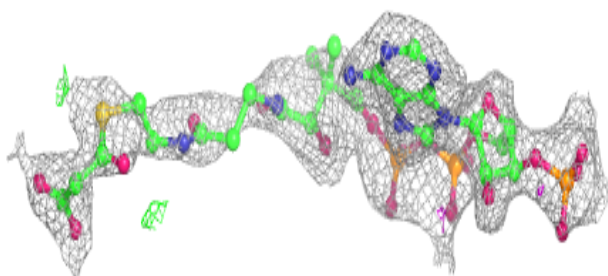
6.5 Other polymers (i)

There are no such residues in this entry.