



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:02 AM GMT

PDB ID : 3KMS  
Title : G62S mutant of foot-and-mouth disease virus RNA-polymerase in complex with a template- primer RNA trigonal structure  
Authors : Ferrer-Orta, C.; Verdaguer, N.; Perez-Luque, R.  
Deposited on : 2009-11-11  
Resolution : 2.20 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

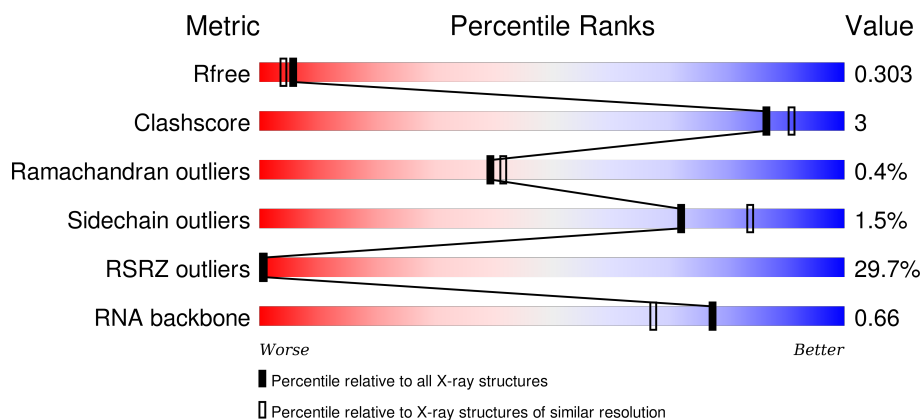
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)
RNA backbone	2183	1062 (2.80-1.60)

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	476	
2	B	7	
3	C	5	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4051 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 3D polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3731	2374	643	693	21			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	SER	GLY	ENGINEERED MUTATION	UNP Q9QCE3
A	471	ALA	-	EXPRESSION TAG	UNP Q9QCE3
A	472	ALA	-	EXPRESSION TAG	UNP Q9QCE3
A	473	LEU	-	EXPRESSION TAG	UNP Q9QCE3
A	474	GLU	-	EXPRESSION TAG	UNP Q9QCE3
A	475	HIS	-	EXPRESSION TAG	UNP Q9QCE3
A	476	HIS	-	EXPRESSION TAG	UNP Q9QCE3

- Molecule 2 is a RNA chain called RNA (5'-R(\*AP\*UP\*GP\*GP\*GP\*CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	7	Total	C	N	O	P	62	0	0
			148	67	28	47	6			

- Molecule 3 is a RNA chain called RNA (5'-R(\*GP\*GP\*CP\*CP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	P	0	0	0
			103	47	19	33	4			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

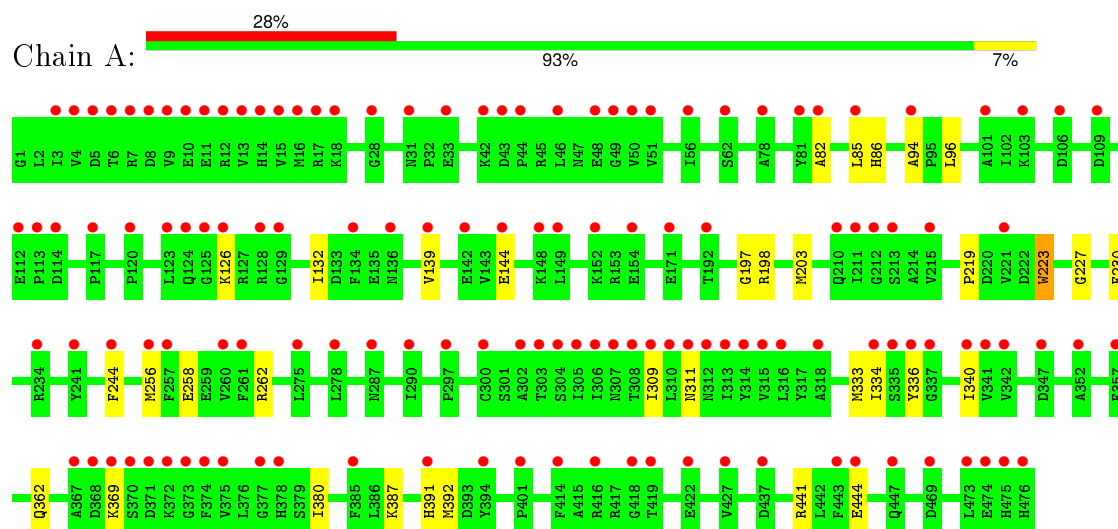
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	59	Total 59	O 59	0	0
5	B	5	Total 5	O 5	0	0
5	C	4	Total 4	O 4	0	0

