



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 20, 2023 – 07:11 PM JST

PDB ID : 7DAE
Title : EPB in complex with tubulin
Authors : Wu, C.; Wang, Y.
Deposited on : 2020-10-16
Resolution : 2.39 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

A user guide is available at

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

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>.

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 : 2.36
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) : 2.36

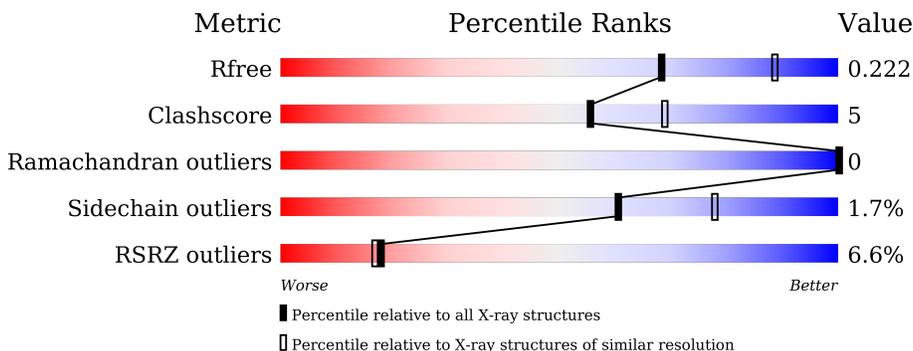
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.39 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	451	 0% 86% 12% .
1	C	451	 87% 10% .
2	B	445	 3% 83% 12% . .
2	D	445	 5% 85% 11% .
3	E	143	 7% 80% 7% 13%
4	F	384	 24% 74% 16% . 9%

2 Entry composition [i](#)

There are 13 unique types of molecules in this entry. The entry contains 18508 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 Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	439	Total	C	N	O	S	0	7	0
			3464	2192	588	660	24			
1	C	440	Total	C	N	O	S	0	11	0
			3475	2201	585	663	26			

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	427	Total	C	N	O	S	0	7	0
			3402	2138	581	656	27			
2	D	430	Total	C	N	O	S	0	5	0
			3388	2124	579	658	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	124	Total	C	N	O	S	0	4	0
			1042	643	188	205	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	initiating methionine	UNP P63042
E	4	ALA	-	expression tag	UNP P63042

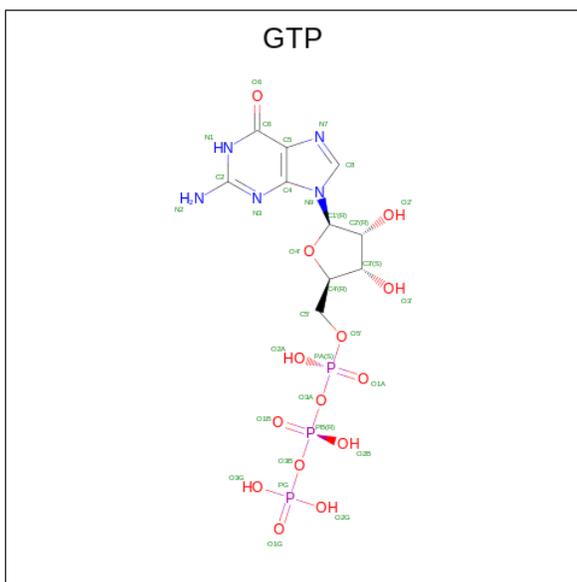
- Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	F	348	Total	C	N	O	S	0	4	0
			2882	1850	494	523	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43
F	383	HIS	-	expression tag	UNP E1BQ43
F	384	HIS	-	expression tag	UNP E1BQ43

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
5	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	1	Total	Mg	0	0
			1	1		
6	B	2	Total	Mg	0	0
			2	2		
6	C	1	Total	Mg	0	0
			1	1		

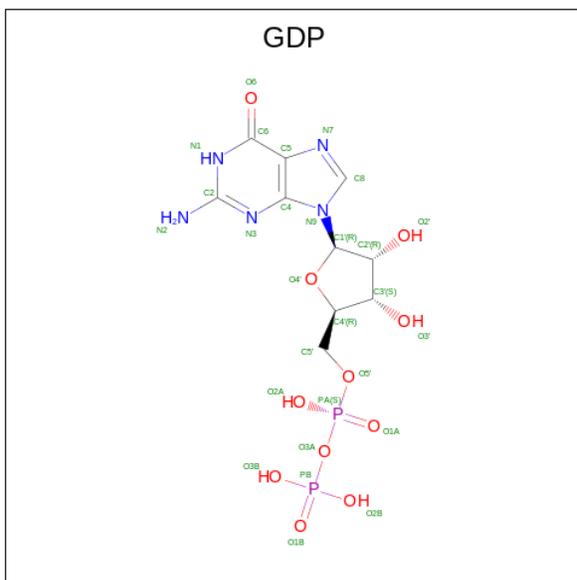
- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Ca 1 1	0	0
7	B	1	Total Ca 1 1	0	0
7	C	1	Total Ca 1 1	0	0
7	E	1	Total Ca 1 1	0	0

- Molecule 8 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

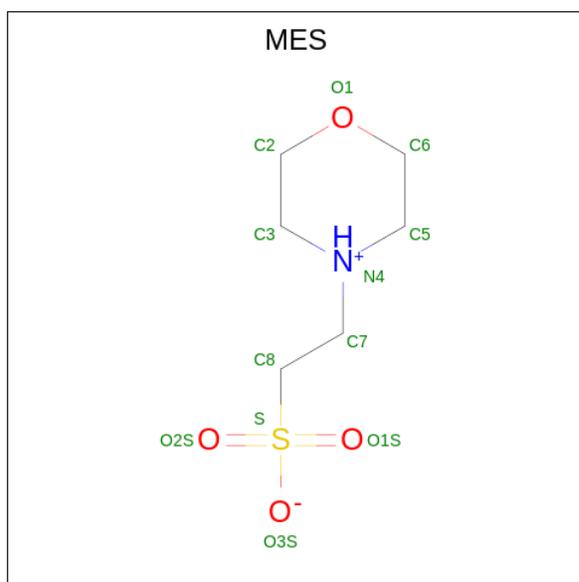
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cl 1 1	0	0

