



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:44 PM GMT

PDB ID : 3UOM  
Title : Ca<sup>2+</sup> complex of Human skeletal calsequestrin  
Authors : Sanchez, E.J.; Lewis, K.M.; Danna, B.R.; Nissen, M.S.; Kang, C.H.  
Deposited on : 2011-11-16  
Resolution : 2.02 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](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

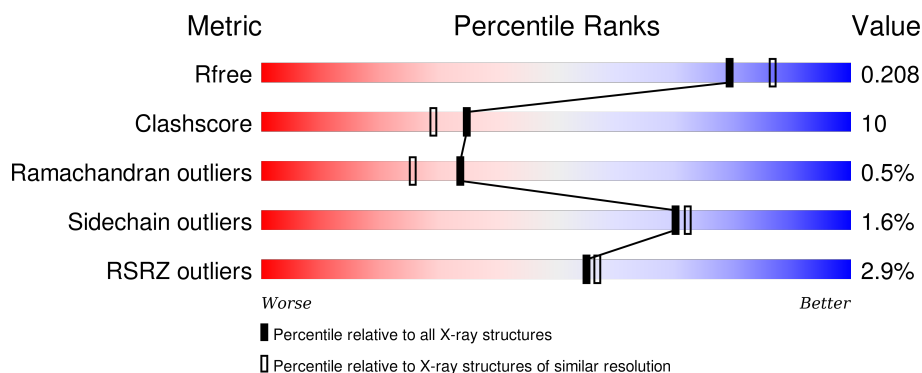
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.02 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	7858 (2.04-2.00)
Clashscore	102246	9060 (2.04-2.00)
Ramachandran outliers	100387	8952 (2.04-2.00)
Sidechain outliers	100360	8951 (2.04-2.00)
RSRZ outliers	91569	7873 (2.04-2.00)

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	362	<div> <div>4%</div> <div>85% 12% ..</div> </div>
1	B	362	<div> <div>4%</div> <div>84% 12% ..</div> </div>
1	C	362	<div> <div>2%</div> <div>82% 14% ...</div> </div>
1	D	362	<div> <div>2%</div> <div>83% 14% .</div> </div>
1	E	362	<div> <div>3%</div> <div>86% 10% ..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	362	

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
2	MRD	A	401	-	-	-	X
2	MRD	B	402	-	-	X	X
2	MRD	B	404	-	-	X	X
2	MRD	B	407	-	-	X	X
2	MRD	C	401	-	-	-	X
2	MRD	C	402	-	-	X	X
2	MRD	D	402	-	-	-	X
2	MRD	D	403	-	-	-	X
2	MRD	D	404	-	-	-	X
2	MRD	D	405	-	-	-	X
2	MRD	D	406	-	-	-	X
2	MRD	D	407	-	-	-	X
2	MRD	E	401	-	-	-	X
2	MRD	E	402	-	-	X	X
2	MRD	E	404	-	-	-	X
2	MRD	E	406	-	-	-	X
2	MRD	F	502	-	-	X	X
2	MRD	F	507	-	-	-	X
3	MPD	A	402	-	-	X	X
3	MPD	A	403	-	-	-	X
3	MPD	B	403	-	-	-	X
3	MPD	B	405	-	-	-	X
3	MPD	B	406	-	-	X	X
3	MPD	C	403	-	-	-	X
3	MPD	C	404	-	-	-	X
3	MPD	C	405	-	-	-	X
3	MPD	E	405	-	-	-	X
3	MPD	F	503	-	-	-	X
3	MPD	F	504	-	-	-	X
3	MPD	F	505	-	-	-	X
4	CA	B	415	-	-	-	X
4	CA	C	413	-	-	-	X
4	CA	D	418	-	-	-	X
4	CA	E	412	-	-	-	X
4	CA	F	515	-	-	-	X

## 2 Entry composition [i](#)

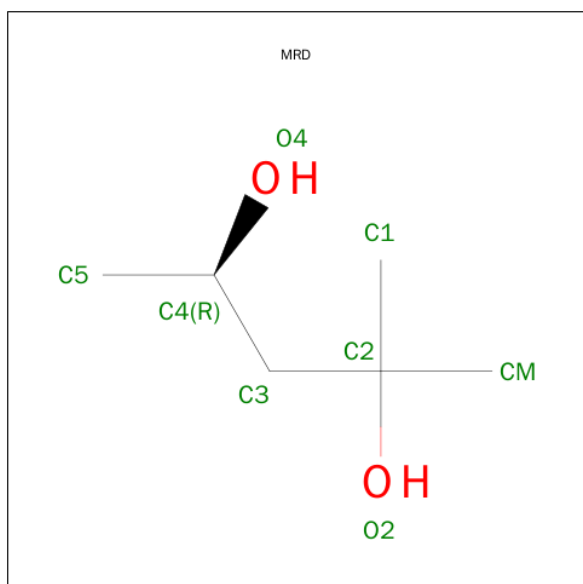
There are 5 unique types of molecules in this entry. The entry contains 18955 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Calsequestrin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	6	0
			2891	1854	429	601	7			
1	B	350	Total	C	N	O	S	0	8	0
			2889	1854	429	598	8			
1	C	351	Total	C	N	O	S	0	8	0
			2898	1860	430	601	7			
1	D	350	Total	C	N	O	S	0	5	0
			2872	1840	429	596	7			
1	E	351	Total	C	N	O	S	0	6	0
			2884	1851	427	599	7			
1	F	350	Total	C	N	O	S	0	7	0
			2884	1850	429	598	7			