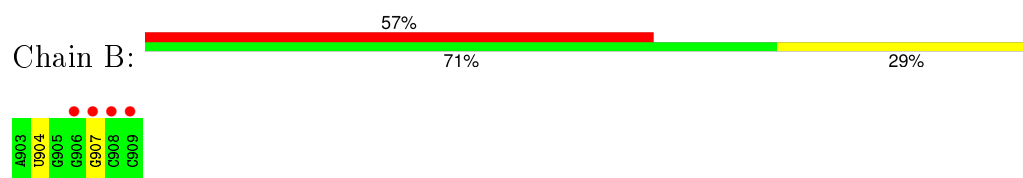
### 3 Residue-property plots [i](#)

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.

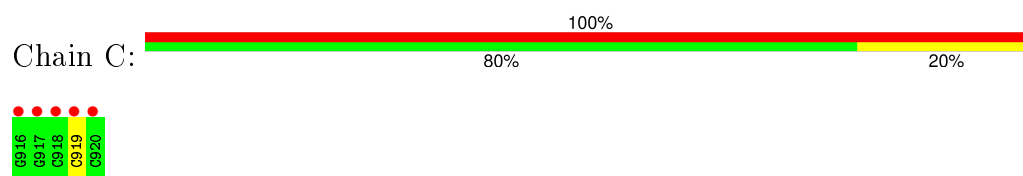
- Molecule 1: 3D polymerase



- Molecule 2: RNA (5'-R(\*AP\*UP\*GP\*GP\*GP\*CP\*C)-3')



- Molecule 3: RNA (5'-R(\*GP\*GP\*CP\*CP\*C)-3')



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.95Å 93.95Å 100.00Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.40 – 2.20 29.39 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.40-2.20) 99.0 (29.39-2.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.51 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.236 , 0.266 0.284 , 0.303	Depositor DCC
$R_{free}$ test set	1318 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	45.3	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 41.5	EDS
Estimated twinning fraction	0.033 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 26076 reflections	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	4051	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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

### 5.1 Standard geometry

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

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	0.33	0/3822	0.46	0/5180
2	B	0.59	0/165	1.00	0/256
3	C	0.60	0/114	0.97	0/176
All	All	0.35	0/4101	0.52	0/5612

There are no bond length outliers.

There are no bond angle outliers.

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	3731	0	3631	21	0
2	B	148	0	78	0	0
3	C	103	0	57	1	0
4	A	1	0	0	0	0
5	A	59	0	0	3	0
5	B	5	0	0	0	0
5	C	4	0	0	0	0
All	All	4051	0	3766	21	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 3.

