



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 21, 2024 – 12:18 AM EDT

PDB ID : 2M2U  
BMRB ID : 18934  
Title : Binary complex of African Swine Fever Virus Pol X with MgdGTP  
Authors : Wu, W.; Su, M.; Tsai, M.  
Deposited on : 2013-01-03

This is a Full wwPDB NMR 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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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 : 1.8.5 (274361), CSD as541be (2020)  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
wwPDB-RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
wwPDB-ShiftChecker : v1.2  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

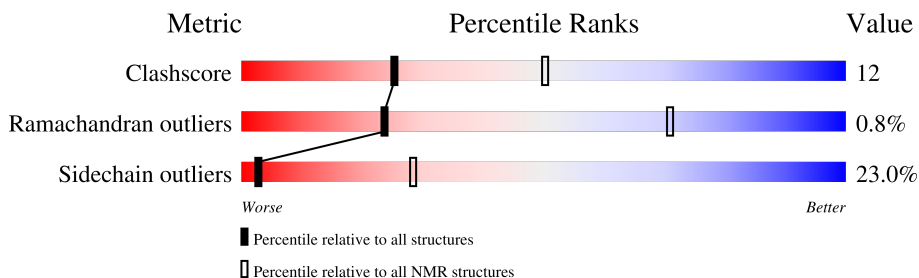
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*


The overall completeness of chemical shifts assignment is 90%.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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  $\leq 5\%$ .

Mol	Chain	Length	Quality of chain
1	A	174	

## 2 Ensemble composition and analysis

This entry contains 20 models. Model 6 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:2-A:174 (173)	0.49	6

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 3 clusters and 6 single-model clusters were found.

Cluster number	Models
1	6, 10, 12, 13, 14, 17, 18
2	1, 5, 8, 11, 20
3	2, 16
Single-model clusters	3; 4; 7; 9; 15; 19

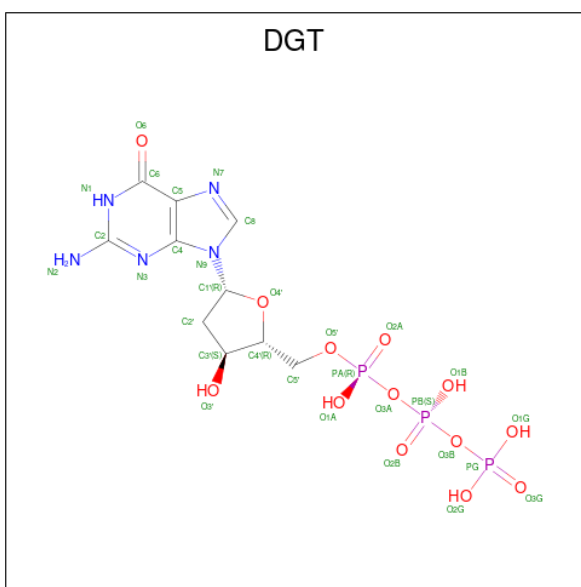
### 3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3048 atoms, of which 1581 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Repair DNA polymerase X.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	174	3003	943	1569	248	239	4	0

- Molecule 2 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).



Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	P
2	A	1	43	10	12	5	13	3

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

Mol	Chain	Residues	Atoms	
			Total	Mg
3	A	2	2	2

## 4 Residue-property plots

### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Repair DNA polymerase X

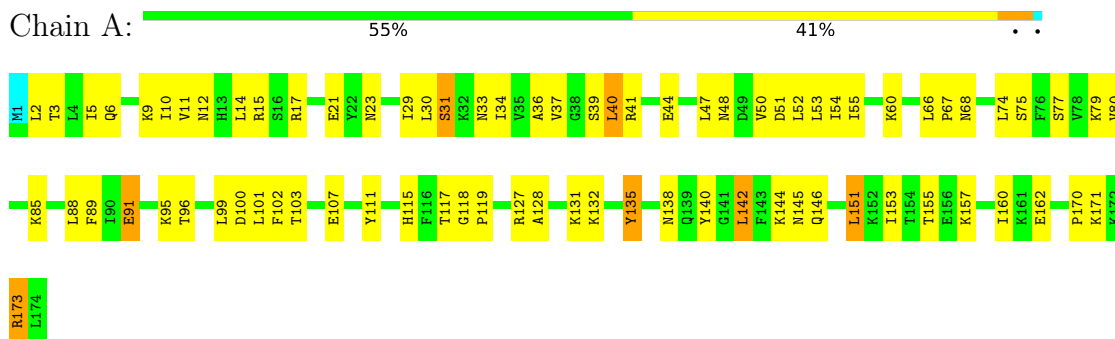


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

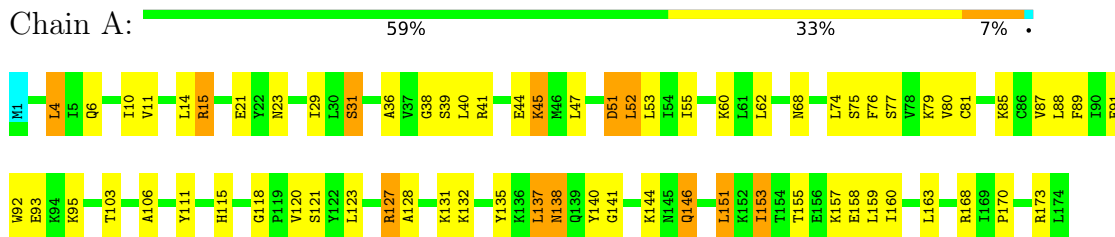
#### 4.2.1 Score per residue for model 1

- Molecule 1: Repair DNA polymerase X



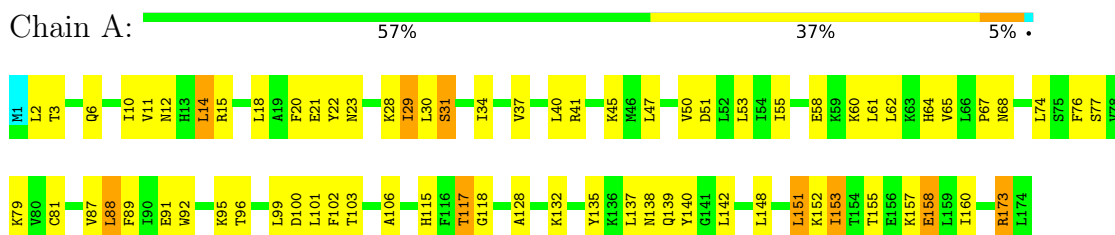
#### 4.2.2 Score per residue for model 2

