



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 26, 2026 – 05:53 AM EDT

PDB ID : 7OK6 / pdb_00007ok6
Title : Crystal structure of UNC119B in complex with LCK peptide
Authors : Yelland, T.; Ismail, S.
Deposited on : 2021-05-17
Resolution : 1.95 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
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

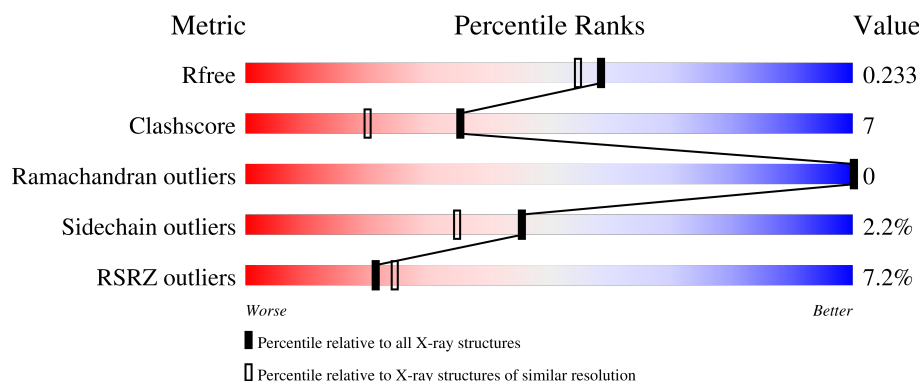
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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	AAA	194	8% 73% 13% • 12%
1	HHH	194	4% 76% 8% 15%
2	BBB	10	10% 50% 50%
2	CCC	10	10% 70% 30%

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	EDO	AAA	403	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3140 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 Protein unc-119 homolog B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HHH	164	Total	C	N	O	S	0	4	0
			1405	900	243	256	6			
1	AAA	170	Total	C	N	O	S	0	3	0
			1447	928	246	267	6			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
HHH	241	LEU	-	expression tag	UNP A6NIH7
HHH	242	GLU	-	expression tag	UNP A6NIH7
HHH	243	HIS	-	expression tag	UNP A6NIH7
HHH	244	HIS	-	expression tag	UNP A6NIH7
HHH	245	HIS	-	expression tag	UNP A6NIH7
HHH	246	HIS	-	expression tag	UNP A6NIH7
HHH	247	HIS	-	expression tag	UNP A6NIH7
HHH	248	HIS	-	expression tag	UNP A6NIH7
AAA	241	LEU	-	expression tag	UNP A6NIH7
AAA	242	GLU	-	expression tag	UNP A6NIH7
AAA	243	HIS	-	expression tag	UNP A6NIH7
AAA	244	HIS	-	expression tag	UNP A6NIH7
AAA	245	HIS	-	expression tag	UNP A6NIH7
AAA	246	HIS	-	expression tag	UNP A6NIH7
AAA	247	HIS	-	expression tag	UNP A6NIH7
AAA	248	HIS	-	expression tag	UNP A6NIH7

- Molecule 2 is a protein called LCK peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BBB	5	Total	C	N	O	S	0	0	0
			26	13	5	6	2			
2	CCC	7	Total	C	N	O	S	0	0	0
			42	22	9	9	2			

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

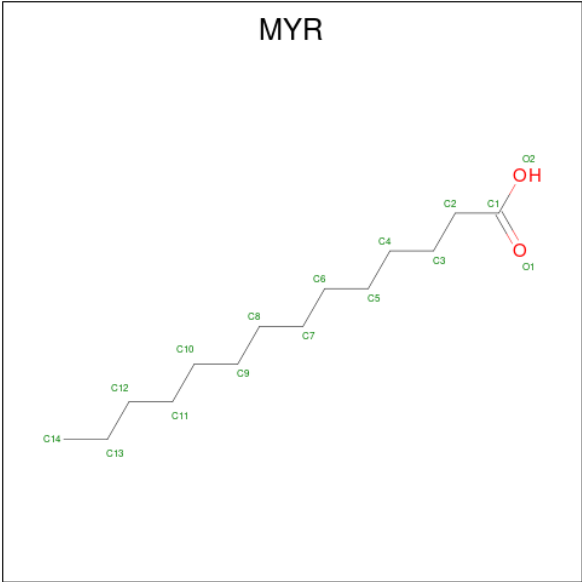


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	AAA	1	Total	C	O	0	0
			4	2	2		
3	AAA	1	Total	C	O	0	0
			4	2	2		
3	AAA	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	1	Total	Ca	0	0
			1	1		

