



wwPDB EM Validation Summary Report ⓘ

Mar 19, 2026 – 09:06 PM UTC

PDB ID : 9GM9 / pdb_00009gm9
EMDB ID : EMD-51445
Title : MukBEF in a DNA capture state
Authors : Burmann, F.; Lowe, J.
Deposited on : 2024-08-28
Resolution : 7.80 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp>

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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

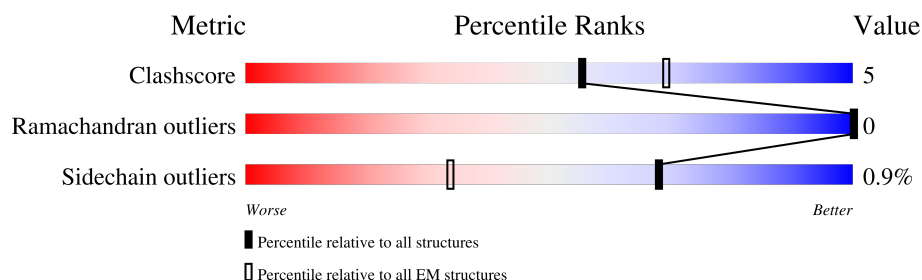
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 7.80 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	1482	61% 7% 33%
1	B	1482	54% 13% 33%
2	C	440	87% 12%
2	D	440	65% 7% 28%
3	E	240	68% 19% 12%
3	F	240	63% 18% 18%
3	Q	240	45% 8% 46%
4	G	78	67% 24% 8%
4	I	78	76% 15% 8%

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Mol	Chain	Length	Quality of chain
5	K	2124	98%
6	L	2124	98%

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
4	4HH	G	36	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 58225 atoms, of which 28572 are hydrogens and 0 are deuteriums.

In the tables below, 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 Chromosome partition protein MukB.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	999	Total	C	H	N	O	S	0	0
			16038	4984	8011	1480	1534	29		
1	B	999	Total	C	H	N	O	S	0	0
			16037	4984	8010	1480	1534	29		

- Molecule 2 is a protein called Chromosome partition protein MukF.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C	440	Total	C	H	N	O	S	0	0
			6982	2218	3451	614	686	13		
2	D	318	Total	C	H	N	O	S	0	0
			5046	1598	2496	448	493	11		

- Molecule 3 is a protein called Chromosome partition protein MukE.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	E	212	Total	C	H	N	O	S	0	0
			3441	1090	1719	301	322	9		
3	F	198	Total	C	H	N	O	S	0	0
			3246	1029	1627	284	298	8		
3	Q	129	Total	C	H	N	O	S	0	0
			2101	653	1060	185	196	7		

- Molecule 4 is a protein called Acyl carrier protein.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	G	72	Total	C	H	N	O	P S	0	0
			1147	360	564	87	133	1 2		
4	I	72	Total	C	H	N	O	P S	0	0
			1147	360	564	87	133	1 2		

- Molecule 5 is a DNA chain called pFB526.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	K	47	Total	C	H	N	O	P	0	0
			1498	460	525	191	275	47		

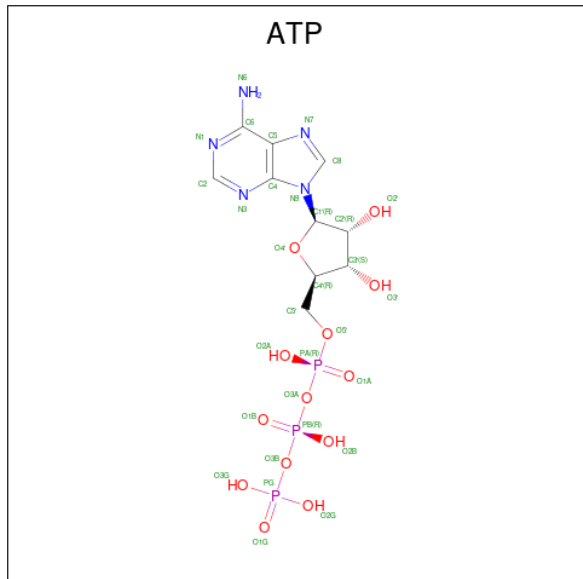
- Molecule 6 is a DNA chain called pFB526.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	L	46	Total	C	H	N	O	P	0	0
			1454	446	521	157	284	46		

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
7	A	1	Total	Mg	0
			1	1	
7	B	1	Total	Mg	0
			1	1	

- Molecule 8 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃) (labeled as "Ligand of Interest" by depositor).

