



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:01 AM GMT

PDB ID : 3GTG  
Title : Backtracked RNA polymerase II complex with 12mer RNA  
Authors : Wang, D.; Bushnell, D.A.; Huang, X.; Westover, K.D.; Levitt, M.; Kornberg, R.D.  
Deposited on : 2009-03-27  
Resolution : 3.78 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.

---

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

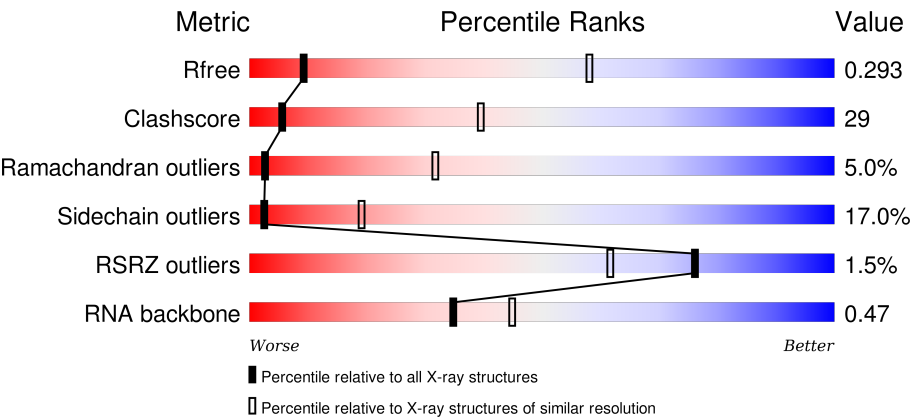
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.78 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.






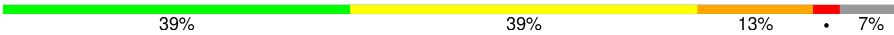





Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1273 (4.06-3.50)
Clashscore	102246	1412 (4.06-3.50)
Ramachandran outliers	100387	1351 (4.06-3.50)
Sidechain outliers	100360	1347 (4.06-3.50)
RSRZ outliers	91569	1281 (4.06-3.50)
RNA backbone	2183	1070 (4.76-2.80)

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  $\geq 3$ , 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	1733	<div><div>2%</div><div><div></div><div>38%</div><div>35%</div><div>9%</div><div>17%</div></div><div>•</div></div>
2	B	1224	<div><div>2%</div><div><div></div><div>41%</div><div>42%</div><div>10%</div><div>6%</div></div><div>•</div></div>
3	C	318	<div><div>%</div><div><div></div><div>36%</div><div>37%</div><div>11%</div><div>15%</div></div><div>•</div></div>
4	E	215	<div><div></div><div><div></div><div>63%</div><div>32%</div><div>5%</div></div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
5	F	155	
6	H	146	
7	I	122	
8	J	70	
9	K	120	
10	L	70	
11	R	12	
12	T	29	
13	N	14	

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
14	ZN	A	1734	-	-	X	-
14	ZN	B	1307	-	-	X	-
14	ZN	J	101	-	-	X	-

## 2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 30067 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 DNA-directed RNA polymerase II subunit RPB1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1442	Total	C	N	O	S	0	0	0
			11332	7133	1982	2156	61			

- Molecule 2 is a protein called DNA-directed RNA polymerase II subunit RPB2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1153	Total	C	N	O	S	0	0	0
			9167	5794	1604	1713	56			

- Molecule 3 is a protein called DNA-directed RNA polymerase II subunit RPB3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	271	Total	C	N	O	S	0	0	0
			2135	1344	355	423	13			

- Molecule 4 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	215	Total	C	N	O	S	0	0	0
			1757	1114	310	322	11			

- Molecule 5 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	85	Total	C	N	O	S	0	0	0
			684	437	116	128	3			

- Molecule 6 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	136	Total	C	N	O	S	0	0	0
			1087	684	183	215	5			

