



## Full wwPDB EM Validation Report ⓘ

May 4, 2024 – 10:53 am BST

PDB ID : 6QD3  
EMDB ID : EMD-4518  
Title : MloK1 model from single particle analysis of 2D crystals, class 7 (intermediate conformation)  
Authors : Righetto, R.; Biyani, N.; Kowal, J.; Chami, M.; Stahlberg, H.  
Deposited on : 2018-12-31  
Resolution : 5.00 Å(reported)  
Based on initial model : 6I9D

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : **FAILED**  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

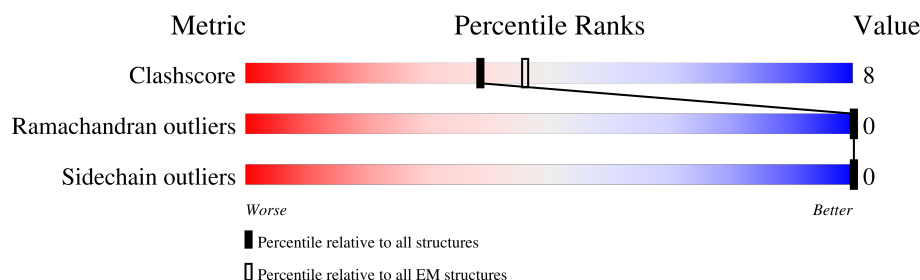
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 5.00 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	355	80% 19%
1	B	355	80% 19%
1	C	355	81% 18%
1	D	355	81% 18%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 21746 atoms, of which 11100 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 Cyclic nucleotide-gated potassium channel mll3241.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	355	Total	C	H	N	O	S	0	0
			5436	1734	2775	455	461	11		
1	B	355	Total	C	H	N	O	S	0	0
			5436	1734	2775	455	461	11		
1	C	355	Total	C	H	N	O	S	0	0
			5436	1734	2775	455	461	11		
1	D	355	Total	C	H	N	O	S	0	0
			5436	1734	2775	455	461	11		

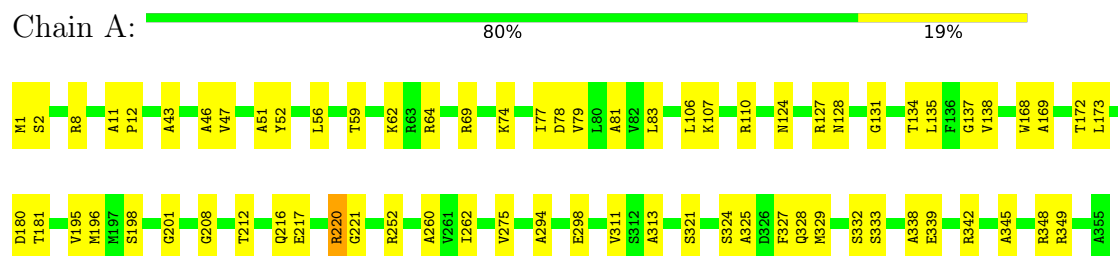
- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
2	A	1	Total	K	0
			1	1	
2	B	1	Total	K	0
			1	1	

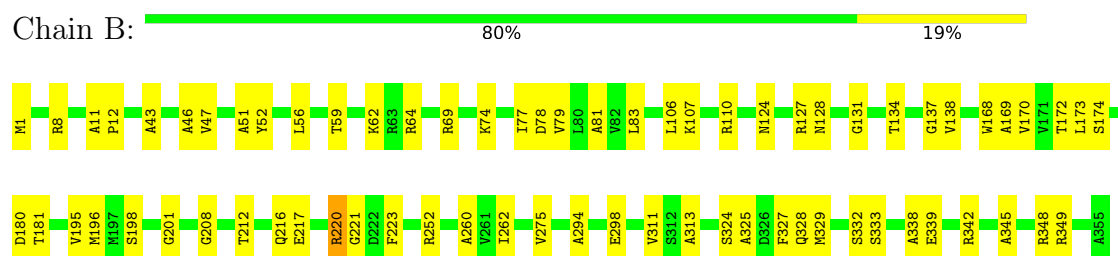
### 3 Residue-property plots

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.

