



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 08:13 pm BST

PDB ID : 3RTX  
Title : Crystal structure of mammalian capping enzyme (Mce1) and Pol II CTD complex  
Authors : Ghosh, A.; Lima, C.D.  
Deposited on : 2011-05-04  
Resolution : 2.81 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

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

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

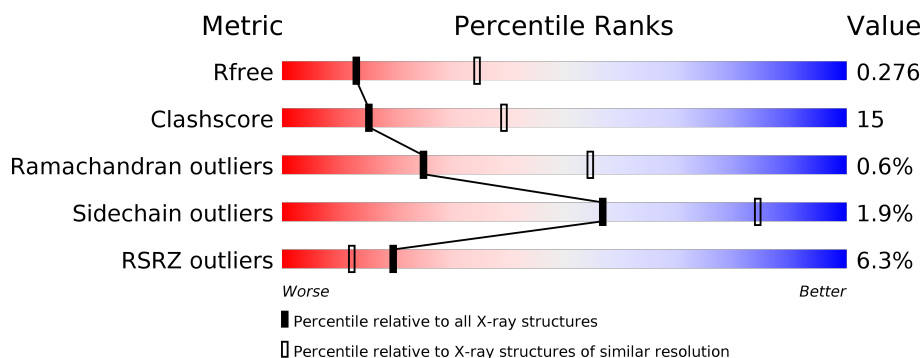
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.81 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))
$R_{free}$	130704	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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 respectively. 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	343	<div> <div>5%</div> <div> <div></div> <div>52%</div> <div>24%</div> <div>•</div> <div>24%</div> </div> </div>
1	B	343	<div> <div>4%</div> <div> <div></div> <div>51%</div> <div>23%</div> <div></div> <div>26%</div> </div> </div>
2	C	18	<div> <div></div> <div> <div></div> <div>61%</div> <div>11%</div> <div></div> <div>28%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4388 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 mRNA-capping enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2094	1336	360	382	16			
1	B	254	Total	C	N	O	S	0	0	0
			2039	1302	351	370	16			

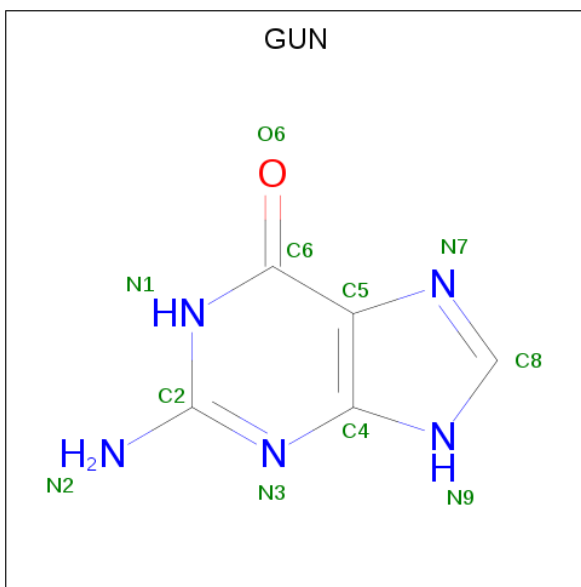
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	225	SER	-	EXPRESSION TAG	UNP O55236
B	225	SER	-	EXPRESSION TAG	UNP O55236

- Molecule 2 is a protein called RNA Polymerase II C-terminal domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	13	Total	C	N	O	P	0	0	0
			111	60	13	34	4			

- Molecule 3 is GUANINE (three-letter code: GUN) (formula: C<sub>5</sub>H<sub>5</sub>N<sub>5</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			11	5	5	1		
3	B	1	Total	C	N	O	0	0
			11	5	5	1		