- Molecule 7 is a protein called DNA-directed RNA polymerase II subunit RPB9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	I	119	Total	C	N	O	S	0	0	0
			971	596	179	186	10			

- Molecule 8 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	J	65	Total	C	N	O	S	0	0	0
			532	339	93	94	6			

- Molecule 9 is a protein called DNA-directed RNA polymerase II subunit RPB11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	K	114	Total	C	N	O	S	0	0	0
			919	590	156	171	2			

- Molecule 10 is a protein called DNA-directed RNA polymerases I, II, and III subunit RPABC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	L	46	Total	C	N	O	S	0	0	0
			363	224	72	63	4			

- Molecule 11 is a RNA chain called RNA (5'-R(\*AP\*UP\*CP\*GP\*AP\*GP\*AP\*GP\*GP\*AP\*UP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	R	12	Total	C	N	O	P	0	0	0
			260	117	52	80	11			

- Molecule 12 is a DNA chain called DNA (28-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	T	28	Total	C	N	O	P	0	0	0
			566	271	104	164	27			

- Molecule 13 is a DNA chain called DNA (5'-D(\*CP\*TP\*GP\*CP\*TP\*TP\*AP\*TP\*CP\*GP\*GP\*TP\*AP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	14	Total	C	N	O	P	0	0	0
			284	137	49	85	13			

- Molecule 14 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	J	1	Total	Zn	0	0
			1	1		
14	B	1	Total	Zn	0	0
			1	1		
14	I	2	Total	Zn	0	0
			2	2		
14	C	1	Total	Zn	0	0
			1	1		
14	A	2	Total	Zn	0	0
			2	2		
14	L	1	Total	Zn	0	0
			1	1		

- Molecule 15 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

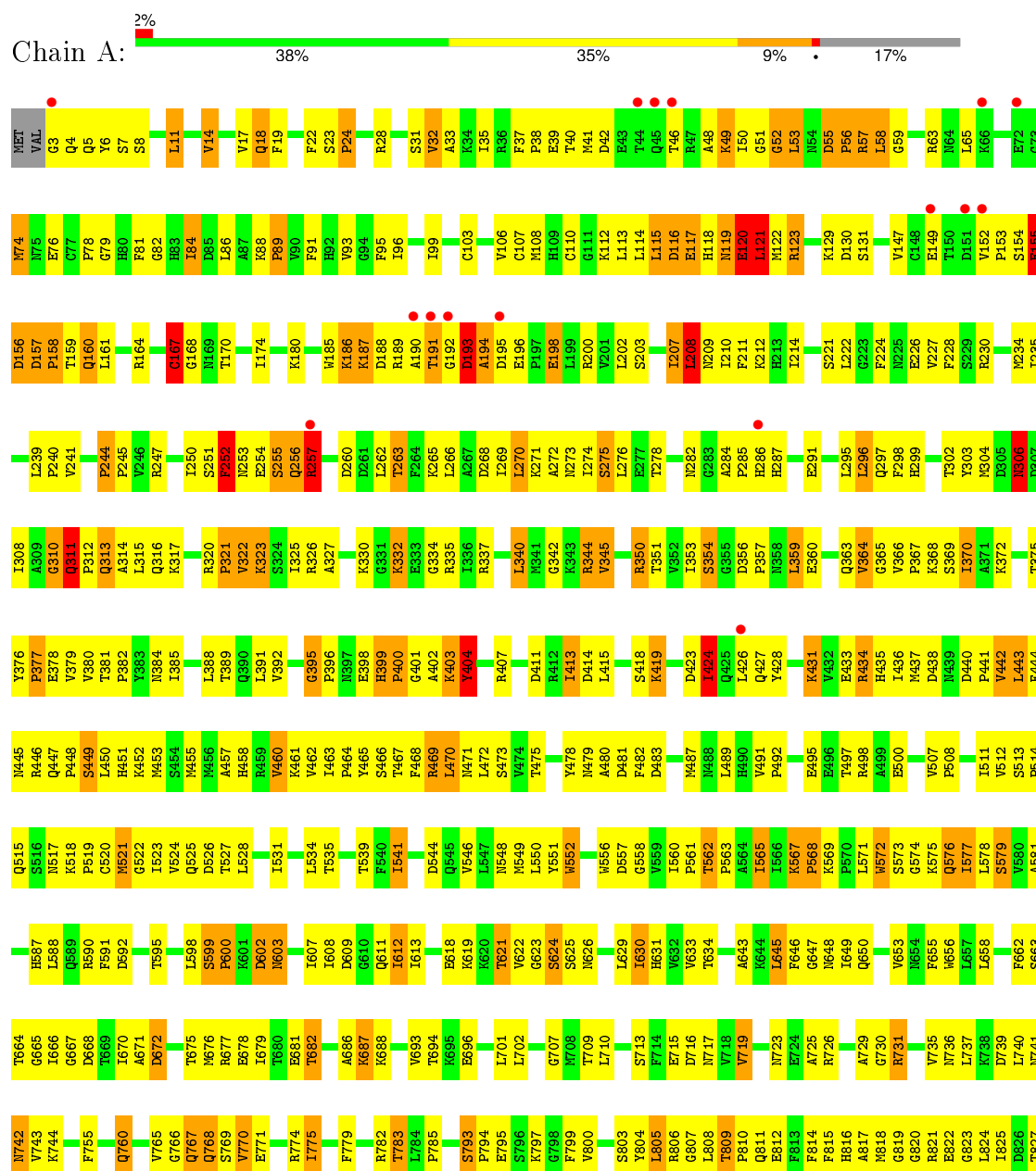
- Molecule 16 is water.