- Molecule 2 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



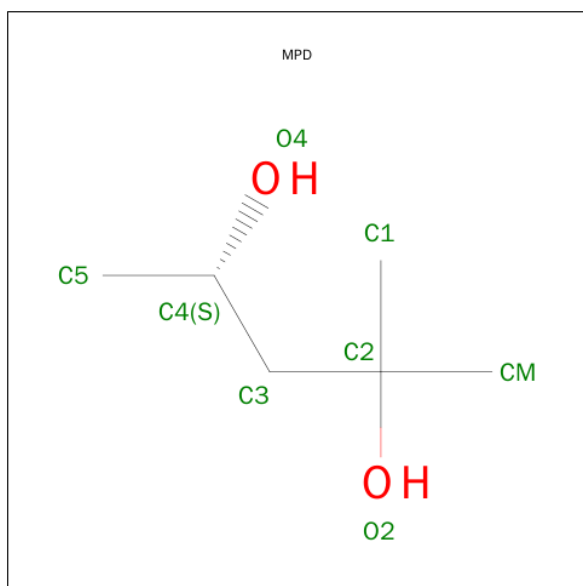
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	F	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	C	O	0	0
			8	6	2		
2	F	1	Total	C	O	0	0
			8	6	2		
2	F	1	Total	C	O	0	0
			8	6	2		
2	F	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 8 6 2	0	0
3	B	1	Total C O 8 6 2	0	0
3	C	1	Total C O 8 6 2	0	0
3	C	1	Total C O 8 6 2	0	0
3	C	1	Total C O 8 6 2	0	0
3	E	1	Total C O 8 6 2	0	0
3	F	1	Total C O 8 6 2	0	0
3	F	1	Total C O 8 6 2	0	0
3	F	1	Total C O 8 6 2	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	15	Total Ca 15 15	0	0
4	E	13	Total Ca 13 13	0	0
4	B	15	Total Ca 16 16	1	1
4	C	15	Total Ca 15 15	0	0
4	A	14	Total Ca 14 14	0	0
4	F	14	Total Ca 14 14	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	198	Total O 198 198	0	0
5	B	184	Total O 184 184	0	0

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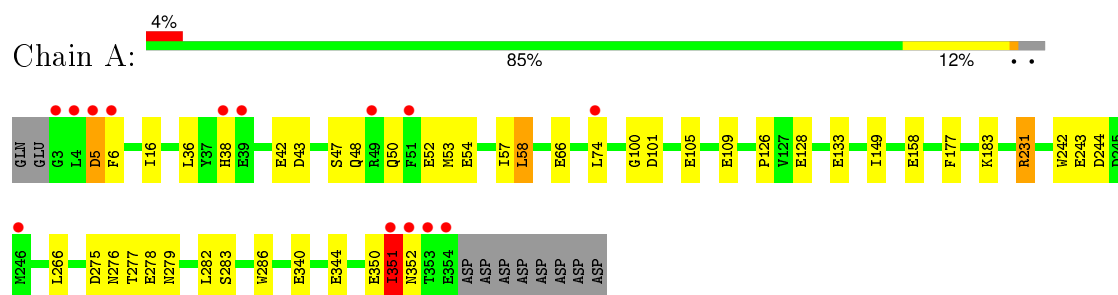
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	207	Total 207	O 207	0	0
5	C	214	Total 214	O 214	0	0
5	E	213	Total 213	O 213	0	0
5	F	198	Total 198	O 198	0	0



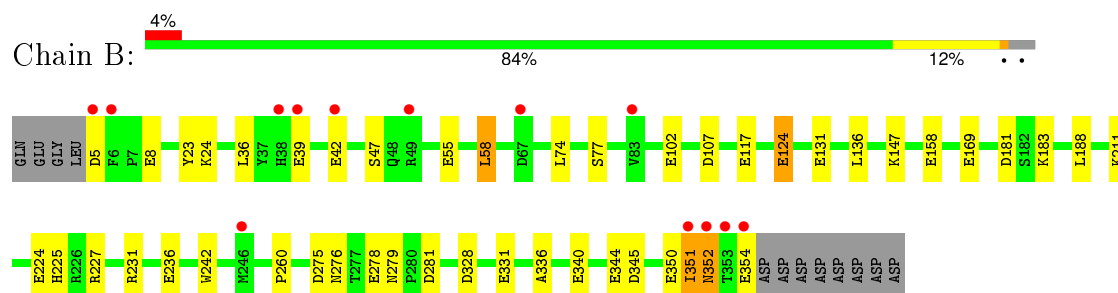
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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.