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



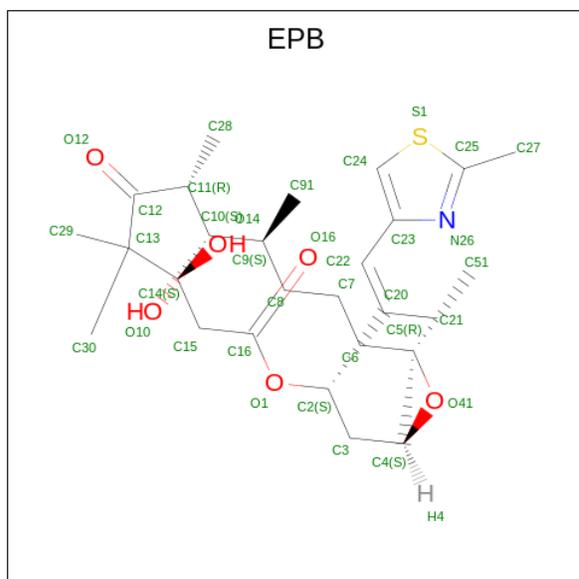
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C N O P 28 10 5 11 2	0	0
9	D	1	Total C N O P 28 10 5 11 2	0	0

- Molecule 10 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



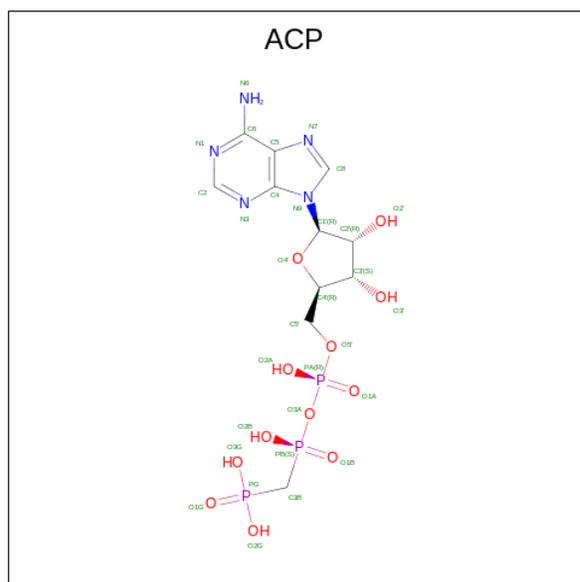
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
10	B	1	12	6	1	4	1	0	0
10	B	1	12	6	1	4	1	0	0

- Molecule 11 is 7,11-DIHYDROXY-8,8,10,12,16-PENTAMETHYL-3-[1-METHYL-2-(2-METHYL-THIAZOL-4-YL)VINYL]-4,17-DIOXABICYCLO[14.1.0]HEPTADECANE-5,9-DIONE (three-letter code: EPB) (formula: C₂₇H₄₁NO₆S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
11	D	1	35	27	1	6	1	0	0

- Molecule 12 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
12	F	1	31	11	5	12	3	0	0

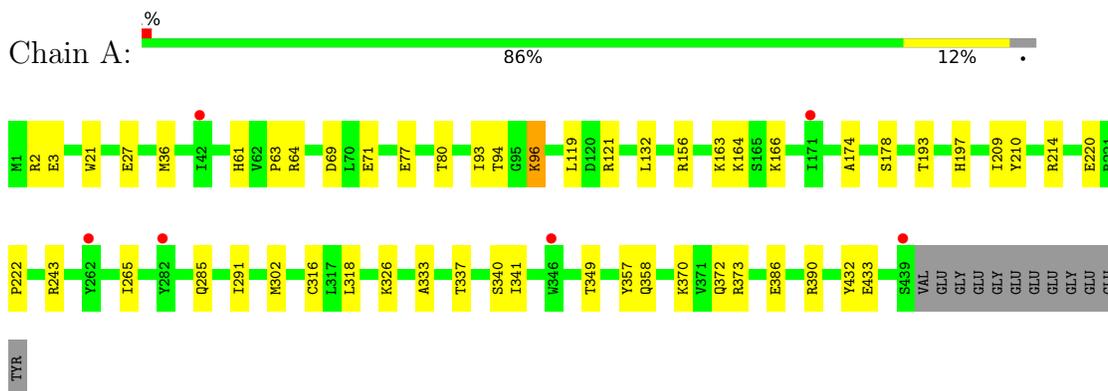
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	138	Total	O	0	0
			138	138		
13	B	123	Total	O	0	0
			123	123		
13	C	215	Total	O	0	0
			215	215		
13	D	71	Total	O	0	0
			71	71		
13	E	26	Total	O	0	0
			26	26		
13	F	63	Total	O	0	0
			63	63		

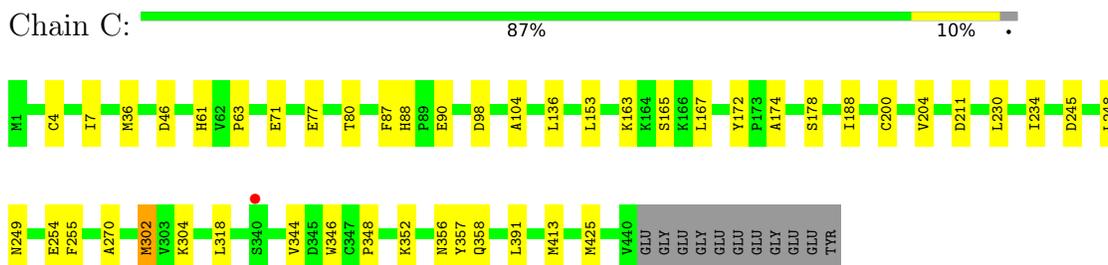
3 Residue-property plots [i](#)

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.

