



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:04 PM GMT

PDB ID : 5C53  
Title : Probing the Structural and Molecular Basis of Nucleotide Selectivity by Human Mitochondrial DNA Polymerase gamma  
Authors : Sohl, C.D.; Szymanski, M.R.; Mislak, A.C.; Shumate, C.K.; Amiralaie, S.; Schinazi, R.F.; Anderson, K.S.; Yin, Y.W.  
Deposited on : 2015-06-19  
Resolution : 3.57 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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
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)	:	rb-20026982

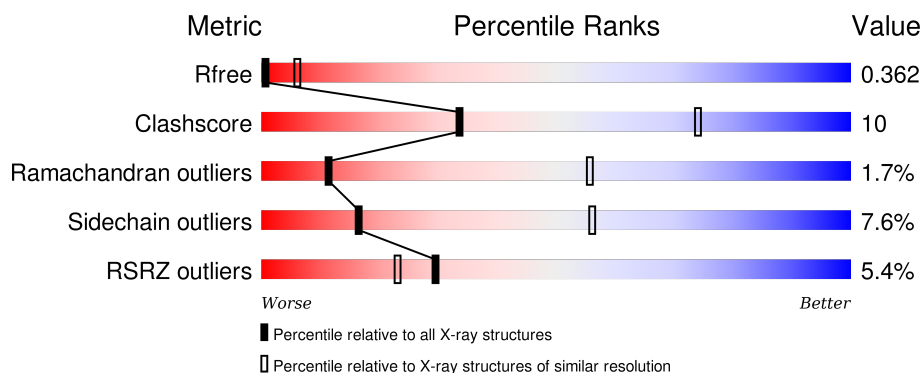
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.57 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	1240 (3.72-3.40)
Clashscore	102246	1057 (3.70-3.42)
Ramachandran outliers	100387	1017 (3.70-3.42)
Sidechain outliers	100360	1017 (3.70-3.42)
RSRZ outliers	91569	1247 (3.72-3.40)

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	1205	<div> <div>5%</div> <div> <div>56%</div> <div>21%</div> <div>•</div> <div>18%</div> </div> </div>
2	B	903	<div> <div>%</div> <div> <div>31%</div> <div>8%</div> <div>•</div> <div>60%</div> </div> </div>
2	C	903	<div> <div>3%</div> <div> <div>29%</div> <div>9%</div> <div>•</div> <div>60%</div> </div> </div>
3	T	26	<div> <div>12%</div> <div> <div>62%</div> <div>38%</div> </div> </div>
4	P	22	<div> <div>68%</div> <div> <div>27%</div> <div>5%</div> </div> </div>

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
6	4Y3	A	4003	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14634 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 polymerase subunit gamma-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	983	Total	C	N	O	S	0	0	0
			7799	4966	1371	1413	49			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098
A	?	-	GLN	deletion	UNP P54098

- Molecule 2 is a protein called Pol gamma B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	363	Total	C	N	O	S	0	0	0
			2942	1885	520	521	16			
2	C	358	Total	C	N	O	S	0	0	0
			2883	1850	506	511	16			

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	26	Total	C	N	O	P	0	0	0
			529	251	93	159	26			

- Molecule 4 is a DNA chain called DNA (5'-D(\*AP\*AP\*AP\*AP\*CP\*GP\*AP\*GP\*GP\*GP\*

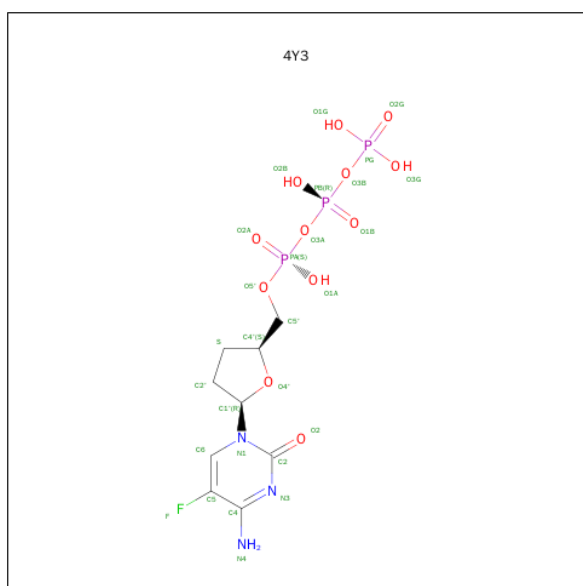
CP\*CP\*AP\*GP\*TP\*GP\*CP\*CP\*GP\*TP\*AP\*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	P	21	Total	C	N	O	P	0	0	0
			433	205	89	119	20			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

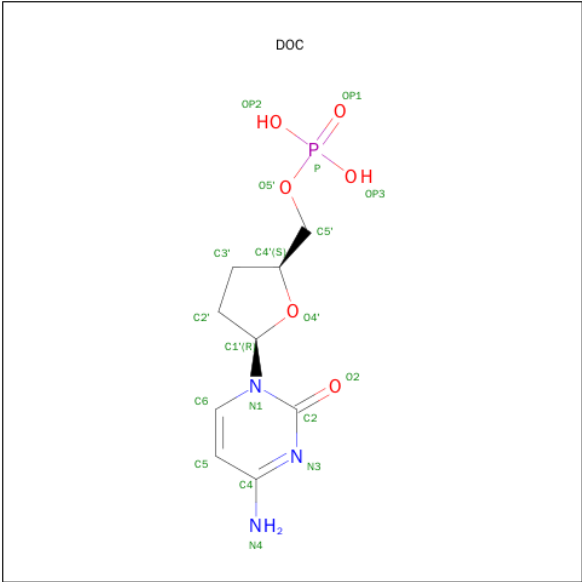
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is [[(2S,5R)-5-(4-azanyl-5-fluoranyl-2-oxidanylidene-pyrimidin-1-yl)oxolan-2-yl]methoxy-oxidanyl-phosphoryl] phosphono hydrogen phosphate (three-letter code: 4Y3) (formula: C<sub>9</sub>H<sub>15</sub>FN<sub>3</sub>O<sub>12</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	A	1	Total	C	F	N	O	P	0	0
			28	9	1	3	12	3		

- Molecule 7 is 2',3'-DIDEOXYCYTIDINE-5'-MONOPHOSPHATE (three-letter code: DOC) (formula: C<sub>9</sub>H<sub>14</sub>N<sub>3</sub>O<sub>6</sub>P).