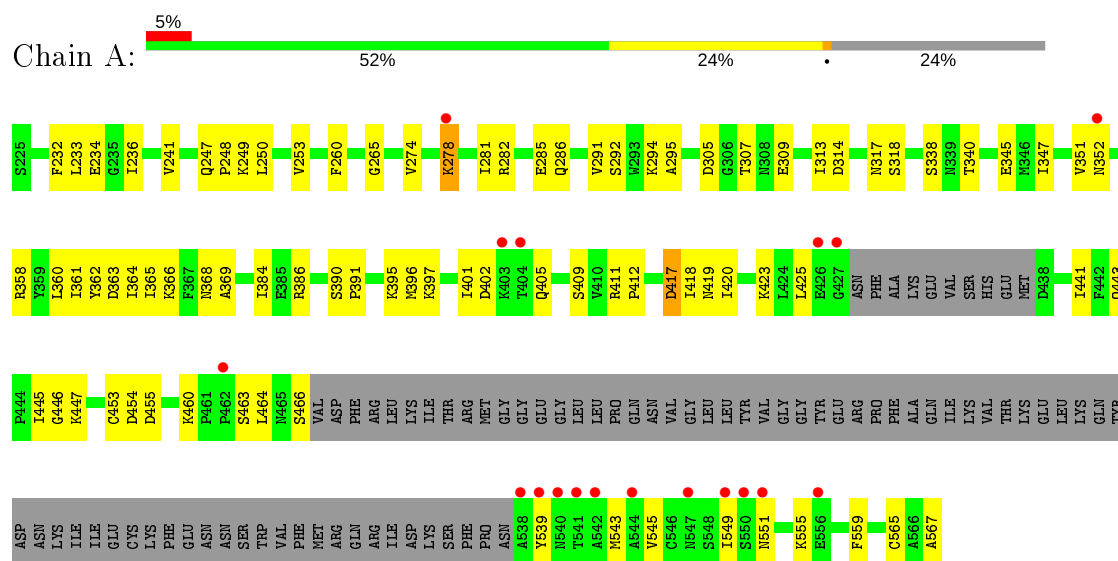
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	59	Total	O	0	0
			59	59		
4	B	63	Total	O	0	0
			63	63		

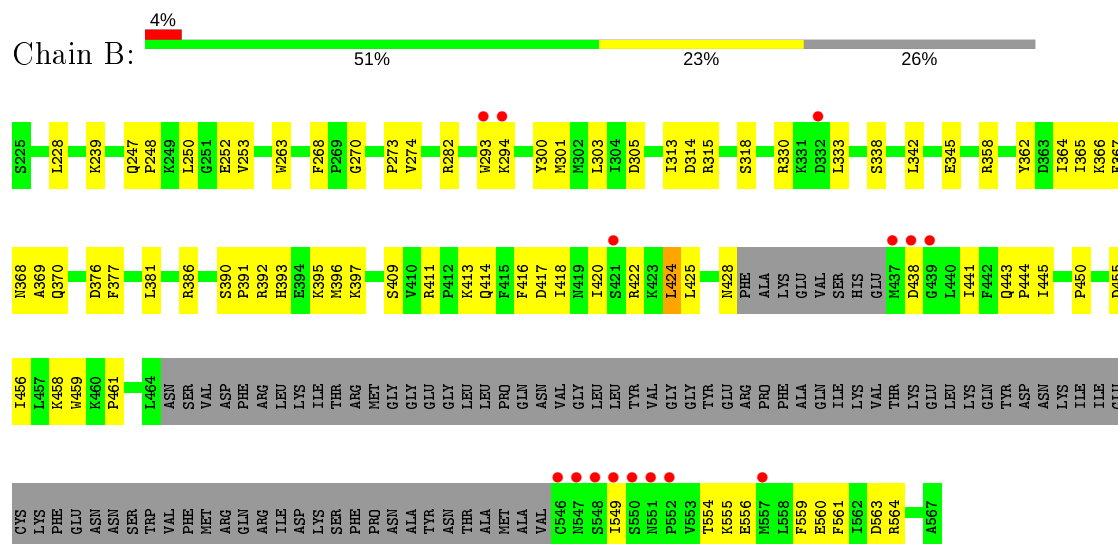
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: mRNA-capping enzyme

