



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2018 – 05:20 am GMT

PDB ID : 5O7T
Title : Crystal structure of KlenTaq mutant M747K in a closed ternary complex with a dG:dCTP base pair
Authors : Betz, K.; Diederichs, K.; Marx, A.
Deposited on : 2017-06-09
Resolution : 1.80 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

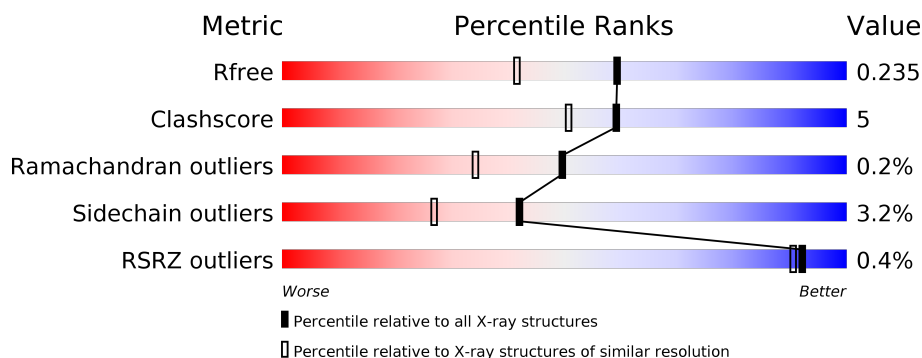
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	111664	5253 (1.80-1.80)
Clashscore	122126	6077 (1.80-1.80)
Ramachandran outliers	120053	6011 (1.80-1.80)
Sidechain outliers	120020	6010 (1.80-1.80)
RSRZ outliers	108989	5157 (1.80-1.80)

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	540	
2	B	12	
3	C	16	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9854 atoms, of which 4684 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 DNA polymerase I, thermostable.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	540	Total	C	H	N	O	S	9	1	0
			8650	2731	4352	773	782	12			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	747	LYS	MET	engineered mutation	UNP P19821

- Molecule 2 is a DNA chain called DNA primer.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	12	Total	C	H	N	O	P	0	0	0
			377	115	134	50	67	11			

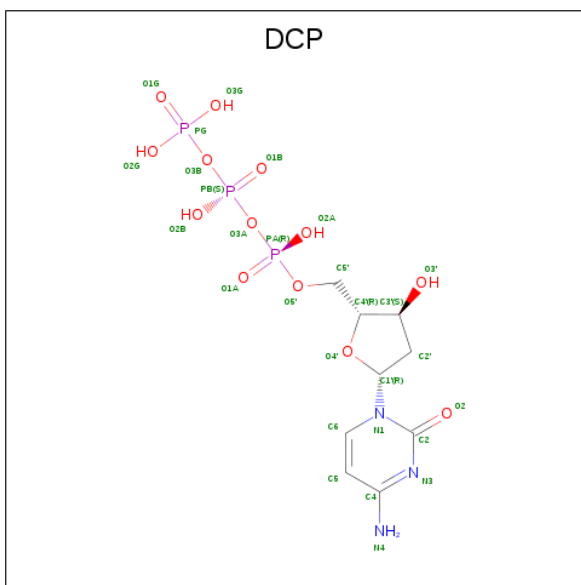
- Molecule 3 is a DNA chain called DNA template.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	16	Total	C	H	N	O	P	0	0	0
			507	155	180	64	93	15			

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

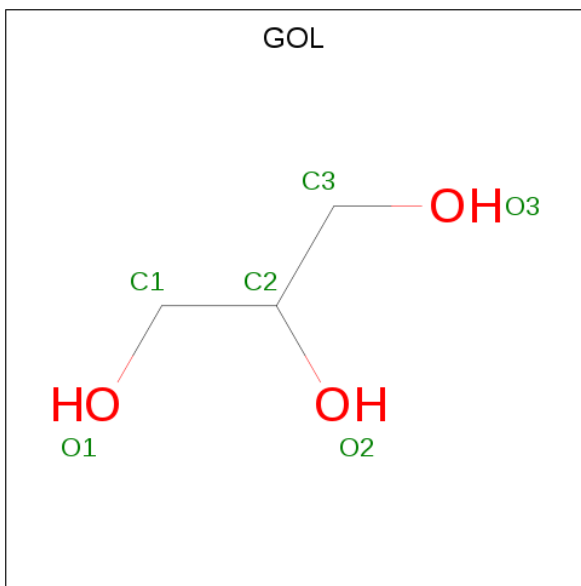
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	2	Total	Mg	0	0
			2	2		

- Molecule 5 is 2'-DEOXYCYTIDINE-5'-TRIPHOSPHATE (three-letter code: DCP) (formula: C₉H₁₆N₃O₁₃P₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	P	0	0
			40	9	12	3	13	3		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	O	0	0
			12	3	6	3		

