



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:56 AM GMT

PDB ID : 3CO2  
Title : Mlotik1 ion channel cyclic-nucleotide binding domain mutant  
Authors : Clayton, G.M.; Alteiri, S.L.; Thomas, L.R.; Morais-Cabral, J.H.  
Deposited on : 2008-03-27  
Resolution : 2.90 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

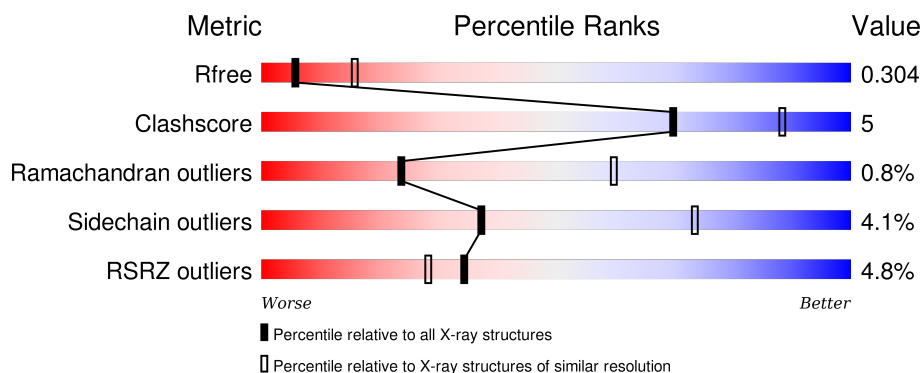
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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))
$R_{free}$	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	140	<div> <div>4%</div> <div>76% 12% • 10%</div> </div>
1	B	140	<div> <div>%</div> <div>84% 8% 9%</div> </div>
1	C	140	<div> <div>9%</div> <div>75% 9% • 15%</div> </div>
1	D	140	<div> <div>4%</div> <div>80% 12% 8%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3519 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 Mlotik1 ion channel protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	126	Total	C	N	O	S	0	0	0
			886	571	147	163	5			
1	B	128	Total	C	N	O	S	0	0	0
			897	579	149	164	5			
1	C	119	Total	C	N	O	S	0	0	0
			811	523	131	153	4			
1	D	129	Total	C	N	O	S	0	0	0
			916	591	153	168	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	307	TRP	ARG	ENGINEERED	UNP Q98GN8
B	307	TRP	ARG	ENGINEERED	UNP Q98GN8
C	307	TRP	ARG	ENGINEERED	UNP Q98GN8
D	307	TRP	ARG	ENGINEERED	UNP Q98GN8

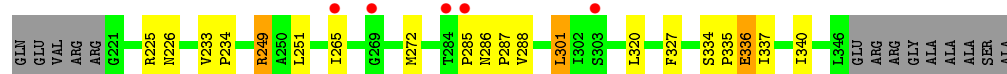
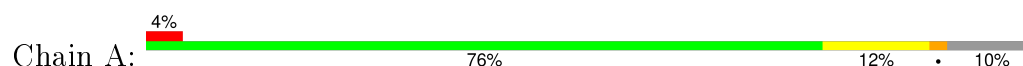
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	3	Total	O	0	0
			3	3		
2	C	1	Total	O	0	0
			1	1		
2	D	1	Total	O	0	0
			1	1		

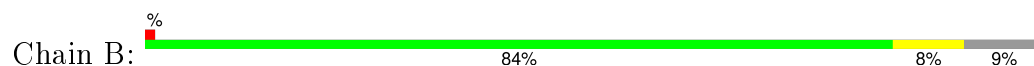
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

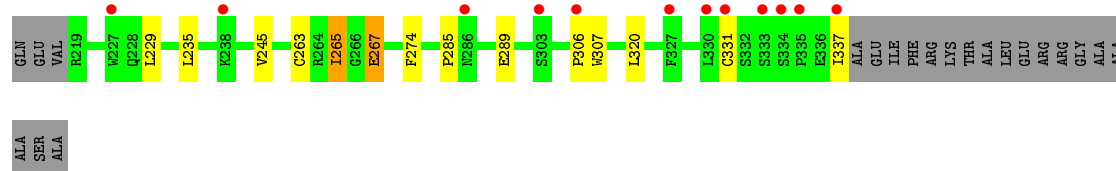
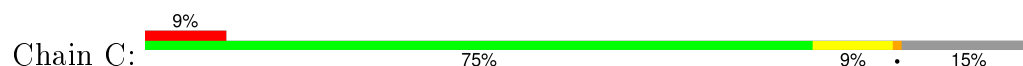
- Molecule 1: Mlotik1 ion channel protein



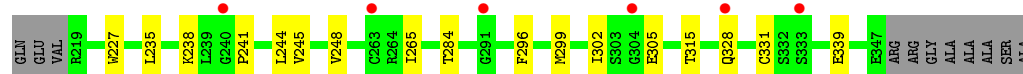
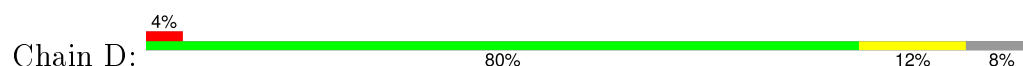
- Molecule 1: Mlotik1 ion channel protein



- Molecule 1: Mlotik1 ion channel protein



- Molecule 1: Mlotik1 ion channel protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	111.47Å 132.35Å 39.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.03 – 2.90 41.02 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.3 (41.03-2.90) 95.5 (41.02-2.47)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.06 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.261 , 0.306 0.263 , 0.304	Depositor DCC
$R_{free}$ test set	694 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	55.0	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 52.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 20960 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3519	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.75% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.36	0/904	0.50	0/1237
1	B	0.35	0/916	0.49	0/1256
1	C	0.38	0/830	0.54	1/1143 (0.1%)
1	D	0.35	0/936	0.51	0/1282
All	All	0.36	0/3586	0.51	1/4918 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	265	ILE	CB-CG1-CD1	5.92	130.47	113.90

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	886	0	852	11	0
1	B	897	0	863	6	0
1	C	811	0	754	7	0
1	D	916	0	890	11	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	3519	0	3359	31	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.