All (21) 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:82:ALA:O	5:A:599:HOH:O	1.59	1.16
1:A:256:MET:HE2	1:A:309:ILE:HG21	1.49	0.94
1:A:230:PHE:HB2	1:A:380:ILE:HD12	1.49	0.92
1:A:387:LYS:HD3	3:C:919:C:H5"	1.77	0.67
1:A:94:ALA:O	1:A:198:ARG:HD2	2.03	0.58
1:A:227:GLY:HA2	1:A:380:ILE:HD13	1.86	0.57
1:A:256:MET:CE	1:A:309:ILE:HG21	2.30	0.56
1:A:441:ARG:O	1:A:444:GLU:HG2	2.08	0.53
1:A:256:MET:HE2	1:A:309:ILE:CG2	2.31	0.53
1:A:244:PHE:HA	1:A:362:GLN:HE22	1.73	0.53
1:A:85:LEU:HD11	1:A:203:MET:SD	2.52	0.49
1:A:132:ILE:HG12	1:A:139:VAL:HG12	1.96	0.47
1:A:86:HIS:HD2	5:A:525:HOH:O	1.98	0.47
1:A:230:PHE:CB	1:A:380:ILE:HD12	2.35	0.47
1:A:82:ALA:C	5:A:599:HOH:O	2.33	0.44
1:A:333:MET:CE	1:A:340:ILE:HD13	2.48	0.44
1:A:333:MET:HE1	1:A:340:ILE:HD13	1.99	0.43
1:A:96:LEU:HD22	1:A:197:GLY:HA3	2.00	0.42
1:A:258:GLU:O	1:A:262:ARG:HG2	2.19	0.42
1:A:219:PRO:O	1:A:223:TRP:HB2	2.19	0.42
1:A:139:VAL:HG23	1:A:144:GLU:HG3	2.03	0.41

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	474/476 (100%)	461 (97%)	11 (2%)	2 (0%)	39	42

All (2) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	126	LYS
1	A	369	LYS

### 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 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	393/400 (98%)	387 (98%)	6 (2%)	72 84

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	223	TRP
1	A	311	ASN
1	A	334	ILE
1	A	336	TYR
1	A	391	HIS
1	A	392	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	86	HIS
1	A	160	GLN
1	A	280	ASN
1	A	311	ASN
1	A	322	HIS
1	A	356	HIS
1	A	362	GLN
1	A	447	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	6/7 (85%)	2 (33%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	4/5 (80%)	0	0
All	All	10/12 (83%)	2 (20%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	904	U
2	B	907	G

There are no RNA pucker outliers to report.

## 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 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.

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

### 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	476/476 (100%)	1.48	135 (28%)  	40, 49, 59, 63	0
2	B	4/7 (57%)	6.61	4 (100%)  	81, 82, 82, 82	4 (100%)
3	C	5/5 (100%)	6.16	5 (100%)  	74, 74, 75, 76	5 (100%)
All	All	485/488 (99%)	1.57	144 (29%)  	40, 49, 60, 82	9 (1%)

All (144) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	916	G	9.6
2	B	909	C	9.6
2	B	907	G	9.0
3	C	917	G	6.8
1	A	370	SER	6.3
3	C	920	C	6.3
1	A	10	GLU	6.0
1	A	394	TYR	5.8
1	A	12	ARG	5.4
1	A	114	ASP	5.3
1	A	113	PRO	5.2
3	C	919	C	5.1
1	A	8	ASP	5.0
1	A	469	ASP	4.9
1	A	6	THR	4.8
1	A	371	ASP	4.8
1	A	369	LYS	4.7
1	A	15	VAL	4.7
1	A	306	ILE	4.7
1	A	7	ARG	4.6
1	A	51	VAL	4.5
2	B	906	G	4.5
1	A	9	VAL	4.5