- Molecule 1: Repair DNA polymerase X



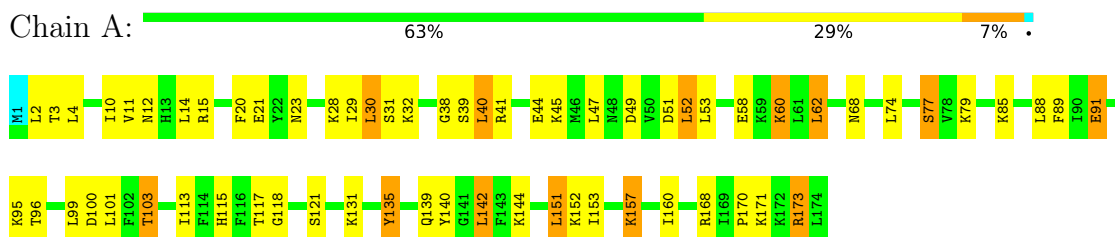
### 4.2.3 Score per residue for model 3

- Molecule 1: Repair DNA polymerase X



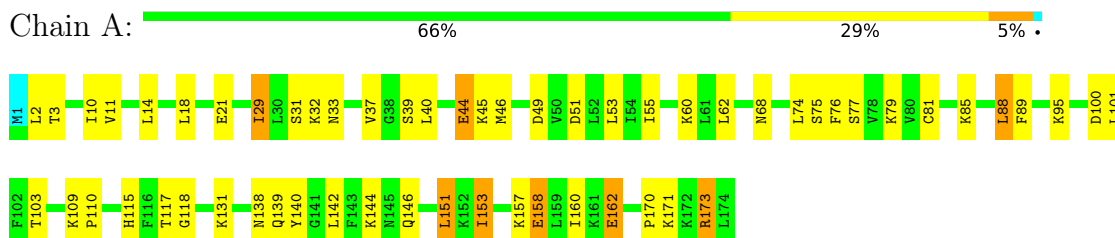
### 4.2.4 Score per residue for model 4

- Molecule 1: Repair DNA polymerase X



### 4.2.5 Score per residue for model 5

- Molecule 1: Repair DNA polymerase X



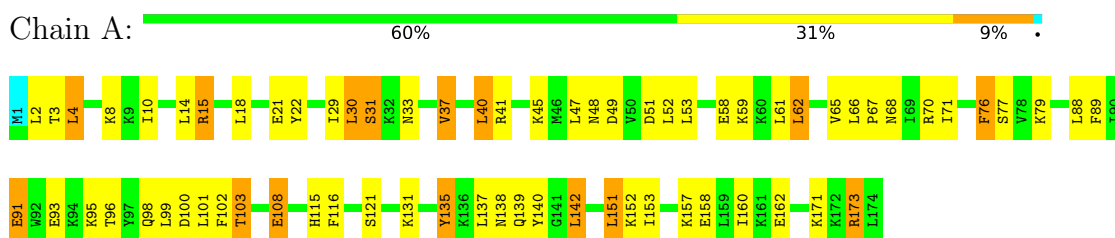
### 4.2.6 Score per residue for model 6 (medoid)

- Molecule 1: Repair DNA polymerase X



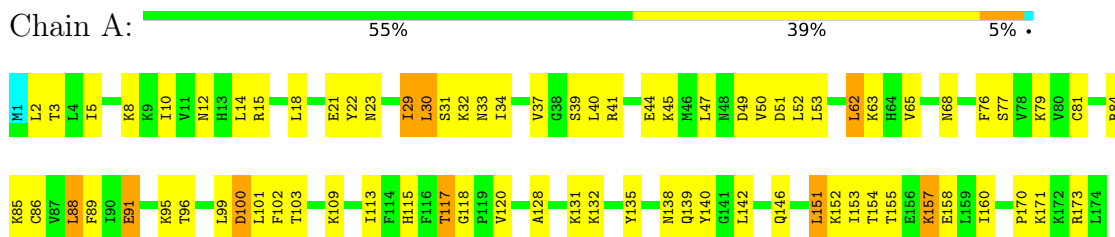
### 4.2.7 Score per residue for model 7

- Molecule 1: Repair DNA polymerase X



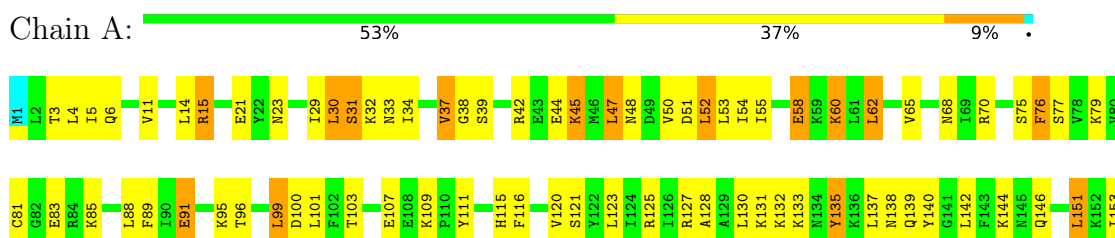
### 4.2.8 Score per residue for model 8

- Molecule 1: Repair DNA polymerase X



### 4.2.9 Score per residue for model 9

- Molecule 1: Repair DNA polymerase X





#### 4.2.10 Score per residue for model 10

- Molecule 1: Repair DNA polymerase X



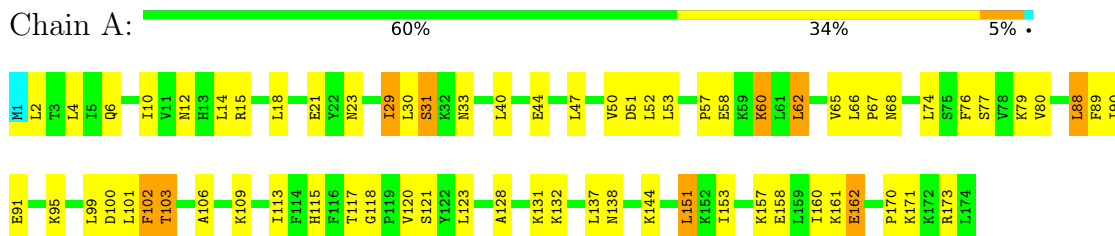
#### 4.2.11 Score per residue for model 11

