



# wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 27, 2020 – 02:11 PM BST

PDB ID : 6UU0  
Title : E. coli sigma-S transcription initiation complex with a 3-nt RNA and a mismatching GTP ("Fresh" crystal soaked with GTP for 1 hour)  
Authors : Zuo, Y.; De, S.; Steitz, T.A.  
Deposited on : 2019-10-30  
Resolution : 3.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<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 : 2.13  
buster-report : 1.1.7 (2018)  
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) : 2.13

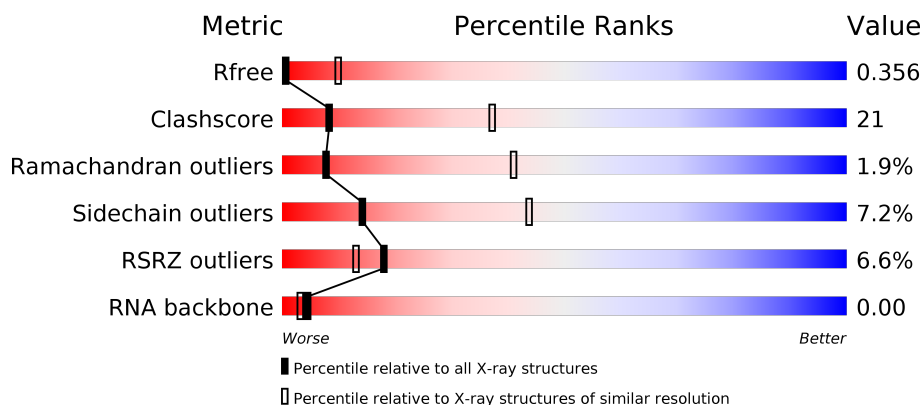
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.90 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	1002 (4.14-3.66)
Clashscore	141614	1004 (4.12-3.68)
Ramachandran outliers	138981	1021 (4.14-3.66)
Sidechain outliers	138945	1014 (4.14-3.66)
RSRZ outliers	127900	1275 (4.20-3.60)
RNA backbone	3102	1040 (4.76-3.00)

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	AAA	242	<div> <div>7%</div> <div>60%</div> <div>30%</div> <div>5%</div> </div>
1	BBB	242	<div> <div>10%</div> <div>61%</div> <div>31%</div> <div>6%</div> </div>
2	CCC	1342	<div> <div>4%</div> <div>63%</div> <div>33%</div> <div>.</div> </div>
3	DDD	1407	<div> <div>7%</div> <div>58%</div> <div>35%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
4	EEE	90	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>58%</div><div>28%</div><div>•</div><div>12%</div></div></div>
5	FFF	336	<div><div><div></div><div></div><div></div></div><div><div>9%</div><div>50%</div><div>29%</div><div>•</div><div>18%</div></div></div>
6	111	50	<div><div><div></div><div></div><div></div></div><div><div>6%</div><div>18%</div><div>46%</div><div></div><div>36%</div></div></div>
7	222	50	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>18%</div><div>52%</div><div></div><div>30%</div></div></div>
8	333	3	<div><div><div></div><div></div><div></div></div><div><div></div><div>33%</div><div>33%</div><div></div><div>33%</div></div></div>

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 28977 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	230	Total	C	N	O	S	0	0	0
			1787	1112	317	352	6			
1	BBB	228	Total	C	N	O	S	0	0	0
			1767	1100	312	349	6			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-6	ALA	-	expression tag	UNP A0A377D9Q8
AAA	-5	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-4	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-3	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-2	HIS	-	expression tag	UNP A0A377D9Q8
AAA	-1	HIS	-	expression tag	UNP A0A377D9Q8
AAA	0	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-6	ALA	-	expression tag	UNP A0A377D9Q8
BBB	-5	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-4	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-3	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-2	HIS	-	expression tag	UNP A0A377D9Q8
BBB	-1	HIS	-	expression tag	UNP A0A377D9Q8
BBB	0	HIS	-	expression tag	UNP A0A377D9Q8

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	CCC	1341	Total	C	N	O	S	0	0	0
			10576	6636	1842	2055	43			

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	DDD	1350	Total	C	N	O	S	0	0	0
			10478	6578	1867	1984	49			