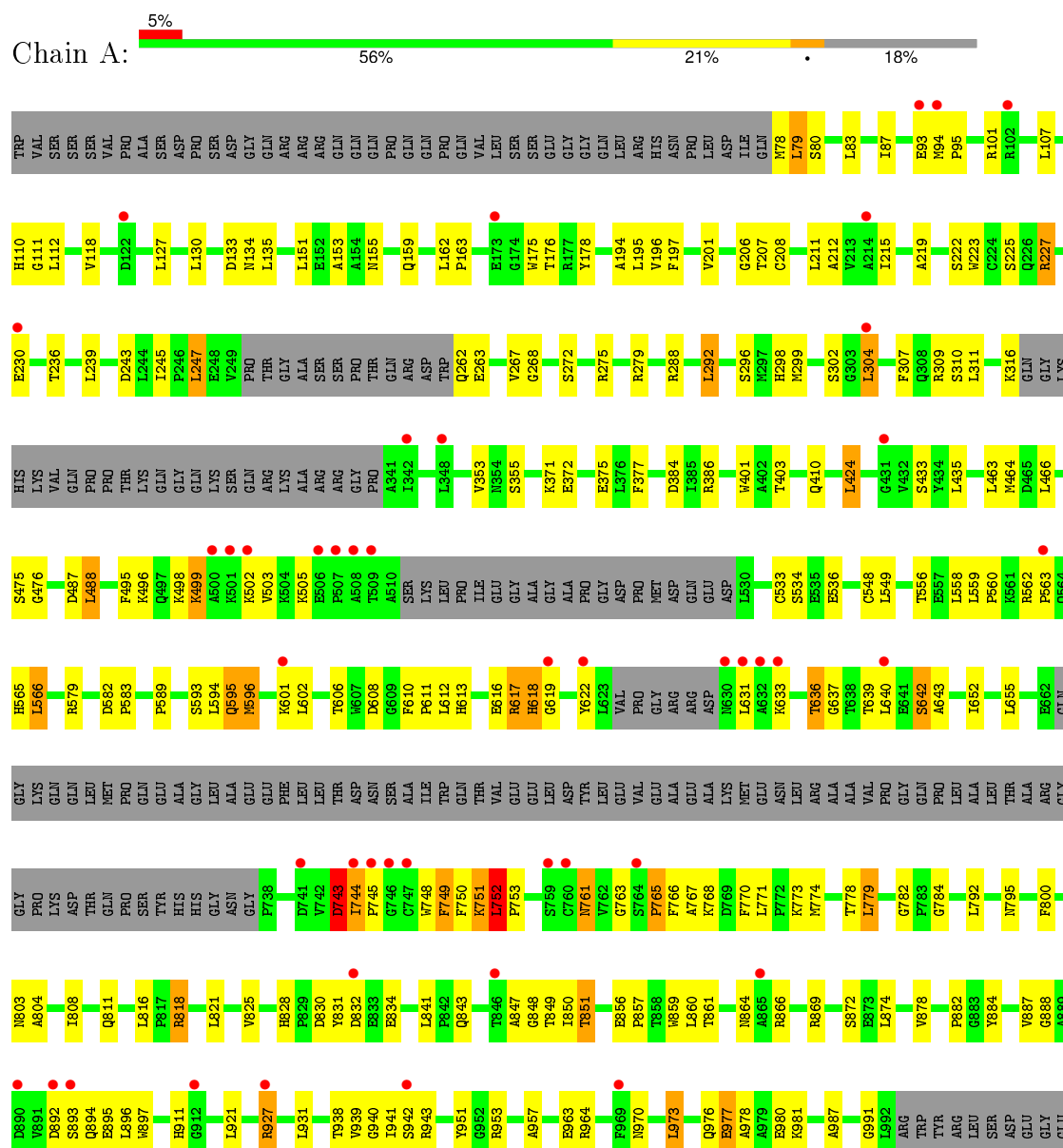


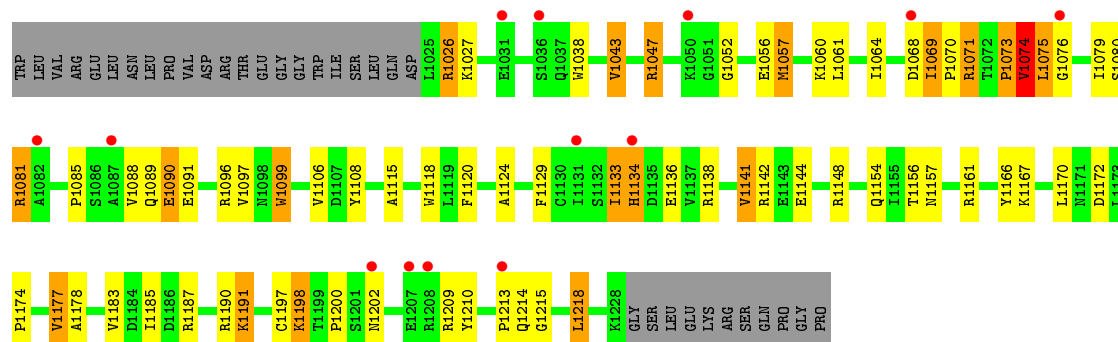
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
7	P	1	18	9	3	5	1	0	0

### 3 Residue-property plots

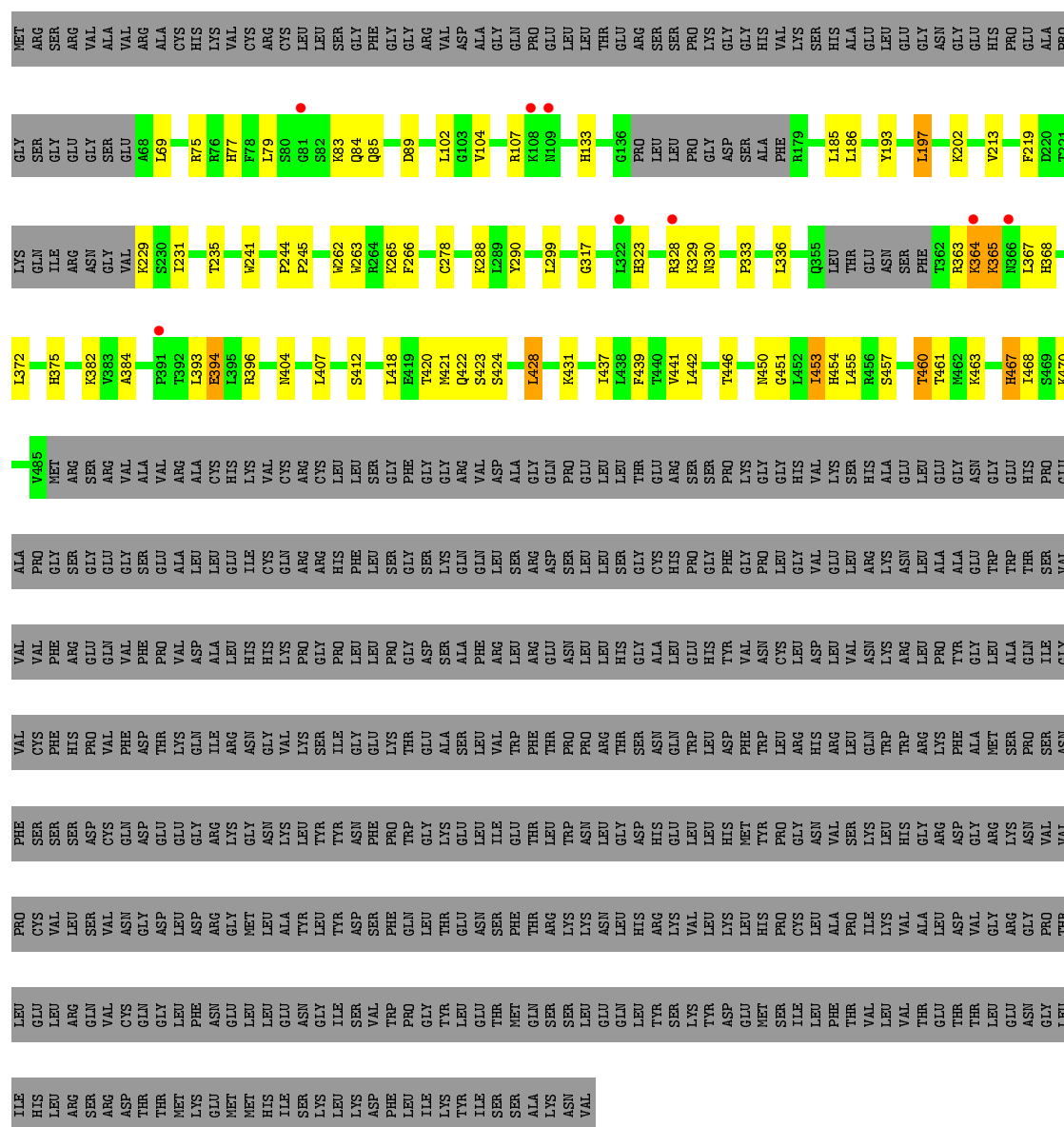
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: DNA polymerase subunit gamma-1



