



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 07:19 PM GMT

PDB ID : 2RD7  
Title : Human Complement Membrane Attack Proteins Share a Common Fold with Bacterial Cytolysins  
Authors : Slade, D.J.; Lovelace, L.L.; Chruszcz, M.; Minor, W.; Lebioda, L.; Sodetz, J.M.  
Deposited on : 2007-09-21  
Resolution : 2.15 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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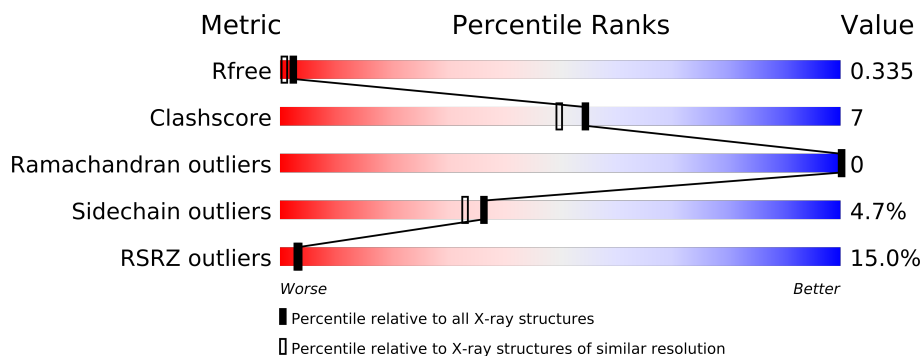
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.15 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))
$R_{free}$	66092	1094 (2.18-2.14)
Clashscore	79885	1299 (2.18-2.14)
Ramachandran outliers	78287	1272 (2.18-2.14)
Sidechain outliers	78261	1272 (2.18-2.14)
RSRZ outliers	66119	1094 (2.18-2.14)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	367	
2	C	184	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4011 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Complement component C8 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	7	0
			2633	1671	439	508	15			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	96	HIS	-	EXPRESSION TAG	UNP P07357
A	97	HIS	-	EXPRESSION TAG	UNP P07357
A	98	HIS	-	EXPRESSION TAG	UNP P07357
A	99	HIS	-	EXPRESSION TAG	UNP P07357
A	100	HIS	-	EXPRESSION TAG	UNP P07357
A	101	HIS	-	EXPRESSION TAG	UNP P07357
A	102	MET	-	EXPRESSION TAG	UNP P07357

- Molecule 2 is a protein called Complement component C8 gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	159	Total	C	N	O	S	0	1	0
			1211	781	206	220	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	MET	-	EXPRESSION TAG	UNP P07360
C	0	ALA	-	EXPRESSION TAG	UNP P07360

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Cl	0	0
			1	1		

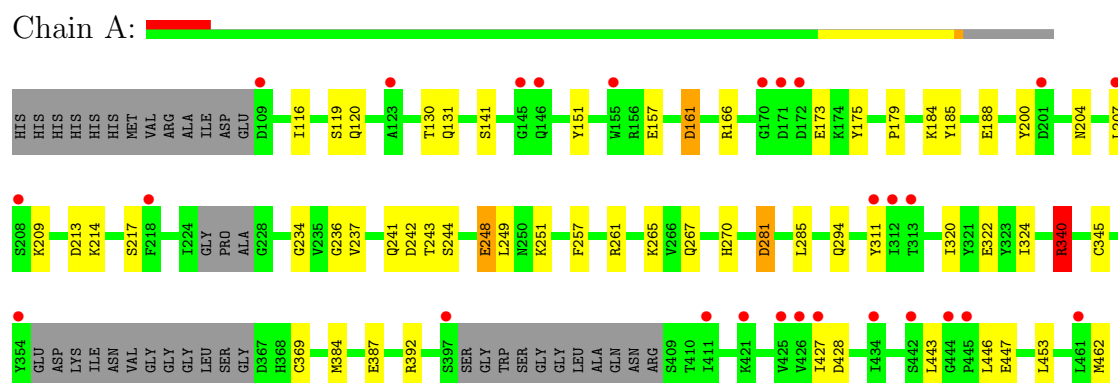
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	129	Total 129	O 129	0	0
4	C	37	Total 37	O 37	0	0