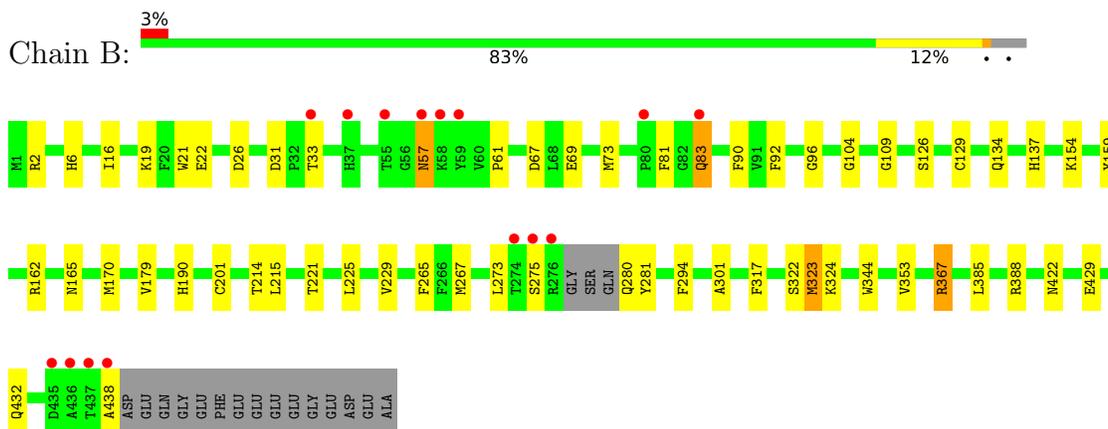
- Molecule 1: Tubulin alpha-1B chain



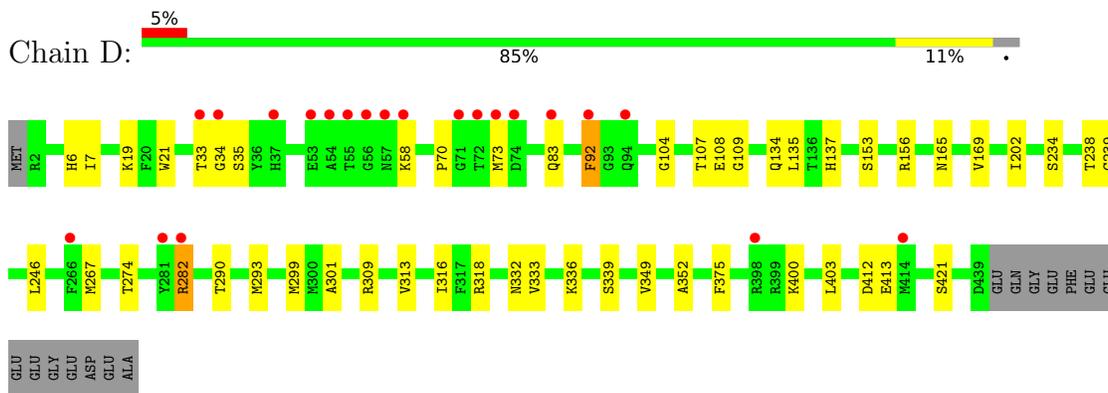
- Molecule 1: Tubulin alpha-1B chain



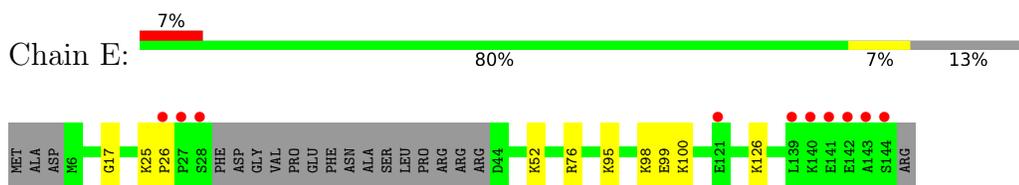
- Molecule 2: Tubulin beta chain



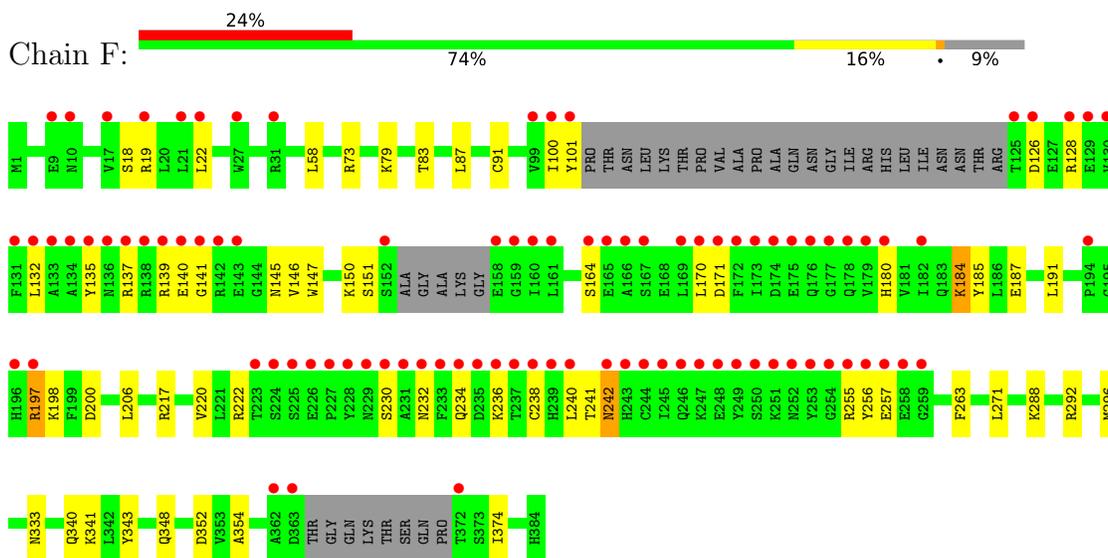
- Molecule 2: Tubulin beta chain



- Molecule 3: Stathmin-4



- Molecule 4: Tubulin tyrosine ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.79Å 157.21Å 181.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.71 – 2.39 49.71 – 2.39	Depositor EDS
% Data completeness (in resolution range)	97.7 (49.71-2.39) 97.7 (49.71-2.39)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.39Å)	Xtrriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.174 , 0.222 0.175 , 0.222	Depositor DCC
R_{free} test set	2000 reflections (1.73%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtrriage
Anisotropy	0.145	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18508	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.47% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EPB, CL, GTP, MES, MG, CA, ACP, GDP

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	0.43	0/3563	0.57	0/4836
1	C	0.49	0/3583	0.60	0/4865
2	B	0.44	0/3494	0.57	1/4731 (0.0%)
2	D	0.41	0/3476	0.57	0/4709
3	E	0.45	0/1063	0.52	0/1411
4	F	0.39	0/2961	0.58	0/3999
All	All	0.43	0/18140	0.57	1/24551 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	31	ASP	CB-CG-OD1	5.97	123.67	118.30

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	3464	0	3388	33	0
1	C	3475	0	3399	28	0
2	B	3402	0	3295	35	0
2	D	3388	0	3266	39	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1042	0	1062	7	0
4	F	2882	0	2851	46	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
6	A	1	0	0	0	0
6	B	2	0	0	0	0
6	C	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	E	1	0	0	0	0
8	A	1	0	0	0	0
9	B	28	0	12	0	0
9	D	28	0	12	0	0
10	B	24	0	24	1	0
11	D	35	0	40	4	0
12	F	31	0	13	4	0
13	A	138	0	0	4	0
13	B	123	0	0	1	0
13	C	215	0	0	1	0
13	D	71	0	0	1	0
13	E	26	0	0	0	0
13	F	63	0	0	3	0
All	All	18508	0	17386	181	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 5.

