



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:21 AM GMT

PDB ID : 3LNZ
Title : Crystal structure of human MDM2 with a 12-mer peptide inhibitor PMI (N8A mutant)
Authors : Pazgier, M.; Lu, W.
Deposited on : 2010-02-03
Resolution : 1.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

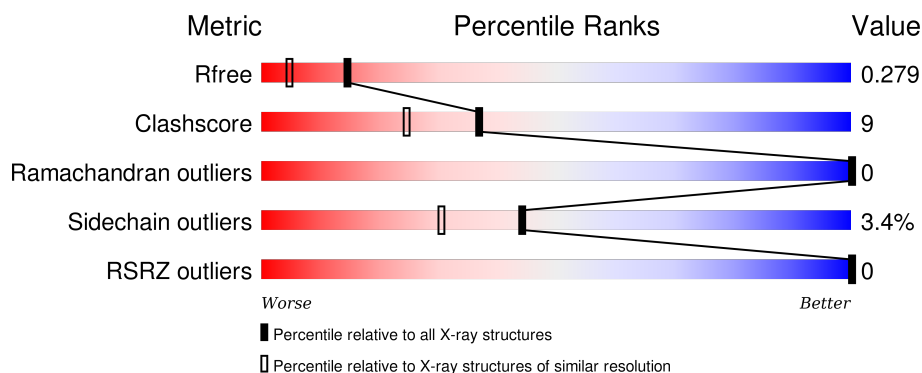
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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 ≥ 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	85	
1	C	85	
1	E	85	
1	G	85	
1	I	85	

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Mol	Chain	Length	Quality of chain
1	K	85	
1	M	85	
1	O	85	
2	B	12	
2	D	12	
2	F	12	
2	H	12	
2	J	12	
2	L	12	
2	N	12	
2	P	12	

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	CL	A	5	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7004 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 E3 ubiquitin-protein ligase Mdm2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	85	Total	C	N	O	S	0	0	0
			706	462	116	124	4			
1	C	82	Total	C	N	O	S	0	0	0
			682	448	113	117	4			
1	E	82	Total	C	N	O	S	0	0	0
			682	448	113	117	4			
1	G	84	Total	C	N	O	S	0	2	0
			712	468	119	121	4			
1	I	83	Total	C	N	O	S	0	0	0
			689	452	114	119	4			
1	K	83	Total	C	N	O	S	0	0	0
			689	452	114	119	4			
1	M	83	Total	C	N	O	S	0	0	0
			689	453	114	118	4			
1	O	83	Total	C	N	O	S	0	1	0
			701	461	115	121	4			

- Molecule 2 is a protein called 12-mer peptide inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	0	0	0
			91	62	12	17			
2	D	11	Total	C	N	O	0	0	0
			91	62	12	17			
2	F	11	Total	C	N	O	0	0	0
			91	62	12	17			
2	H	12	Total	C	N	O	0	0	0
			99	67	13	19			
2	J	11	Total	C	N	O	0	0	0
			91	62	12	17			
2	L	12	Total	C	N	O	0	0	0
			99	67	13	19			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	N	11	Total	C	N	O	0	0	0
			91	62	12	17			
2	P	11	Total	C	N	O	0	0	0
			91	62	12	17			

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Cl	0	0
			1	1		
3	K	1	Total	Cl	0	0
			1	1		
3	E	1	Total	Cl	0	0
			1	1		
3	I	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		
3	A	1	Total	Cl	0	0
			1	1		
3	M	2	Total	Cl	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	81	Total	O	0	0
			81	81		
4	B	20	Total	O	0	0
			20	20		
4	C	63	Total	O	0	0
			63	63		
4	D	14	Total	O	0	0
			14	14		
4	G	83	Total	O	0	0
			83	83		
4	E	83	Total	O	0	0
			83	83		
4	F	18	Total	O	0	0
			18	18		
4	H	15	Total	O	0	0
			15	15		

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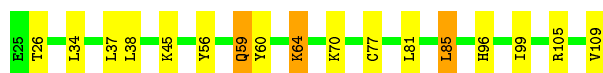
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	I	70	Total 70	O 70	0	0
4	J	8	Total 8	O 8	0	0
4	K	57	Total 57	O 57	0	0
4	L	13	Total 13	O 13	0	0
4	M	76	Total 76	O 76	0	0
4	N	15	Total 15	O 15	0	0
4	O	72	Total 72	O 72	0	0
4	P	14	Total 14	O 14	0	0

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: E3 ubiquitin-protein ligase Mdm2

Chain A: 




- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain C: 




- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain E: 




- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain G: 




- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain I: 



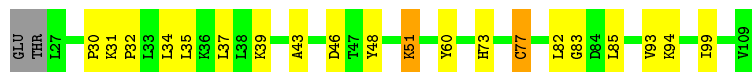
- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain K: 



- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain M: 74% 21% ..