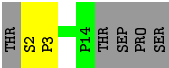


#### • Molecule 1: mRNA-capping enzyme



#### • Molecule 2: RNA Polymerase II C-terminal domain





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	82.98Å 114.75Å 150.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.81 45.89 – 2.81	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-2.81) 98.9 (45.89-2.81)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.32 (at 2.81Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, $R_{free}$	0.224 , 0.280 0.218 , 0.276	Depositor DCC
$R_{free}$ test set	910 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.3	Xtriage
Anisotropy	0.671	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 52.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4388	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.87% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.30	0/2137	0.52	0/2878
1	B	0.30	0/2081	0.52	0/2800
2	C	0.31	0/73	0.54	0/94
All	All	0.30	0/4291	0.52	0/5772

There are no bond length outliers.

There are no bond angle outliers.

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	2094	0	2108	70	0
1	B	2039	0	2057	65	0
2	C	111	0	78	4	0
3	A	11	0	5	0	0
3	B	11	0	5	0	0
4	A	59	0	0	1	0
4	B	63	0	0	3	0
All	All	4388	0	4253	127	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 15.



All (127) 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:423:LYS:HE2	1:B:428:ASN:HD22	1.31	0.93
1:A:420:ILE:HD11	1:B:414:GLN:HE22	1.46	0.80
1:A:286:GLN:HA	1:B:397:LYS:HD3	1.66	0.77
1:A:305:ASP:HA	1:A:338:SER:HA	1.67	0.75
1:B:358:ARG:HG2	1:B:409:SER:HB3	1.69	0.73
1:A:420:ILE:HG22	1:A:420:ILE:O	1.88	0.72
1:B:397:LYS:HB3	1:B:397:LYS:NZ	2.06	0.70
1:A:390:SER:HB3	1:A:391:PRO:HD3	1.74	0.70
1:A:386:ARG:HH12	2:C:3:PRO:HD2	1.57	0.70
1:B:390:SER:HB2	1:B:391:PRO:HD3	1.72	0.70
1:A:386:ARG:HH22	2:C:2:SEP:HA	1.57	0.69
1:A:285:GLU:HB3	1:A:565:CYS:SG	2.33	0.68
1:A:247:GLN:OE1	1:A:250:LEU:HB3	1.94	0.67
1:A:395:LYS:HB3	1:A:401:ILE:HD12	1.75	0.67
1:B:422:ARG:NH2	1:B:563:ASP:HB2	2.12	0.65
1:B:416:PHE:HB3	1:B:420:ILE:HD12	1.77	0.65
1:B:392:ARG:O	1:B:396:MET:HG3	1.96	0.65
1:B:315:ARG:HG3	4:B:100:HOH:O	1.97	0.64
1:A:395:LYS:HD3	1:A:401:ILE:HD11	1.80	0.63
1:B:268:PHE:CE2	1:B:270:GLY:HA3	2.33	0.63
1:A:278:LYS:HD3	1:A:551:ASN:HB3	1.80	0.62