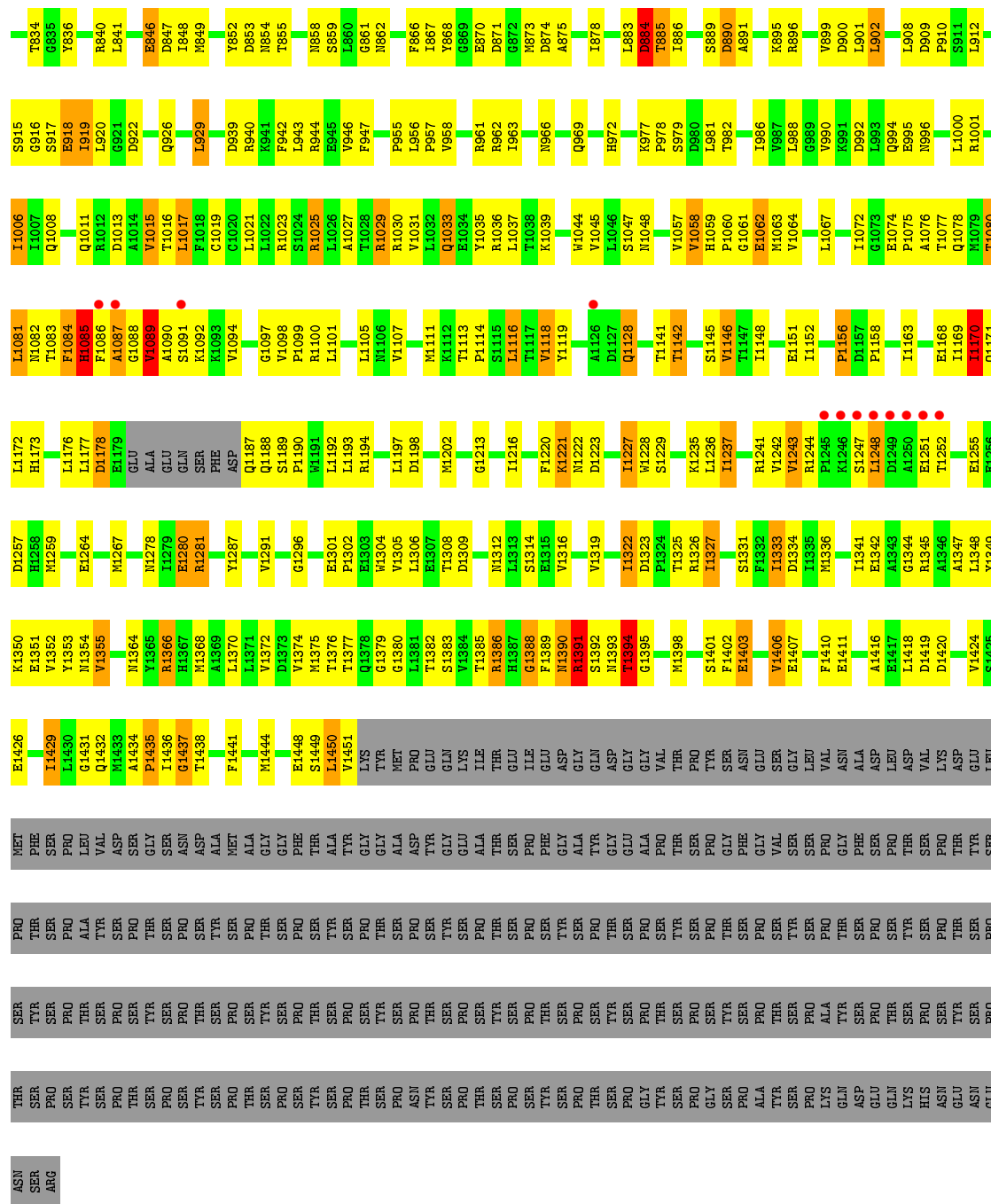
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
16	R	1	Total	O	0	0
			1	1		

