



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 07:09 PM UTC

PDB ID : 6GVN / pdb_00006gvn
Title : Tubulin:TM-3 DARPin complex
Authors : Gigant, B.; Cantos Fernandes, S.; Campanacci, V.
Deposited on : 2018-06-21
Resolution : 2.69 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

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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

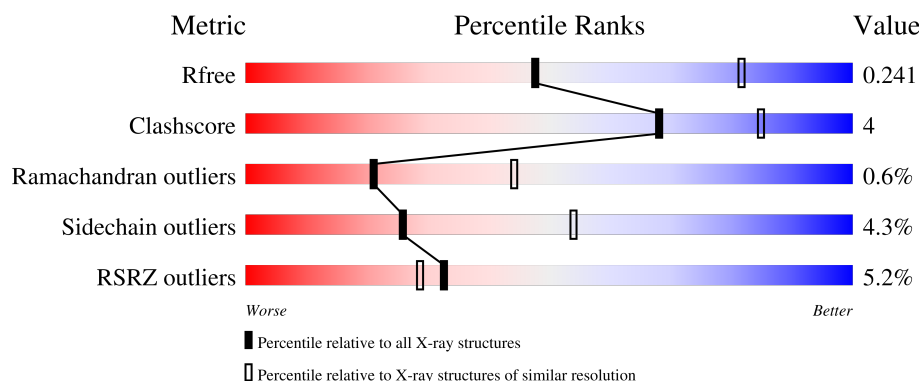
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

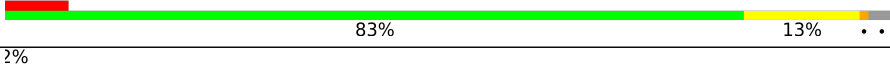
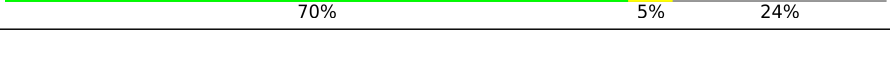
The reported resolution of this entry is 2.69 Å.

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}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	
2	B	445	
3	F	169	

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7890 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 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	434	Total	C	N	O	S	0	0	0
			3363	2132	569	640	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	SER	GLY	conflict	UNP D0VWZ0
A	340	SER	THR	conflict	UNP D0VWZ0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	431	Total	C	N	O	S	0	0	0
			3371	2117	575	653	26			

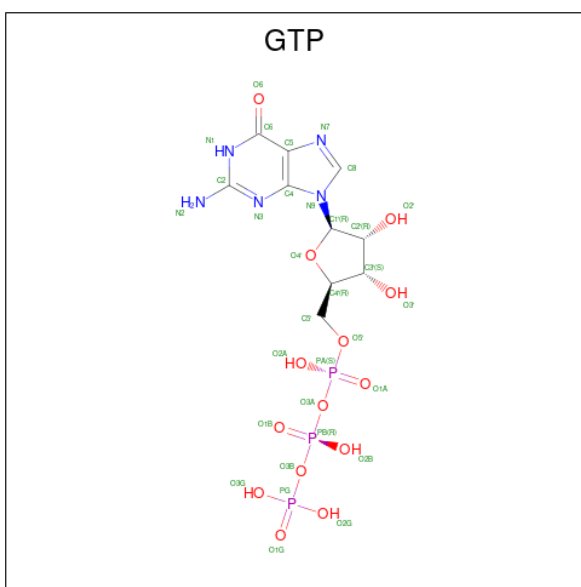
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	203	CYS	SER	conflict	UNP D0VWY9
B	318	ILE	VAL	conflict	UNP D0VWY9

- Molecule 3 is a protein called TM-3 DARPIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	128	Total	C	N	O	S	0	0	0
			946	597	165	181	3			