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	EEE	79	Total	C	N	O	S	0	0	0
			627	382	118	126	1			

- Molecule 5 is a protein called RNA polymerase sigma factor RpoS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	FFF	277	Total	C	N	O	S	0	0	0
			2253	1411	415	423	4			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
FFF	2	GLY	SER	conflict	UNP P13445
FFF	33	GLU	GLN	conflict	UNP P13445
FFF	329	LEU	-	expression tag	UNP P13445
FFF	330	GLU	-	expression tag	UNP P13445
FFF	331	HIS	-	expression tag	UNP P13445
FFF	332	HIS	-	expression tag	UNP P13445
FFF	333	HIS	-	expression tag	UNP P13445
FFF	334	HIS	-	expression tag	UNP P13445
FFF	335	HIS	-	expression tag	UNP P13445
FFF	336	HIS	-	expression tag	UNP P13445

- Molecule 6 is a DNA chain called Synthetic DNA 50-MER (promoter non-template strand).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	111	32	Total	C	N	O	P	0	0	0
			660	313	122	193	32			

- Molecule 7 is a DNA chain called Synthetic DNA 50-MER (promoter template strand).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	222	35	Total	C	N	O	P	0	0	0
			716	342	132	208	34			

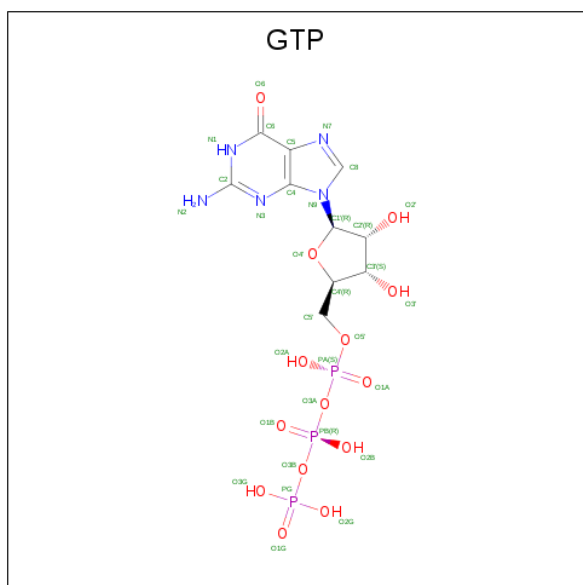
- Molecule 8 is a RNA chain called RNA 3-mer (de novo synthesized).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	333	3	Total	C	N	O	P	0	0	0
			77	30	15	27	5			

- Molecule 9 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	CCC	1	Total	Mg	0	0
			1	1		
9	333	1	Total	Mg	0	0
			1	1		


- Molecule 10 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>14</sub>P<sub>3</sub>).