### 3 Residue-property plots

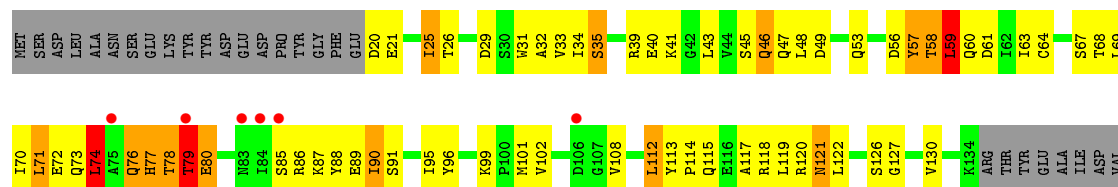
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: DNA-directed RNA polymerase II subunit RPB1

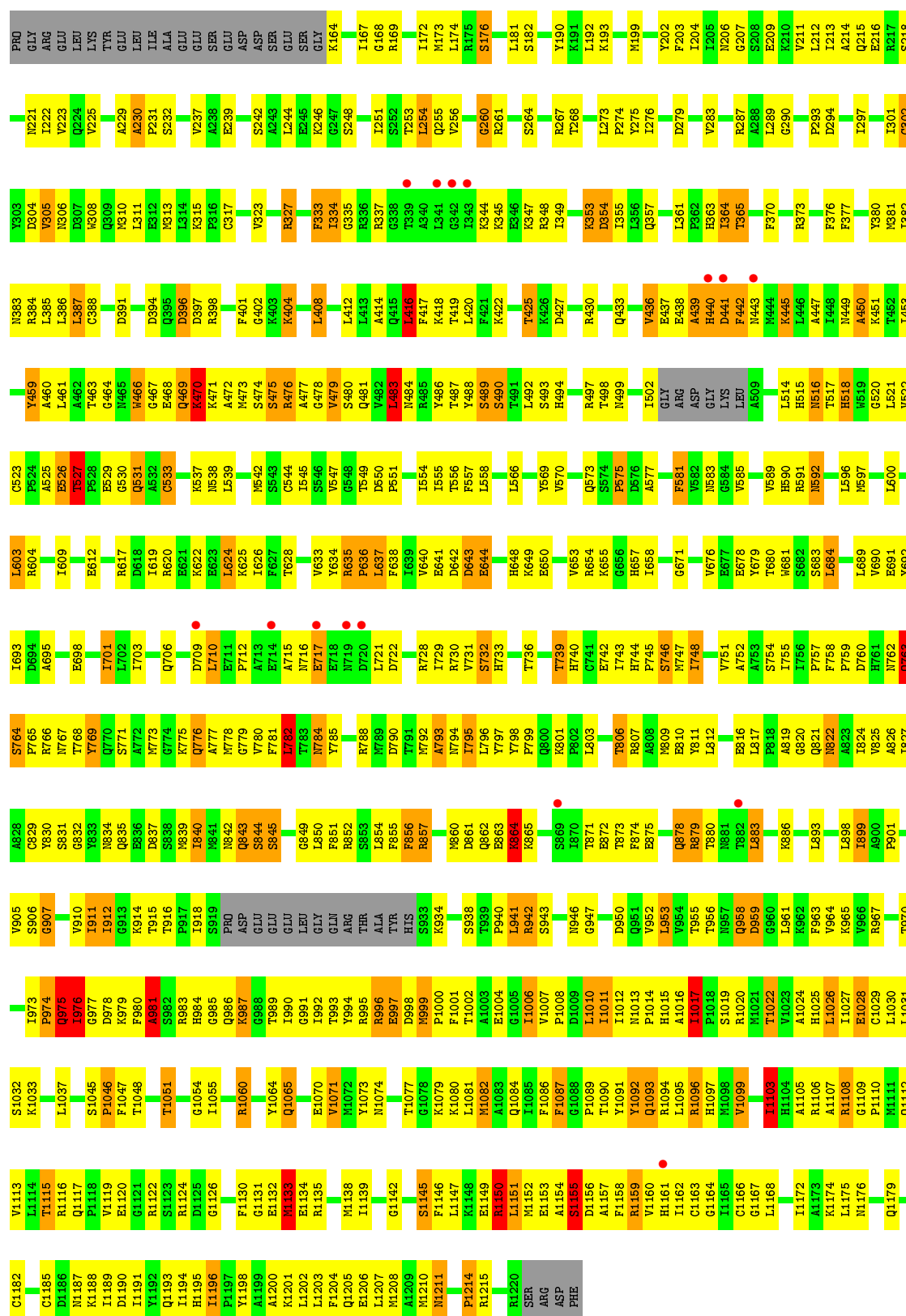




● Molecule 2: DNA-directed RNA polymerase II subunit RPB2





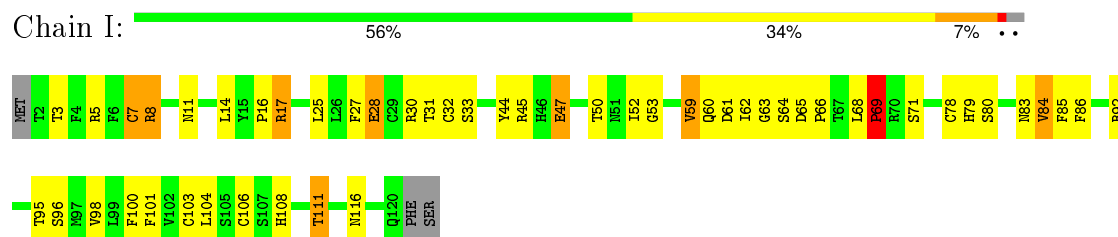


• Molecule 3: DNA-directed RNA polymerase II subunit RPB3

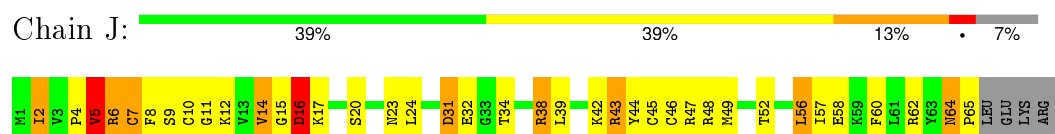




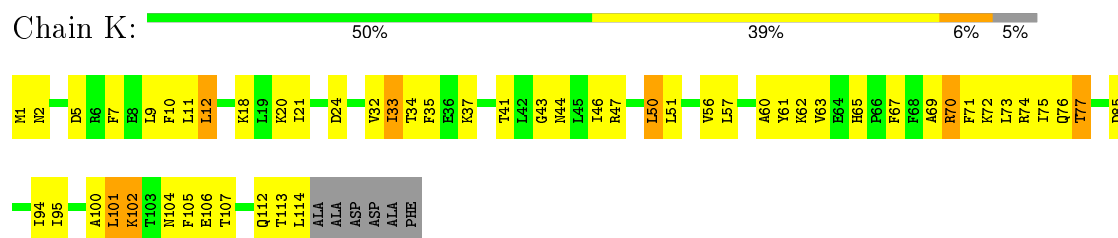
- Molecule 7: DNA-directed RNA polymerase II subunit RPB9