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



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

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

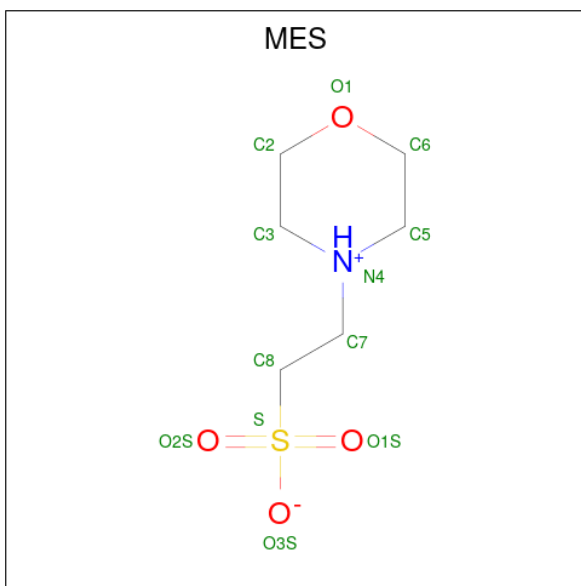
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0
5	B	1	Total Mg 1 1	0	0

- Molecule 6 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: C₆H₁₃NO₄S).



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

- Molecule 8 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			6	3	3		
8	F	1	Total	C	O	0	0
			6	3	3		

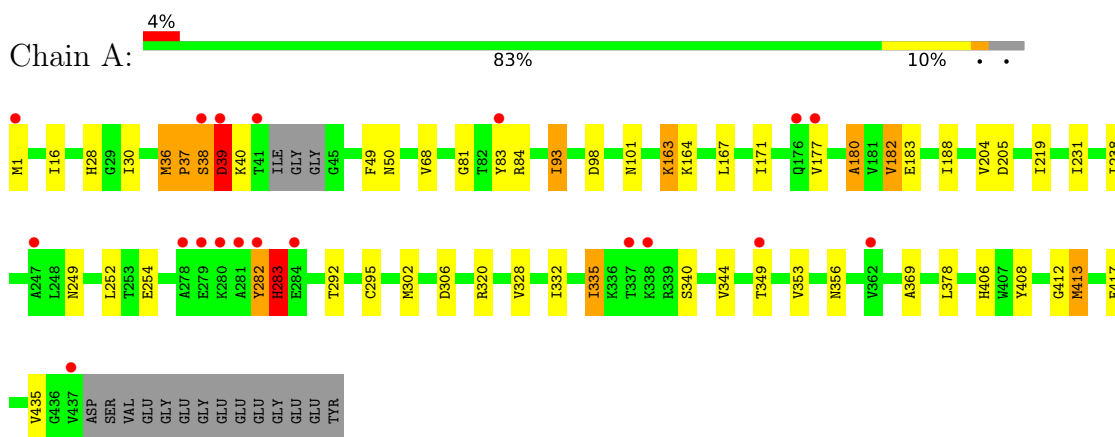
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	51	Total	O	0	0
			51	51		
9	B	46	Total	O	0	0
			46	46		
9	F	18	Total	O	0	0
			18	18		

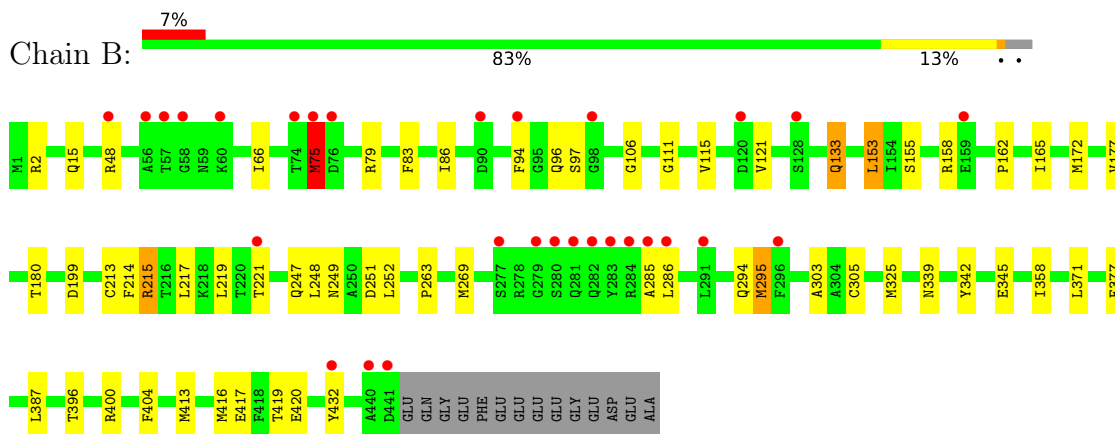
3 Residue-property plots [i](#)

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.