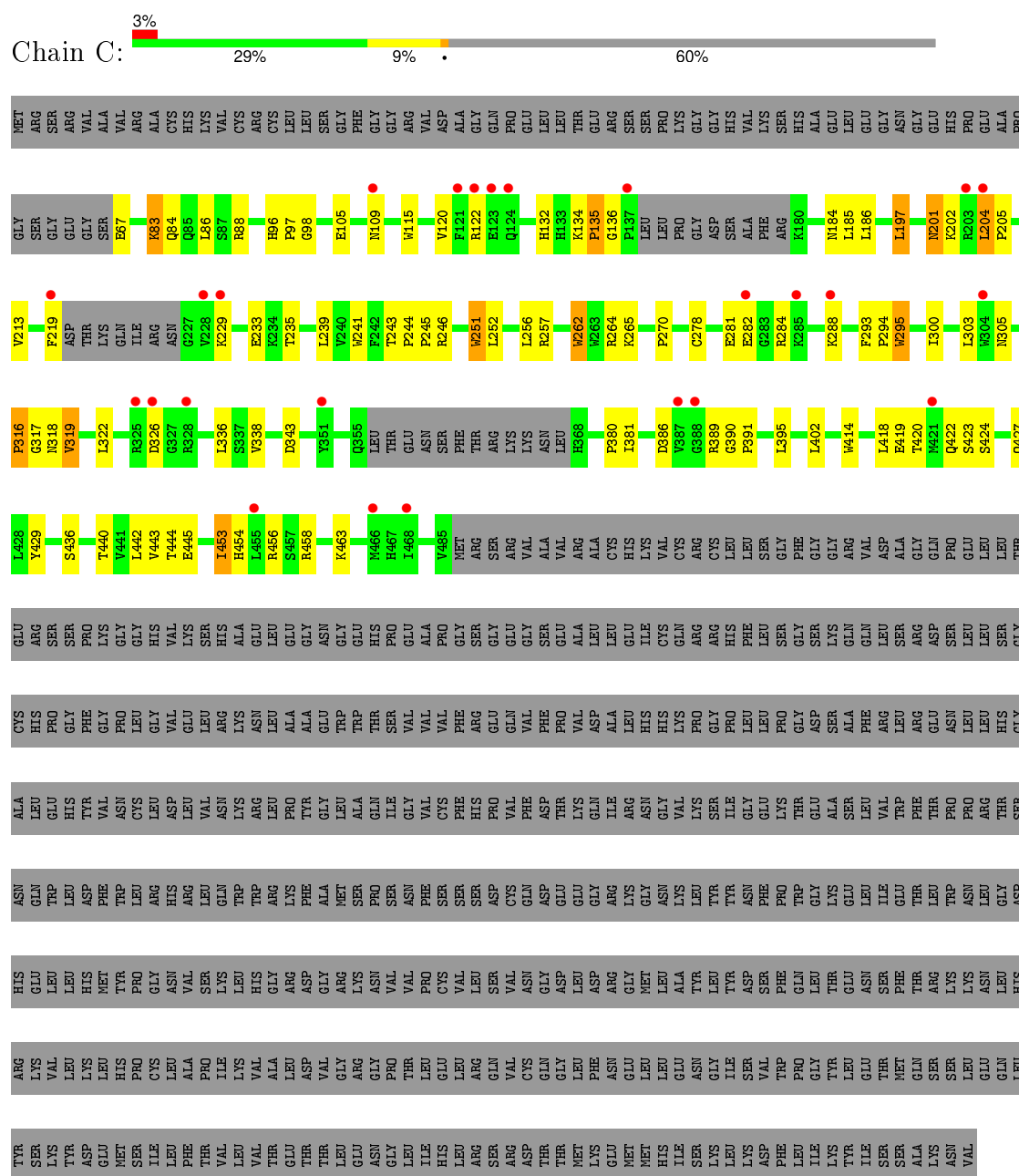


• Molecule 2: Pol gamma B

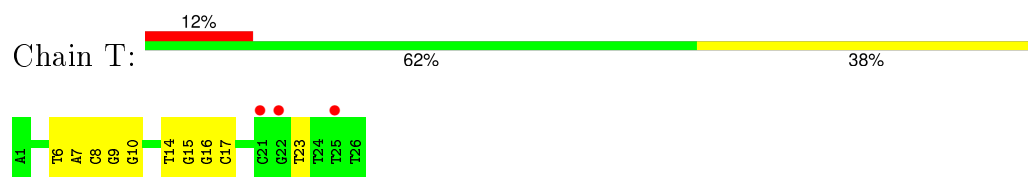


• Molecule 2: Pol gamma B



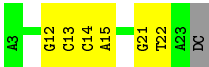


• Molecule 3: DNA (26-MER)



• Molecule 4: DNA (5'-D(\*AP\*AP\*AP\*AP\*CP\*GP\*AP\*GP\*GP\*GP\*CP\*CP\*AP\*GP\*TP\*GP\*CP\*CP\*GP\*TP\*AP\*C)-3')





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	217.45Å 217.45Å 163.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 3.57 48.91 – 3.57	Depositor EDS
% Data completeness (in resolution range)	99.0 (48.91-3.57) 85.1 (48.91-3.57)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 3.57Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.300 , 0.338 0.342 , 0.362	Depositor DCC
$R_{free}$ test set	2000 reflections (5.20%)	DCC
Wilson B-factor (Å <sup>2</sup> )	137.1	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 7.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 46866 reflections	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	14634	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.40% 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: DOC, MG, 4Y3

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	0.22	0/7999	0.43	1/10852 (0.0%)
2	B	0.22	0/3015	0.39	0/4074
2	C	0.23	0/2956	0.42	2/3997 (0.1%)
3	T	0.51	0/591	0.88	0/909
4	P	0.49	0/488	0.75	0/752
All	All	0.25	0/15049	0.47	3/20584 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	135	PRO	CA-N-CD	-8.64	99.41	111.50
2	C	96	HIS	C-N-CD	-7.46	104.20	120.60
1	A	752	LEU	C-N-CD	-6.44	106.44	120.60

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	7799	0	7692	184	0
2	B	2942	0	2937	44	0
2	C	2883	0	2858	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	T	529	0	291	10	0
4	P	433	0	234	6	0
5	A	2	0	0	0	0
6	A	28	0	11	4	0
7	P	18	0	12	1	0
All	All	14634	0	14035	292	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 10.