- Molecule 5 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	BBB	1	Total	C	O	0	0
			15	14	1		
5	CCC	1	Total	C	O	0	0
			15	14	1		

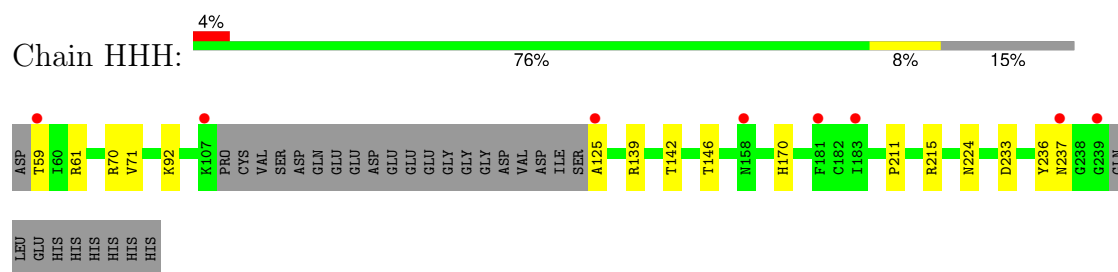
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	HHH	92	Total	O	0	0
			92	92		
6	AAA	81	Total	O	0	0
			81	81		
6	BBB	2	Total	O	0	0
			2	2		
6	CCC	2	Total	O	0	0
			2	2		

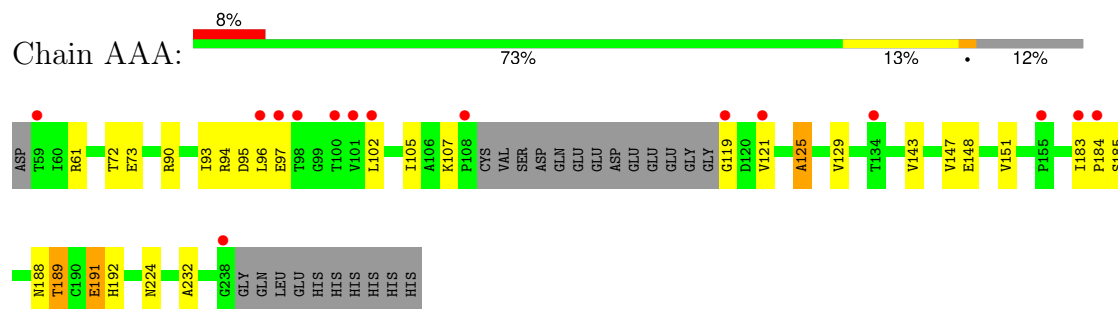
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Protein unc-119 homolog B



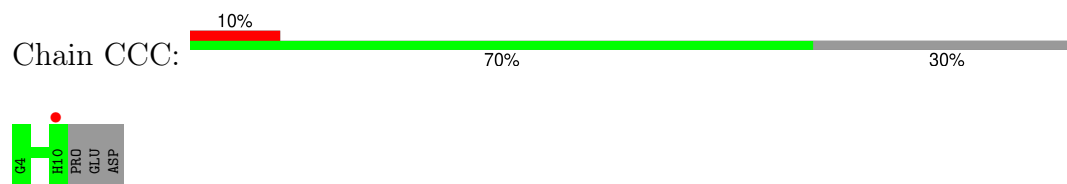
- Molecule 1: Protein unc-119 homolog B



- Molecule 2: LCK peptide



- Molecule 2: LCK peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.08Å 67.00Å 106.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.74 – 1.95 56.74 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.9 (56.74-1.95) 99.9 (56.74-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.181 , 0.224 0.194 , 0.233	Depositor DCC
R_{free} test set	1478 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	27.8	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3140	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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: CA, MYR, EDO