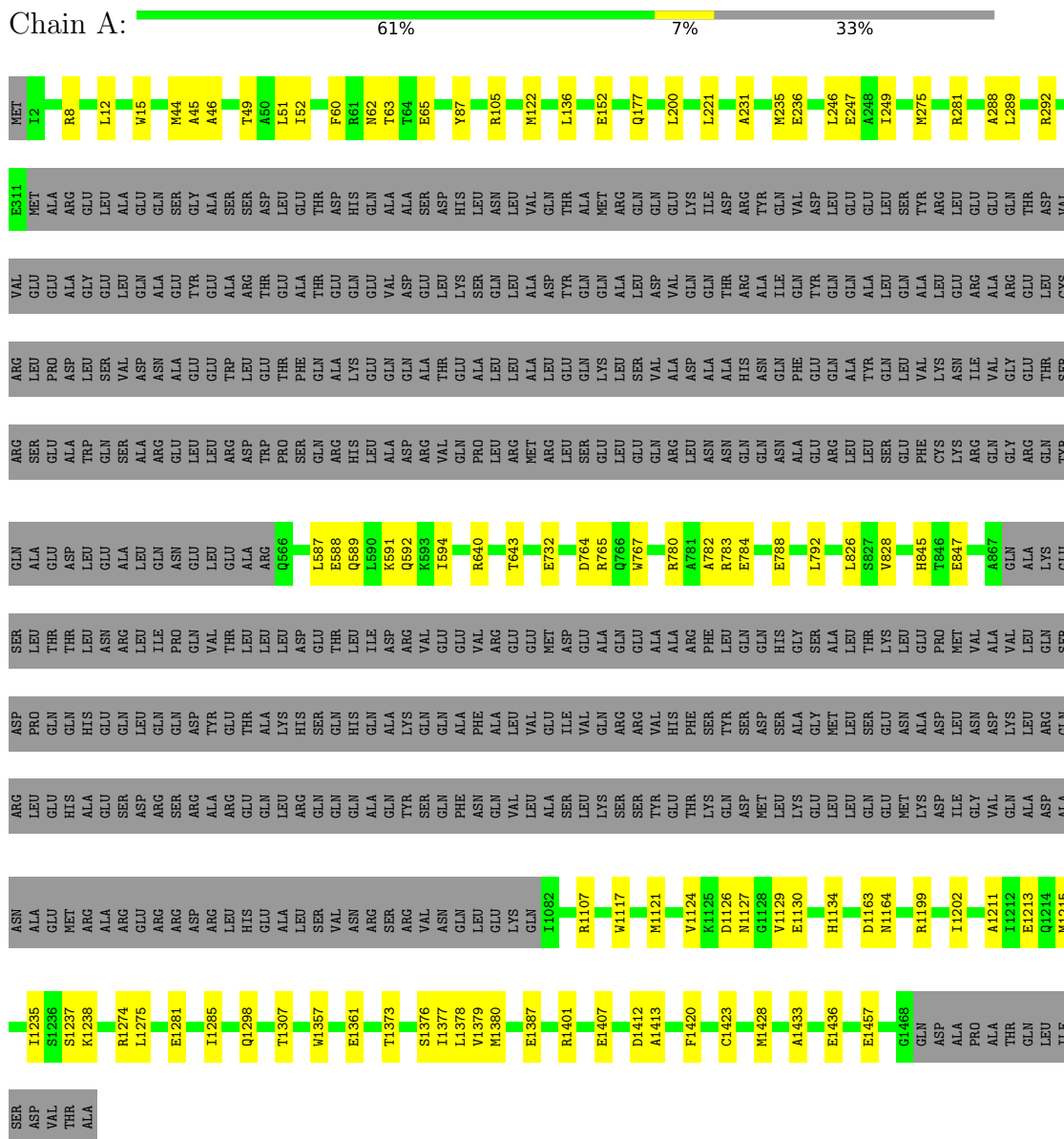


Mol	Chain	Residues	Atoms						AltConf
8	A	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	
8	B	1	Total	C	H	N	O	P	0
			43	10	12	5	13	3	