1:A:351:VAL:HG12	1:A:352:ASN:ND2	2.16	0.60
1:A:402:ASP:HB3	1:A:405:GLN:HG2	1.82	0.60
1:A:420:ILE:CD1	1:B:414:GLN:HE22	2.13	0.60
1:A:567:ALA:O	1:B:411:ARG:HD3	2.02	0.59
1:B:345:GLU:HG2	1:B:362:TYR:HE2	1.69	0.58
1:B:444:PRO:HG3	1:B:455:ASP:HB3	1.84	0.58
1:B:239:LYS:HA	4:B:34:HOH:O	2.04	0.57
1:B:397:LYS:HB3	1:B:397:LYS:HZ2	1.68	0.57
1:B:247:GLN:HG3	1:B:248:PRO:HA	1.85	0.57
1:A:247:GLN:HG3	1:A:248:PRO:HA	1.85	0.57
1:B:314:ASP:OD2	1:B:318:SER:HB2	2.05	0.56
1:A:233:LEU:HD13	1:A:236:ILE:HD11	1.86	0.56
1:A:286:GLN:HA	1:B:397:LYS:CD	2.33	0.56
1:A:286:GLN:HG2	1:B:397:LYS:HD2	1.88	0.56
1:A:291:VAL:HG22	1:A:292:SER:N	2.20	0.56
1:A:294:LYS:NZ	1:A:460:LYS:HE3	2.21	0.56
1:B:330:ARG:HD3	1:B:386:ARG:O	2.07	0.55
1:A:340:THR:HA	1:A:366:LYS:O	2.07	0.55
1:B:559:PHE:O	1:B:563:ASP:HB2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:GLU:HG2	1:A:362:TYR:HE2	1.72	0.54
1:A:555:LYS:HB3	1:A:555:LYS:NZ	2.22	0.54
1:A:313:ILE:HD12	1:A:313:ILE:N	2.23	0.54
1:A:358:ARG:HG2	1:A:409:SER:OG	2.08	0.54
1:A:423:LYS:HE2	1:B:428:ASN:ND2	2.12	0.53
1:B:376:ASP:OD1	1:B:445:ILE:HB	2.08	0.53
1:A:417:ASP:HB3	1:A:419:ASN:OD1	2.09	0.52
1:B:274:VAL:O	1:B:458:LYS:HG2	2.10	0.52
1:B:333:LEU:HB3	1:B:395:LYS:HE3	1.92	0.52
1:A:453:CYS:C	1:A:455:ASP:H	2.12	0.52
1:B:422:ARG:HH22	1:B:563:ASP:CG	2.14	0.51
1:A:274:VAL:HG21	1:A:454:ASP:HA	1.92	0.51
1:B:365:ILE:HD12	1:B:365:ILE:N	2.25	0.51
1:B:300:TYR:CE1	1:B:314:ASP:HB3	2.46	0.51
1:B:555:LYS:HB3	1:B:555:LYS:NZ	2.26	0.50
1:B:422:ARG:HH22	1:B:563:ASP:HB2	1.75	0.50
1:B:425:LEU:HD12	1:B:559:PHE:HZ	1.76	0.50
1:A:420:ILE:CG2	1:A:420:ILE:O	2.59	0.50
1:B:247:GLN:OE1	1:B:250:LEU:HB3	2.12	0.50
1:B:253:VAL:HG13	1:B:303:LEU:HD23	1.93	0.50
1:A:445:ILE:HD12	1:A:446:GLY:N	2.27	0.50
1:A:364:ILE:O	1:A:364:ILE:HG23	2.12	0.50
1:A:232:PHE:CD2	1:A:241:VAL:HG11	2.48	0.49
1:A:232:PHE:CG	1:A:241:VAL:HG11	2.47	0.49
1:B:368:ASN:O	1:B:369:ALA:HB3	2.12	0.49
1:B:315:ARG:HD3	4:B:16:HOH:O	2.11	0.49
1:A:446:GLY:HA3	4:A:88:HOH:O	2.12	0.49
1:B:342:LEU:HD23	1:B:364:ILE:HG13	1.95	0.49
1:A:361:ILE:HG22	1:A:384:ILE:HD13	1.95	0.48
1:B:248:PRO:O	1:B:252:GLU:HG3	2.13	0.48
1:A:386:ARG:NH1	2:C:3:PRO:HD2	2.25	0.48
1:B:386:ARG:HH11	1:B:386:ARG:HG3	1.78	0.48
1:B:556:GLU:O	1:B:560:GLU:HG2	2.14	0.48
1:B:268:PHE:CE1	1:B:301:MET:HG3	2.49	0.48