The worst 5 of 181 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:D:282:ARG:HD3	11:D:502:EPB:H272	1.61	0.82
4:F:197:ARG:NH2	4:F:256:TYR:HB2	1.95	0.81
2:D:293:MET:HE2	2:D:375:PHE:HB2	1.68	0.75
1:C:234:ILE:HG21	1:C:302[B]:MET:SD	2.27	0.74
2:D:238[B]:THR:HG21	2:D:318:ARG:HD2	1.70	0.72

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	444/451 (98%)	436 (98%)	8 (2%)	0	100	100
1	C	448/451 (99%)	438 (98%)	10 (2%)	0	100	100
2	B	430/445 (97%)	418 (97%)	12 (3%)	0	100	100
2	D	432/445 (97%)	424 (98%)	8 (2%)	0	100	100
3	E	124/143 (87%)	122 (98%)	2 (2%)	0	100	100
4	F	344/384 (90%)	333 (97%)	11 (3%)	0	100	100
All	All	2222/2319 (96%)	2171 (98%)	51 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	377/379 (100%)	374 (99%)	3 (1%)	81	91
1	C	380/379 (100%)	373 (98%)	7 (2%)	59	76
2	B	376/383 (98%)	368 (98%)	8 (2%)	53	72
2	D	374/383 (98%)	369 (99%)	5 (1%)	69	84
3	E	115/127 (91%)	112 (97%)	3 (3%)	46	66
4	F	318/342 (93%)	307 (96%)	11 (4%)	36	55
All	All	1940/1993 (97%)	1903 (98%)	37 (2%)	60	75

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	F	171	ASP
4	F	271[A]	LEU
4	F	184	LYS
4	F	230	SER
1	C	165[B]	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	332	ASN
4	F	229	ASN
4	F	348	GLN
4	F	232	ASN
2	D	83	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 9 are monoatomic - leaving 8 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	MES	B	504	-	12,12,12	4.52	7 (58%)	14,16,16	1.46	2 (14%)
11	EPB	D	502	-	33,37,37	3.15	13 (39%)	42,56,56	3.35	13 (30%)
9	GDP	B	501	6	24,30,30	1.03	3 (12%)	30,47,47	1.24	4 (13%)
5	GTP	A	501	6	26,34,34	1.09	2 (7%)	32,54,54	1.40	5 (15%)
10	MES	B	505	-	12,12,12	4.52	7 (58%)	14,16,16	2.23	3 (21%)
12	ACP	F	401	-	27,33,33	4.72	9 (33%)	32,52,52	1.99	4 (12%)
9	GDP	D	501	-	24,30,30	1.00	0	30,47,47	1.10	3 (10%)
5	GTP	C	501	6	26,34,34	1.05	2 (7%)	32,54,54	1.25	3 (9%)

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	MES	B	504	-	-	3/6/14/14	0/1/1/1
11	EPB	D	502	-	-	8/50/59/59	0/2/3/3
9	GDP	B	501	6	-	5/12/32/32	0/3/3/3
5	GTP	A	501	6	-	5/18/38/38	0/3/3/3
10	MES	B	505	-	-	0/6/14/14	0/1/1/1
12	ACP	F	401	-	-	4/15/38/38	0/3/3/3
9	GDP	D	501	-	-	4/12/32/32	0/3/3/3
5	GTP	C	501	6	-	8/18/38/38	0/3/3/3

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	F	401	ACP	C2'-C1'	-15.03	1.31	1.53
12	F	401	ACP	O4'-C1'	14.82	1.61	1.41
11	D	502	EPB	C24-S1	-10.09	1.54	1.70
10	B	505	MES	C7-N4	-8.26	1.28	1.47
10	B	504	MES	C7-N4	-8.26	1.28	1.47

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	502	EPB	C6-C5-C4	9.69	135.43	119.02
11	D	502	EPB	O41-C4-C3	8.66	136.27	116.44
11	D	502	EPB	C3-C2-C20	-8.07	102.29	113.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	D	502	EPB	C3-C4-C5	-7.50	111.73	125.89
12	F	401	ACP	C5-C6-N6	6.71	130.56	120.35

There are no chirality outliers.

5 of 37 torsion outliers are listed below:

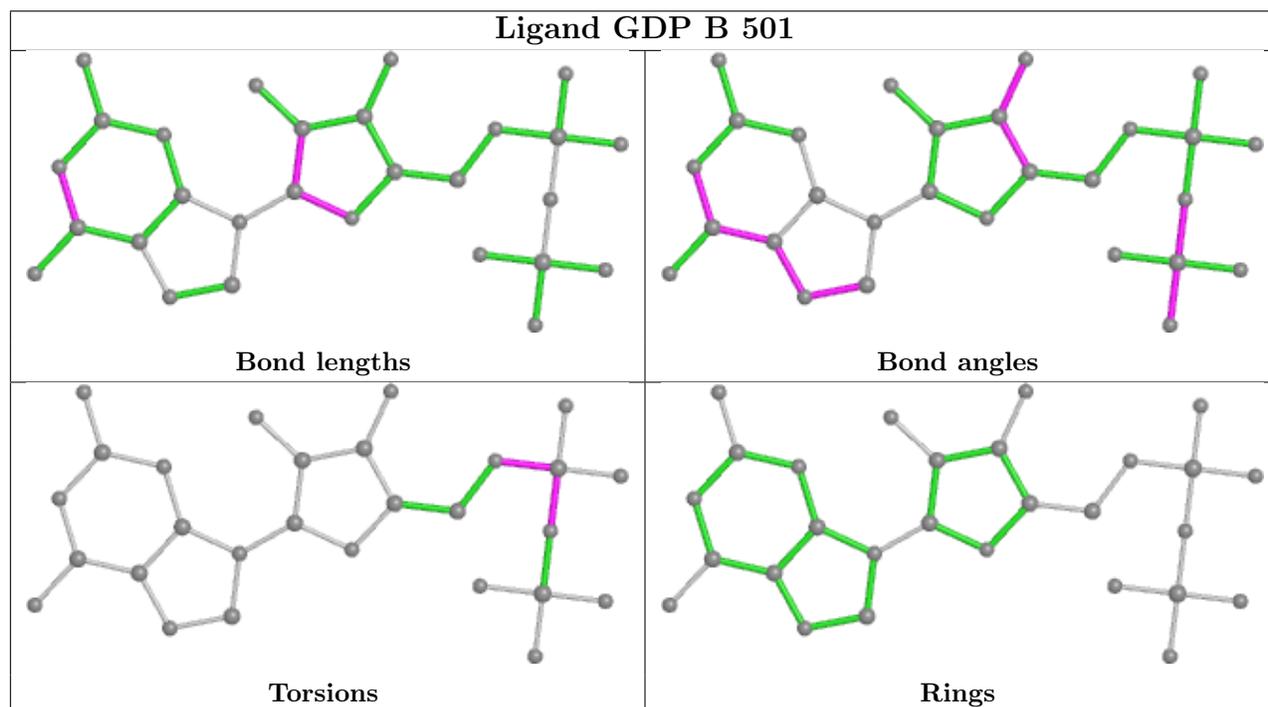
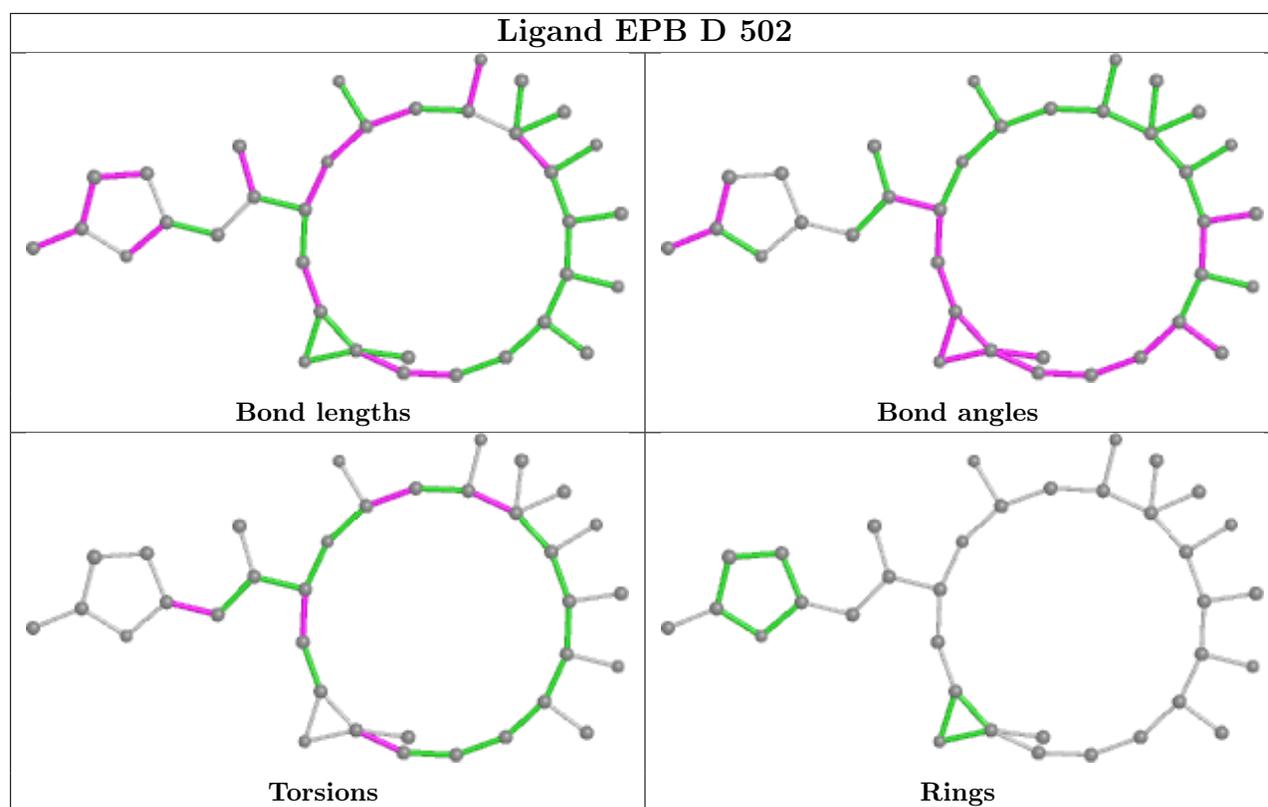
Mol	Chain	Res	Type	Atoms
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O2A
9	B	501	GDP	C5'-O5'-PA-O1A

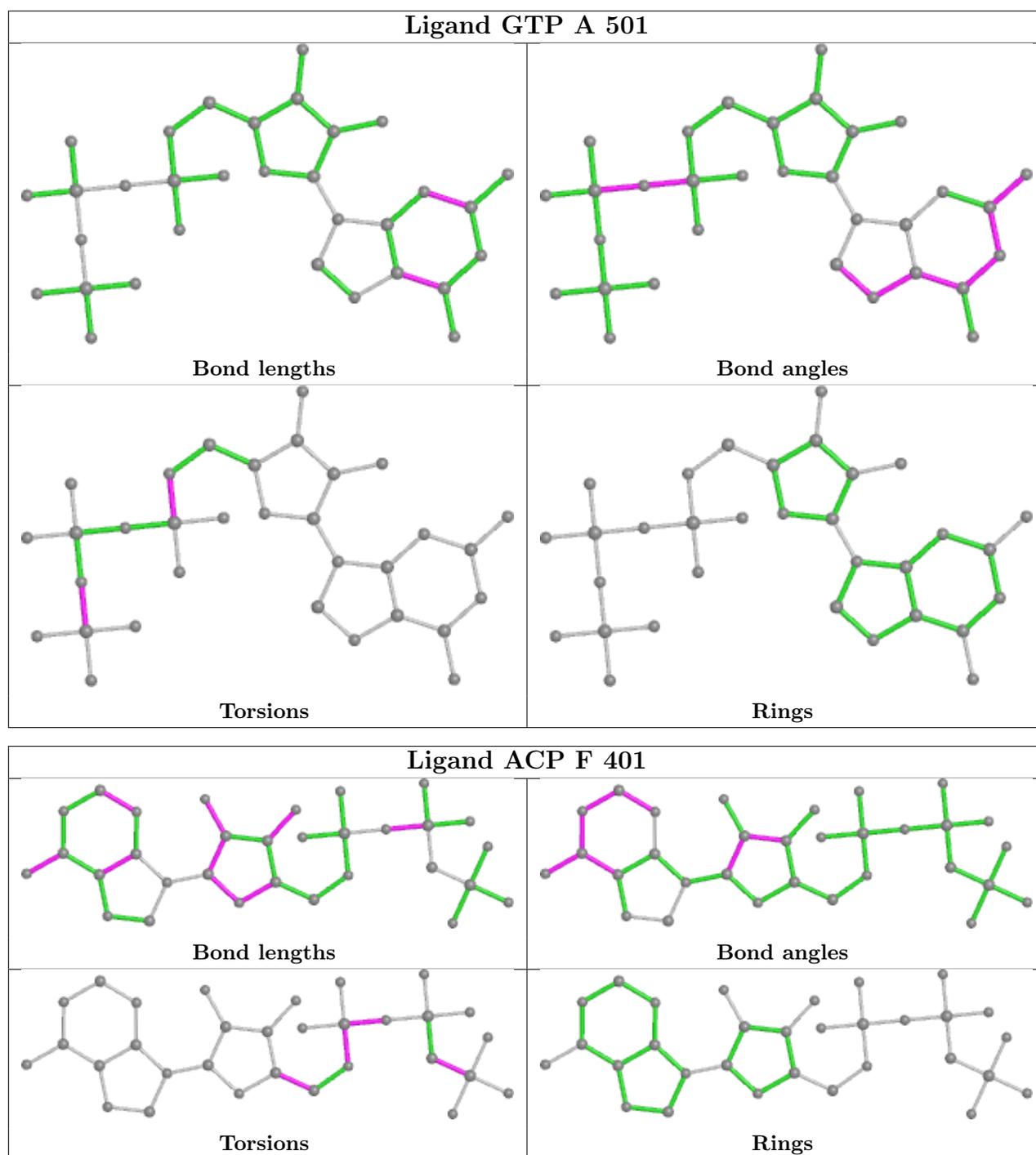
There are no ring outliers.