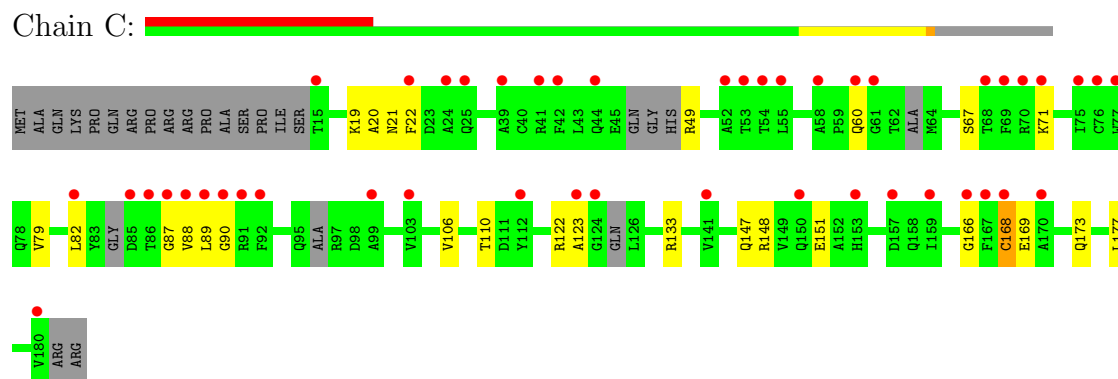
### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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: Complement component C8 alpha chain



- Molecule 2: Complement component C8 gamma chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	96.55Å 126.09Å 51.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.00 – 2.15 32.66 – 2.15	Depositor EDS
% Data completeness (in resolution range)	91.9 (34.00-2.15) 91.9 (32.66-2.15)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.94 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.2.0005, COOT	Depositor
R, $R_{free}$	0.206 , 0.261 0.282 , 0.335	Depositor DCC
$R_{free}$ test set	1617 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	39.8	Xtriage
Anisotropy	0.471	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 52.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 32351 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4011	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 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	0.94	4/2687 (0.1%)	0.87	3/3624 (0.1%)
2	C	0.80	1/1234 (0.1%)	0.80	2/1672 (0.1%)
All	All	0.90	5/3921 (0.1%)	0.85	5/5296 (0.1%)

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
2	C	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	168	CYS	CB-SG	-6.03	1.72	1.82
1	A	311	TYR	CE2-CZ	-5.05	1.31	1.38
1	A	447	GLU	CG-CD	5.04	1.59	1.51
1	A	281[A]	ASP	CB-CG	5.03	1.62	1.51
1	A	281[B]	ASP	CB-CG	5.03	1.62	1.51

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	133	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	428	ASP	CB-CG-OD2	-5.28	113.54	118.30
1	A	161	ASP	CB-CG-OD2	-5.03	113.77	118.30
1	A	340	ARG	NE-CZ-NH1	5.01	122.81	120.30
2	C	148	ARG	NE-CZ-NH2	-5.01	117.80	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	87	GLY	Peptide