1:B:293:TRP:HB2	1:B:424:LEU:HD21	1.95	0.48
1:B:263:TRP:CE3	1:B:450:PRO:HB2	2.48	0.48
1:A:386:ARG:NH2	2:C:2:SEP:HA	2.29	0.47
1:B:362:TYR:CZ	1:B:413:LYS:HE2	2.51	0.46
1:A:305:ASP:OD1	1:A:338:SER:HB2	2.16	0.46
1:A:418:ILE:C	1:A:420:ILE:H	2.19	0.46
1:B:441:ILE:HD11	1:B:456:ILE:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:ARG:HG3	1:A:412:PRO:HD2	1.99	0.45
1:B:422:ARG:HH22	1:B:563:ASP:CB	2.29	0.45
1:A:539:TYR:O	1:A:543:MET:HB2	2.17	0.45
1:A:282:ARG:O	1:A:285:GLU:HG2	2.16	0.45
1:A:314:ASP:OD2	1:A:318:SER:HB2	2.17	0.45
1:A:368:ASN:O	1:A:369:ALA:HB3	2.17	0.44
1:A:281:ILE:HG12	1:A:281:ILE:O	2.16	0.44
1:A:294:LYS:HZ3	1:A:460:LYS:HE3	1.81	0.44
1:B:294:LYS:O	1:B:438:ASP:HB2	2.17	0.44
1:B:366:LYS:HG3	1:B:370:GLN:O	2.18	0.44
1:B:560:GLU:O	1:B:564:ARG:HG3	2.17	0.44
1:A:425:LEU:HD12	1:A:559:PHE:HZ	1.82	0.44
1:A:397:LYS:HB3	1:A:397:LYS:NZ	2.32	0.43
1:B:459:TRP:CH2	1:B:461:PRO:HG3	2.53	0.43
1:A:441:ILE:O	1:A:441:ILE:HG23	2.18	0.43
1:B:367:PHE:O	1:B:370:GLN:N	2.48	0.43
1:B:377:PHE:CE2	1:B:381:LEU:HD11	2.53	0.43
1:A:463:SER:O	1:A:464:LEU:HB2	2.18	0.43
1:A:345:GLU:HG2	1:A:362:TYR:CE2	2.52	0.43
1:B:228:LEU:N	1:B:228:LEU:HD12	2.34	0.43
1:B:313:ILE:HD12	1:B:313:ILE:N	2.33	0.43
1:A:545:VAL:O	1:A:549:ILE:HG13	2.18	0.43
1:A:347:ILE:HD13	1:A:360:LEU:HD11	2.01	0.43
1:A:453:CYS:C	1:A:455:ASP:N	2.71	0.43
1:B:273:PRO:HB3	1:B:456:ILE:HG22	2.01	0.42
1:A:365:ILE:HD12	1:A:365:ILE:N	2.34	0.42
1:B:459:TRP:CZ3	1:B:461:PRO:HG3	2.54	0.42
1:A:249:LYS:O	1:A:253:VAL:HG23	2.19	0.42
1:B:393:HIS:HA	1:B:396:MET:HE3	2.02	0.42
1:B:282:ARG:HA	1:B:561:PHE:CZ	2.55	0.42
1:A:555:LYS:HB3	1:A:555:LYS:HZ3	1.84	0.42
1:A:358:ARG:HH11	1:A:358:ARG:HG2	1.84	0.41
1:B:554:THR:C	1:B:556:GLU:N	2.73	0.41
1:B:416:PHE:CD1	1:B:416:PHE:N	2.88	0.41
1:A:402:ASP:O	1:A:405:GLN:HG2	2.20	0.41
1:B:420:ILE:O	1:B:420:ILE:HG22	2.21	0.41
1:A:278:LYS:CD	1:A:551:ASN:HB3	2.49	0.41
1:B:305:ASP:HA	1:B:338:SER:HA	2.03	0.41
1:A:295:ALA:HB3	1:A:345:GLU:OE1	2.20	0.41
1:A:351:VAL:HG21	1:A:358:ARG:NH2	2.36	0.41
1:A:466:SER:C	1:A:545:VAL:HG11	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:MET:HG2	1:A:401:ILE:HG22	2.01	0.41
1:A:260:PHE:HA	1:A:366:LYS:HE3	2.03	0.41
1:A:307:THR:O	1:A:309:GLU:HG2	2.21	0.40
1:B:549:ILE:HG22	1:B:549:ILE:O	2.21	0.40
1:B:554:THR:C	1:B:556:GLU:H	2.23	0.40