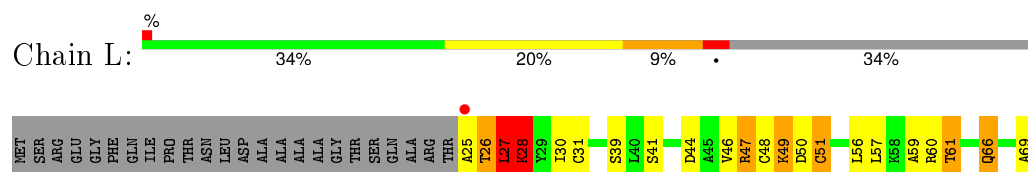
- Molecule 8: DNA-directed RNA polymerases I, II, and III subunit RPABC5



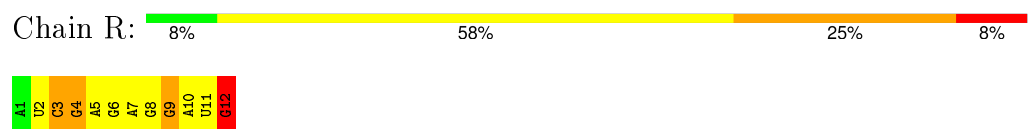
- Molecule 9: DNA-directed RNA polymerase II subunit RPB11



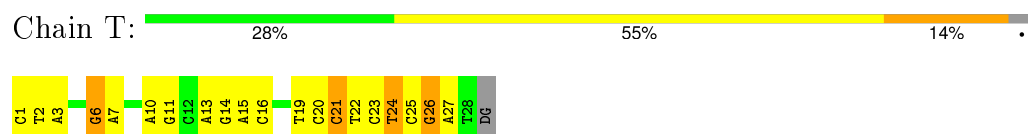
- Molecule 10: DNA-directed RNA polymerases I, II, and III subunit RPABC4



- Molecule 11: RNA (5'-R(\*AP\*UP\*CP\*GP\*AP\*GP\*AP\*GP\*GP\*AP\*UP\*G)-3')



- Molecule 12: DNA (28-MER)



- Molecule 13: DNA (5'-D(\*CP\*TP\*GP\*CP\*TP\*TP\*AP\*TP\*CP\*GP\*GP\*TP\*AP\*G)-3')