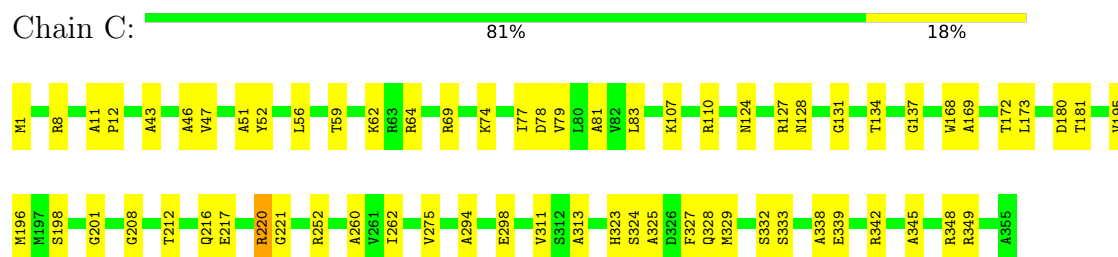
- Molecule 1: Cyclic nucleotide-gated potassium channel mll3241



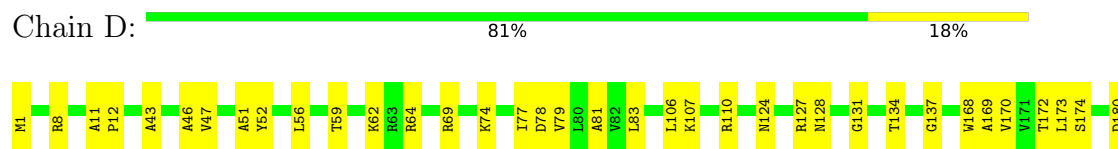
- Molecule 1: Cyclic nucleotide-gated potassium channel mll3241



- Molecule 1: Cyclic nucleotide-gated potassium channel mll3241



- Molecule 1: Cyclic nucleotide-gated potassium channel mll3241



T181	V196	M196	M197	S198	G201	G208	T212	Q216	E217	R220	G221	R252	A260	V261	I262	E298	V311	S312	A313	S324	A325	D326	F327	Q328	M329	S332	S333	A338	E339	R342	A345	R348	R349	A355
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	31417	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; The defocus at the center of each particle box was estimated based on the tilt geometry.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45	Depositor
Minimum defocus (nm)	750	Depositor
Maximum defocus (nm)	4300	Depositor
Magnification	50000	Depositor
Image detector	GATAN K2 SUMMIT (4k 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:  
K

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	0.43	0/2720	0.63	1/3713 (0.0%)
1	B	0.43	0/2720	0.63	1/3713 (0.0%)
1	C	0.43	0/2720	0.63	1/3713 (0.0%)
1	D	0.43	0/2720	0.63	1/3713 (0.0%)
All	All	0.43	0/10880	0.63	4/14852 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	220	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	D	220	ARG	NE-CZ-NH2	-6.94	116.83	120.30
1	B	220	ARG	NE-CZ-NH2	-6.93	116.83	120.30
1	A	220	ARG	NE-CZ-NH2	-6.89	116.86	120.30

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	A	2661	2775	2775	49	0
1	B	2661	2775	2775	48	0
1	C	2661	2775	2775	45	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	2661	2775	2775	46	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
All	All	10646	11100	11100	172	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 8.

All (172) 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:B:64:ARG:O	1:B:69:ARG:NH1	2.11	0.84
1:D:64:ARG:O	1:D:69:ARG:NH1	2.11	0.83
1:C:64:ARG:O	1:C:69:ARG:NH1	2.11	0.83
1:A:64:ARG:O	1:A:69:ARG:NH1	2.11	0.83
1:B:208:GLY:O	1:B:212:THR:OG1	1.98	0.82
1:C:208:GLY:O	1:C:212:THR:OG1	1.98	0.81
1:A:208:GLY:O	1:A:212:THR:OG1	1.98	0.81
1:D:208:GLY:O	1:D:212:THR:OG1	1.98	0.80
1:C:56:LEU:O	1:C:59:THR:OG1	1.99	0.79
1:A:56:LEU:O	1:A:59:THR:OG1	2.00	0.78
1:B:56:LEU:O	1:B:59:THR:OG1	2.00	0.77
1:D:56:LEU:O	1:D:59:THR:OG1	1.99	0.77
1:B:77:ILE:O	1:B:81:ALA:N	2.21	0.74
1:A:77:ILE:O	1:A:81:ALA:N	2.21	0.74
1:C:77:ILE:O	1:C:81:ALA:N	2.21	0.74
1:D:195:VAL:O	1:D:198:SER:OG	2.04	0.73
1:C:195:VAL:O	1:C:198:SER:OG	2.04	0.73
1:D:77:ILE:O	1:D:81:ALA:N	2.21	0.73
1:A:127:ARG:NH1	1:A:128:ASN:OD1	2.23	0.72
1:C:127:ARG:NH1	1:C:128:ASN:OD1	2.23	0.72
1:D:127:ARG:NH1	1:D:128:ASN:OD1	2.23	0.72
1:B:127:ARG:NH1	1:B:128:ASN:OD1	2.23	0.71
1:B:195:VAL:O	1:B:198:SER:OG	2.04	0.70
1:B:168:TRP:O	1:B:172:THR:OG1	2.06	0.69
1:C:124:ASN:OD1	1:D:252:ARG:NH1	2.26	0.69
1:D:168:TRP:O	1:D:172:THR:OG1	2.06	0.69
1:A:124:ASN:OD1	1:B:252:ARG:NH1	2.26	0.69
1:B:124:ASN:OD1	1:C:252:ARG:NH1	2.26	0.68
1:C:52:TYR:O	1:C:56:LEU:N	2.27	0.68
1:B:339:GLU:OE2	1:B:342:ARG:NH2	2.28	0.67