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2633	0	2479	38	0
2	C	1211	0	1146	12	0
3	C	1	0	0	0	0
4	A	129	0	0	4	0
4	C	37	0	0	0	0
All	All	4011	0	3625	50	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (50) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:147:GLN:O	2:C:151:GLU:HG3	1.69	0.92
1:A:340:ARG:HG3	1:A:340:ARG:HH11	1.40	0.85
1:A:345:CYS:HG	1:A:369:CYS:HG	0.87	0.84
2:C:88:VAL:HG12	2:C:89:LEU:H	1.55	0.71
1:A:340:ARG:CG	1:A:340:ARG:HH11	2.11	0.63
1:A:241:GLN:NE2	4:A:525:HOH:O	2.29	0.63
2:C:90:GLY:O	2:C:106:VAL:HA	2.03	0.59
2:C:19:LYS:NZ	2:C:110:THR:O	2.30	0.59
1:A:188[A]:GLU:OE2	1:A:270:HIS:CE1	2.56	0.59
1:A:242:ASP:N	4:A:557:HOH:O	2.32	0.57
1:A:261:ARG:HG3	1:A:324:ILE:HD13	1.85	0.57
1:A:294[A]:GLN:O	1:A:294[A]:GLN:HG2	2.03	0.57
1:A:285:LEU:CD2	1:A:443:LEU:HD11	2.36	0.56
1:A:116[A]:ILE:HG22	1:A:119:SER:HB3	1.87	0.56
1:A:130:THR:O	1:A:241:GLN:HG2	2.09	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:116[A]:ILE:HG13	1:A:185:TYR:CE2	2.44	0.52
2:C:71:LYS:HG3	2:C:168:CYS:SG	2.48	0.52
2:C:173:GLN:CD	2:C:173:GLN:N	2.63	0.52
1:A:161:ASP:HB3	1:A:166:ARG:HB3	1.93	0.51
1:A:265:LYS:HE2	1:A:427[B]:ILE:HD13	1.92	0.50
1:A:267:GLN:HG2	1:A:427[B]:ILE:HD11	1.94	0.50
1:A:462:MET:HE2	4:A:496:HOH:O	2.13	0.48
1:A:248:GLU:OE1	1:A:251:LYS:NZ	2.46	0.48
1:A:345:CYS:CB	1:A:369:CYS:HG	2.24	0.48
1:A:116[A]:ILE:HG12	1:A:185:TYR:CG	2.48	0.47
1:A:130:THR:C	1:A:131:GLN:HG2	2.35	0.47
2:C:22:PHE:HB3	2:C:89:LEU:HB3	1.97	0.47
2:C:122:ARG:CG	2:C:123:ALA:H	2.28	0.46
1:A:213:ASP:O	1:A:217:SER:HB2	2.17	0.44
1:A:157:GLU:OE1	1:A:157:GLU:HA	2.17	0.43
2:C:67:SER:HA	2:C:79:VAL:O	2.18	0.43
1:A:204:ASN:HA	1:A:207:LEU:HD12	1.99	0.43
1:A:340:ARG:CG	1:A:340:ARG:NH1	2.75	0.43
2:C:122:ARG:CG	2:C:123:ALA:N	2.81	0.43
1:A:427[A]:ILE:HA	1:A:427[A]:ILE:HD12	1.94	0.42
1:A:257:PHE:HE1	1:A:387:GLU:HG3	1.84	0.42
1:A:257:PHE:CE1	1:A:387:GLU:HG3	2.54	0.42
1:A:234:GLY:HA3	1:A:237:VAL:HG21	2.01	0.42
1:A:151:TYR:HB2	1:A:175:TYR:HE2	1.85	0.42
1:A:116[A]:ILE:CG1	1:A:185:TYR:CD2	3.03	0.42
1:A:270:HIS:HB3	4:A:473:HOH:O	2.20	0.42
2:C:71:LYS:HE3	2:C:166:GLY:O	2.20	0.42
1:A:236:GLY:HA2	1:A:265:LYS:HE3	2.01	0.41
1:A:116[B]:ILE:HG12	1:A:179:PRO:HD3	2.02	0.41
2:C:20:ALA:O	2:C:21:ASN:HB2	2.20	0.41
1:A:200:TYR:OH	1:A:209:LYS:HG2	2.20	0.41
1:A:320:ILE:CD1	1:A:427[A]:ILE:HD11	2.51	0.41
1:A:214:LYS:HA	1:A:217:SER:HB2	2.03	0.41
1:A:261:ARG:HG3	1:A:324:ILE:CD1	2.51	0.40
1:A:322:GLU:OE2	1:A:392:ARG:NH1	2.54	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	327/367 (89%)	321 (98%)	6 (2%)	0	100	100
2	C	148/184 (80%)	136 (92%)	12 (8%)	0	100	100
All	All	475/551 (86%)	457 (96%)	18 (4%)	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	273/312 (88%)	259 (95%)	14 (5%)	33	29
2	C	119/150 (79%)	114 (96%)	5 (4%)	40	39
All	All	392/462 (85%)	373 (95%)	19 (5%)	36	32