3 Residue-property plots

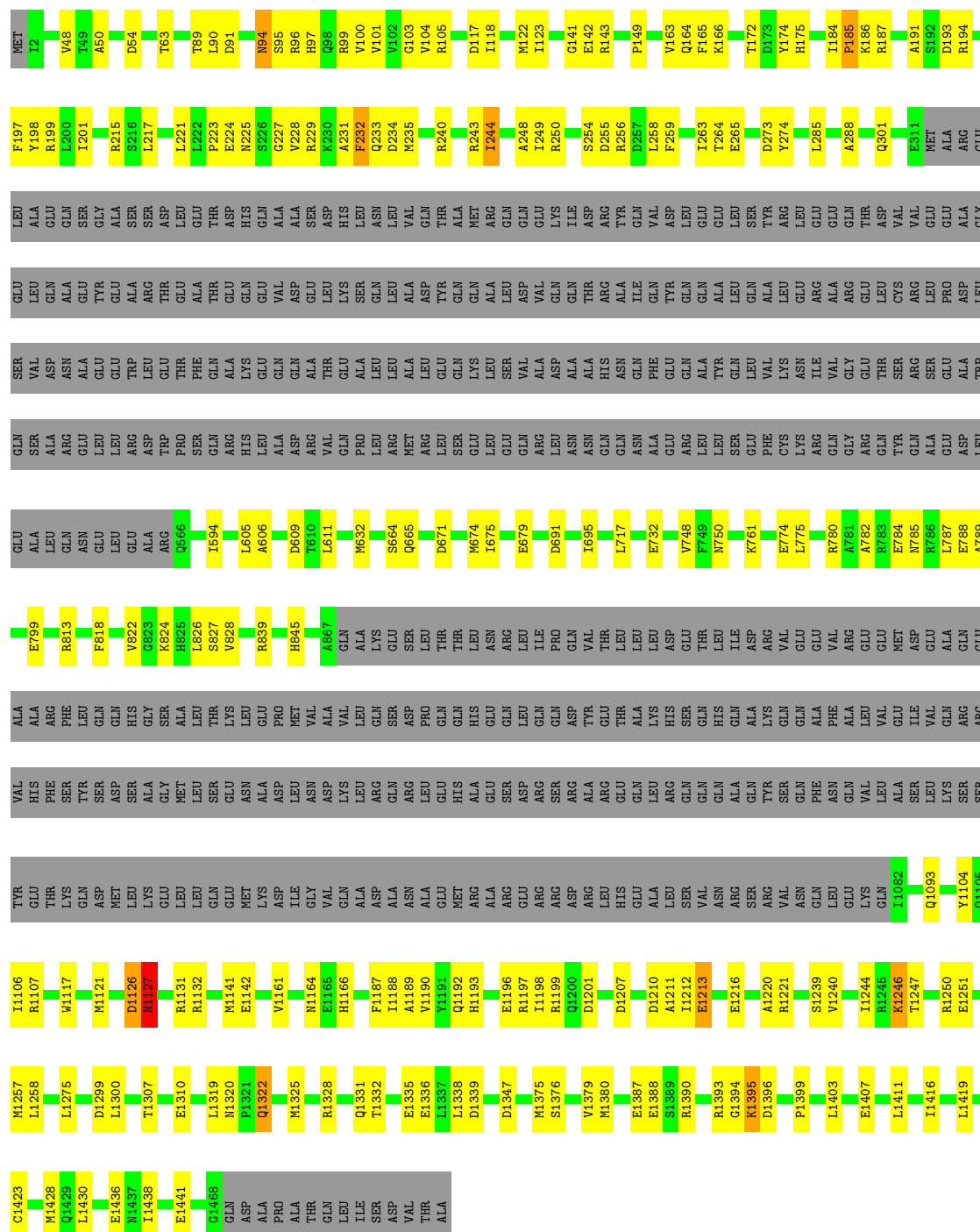
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: Chromosome partition protein MukB