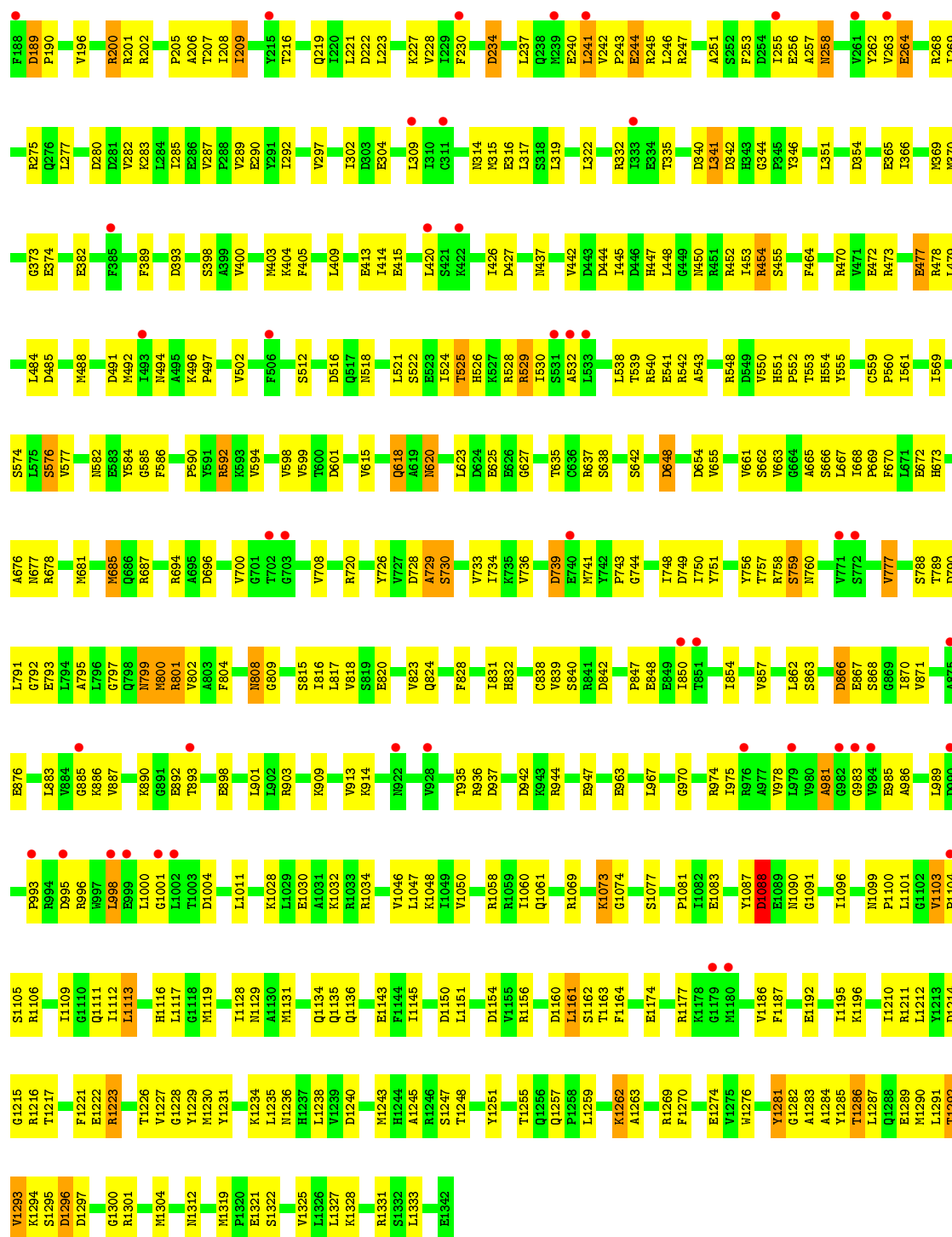


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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.

- Chain AAA:
- 
- 7% 60% 30% 5%
- ALA HIS HIS HIS HIS HIS HIS MET GLY SER VAL T6 L9 K10 P11 R12 Q18 T22 K25 L28 E29 P30 I31 E32 H37 N41 A42 L43 R44 R45 I46 L47 S50 M51 P52 A55 V56 T57 E58 V59 I61 V64 T70 Q75 P76 P77

- Chain BBB: 