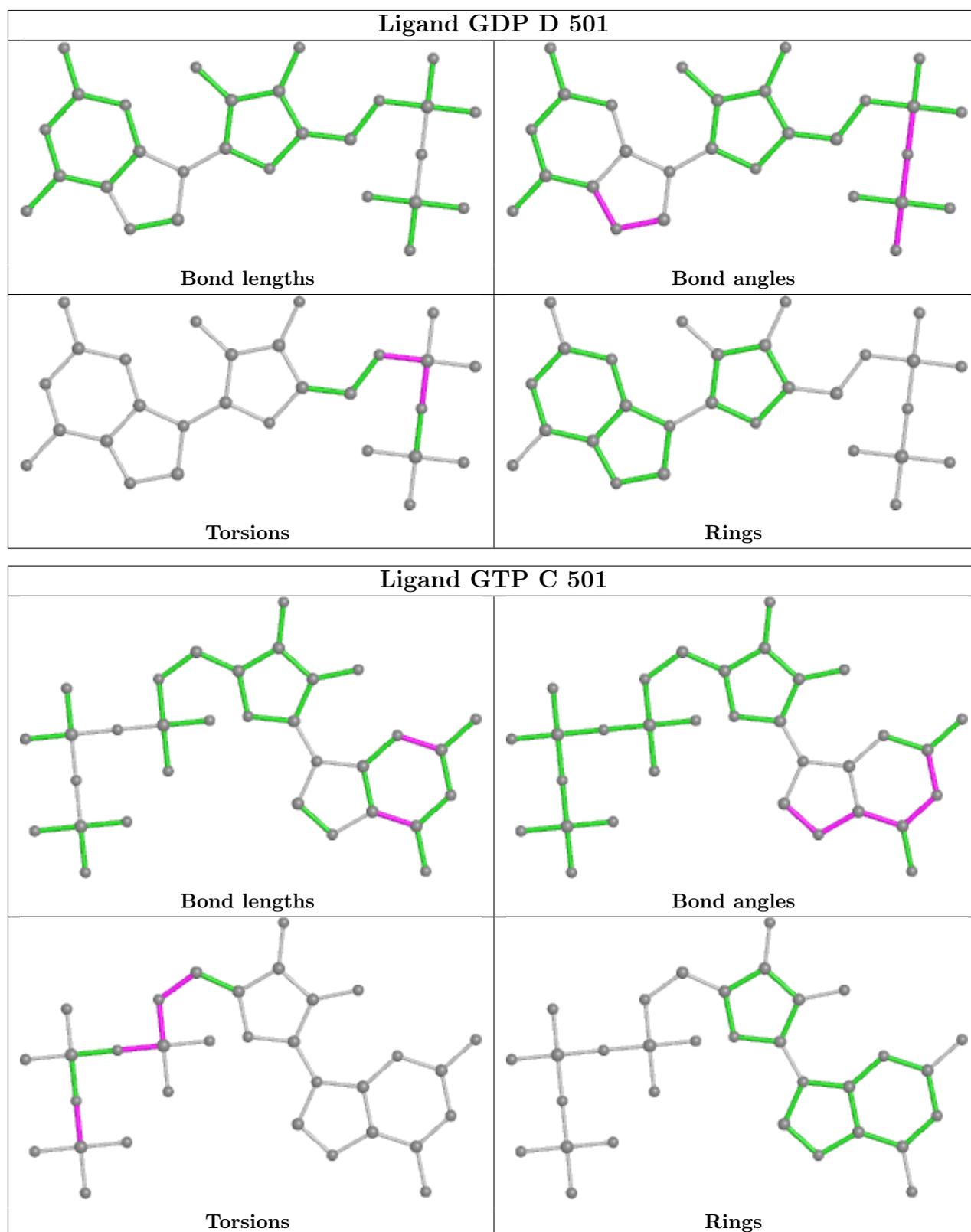
3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	D	502	EPB	4	0
10	B	505	MES	1	0
12	F	401	ACP	4	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

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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 ²)	Q<0.9
1	A	439/451 (97%)	0.01	6 (1%) 75 73	24, 36, 56, 95	0
1	C	440/451 (97%)	-0.27	1 (0%) 95 94	21, 30, 49, 69	0
2	B	427/445 (95%)	0.02	15 (3%) 44 43	21, 37, 63, 92	2 (0%)
2	D	430/445 (96%)	0.31	21 (4%) 29 28	28, 44, 72, 94	5 (1%)
3	E	124/143 (86%)	0.24	10 (8%) 12 11	28, 50, 77, 98	0
4	F	348/384 (90%)	0.98	93 (26%) 0 0	29, 56, 101, 112	0
All	All	2208/2319 (95%)	0.18	146 (6%) 18 17	21, 40, 78, 112	7 (0%)

The worst 5 of 146 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	249	TYR	7.5
2	B	437	THR	7.3
4	F	173	ILE	6.5
4	F	169	LEU	6.1
3	E	143	ALA	6.1

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 monosaccharides in this entry.