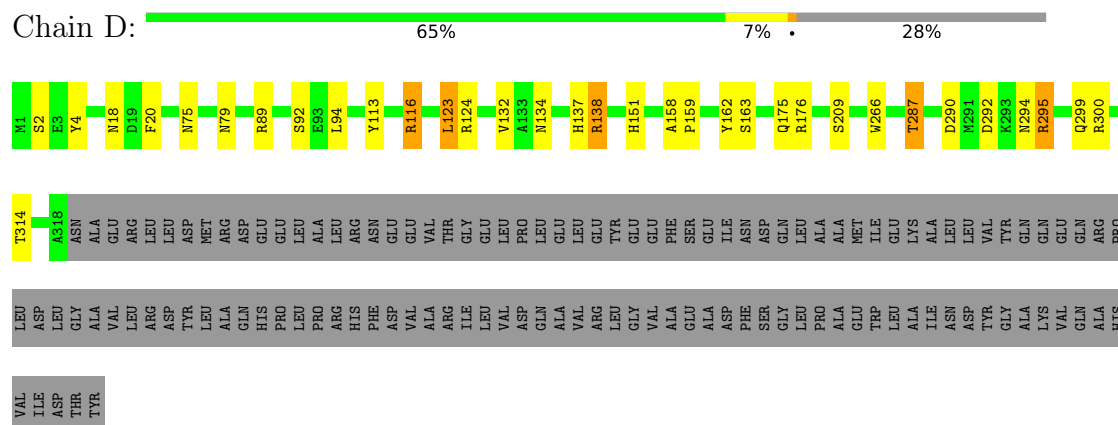


- Molecule 1: Chromosome partition protein MukB

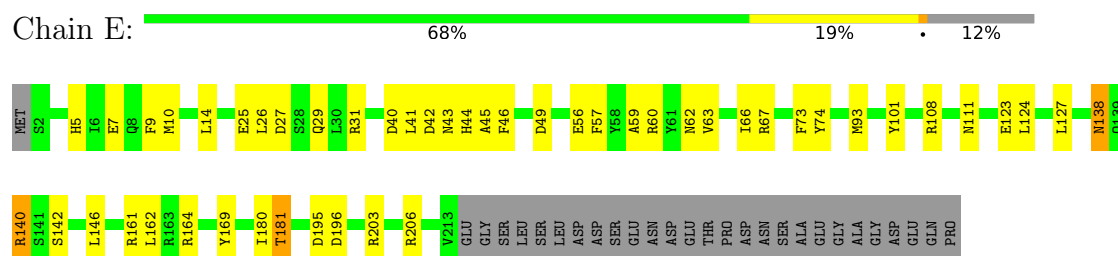




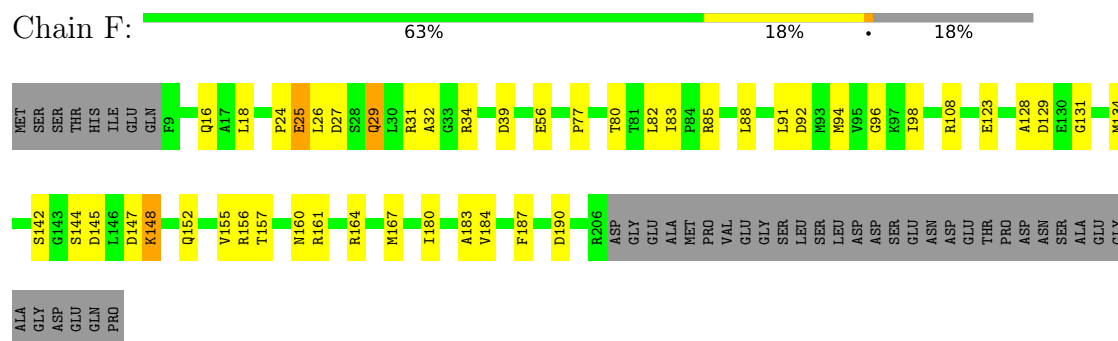
- Molecule 2: Chromosome partition protein MukF