All (292) 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)
2:C:134:LYS:CD	2:C:135:PRO:HD3	1.82	1.08
2:C:135:PRO:HD2	2:C:136:GLY:H	1.11	1.06
2:C:134:LYS:HD2	2:C:135:PRO:CD	1.92	1.00
2:C:134:LYS:HD2	2:C:135:PRO:HD3	1.01	1.00
2:C:419:GLU:H	2:C:420:THR:HA	1.35	0.92
2:C:135:PRO:HD2	2:C:136:GLY:N	1.88	0.86
2:C:134:LYS:NZ	2:C:135:PRO:HD2	1.92	0.85
2:C:134:LYS:CD	2:C:135:PRO:CD	2.57	0.78
2:C:443:VAL:HG22	2:C:453:ILE:HD11	1.66	0.77
1:A:243:ASP:HB3	1:A:279:ARG:HE	1.49	0.77
2:C:135:PRO:CD	2:C:136:GLY:H	1.94	0.74
2:C:442:LEU:HB3	2:C:454:HIS:HB2	1.69	0.73
1:A:464:MET:HB2	1:A:589:PRO:HG2	1.71	0.73
1:A:487:ASP:OD2	1:A:601:LYS:NZ	2.22	0.72
1:A:849:THR:HG22	1:A:850:ILE:HD13	1.71	0.72
1:A:1068:ASP:HA	1:A:1085:PRO:HG2	1.72	0.71
2:C:134:LYS:HZ2	2:C:135:PRO:HD2	1.56	0.70
1:A:153:ALA:HB1	1:A:194:ALA:HB2	1.74	0.69
2:C:134:LYS:NZ	2:C:135:PRO:CD	2.55	0.69
1:A:938:THR:H	1:A:939:VAL:HA	1.61	0.66
2:B:77:HIS:HE1	2:B:431:LYS:HG3	1.61	0.65
1:A:1161:ARG:HE	1:A:1177:VAL:HG22	1.61	0.65
1:A:533:CYS:SG	1:A:534:SER:N	2.69	0.65
2:C:213:VAL:HG22	2:C:235:THR:HG22	1.77	0.65
1:A:856:GLU:OE1	1:A:859:TRP:N	2.26	0.65
2:B:197:LEU:HD22	2:B:202:LYS:HA	1.79	0.64
1:A:896:LEU:HD21	1:A:931:LEU:HD23	1.79	0.64
1:A:800:PHE:HB2	1:A:869:ARG:HE	1.63	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:83:LYS:HG2	2:C:84:GLN:HG2	1.79	0.64
2:C:134:LYS:HZ3	2:C:135:PRO:CD	2.11	0.63
1:A:230:GLU:OE2	1:A:386:ARG:NH1	2.32	0.62
2:B:442:LEU:HB3	2:B:454:HIS:HB2	1.82	0.62
1:A:1057:MET:SD	1:A:1057:MET:N	2.73	0.62
1:A:884:TYR:HA	1:A:1142:ARG:HA	1.80	0.62
1:A:850:ILE:HG22	3:T:6:DT:H4'	1.81	0.61
1:A:79:LEU:H	1:A:83:LEU:HG	1.65	0.61
2:C:135:PRO:CD	2:C:136:GLY:N	2.56	0.61
2:C:429:TYR:HE1	2:C:463:LYS:HZ3	1.47	0.60
1:A:963:GLU:HG3	1:A:981:LYS:HZ3	1.66	0.60
1:A:978:ALA:HA	1:A:981:LYS:HD2	1.83	0.60
1:A:1142:ARG:NH1	1:A:1144:GLU:OE1	2.34	0.59
1:A:502:LYS:HB3	1:A:503:VAL:HB	1.83	0.59
1:A:1108:TYR:OH	1:A:1161:ARG:NH1	2.34	0.59
1:A:744:ILE:HG23	1:A:745:PRO:HD3	1.83	0.59
1:A:1069:ILE:O	1:A:1071:ARG:N	2.35	0.59
1:A:743:ASP:OD1	1:A:743:ASP:N	2.36	0.59
2:B:75:ARG:NH1	2:B:84:GLN:OE1	2.35	0.59
1:A:134:ASN:ND2	1:A:1166:TYR:OH	2.32	0.59
1:A:938:THR:N	1:A:939:VAL:HA	2.16	0.59
1:A:463:LEU:HD21	1:A:594:LEU:HD23	1.84	0.58
2:C:219:PHE:HD1	2:C:229:LYS:HG2	1.69	0.58
1:A:107:LEU:O	1:A:112:LEU:N	2.36	0.57
1:A:208:CYS:SG	1:A:227:ARG:NH2	2.77	0.57
1:A:921:LEU:HD22	1:A:1174:PRO:HG2	1.86	0.57
2:C:197:LEU:HD12	2:C:202:LYS:HG2	1.86	0.57
1:A:831:TYR:H	1:A:832:ASP:HA	1.69	0.57
1:A:951:TYR:CD2	6:A:4003:4Y3:H7	2.40	0.57
2:B:363:ARG:HD3	2:B:364:LYS:H	1.70	0.56
2:B:428:LEU:HD13	2:B:428:LEU:H	1.70	0.56
1:A:887:VAL:HG22	1:A:1185:ILE:HG23	1.87	0.56
1:A:488:LEU:H	1:A:488:LEU:HD13	1.69	0.55
2:B:185:LEU:H	2:B:185:LEU:HD23	1.71	0.55
2:C:319:VAL:HA	2:C:322:LEU:HD13	1.88	0.55
1:A:1079:ILE:HG12	1:A:1099:TRP:CZ3	2.42	0.55
1:A:869:ARG:NH1	4:P:22:DT:OP1	2.41	0.54
2:B:104:VAL:HG23	2:B:107:ARG:HH21	1.72	0.54
1:A:1073:PRO:HA	1:A:1074:VAL:HG13	1.89	0.54
1:A:162:LEU:HG	1:A:401:TRP:CZ3	2.42	0.54
1:A:1096:ARG:HA	1:A:1099:TRP:HB3	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:278:CYS:SG	2:C:288:LYS:NZ	2.81	0.54
1:A:239:LEU:O	1:A:279:ARG:NH1	2.41	0.54
2:B:241:TRP:HB3	2:B:336:LEU:HB3	1.90	0.54
1:A:466:LEU:HB3	1:A:602:LEU:HD21	1.89	0.53
2:B:323:HIS:HB3	2:B:330:ASN:HB2	1.90	0.53
2:C:424:SER:HB3	2:C:427:GLN:HG2	1.90	0.53
1:A:861:THR:HG21	3:T:8:DC:H1'	1.91	0.52
2:B:262:TRP:HA	2:B:265:LYS:HE2	1.91	0.52
2:C:184:ASN:OD1	2:C:185:LEU:N	2.41	0.52
1:A:1089:GLN:N	1:A:1090:GLU:HA	2.24	0.52
1:A:911:HIS:NE2	1:A:1172:ASP:O	2.37	0.52
1:A:977:GLU:HB3	1:A:981:LYS:HZ2	1.74	0.52
1:A:761:ASN:N	1:A:761:ASN:OD1	2.43	0.52
1:A:549:LEU:HD11	2:B:468:ILE:HG21	1.92	0.52
1:A:752:LEU:HB2	1:A:753:PRO:HA	1.90	0.52
1:A:834:GLU:HG3	2:B:328:ARG:HH21	1.75	0.52
1:A:353:VAL:HG13	1:A:355:SER:H	1.75	0.52
1:A:895:GLU:CG	6:A:4003:4Y3:H4	2.23	0.52
2:C:419:GLU:N	2:C:420:THR:HA	2.07	0.52
2:B:83:LYS:HG2	2:B:85:GLN:H	1.74	0.51
1:A:196:VAL:HG22	1:A:215:ILE:HG12	1.93	0.51
1:A:866:ARG:HH21	1:A:869:ARG:HD2	1.75	0.51
1:A:562:ARG:HH11	1:A:563:PRO:HD2	1.74	0.51
1:A:622:TYR:HB2	1:A:770:PHE:HE2	1.75	0.51
1:A:93:GLU:HA	1:A:94:MET:HB2	1.93	0.51
1:A:296:SER:HB2	1:A:847:ALA:HB3	1.93	0.51
1:A:212:ALA:HB3	1:A:223:TRP:HB3	1.92	0.51
1:A:1061:LEU:HB3	1:A:1097:VAL:HG13	1.92	0.51
1:A:495:PHE:HB3	1:A:496:LYS:HB2	1.92	0.51