- Molecule 1: Repair DNA polymerase X



#### 4.2.12 Score per residue for model 12

- Molecule 1: Repair DNA polymerase X

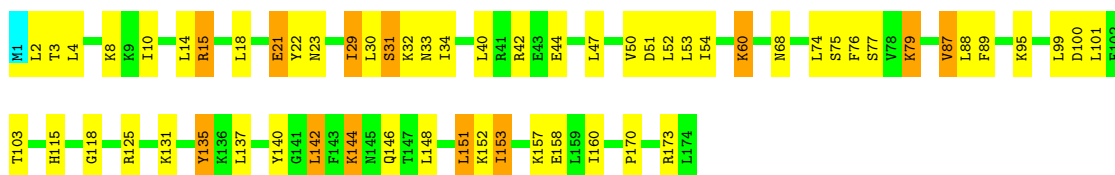


#### 4.2.13 Score per residue for model 13

- Molecule 1: Repair DNA polymerase X



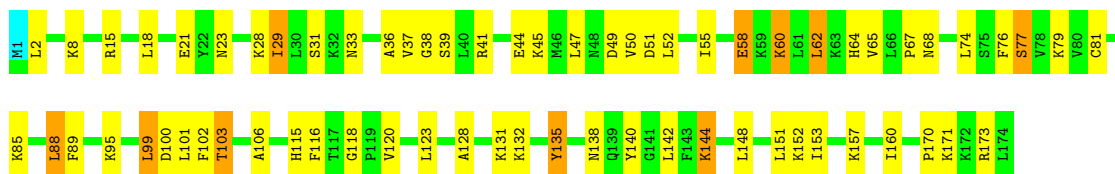




#### 4.2.14 Score per residue for model 14

- Molecule 1: Repair DNA polymerase X

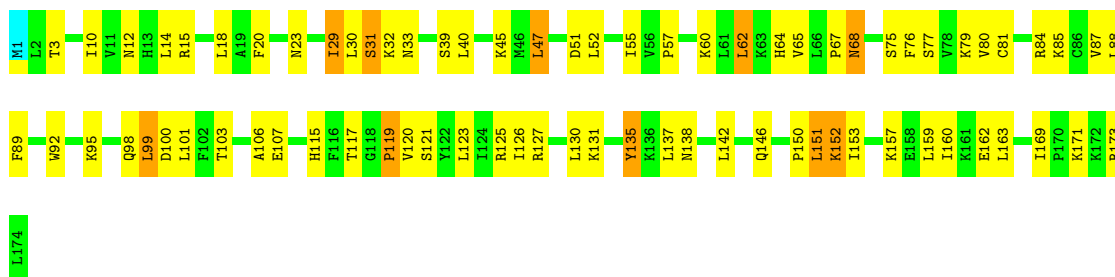
Chain A: 61% 33% 6%



#### 4.2.15 Score per residue for model 15

- Molecule 1: Repair DNA polymerase X

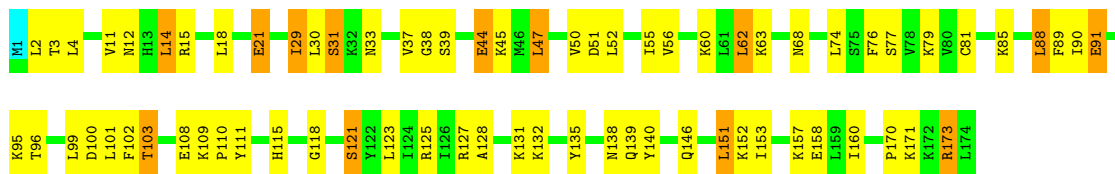
Chain A: 56% 37% 6%



#### 4.2.16 Score per residue for model 16

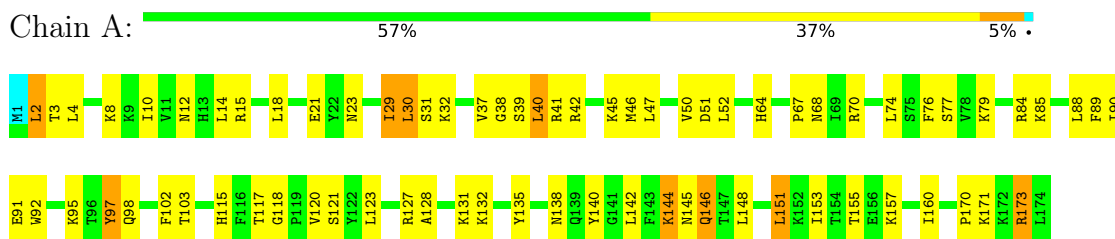
- Molecule 1: Repair DNA polymerase X

Chain A: 58% 34% 7%



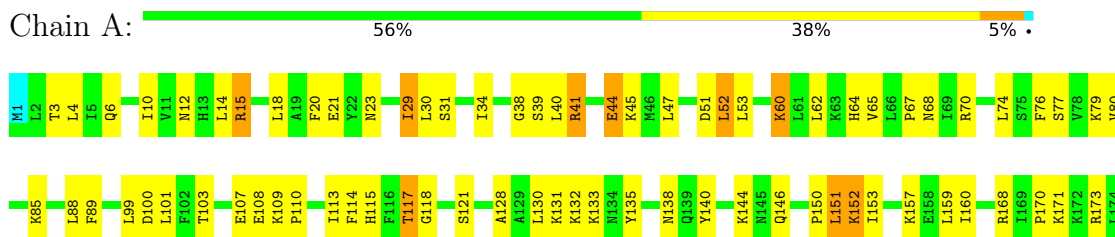
## 4.2.17 Score per residue for model 17

- Molecule 1: Repair DNA polymerase X



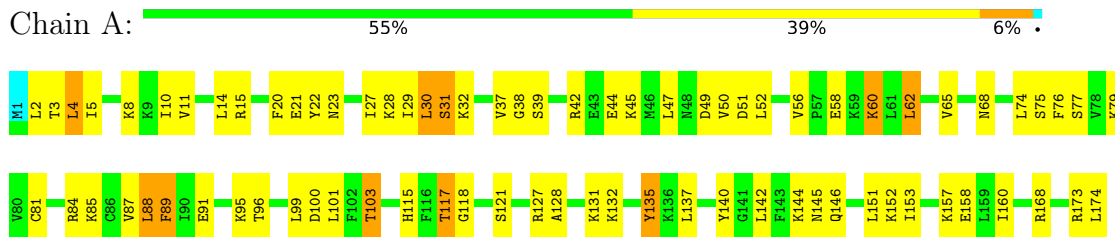
## 4.2.18 Score per residue for model 18

- Molecule 1: Repair DNA polymerase X



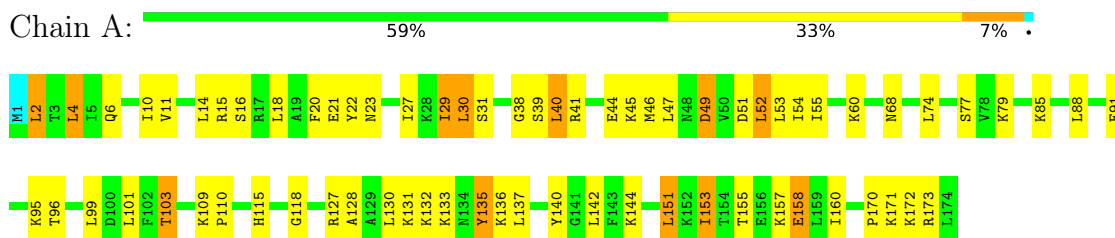
## 4.2.19 Score per residue for model 19

- Molecule 1: Repair DNA polymerase X



## 4.2.20 Score per residue for model 20

- Molecule 1: Repair DNA polymerase X



## 5 Refinement protocol and experimental data overview

The models were refined using the following method: *distance geometry*.