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	AAA	0.98	0/1483	1.24	2/2003 (0.1%)
1	HHH	0.96	0/1440	1.24	5/1945 (0.3%)
2	BBB	1.06	0/25	1.43	0/31
2	CCC	1.03	0/42	1.38	0/54
All	All	0.97	0/2990	1.24	7/4033 (0.2%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	HHH	236	TYR	CA-C-N	6.46	133.44	122.26
1	HHH	236	TYR	C-N-CA	6.46	133.44	122.26
1	HHH	59	THR	CA-C-N	5.87	128.59	120.49
1	HHH	59	THR	C-N-CA	5.87	128.59	120.49
1	HHH	233	ASP	CA-CB-CG	5.70	118.30	112.60
1	AAA	125	ALA	CA-C-N	5.65	126.35	120.03
1	AAA	125	ALA	C-N-CA	5.65	126.35	120.03

There are no chirality outliers.

There are no planarity outliers.

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	AAA	1447	0	1393	29	0
1	HHH	1405	0	1353	15	0
2	BBB	26	0	20	0	0
2	CCC	42	0	32	0	0
3	AAA	12	0	18	7	0
4	AAA	1	0	0	0	0
5	BBB	15	0	27	0	0
5	CCC	15	0	27	0	0
6	AAA	81	0	0	5	0
6	BBB	2	0	0	0	0
6	CCC	2	0	0	0	0
6	HHH	92	0	0	8	0
All	All	3140	0	2870	43	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 7.

All (43) 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:AAA:102:LEU:O	1:AAA:119:GLY:HA3	1.68	0.91
1:AAA:183:ILE:H	1:AAA:188:ASN:HD21	1.20	0.88
1:AAA:72:THR:HB	3:AAA:403:EDO:H22	1.65	0.77
1:HHH:146[A]:THR:HG23	6:HHH:372:HOH:O	1.83	0.77
1:AAA:90:ARG:HD2	6:AAA:574:HOH:O	1.85	0.77
1:AAA:73:GLU:H	3:AAA:403:EDO:H21	1.52	0.74
1:AAA:189:THR:CG2	6:AAA:575:HOH:O	2.41	0.69
1:HHH:125:ALA:HB3	6:HHH:389:HOH:O	1.92	0.68
1:AAA:73:GLU:N	3:AAA:403:EDO:H21	2.08	0.67
1:AAA:61:ARG:HH11	1:AAA:224:ASN:HD22	1.45	0.63
1:AAA:189:THR:HG22	6:AAA:575:HOH:O	1.99	0.62
1:AAA:183:ILE:H	1:AAA:188:ASN:ND2	1.96	0.61
1:HHH:170:HIS:CE1	6:HHH:331:HOH:O	2.54	0.60
1:AAA:94:ARG:NH2	1:AAA:191[A]:GLU:OE1	2.32	0.60
1:HHH:92:LYS:HE2	1:HHH:146[B]:THR:HG21	1.86	0.58
1:HHH:139:ARG:HD3	6:HHH:361:HOH:O	2.03	0.57
1:AAA:90:ARG:HB3	1:AAA:148:GLU:HB3	1.86	0.57