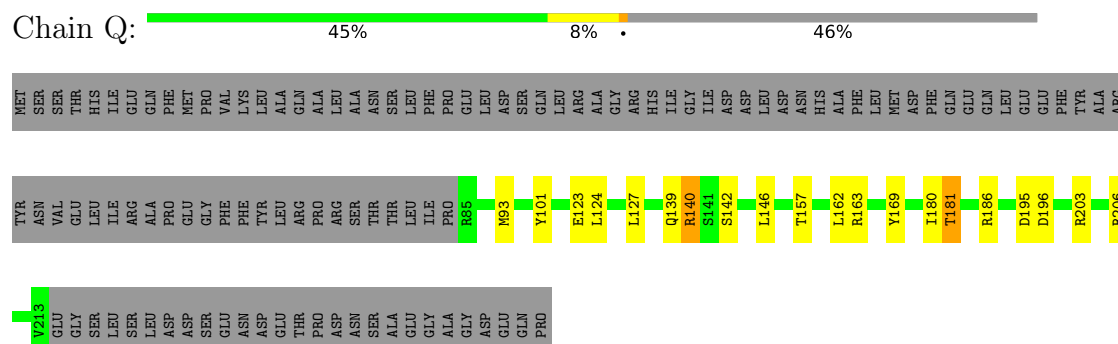
- Molecule 3: Chromosome partition protein MukE



- Molecule 3: Chromosome partition protein MukE



- Molecule 3: Chromosome partition protein MukE



- Molecule 6: pFB526

98%

[illegible]



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7508	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, 4HH, 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	A	0.33	2/8143 (0.0%)	0.67	3/10968 (0.0%)
1	B	1.20	65/8143 (0.8%)	1.29	133/10968 (1.2%)
2	C	0.83	2/3592 (0.1%)	1.30	21/4862 (0.4%)
2	D	0.87	1/2593 (0.0%)	1.44	16/3504 (0.5%)
3	E	1.50	19/1753 (1.1%)	1.71	44/2361 (1.9%)
3	F	1.64	24/1648 (1.5%)	1.68	49/2218 (2.2%)
3	Q	0.99	6/1054 (0.6%)	1.42	7/1413 (0.5%)
4	G	0.13	0/558	0.28	0/754
4	I	0.13	0/558	0.27	0/754
5	K	0.70	0/1095	1.71	8/1689 (0.5%)
6	L	0.71	0/1041	1.71	10/1603 (0.6%)
All	All	0.95	119/30178 (0.4%)	1.25	291/41094 (0.7%)

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
2	C	0	6
2	D	0	5
3	E	0	4
3	Q	0	2
5	K	0	13
6	L	0	12
All	All	0	42

The worst 5 of 119 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	295	ARG	C-N	-24.36	1.03	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	295	ARG	C-N	-24.36	1.03	1.33
1	A	589	GLN	C-N	13.54	1.51	1.33
3	E	44	HIS	CE1-NE2	-8.90	1.23	1.32
1	B	175	HIS	CE1-NE2	-8.88	1.23	1.32

The worst 5 of 291 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	295	ARG	CA-C-N	22.14	147.89	120.88
2	C	295	ARG	C-N-CA	22.14	147.89	120.88
2	D	295	ARG	CA-C-N	22.07	147.81	120.88
2	D	295	ARG	C-N-CA	22.07	147.81	120.88
1	A	589	GLN	O-C-N	9.98	132.35	122.07

There are no chirality outliers.

5 of 42 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	120	PHE	Sidechain
2	C	138	ARG	Sidechain
2	C	300	ARG	Sidechain
2	C	4	TYR	Sidechain
2	C	89	ARG	Sidechain

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	8027	8011	8007	76	0
1	B	8027	8010	8007	92	0
2	C	3531	3451	3450	69	0
2	D	2550	2496	2495	57	0
3	E	1722	1719	1718	15	0
3	F	1619	1627	1626	14	0
3	Q	1041	1060	1059	8	0
4	G	583	564	563	26	0
4	I	583	564	563	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	K	973	525	526	4	0
6	L	933	521	520	5	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
8	A	31	12	12	0	0
8	B	31	12	12	0	0
All	All	29653	28572	28558	293	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 293 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)
2:C:158:ALA:HB1	2:D:123:LEU:HG	1.19	1.18
2:C:162:TYR:HB3	2:D:124:ARG:HG3	1.23	1.17
2:C:158:ALA:CB	2:D:123:LEU:HG	1.82	1.08
2:C:131:ILE:HD11	2:D:163:SER:OG	1.56	1.05
4:G:36:4HH:CL3	4:G:40:VAL:HG21	1.87	1.04

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 PDB entries followed by that with respect to all EM entries.