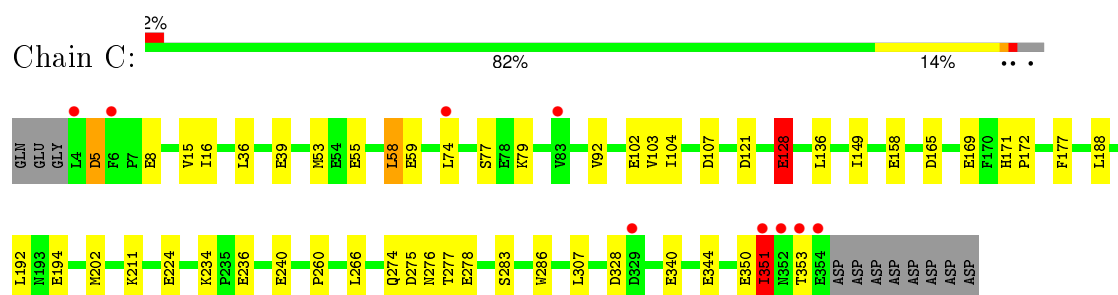
#### • Molecule 1: Calsequestrin-1



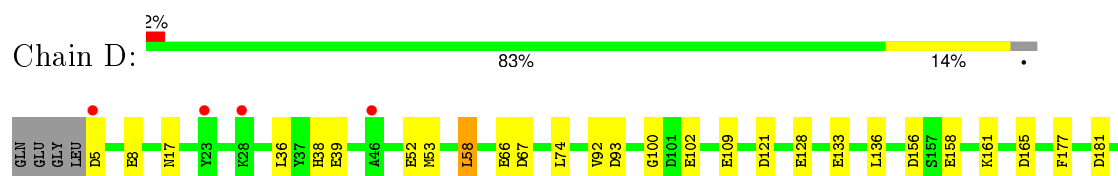
#### • Molecule 1: Calsequestrin-1

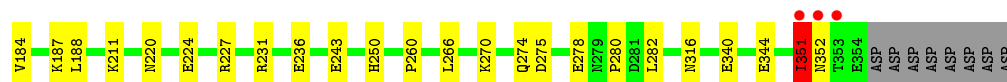


#### • Molecule 1: Calsequestrin-1

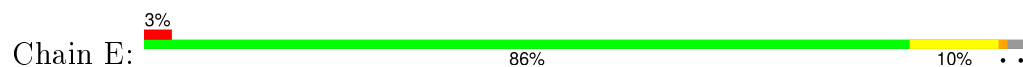


#### • Molecule 1: Calsequestrin-1

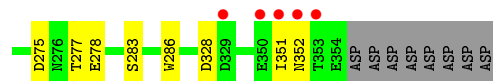
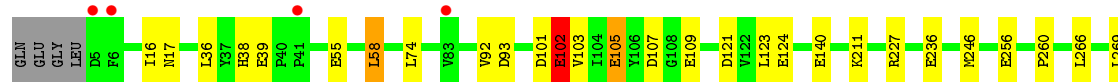
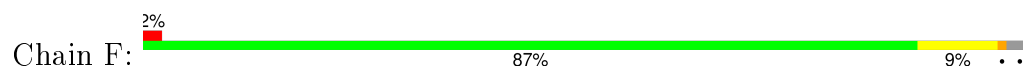




● Molecule 1: Calsequestrin-1



● Molecule 1: Calsequestrin-1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.80Å 89.79Å 119.16Å 90.13° 89.90° 60.05°	Depositor
Resolution (Å)	38.90 – 2.02 38.90 – 2.01	Depositor EDS
% Data completeness (in resolution range)	91.8 (38.90-2.02) 90.8 (38.90-2.01)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 2.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.6.1_357)	Depositor
R, $R_{free}$	0.182 , 0.213 0.182 , 0.208	Depositor DCC
$R_{free}$ test set	1995 reflections (1.03%)	DCC
Wilson B-factor (Å <sup>2</sup> )	30.9	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.012 for k,-h+k,l 0.012 for h-k,h,l 0.448 for -h+k,-h,l 0.448 for -k,h-k,l 0.459 for -h+k,k,-l 0.467 for h,h-k,-l 0.013 for -h,-k,l 0.448 for -k,-h,-l 0.013 for k,h,-l 0.013 for h-k,-k,-l 0.013 for -h,-h+k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 204132 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	18955	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MRD, CA, MPD

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	0.44	0/2971	0.51	0/4032
1	B	0.43	1/2978 (0.0%)	0.51	0/4040
1	C	0.45	1/2987 (0.0%)	0.52	0/4053
1	D	0.46	0/2952	0.51	0/4006
1	E	0.41	0/2967	0.50	0/4027
1	F	0.53	5/2970 (0.2%)	0.60	8/4030 (0.2%)
All	All	0.45	7/17825 (0.0%)	0.53	8/24188 (0.0%)