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Mol	Chain	Res	Type	RSRZ
1	A	5	ASP	4.4
1	A	309	ILE	4.2
1	A	313	ILE	4.1
1	A	149	LEU	4.1
1	A	287	ASN	4.0
1	A	16	MET	4.0
1	A	310	LEU	4.0
1	A	372	LYS	3.9
1	A	475	HIS	3.9
1	A	303	THR	3.9
1	A	308	THR	3.8
1	A	18	LYS	3.8
1	A	49	GLY	3.8
1	A	305	ILE	3.7
1	A	17	ARG	3.7
1	A	473	LEU	3.6
1	A	109	ASP	3.6
1	A	123	LEU	3.6
1	A	28	GLY	3.6
1	A	302	ALA	3.5
1	A	368	ASP	3.5
1	A	373	GLY	3.4
1	A	378	HIS	3.4
1	A	101	ALA	3.4
1	A	134	PHE	3.4
1	A	46	LEU	3.4
1	A	340	ILE	3.4
1	A	447	GLN	3.3
2	B	908	C	3.3
1	A	314	TYR	3.3
1	A	278	LEU	3.3
1	A	106	ASP	3.3
1	A	125	GLY	3.2
1	A	367	ALA	3.2
1	A	257	PHE	3.2
1	A	416	ARG	3.2
1	A	81	TYR	3.2
3	C	918	C	3.1
1	A	275	LEU	3.0
1	A	352	ALA	3.0
1	A	14	HIS	3.0
1	A	139	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	4	VAL	2.9
1	A	341	VAL	2.9
1	A	307	ASN	2.9
1	A	244	PHE	2.9
1	A	128	ARG	2.9
1	A	290	ILE	2.9
1	A	347	ASP	2.9
1	A	13	VAL	2.8
1	A	48	GLU	2.8
1	A	474	GLU	2.8
1	A	152	LYS	2.8
1	A	315	VAL	2.8
1	A	154	GLU	2.8
1	A	335	SER	2.8
1	A	148	LYS	2.8
1	A	82	ALA	2.8
1	A	144	GLU	2.8
1	A	126	LYS	2.7
1	A	385	PHE	2.7
1	A	375	VAL	2.7
1	A	418	GLY	2.7
1	A	336	TYR	2.6
1	A	171	GLU	2.6
1	A	256	MET	2.6
1	A	391	HIS	2.6
1	A	437	ASP	2.6
1	A	334	ILE	2.6
1	A	422	GLU	2.5
1	A	312	ASN	2.5
1	A	261	PHE	2.5
1	A	11	GLU	2.5
1	A	136	ASN	2.4
1	A	337	GLY	2.4
1	A	103	LYS	2.4
1	A	304	SER	2.4
1	A	31	ASN	2.3
1	A	221	VAL	2.3
1	A	117	PRO	2.3
1	A	78	ALA	2.3
1	A	94	ALA	2.3
1	A	318	ALA	2.3
1	A	311	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	210	GLN	2.3
1	A	414	PHE	2.3
1	A	85	LEU	2.3
1	A	444	GLU	2.3
1	A	215	VAL	2.2
1	A	374	PHE	2.2
1	A	213	SER	2.2
1	A	427	VAL	2.2
1	A	357	PHE	2.2
1	A	44	PRO	2.2
1	A	112	GLU	2.2
1	A	241	TYR	2.2
1	A	377	GLY	2.2
1	A	62	SER	2.2
1	A	124	GLN	2.2
1	A	401	PRO	2.2
1	A	33	GLU	2.2
1	A	50	VAL	2.1
1	A	120	PRO	2.1
1	A	142	GLU	2.1
1	A	211	ILE	2.1
1	A	260	VAL	2.1
1	A	342	VAL	2.1
1	A	419	THR	2.1
1	A	56	ILE	2.1
1	A	43	ASP	2.1
1	A	129	GLY	2.1
1	A	300	CYS	2.1
1	A	3	ILE	2.1
1	A	297	PRO	2.1
1	A	192	THR	2.1
1	A	234	ARG	2.0
1	A	476	HIS	2.0
1	A	212	GLY	2.0
1	A	42	LYS	2.0
1	A	316	LEU	2.0
1	A	443	PHE	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 [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, 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( $\text{\AA}^2$ )	Q<0.9
4	MG	A	950	1/1	0.76	0.33	1.74	67,67,67,67	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.