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:TYR:O	1:A:56:LEU:N	2.27	0.67
1:A:339:GLU:OE2	1:A:342:ARG:NH2	2.28	0.67
1:A:168:TRP:O	1:A:172:THR:OG1	2.06	0.67
1:B:52:TYR:O	1:B:56:LEU:N	2.27	0.67
1:A:195:VAL:O	1:A:198:SER:OG	2.04	0.67
1:C:339:GLU:OE2	1:C:342:ARG:NH2	2.28	0.67
1:C:168:TRP:O	1:C:172:THR:OG1	2.06	0.67
1:D:52:TYR:O	1:D:56:LEU:N	2.27	0.66
1:B:217:GLU:O	1:B:221:GLY:N	2.29	0.66
1:D:217:GLU:O	1:D:221:GLY:N	2.29	0.66
1:A:217:GLU:O	1:A:221:GLY:N	2.29	0.66
1:D:339:GLU:OE2	1:D:342:ARG:NH2	2.28	0.66
1:A:252:ARG:NH1	1:D:124:ASN:O	2.28	0.66
1:C:217:GLU:O	1:C:221:GLY:N	2.29	0.66
1:D:62:LYS:O	1:D:69:ARG:NH2	2.29	0.66
1:A:62:LYS:O	1:A:69:ARG:NH2	2.29	0.65
1:B:62:LYS:O	1:B:69:ARG:NH2	2.29	0.65
1:C:62:LYS:O	1:C:69:ARG:NH2	2.29	0.65
1:A:74:LYS:O	1:A:110:ARG:NE	2.30	0.64
1:B:74:LYS:O	1:B:110:ARG:NE	2.30	0.64
1:C:74:LYS:O	1:C:110:ARG:NE	2.30	0.64
1:D:74:LYS:O	1:D:110:ARG:NE	2.30	0.64
1:C:329:MET:O	1:C:332:SER:OG	2.11	0.64
1:A:252:ARG:NH1	1:D:124:ASN:OD1	2.31	0.63
1:A:298:GLU:OE2	1:A:348:ARG:NH1	2.33	0.62
1:D:47:VAL:O	1:D:51:ALA:N	2.33	0.62
1:D:298:GLU:OE2	1:D:348:ARG:NH1	2.33	0.62
1:A:47:VAL:O	1:A:51:ALA:N	2.33	0.62
1:B:298:GLU:OE2	1:B:348:ARG:NH1	2.33	0.61
1:C:298:GLU:OE2	1:C:348:ARG:NH1	2.33	0.61
1:B:47:VAL:O	1:B:51:ALA:N	2.33	0.61
1:C:47:VAL:O	1:C:51:ALA:N	2.33	0.61
1:C:124:ASN:O	1:D:252:ARG:NH1	2.35	0.60
1:B:124:ASN:O	1:C:252:ARG:NH1	2.35	0.60
1:A:329:MET:O	1:A:332:SER:OG	2.11	0.59
1:B:329:MET:O	1:B:332:SER:OG	2.11	0.59
1:D:329:MET:O	1:D:332:SER:OG	2.11	0.58
1:D:345:ALA:O	1:D:349:ARG:NE	2.36	0.58
1:A:78:ASP:OD1	1:A:107:LYS:NZ	2.36	0.58
1:A:124:ASN:O	1:B:252:ARG:NH1	2.37	0.58
1:B:78:ASP:OD1	1:B:107:LYS:NZ	2.37	0.58