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	993/1482 (67%)	962 (97%)	31 (3%)	0	100	100
1	B	993/1482 (67%)	953 (96%)	40 (4%)	0	100	100
2	C	438/440 (100%)	426 (97%)	12 (3%)	0	100	100
2	D	316/440 (72%)	309 (98%)	7 (2%)	0	100	100
3	E	210/240 (88%)	206 (98%)	4 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	196/240 (82%)	191 (97%)	5 (3%)	0	100	100
3	Q	127/240 (53%)	123 (97%)	4 (3%)	0	100	100
4	G	69/78 (88%)	68 (99%)	1 (1%)	0	100	100
4	I	69/78 (88%)	66 (96%)	3 (4%)	0	100	100
All	All	3411/4720 (72%)	3304 (97%)	107 (3%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	861/1281 (67%)	860 (100%)	1 (0%)	88	89
1	B	861/1281 (67%)	859 (100%)	2 (0%)	87	87
2	C	376/376 (100%)	369 (98%)	7 (2%)	50	67
2	D	274/376 (73%)	268 (98%)	6 (2%)	45	64
3	E	189/212 (89%)	184 (97%)	5 (3%)	40	62
3	F	177/212 (84%)	175 (99%)	2 (1%)	65	76
3	Q	116/212 (55%)	112 (97%)	4 (3%)	32	54
4	G	62/66 (94%)	62 (100%)	0	100	100
4	I	62/66 (94%)	62 (100%)	0	100	100
All	All	2978/4082 (73%)	2951 (99%)	27 (1%)	68	79

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	209	SER
3	E	138	ASN
3	Q	162	LEU
3	E	123	GLU
3	E	162	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	111	ASN
3	E	152	GLN
1	B	766	GLN
1	B	566	GLN
3	Q	111	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
4	4HH	I	36	4	22,26,27	0.47	0	27,35,37	1.74	3 (11%)
4	4HH	G	36	4	22,26,27	0.45	0	27,35,37	3.17	4 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	4HH	I	36	4	-	6/33/35/37	-
4	4HH	G	36	4	-	5/33/35/37	-

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	G	36	4HH	O1P-P-OG	11.98	161.86	107.57
4	G	36	4HH	OG-P-O2P	-8.70	74.46	108.94
4	G	36	4HH	P-OG-CB	6.32	157.57	121.35
4	I	36	4HH	P-OG-CB	-5.47	90.01	121.35
4	I	36	4HH	O1P-P-OG	4.80	129.31	107.57

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	G	36	4HH	CB-OG-P-O3P
4	I	36	4HH	N-CA-CB-OG
4	I	36	4HH	CB-OG-P-O1P
4	I	36	4HH	CO-CP-CQ-NR
4	G	36	4HH	ON-CL3-CM-OM

There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	I	36	4HH	1	0
4	G	36	4HH	16	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	$\# Z > 2$
8	ATP	B	1502	7	32,33,33	0.56	1 (3%)	48,52,52	0.74	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	ATP	A	1502	7	32,33,33	0.58	1 (3%)	48,52,52	0.75	2 (4%)

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
8	ATP	B	1502	7	-	2/22/38/38	0/3/3/3
8	ATP	A	1502	7	-	2/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1502	ATP	PB-O3B	-2.37	1.56	1.59
8	B	1502	ATP	PB-O3B	-2.07	1.57	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	1502	ATP	O2'-C2'-C3'	-2.34	104.31	111.82
8	B	1502	ATP	O2'-C2'-C3'	-2.20	104.76	111.82
8	B	1502	ATP	O3'-C3'-C2'	-2.16	104.90	111.82
8	A	1502	ATP	O3'-C3'-C2'	-2.09	105.13	111.82

There are no chirality outliers.