Of the 2000 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	
HADDOCK	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	2357
Number of shifts mapped to atoms	2357
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

## 6 Model quality i

### 6.1 Standard geometry i

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

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	1426	1558	1558	32±4
2	A	31	12	12	9±2
3	A	2	0	0	1±0
All	All	29180	31400	31400	698

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 12.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:201:DGT:O3G	3:A:203:MG:MG	0.78	1.27	13	17
1:A:91:GLU:HB2	1:A:96:THR:HG22	0.71	1.61	3	8
1:A:115:HIS:CD2	2:A:201:DGT:H8	0.69	2.22	3	12
1:A:10:ILE:HG22	1:A:92:TRP:HZ2	0.69	1.47	3	1
2:A:201:DGT:O2B	2:A:201:DGT:O3G	0.69	2.10	17	1
1:A:128:ALA:O	1:A:132:LYS:HG2	0.67	1.89	11	14
1:A:107:GLU:O	1:A:151:LEU:HD11	0.67	1.90	15	2
2:A:201:DGT:O2G	3:A:203:MG:MG	0.66	1.36	8	1
1:A:81:CYS:HB2	1:A:87:VAL:HG23	0.65	1.67	10	3
1:A:51:ASP:OD2	1:A:100:ASP:HB2	0.65	1.92	7	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:11:VAL:CG2	1:A:50:VAL:HG11	0.64	2.23	19	6
1:A:51:ASP:CG	2:A:201:DGT:O2A	0.64	2.36	14	13
1:A:14:LEU:HD11	1:A:90:ILE:HD13	0.64	1.70	6	3
1:A:77:SER:O	1:A:88:LEU:HG	0.63	1.92	12	19
1:A:4:LEU:HD21	1:A:40:LEU:HA	0.63	1.69	7	3
2:A:201:DGT:H2'A	2:A:201:DGT:N3	0.63	2.07	20	10
1:A:52:LEU:HD11	1:A:99:LEU:HD11	0.62	1.69	20	2
1:A:157:LYS:O	1:A:160:ILE:HG13	0.62	1.94	11	20
1:A:4:LEU:HD22	1:A:40:LEU:HD22	0.62	1.72	4	2
1:A:38:GLY:HA2	2:A:201:DGT:O1B	0.61	1.95	17	11
2:A:201:DGT:O3G	2:A:201:DGT:O2B	0.61	2.17	15	3
1:A:85:LYS:NZ	2:A:201:DGT:O6	0.61	2.33	19	10
1:A:14:LEU:O	1:A:18:LEU:HG	0.61	1.95	12	5
1:A:85:LYS:HE3	1:A:102:PHE:CZ	0.61	2.31	17	1
1:A:79:LYS:HB3	1:A:87:VAL:HG23	0.61	1.72	13	1
1:A:115:HIS:NE2	2:A:201:DGT:H8	0.60	2.12	8	20
1:A:70:ARG:HB2	1:A:76:PHE:CZ	0.60	2.31	7	2
1:A:10:ILE:O	1:A:14:LEU:HG	0.60	1.97	2	13
1:A:18:LEU:HB2	1:A:29:ILE:O	0.60	1.97	11	12
1:A:10:ILE:HG21	1:A:97:TYR:HE2	0.60	1.57	17	1
1:A:113:ILE:O	1:A:117:THR:HB	0.60	1.97	18	1
1:A:2:LEU:HD13	1:A:50:VAL:HG23	0.60	1.74	1	1
1:A:15:ARG:O	1:A:30:LEU:HA	0.59	1.98	17	11
1:A:108:GLU:HB2	1:A:139:GLN:O	0.59	1.97	7	2
1:A:76:PHE:HA	1:A:89:PHE:O	0.58	1.98	14	17
1:A:47:LEU:HB2	2:A:201:DGT:O2G	0.58	1.99	14	2
1:A:118:GLY:HA3	1:A:170:PRO:HB3	0.57	1.75	17	13
1:A:130:LEU:HB3	1:A:135:TYR:CD1	0.57	2.34	15	1
1:A:51:ASP:OD2	2:A:201:DGT:O1A	0.57	2.22	6	14
1:A:15:ARG:NE	1:A:31:SER:HB3	0.57	2.14	19	1
1:A:62:LEU:O	1:A:65:VAL:HG22	0.56	1.99	7	11
1:A:51:ASP:CG	2:A:201:DGT:PA	0.56	2.83	13	17
1:A:118:GLY:CA	1:A:170:PRO:HB3	0.56	2.30	16	2
1:A:10:ILE:HG22	1:A:92:TRP:CZ2	0.56	2.34	3	2
2:A:201:DGT:C5'	2:A:201:DGT:O1B	0.56	2.54	11	3
1:A:132:LYS:N	1:A:132:LYS:HE2	0.56	2.16	11	1
1:A:92:TRP:CD1	1:A:93:GLU:HG3	0.55	2.37	2	1
1:A:55:ILE:CG2	1:A:106:ALA:HA	0.55	2.31	2	4
1:A:21:GLU:HB3	1:A:68:ASN:HB3	0.55	1.78	19	7
1:A:62:LEU:HD11	1:A:103:THR:HB	0.54	1.79	14	5
1:A:39:SER:HB2	1:A:47:LEU:HD11	0.54	1.79	15	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:123:LEU:O	1:A:127:ARG:HD2	0.54	2.02	2	1
1:A:137:LEU:HG	1:A:138:ASN:N	0.53	2.17	2	1
1:A:10:ILE:HD11	1:A:50:VAL:HG21	0.53	1.80	12	6
1:A:120:VAL:HB	2:A:201:DGT:O3'	0.53	2.03	6	7
1:A:153:ILE:HG22	1:A:158:GLU:HG3	0.53	1.80	5	1
1:A:135:TYR:HD1	1:A:142:LEU:HD12	0.53	1.64	20	1
1:A:22:TYR:HB3	1:A:27:ILE:HD11	0.53	1.79	19	2
1:A:50:VAL:HG13	1:A:99:LEU:HD12	0.52	1.81	14	1
1:A:30:LEU:HG	1:A:31:SER:N	0.52	2.19	12	1
1:A:21:GLU:CB	1:A:68:ASN:HB3	0.52	2.35	3	9
1:A:52:LEU:O	1:A:101:LEU:HA	0.52	2.05	18	4
1:A:6:GLN:O	1:A:10:ILE:HG23	0.52	2.04	12	6
1:A:58:GLU:OE1	1:A:60:LYS:HE3	0.52	2.04	12	4