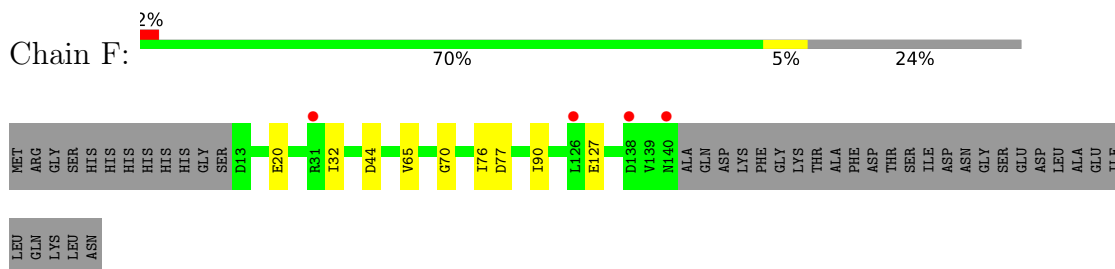
• Molecule 1: Tubulin alpha chain



• Molecule 2: Tubulin beta chain



• Molecule 3: TM-3 DARPIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.10Å 84.26Å 81.98Å 90.00° 99.00° 90.00°	Depositor
Resolution (Å)	43.08 – 2.69 43.08 – 2.69	Depositor EDS
% Data completeness (in resolution range)	98.1 (43.08-2.69) 98.3 (43.08-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.69Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.193 , 0.216 0.219 , 0.241	Depositor DCC
R_{free} test set	1349 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	40.5	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 72.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7890	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.94% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, GOL, SO4, MES

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	0.89	2/3438 (0.1%)	1.39	17/4671 (0.4%)
2	B	0.85	1/3446 (0.0%)	1.33	10/4671 (0.2%)
3	F	0.94	0/959	1.47	6/1306 (0.5%)
All	All	0.88	3/7843 (0.0%)	1.37	33/10648 (0.3%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	177	VAL	CA-CB	5.49	1.61	1.54
2	B	413	MET	SD-CE	-5.44	1.66	1.79
1	A	36	MET	SD-CE	-5.37	1.66	1.79

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	340	SER	N-CA-C	-8.96	99.24	111.87
1	A	412	GLY	CA-C-N	8.15	132.39	120.90
1	A	412	GLY	C-N-CA	8.15	132.39	120.90
1	A	205	ASP	CA-CB-CG	7.05	119.65	112.60
1	A	39	ASP	CA-CB-CG	6.70	119.30	112.60
2	B	180	THR	N-CA-C	-6.69	97.82	108.73
3	F	77	ASP	CA-CB-CG	6.54	119.14	112.60
1	A	98	ASP	CA-CB-CG	6.42	119.02	112.60
2	B	75	MET	CA-C-N	6.23	128.54	120.44
2	B	75	MET	C-N-CA	6.23	128.54	120.44
3	F	44	ASP	CA-CB-CG	6.17	118.77	112.60
3	F	127	GLU	CB-CG-CD	5.81	122.48	112.60
1	A	37	PRO	CA-C-N	5.74	132.51	121.54
1	A	37	PRO	C-N-CA	5.74	132.51	121.54
2	B	358	ILE	N-CA-C	5.71	112.76	107.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	251	ASP	CA-CB-CG	5.62	118.22	112.60
1	A	306	ASP	CA-CB-CG	5.57	118.17	112.60
2	B	177	VAL	CB-CA-C	5.56	116.63	111.30
2	B	162	PRO	CA-C-N	5.51	132.35	122.38
2	B	162	PRO	C-N-CA	5.51	132.35	122.38
2	B	249	ASN	CA-C-N	5.42	127.98	120.29
2	B	249	ASN	C-N-CA	5.42	127.98	120.29
1	A	81	GLY	CA-C-N	5.39	127.50	120.28
1	A	81	GLY	C-N-CA	5.39	127.50	120.28
3	F	44	ASP	CA-C-N	5.33	127.68	120.38
3	F	44	ASP	C-N-CA	5.33	127.68	120.38
1	A	219	ILE	CA-C-N	5.24	127.61	120.54
1	A	219	ILE	C-N-CA	5.24	127.61	120.54
1	A	180	ALA	N-CA-C	5.21	117.92	109.06
1	A	38	SER	CA-C-N	5.14	131.35	121.54
1	A	38	SER	C-N-CA	5.14	131.35	121.54
3	F	70	GLY	N-CA-C	5.02	122.28	115.30
1	A	413	MET	N-CA-C	5.01	117.30	110.24