6.4 Ligands

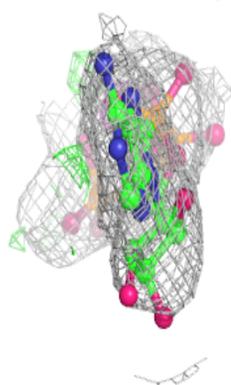
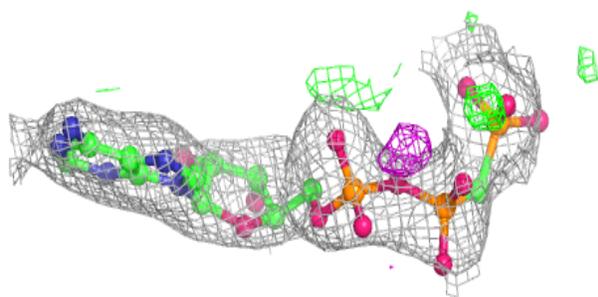
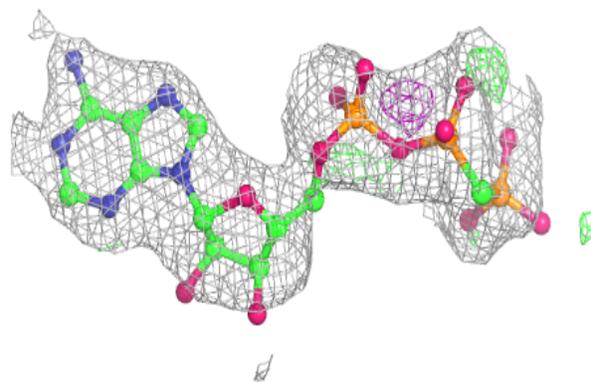
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	MG	B	506	1/1	0.71	0.19	63,63,63,63	0
12	ACP	F	401	31/31	0.88	0.23	69,88,116,127	0
7	CA	E	201	1/1	0.90	0.05	77,77,77,77	0
7	CA	B	503	1/1	0.90	0.13	83,83,83,83	0
8	CL	A	504	1/1	0.92	0.06	58,58,58,58	0
11	EPB	D	502	35/35	0.93	0.15	46,64,73,78	0
6	MG	B	502	1/1	0.93	0.28	27,27,27,27	0
6	MG	C	502	1/1	0.94	0.19	25,25,25,25	0
10	MES	B	504	12/12	0.97	0.12	36,44,47,59	0
10	MES	B	505	12/12	0.97	0.14	45,53,59,80	0
7	CA	A	503	1/1	0.97	0.03	47,47,47,47	0
6	MG	A	502	1/1	0.97	0.13	26,26,26,26	0
9	GDP	D	501	28/28	0.98	0.11	31,40,47,52	0
5	GTP	A	501	32/32	0.99	0.16	22,28,33,39	0
5	GTP	C	501	32/32	0.99	0.13	17,24,27,28	0
9	GDP	B	501	28/28	0.99	0.14	21,27,32,36	0
7	CA	C	503	1/1	0.99	0.06	39,39,39,39	0

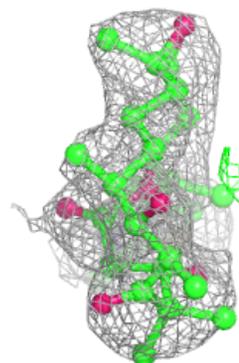
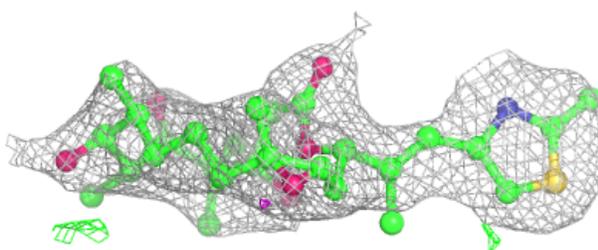
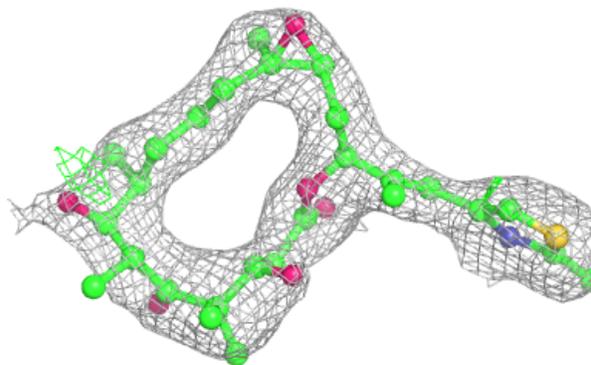
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ACP F 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

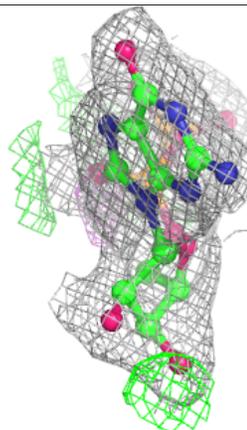
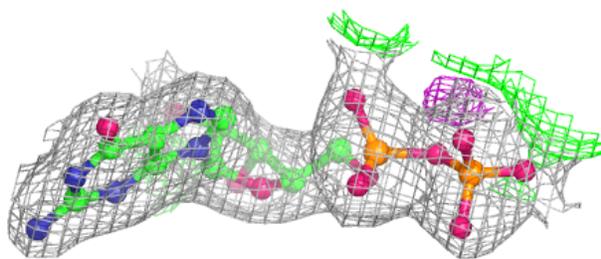
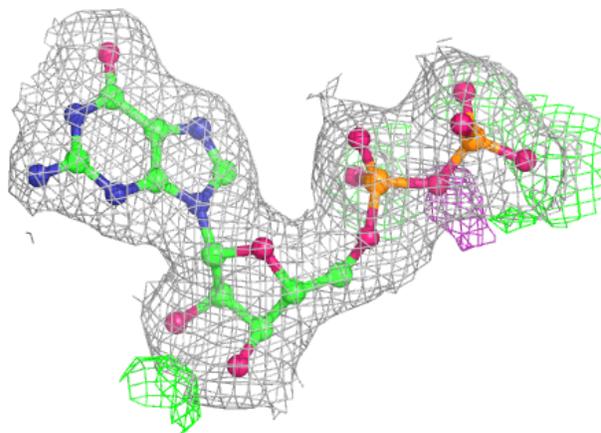
**Electron density around EPB D 502:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