1:A:51:ASP:O	1:A:52:LEU:HD12	0.52	2.04	8	6
1:A:57:PRO:HA	1:A:106:ALA:HB2	0.52	1.80	12	2
1:A:36:ALA:HA	1:A:52:LEU:HD23	0.52	1.80	14	2
1:A:53:LEU:HD23	1:A:102:PHE:HB2	0.51	1.82	7	5
1:A:51:ASP:C	1:A:52:LEU:HD12	0.51	2.26	8	6
1:A:61:LEU:O	1:A:65:VAL:HG23	0.51	2.06	3	1
2:A:201:DGT:O2G	2:A:201:DGT:O2B	0.51	2.27	20	2
1:A:135:TYR:HE2	1:A:142:LEU:HD13	0.51	1.65	15	1
1:A:11:VAL:O	1:A:15:ARG:HG2	0.51	2.06	20	1
1:A:135:TYR:CD1	1:A:142:LEU:HD12	0.51	2.41	6	7
1:A:142:LEU:O	1:A:148:LEU:HD12	0.51	2.06	13	5
1:A:21:GLU:HB2	1:A:68:ASN:CB	0.50	2.36	4	1
1:A:151:LEU:N	1:A:151:LEU:HD13	0.50	2.21	12	12
1:A:20:PHE:HB2	1:A:68:ASN:O	0.50	2.07	10	7
1:A:15:ARG:HD2	1:A:31:SER:OG	0.50	2.07	16	2
1:A:12:ASN:O	1:A:15:ARG:HG3	0.50	2.07	18	4
1:A:21:GLU:HB3	1:A:68:ASN:CB	0.50	2.36	19	1
1:A:15:ARG:HG2	1:A:31:SER:CA	0.49	2.37	2	3
1:A:30:LEU:H	1:A:30:LEU:HD23	0.49	1.66	20	2
1:A:38:GLY:CA	2:A:201:DGT:O1B	0.49	2.60	17	1
1:A:45:LYS:HE3	1:A:45:LYS:H	0.49	1.68	9	1
1:A:39:SER:HB3	1:A:44:GLU:HB2	0.49	1.84	8	8
1:A:117:THR:HG22	1:A:118:GLY:N	0.49	2.22	19	2
1:A:115:HIS:CD2	2:A:201:DGT:H1'	0.49	2.43	18	6
1:A:41:ARG:HD2	1:A:117:THR:O	0.49	2.08	18	1
1:A:4:LEU:CD2	1:A:40:LEU:HA	0.49	2.38	17	3
1:A:117:THR:HG23	1:A:118:GLY:N	0.49	2.22	17	1
1:A:10:ILE:HG13	1:A:11:VAL:N	0.48	2.21	5	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:201:DGT:O1B	2:A:201:DGT:C5'	0.48	2.61	10	5
1:A:4:LEU:HB2	1:A:44:GLU:O	0.48	2.07	10	4
1:A:18:LEU:HD23	1:A:29:ILE:HD12	0.48	1.84	14	1
1:A:40:LEU:HD23	1:A:47:LEU:HD21	0.48	1.85	1	1
1:A:118:GLY:HA3	1:A:170:PRO:CB	0.48	2.38	4	5
1:A:130:LEU:HA	1:A:133:LYS:HG2	0.48	1.86	6	4
1:A:21:GLU:HB2	1:A:68:ASN:HB3	0.48	1.85	18	3
1:A:4:LEU:HD23	1:A:44:GLU:O	0.48	2.08	19	2
1:A:151:LEU:H	1:A:151:LEU:HD13	0.48	1.68	7	1
1:A:81:CYS:SG	1:A:85:LYS:HE3	0.48	2.48	9	1
1:A:34:ILE:HG12	1:A:54:ILE:HG23	0.48	1.84	6	3
1:A:56:VAL:HG21	1:A:62:LEU:HA	0.48	1.85	19	2
1:A:66:LEU:N	1:A:67:PRO:HD2	0.48	2.23	7	4
1:A:51:ASP:HB2	2:A:201:DGT:O2A	0.48	2.08	20	5
1:A:88:LEU:HD13	1:A:101:LEU:HD21	0.47	1.85	9	7
1:A:113:ILE:O	1:A:117:THR:HG23	0.47	2.08	8	2
1:A:2:LEU:O	1:A:46:MET:HG3	0.47	2.10	17	3
2:A:201:DGT:O1B	2:A:201:DGT:H5'A	0.47	2.10	1	1
1:A:59:LYS:H	1:A:59:LYS:HD2	0.47	1.69	7	1
1:A:146:GLN:NE2	1:A:146:GLN:HA	0.47	2.24	15	2
1:A:51:ASP:OD1	2:A:201:DGT:PA	0.47	2.73	13	2
1:A:51:ASP:OD2	1:A:100:ASP:CB	0.47	2.63	8	2
1:A:51:ASP:CB	2:A:201:DGT:O2A	0.47	2.62	13	5
1:A:64:HIS:O	1:A:67:PRO:HD2	0.46	2.09	17	5
1:A:52:LEU:HD13	1:A:99:LEU:HD11	0.46	1.85	15	1
1:A:4:LEU:HG	1:A:44:GLU:O	0.46	2.10	2	1
1:A:110:PRO:HG2	1:A:151:LEU:HD12	0.46	1.87	18	1
1:A:15:ARG:HD3	1:A:31:SER:OG	0.46	2.09	15	3
1:A:37:VAL:O	1:A:51:ASP:HB2	0.46	2.11	3	1
1:A:51:ASP:CG	2:A:201:DGT:O1A	0.46	2.54	6	2
1:A:39:SER:OG	1:A:47:LEU:HB3	0.46	2.11	11	1
1:A:151:LEU:HD13	1:A:151:LEU:H	0.46	1.71	1	4
1:A:151:LEU:HD13	1:A:151:LEU:N	0.46	2.25	7	1
1:A:111:TYR:CZ	1:A:141:GLY:HA2	0.46	2.46	2	1
1:A:159:LEU:O	1:A:163:LEU:HG	0.46	2.10	2	2
2:A:201:DGT:N3	2:A:201:DGT:H2'A	0.46	2.25	11	3
1:A:49:ASP:HB2	1:A:98:GLN:HG2	0.46	1.87	11	1
1:A:55:ILE:HG21	1:A:109:LYS:CG	0.46	2.41	9	1
1:A:45:LYS:N	1:A:45:LYS:HE3	0.46	2.26	2	1
1:A:123:LEU:O	1:A:127:ARG:HG2	0.46	2.10	17	2
1:A:158:GLU:O	1:A:162:GLU:HB2	0.45	2.11	12	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:A:201:DGT:N3	2:A:201:DGT:O5'	0.45	2.49	19	1
1:A:61:LEU:O	1:A:65:VAL:HG13	0.45	2.11	7	1
1:A:8:LYS:HD2	1:A:8:LYS:C	0.45	2.32	13	1
1:A:135:TYR:CD1	1:A:135:TYR:C	0.45	2.90	15	1
1:A:59:LYS:HD2	1:A:59:LYS:N	0.45	2.27	7	1
1:A:111:TYR:CZ	1:A:151:LEU:HD12	0.45	2.47	9	2
1:A:121:SER:O	1:A:125:ARG:HG2	0.45	2.11	9	2
1:A:151:LEU:HD22	1:A:151:LEU:H	0.45	1.72	9	1
1:A:151:LEU:CD2	1:A:151:LEU:H	0.45	2.25	15	2