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
1	F	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	102[A]	GLU	N-CA	9.35	1.65	1.46
1	F	102[B]	GLU	N-CA	9.35	1.65	1.46
1	F	124	GLU	C-N	-5.82	1.20	1.34
1	F	102[A]	GLU	C-N	-5.33	1.21	1.34
1	F	102[B]	GLU	C-N	-5.33	1.21	1.34

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	102[A]	GLU	O-C-N	-7.73	110.34	122.70
1	F	102[B]	GLU	O-C-N	-7.73	110.34	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	102[A]	GLU	N-CA-CB	-7.35	97.36	110.60
1	F	102[B]	GLU	N-CA-CB	-7.35	97.36	110.60
1	F	102[A]	GLU	CB-CA-C	5.97	122.34	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	102[A]	GLU	Mainchain
1	F	102[B]	GLU	Mainchain

## 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	2891	0	2717	55	1
1	B	2889	0	2724	53	0
1	C	2898	0	2734	70	0
1	D	2872	0	2698	52	0
1	E	2884	0	2715	49	1
1	F	2884	0	2716	44	2
2	A	16	0	28	3	0
2	B	24	0	40	23	0
2	C	32	0	56	15	0
2	D	56	0	98	11	0
2	E	40	0	70	15	0
2	F	40	0	70	14	0
3	A	40	0	70	16	0
3	B	32	0	56	14	0
3	C	24	0	42	4	0
3	E	8	0	14	3	0
3	F	24	0	42	2	0
4	A	14	0	0	0	0
4	B	16	0	0	0	0
4	C	15	0	0	0	0
4	D	15	0	0	0	0
4	E	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	14	0	0	0	0
5	A	198	0	0	13	2
5	B	184	0	0	9	1
5	C	214	0	0	11	1
5	D	207	0	0	8	1
5	E	213	0	0	6	0
5	F	198	0	0	10	1
All	All	18955	0	16890	341	5

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 10.

The worst 5 of 341 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:406:MRD:C5	2:C:406:MRD:H1C1	1.49	1.37
2:B:407:MRD:H1C1	2:B:407:MRD:C5	1.51	1.33
2:C:406:MRD:H5C3	2:C:406:MRD:C1	1.55	1.22
2:B:407:MRD:H5C3	2:B:407:MRD:C1	1.79	1.12
1:A:58:LEU:HD23	1:A:58:LEU:N	1.62	1.11

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:102[A]:GLU:OE2	5:A:609:HOH:O[1_654]	1.39	0.81
5:B:624:HOH:O	5:C:648:HOH:O[1_455]	1.68	0.52
1:E:102[B]:GLU:OE1	5:D:626:HOH:O[1_565]	1.98	0.22
1:F:101:ASP:OD1	5:A:549:HOH:O[1_654]	2.11	0.09
1:A:101:ASP:OD1	5:F:671:HOH:O[1_546]	2.19	0.01

## 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	356/362 (98%)	346 (97%)	8 (2%)	2 (1%)	30	21
1	B	356/362 (98%)	349 (98%)	5 (1%)	2 (1%)	30	21
1	C	357/362 (99%)	349 (98%)	5 (1%)	3 (1%)	24	15
1	D	353/362 (98%)	344 (98%)	8 (2%)	1 (0%)	46	40
1	E	355/362 (98%)	350 (99%)	5 (1%)	0	100	100
1	F	355/362 (98%)	349 (98%)	4 (1%)	2 (1%)	30	21
All	All	2132/2172 (98%)	2087 (98%)	35 (2%)	10 (0%)	34	26

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	351	ILE
1	A	352	ASN
1	B	352	ASN
1	C	5	ASP
1	D	351	ILE

### 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	317/324 (98%)	309 (98%)	8 (2%)	55	54
1	B	318/324 (98%)	310 (98%)	8 (2%)	55	54
1	C	319/324 (98%)	316 (99%)	3 (1%)	84	87
1	D	315/324 (97%)	310 (98%)	5 (2%)	70	72
1	E	317/324 (98%)	313 (99%)	4 (1%)	76	78
1	F	317/324 (98%)	314 (99%)	3 (1%)	84	87
All	All	1903/1944 (98%)	1872 (98%)	31 (2%)	70	72

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	169[B]	GLU
1	C	128	GLU
1	F	58	LEU
1	B	211	LYS
1	C	351	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	316	ASN
1	F	193	ASN
1	F	25	ASN
1	E	141	ASN
1	F	38	HIS