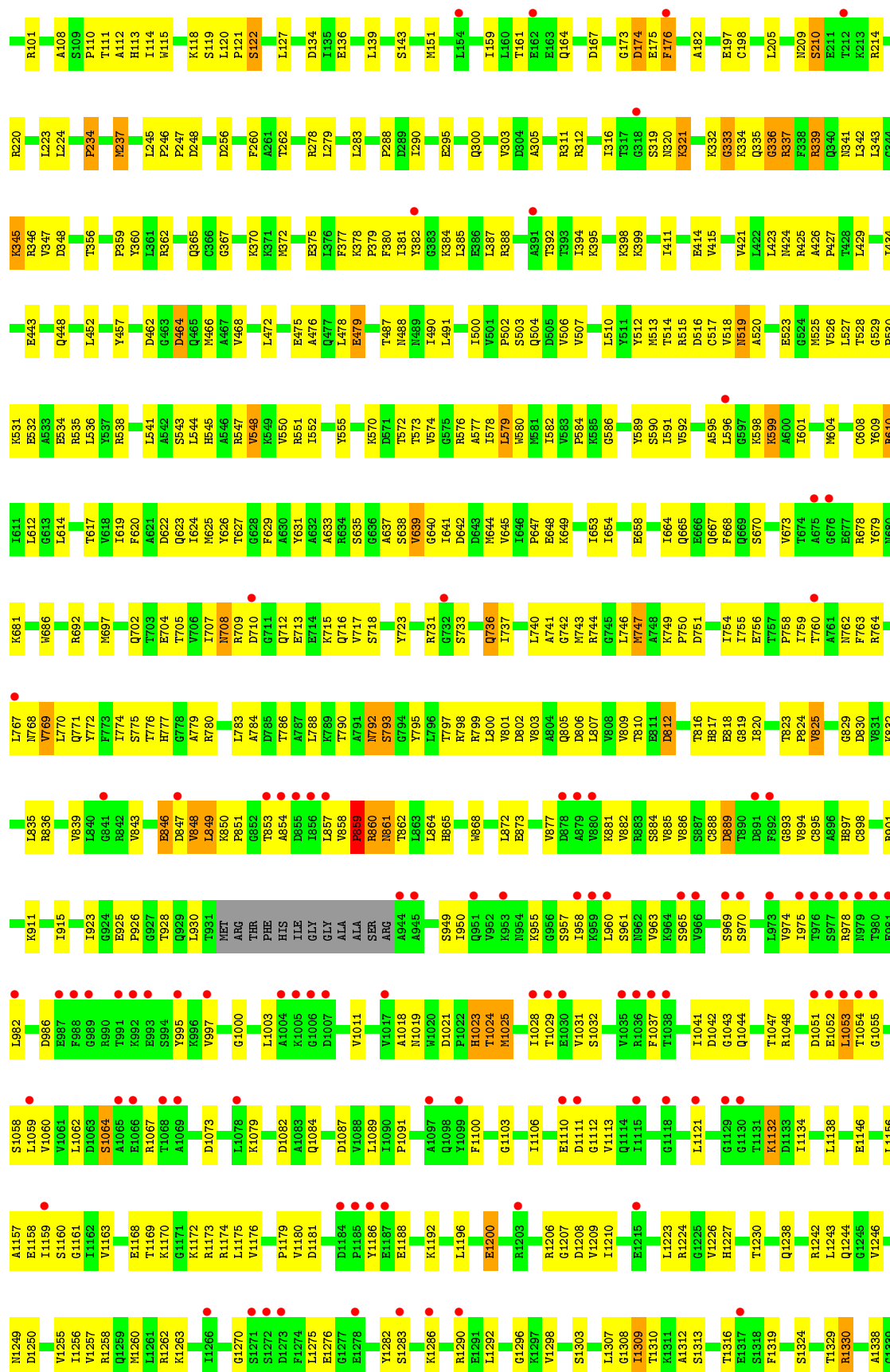
- Chain CCC: 



- Molecule 3: DNA-directed RNA polymerase subunit beta'











## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.80Å 156.16Å 233.37Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.20 – 3.90 49.43 – 3.90	Depositor EDS
% Data completeness (in resolution range)	98.2 (49.20-3.90) 98.3 (49.43-3.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.05 (at 3.88Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, $R_{free}$	0.314 , 0.368 0.306 , 0.356	Depositor DCC
$R_{free}$ test set	2123 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	168.6	Xtriage
Anisotropy	0.188	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 190.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.31$ , $\langle L^2 \rangle = 0.15$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	28977	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	287.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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: GTP, ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	AAA	0.64	0/1809	0.75	0/2450
1	BBB	0.65	0/1789	0.73	0/2425
2	CCC	0.63	0/10745	0.80	5/14499 (0.0%)
3	DDD	0.63	0/10636	0.77	0/14362
4	EEE	0.62	0/629	0.78	0/847
5	FFF	0.65	0/2282	0.67	0/3076
6	111	0.31	0/739	0.64	0/1137
7	222	0.32	0/803	0.61	0/1238
8	333	0.43	0/50	0.62	0/76
All	All	0.62	0/29482	0.76	5/40110 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	CCC	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CCC	153	PRO	N-CD-CG	-6.65	93.23	103.20
2	CCC	1088	ASP	CB-CA-C	-5.99	98.42	110.40
2	CCC	1048	LYS	CB-CA-C	-5.52	99.35	110.40
2	CCC	454	ARG	CB-CA-C	-5.40	99.60	110.40
2	CCC	1222	GLU	CB-CA-C	5.25	120.89	110.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	CCC	1282	GLY	Peptide