1:A:51:ASP:OD1	2:A:201:DGT:O2A	0.45	2.35	7	1
1:A:81:CYS:HB2	1:A:87:VAL:CG2	0.44	2.43	3	3
1:A:39:SER:HB2	1:A:47:LEU:HG	0.44	1.88	16	1
1:A:12:ASN:O	1:A:15:ARG:HG2	0.44	2.12	4	3
1:A:135:TYR:CZ	1:A:144:LYS:HB2	0.44	2.47	14	1
1:A:39:SER:HB2	1:A:47:LEU:HD23	0.44	1.89	14	1
1:A:111:TYR:CE1	1:A:151:LEU:HB3	0.44	2.47	11	1
1:A:100:ASP:HB3	1:A:102:PHE:CZ	0.44	2.48	14	1
1:A:60:LYS:H	1:A:60:LYS:HD2	0.44	1.73	15	2
1:A:150:PRO:O	1:A:152:LYS:HE2	0.44	2.12	18	2
1:A:144:LYS:O	1:A:146:GLN:N	0.44	2.51	17	1
1:A:115:HIS:O	1:A:123:LEU:HD11	0.43	2.11	9	1
1:A:20:PHE:CD2	1:A:65:VAL:HA	0.43	2.48	3	1
1:A:120:VAL:HA	1:A:123:LEU:HD12	0.43	1.90	12	3
1:A:153:ILE:HB	1:A:158:GLU:HB3	0.43	1.89	3	3
1:A:15:ARG:HG2	1:A:16:SER:N	0.43	2.28	6	1
1:A:4:LEU:CD1	1:A:40:LEU:HA	0.43	2.44	10	1
1:A:22:TYR:HB3	1:A:27:ILE:CD1	0.43	2.43	19	1
1:A:109:LYS:HB3	1:A:110:PRO:CD	0.43	2.44	16	4
1:A:58:GLU:OE1	1:A:60:LYS:HG2	0.43	2.13	19	1
1:A:85:LYS:HG2	1:A:102:PHE:CE2	0.43	2.48	1	1
1:A:30:LEU:HD23	1:A:30:LEU:N	0.43	2.28	20	1
1:A:151:LEU:HB2	1:A:153:ILE:CD1	0.43	2.44	2	1
1:A:47:LEU:HD13	1:A:49:ASP:O	0.43	2.14	8	2
1:A:89:PHE:CE2	1:A:98:GLN:HG2	0.43	2.49	7	1
1:A:55:ILE:HG22	1:A:106:ALA:HA	0.43	1.91	15	2
1:A:135:TYR:CE1	1:A:144:LYS:HG2	0.43	2.49	13	1
1:A:64:HIS:C	1:A:67:PRO:HD2	0.43	2.34	3	1
1:A:97:TYR:N	1:A:97:TYR:CD1	0.43	2.87	17	1
1:A:70:ARG:HB2	1:A:76:PHE:CE2	0.42	2.49	7	1
1:A:109:LYS:O	1:A:113:ILE:HG12	0.42	2.14	12	2
1:A:81:CYS:O	1:A:85:LYS:HB2	0.42	2.14	5	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:169:ILE:O	1:A:169:ILE:HG13	0.42	2.15	15	1
1:A:44:GLU:OE1	1:A:44:GLU:HA	0.42	2.14	16	1
1:A:12:ASN:HA	1:A:15:ARG:NE	0.42	2.30	17	3
1:A:51:ASP:HA	1:A:100:ASP:O	0.42	2.14	7	1
1:A:117:THR:HG23	1:A:118:GLY:H	0.42	1.74	17	1
1:A:51:ASP:OD1	1:A:51:ASP:N	0.42	2.52	7	1
1:A:91:GLU:HB3	1:A:96:THR:HG22	0.42	1.91	9	1
1:A:127:ARG:CZ	1:A:137:LEU:HD22	0.42	2.45	2	1
1:A:45:LYS:HE3	1:A:45:LYS:N	0.42	2.29	9	1
1:A:135:TYR:CE1	1:A:144:LYS:HB2	0.42	2.49	9	1
1:A:31:SER:HA	1:A:34:ILE:O	0.42	2.15	3	1
1:A:109:LYS:HE3	1:A:154:THR:OG1	0.41	2.15	8	1
1:A:42:ARG:HH21	1:A:117:THR:HG23	0.41	1.75	19	1
1:A:51:ASP:O	1:A:52:LEU:HG	0.41	2.14	16	1
1:A:111:TYR:OH	1:A:142:LEU:HD23	0.41	2.16	10	1
2:A:201:DGT:N3	2:A:201:DGT:C2'	0.41	2.83	3	1
1:A:45:LYS:N	1:A:45:LYS:HD3	0.41	2.29	6	1
1:A:37:VAL:HB	1:A:116:PHE:HB3	0.41	1.90	9	3
2:A:201:DGT:N3	2:A:201:DGT:O1A	0.41	2.53	19	1
1:A:4:LEU:HD12	1:A:40:LEU:HA	0.41	1.92	10	1
1:A:145:ASN:O	1:A:146:GLN:HB2	0.41	2.15	11	2
1:A:111:TYR:OH	1:A:151:LEU:HG	0.41	2.15	2	1
1:A:77:SER:O	1:A:88:LEU:HD23	0.41	2.16	14	1
1:A:39:SER:HB3	1:A:44:GLU:HB3	0.41	1.92	18	1
1:A:2:LEU:HD12	1:A:48:ASN:O	0.41	2.16	1	1
1:A:34:ILE:HG21	1:A:52:LEU:HD23	0.41	1.91	8	1
1:A:5:ILE:HG13	1:A:6:GLN:N	0.41	2.31	9	1
1:A:111:TYR:CD1	1:A:111:TYR:N	0.41	2.89	16	1
1:A:54:ILE:HG22	1:A:103:THR:HA	0.41	1.92	20	1
1:A:15:ARG:HG3	1:A:31:SER:N	0.41	2.31	9	1
1:A:47:LEU:HD23	1:A:48:ASN:H	0.41	1.76	9	1
2:A:201:DGT:O1B	2:A:201:DGT:H5'	0.41	2.16	12	1
1:A:60:LYS:N	1:A:60:LYS:HD3	0.41	2.30	13	1
1:A:20:PHE:CE2	1:A:27:ILE:HD13	0.41	2.50	19	1
1:A:119:PRO:O	1:A:123:LEU:HG	0.41	2.16	15	1
1:A:47:LEU:HD22	1:A:49:ASP:O	0.40	2.16	7	1
1:A:62:LEU:CD1	1:A:103:THR:HB	0.40	2.47	7	1
1:A:130:LEU:HD13	1:A:135:TYR:CE1	0.40	2.52	15	1
1:A:20:PHE:CE1	1:A:27:ILE:HD13	0.40	2.51	20	1
1:A:37:VAL:HG11	1:A:53:LEU:HD12	0.40	1.92	1	1
1:A:114:PHE:HB2	1:A:159:LEU:CD2	0.40	2.47	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:TYR:OH	1:A:151:LEU:HB3	0.40	2.17	16	1
1:A:168:ARG:HB3	1:A:174:LEU:OXT	0.40	2.16	19	1
1:A:36:ALA:HA	1:A:52:LEU:HB3	0.40	1.92	2	1
1:A:34:ILE:HG13	1:A:54:ILE:HG12	0.40	1.93	9	1
2:A:201:DGT:O1A	2:A:201:DGT:C2	0.40	2.70	19	1