### 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](#)

Of 129 ligands modelled in this entry, 87 are monoatomic - leaving 42 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
2	MRD	A	401	-	6,7,7	0.28	0	7,10,10	0.35	0
3	MPD	A	402	-	6,7,7	0.30	0	7,10,10	0.53	0
3	MPD	A	403	-	6,7,7	0.27	0	7,10,10	0.47	0
3	MPD	A	404	-	6,7,7	0.27	0	7,10,10	0.28	0
3	MPD	A	405	-	6,7,7	0.29	0	7,10,10	0.38	0
3	MPD	A	406	-	6,7,7	0.27	0	7,10,10	0.43	0
2	MRD	A	407	-	6,7,7	0.35	0	7,10,10	0.68	0
3	MPD	B	401	-	6,7,7	0.26	0	7,10,10	0.51	0
2	MRD	B	402	-	6,7,7	0.41	0	7,10,10	0.43	0
3	MPD	B	403	-	6,7,7	0.42	0	7,10,10	0.48	0
2	MRD	B	404	-	6,7,7	0.26	0	7,10,10	0.46	0
3	MPD	B	405	-	6,7,7	0.30	0	7,10,10	0.21	0
3	MPD	B	406	-	6,7,7	1.00	1 (16%)	7,10,10	0.52	0
2	MRD	B	407	-	6,7,7	0.26	0	7,10,10	0.46	0
2	MRD	C	401	-	6,7,7	0.28	0	7,10,10	0.38	0
2	MRD	C	402	-	6,7,7	0.33	0	7,10,10	0.52	0
3	MPD	C	403	-	6,7,7	0.28	0	7,10,10	0.41	0
3	MPD	C	404	-	6,7,7	0.26	0	7,10,10	0.44	0
3	MPD	C	405	-	6,7,7	0.28	0	7,10,10	0.40	0
2	MRD	C	406	-	6,7,7	0.43	0	7,10,10	0.72	0
2	MRD	C	407	-	6,7,7	0.29	0	7,10,10	0.45	0
2	MRD	D	401	-	6,7,7	0.28	0	7,10,10	0.36	0
2	MRD	D	402	-	6,7,7	0.40	0	7,10,10	0.25	0
2	MRD	D	403	-	6,7,7	0.28	0	7,10,10	0.42	0
2	MRD	D	404	-	6,7,7	0.28	0	7,10,10	0.47	0
2	MRD	D	405	-	6,7,7	0.27	0	7,10,10	0.45	0
2	MRD	D	406	-	6,7,7	0.34	0	7,10,10	0.45	0
2	MRD	D	407	-	6,7,7	0.32	0	7,10,10	0.20	0
2	MRD	E	401	-	6,7,7	0.28	0	7,10,10	0.25	0
2	MRD	E	402	-	6,7,7	0.35	0	7,10,10	0.50	0
2	MRD	E	403	-	6,7,7	0.30	0	7,10,10	0.41	0
2	MRD	E	404	-	6,7,7	0.27	0	7,10,10	0.32	0
3	MPD	E	405	-	6,7,7	0.30	0	7,10,10	0.32	0
2	MRD	E	406	-	6,7,7	0.30	0	7,10,10	0.33	0
2	MRD	F	501	-	6,7,7	0.26	0	7,10,10	0.30	0
2	MRD	F	502	-	6,7,7	0.29	0	7,10,10	0.47	0
3	MPD	F	503	-	6,7,7	0.27	0	7,10,10	0.47	0
3	MPD	F	504	-	6,7,7	0.26	0	7,10,10	0.60	0
3	MPD	F	505	-	6,7,7	0.28	0	7,10,10	0.28	0
2	MRD	F	506	-	6,7,7	0.28	0	7,10,10	0.20	0
2	MRD	F	507	-	6,7,7	0.28	0	7,10,10	0.38	0
2	MRD	F	508	-	6,7,7	0.31	0	7,10,10	0.33	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
2	MRD	A	401	-	-	0/5/5/5	0/0/0/0
3	MPD	A	402	-	-	0/5/5/5	0/0/0/0
3	MPD	A	403	-	-	0/5/5/5	0/0/0/0
3	MPD	A	404	-	-	0/5/5/5	0/0/0/0
3	MPD	A	405	-	-	0/5/5/5	0/0/0/0
3	MPD	A	406	-	-	0/5/5/5	0/0/0/0
2	MRD	A	407	-	-	0/5/5/5	0/0/0/0
3	MPD	B	401	-	-	0/5/5/5	0/0/0/0
2	MRD	B	402	-	-	0/5/5/5	0/0/0/0
3	MPD	B	403	-	-	0/5/5/5	0/0/0/0
2	MRD	B	404	-	-	0/5/5/5	0/0/0/0
3	MPD	B	405	-	-	0/5/5/5	0/0/0/0
3	MPD	B	406	-	-	0/5/5/5	0/0/0/0
2	MRD	B	407	-	-	0/5/5/5	0/0/0/0
2	MRD	C	401	-	-	0/5/5/5	0/0/0/0
2	MRD	C	402	-	-	0/5/5/5	0/0/0/0
3	MPD	C	403	-	-	0/5/5/5	0/0/0/0
3	MPD	C	404	-	-	0/5/5/5	0/0/0/0
3	MPD	C	405	-	-	0/5/5/5	0/0/0/0
2	MRD	C	406	-	-	0/5/5/5	0/0/0/0
2	MRD	C	407	-	-	0/5/5/5	0/0/0/0
2	MRD	D	401	-	-	0/5/5/5	0/0/0/0
2	MRD	D	402	-	-	0/5/5/5	0/0/0/0
2	MRD	D	403	-	-	0/5/5/5	0/0/0/0
2	MRD	D	404	-	-	0/5/5/5	0/0/0/0
2	MRD	D	405	-	-	0/5/5/5	0/0/0/0
2	MRD	D	406	-	-	0/5/5/5	0/0/0/0
2	MRD	D	407	-	-	0/5/5/5	0/0/0/0
2	MRD	E	401	-	-	0/5/5/5	0/0/0/0
2	MRD	E	402	-	-	0/5/5/5	0/0/0/0
2	MRD	E	403	-	-	0/5/5/5	0/0/0/0
2	MRD	E	404	-	-	0/5/5/5	0/0/0/0
3	MPD	E	405	-	-	0/5/5/5	0/0/0/0
2	MRD	E	406	-	-	0/5/5/5	0/0/0/0
2	MRD	F	501	-	-	0/5/5/5	0/0/0/0
2	MRD	F	502	-	-	0/5/5/5	0/0/0/0
3	MPD	F	503	-	-	0/5/5/5	0/0/0/0
3	MPD	F	504	-	-	0/5/5/5	0/0/0/0
3	MPD	F	505	-	-	0/5/5/5	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MRD	F	506	-	-	0/5/5/5	0/0/0/0
2	MRD	F	507	-	-	0/5/5/5	0/0/0/0
2	MRD	F	508	-	-	0/5/5/5	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	406	MPD	O2-C2	-2.17	1.38	1.44