- Molecule 1: E3 ubiquitin-protein ligase Mdm2

Chain O: 68% 28% ..



- Molecule 2: 12-mer peptide inhibitor

Chain B: 75% 17% 8%



- Molecule 2: 12-mer peptide inhibitor

Chain D: 92% 8%



- Molecule 2: 12-mer peptide inhibitor

Chain F: 58% 25% 8% 8%



- Molecule 2: 12-mer peptide inhibitor

Chain H: 83% 17%




- Molecule 2: 12-mer peptide inhibitor

Chain J: 92% 8%



- Molecule 2: 12-mer peptide inhibitor

Chain L:  83% 17%



- Molecule 2: 12-mer peptide inhibitor

Chain N:  92% 8%



- Molecule 2: 12-mer peptide inhibitor

Chain P:  58% 33% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	90.54Å 90.54Å 196.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.95 41.13 – 1.95	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-1.95) 100.0 (41.13-1.95)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.82 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.220 , 0.267 0.228 , 0.279	Depositor DCC
R_{free} test set	3421 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 28.0	EDS
Estimated twinning fraction	0.456 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	2 of 67730 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7004	wwPDB-VP
Average B, all atoms (Å ²)	27.0	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 20.98 % 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 7.7275e-03.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section:
CL

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	1.05	1/720 (0.1%)	0.98	3/968 (0.3%)
1	C	0.85	0/696	0.90	1/936 (0.1%)
1	E	0.90	0/696	0.91	1/936 (0.1%)
1	G	0.89	0/729	0.99	1/981 (0.1%)
1	I	0.91	0/703	0.85	0/946
1	K	0.94	0/703	0.95	2/946 (0.2%)
1	M	1.02	1/703 (0.1%)	0.92	0/946
1	O	0.94	0/716	0.83	0/964
2	B	1.12	0/94	0.83	0/128
2	D	0.80	0/94	0.72	0/128
2	F	0.95	0/94	0.98	1/128 (0.8%)
2	H	1.07	0/103	0.73	0/140
2	J	0.99	0/94	0.73	0/128
2	L	1.07	0/103	0.69	0/140
2	N	1.05	0/94	0.92	0/128
2	P	1.16	0/94	0.83	0/128
All	All	0.95	2/6436 (0.0%)	0.91	9/8671 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	77	CYS	CB-SG	-9.98	1.65	1.82
1	A	77	CYS	CB-SG	-9.45	1.66	1.82

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	85	LEU	CA-CB-CG	5.98	129.05	115.30
1	K	85	LEU	CA-CB-CG	-5.44	102.78	115.30
1	G	107	LEU	CA-CB-CG	5.35	127.60	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	10	LEU	CA-CB-CG	-5.34	103.01	115.30
1	A	59	GLN	CB-CA-C	-5.28	99.84	110.40

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	706	0	740	22	0
1	C	682	0	718	19	0
1	E	682	0	718	7	0
1	G	712	0	757	21	0
1	I	689	0	725	9	0
1	K	689	0	725	12	0
1	M	689	0	727	16	0
1	O	701	0	733	19	0
2	B	91	0	85	3	0
2	D	91	0	85	0	0
2	F	91	0	85	5	0
2	H	99	0	92	3	0
2	J	91	0	85	0	0
2	L	99	0	92	4	0
2	N	91	0	85	0	0
2	P	91	0	85	2	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
3	K	1	0	0	0	0
3	M	2	0	0	1	0
4	A	81	0	0	3	0
4	B	20	0	0	1	0
4	C	63	0	0	3	0
4	D	14	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	83	0	0	3	0
4	F	18	0	0	0	0
4	G	83	0	0	6	0
4	H	15	0	0	0	0
4	I	70	0	0	5	0
4	J	8	0	0	0	0
4	K	57	0	0	2	0
4	L	13	0	0	0	0
4	M	76	0	0	2	0
4	N	15	0	0	0	0
4	O	72	0	0	1	0
4	P	14	0	0	0	0
All	All	7004	0	6537	121	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 9.