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	3363	0	3255	33	0
2	B	3371	0	3233	23	0
3	F	946	0	961	1	0
4	A	32	0	12	0	0
4	B	32	0	12	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	5	0	0	0	0
7	B	12	0	13	1	0
8	B	6	0	8	0	0
8	F	6	0	8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	51	0	0	0	0
9	B	46	0	0	2	0
9	F	18	0	0	0	0
All	All	7890	0	7502	55	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 4.

All (55) 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:30:ILE:HG12	1:A:36:MET:HE2	1.64	0.79
1:A:30:ILE:CG1	1:A:36:MET:HE2	2.18	0.74
2:B:199:ASP:OD1	7:B:503:MES:H32	1.92	0.68
1:A:101:ASN:ND2	1:A:180:ALA:HB2	2.10	0.67
1:A:163:LYS:H	1:A:163:LYS:HD2	1.61	0.64
1:A:332:ILE:O	1:A:335:ILE:HG12	1.99	0.62
2:B:106:GLY:O	2:B:111:GLY:HA3	1.99	0.62
1:A:36:MET:HE1	1:A:49:PHE:CE1	2.37	0.60
1:A:182:VAL:HG13	1:A:408:TYR:OH	2.02	0.60
1:A:282:TYR:O	1:A:283:HIS:HB2	2.01	0.59
2:B:213:CYS:HA	2:B:217:LEU:HD12	1.83	0.59
1:A:68:VAL:HG22	1:A:93:ILE:HG13	1.82	0.59
2:B:295:MET:HG2	2:B:377:PHE:HB2	1.84	0.58
1:A:36:MET:HE1	1:A:49:PHE:CZ	2.39	0.56
1:A:163:LYS:HD3	1:A:164:LYS:HE3	1.87	0.56
1:A:180:ALA:HB3	1:A:183:GLU:HG3	1.86	0.56
2:B:214:PHE:HD2	2:B:215:ARG:HE	1.51	0.56
1:A:332:ILE:CD1	1:A:353:VAL:HG21	2.36	0.55
2:B:115:VAL:HG23	2:B:153:LEU:HD22	1.87	0.55
1:A:344:VAL:HG11	1:A:435:VAL:CG1	2.37	0.55
1:A:413:MET:HE3	1:A:417:GLU:HB3	1.90	0.54
2:B:417:GLU:HA	2:B:420:GLU:HG2	1.90	0.52
2:B:269:MET:HG3	2:B:303:ALA:HB3	1.92	0.52
1:A:344:VAL:HG11	1:A:435:VAL:HG12	1.93	0.51
2:B:263:PRO:HG2	9:B:640:HOH:O	2.09	0.51
1:A:320:ARG:HA	1:A:356:ASN:O	2.11	0.51
2:B:339:ASN:HB3	2:B:342:TYR:HD1	1.76	0.51
1:A:282:TYR:CE1	1:A:369:ALA:HB1	2.46	0.50
2:B:75:MET:HG3	2:B:94:PHE:CD1	2.48	0.49