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	170.96Å 223.00Å 195.41Å 90.00° 102.28° 90.00°	Depositor
Resolution (Å)	50.00 – 3.78 42.41 – 3.79	Depositor EDS
% Data completeness (in resolution range)	95.4 (50.00-3.78) 95.5 (42.41-3.79)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.47 (at 3.76Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.253 , 0.300 0.254 , 0.293	Depositor DCC
$R_{free}$ test set	3441 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	108.9	Xtriage
Anisotropy	0.100	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 78.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	4 of 67913 reflections (0.006%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	30067	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	143.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.53% 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: ZN, 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	0.53	0/11536	0.76	14/15605 (0.1%)
2	B	0.60	0/9347	0.79	15/12609 (0.1%)
3	C	0.63	0/2174	0.76	1/2946 (0.0%)
4	E	0.47	0/1793	0.64	1/2413 (0.0%)
5	F	0.47	0/696	0.74	1/940 (0.1%)
6	H	0.47	0/1105	0.79	2/1495 (0.1%)
7	I	0.53	0/989	0.72	0/1331
8	J	0.67	0/541	0.91	2/727 (0.3%)
9	K	0.65	0/937	0.71	1/1265 (0.1%)
10	L	0.58	0/365	0.90	2/485 (0.4%)
11	R	0.95	0/292	1.67	5/455 (1.1%)
12	T	0.96	1/634 (0.2%)	1.67	13/975 (1.3%)
13	N	0.91	0/317	1.53	4/488 (0.8%)
All	All	0.58	1/30726 (0.0%)	0.82	61/41734 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	T	23	DC	C1'-N1	5.72	1.56	1.49

The worst 5 of 61 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	59	ILE	CB-CA-C	-9.58	92.45	111.60
12	T	24	DT	O4'-C1'-N1	9.42	114.59	108.00
1	A	885	THR	N-CA-CB	-9.25	92.73	110.30
2	B	974	PRO	N-CA-C	-9.20	88.18	112.10
12	T	25	DC	O4'-C1'-N1	9.20	114.44	108.00

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	11332	0	11392	764	1
2	B	9167	0	9178	660	0
3	C	2135	0	2090	155	1
4	E	1757	0	1781	55	0
5	F	684	0	703	27	0
6	H	1087	0	1062	46	0
7	I	971	0	929	30	0
8	J	532	0	545	55	0
9	K	919	0	929	57	0
10	L	363	0	387	24	0
11	R	260	0	132	22	0
12	T	566	0	316	15	0
13	N	284	0	161	3	0
14	A	2	0	0	3	0
14	B	1	0	0	2	0
14	C	1	0	0	0	0
14	I	2	0	0	0	0
14	J	1	0	0	2	0
14	L	1	0	0	0	0
15	A	1	0	0	0	0
16	R	1	0	0	0	0
All	All	30067	0	29605	1752	1

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 29.

The worst 5 of 1752 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:399:HIS:CG	1:A:400:PRO:HD3	1.52	1.43
2:B:439:ALA:CB	2:B:440:HIS:HA	1.41	1.42
1:A:399:HIS:CD2	1:A:400:PRO:HD3	1.62	1.34

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1081:LEU:CD2	1:A:1082:ASN:H	1.47	1.27
2:B:439:ALA:HB3	2:B:440:HIS:CA	1.66	1.24

All (1) 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:A:418:SER:OG	3:C:87:PHE:O[2_555]	2.17	0.03

## 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	1438/1733 (83%)	1054 (73%)	303 (21%)	81 (6%)	2	29
2	B	1145/1224 (94%)	855 (75%)	231 (20%)	59 (5%)	2	30
3	C	269/318 (85%)	207 (77%)	48 (18%)	14 (5%)	2	30
4	E	213/215 (99%)	175 (82%)	33 (16%)	5 (2%)	8	51
5	F	83/155 (54%)	66 (80%)	14 (17%)	3 (4%)	4	41
6	H	132/146 (90%)	104 (79%)	22 (17%)	6 (4%)	3	34
7	I	117/122 (96%)	84 (72%)	29 (25%)	4 (3%)	5	43
8	J	63/70 (90%)	48 (76%)	12 (19%)	3 (5%)	3	33
9	K	112/120 (93%)	86 (77%)	24 (21%)	2 (2%)	11	55
10	L	44/70 (63%)	31 (70%)	9 (20%)	4 (9%)	1	16
All	All	3616/4173 (87%)	2710 (75%)	725 (20%)	181 (5%)	3	32