2:B:407:LEU:HD13	2:C:120:VAL:HG12	1.92	0.51
2:C:262:TRP:HA	2:C:265:LYS:HE2	1.93	0.51
1:A:299:MET:HG2	1:A:848:GLY:HA2	1.93	0.51
2:B:365:LYS:H	2:B:365:LYS:HD2	1.75	0.50
2:B:219:PHE:HA	2:B:229:LYS:N	2.27	0.50
2:C:444:THR:OG1	2:C:445:GLU:OE2	2.28	0.50
1:A:963:GLU:HG3	1:A:981:LYS:NZ	2.27	0.50
1:A:1200:PRO:O	1:A:1202:ASN:N	2.44	0.50
2:C:252:LEU:HD22	2:C:305:ASN:HB2	1.93	0.50
2:C:389:ARG:HD3	2:C:395:LEU:HD11	1.93	0.50
2:B:404:ASN:HA	2:B:407:LEU:HG	1.93	0.50
2:C:444:THR:OG1	2:C:445:GLU:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:134:LYS:HZ3	2:C:135:PRO:HD2	1.70	0.49
2:B:393:LEU:HD12	2:B:394:GLU:HG2	1.93	0.49
1:A:262:GLN:HB2	1:A:263:GLU:HG2	1.94	0.49
2:C:201:ASN:ND2	2:C:201:ASN:O	2.42	0.49
2:C:134:LYS:CG	2:C:135:PRO:CD	2.91	0.49
1:A:750:PHE:HD1	1:A:751:LYS:HG2	1.76	0.49
1:A:608:ASP:OD1	1:A:778:THR:OG1	2.29	0.49
1:A:1088:VAL:HG12	1:A:1090:GLU:HA	1.94	0.49
1:A:556:THR:HA	1:A:559:LEU:HD13	1.95	0.49
2:C:241:TRP:HD1	2:C:336:LEU:HD22	1.77	0.49
2:C:205:PRO:HB3	2:C:243:THR:HA	1.95	0.49
1:A:94:MET:HG3	1:A:1170:LEU:HD11	1.95	0.49
1:A:953:ARG:HG3	1:A:957:ALA:HB2	1.93	0.49
1:A:1115:ALA:HB3	1:A:1156:THR:HG23	1.95	0.49
1:A:987:ALA:HB1	1:A:1056:GLU:HG2	1.95	0.49
1:A:275:ARG:NH2	1:A:433:SER:O	2.42	0.49
2:B:441:VAL:HG23	2:B:453:ILE:HG13	1.94	0.48
1:A:856:GLU:H	1:A:860:LEU:HD12	1.78	0.48
2:C:436:SER:OG	2:C:458:ARG:NH1	2.46	0.48
1:A:1075:LEU:HD23	1:A:1075:LEU:H	1.78	0.48
2:B:457:SER:OG	2:B:460:THR:O	2.32	0.48
1:A:1154:GLN:HG3	1:A:1218:LEU:HD21	1.95	0.48
2:C:134:LYS:HG3	2:C:135:PRO:HD2	1.96	0.48
2:B:213:VAL:HA	2:B:235:THR:HA	1.95	0.48
2:B:384:ALA:HB2	2:B:437:ILE:HD13	1.94	0.48
2:C:105:GLU:O	2:C:109:ASN:ND2	2.43	0.48
1:A:869:ARG:HB2	1:A:872:SER:HB2	1.96	0.48
1:A:825:VAL:HG13	1:A:882:PRO:HG2	1.95	0.48
1:A:175:TRP:CD2	1:A:223:TRP:HB2	2.48	0.48
1:A:991:GLY:HA2	1:A:1052:GLY:HA2	1.96	0.48
1:A:1134:HIS:HD2	7:P:101:DOC:H1'	1.78	0.48
1:A:616:GLU:HB2	1:A:617:ARG:HD3	1.96	0.48
2:C:317:GLY:HA3	2:C:318:ASN:HA	1.58	0.48
1:A:849:THR:OG1	3:T:7:DA:OP1	2.23	0.47
1:A:803:ASN:HA	3:T:10:DG:H4'	1.95	0.47
1:A:887:VAL:HG13	1:A:1185:ILE:HG12	1.95	0.47
1:A:178:TYR:O	1:A:219:ALA:HB1	2.14	0.47
1:A:475:SER:HA	1:A:476:GLY:HA2	1.49	0.47
1:A:1183:VAL:HB	1:A:1214:GLN:HB3	1.96	0.47
1:A:1183:VAL:N	1:A:1214:GLN:O	2.47	0.47
1:A:1090:GLU:O	1:A:1091:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:611:PRO:HG3	1:A:652:ILE:HD13	1.97	0.47
2:C:235:THR:OG1	2:C:343:ASP:OD1	2.29	0.47
1:A:272:SER:HB3	1:A:843:GLN:HA	1.97	0.46
1:A:804:ALA:O	1:A:808:ILE:HG12	2.14	0.46
1:A:642:SER:HA	1:A:643:ALA:HA	1.58	0.46
1:A:765:PRO:HA	1:A:766:PHE:HA	1.58	0.46
2:C:246:ARG:NH2	2:C:326:ASP:OD2	2.46	0.46
2:B:428:LEU:HA	2:B:431:LYS:HB3	1.96	0.46
1:A:939:VAL:HA	1:A:940:GLY:HA3	1.71	0.46
1:A:593:SER:HB2	1:A:596:MET:HB2	1.97	0.46
1:A:866:ARG:HE	1:A:869:ARG:HD2	1.79	0.46
1:A:135:LEU:HD23	1:A:135:LEU:H	1.79	0.46
1:A:977:GLU:HB3	1:A:981:LYS:NZ	2.31	0.46
4:P:14:DC:H2'	4:P:15:DA:C8	2.50	0.46
1:A:897:TRP:CD1	1:A:1177:VAL:HG21	2.50	0.46
1:A:636:THR:OG1	1:A:637:GLY:N	2.49	0.46
2:B:193:TYR:OH	2:B:333:PRO:HG3	2.15	0.46
1:A:888:GLY:HA3	1:A:1138:ARG:HD2	1.97	0.46
1:A:302:SER:HB2	1:A:1081:ARG:HD3	1.96	0.46
2:B:266:PHE:HA	2:B:375:HIS:CD2	2.51	0.46
1:A:606:THR:HB	1:A:612:LEU:HD13	1.97	0.46
2:B:197:LEU:HA	2:B:197:LEU:HD23	1.84	0.45
2:B:364:LYS:HB2	2:B:364:LYS:HE2	1.65	0.45
1:A:618:HIS:CD2	1:A:619:GLY:H	2.34	0.45
3:T:16:DG:H1	4:P:13:DC:H42	1.63	0.45
2:C:381:ILE:HG21	2:C:414:TRP:HB2	1.97	0.45
2:B:278:CYS:SG	2:B:288:LYS:NZ	2.87	0.45
1:A:942:SER:HA	1:A:943:ARG:HA	1.58	0.45
2:B:420:THR:HG23	2:B:421:MET:HG2	1.99	0.45
2:B:467:HIS:HB3	2:B:470:LYS:HB2	1.97	0.45
1:A:617:ARG:HB2	1:A:763:GLY:HA3	1.99	0.45
1:A:894:GLN:HG3	1:A:895:GLU:H	1.81	0.45
1:A:384:ASP:OD1	1:A:384:ASP:N	2.42	0.45
1:A:262:GLN:HA	1:A:263:GLU:HA	1.51	0.45
1:A:110:HIS:HB3	1:A:111:GLY:HA2	1.98	0.45
1:A:778:THR:HA	1:A:779:LEU:HA	1.61	0.45
1:A:435:LEU:HD22	1:A:878:VAL:HG11	1.98	0.45
2:B:244:PRO:HA	2:B:245:PRO:HD3	1.86	0.45
1:A:895:GLU:CD	6:A:4003:4Y3:H4	2.21	0.45
1:A:976:GLN:O	1:A:980:GLU:HG2	2.17	0.45
2:C:67:GLU:N	2:C:88:ARG:HH21	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:389:ARG:HB3	2:C:395:LEU:HD11	1.98	0.44
1:A:1124:ALA:O	1:A:1148:ARG:NH2	2.44	0.44
1:A:1214:GLN:HA	1:A:1215:GLY:HA3	1.58	0.44
1:A:268:GLY:HA2	1:A:403:THR:HG21	1.99	0.44
2:C:293:PHE:HB3	2:C:295:TRP:H	1.82	0.44
1:A:307:PHE:O	1:A:310:SER:OG	2.34	0.44