## 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	AAA	1787	0	1813	72	0
1	BBB	1767	0	1789	79	0
2	CCC	10576	0	10591	443	0
3	DDD	10478	0	10691	561	2
4	EEE	627	0	634	22	0
5	FFF	2253	0	2298	115	1
6	111	660	0	362	56	1
7	222	716	0	396	58	1
8	333	77	0	32	7	0
9	333	1	0	0	0	0
9	CCC	1	0	0	0	0
10	CCC	32	0	12	7	0
11	DDD	2	0	0	1	0
All	All	28977	0	28618	1207	3

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 21.

The worst 5 of 1207 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:525:MET:O	3:DDD:548:VAL:HG22	1.37	1.23
3:DDD:572:THR:HG21	3:DDD:589:TYR:OH	1.35	1.22
3:DDD:525:MET:N	3:DDD:548:VAL:HG23	1.58	1.18
3:DDD:825:VAL:HG11	3:DDD:1242:ARG:NH1	1.60	1.17
2:CCC:1106:ARG:NH1	10:CCC:1402:GTP:O1G	1.79	1.16

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:DDD:1174:ARG:NH2	7:222:32:DA:OP1[3_644]	1.88	0.32
3:DDD:210:SER:OG	6:111:28:DA:OP2[3_644]	1.89	0.31
5:FFF:67:TYR:O	5:FFF:299:ARG:NH2[3_644]	2.06	0.14

## 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	AAA	228/242 (94%)	211 (92%)	11 (5%)	6 (3%)	5	35
1	BBB	226/242 (93%)	207 (92%)	14 (6%)	5 (2%)	6	38
2	CCC	1339/1342 (100%)	1244 (93%)	68 (5%)	27 (2%)	7	40
3	DDD	1346/1407 (96%)	1231 (92%)	90 (7%)	25 (2%)	8	41
4	EEE	77/90 (86%)	73 (95%)	4 (5%)	0	100	100
5	FFF	275/336 (82%)	251 (91%)	20 (7%)	4 (2%)	10	45
All	All	3491/3659 (95%)	3217 (92%)	207 (6%)	67 (2%)	8	41

5 of 67 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	117	HIS
1	BBB	193	GLU
1	BBB	194	GLN
2	CCC	46	GLN
2	CCC	247	ARG

### 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	AAA	198/208 (95%)	178 (90%)	20 (10%)	7	30
1	BBB	196/208 (94%)	182 (93%)	14 (7%)	14	44
2	CCC	1156/1157 (100%)	1066 (92%)	90 (8%)	12	41
3	DDD	1127/1168 (96%)	1054 (94%)	73 (6%)	17	46
4	EEE	67/74 (90%)	64 (96%)	3 (4%)	27	56
5	FFF	240/292 (82%)	226 (94%)	14 (6%)	20	50
All	All	2984/3107 (96%)	2770 (93%)	214 (7%)	14	44

5 of 214 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	CCC	801	ARG
2	CCC	1286	THR
4	EEE	8	ASP
2	CCC	815	SER
2	CCC	1073	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
8	333	1/3 (33%)	1 (100%)	0

All (1) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	333	16	G

There are no RNA pucker outliers to report.

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

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



## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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$
10	GTP	CCC	1402	9	26,34,34	1.14	1 (3%)	33,54,54	2.33	8 (24%)

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
10	GTP	CCC	1402	9	-	4/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	CCC	1402	GTP	C6-C5	4.16	1.48	1.41

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	CCC	1402	GTP	C6-C5-C4	-7.08	114.04	120.80
10	CCC	1402	GTP	C1'-N9-C4	-4.43	118.87	126.64
10	CCC	1402	GTP	C6-N1-C2	4.37	122.87	115.93
10	CCC	1402	GTP	C5-C6-N1	-3.98	117.99	123.43
10	CCC	1402	GTP	N3-C2-N1	-3.47	122.59	127.22

There are no chirality outliers.