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

31 monomers are involved in 120 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	MPD	8	0
3	A	403	MPD	2	0
3	A	404	MPD	4	0
3	A	406	MPD	2	0
2	A	407	MRD	3	0
3	B	401	MPD	1	0
2	B	402	MRD	7	0
3	B	403	MPD	4	0
2	B	404	MRD	8	0
3	B	405	MPD	1	0
3	B	406	MPD	8	0
2	B	407	MRD	8	0
2	C	402	MRD	10	0
3	C	403	MPD	1	0
3	C	405	MPD	3	0
2	C	406	MRD	3	0
2	C	407	MRD	2	0
2	D	402	MRD	4	0
2	D	403	MRD	3	0
2	D	404	MRD	1	0
2	D	405	MRD	2	0
2	D	406	MRD	1	0
2	E	402	MRD	10	0
2	E	403	MRD	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	404	MRD	2	0
3	E	405	MPD	3	0
2	E	406	MRD	1	0
2	F	502	MRD	6	0
3	F	505	MPD	2	0
2	F	507	MRD	4	0
2	F	508	MRD	4	0

## 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	352/362 (97%)	0.28	14 (3%) 42 44	21, 36, 77, 101	0
1	B	350/362 (96%)	0.22	13 (3%) 45 47	21, 36, 75, 97	0
1	C	351/362 (96%)	0.27	9 (2%) 59 61	21, 35, 76, 109	0
1	D	350/362 (96%)	0.22	7 (2%) 68 69	20, 36, 75, 99	0
1	E	351/362 (96%)	0.15	10 (2%) 56 58	22, 36, 76, 102	0
1	F	350/362 (96%)	0.19	9 (2%) 59 61	21, 35, 72, 99	0
All	All	2104/2172 (96%)	0.22	62 (2%) 55 57	20, 36, 77, 109	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	353	THR	13.8
1	D	353	THR	10.2
1	B	351	ILE	8.8
1	A	354	GLU	7.5
1	C	353	THR	7.1