All (4) torsion outliers are listed below:

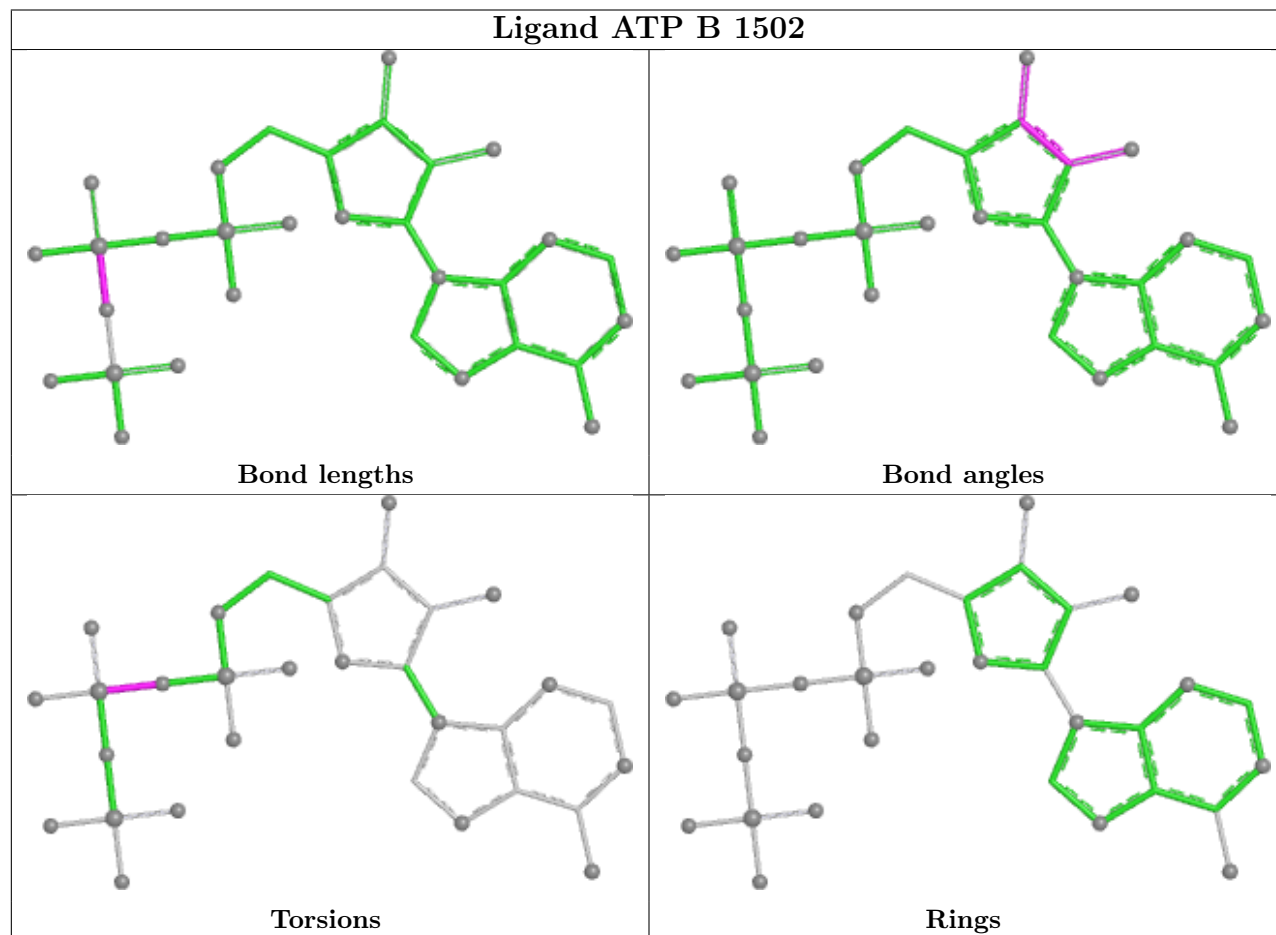
Mol	Chain	Res	Type	Atoms
8	A	1502	ATP	PA-O3A-PB-O2B
8	B	1502	ATP	PA-O3A-PB-O1B
8	B	1502	ATP	PA-O3A-PB-O2B
8	A	1502	ATP	PA-O3A-PB-O1B