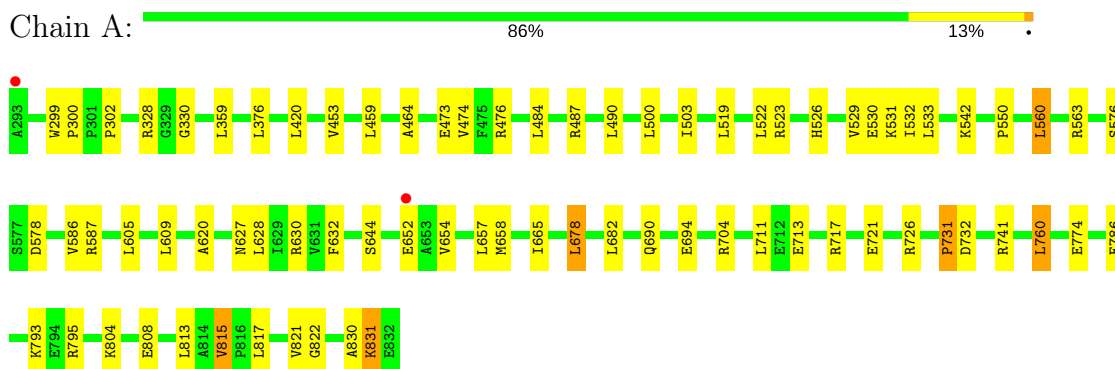
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	189	Total 189	O 189	0	0
7	B	30	Total 30	O 30	0	0
7	C	46	Total 46	O 46	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 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: DNA polymerase I, thermostable



- Molecule 2: DNA primer



- Molecule 3: DNA template



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	109.48Å 109.48Å 91.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.40 – 1.80 47.40 – 1.80	Depositor EDS
% Data completeness (in resolution range)	98.2 (47.40-1.80) 98.0 (47.40-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.97 (at 1.79Å)	Xtriage
Refinement program	PHENIX (dev_2747: ???)	Depositor
R, R_{free}	0.177 , 0.235 0.177 , 0.235	Depositor DCC
R_{free} test set	2934 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9854	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, MG, DDG, DCP

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	0.55	0/4391	0.68	3/5947 (0.1%)
2	B	1.47	2/249 (0.8%)	1.19	2/382 (0.5%)
3	C	1.39	0/367	1.28	6/565 (1.1%)
All	All	0.72	2/5007 (0.0%)	0.79	11/6894 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	103	DC	C3'-O3'	-5.97	1.36	1.44
2	B	110	DG	C8-N7	5.50	1.34	1.30

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	212	DT	O5'-P-OP2	-6.87	99.52	105.70
3	C	215	DT	O5'-P-OP2	-6.74	99.64	105.70
3	C	210	DC	O5'-P-OP1	-6.22	100.11	105.70
1	A	760	LEU	CA-CB-CG	6.03	129.16	115.30
3	C	204	DG	O5'-P-OP2	-5.80	100.48	105.70
2	B	108	DG	O4'-C1'-N9	5.32	111.72	108.00
3	C	214	DG	O4'-C1'-N9	5.23	111.66	108.00
2	B	105	DA	OP2-P-O3'	5.16	116.54	105.20
1	A	741	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	560	LEU	CA-CB-CG	5.11	127.05	115.30
3	C	209	DC	OP2-P-O3'	5.09	116.39	105.20

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	4298	4352	4351	41	0
2	B	243	134	134	3	0
3	C	327	180	180	5	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
5	A	28	12	12	0	0
6	B	6	6	8	1	0
7	A	189	0	0	3	0
7	B	30	0	0	1	0
7	C	46	0	0	4	0
All	All	5170	4684	4685	49	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 5.