1:HHH:215:ARG:HD3	6:HHH:307:HOH:O	2.05	0.56
1:HHH:92:LYS:HB3	1:HHH:146[B]:THR:HG23	1.89	0.55
1:HHH:92:LYS:HE2	1:HHH:146[B]:THR:CG2	2.37	0.54
1:AAA:151:VAL:HG23	1:AAA:184:PRO:HA	1.89	0.54
1:HHH:142[B]:THR:HG21	1:AAA:125:ALA:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:HHH:92:LYS:HB3	1:HHH:146[B]:THR:CG2	2.39	0.53
1:AAA:73:GLU:H	3:AAA:403:EDO:C2	2.22	0.51
1:AAA:90:ARG:NH1	6:AAA:501:HOH:O	2.46	0.48
1:HHH:61:ARG:HD3	1:HHH:224:ASN:O	2.13	0.47
1:AAA:72:THR:CB	3:AAA:403:EDO:H22	2.41	0.47
1:AAA:93:ILE:HG23	1:AAA:143:VAL:HG13	1.97	0.47
1:AAA:183:ILE:N	1:AAA:188:ASN:HD21	2.00	0.47
1:AAA:95:ASP:OD1	1:AAA:97:GLU:HG3	2.15	0.46
1:AAA:105:ILE:HG23	3:AAA:401:EDO:H12	1.98	0.46
1:AAA:102:LEU:C	1:AAA:119:GLY:HA3	2.39	0.45
1:AAA:61:ARG:HH11	1:AAA:224:ASN:ND2	2.13	0.45
1:AAA:192:HIS:HD2	6:AAA:542:HOH:O	2.00	0.43
1:AAA:73:GLU:HB2	3:AAA:403:EDO:H21	1.99	0.43
1:HHH:70:ARG:CD	6:HHH:339:HOH:O	2.65	0.43
1:HHH:211:PRO:HG3	1:HHH:237:ASN:ND2	2.35	0.42
1:AAA:129:VAL:O	1:AAA:232:ALA:HA	2.20	0.42
1:HHH:146[A]:THR:HG21	6:HHH:347:HOH:O	2.20	0.42
1:AAA:147:VAL:O	1:AAA:189:THR:HA	2.20	0.42
1:AAA:61:ARG:NH1	1:AAA:224:ASN:HD22	2.15	0.41
1:HHH:170:HIS:HE1	6:HHH:331:HOH:O	1.98	0.41
1:AAA:93:ILE:HG23	1:AAA:143:VAL:CG1	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AAA	169/194 (87%)	166 (98%)	3 (2%)	0	100	100
1	HHH	164/194 (84%)	162 (99%)	2 (1%)	0	100	100
2	BBB	3/10 (30%)	3 (100%)	0	0	100	100
2	CCC	5/10 (50%)	5 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	341/408 (84%)	336 (98%)	5 (2%)	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 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	AAA	160/178 (90%)	153 (96%)	7 (4%)	25	12
1	HHH	154/178 (86%)	153 (99%)	1 (1%)	78	78
2	BBB	3/8 (38%)	3 (100%)	0	100	100
2	CCC	5/8 (62%)	5 (100%)	0	100	100
All	All	322/372 (87%)	314 (98%)	8 (2%)	45	29