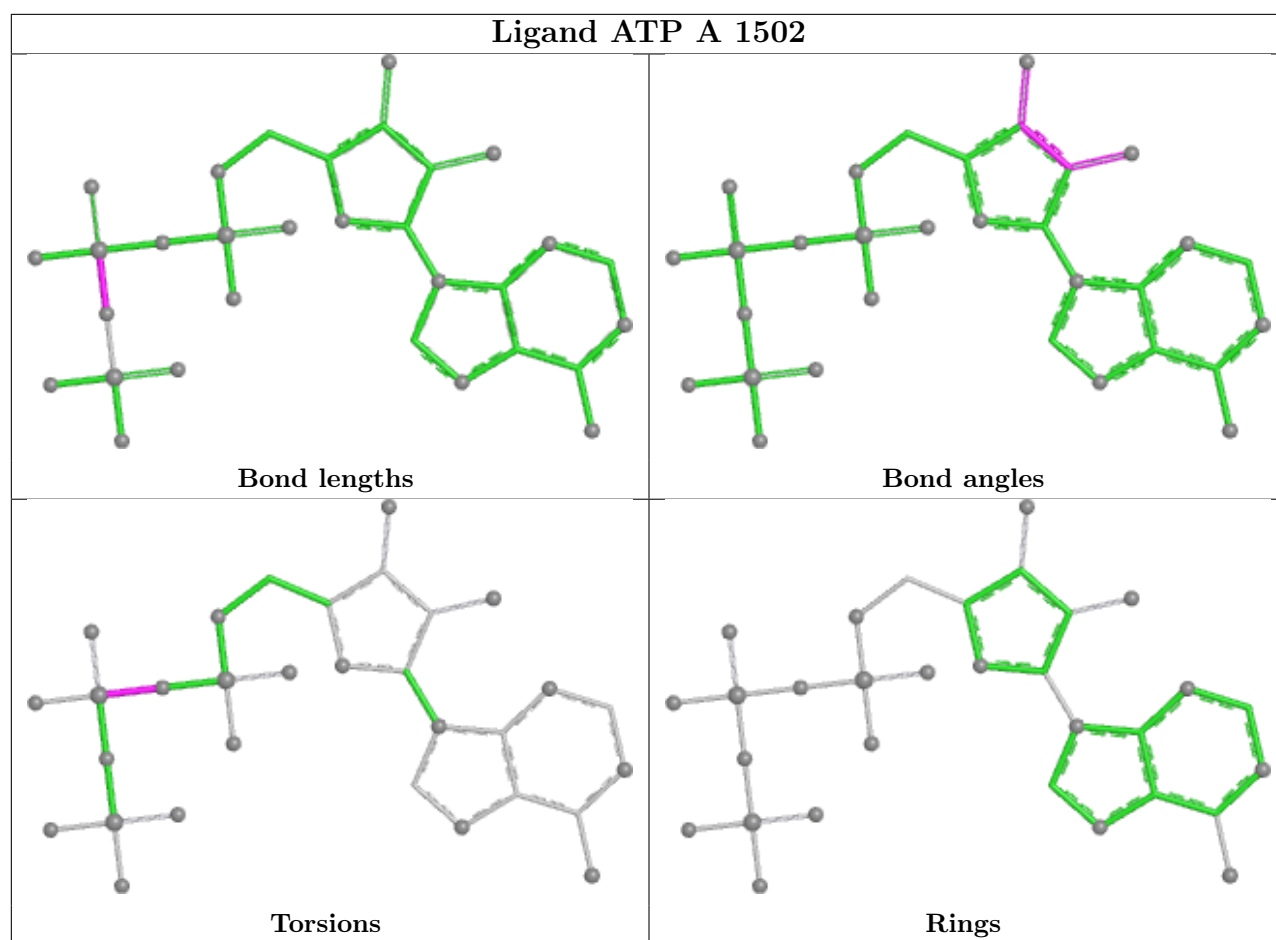
There are no ring outliers.

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	C	1
2	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	295:ARG	C	296:ILE	N	1.03
1	D	295:ARG	C	296:ILE	N	1.03

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-51445. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.