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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, 95<sup>th</sup> 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(Å <sup>2</sup> )	Q<0.9
2	MRD	D	406	8/8	0.78	0.33	26.47	57,60,64,65	0
4	CA	B	415	1/1	0.91	0.24	15.76	59,59,59,59	0
4	CA	C	413	1/1	0.78	0.31	14.96	64,64,64,64	0
3	MPD	B	406	8/8	0.66	0.49	11.56	54,63,72,72	0
2	MRD	F	502	8/8	0.67	0.37	9.91	52,62,72,74	0
3	MPD	F	505	8/8	0.89	0.27	8.33	51,58,66,68	0
2	MRD	D	402	8/8	0.58	0.29	8.17	47,57,68,75	0
3	MPD	C	405	8/8	0.87	0.39	7.91	54,61,65,69	0
3	MPD	A	403	8/8	0.71	0.30	7.68	46,57,65,69	0
3	MPD	E	405	8/8	0.87	0.31	6.71	49,57,62,63	0
3	MPD	B	405	8/8	0.81	0.27	6.18	51,58,67,69	0
3	MPD	A	402	8/8	0.65	0.31	6.01	37,54,62,65	0
2	MRD	A	401	8/8	0.94	0.18	5.59	34,41,46,47	0
2	MRD	E	406	8/8	0.88	0.27	5.51	50,57,64,67	0
4	CA	F	515	1/1	0.89	0.27	5.32	62,62,62,62	0
3	MPD	F	503	8/8	0.89	0.35	5.18	48,57,61,64	0
2	MRD	C	402	8/8	0.77	0.29	4.33	50,55,64,82	0
2	MRD	D	403	8/8	0.82	0.26	4.14	50,59,66,68	0
4	CA	E	412	1/1	0.84	0.28	4.00	63,63,63,63	0
4	CA	D	418	1/1	0.99	0.13	4.00	29,29,29,29	0
2	MRD	D	405	8/8	0.89	0.24	3.83	52,62,69,71	0
2	MRD	B	407	8/8	0.88	0.36	3.71	59,71,77,81	0
2	MRD	E	404	8/8	0.79	0.23	3.48	60,66,73,76	0
2	MRD	B	404	8/8	0.88	0.30	3.35	52,63,68,69	0
2	MRD	E	401	8/8	0.92	0.18	3.16	37,42,46,48	0
2	MRD	D	404	8/8	0.89	0.20	3.16	52,65,68,75	0
2	MRD	E	402	8/8	0.79	0.23	2.97	45,58,69,73	0
2	MRD	D	407	8/8	0.82	0.26	2.90	60,69,74,76	0
3	MPD	B	403	8/8	0.75	0.24	2.79	43,54,62,68	0
2	MRD	F	507	8/8	0.83	0.27	2.59	62,72,78,79	0
3	MPD	C	403	8/8	0.86	0.25	2.54	43,56,64,74	0
2	MRD	B	402	8/8	0.75	0.28	2.37	40,52,65,69	0
3	MPD	C	404	8/8	0.91	0.23	2.34	48,57,65,75	0
2	MRD	C	401	8/8	0.91	0.15	2.25	36,40,43,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MPD	F	504	8/8	0.89	0.19	2.20	51,62,67,74	0
3	MPD	A	404	8/8	0.89	0.17	1.63	52,58,66,67	0
4	CA	D	414	1/1	0.99	0.15	1.44	55,55,55,55	0
3	MPD	A	406	8/8	0.77	0.26	1.35	65,73,76,79	0
4	CA	A	413	1/1	0.97	0.16	0.84	61,61,61,61	0
4	CA	A	417	1/1	0.99	0.11	0.64	29,29,29,29	0
2	MRD	F	501	8/8	0.89	0.17	0.59	37,45,48,51	0
3	MPD	B	401	8/8	0.93	0.16	0.48	36,44,49,59	0
4	CA	E	418	1/1	0.99	0.15	0.46	33,33,33,33	0
4	CA	B	417	1/1	0.92	0.12	-0.06	57,57,57,57	0
4	CA	F	521	1/1	0.98	0.13	-0.13	31,31,31,31	0
4	CA	C	408	1/1	0.88	0.12	-0.13	53,53,53,53	0
4	CA	C	419	1/1	0.98	0.12	-0.17	32,32,32,32	0
4	CA	A	420	1/1	0.98	0.13	-0.40	35,35,35,35	0
4	CA	D	419	1/1	0.98	0.11	-0.43	34,34,34,34	0
2	MRD	E	403	8/8	0.89	0.14	-0.45	50,57,62,64	0
4	CA	A	411	1/1	0.98	0.09	-0.50	41,41,41,41	0
4	CA	C	414	1/1	0.93	0.12	-0.52	65,65,65,65	0
4	CA	C	416	1/1	0.97	0.09	-0.62	37,37,37,37	0
4	CA	F	517	1/1	0.93	0.10	-0.77	55,55,55,55	0
4	CA	C	412	1/1	0.97	0.13	-0.78	42,42,42,42	0
4	CA	D	421	1/1	1.00	0.11	-0.87	34,34,34,34	0
4	CA	D	420	1/1	0.97	0.10	-0.87	33,33,33,33	0
4	CA	B	416	1/1	0.96	0.10	-0.91	66,66,66,66	0
4	CA	F	510	1/1	0.88	0.10	-0.93	50,50,50,50	0
4	CA	B	422	1/1	0.98	0.11	-1.07	32,32,32,32	0
4	CA	D	422	1/1	0.98	0.10	-1.12	34,34,34,34	0
4	CA	A	419	1/1	0.95	0.10	-1.16	31,31,31,31	0