2:B:2:ARG:HB3	2:B:133:GLN:HE21	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:VAL:HG11	1:A:353:VAL:HG11	1.95	0.48
2:B:83:PHE:O	2:B:86:ILE:HG22	2.13	0.48
1:A:28:HIS:CE1	1:A:49:PHE:HB3	2.48	0.47
1:A:204:VAL:HG11	1:A:231:ILE:HG12	1.97	0.47
2:B:396:THR:O	2:B:400:ARG:HG3	2.14	0.47
1:A:406:HIS:CG	2:B:263:PRO:HD3	2.51	0.46
2:B:66:ILE:HG12	2:B:121:VAL:HG12	1.97	0.46
1:A:36:MET:SD	1:A:39:ASP:HB3	2.56	0.46
1:A:238:ILE:HG12	1:A:378:LEU:HD21	1.99	0.45
2:B:404:PHE:HE1	3:F:90:ILE:HD12	1.81	0.45
2:B:172:MET:HG3	2:B:387:LEU:HD21	1.99	0.44
2:B:416:MET:HA	2:B:419:THR:OG1	2.17	0.44
1:A:332:ILE:HD11	1:A:353:VAL:CG2	2.47	0.44
1:A:332:ILE:CD1	1:A:353:VAL:CG2	2.96	0.44
1:A:16:ILE:HD13	1:A:171:ILE:HD11	2.00	0.43
1:A:292:THR:O	1:A:295:CYS:HB2	2.18	0.43
2:B:432:TYR:HE1	9:B:601:HOH:O	2.02	0.43
2:B:286:LEU:HD21	2:B:294:GLN:NE2	2.33	0.42
1:A:167:LEU:HD13	1:A:252:LEU:HD22	2.01	0.42
1:A:249:ASN:HA	1:A:254:GLU:HB3	2.02	0.42
1:A:39:ASP:CG	1:A:40:LYS:H	2.28	0.42
1:A:163:LYS:H	1:A:163:LYS:CD	2.25	0.42
1:A:30:ILE:HG13	1:A:36:MET:HE2	1.96	0.42
2:B:213:CYS:HB3	2:B:219:LEU:HD12	2.01	0.42
2:B:165:ILE:HG21	2:B:252:LEU:HB3	2.01	0.41

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	430/451 (95%)	407 (95%)	18 (4%)	5 (1%)	10 27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	429/445 (96%)	416 (97%)	12 (3%)	1 (0%)	43	68
3	F	126/169 (75%)	124 (98%)	2 (2%)	0	100	100
All	All	985/1065 (92%)	947 (96%)	32 (3%)	6 (1%)	21	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	283	HIS
1	A	37	PRO
1	A	39	ASP
1	A	38	SER
1	A	282	TYR
2	B	285	ALA

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	358/379 (94%)	346 (97%)	12 (3%)	32	62
2	B	367/383 (96%)	348 (95%)	19 (5%)	21	47
3	F	98/132 (74%)	94 (96%)	4 (4%)	27	56
All	All	823/894 (92%)	788 (96%)	35 (4%)	26	54