All (31) 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:A:249:ARG:HH21	1:A:249:ARG:HG2	1.33	0.94
1:A:249:ARG:HH21	1:A:249:ARG:CG	1.88	0.85
1:A:249:ARG:NH2	1:A:249:ARG:HG2	1.96	0.78
1:B:274:PHE:HB2	1:B:320:LEU:HB2	1.83	0.61
1:C:331:CYS:SG	1:C:337:ILE:HG12	2.40	0.61
1:D:227:TRP:HH2	1:D:241:PRO:HA	1.66	0.59
1:A:327:PHE:CE1	1:A:337:ILE:HD12	2.41	0.56
1:B:262:ILE:HG23	1:B:319:LEU:HD11	1.88	0.56
1:D:339:GLU:OE1	1:D:339:GLU:HA	2.06	0.55
1:A:225:ARG:NH1	1:A:226:ASN:OD1	2.43	0.51
1:D:227:TRP:CH2	1:D:241:PRO:HA	2.45	0.50
1:C:267:GLU:O	1:C:306:PRO:HA	2.11	0.50
1:D:328:GLN:NE2	1:D:331:CYS:SG	2.85	0.50
1:B:251:LEU:HD13	1:B:320:LEU:HD13	1.94	0.50
1:C:245:VAL:HG21	1:D:245:VAL:CG2	2.42	0.49
1:C:274:PHE:HB2	1:C:320:LEU:HB2	1.95	0.48
1:B:230:VAL:HG12	1:B:244:LEU:HD22	1.98	0.46
1:D:235:LEU:HD21	1:D:302:ILE:HD11	1.98	0.45
1:B:299:MET:N	1:B:299:MET:SD	2.87	0.44
1:D:227:TRP:CD1	1:D:227:TRP:C	2.90	0.44
1:C:245:VAL:HG21	1:D:245:VAL:HG21	2.00	0.44
1:A:251:LEU:HD13	1:A:320:LEU:HD13	1.98	0.43
1:A:272:MET:HB2	1:A:301:LEU:HG	2.00	0.43
1:A:288:VAL:HA	1:D:296:PHE:HB3	2.00	0.43
1:B:309:ALA:HB2	1:C:285:PRO:HB2	2.00	0.43
1:D:244:LEU:O	1:D:248:VAL:HG23	2.18	0.42
1:D:299:MET:HB3	1:D:305:GLU:HG3	2.00	0.42
1:C:263:CYS:HB2	1:C:307:TRP:CD2	2.55	0.42
1:A:233:VAL:HA	1:A:234:PRO:HD2	1.86	0.41
1:A:334:SER:HA	1:A:335:PRO:HD2	1.86	0.41
1:A:336:GLU:O	1:A:340:ILE:HG12	2.21	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	A	124/140 (89%)	116 (94%)	5 (4%)	3 (2%)	7	29
1	B	126/140 (90%)	120 (95%)	6 (5%)	0	100	100
1	C	117/140 (84%)	105 (90%)	11 (9%)	1 (1%)	21	57
1	D	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
All	All	494/560 (88%)	464 (94%)	26 (5%)	4 (1%)	24	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	285	PRO
1	A	286	ASN
1	A	287	PRO
1	C	267	GLU

### 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	86/109 (79%)	82 (95%)	4 (5%)	32	68
1	B	88/109 (81%)	86 (98%)	2 (2%)	58	87
1	C	78/109 (72%)	74 (95%)	4 (5%)	29	65
1	D	91/109 (84%)	87 (96%)	4 (4%)	35	70
All	All	343/436 (79%)	329 (96%)	14 (4%)	37	73



All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	249	ARG
1	A	265	ILE
1	A	301	LEU
1	A	336	GLU
1	B	276	VAL
1	B	328	GLN
1	C	229	LEU
1	C	235	LEU
1	C	265	ILE
1	C	289	GLU
1	D	238	LYS
1	D	265	ILE
1	D	284	THR
1	D	315	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	126/140 (90%)	0.31	5 (3%) 42 35	11, 12, 13, 13	0
1	B	128/140 (91%)	0.12	1 (0%) 87 86	11, 12, 13, 15	0
1	C	119/140 (85%)	0.45	12 (10%) 9 5	12, 12, 13, 16	0
1	D	129/140 (92%)	0.42	6 (4%) 35 29	11, 12, 13, 14	0
All	All	502/560 (89%)	0.32	24 (4%) 34 28	11, 12, 13, 16	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	328	GLN	6.4
1	A	284	THR	4.9
1	C	303	SER	3.0
1	C	330	LEU	2.9
1	B	333	SER	2.7
1	D	333	SER	2.6
1	C	327	PHE	2.6
1	D	291	GLY	2.5
1	C	227	TRP	2.5
1	C	331	CYS	2.4
1	C	238	LYS	2.4
1	A	303	SER	2.4
1	A	265	ILE	2.3
1	C	333	SER	2.3
1	A	269	GLY	2.2
1	A	285	PRO	2.2
1	C	286	ASN	2.2
1	D	304	GLY	2.2
1	C	334	SER	2.2
1	D	240	GLY	2.1
1	C	335	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	337	ILE	2.1
1	C	306	PRO	2.0
1	D	263	CYS	2.0

## 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 carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.