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	141	SER
1	A	173	GLU
1	A	184	LYS
1	A	243	THR
1	A	244	SER
1	A	248	GLU
1	A	249	LEU
1	A	281[A]	ASP
1	A	281[B]	ASP
1	A	340	ARG

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Mol	Chain	Res	Type
1	A	384	MET
1	A	446	LEU
1	A	453	LEU
2	C	49	ARG
2	C	60	GLN
2	C	82	LEU
2	C	169	GLU
2	C	177	LEU

Some 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 chains 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 ⓘ

There are no carbohydrates in this entry.

### 5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is 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.

### 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 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	328/367 (89%)	0.77	27 (8%) 12 13	35, 51, 73, 89	0
2	C	159/184 (86%)	1.24	46 (28%) 1 1	27, 44, 57, 62	0
All	All	487/551 (88%)	0.92	73 (14%) 3 3	27, 50, 70, 89	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	85	ASP	4.6
2	C	89	LEU	4.5
2	C	88	VAL	4.3
2	C	61	GLY	3.9
1	A	312	ILE	3.8
2	C	168	CYS	3.7
2	C	167	PHE	3.5
2	C	52	ALA	3.5
1	A	397	SER	3.5
1	A	445	PRO	3.4
1	A	218[A]	PHE	3.4
2	C	53	THR	3.2
1	A	427[A]	ILE	3.2
2	C	86	THR	3.2
2	C	42	PHE	3.1
1	A	207	LEU	3.1
2	C	41	ARG	3.1
1	A	155	TRP	3.0
2	C	141	VAL	3.0
2	C	76	CYS	2.9
2	C	124	GLY	2.9
2	C	157	ASP	2.9
2	C	75	ILE	2.9
2	C	99	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
2	C	39	ALA	2.8
1	A	425	VAL	2.8
2	C	87	GLY	2.8
1	A	354	TYR	2.8
2	C	112	TYR	2.8
2	C	24	ALA	2.7
2	C	70	ARG	2.6
1	A	145	GLY	2.6
1	A	421	LYS	2.6
2	C	68	THR	2.6
1	A	109	ASP	2.5
1	A	172	ASP	2.5
2	C	180	VAL	2.5
2	C	60	GLN	2.5
1	A	123	ALA	2.5
2	C	77	TRP	2.5
1	A	208	SER	2.4
2	C	170	ALA	2.4
2	C	69	PHE	2.4
2	C	58	ALA	2.4
1	A	171	ASP	2.4
1	A	170	GLY	2.4
2	C	44	GLN	2.3
2	C	150	GLN	2.3
1	A	442	SER	2.3
2	C	55	LEU	2.3
2	C	153	HIS	2.3
2	C	166	GLY	2.3
1	A	461	LEU	2.3
1	A	426	VAL	2.2
1	A	311	TYR	2.2
1	A	146	GLN	2.2
2	C	25	GLN	2.2
2	C	71	LYS	2.2
2	C	159	ILE	2.2
1	A	313	THR	2.2
2	C	22	PHE	2.2
2	C	90	GLY	2.2
1	A	411	ILE	2.2
2	C	92	PHE	2.1
1	A	434	ILE	2.1
2	C	103	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	444	GLY	2.1
2	C	54	THR	2.1
1	A	201	ASP	2.1
2	C	123	ALA	2.1
2	C	15	THR	2.1
2	C	82	LEU	2.0
2	C	91	ARG	2.0

## 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	CL	C	183	1/1	0.14	-1.61	57,57,57,57	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.