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	HHH	71	VAL
1	AAA	96	LEU
1	AAA	107	LYS
1	AAA	121	VAL
1	AAA	185	SER
1	AAA	189	THR
1	AAA	191[A]	GLU
1	AAA	191[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

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](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	$\# Z > 2$
5	MYR	CCC	301	2	13,14,15	0.96	1 (7%)	12,13,15	0.50	0
5	MYR	BBB	301	2	13,14,15	0.76	0	12,13,15	0.43	0
3	EDO	AAA	401	-	3,3,3	0.19	0	2,2,2	0.17	0
3	EDO	AAA	403	-	3,3,3	0.27	0	2,2,2	0.69	0
3	EDO	AAA	402	-	3,3,3	0.15	0	2,2,2	0.24	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
5	MYR	CCC	301	2	-	8/12/12/13	-
5	MYR	BBB	301	2	-	6/12/12/13	-
3	EDO	AAA	401	-	-	0/1/1/1	-
3	EDO	AAA	403	-	-	0/1/1/1	-
3	EDO	AAA	402	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	CCC	301	MYR	C3-C2	-2.33	1.42	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

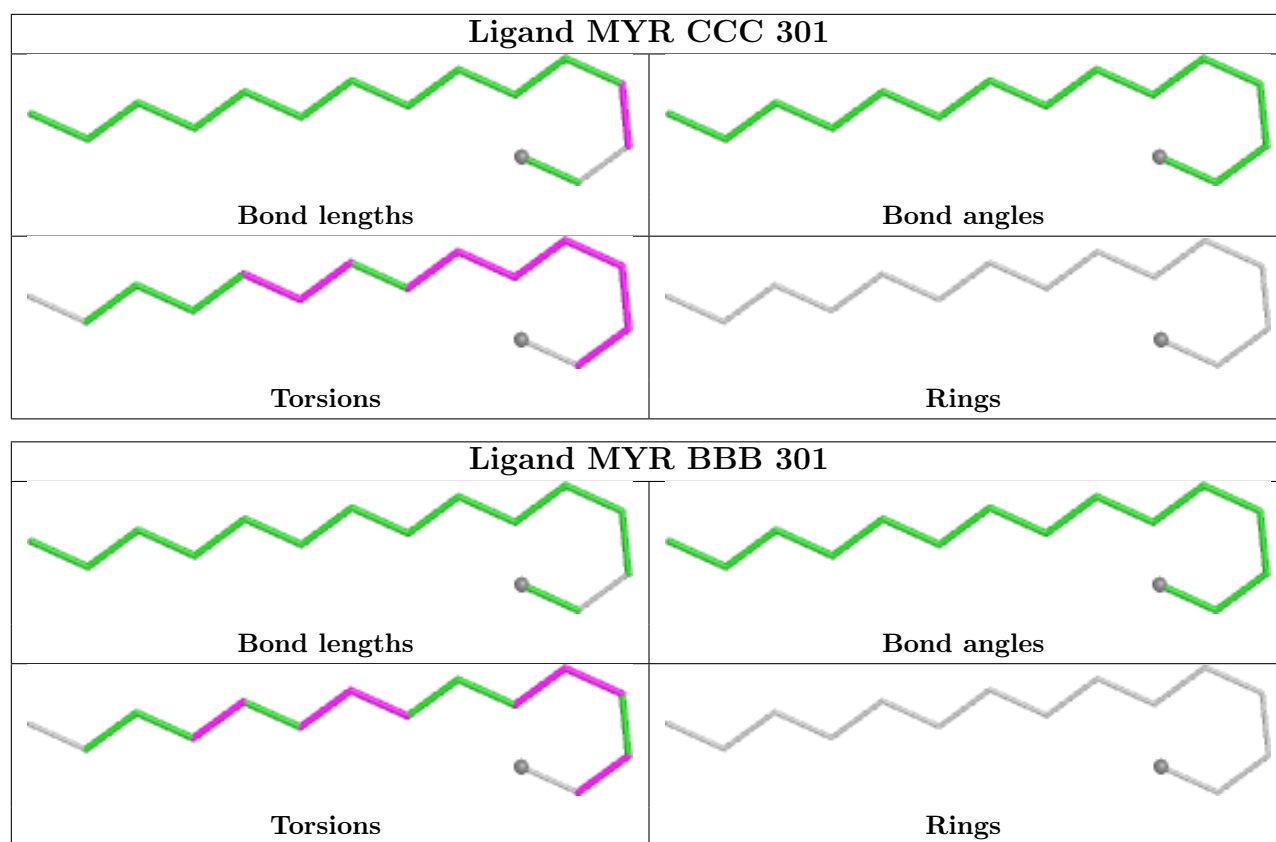
Mol	Chain	Res	Type	Atoms
5	BBB	301	MYR	O1-C1-C2-C3
5	CCC	301	MYR	O1-C1-C2-C3
5	CCC	301	MYR	C2-C3-C4-C5
5	CCC	301	MYR	C11-C10-C9-C8
5	BBB	301	MYR	C7-C8-C9-C10
5	BBB	301	MYR	C9-C10-C11-C12
3	AAA	402	EDO	O1-C1-C2-O2
5	BBB	301	MYR	C3-C4-C5-C6
5	CCC	301	MYR	C3-C4-C5-C6
5	CCC	301	MYR	C5-C6-C7-C8
5	CCC	301	MYR	C1-C2-C3-C4
5	BBB	301	MYR	C6-C7-C8-C9
5	BBB	301	MYR	C2-C3-C4-C5
5	CCC	301	MYR	C7-C8-C9-C10
5	CCC	301	MYR	C4-C5-C6-C7