4	CA	A	418	1/1	0.98	0.10	-1.21	34,34,34,34	0
4	CA	F	520	1/1	0.96	0.10	-1.25	34,34,34,34	0
4	CA	D	412	1/1	0.97	0.07	-1.30	40,40,40,40	0
4	CA	C	418	1/1	0.97	0.08	-1.32	35,35,35,35	0
4	CA	B	421	1/1	0.96	0.10	-1.34	31,31,31,31	0
4	CA	E	415	1/1	0.96	0.07	-1.40	35,35,35,35	0
4	CA	B	418	1/1	0.96	0.10	-1.44	37,37,37,37	0
4	CA	F	522	1/1	0.99	0.10	-1.45	34,34,34,34	0
4	CA	B	413	1/1	0.98	0.06	-1.49	40,40,40,40	0
4	CA	E	417	1/1	0.92	0.08	-1.54	35,35,35,35	0
4	CA	F	513	1/1	0.92	0.09	-1.72	41,41,41,41	0
4	CA	C	411	1/1	0.99	0.06	-1.76	39,39,39,39	0
4	CA	F	519	1/1	0.99	0.09	-1.78	30,30,30,30	0
4	CA	C	420	1/1	0.99	0.06	-1.99	32,32,32,32	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	CA	E	413	1/1	0.91	0.05	-2.11	58,58,58,58	0
2	MRD	D	401	8/8	0.98	0.10	-2.14	33,41,42,47	0
4	CA	A	414	1/1	0.95	0.05	-2.15	61,61,61,61	0
4	CA	C	417	1/1	1.00	0.07	-2.16	30,30,30,30	0
4	CA	D	415	1/1	0.92	0.04	-2.17	58,58,58,58	0
4	CA	E	410	1/1	0.93	0.06	-2.17	38,38,38,38	0
4	CA	D	409	1/1	0.96	0.08	-2.23	52,52,52,52	0
4	CA	E	414	1/1	0.93	0.07	-2.35	52,52,52,52	0
4	CA	B	414	1/1	0.88	0.08	-2.45	54,54,54,54	1
4	CA	A	415	1/1	0.93	0.09	-2.61	57,57,57,57	0
4	CA	D	416	1/1	0.90	0.07	-2.73	54,54,54,54	0
4	CA	F	518	1/1	0.98	0.08	-2.84	36,36,36,36	0
4	CA	F	516	1/1	0.99	0.04	-3.08	63,63,63,63	0
4	CA	D	417	1/1	0.90	0.08	-3.25	36,36,36,36	0
4	CA	A	416	1/1	0.96	0.07	-3.27	36,36,36,36	0
4	CA	E	416	1/1	0.95	0.08	-3.28	30,30,30,30	0
4	CA	B	419	1/1	0.99	0.05	-3.85	30,30,30,30	0
4	CA	B	420	1/1	0.98	0.06	-3.99	32,32,32,32	0
4	CA	C	415	1/1	0.95	0.05	-4.00	53,53,53,53	0
4	CA	E	411	1/1	0.81	0.18	-	35,35,35,35	1
4	CA	F	511	1/1	0.95	0.15	-	56,56,56,56	0
4	CA	C	410	1/1	0.92	0.09	-	56,56,56,56	0
4	CA	E	409	1/1	0.90	0.10	-	57,57,57,57	0
4	CA	A	412	1/1	0.81	0.13	-	60,60,60,60	0
4	CA	F	509	1/1	0.95	0.09	-	49,49,49,49	0
3	MPD	A	405	8/8	0.88	0.27	-	47,59,66,69	0
4	CA	F	512	1/1	0.79	0.10	-	57,57,57,57	0
4	CA	C	422	1/1	0.89	0.22	-	57,57,57,57	1
4	CA	D	411	1/1	0.93	0.06	-	60,60,60,60	0
2	MRD	A	407	8/8	0.85	0.20	-	64,69,73,75	0
4	CA	C	421	1/1	0.85	0.10	-	49,49,49,49	0
4	CA	E	419	1/1	0.98	0.09	-	49,49,49,49	0
4	CA	B	412	1/1	0.92	0.06	-	63,63,63,63	0
4	CA	E	407	1/1	0.95	0.11	-	52,52,52,52	0
4	CA	E	408	1/1	0.85	0.15	-	54,54,54,54	0
4	CA	C	409	1/1	0.92	0.14	-	54,54,54,54	0
2	MRD	F	508	8/8	0.84	0.20	-	62,66,68,71	0
4	CA	D	408	1/1	0.91	0.09	-	49,49,49,49	0
4	CA	A	410	1/1	0.92	0.08	-	56,56,56,56	0
4	CA	B	409[B]	1/1	0.69	0.13	-	57,57,57,57	1
4	CA	B	409[A]	1/1	0.69	0.13	-	57,57,57,57	1
2	MRD	C	406	8/8	0.89	0.34	-	26,59,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CA	A	409	1/1	0.96	0.26	-	57,57,57,57	0
4	CA	D	410	1/1	0.96	0.10	-	56,56,56,56	0
4	CA	B	410	1/1	0.97	0.08	-	51,51,51,51	0
4	CA	D	413	1/1	0.85	0.19	-	32,32,32,32	1
2	MRD	F	506	8/8	0.81	0.23	-	44,57,67,69	0
4	CA	F	514	1/1	0.86	0.35	-	32,32,32,32	1
4	CA	B	408	1/1	0.88	0.08	-	50,50,50,50	0
4	CA	A	421	1/1	0.90	0.06	-	48,48,48,48	0
4	CA	B	411	1/1	0.88	0.15	-	57,57,57,57	0
2	MRD	C	407	8/8	0.83	0.24	-	67,73,75,78	0
4	CA	A	408	1/1	0.97	0.08	-	51,51,51,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.