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	50	ASN
1	A	83	TYR
1	A	84	ARG
1	A	93	ILE
1	A	163	LYS
1	A	182	VAL
1	A	188	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	283	HIS
1	A	302	MET
1	A	335	ILE
1	A	349	THR
2	B	15	GLN
2	B	48	ARG
2	B	75	MET
2	B	79	ARG
2	B	96	GLN
2	B	97	SER
2	B	133	GLN
2	B	153	LEU
2	B	155	SER
2	B	158	ARG
2	B	215	ARG
2	B	221	THR
2	B	247	GLN
2	B	248	LEU
2	B	295	MET
2	B	305	CYS
2	B	325	MET
2	B	345	GLU
2	B	371	LEU
3	F	20	GLU
3	F	32	ILE
3	F	65	VAL
3	F	76	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
1	A	107	HIS
1	A	197	HIS
1	A	256	GLN
1	A	372	GLN
1	A	393	HIS
2	B	8	GLN
2	B	11	GLN
2	B	14	ASN
2	B	91	ASN
2	B	136	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	167	ASN
2	B	192	HIS
2	B	229	HIS
2	B	258	ASN
2	B	294	GLN
2	B	300	ASN
2	B	331	GLN
2	B	336	GLN
2	B	424	ASN
3	F	140	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	$\# Z > 2$
4	GTP	A	501	5	33,34,34	0.51	0	50,54,54	0.50	0
7	MES	B	503	-	12,12,12	0.72	0	15,16,16	0.36	0
8	GOL	F	201	-	5,5,5	0.15	0	5,5,5	0.29	0
