



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 7, 2017 – 08:42 AM EST

PDB ID : 4GV8  
Title : DUTPase from phage phi11 of S.aureus: visualization of the species-specific insert  
Authors : Leveles, I.; Harmat, V.; Nemeth, V.; Bendes, A.; Szabo, J.; Kadar, V.; Zagyva, I.; Rona, G.; Toth, J.; Vertessy, B.G.  
Deposited on : unknown  
Resolution : 2.10 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : rb-20030345

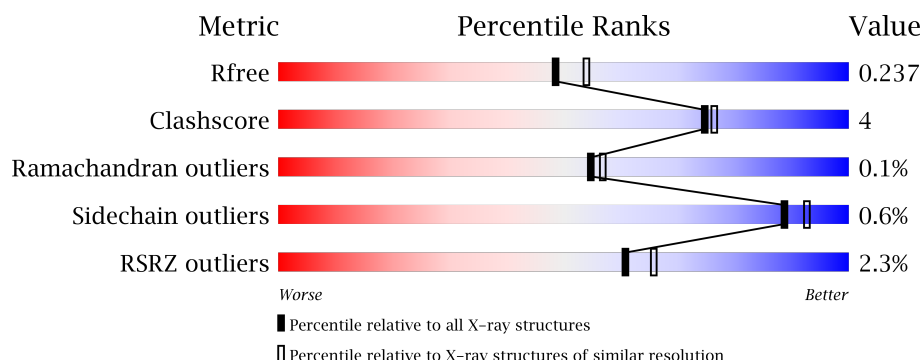
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
$R_{free}$	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	169	
1	B	169	
1	C	169	
1	D	169	
1	E	169	

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Mol	Chain	Length	Quality of chain
1	F	169	

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	MG	A	203	-	-	-	X
3	MG	D	203	-	-	-	X

## 2 Entry composition [i](#)

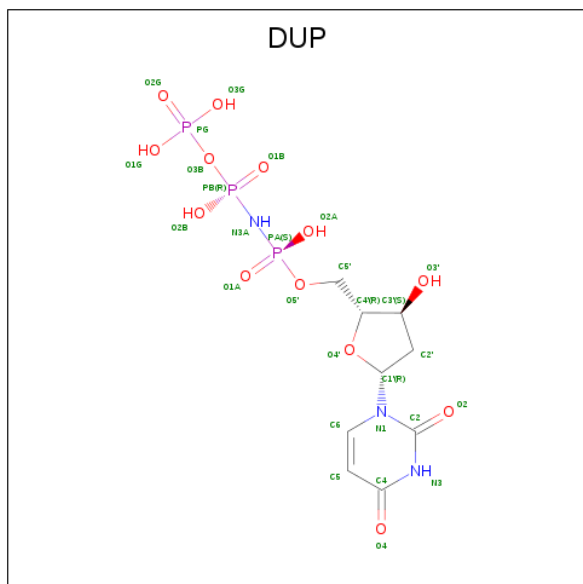
There are 4 unique types of molecules in this entry. The entry contains 7352 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DUTPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	1	0
			1139	721	194	223	1			
1	B	154	Total	C	N	O	S	0	0	0
			1159	731	193	234	1			
1	C	154	Total	C	N	O	S	0	0	0
			1137	721	192	223	1			
1	D	152	Total	C	N	O	S	0	0	0
			1117	704	188	224	1			
1	E	154	Total	C	N	O	S	0	0	0
			1126	713	191	221	1			
1	F	153	Total	C	N	O	S	0	1	0
			1122	713	191	217	1			

- Molecule 2 is 2'-DEOXYURIDINE 5'-ALPHA,BETA-IMIDO-TRIPHOSPHATE (three-letter code: DUP) (formula: C<sub>9</sub>H<sub>16</sub>N<sub>3</sub>O<sub>13</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	B	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	C	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	D	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	E	1	Total	C	N	O	P	0	0
			28	9	3	13	3		
2	F	1	Total	C	N	O	P	0	0
			28	9	3	13	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	2	Total	Mg	0	0
			2	2		
3	E	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	A	2	Total	Mg	0	0
			2	2		
3	F	1	Total	Mg	0	0
			1	1		


- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	85	Total	O	0	0
			85	85		
4	B	87	Total	O	0	0
			87	87		
4	C	82	Total	O	0	0
			82	82		
4	D	37	Total	O	0	0
			37	37		
4	E	43	Total	O	0	0
			43	43		
4	F	42	Total	O	0	0
			42	42		

### 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 the various outlier classes 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: DUTPase

Chain A: 




- Molecule 1: DUTPase

Chain B: 