There are no symmetry-related clashes.

## 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	256/343 (75%)	234 (91%)	20 (8%)	2 (1%)	19	47
1	B	248/343 (72%)	219 (88%)	28 (11%)	1 (0%)	34	64
2	C	8/18 (44%)	6 (75%)	2 (25%)	0	100	100
All	All	512/704 (73%)	459 (90%)	50 (10%)	3 (1%)	25	54

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	GLY
1	B	418	ILE
1	A	278	LYS

### 5.3.2 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 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	234/307 (76%)	228 (97%)	6 (3%)	46	78
1	B	229/307 (75%)	226 (99%)	3 (1%)	69	90
2	C	9/13 (69%)	9 (100%)	0	100	100
All	All	472/627 (75%)	463 (98%)	9 (2%)	57	84

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	GLU
1	A	317	ASN
1	A	363	ASP
1	A	417	ASP
1	A	443	GLN
1	A	447	LYS
1	B	417	ASP
1	B	424	LEU
1	B	443	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	321	HIS
1	A	352	ASN
1	A	368	ASN
1	A	382	GLN
1	A	443	GLN
1	B	254	GLN
1	B	317	ASN
1	B	352	ASN
1	B	368	ASN
1	B	428	ASN
1	B	443	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SEP	C	9	2	8,9,10	2.25	1 (12%)	8,12,14	4.92	3 (37%)
2	SEP	C	6	2	8,9,10	2.24	1 (12%)	8,12,14	5.01	3 (37%)
2	SEP	C	2	2	8,9,10	2.21	1 (12%)	8,12,14	5.04	3 (37%)
2	SEP	C	13	2	8,9,10	2.19	1 (12%)	8,12,14	5.07	3 (37%)

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	SEP	C	9	2	-	5/5/8/10	-
2	SEP	C	6	2	-	2/5/8/10	-
2	SEP	C	2	2	-	5/5/8/10	-
2	SEP	C	13	2	-	3/5/8/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	9	SEP	OG-CB	-5.73	1.22	1.44
2	C	6	SEP	OG-CB	-5.72	1.22	1.44
2	C	2	SEP	OG-CB	-5.61	1.23	1.44
2	C	13	SEP	OG-CB	-5.54	1.23	1.44

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	13	SEP	OG-CB-CA	13.70	121.47	108.14
2	C	2	SEP	OG-CB-CA	13.65	121.43	108.14
2	C	6	SEP	OG-CB-CA	13.60	121.38	108.14
2	C	9	SEP	OG-CB-CA	13.31	121.10	108.14
2	C	9	SEP	O3P-P-O1P	2.65	121.07	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	6	SEP	O3P-P-O1P	2.63	120.97	110.68
2	C	2	SEP	O3P-P-O1P	2.62	120.93	110.68
2	C	13	SEP	O3P-P-O1P	2.62	120.92	110.68
2	C	13	SEP	O2P-P-OG	2.15	112.46	106.73
2	C	2	SEP	O2P-P-OG	2.12	112.36	106.73
2	C	9	SEP	O2P-P-OG	2.01	112.09	106.73
2	C	6	SEP	O2P-P-OG	2.01	112.09	106.73

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	9	SEP	N-CA-CB-OG
2	C	9	SEP	CB-OG-P-O2P
2	C	9	SEP	CB-OG-P-O3P
2	C	2	SEP	N-CA-CB-OG
2	C	2	SEP	CB-OG-P-O3P
2	C	13	SEP	CB-OG-P-O2P
2	C	13	SEP	CB-OG-P-O3P
2	C	2	SEP	CB-OG-P-O1P
2	C	13	SEP	CB-OG-P-O1P
2	C	9	SEP	CA-CB-OG-P
2	C	6	SEP	CA-CB-OG-P
2	C	6	SEP	N-CA-CB-OG
2	C	2	SEP	CB-OG-P-O2P
2	C	9	SEP	CB-OG-P-O1P
2	C	2	SEP	CA-CB-OG-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	2	SEP	2	0