All (4) torsion outliers are listed below:

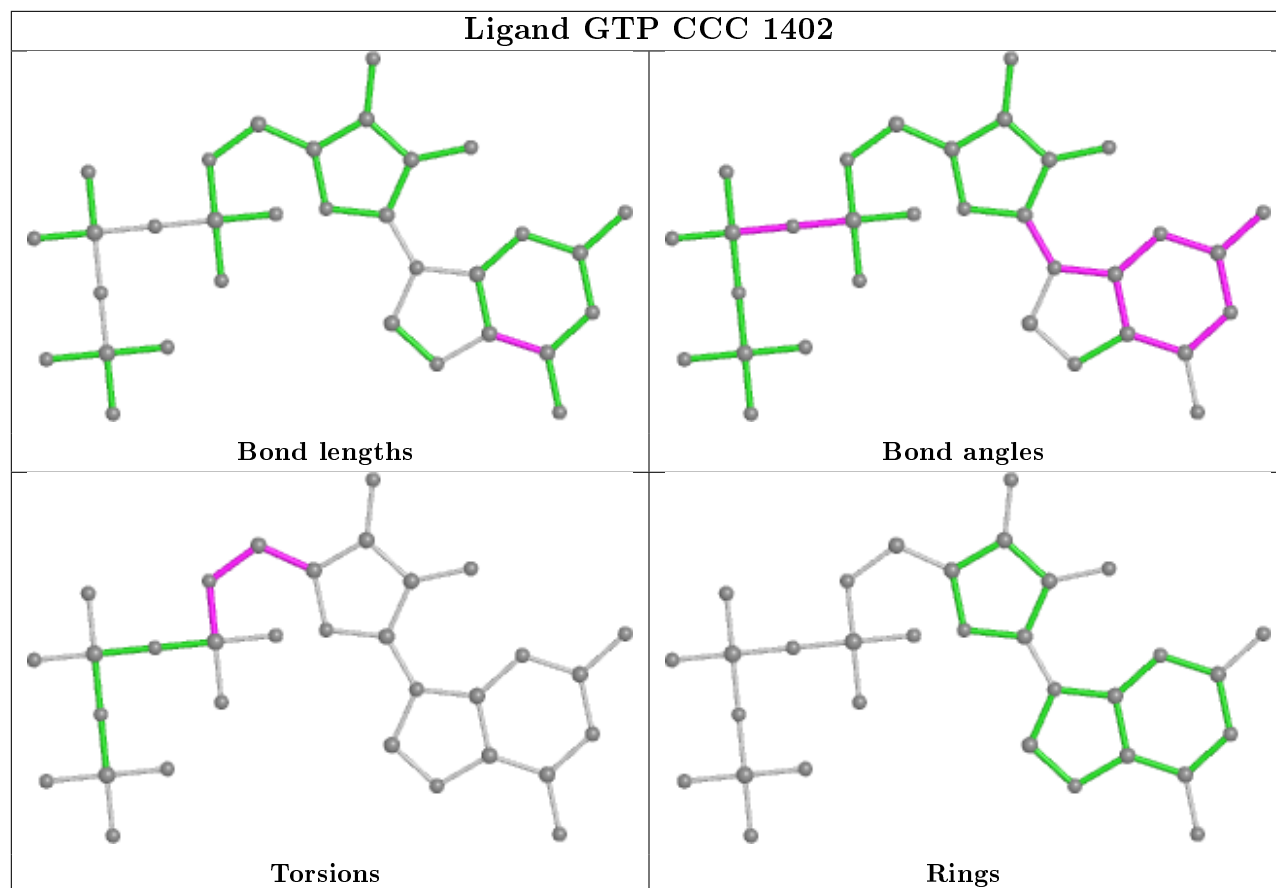
Mol	Chain	Res	Type	Atoms
10	CCC	1402	GTP	C5'-O5'-PA-O3A
10	CCC	1402	GTP	C5'-O5'-PA-O2A
10	CCC	1402	GTP	C4'-C5'-O5'-PA
10	CCC	1402	GTP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	CCC	1402	GTP	7	0

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.