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	AAA	401	EDO	1	0
3	AAA	403	EDO	6	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AAA	170/194 (87%)	0.50	15 (8%) 15 17	16, 33, 55, 75	3 (1%)
1	HHH	164/194 (84%)	0.29	8 (4%) 35 39	15, 29, 56, 74	4 (2%)
2	BBB	5/10 (50%)	0.64	1 (20%) 3 3	24, 28, 41, 65	0
2	CCC	7/10 (70%)	0.33	1 (14%) 6 7	23, 26, 37, 67	0
All	All	346/408 (84%)	0.40	25 (7%) 21 24	15, 31, 56, 75	7 (2%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	119	GLY	5.0
1	AAA	121	VAL	4.2
1	AAA	108	PRO	3.9
1	HHH	181	PHE	3.9
1	HHH	107	LYS	3.8
1	HHH	125	ALA	3.6
2	BBB	4	SER	3.4
1	HHH	183	ILE	3.4
1	HHH	237	ASN	3.3
1	HHH	59	THR	3.0
2	CCC	10	HIS	2.8
1	HHH	239	GLY	2.8
1	AAA	59	THR	2.8
1	AAA	184	PRO	2.8
1	AAA	238	GLY	2.7
1	AAA	134	THR	2.6
1	AAA	98	THR	2.5
1	AAA	183	ILE	2.3
1	AAA	155	PRO	2.3
1	AAA	96	LEU	2.3
1	HHH	158	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	AAA	102	LEU	2.2
1	AAA	100	THR	2.1
1	AAA	101	VAL	2.1
1	AAA	97	GLU	2.1

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](#)

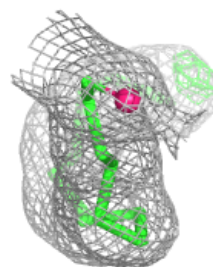
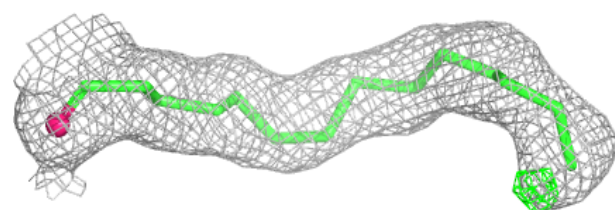
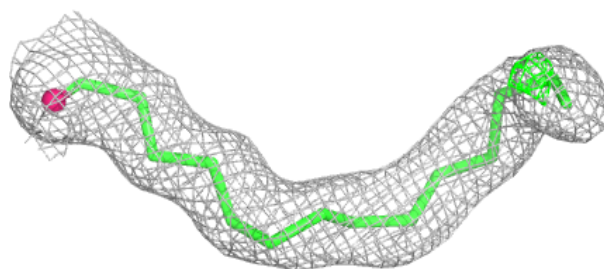
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	EDO	AAA	401	4/4	0.90	0.13	38,41,43,45	0
3	EDO	AAA	403	4/4	0.92	0.10	37,41,44,45	0
5	MYR	BBB	301	15/16	0.93	0.11	23,37,40,41	0
5	MYR	CCC	301	15/16	0.94	0.11	22,35,48,49	0
3	EDO	AAA	402	4/4	0.95	0.11	32,39,40,40	0
4	CA	AAA	404	1/1	0.99	0.11	33,33,33,33	0

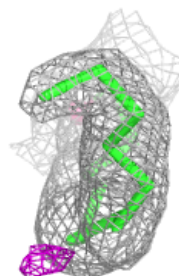
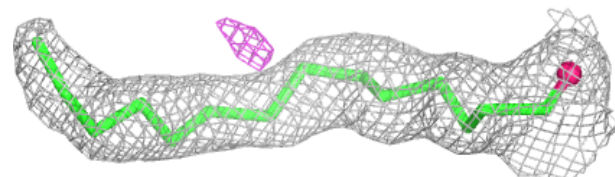
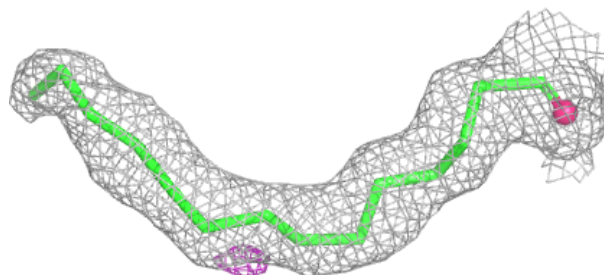
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MYR BBB 301:

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

**Electron density around MYR CCC 301:**

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



6.5 Other polymers ⓘ

There are no such residues in this entry.