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:345:ALA:O	1:B:349:ARG:NE	2.36	0.58
1:C:345:ALA:O	1:C:349:ARG:NE	2.36	0.58
1:D:78:ASP:OD1	1:D:107:LYS:NZ	2.36	0.58
1:C:78:ASP:OD1	1:C:107:LYS:NZ	2.36	0.57
1:A:345:ALA:O	1:A:349:ARG:NE	2.36	0.57
1:B:131:GLY:O	1:B:134:THR:OG1	2.22	0.57
1:C:298:GLU:N	1:C:298:GLU:OE1	2.37	0.57
1:A:131:GLY:O	1:A:134:THR:OG1	2.22	0.57
1:C:131:GLY:O	1:C:134:THR:OG1	2.22	0.56
1:D:131:GLY:O	1:D:134:THR:OG1	2.22	0.56
1:B:324:SER:O	1:B:327:PHE:N	2.39	0.56
1:D:298:GLU:OE1	1:D:298:GLU:N	2.37	0.55
1:A:324:SER:O	1:A:327:PHE:N	2.39	0.55
1:C:324:SER:O	1:C:327:PHE:N	2.39	0.55
1:A:298:GLU:OE1	1:A:298:GLU:N	2.37	0.55
1:D:169:ALA:O	1:D:173:LEU:N	2.40	0.54
1:D:324:SER:O	1:D:327:PHE:N	2.39	0.54
1:A:216:GLN:NE2	1:B:1:MET:SD	2.79	0.54
1:A:169:ALA:O	1:A:173:LEU:N	2.40	0.54
1:B:298:GLU:OE1	1:B:298:GLU:N	2.37	0.53
1:B:216:GLN:NE2	1:C:1:MET:SD	2.77	0.53
1:B:216:GLN:O	1:B:220:ARG:N	2.42	0.52
1:D:216:GLN:O	1:D:220:ARG:N	2.42	0.52
1:C:169:ALA:O	1:C:173:LEU:N	2.40	0.52
1:A:1:MET:SD	1:D:216:GLN:NE2	2.81	0.52
1:C:180:ASP:OD1	1:C:181:THR:N	2.43	0.52
1:B:169:ALA:O	1:B:173:LEU:N	2.40	0.52
1:C:216:GLN:NE2	1:D:1:MET:SD	2.80	0.51
1:C:260:ALA:O	1:C:313:ALA:N	2.42	0.51
1:C:216:GLN:O	1:C:220:ARG:N	2.42	0.51
1:B:260:ALA:O	1:B:313:ALA:N	2.42	0.51
1:D:324:SER:O	1:D:328:GLN:N	2.38	0.51
1:B:180:ASP:OD1	1:B:181:THR:N	2.43	0.51
1:C:324:SER:O	1:C:328:GLN:N	2.38	0.51
1:A:325:ALA:O	1:A:329:MET:N	2.42	0.51
1:D:180:ASP:OD1	1:D:181:THR:N	2.43	0.50
1:D:325:ALA:O	1:D:329:MET:N	2.42	0.50
1:A:324:SER:O	1:A:328:GLN:N	2.38	0.49
1:C:196:MET:SD	1:C:196:MET:N	2.86	0.49
1:A:216:GLN:O	1:A:220:ARG:N	2.42	0.49
1:A:180:ASP:OD1	1:A:181:THR:N	2.43	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:260:ALA:O	1:D:313:ALA:N	2.42	0.49
1:C:325:ALA:O	1:C:329:MET:N	2.42	0.49
1:A:260:ALA:O	1:A:313:ALA:N	2.42	0.48
1:C:338:ALA:O	1:C:342:ARG:N	2.45	0.48
1:B:325:ALA:O	1:B:329:MET:N	2.42	0.47
1:A:196:MET:N	1:A:196:MET:SD	2.86	0.47
1:D:338:ALA:O	1:D:342:ARG:N	2.45	0.47
1:D:196:MET:SD	1:D:196:MET:N	2.86	0.47
1:B:196:MET:SD	1:B:196:MET:N	2.86	0.46
1:B:324:SER:O	1:B:328:GLN:N	2.38	0.46
1:B:338:ALA:O	1:B:342:ARG:N	2.45	0.45
1:A:338:ALA:O	1:A:342:ARG:N	2.45	0.45
1:B:134:THR:O	1:B:137:GLY:N	2.50	0.45
1:C:134:THR:O	1:C:137:GLY:N	2.50	0.45
1:D:134:THR:O	1:D:137:GLY:N	2.50	0.45
1:D:198:SER:O	1:D:201:GLY:N	2.50	0.45
1:A:134:THR:O	1:A:137:GLY:N	2.50	0.45
1:B:134:THR:O	1:B:138:VAL:N	2.43	0.45
1:B:170:VAL:O	1:B:174:SER:OG	2.28	0.45
1:D:79:VAL:HG12	1:D:83:LEU:HD12	2.00	0.44
1:A:275:VAL:N	1:A:294:ALA:O	2.50	0.44
1:A:79:VAL:HG12	1:A:83:LEU:HD12	2.00	0.44
1:B:198:SER:O	1:B:201:GLY:N	2.50	0.44
1:D:329:MET:O	1:D:333:SER:N	2.51	0.44
1:B:329:MET:O	1:B:333:SER:N	2.51	0.44
1:A:329:MET:O	1:A:333:SER:N	2.51	0.44
1:C:79:VAL:HG12	1:C:83:LEU:HD12	2.00	0.44
1:B:275:VAL:N	1:B:294:ALA:O	2.50	0.43
1:A:8:ARG:O	1:A:11:ALA:HB2	2.18	0.43
1:A:198:SER:O	1:A:201:GLY:N	2.50	0.43
1:C:329:MET:O	1:C:333:SER:N	2.51	0.43
1:B:79:VAL:HG12	1:B:83:LEU:HD12	2.00	0.43
1:D:43:ALA:O	1:D:46:ALA:N	2.52	0.43
1:C:43:ALA:O	1:C:46:ALA:N	2.52	0.43
1:C:8:ARG:O	1:C:11:ALA:HB2	2.18	0.43
1:D:8:ARG:O	1:D:11:ALA:HB2	2.18	0.43
1:A:134:THR:O	1:A:138:VAL:N	2.43	0.42
1:B:8:ARG:O	1:B:11:ALA:HB2	2.18	0.42
1:A:325:ALA:HB3	1:D:220:ARG:CZ	2.49	0.42
1:B:43:ALA:O	1:B:46:ALA:N	2.52	0.42
1:C:262:ILE:HD12	1:C:311:VAL:HG12	2.02	0.42