2:B:454:HIS:ND1	2:B:463:LYS:HE3	2.33	0.44
1:A:808:ILE:HD12	1:A:874:LEU:HG	1.99	0.44
1:A:612:LEU:HA	1:A:612:LEU:HD12	1.76	0.44
1:A:372:GLU:HG3	1:A:375:GLU:H	1.82	0.44
1:A:856:GLU:HA	1:A:857:PRO:HD3	1.85	0.44
1:A:162:LEU:HD22	1:A:163:PRO:HD2	1.99	0.44
2:B:421:MET:HA	2:B:422:GLN:HB3	1.99	0.44
1:A:582:ASP:HA	1:A:583:PRO:HD3	1.90	0.44
2:C:239:LEU:HB3	2:C:338:VAL:HB	1.99	0.44
2:B:365:LYS:HG2	2:B:367:LEU:H	1.82	0.44
1:A:1133:ILE:HG12	1:A:1136:GLU:HB3	1.98	0.44
2:C:303:LEU:HD22	2:C:338:VAL:HG22	2.00	0.44
1:A:579:ARG:NH1	4:P:12:DG:OP1	2.51	0.44
1:A:1187:ARG:HH11	1:A:1209:ARG:HH12	1.66	0.44
1:A:267:VAL:HG12	1:A:292:LEU:HB3	1.98	0.44
1:A:536:GLU:HG3	2:C:257:ARG:HH12	1.82	0.43
1:A:773:LYS:HD2	1:A:773:LYS:HA	1.89	0.43
1:A:892:ASP:HA	1:A:893:SER:HA	1.66	0.43
1:A:856:GLU:N	1:A:860:LEU:HD12	2.33	0.43
1:A:566:LEU:HD13	1:A:566:LEU:H	1.81	0.43
1:A:973:LEU:HD21	1:A:976:GLN:HG3	1.99	0.43
1:A:895:GLU:HG3	6:A:4003:4Y3:H4	1.81	0.43
1:A:1047:ARG:H	1:A:1047:ARG:HG3	1.64	0.43
1:A:505:LYS:HD3	1:A:505:LYS:HA	1.78	0.43
2:C:134:LYS:CE	2:C:135:PRO:HD3	2.47	0.43
2:C:419:GLU:OE2	2:C:422:GLN:HB2	2.18	0.43
1:A:831:TYR:N	1:A:832:ASP:HA	2.30	0.43
3:T:9:DG:H2'	3:T:10:DG:C8	2.53	0.43
2:C:316:PRO:HA	2:C:317:GLY:HA2	1.57	0.43
2:C:134:LYS:HG3	2:C:135:PRO:CD	2.49	0.43
4:P:21:DG:H2'	4:P:22:DT:C6	2.53	0.43
1:A:1079:ILE:HG12	1:A:1099:TRP:CE3	2.54	0.43
1:A:1198:LYS:HB3	1:A:1198:LYS:HE3	1.81	0.43
2:B:418:LEU:HD22	2:C:204:LEU:HD12	1.99	0.43
3:T:17:DC:H42	4:P:12:DG:H1	1.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1026:ARG:HD2	1:A:1026:ARG:O	2.20	0.42
1:A:498:LYS:HD3	3:T:23:DT:OP1	2.19	0.42
1:A:864:ASN:HB3	1:A:1191:LYS:HD3	2.01	0.42
1:A:782:GLY:HA2	1:A:784:GLY:HA2	2.01	0.42
1:A:1060:LYS:HE2	1:A:1064:ILE:HD11	2.01	0.42
2:C:205:PRO:HB3	2:C:244:PRO:HD3	2.01	0.42
1:A:963:GLU:HA	1:A:981:LYS:HE2	2.02	0.42
2:C:243:THR:HG1	2:C:251:TRP:HE3	1.64	0.42
1:A:155:ASN:O	1:A:159:GLN:HG2	2.20	0.42
1:A:299:MET:SD	1:A:849:THR:HG23	2.59	0.42
1:A:206:GLY:HA3	1:A:207:THR:HA	1.82	0.42
2:B:133:HIS:ND1	2:C:233:GLU:OE2	2.51	0.42
1:A:828:HIS:O	1:A:830:ASP:N	2.45	0.41
1:A:87:ILE:HD13	1:A:127:LEU:HD22	2.01	0.41
1:A:79:LEU:HD13	1:A:80:SER:H	1.84	0.41
1:A:818:ARG:H	1:A:818:ARG:HE	1.68	0.41
1:A:288:ARG:HA	1:A:288:ARG:HE	1.86	0.41
1:A:176:THR:OG1	1:A:222:SER:OG	2.36	0.41
2:B:213:VAL:HG11	2:C:132:HIS:CE1	2.55	0.41
1:A:298:HIS:HB2	1:A:410:GLN:HE22	1.85	0.41
1:A:371:LYS:HA	1:A:371:LYS:HD2	1.97	0.41
1:A:595:GLN:OE1	1:A:795:ASN:ND2	2.37	0.41
1:A:247:LEU:H	1:A:247:LEU:HD13	1.85	0.41
3:T:14:DT:H2''	3:T:15:DG:C8	2.55	0.41
2:C:418:LEU:N	2:C:419:GLU:HA	2.36	0.41
1:A:78:MET:HA	1:A:79:LEU:HA	1.77	0.41
2:C:389:ARG:HG2	2:C:390:GLY:N	2.35	0.41
1:A:850:ILE:HA	1:A:851:THR:HA	1.76	0.41
3:T:6:DT:H2'	3:T:7:DA:O4'	2.20	0.41
1:A:1074:VAL:HB	1:A:1167:LYS:HB3	2.01	0.41
2:B:439:PHE:HB3	2:B:455:LEU:HD11	2.03	0.41
1:A:499:LYS:H	1:A:499:LYS:HG3	1.59	0.41
1:A:851:THR:O	1:A:1106:VAL:HG21	2.21	0.41
1:A:864:ASN:O	1:A:872:SER:OG	2.38	0.41
1:A:1075:LEU:HB2	1:A:1076:GLY:HA3	2.02	0.41
2:C:440:THR:OG1	2:C:456:ARG:HB3	2.20	0.41
2:B:79:LEU:HG	2:B:102:LEU:HB2	2.03	0.41
1:A:1064:ILE:HG22	1:A:1071:ARG:HB3	2.03	0.41
1:A:749:PHE:HB2	1:A:750:PHE:H	1.60	0.41
2:C:264:ARG:HG3	2:C:270:PRO:HB3	2.02	0.41
1:A:225:SER:HB3	1:A:227:ARG:NH2	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1213:PRO:O	1:A:1214:GLN:NE2	2.54	0.40
1:A:211:LEU:HD12	1:A:377:PHE:HZ	1.86	0.40
1:A:502:LYS:HA	1:A:503:VAL:HA	1.94	0.40
2:C:293:PHE:N	2:C:294:PRO:HA	2.37	0.40
2:B:382:LYS:H	2:B:412:SER:HB2	1.86	0.40
1:A:299:MET:HG3	1:A:849:THR:HG23	2.03	0.40
1:A:771:LEU:HD21	1:A:792:LEU:HB3	2.02	0.40
1:A:304:LEU:HD13	1:A:309:ARG:HG2	2.02	0.40
1:A:151:LEU:HA	1:A:151:LEU:HD23	1.95	0.40
1:A:1157:ASN:ND2	1:A:1178:ALA:O	2.55	0.40
1:A:175:TRP:CE3	1:A:223:TRP:HB2	2.57	0.40
1:A:631:LEU:HB3	1:A:633:LYS:NZ	2.35	0.40
2:B:446:THR:O	2:B:450:ASN:ND2	2.53	0.40
2:C:244:PRO:HA	2:C:245:PRO:HD3	1.81	0.40
1:A:1136:GLU:OE2	1:A:1138:ARG:NH1	2.55	0.40
1:A:151:LEU:HD21	1:A:424:LEU:HD11	2.04	0.40
2:B:290:TYR:HD1	2:B:299:LEU:HA	1.87	0.40
2:B:423:SER:OG	2:B:424:SER:N	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	969/1205 (80%)	835 (86%)	114 (12%)	20 (2%)	9	52
2	B	355/903 (39%)	326 (92%)	27 (8%)	2 (1%)	30	74
2	C	350/903 (39%)	325 (93%)	18 (5%)	7 (2%)	9	53
All	All	1674/3011 (56%)	1486 (89%)	159 (10%)	29 (2%)	11	56