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GUN	A	1	-	9,12,12	1.50	2 (22%)	8,17,17	3.41	5 (62%)
3	GUN	B	2	-	9,12,12	1.51	2 (22%)	8,17,17	3.34	5 (62%)

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
3	GUN	A	1	-	-	-	0/2/2/2
3	GUN	B	2	-	-	-	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	GUN	C6-N1	3.46	1.39	1.33
3	B	2	GUN	C6-N1	3.46	1.39	1.33
3	A	1	GUN	C4-N3	2.17	1.40	1.36
3	B	2	GUN	C4-N3	2.12	1.40	1.36

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	GUN	N3-C2-N1	-5.74	119.56	127.22
3	B	2	GUN	N3-C2-N1	-5.70	119.62	127.22
3	A	1	GUN	C2-N3-C4	4.94	121.00	115.36
3	B	2	GUN	C2-N3-C4	4.78	120.82	115.36
3	A	1	GUN	C6-N1-C2	3.54	121.55	115.93
3	B	2	GUN	C6-N1-C2	3.49	121.47	115.93
3	A	1	GUN	C6-C5-C4	-2.98	117.95	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2	GUN	C6-C5-C4	-2.81	118.12	120.80
3	B	2	GUN	C5-C6-N1	-2.36	120.20	123.43
3	A	1	GUN	C5-C6-N1	-2.36	120.21	123.43

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

### 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	262/343 (76%)	0.03	18 (6%) 16 10	27, 52, 106, 122	2 (0%)
1	B	254/343 (74%)	-0.03	15 (5%) 22 14	29, 51, 107, 143	0
2	C	9/18 (50%)	0.18	0 100 100	64, 89, 107, 111	0
All	All	525/704 (74%)	0.00	33 (6%) 20 12	27, 52, 107, 143	2 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	541	THR	5.4
1	B	546	CYS	5.2
1	B	438	ASP	4.4
1	A	539	TYR	4.3
1	B	550	SER	4.1
1	B	551	ASN	3.9
1	A	427	GLY	3.8
1	B	437	MET	3.6
1	A	352	ASN	3.5
1	A	540	ASN	3.4
1	A	404	THR	3.2
1	A	426	GLU	3.2
1	A	462	PRO	3.0
1	B	548	SER	3.0
1	A	551	ASN	2.9
1	A	278	LYS	2.9
1	A	403	LYS	2.7
1	A	538	ALA	2.5
1	B	332	ASP	2.5
1	B	549	ILE	2.4
1	B	547	ASN	2.4
1	B	557	MET	2.4
1	A	542	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	439	GLY	2.4
1	A	550	SER	2.3
1	B	552	PRO	2.2
1	A	549	ILE	2.2
1	B	294	LYS	2.1
1	A	556	GLU	2.1
1	A	544	ALA	2.1
1	B	421	SER	2.1
1	B	293	TRP	2.0
1	A	547	ASN	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors(Å <sup>2</sup> )	Q<0.9
2	SEP	C	13	10/11	0.64	0.27	98,108,120,121	0
2	SEP	C	2	10/11	0.69	0.26	116,122,134,135	0
2	SEP	C	6	10/11	0.86	0.16	85,94,116,117	0
2	SEP	C	9	10/11	0.92	0.13	87,89,91,91	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors(Å <sup>2</sup> )	Q<0.9
3	GUN	A	1	11/11	0.86	0.24	90,96,98,98	0
3	GUN	B	2	11/11	0.87	0.23	80,89,96,97	0

## 6.5 Other polymers

There are no such residues in this entry.