8	GOL	B	504	-	5,5,5	0.22	0	5,5,5	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	SO4	A	503	-	4,4,4	0.29	0	6,6,6	0.18	0
4	GTP	B	501	5	33,34,34	0.55	0	50,54,54	0.68	2 (4%)

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
4	GTP	A	501	5	-	9/22/38/38	0/3/3/3
7	MES	B	503	-	-	2/6/14/14	0/1/1/1
8	GOL	F	201	-	-	0/4/4/4	-
8	GOL	B	504	-	-	0/4/4/4	-
4	GTP	B	501	5	-	3/22/38/38	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	501	GTP	O2G-PG-O3B	2.89	114.34	104.64
4	B	501	GTP	O5'-PA-O1A	2.01	116.91	108.94

There are no chirality outliers.

All (14) torsion outliers are listed below:

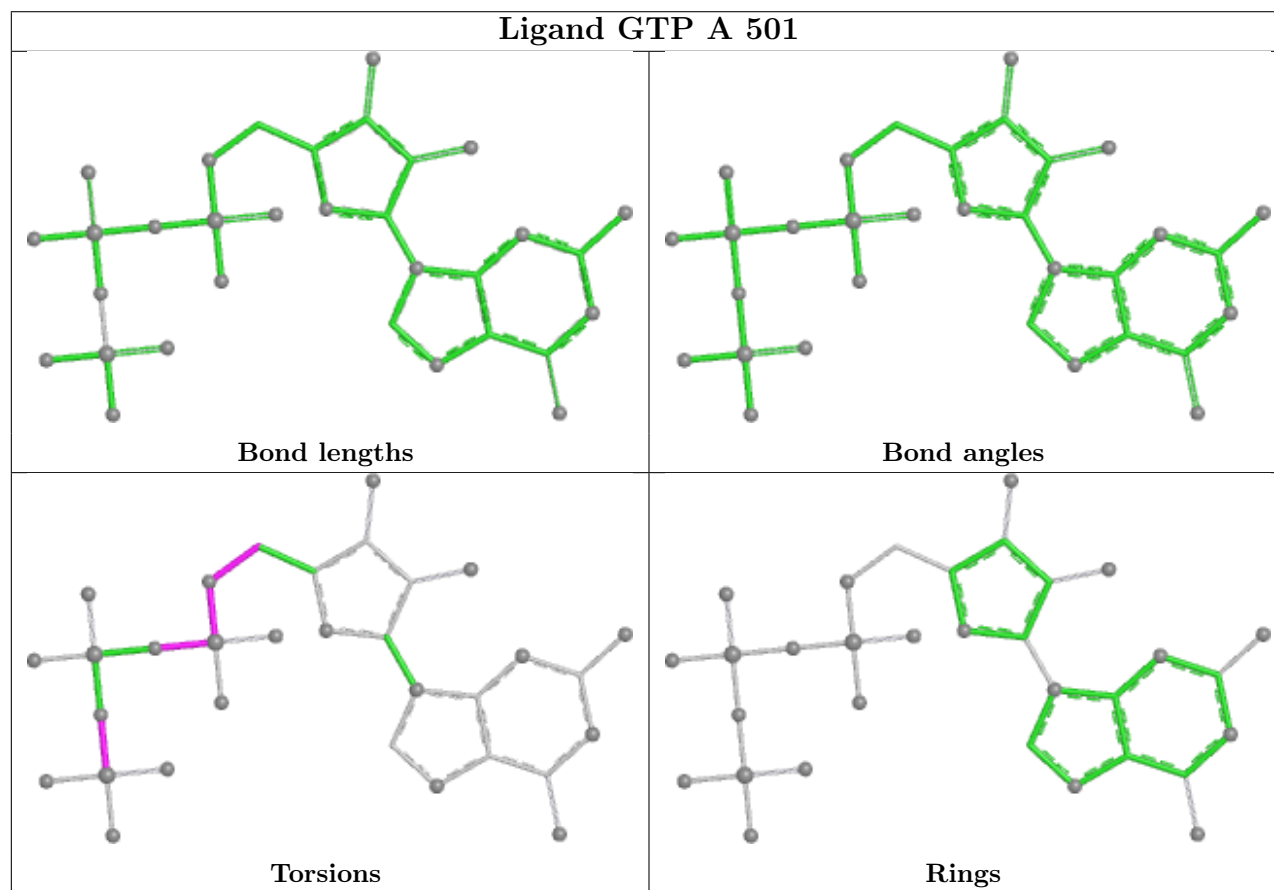
Mol	Chain	Res	Type	Atoms
4	A	501	GTP	PB-O3B-PG-O2G
4	A	501	GTP	C5'-O5'-PA-O3A
4	A	501	GTP	C5'-O5'-PA-O1A
4	A	501	GTP	C5'-O5'-PA-O2A
4	B	501	GTP	C5'-O5'-PA-O3A
4	B	501	GTP	C5'-O5'-PA-O1A
7	B	503	MES	C8-C7-N4-C3
7	B	503	MES	C8-C7-N4-C5
4	B	501	GTP	C5'-O5'-PA-O2A
4	A	501	GTP	PB-O3B-PG-O3G
4	A	501	GTP	PB-O3A-PA-O2A
4	A	501	GTP	PB-O3B-PG-O1G
4	A	501	GTP	C4'-C5'-O5'-PA
4	A	501	GTP	PB-O3A-PA-O1A