## 6.3 Torsion angles [i](#)

### 6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	172/174 (99%)	163±1 (95±1%)	8±1 (5±1%)	1±1 (1±0%)	24	71
All	All	3440/3480 (99%)	3251 (95%)	161 (5%)	28 (1%)	24	71

All 5 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	173	ARG	19
1	A	117	THR	4
1	A	119	PRO	2
1	A	145	ASN	2
1	A	146	GLN	1

### 6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. 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	158/159 (99%)	122±3 (77±2%)	36±3 (23±2%)	3	28
All	All	3160/3180 (99%)	2433 (77%)	727 (23%)	3	28

All 97 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	29	ILE	20
1	A	79	LYS	20
1	A	103	THR	20
1	A	151	LEU	20
1	A	153	ILE	20
1	A	31	SER	19
1	A	95	LYS	19
1	A	131	LYS	19
1	A	140	TYR	18
1	A	23	ASN	17
1	A	74	LEU	16
1	A	135	TYR	16
1	A	45	LYS	16
1	A	3	THR	15
1	A	60	LYS	15
1	A	99	LEU	15
1	A	138	ASN	15
1	A	171	LYS	15
1	A	62	LEU	15
1	A	40	LEU	14
1	A	30	LEU	14
1	A	33	ASN	13
1	A	144	LYS	13
1	A	47	LEU	13
1	A	2	LEU	13
1	A	121	SER	11
1	A	137	LEU	11
1	A	152	LYS	11
1	A	41	ARG	10
1	A	91	GLU	10
1	A	173	ARG	10
1	A	146	GLN	10
1	A	88	LEU	10
1	A	75	SER	9
1	A	53	LEU	9
1	A	158	GLU	9
1	A	142	LEU	8
1	A	4	LEU	8
1	A	15	ARG	8
1	A	101	LEU	8
1	A	32	LYS	8

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Mol	Chain	Res	Type	Models (Total)
1	A	37	VAL	8
1	A	127	ARG	7
1	A	155	THR	7
1	A	162	GLU	7
1	A	55	ILE	6
1	A	100	ASP	6
1	A	139	GLN	6
1	A	49	ASP	6
1	A	80	VAL	5
1	A	117	THR	5
1	A	52	LEU	5
1	A	14	LEU	5
1	A	22	TYR	5
1	A	8	LYS	5
1	A	5	ILE	4
1	A	39	SER	4
1	A	28	LYS	4
1	A	58	GLU	4
1	A	84	ARG	4
1	A	42	ARG	4
1	A	89	PHE	3
1	A	168	ARG	3
1	A	44	GLU	3
1	A	21	GLU	3
1	A	102	PHE	3
1	A	98	GLN	3
1	A	107	GLU	2
1	A	77	SER	2
1	A	157	LYS	2
1	A	48	ASN	2
1	A	76	PHE	2
1	A	108	GLU	2
1	A	63	LYS	2
1	A	68	ASN	2
1	A	126	ILE	2
1	A	161	LYS	2
1	A	125	ARG	2
1	A	70	ARG	2
1	A	9	LYS	1
1	A	17	ARG	1
1	A	6	GLN	1
1	A	51	ASP	1

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Mol	Chain	Res	Type	Models (Total)
1	A	71	ILE	1
1	A	93	GLU	1
1	A	86	CYS	1
1	A	83	GLU	1
1	A	174	LEU	1
1	A	13	HIS	1
1	A	87	VAL	1
1	A	90	ILE	1
1	A	92	TRP	1
1	A	97	TYR	1
1	A	34	ILE	1
1	A	16	SER	1
1	A	136	LYS	1
1	A	172	LYS	1

### 6.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	DGT	A	201	3	26,33,33	1.88±0.02	3±0 (11±1%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	DGT	A	201	3	32,52,52	1.93±0.05	8±1 (26±3%)

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	DGT	A	201	3	-	0±0,18,34,34	0±0,3,3,3

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	A	201	DGT	C5-C6	7.20	1.32	1.47	20	20
2	A	201	DGT	C5-C4	3.84	1.33	1.43	20	20
2	A	201	DGT	PG-O3G	3.66	1.62	1.50	13	20
2	A	201	DGT	C6-N1	2.20	1.41	1.37	17	2

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	201	DGT	PB-O3B-PG	6.85	109.33	132.83	11	20
2	A	201	DGT	C2-N1-C6	3.93	117.86	125.10	14	20
2	A	201	DGT	C5-C6-N1	3.33	119.83	113.95	1	20
2	A	201	DGT	O2G-PG-O1G	3.22	119.95	107.64	12	20
2	A	201	DGT	C8-N7-C5	3.13	108.95	102.99	14	20