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	752	LEU
1	A	1070	PRO
2	C	97	PRO
1	A	749	PHE
1	A	1177	VAL
2	C	98	GLY
2	C	423	SER
1	A	642	SER
1	A	767	ALA
1	A	1073	PRO
1	A	1080	SER
1	A	1134	HIS
2	C	316	PRO
2	C	319	VAL
2	C	391	PRO
1	A	95	PRO
1	A	610	PHE
1	A	618	HIS
1	A	811	GLN
1	A	927	ARG
1	A	1074	VAL
1	A	743	ASP
1	A	765	PRO
2	B	317	GLY
2	C	380	PRO
2	B	451	GLY
1	A	560	PRO
1	A	1043	VAL
1	A	1141	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	823/1017 (81%)	749 (91%)	74 (9%)	12	49
2	B	325/791 (41%)	307 (94%)	18 (6%)	27	68
2	C	316/791 (40%)	297 (94%)	19 (6%)	24	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	1464/2599 (56%)	1353 (92%)	111 (8%)	16	56

All (111) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	LEU
1	A	101	ARG
1	A	118	VAL
1	A	130	LEU
1	A	133	ASP
1	A	195	LEU
1	A	197	PHE
1	A	201	VAL
1	A	227	ARG
1	A	236	THR
1	A	245	ILE
1	A	247	LEU
1	A	292	LEU
1	A	304	LEU
1	A	311	LEU
1	A	316	LYS
1	A	424	LEU
1	A	488	LEU
1	A	499	LYS
1	A	548	CYS
1	A	558	LEU
1	A	565	HIS
1	A	566	LEU
1	A	595	GLN
1	A	596	MET
1	A	613	HIS
1	A	617	ARG
1	A	636	THR
1	A	639	THR
1	A	640	LEU
1	A	655	LEU
1	A	743	ASP
1	A	744	ILE
1	A	748	TRP
1	A	751	LYS
1	A	761	ASN
1	A	768	LYS