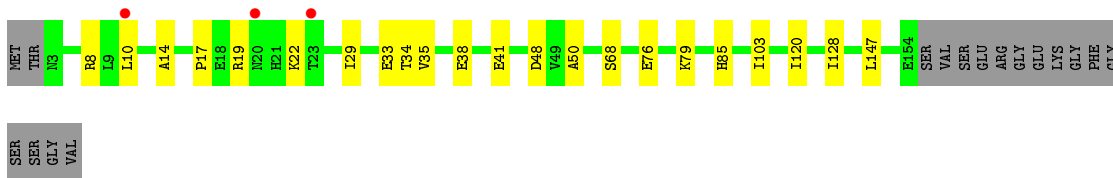
- Molecule 1: DUTPase

Chain C: 




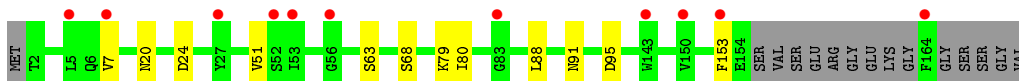
- Molecule 1: DUTPase

Chain D: 

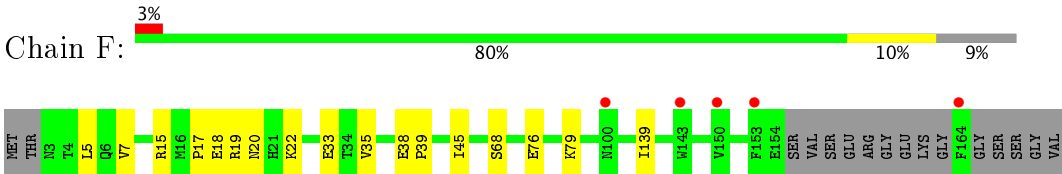


- Molecule 1: DUTPase

Chain E: 



- Molecule 1: DUTPase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.66 Å   109.66 Å   169.27 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	47.10 – 2.10 47.10 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.10-2.10) 100.0 (47.10-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.18 (at 2.10 Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.183   ,   0.232 0.189   ,   0.237	Depositor DCC
$R_{free}$ test set	3140 reflections (5.44%)	DCC
Wilson B-factor (Å <sup>2</sup> )	41.4	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 60.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7352	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: DUP, 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	0.94	1/1160 (0.1%)	0.90	1/1580 (0.1%)
1	B	0.89	0/1177	0.91	1/1602 (0.1%)
1	C	0.97	0/1154	0.95	4/1573 (0.3%)
1	D	0.73	0/1134	0.80	0/1547
1	E	0.75	0/1144	0.81	1/1560 (0.1%)
1	F	0.78	0/1142	0.86	0/1557
All	All	0.85	1/6911 (0.0%)	0.87	7/9419 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	143	TRP	CD2-CE2	6.33	1.49	1.41

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	121	ARG	NE-CZ-NH1	5.95	123.27	120.30
1	C	121	ARG	NE-CZ-NH2	-5.80	117.40	120.30
1	A	15	ARG	NE-CZ-NH1	5.59	123.10	120.30
1	E	95	ASP	CB-CG-OD2	5.33	123.09	118.30
1	C	118	ASP	CB-CG-OD1	5.10	122.89	118.30

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	1139	0	1106	6	0
1	B	1159	0	1114	7	0
1	C	1137	0	1091	7	0
1	D	1117	0	1052	18	0
1	E	1126	0	1054	8	0
1	F	1122	0	1067	14	0
2	A	28	0	12	1	0
2	B	28	0	12	0	0
2	C	28	0	12	1	0
2	D	28	0	12	0	0
2	E	28	0	12	0	0
2	F	28	0	12	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	85	0	0	0	0
4	B	87	0	0	0	0
4	C	82	0	0	1	0
4	D	37	0	0	2	0
4	E	43	0	0	1	0
4	F	42	0	0	0	0
All	All	7352	0	6556	50	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 4.

The worst 5 of 50 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:D:103:ILE:HD12	1:D:120:ILE:HG22	1.76	0.68
1:D:103:ILE:HD12	1:D:120:ILE:CG2	2.27	0.63
1:E:20:ASN:HB3	1:E:24:ASP:OD2	1.99	0.63
1:E:80:ILE:HD12	1:E:88:LEU:HD22	1.82	0.62
1:C:36:VAL:HG12	4:C:343:HOH:O	2.00	0.61

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	152/169 (90%)	151 (99%)	1 (1%)	0	100	100
1	B	151/169 (89%)	150 (99%)	1 (1%)	0	100	100
1	C	151/169 (89%)	148 (98%)	3 (2%)	0	100	100
1	D	150/169 (89%)	148 (99%)	2 (1%)	0	100	100
1	E	151/169 (89%)	145 (96%)	6 (4%)	0	100	100
1	F	151/169 (89%)	147 (97%)	3 (2%)	1 (1%)	25	20
All	All	906/1014 (89%)	889 (98%)	16 (2%)	1 (0%)	55	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	20	ASN