All (49) 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)
3:C:214:DG:N7	7:C:303:HOH:O	2.23	0.72
3:C:211:DG:OP2	7:C:301:HOH:O	2.10	0.70
1:A:302:PRO:HG2	1:A:328:ARG:HD3	1.81	0.63
3:C:212:DT:OP2	7:C:302:HOH:O	2.16	0.61
1:A:578:ASP:OD1	7:A:1001:HOH:O	2.16	0.60
1:A:804:LYS:NZ	1:A:808:GLU:OE2	2.33	0.60
1:A:523:ARG:NH1	1:A:530:GLU:OE1	2.35	0.59
1:A:731:PRO:O	1:A:732:ASP:HB2	2.08	0.53
3:C:210:DC:H2'	3:C:211:DG:C8	2.44	0.53
1:A:473:GLU:OE2	1:A:476:ARG:NH2	2.28	0.52
2:B:103:DC:P	7:B:302:HOH:O	2.68	0.51
1:A:376:LEU:HD22	1:A:420:LEU:HD12	1.93	0.50
1:A:690:GLN:O	1:A:694:GLU:HG2	2.10	0.50
1:A:522:LEU:HD12	1:A:522:LEU:O	2.12	0.49
2:B:103:DC:H5''	2:B:103:DC:H6	1.77	0.49
1:A:721:GLU:HA	1:A:726:ARG:O	2.13	0.49
1:A:330:GLY:N	7:A:1014:HOH:O	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:609:LEU:HG	1:A:821:VAL:HG12	1.95	0.48
1:A:523:ARG:HG2	1:A:523:ARG:O	2.13	0.48
1:A:813:LEU:HD12	1:A:817:LEU:HD21	1.97	0.47
1:A:713:GLU:O	1:A:717:ARG:HG3	2.14	0.46
1:A:632:PHE:HB2	1:A:815:VAL:HG22	1.96	0.46
1:A:654:VAL:HA	1:A:658:MET:HE2	1.97	0.45
1:A:795:ARG:HG2	1:A:795:ARG:HH11	1.81	0.45
1:A:786:GLU:CD	1:A:831:LYS:HE3	2.36	0.45
1:A:632:PHE:HB2	1:A:815:VAL:CG2	2.46	0.45
1:A:453:VAL:HG13	1:A:550:PRO:HB3	2.00	0.44
1:A:786:GLU:OE2	1:A:831:LYS:HE3	2.18	0.44
1:A:299:TRP:CG	1:A:300:PRO:HA	2.53	0.44
1:A:490:LEU:HD11	1:A:532:ILE:HD13	1.99	0.43
1:A:678:LEU:HD22	1:A:682:LEU:HG	2.00	0.43
1:A:522:LEU:CD1	1:A:529:VAL:HG21	2.48	0.43
1:A:704:ARG:HG3	7:A:1166:HOH:O	2.19	0.43
6:B:202:GOL:H12	7:C:326:HOH:O	2.17	0.43
1:A:665:ILE:HG13	1:A:682:LEU:HD21	1.99	0.43
1:A:620:ALA:HB2	1:A:628:LEU:HG	2.01	0.42
1:A:605:LEU:HG	1:A:793:LYS:HG2	2.02	0.42
2:B:103:DC:H2''	2:B:104:DC:H5'	2.02	0.42
1:A:563:ARG:O	1:A:576:SER:HA	2.20	0.41
1:A:657:LEU:H	1:A:657:LEU:HD22	1.85	0.41
1:A:519:LEU:HB2	1:A:533:LEU:HD21	2.02	0.41
1:A:576:SER:O	3:C:208:DG:H4'	2.20	0.41
1:A:474:VAL:HG11	1:A:484:LEU:HD21	2.03	0.41
1:A:359:LEU:HD23	1:A:359:LEU:C	2.40	0.41
1:A:503:ILE:HD11	1:A:522:LEU:HD23	2.03	0.40
1:A:464:ALA:HB2	1:A:542:LYS:HE3	2.03	0.40
1:A:627:ASN:OD1	1:A:630:ARG:NH2	2.54	0.40
1:A:500:LEU:HD21	1:A:526:HIS:HB2	2.04	0.40
1:A:822:GLY:HA3	1:A:830:ALA:O	2.22	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	539/540 (100%)	521 (97%)	17 (3%)	1 (0%)	49 34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	586	VAL

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	442/441 (100%)	428 (97%)	14 (3%)	42 27

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	459	LEU
1	A	487	ARG
1	A	531	LYS
1	A	560	LEU
1	A	587	ARG
1	A	644	SER
1	A	652	GLU
1	A	678	LEU
1	A	711	LEU
1	A	731	PRO
1	A	760	LEU
1	A	774	GLU
1	A	815	VAL
1	A	831	LYS

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 molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	DDG	B	112	3,2	17,23,24	0.70	0	12,33,36	0.90	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	DDG	B	112	3,2	-	0/3/18/19	0/3/3/3

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.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\# Z > 2$
5	DCP	A	903	4	23,29,29	0.83	0	28,45,45	0.67	0
6	GOL	B	202	-	5,5,5	1.19	0	5,5,5	0.70	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
5	DCP	A	903	4	-	0/18/34/34	0/2/2/2
6	GOL	B	202	-	-	0/4/4/4	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	202	GOL	1	0

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 [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	540/540 (100%)	-0.32	2 (0%) 92 90	30, 50, 93, 136	0
2	B	11/12 (91%)	-0.64	0 100 100	34, 36, 67, 72	0
3	C	16/16 (100%)	-0.43	0 100 100	31, 39, 98, 101	0
All	All	567/568 (99%)	-0.33	2 (0%) 92 90	30, 49, 95, 136	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	293	ALA	7.0
1	A	652	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	B-factors(Å ²)	Q<0.9
2	DDG	B	112	21/22	0.99	0.10	29,35,45,48	0

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. 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	B-factors(Å ²)	Q<0.9
6	GOL	B	202	6/6	0.90	0.16	70,82,99,99	0
4	MG	A	901	1/1	0.94	0.05	37,37,37,37	0
4	MG	A	902	1/1	0.97	0.09	47,47,47,47	0
4	MG	B	201	1/1	0.98	0.08	52,52,52,52	0
5	DCP	A	903	28/28	0.98	0.10	27,36,46,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.