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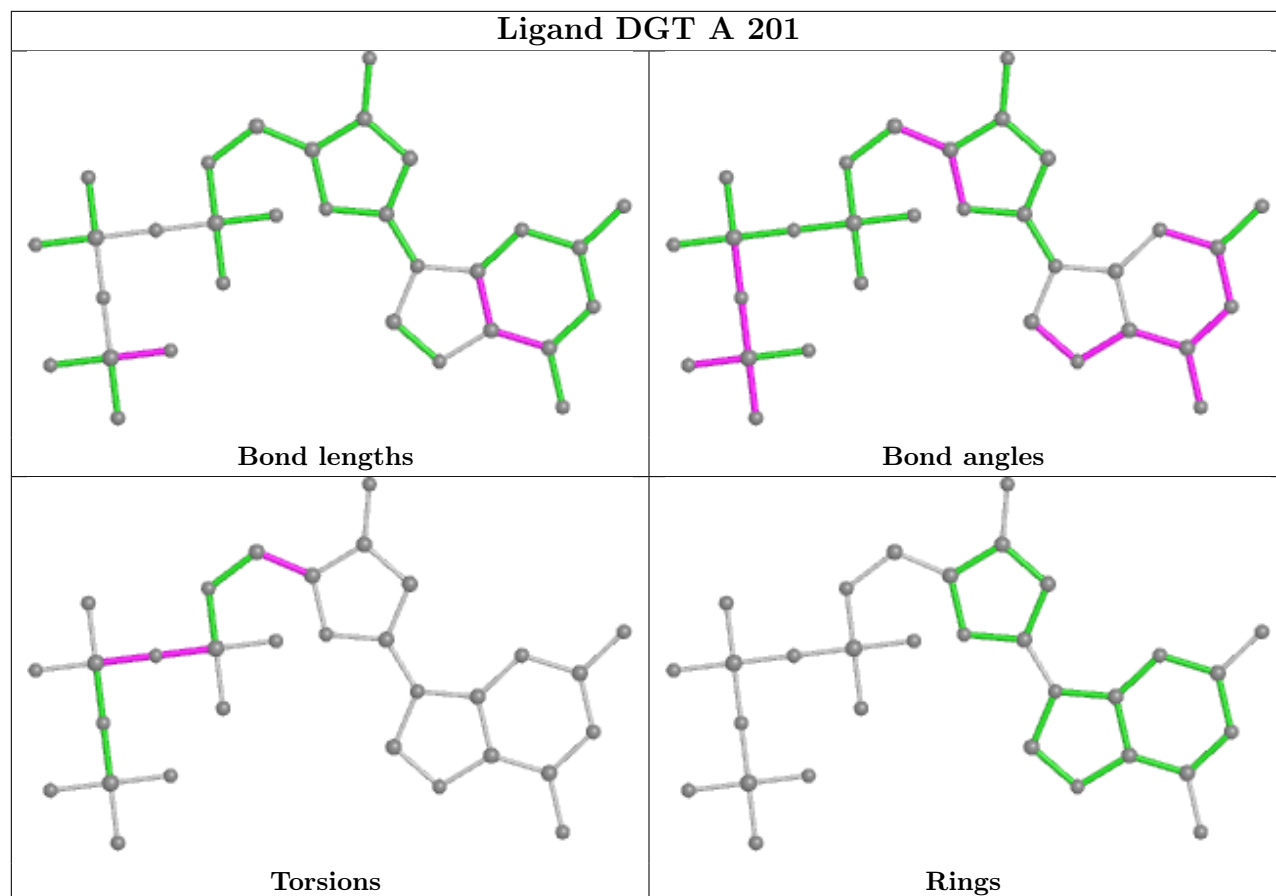
Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	A	201	DGT	PA-O3A-PB	3.04	122.40	132.83	7	4
2	A	201	DGT	O4'-C4'-C5'	2.79	100.19	109.37	2	8
2	A	201	DGT	C2'-C1'-N9	2.72	107.99	114.27	12	4
2	A	201	DGT	O5'-C5'-C4'	2.72	99.64	108.99	3	6
2	A	201	DGT	N1-C2-N3	2.60	118.46	123.32	12	19
2	A	201	DGT	O2G-PG-O3B	2.41	112.70	104.64	9	7
2	A	201	DGT	O4'-C1'-C2'	2.40	101.71	106.25	6	4
2	A	201	DGT	O6-C6-C5	2.32	119.84	124.37	3	3
2	A	201	DGT	O3B-PG-O3G	2.31	98.39	111.19	9	7
2	A	201	DGT	O1G-PG-O3B	2.25	112.17	104.64	10	2
2	A	201	DGT	N2-C2-N1	2.21	121.43	116.71	20	3

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 6.7 Other polymers [i](#)

There are no such molecules in this entry.

## 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 7 Chemical shift validation i

The completeness of assignment taking into account all chemical shift lists is 90% for the well-defined parts and 89% for the entire structure.

### 7.1 Chemical shift list 1

File name: working\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping i

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	2357
Number of shifts mapped to atoms	2357
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	19

#### 7.1.2 Chemical shift referencing i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	174	$2.46 \pm 0.15$	Should be applied
$^{13}\text{C}_\beta$	166	$2.80 \pm 0.13$	Should be applied
$^{13}\text{C}'$	149	$2.88 \pm 0.13$	Should be applied
$^{15}\text{N}$	167	$0.70 \pm 0.50$	None needed (imprecise)

#### 7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 90%, i.e. 2349 atoms were assigned a chemical shift out of a possible 2621. 0 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	837/861 (97%)	348/348 (100%)	322/346 (93%)	167/167 (100%)
Sidechain	1386/1584 (88%)	950/1032 (92%)	424/485 (87%)	12/67 (18%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	126/176 (72%)	78/86 (91%)	47/86 (55%)	1/4 (25%)
Overall	2349/2621 (90%)	1376/1466 (94%)	793/917 (86%)	180/238 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 89%, i.e. 2357 atoms were assigned a chemical shift out of a possible 2636. 0 out of 38 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	839/866 (97%)	349/350 (100%)	323/348 (93%)	167/168 (99%)
Sidechain	1392/1594 (87%)	954/1039 (92%)	426/488 (87%)	12/67 (18%)
Aromatic	126/176 (72%)	78/86 (91%)	47/86 (55%)	1/4 (25%)
Overall	2357/2636 (89%)	1381/1475 (94%)	796/922 (86%)	180/239 (75%)

#### 7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	168	ARG	CD	33.07	38.57 – 47.75	-11.0
1	A	8	LYS	CD	40.58	23.50 – 34.42	10.6
1	A	42	ARG	CD	34.13	38.57 – 47.75	-9.8
1	A	170	PRO	CD	41.64	45.11 – 55.58	-8.3
1	A	8	LYS	HD2	3.14	0.58 – 2.64	7.4
1	A	8	LYS	HD3	3.14	0.54 – 2.65	7.3
1	A	141	GLY	HA3	1.50	2.08 – 5.71	-6.6
1	A	168	ARG	HD2	1.72	1.97 – 4.26	-6.1
1	A	173	ARG	HD3	1.55	1.81 – 4.39	-6.0
1	A	93	GLU	HG3	1.00	1.20 – 3.30	-5.9
1	A	70	ARG	HD2	1.77	1.97 – 4.26	-5.9
1	A	173	ARG	HD2	1.77	1.97 – 4.26	-5.9
1	A	127	ARG	HD2	1.78	1.97 – 4.26	-5.8
1	A	42	ARG	CG	33.88	21.24 – 33.19	5.6
1	A	168	ARG	HD3	1.72	1.81 – 4.39	-5.4
1	A	70	ARG	HD3	1.77	1.81 – 4.39	-5.2
1	A	17	ARG	HD2	4.30	1.97 – 4.26	5.2
1	A	127	ARG	HD3	1.78	1.81 – 4.39	-5.1
1	A	10	ILE	HG13	-0.86	-0.82 – 3.23	-5.1

### 7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