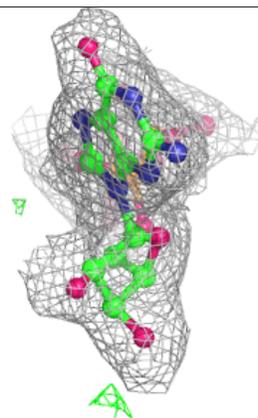
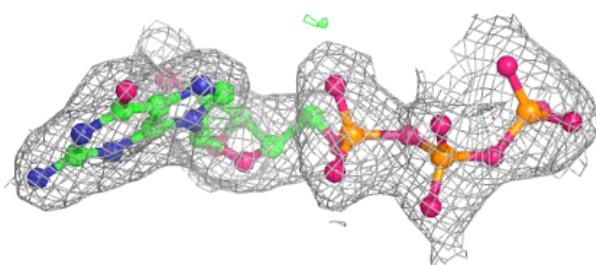
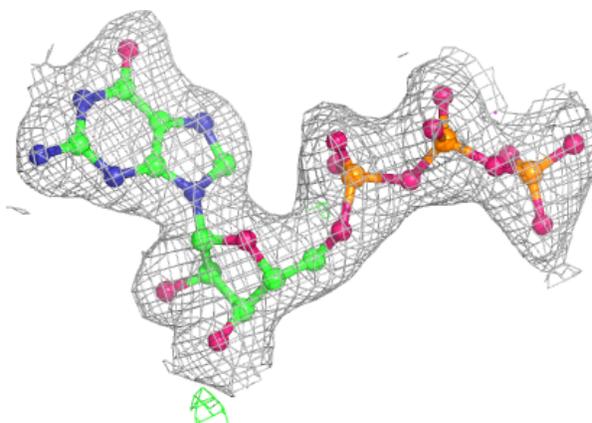
Electron density around GDP D 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

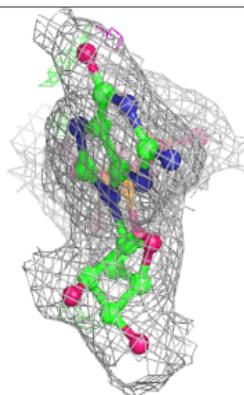
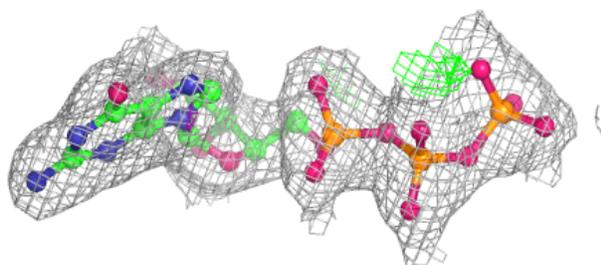
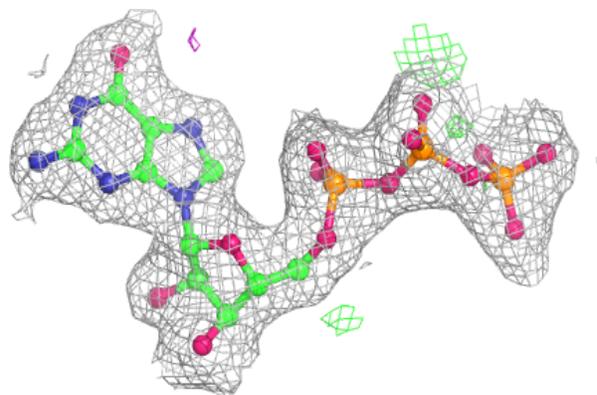


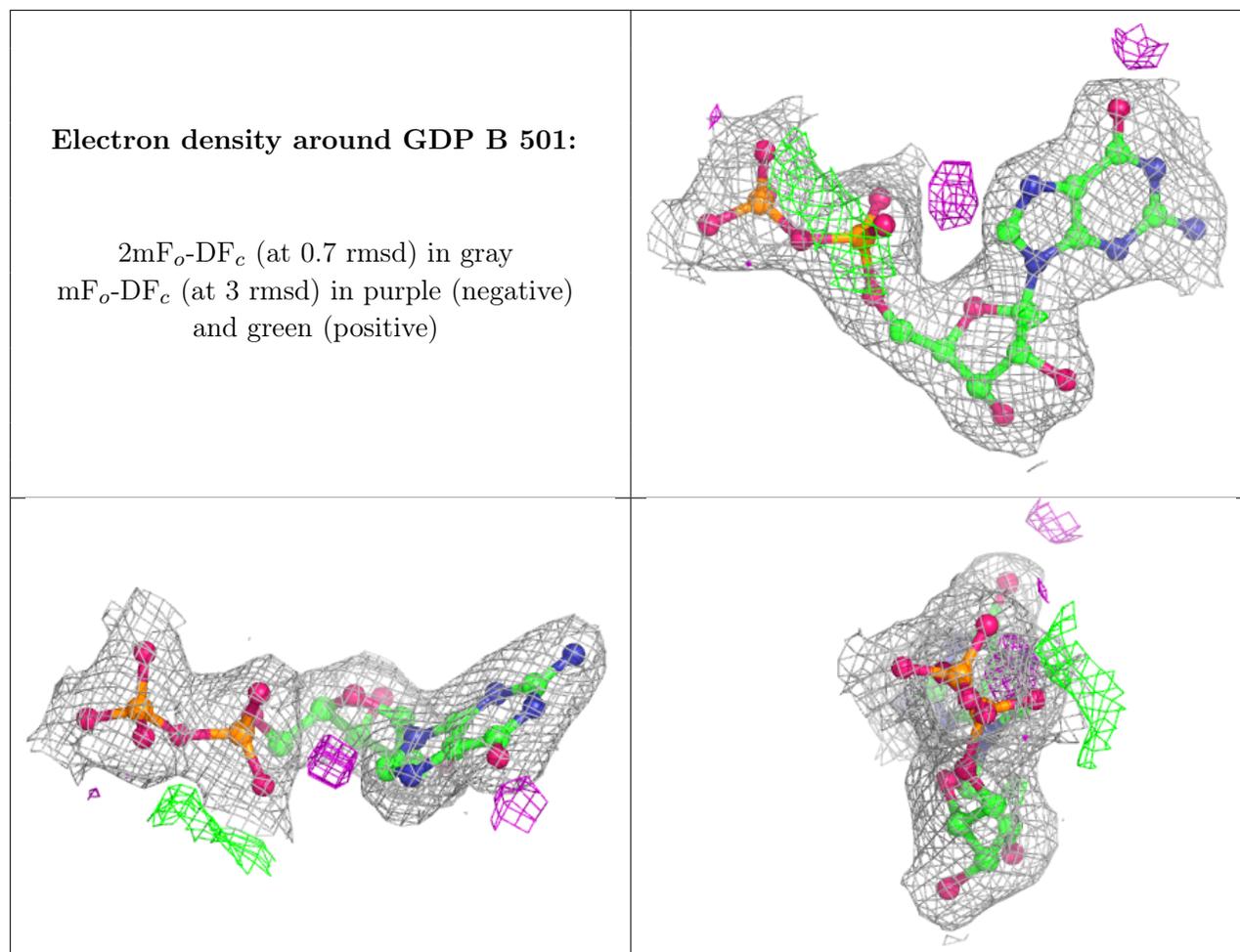
Electron density around GTP A 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around GTP C 501:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.