### 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	117/142 (82%)	115 (98%)	2 (2%)	66	72
1	B	122/142 (86%)	121 (99%)	1 (1%)	85	89
1	C	115/142 (81%)	114 (99%)	1 (1%)	82	87
1	D	110/142 (78%)	110 (100%)	0	100	100
1	E	109/142 (77%)	109 (100%)	0	100	100
1	F	110/142 (78%)	110 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	683/852 (80%)	679 (99%)	4 (1%)	89	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	54	PRO
1	B	164	PHE
1	C	164	PHE

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

Mol	Chain	Res	Type
1	B	136	GLN
1	E	91	ASN

### 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 14 ligands modelled in this entry, 8 are monoatomic - leaving 6 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	DUP	A	201	3	29,29,29	3.30	11 (37%)	37,45,45	2.66	10 (27%)
2	DUP	B	201	3	29,29,29	3.64	11 (37%)	37,45,45	2.68	11 (29%)
2	DUP	C	201	3	29,29,29	3.57	12 (41%)	37,45,45	2.73	15 (40%)
2	DUP	D	201	3	29,29,29	3.59	12 (41%)	37,45,45	2.51	8 (21%)
2	DUP	E	201	3	29,29,29	3.51	11 (37%)	37,45,45	2.81	13 (35%)
2	DUP	F	201	3	29,29,29	3.48	11 (37%)	37,45,45	2.54	11 (29%)

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	DUP	A	201	3	-	0/18/34/34	0/2/2/2
2	DUP	B	201	3	-	0/18/34/34	0/2/2/2
2	DUP	C	201	3	-	0/18/34/34	0/2/2/2
2	DUP	D	201	3	-	0/18/34/34	0/2/2/2
2	DUP	E	201	3	-	0/18/34/34	0/2/2/2
2	DUP	F	201	3	-	0/18/34/34	0/2/2/2

The worst 5 of 68 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	201	DUP	C6-N1	-9.58	1.35	1.47
2	C	201	DUP	C6-N1	-9.47	1.35	1.47
2	E	201	DUP	C6-N1	-9.32	1.35	1.47
2	B	201	DUP	C6-N1	-9.23	1.35	1.47
2	B	201	DUP	C6-C5	-9.11	1.35	1.52

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	201	DUP	C4-N3-C2	-6.27	120.44	125.81
2	A	201	DUP	C4-N3-C2	-6.07	120.61	125.81
2	E	201	DUP	C4-N3-C2	-5.91	120.75	125.81
2	F	201	DUP	C2'-C1'-N1	-5.70	108.64	115.61
2	D	201	DUP	C4-N3-C2	-5.17	121.38	125.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	DUP	1	0
2	C	201	DUP	1	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	153/169 (90%)	-0.50	0 100 100	37, 48, 71, 100	0
1	B	154/169 (91%)	-0.39	0 100 100	36, 50, 78, 101	0
1	C	154/169 (91%)	-0.30	2 (1%) 77 81	35, 46, 80, 95	0
1	D	152/169 (89%)	-0.00	3 (1%) 65 70	53, 79, 111, 136	0
1	E	154/169 (91%)	0.13	11 (7%) 17 21	47, 68, 112, 130	0
1	F	153/169 (90%)	-0.05	5 (3%) 47 54	46, 64, 100, 112	0
All	All	920/1014 (90%)	-0.19	21 (2%) 61 66	35, 58, 101, 136	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	143	TRP	4.1
1	E	150	VAL	3.9
1	D	23	THR	3.7
1	E	52	SER	3.6
1	E	153	PHE	3.4

### 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 [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(Å <sup>2</sup> )	Q<0.9
3	MG	A	203	1/1	1.00	0.26	7.36	25,25,25,25	0
3	MG	D	203	1/1	0.99	0.21	6.08	32,32,32,32	0
3	MG	D	202	1/1	0.96	0.11	0.70	80,80,80,80	0
2	DUP	D	201	28/28	0.97	0.10	-0.48	69,74,78,83	0
2	DUP	A	201	28/28	0.99	0.08	-0.60	34,40,49,56	0
2	DUP	B	201	28/28	0.98	0.07	-0.78	40,44,54,61	0
2	DUP	C	201	28/28	0.99	0.07	-0.93	34,39,50,54	0
2	DUP	E	201	28/28	0.97	0.09	-1.34	64,69,81,82	0
2	DUP	F	201	28/28	0.97	0.07	-1.46	52,62,67,70	0
3	MG	E	202	1/1	0.91	0.07	-	73,73,73,73	0
3	MG	B	202	1/1	0.98	0.07	-	47,47,47,47	0
3	MG	F	202	1/1	0.96	0.03	-	65,65,65,65	0
3	MG	A	202	1/1	0.99	0.07	-	42,42,42,42	0
3	MG	C	202	1/1	0.99	0.05	-	43,43,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.