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:ALA:O	1:A:46:ALA:N	2.52	0.42
1:B:223:PHE:CD2	1:C:325:ALA:HB2	2.54	0.42
1:B:262:ILE:HD12	1:B:311:VAL:HG12	2.02	0.42
1:A:262:ILE:HD12	1:A:311:VAL:HG12	2.02	0.42
1:C:11:ALA:HB3	1:C:12:PRO:HD3	2.02	0.42
1:C:275:VAL:N	1:C:294:ALA:O	2.50	0.42
1:D:11:ALA:HB3	1:D:12:PRO:HD3	2.02	0.42
1:D:262:ILE:HD12	1:D:311:VAL:HG12	2.02	0.42
1:C:198:SER:O	1:C:201:GLY:N	2.50	0.41
1:A:325:ALA:H	1:D:220:ARG:HH21	1.68	0.41
1:B:106:LEU:O	1:B:110:ARG:N	2.54	0.41
1:A:11:ALA:HB3	1:A:12:PRO:HD3	2.02	0.41
1:A:2:SER:O	1:A:321:SER:OG	2.32	0.41
1:B:11:ALA:HB3	1:B:12:PRO:HD3	2.02	0.41
1:D:106:LEU:O	1:D:110:ARG:N	2.54	0.41
1:A:106:LEU:O	1:A:110:ARG:N	2.54	0.41
1:B:220:ARG:NH2	1:C:323:HIS:HB3	2.36	0.41
1:D:170:VAL:O	1:D:174:SER:OG	2.28	0.41
1:A:134:THR:HG1	1:A:135:LEU:H	1.69	0.40

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	353/355 (99%)	307 (87%)	46 (13%)	0	100	100
1	B	353/355 (99%)	307 (87%)	46 (13%)	0	100	100
1	C	353/355 (99%)	307 (87%)	46 (13%)	0	100	100
1	D	353/355 (99%)	307 (87%)	46 (13%)	0	100	100
All	All	1412/1420 (99%)	1228 (87%)	184 (13%)	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 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	273/273 (100%)	273 (100%)	0	100	100
1	B	273/273 (100%)	273 (100%)	0	100	100
1	C	273/273 (100%)	273 (100%)	0	100	100
1	D	273/273 (100%)	273 (100%)	0	100	100
All	All	1092/1092 (100%)	1092 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	GLN
1	B	328	GLN
1	C	328	GLN
1	D	328	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

## 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 Map visualisation

This section contains visualisations of the EMDB entry EMD-4518. 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.