## 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	AAA	230/242 (95%)	0.17	17 (7%) 14 11	226, 314, 364, 413	0
1	BBB	228/242 (94%)	0.35	24 (10%) 6 5	225, 304, 376, 418	0
2	CCC	1341/1342 (99%)	0.05	54 (4%) 38 30	142, 264, 377, 490	0
3	DDD	1350/1407 (95%)	0.20	104 (7%) 13 10	159, 274, 397, 472	0
4	EEE	79/90 (87%)	-0.30	1 (1%) 77 68	206, 300, 449, 524	0
5	FFF	277/336 (82%)	0.38	31 (11%) 5 5	207, 306, 397, 435	0
6	111	32/50 (64%)	-0.17	3 (9%) 8 7	241, 310, 392, 431	0
7	222	35/50 (70%)	-0.16	1 (2%) 51 40	224, 303, 435, 475	0
8	333	2/3 (66%)	-0.18	0 100 100	261, 261, 261, 291	0
All	All	3574/3762 (95%)	0.15	235 (6%) 18 13	142, 283, 392, 524	0

The worst 5 of 235 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	CCC	1001	GLY	10.4
3	DDD	1054	THR	9.2
3	DDD	1055	GLY	8.2
3	DDD	1066	GLU	6.4
6	111	46	DG	6.4

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

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

### 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

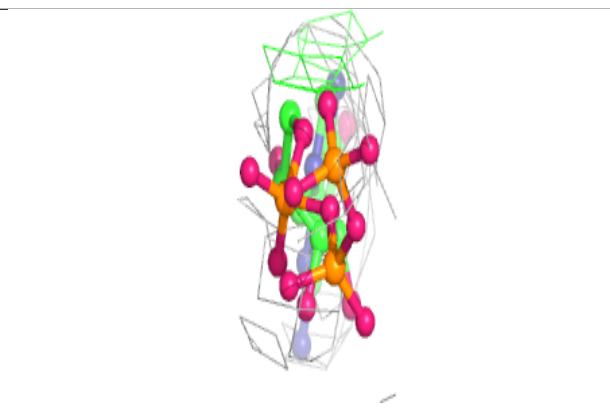
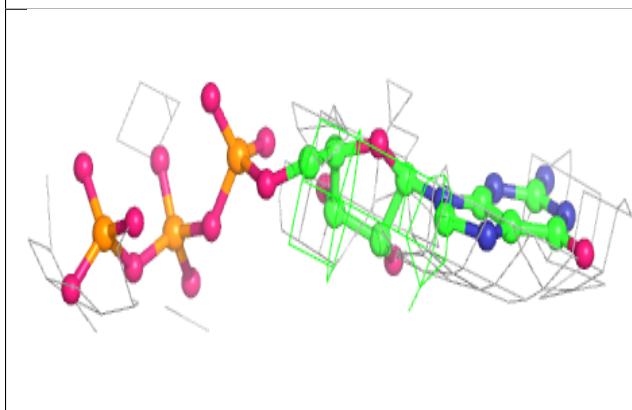
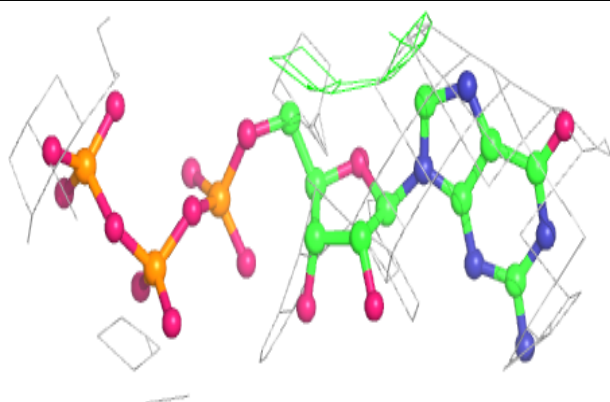
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
10	GTP	CCC	1402	32/32	0.91	0.28	180,256,340,342	0
11	ZN	DDD	1501	1/1	0.97	0.07	436,436,436,436	0
9	MG	333	101	1/1	0.98	0.20	154,154,154,154	0
9	MG	CCC	1401	1/1	1.00	0.16	309,309,309,309	0
11	ZN	DDD	1502	1/1	1.00	0.17	351,351,351,351	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

### Electron density around GTP CCC 1402:

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.