The worst 5 of 121 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)
4:A:452:HOH:O	2:B:11:SER:HB2	1.58	1.02
1:C:46:ASP:HB3	4:C:184:HOH:O	1.63	0.97
1:C:79:ASN:HB3	4:C:661:HOH:O	1.65	0.96
1:G:54[A]:LEU:HD13	2:H:12:PRO:HD3	1.53	0.88
1:K:54:LEU:CD1	2:L:12:PRO:HD3	2.04	0.88

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 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	83/85 (98%)	83 (100%)	0	0	100	100
1	C	80/85 (94%)	79 (99%)	1 (1%)	0	100	100
1	E	80/85 (94%)	79 (99%)	1 (1%)	0	100	100
1	G	84/85 (99%)	84 (100%)	0	0	100	100
1	I	81/85 (95%)	77 (95%)	4 (5%)	0	100	100
1	K	81/85 (95%)	80 (99%)	1 (1%)	0	100	100
1	M	81/85 (95%)	81 (100%)	0	0	100	100
1	O	82/85 (96%)	81 (99%)	1 (1%)	0	100	100
2	B	9/12 (75%)	9 (100%)	0	0	100	100
2	D	9/12 (75%)	9 (100%)	0	0	100	100
2	F	9/12 (75%)	9 (100%)	0	0	100	100
2	H	10/12 (83%)	10 (100%)	0	0	100	100
2	J	9/12 (75%)	9 (100%)	0	0	100	100
2	L	10/12 (83%)	10 (100%)	0	0	100	100
2	N	9/12 (75%)	8 (89%)	1 (11%)	0	100	100
2	P	9/12 (75%)	9 (100%)	0	0	100	100
All	All	726/776 (94%)	717 (99%)	9 (1%)	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	A	80/80 (100%)	77 (96%)	3 (4%)	40	25
1	C	77/80 (96%)	74 (96%)	3 (4%)	39	24
1	E	77/80 (96%)	75 (97%)	2 (3%)	54	43
1	G	81/80 (101%)	79 (98%)	2 (2%)	55	45
1	I	78/80 (98%)	74 (95%)	4 (5%)	29	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	78/80 (98%)	75 (96%)	3 (4%)	40	25
1	M	78/80 (98%)	77 (99%)	1 (1%)	76	72
1	O	79/80 (99%)	74 (94%)	5 (6%)	22	8
2	B	9/10 (90%)	9 (100%)	0	100	100
2	D	9/10 (90%)	9 (100%)	0	100	100
2	F	9/10 (90%)	9 (100%)	0	100	100
2	H	10/10 (100%)	10 (100%)	0	100	100
2	J	9/10 (90%)	9 (100%)	0	100	100
2	L	10/10 (100%)	10 (100%)	0	100	100
2	N	9/10 (90%)	9 (100%)	0	100	100
2	P	9/10 (90%)	8 (89%)	1 (11%)	8	1
All	All	702/720 (98%)	678 (97%)	24 (3%)	44	30

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	44	GLN
1	I	98	LYS
1	O	90	SER
1	I	65	ARG
1	I	88	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	ASN
1	E	71	GLN

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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 8 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	A	85/85 (100%)	-0.28	0 100 100	20, 24, 32, 45	0
1	C	82/85 (96%)	-0.04	0 100 100	22, 29, 36, 41	0
1	E	82/85 (96%)	-0.22	0 100 100	21, 26, 34, 37	0
1	G	84/85 (98%)	-0.25	0 100 100	20, 25, 32, 39	0
1	I	83/85 (97%)	-0.27	0 100 100	17, 24, 31, 36	0
1	K	83/85 (97%)	-0.22	0 100 100	21, 25, 34, 39	0
1	M	83/85 (97%)	-0.27	0 100 100	19, 25, 33, 35	0
1	O	83/85 (97%)	-0.15	0 100 100	20, 28, 33, 35	0
2	B	11/12 (91%)	-0.28	0 100 100	25, 28, 34, 41	0
2	D	11/12 (91%)	-0.17	0 100 100	33, 35, 42, 48	0
2	F	11/12 (91%)	-0.05	0 100 100	29, 34, 42, 46	0
2	H	12/12 (100%)	-0.12	0 100 100	23, 28, 35, 38	0
2	J	11/12 (91%)	-0.01	0 100 100	29, 33, 48, 53	0
2	L	12/12 (100%)	-0.19	0 100 100	27, 29, 35, 36	0
2	N	11/12 (91%)	-0.05	0 100 100	25, 28, 36, 44	0
2	P	11/12 (91%)	-0.13	0 100 100	28, 34, 39, 43	0
All	All	755/776 (97%)	-0.20	0 100 100	17, 27, 36, 53	0

There are no RSRZ outliers to report.

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
3	CL	A	5	1/1	0.95	0.13	2.78	43,43,43,43	0
3	CL	K	7	1/1	0.92	0.15	1.72	48,48,48,48	0
3	CL	I	1	1/1	0.96	0.09	-0.14	32,32,32,32	0
3	CL	E	2	1/1	0.99	0.09	-0.53	30,30,30,30	0
3	CL	M	6	1/1	0.94	0.08	-1.63	42,42,42,42	0
3	CL	G	4	1/1	0.99	0.06	-2.48	45,45,45,45	0
3	CL	C	8	1/1	0.97	0.03	-3.23	39,39,39,39	0
3	CL	M	3	1/1	0.98	0.05	-	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.