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Mol	Chain	Res	Type
1	A	774	MET
1	A	779	LEU
1	A	816	LEU
1	A	818	ARG
1	A	821	LEU
1	A	841	LEU
1	A	851	THR
1	A	927	ARG
1	A	941	ILE
1	A	964	ARG
1	A	970	ASN
1	A	973	LEU
1	A	977	GLU
1	A	1026	ARG
1	A	1027	LYS
1	A	1038	TRP
1	A	1043	VAL
1	A	1047	ARG
1	A	1057	MET
1	A	1069	ILE
1	A	1071	ARG
1	A	1074	VAL
1	A	1075	LEU
1	A	1081	ARG
1	A	1090	GLU
1	A	1099	TRP
1	A	1118	TRP
1	A	1120	PHE
1	A	1129	PHE
1	A	1133	ILE
1	A	1141	VAL
1	A	1190	ARG
1	A	1191	LYS
1	A	1197	CYS
1	A	1198	LYS
1	A	1210	TYR
1	A	1218	LEU
2	B	69	LEU
2	B	89	ASP
2	B	186	LEU
2	B	197	LEU
2	B	231	ILE

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Mol	Chain	Res	Type
2	B	263	TRP
2	B	329	LYS
2	B	364	LYS
2	B	365	LYS
2	B	368	HIS
2	B	372	LEU
2	B	394	GLU
2	B	396	ARG
2	B	428	LEU
2	B	453	ILE
2	B	460	THR
2	B	461	THR
2	B	467	HIS
2	C	83	LYS
2	C	86	LEU
2	C	115	TRP
2	C	122	ARG
2	C	186	LEU
2	C	197	LEU
2	C	201	ASN
2	C	204	LEU
2	C	251	TRP
2	C	256	LEU
2	C	262	TRP
2	C	281	GLU
2	C	282	GLU
2	C	284	ARG
2	C	295	TRP
2	C	300	ILE
2	C	386	ASP
2	C	402	LEU
2	C	453	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	264	GLN
1	A	1134	HIS
2	C	96	HIS



### 5.3.3 RNA ⓘ

There are no RNA molecules 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 4 ligands modelled in this entry, 2 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	$\# Z  > 2$
6	4Y3	A	4003	5	21,29,29	3.28	5 (23%)	22,45,45	1.32	2 (9%)
7	DOC	P	101	4	12,19,20	0.79	0	14,26,29	0.45	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
6	4Y3	A	4003	5	-	0/18/31/31	0/2/2/2
7	DOC	P	101	4	-	0/3/18/19	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	4003	4Y3	C2'-C1'	-8.07	1.33	1.51
6	A	4003	4Y3	O4'-C4'	-6.83	1.29	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	4003	4Y3	C2-N3	-2.24	1.33	1.38
6	A	4003	4Y3	C4-N4	4.45	1.46	1.34
6	A	4003	4Y3	O4'-C1'	8.50	1.62	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	4003	4Y3	N4-C4-N3	2.41	120.46	116.92
6	A	4003	4Y3	S-C2'-C1'	3.36	106.55	102.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	4003	4Y3	4	0
7	P	101	DOC	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	983/1205 (81%)	0.31	58 (5%) 26 20	44, 73, 91, 163	0
2	B	363/903 (40%)	0.21	8 (2%) 65 55	47, 65, 87, 101	0
2	C	358/903 (39%)	0.32	25 (6%) 19 15	54, 73, 86, 96	0
3	T	26/26 (100%)	0.72	3 (11%) 6 6	84, 107, 126, 131	0
4	P	21/22 (95%)	0.16	0 100 100	92, 105, 127, 166	0
All	All	1751/3059 (57%)	0.30	94 (5%) 29 23	44, 72, 94, 166	0

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	745	PRO	11.2
1	A	630	ASN	9.4
1	A	746	GLY	9.0
1	A	747	CYS	7.9
1	A	632	ALA	6.6
2	C	282	GLU	5.8
1	A	501	LYS	5.6
1	A	631	LEU	5.5
1	A	744	ILE	5.2
2	C	228	VAL	5.0
1	A	622	TYR	4.5
1	A	500	ALA	4.5
1	A	509	THR	4.4
1	A	741	ASP	4.4
2	B	366	ASN	4.3
1	A	619	GLY	4.1
1	A	508	ALA	4.1
2	C	121	PHE	4.0
1	A	1202	ASN	3.8
1	A	865	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	640	LEU	3.7
1	A	230	GLU	3.7
1	A	506	GLU	3.5
1	A	1031	GLU	3.4
1	A	102	ARG	3.4
1	A	759	SER	3.4
2	C	123	GLU	3.3
1	A	1087	ALA	3.3
1	A	214	ALA	3.2
1	A	1207	GLU	3.1
1	A	94	MET	3.1
1	A	507	PRO	3.1
1	A	431	GLY	3.1
2	C	325	ARG	3.0
2	B	328	ARG	3.0
1	A	760	CYS	3.0
2	C	288	LYS	2.9
1	A	601	LYS	2.9
1	A	764	SER	2.8
2	C	124	GLN	2.8
2	C	229	LYS	2.8
2	C	328	ARG	2.8
2	B	322	LEU	2.8
2	C	421	MET	2.8
1	A	969	PHE	2.8
2	B	108	LYS	2.7
1	A	633	LYS	2.7
2	C	388	GLY	2.6
2	C	455	LEU	2.6
2	C	468	ILE	2.6
1	A	1213	PRO	2.6
2	C	304	TRP	2.6
2	C	351	TYR	2.6
2	C	204	LEU	2.6
1	A	1082	ALA	2.6
1	A	893	SER	2.5
2	C	466	MET	2.5
1	A	173	GLU	2.5
1	A	502	LYS	2.5
2	C	137	PRO	2.5
2	C	122	ARG	2.5
3	T	25	DT	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1208	ARG	2.5
1	A	1076	GLY	2.4
2	C	285	LYS	2.4
1	A	846	THR	2.4
2	C	219	PHE	2.3
2	B	81	GLY	2.3
1	A	890	ASP	2.3
1	A	304	LEU	2.3
1	A	927	ARG	2.3
2	B	109	ASN	2.3
1	A	1134	HIS	2.2
1	A	342	ILE	2.2
1	A	1050	LYS	2.2
1	A	563	PRO	2.2
1	A	348	LEU	2.2
1	A	832	ASP	2.2
1	A	942	SER	2.2
2	B	391	PRO	2.2
2	C	387	VAL	2.1
1	A	1036	SER	2.1
1	A	912	GLY	2.1
1	A	122	ASP	2.1
2	C	326	ASP	2.1
3	T	22	DG	2.1
2	C	203	ARG	2.1
1	A	1068	ASP	2.1
1	A	892	ASP	2.0
1	A	93	GLU	2.0
2	C	109	ASN	2.0
3	T	21	DC	2.0
1	A	1131	ILE	2.0
2	B	364	LYS	2.0

## 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
6	4Y3	A	4003	28/28	0.83	0.42	0.89	80,100,106,107	0
7	DOC	P	101	18/19	0.84	0.35	0.03	91,94,98,99	0
5	MG	A	4002	1/1	0.88	0.34	-	60,60,60,60	0
5	MG	A	4001	1/1	0.92	0.20	-	70,70,70,70	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.