5 of 181 Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	A	56	PRO
1	A	115	LEU
1	A	116	ASP
1	A	117	GLU
1	A	119	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	1258/1520 (83%)	1041 (83%)	217 (17%)	2	18
2	B	1000/1061 (94%)	822 (82%)	178 (18%)	2	17
3	C	238/274 (87%)	188 (79%)	50 (21%)	1	10
4	E	196/197 (100%)	174 (89%)	22 (11%)	7	38
5	F	74/137 (54%)	66 (89%)	8 (11%)	8	40
6	H	119/128 (93%)	107 (90%)	12 (10%)	9	43
7	I	113/116 (97%)	96 (85%)	17 (15%)	3	26
8	J	60/65 (92%)	48 (80%)	12 (20%)	1	12
9	K	99/102 (97%)	81 (82%)	18 (18%)	2	15
10	L	40/57 (70%)	31 (78%)	9 (22%)	1	9
All	All	3197/3657 (87%)	2654 (83%)	543 (17%)	2	19

5 of 543 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	253	THR
2	B	625	LYS
7	I	92	ARG
2	B	305	VAL
2	B	425	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	278	GLN
2	B	744	HIS
6	H	11	GLN
2	B	395	GLN
2	B	515	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	R	11/12 (91%)	3 (27%)	0

All (3) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	R	4	G
11	R	10	A
11	R	12	G

There are no RNA pucker outliers to report.

## 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 9 ligands modelled in this entry, 9 are 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 [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, 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	1442/1733 (83%)	-0.26	28 (1%) 70 54	72, 131, 247, 370	0
2	B	1153/1224 (94%)	-0.21	21 (1%) 71 56	71, 114, 240, 374	0
3	C	271/318 (85%)	-0.41	3 (1%) 82 69	80, 106, 165, 306	0
4	E	215/215 (100%)	-0.31	0 100 100	106, 165, 276, 316	0
5	F	85/155 (54%)	-0.34	0 100 100	107, 137, 170, 200	0
6	H	136/146 (93%)	-0.12	3 (2%) 65 49	126, 169, 276, 299	0
7	I	119/122 (97%)	-0.33	0 100 100	109, 150, 180, 237	0
8	J	65/70 (92%)	-0.48	0 100 100	80, 94, 135, 153	0
9	K	114/120 (95%)	-0.44	0 100 100	83, 112, 136, 139	0
10	L	46/70 (65%)	-0.17	1 (2%) 65 49	99, 175, 228, 246	0
11	R	12/12 (100%)	-0.49	0 100 100	104, 119, 182, 208	0
12	T	28/29 (96%)	-0.12	0 100 100	102, 222, 413, 422	0
13	N	14/14 (100%)	-0.13	0 100 100	270, 329, 352, 379	0
All	All	3700/4228 (87%)	-0.26	56 (1%) 76 62	71, 128, 251, 422	0

The worst 5 of 56 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1250	ALA	6.2
2	B	882	THR	6.0
1	A	1249	ASP	5.3
1	A	44	THR	5.2
2	B	441	ASP	5.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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
14	ZN	C	319	1/1	0.99	0.11	-0.43	118,118,118,118	0
14	ZN	I	203	1/1	0.99	0.09	-1.15	103,103,103,103	0
14	ZN	L	105	1/1	0.94	0.09	-1.18	155,155,155,155	0
14	ZN	B	1307	1/1	0.90	0.03	-1.27	163,163,163,163	0
14	ZN	I	204	1/1	0.98	0.06	-1.41	125,125,125,125	0
14	ZN	A	1734	1/1	0.92	0.04	-1.78	232,232,232,232	0
14	ZN	J	101	1/1	0.75	0.16	-2.00	218,218,218,218	0
14	ZN	A	1735	1/1	0.97	0.08	-	136,136,136,136	0
15	MG	A	1736	1/1	0.99	0.14	-	113,113,113,113	0

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

There are no such residues in this entry.