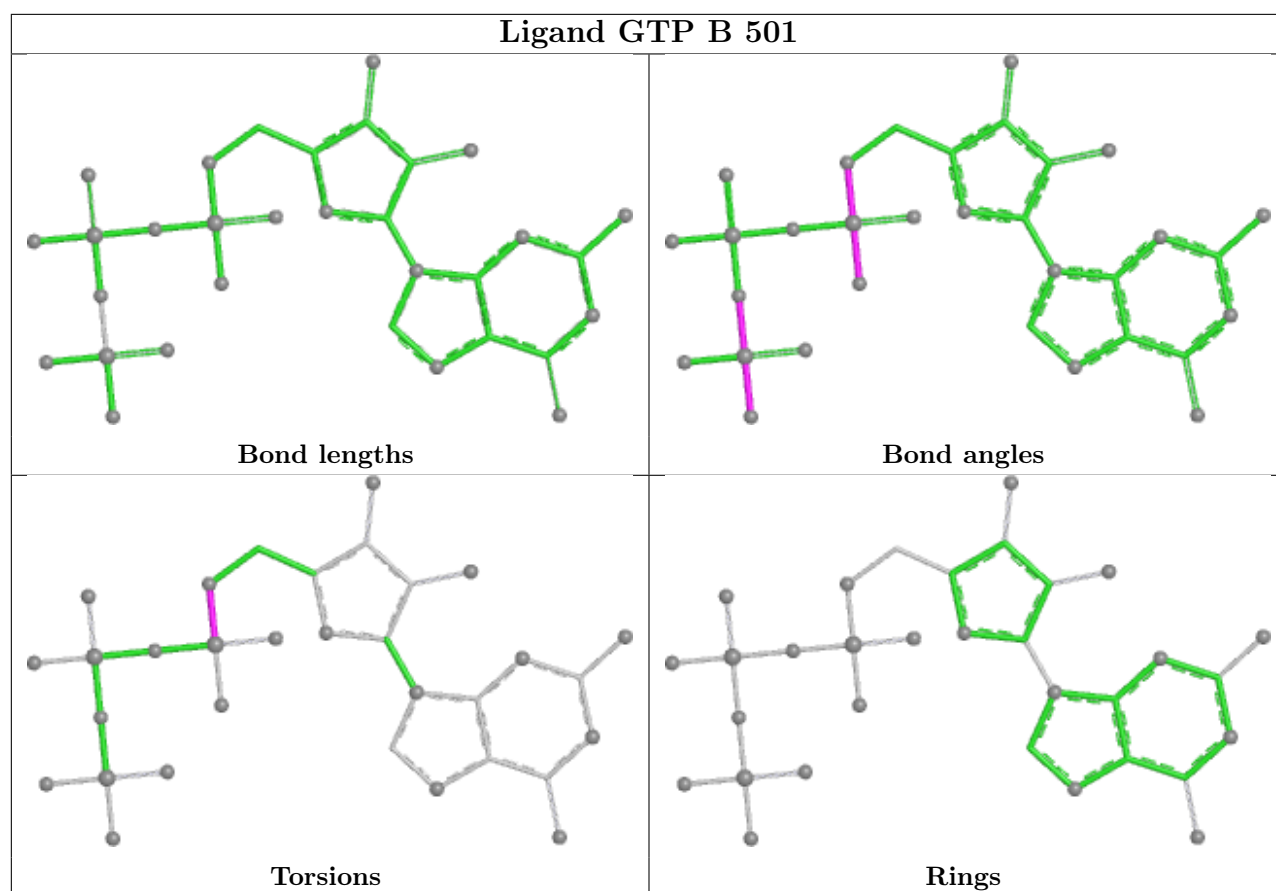
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	503	MES	1	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, 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	434/451 (96%)	0.29	19 (4%)	39 35	26, 46, 75, 105	0
2	B	431/445 (96%)	0.43	29 (6%)	24 21	32, 52, 88, 121	0
3	F	128/169 (75%)	0.13	4 (3%)	51 48	32, 44, 69, 111	0
All	All	993/1065 (93%)	0.33	52 (5%)	33 29	26, 47, 81, 121	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	437	VAL	5.2
1	A	41	THR	4.9
2	B	57	THR	4.4
2	B	279	GLY	4.1
2	B	280	SER	3.8
2	B	56	ALA	3.5
1	A	338	LYS	3.5
2	B	440	ALA	3.3
1	A	282	TYR	3.3
1	A	177	VAL	3.3
1	A	38	SER	3.1
2	B	281	GLN	3.1
1	A	39	ASP	3.0
2	B	120	ASP	3.0
1	A	1	MET	2.9
2	B	283	TYR	2.9
2	B	159	GLU	2.8
3	F	140	ASN	2.8
1	A	280	LYS	2.7
2	B	441	ASP	2.6
1	A	83	TYR	2.6
1	A	337	THR	2.6
2	B	75	MET	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	60	LYS	2.6
1	A	284	GLU	2.5
2	B	285	ALA	2.5
2	B	296	PHE	2.5
3	F	31	ARG	2.5
2	B	74	THR	2.5
2	B	94	PHE	2.5
1	A	278	ALA	2.4
2	B	284	ARG	2.4
2	B	286	LEU	2.4
1	A	362	VAL	2.4
2	B	128	SER	2.3
1	A	279	GLU	2.3
2	B	98	GLY	2.3
3	F	126	LEU	2.2
2	B	48	ARG	2.2
1	A	176	GLN	2.1
2	B	432	TYR	2.1
2	B	291	LEU	2.1
2	B	90	ASP	2.1
2	B	58	GLY	2.1
2	B	76	ASP	2.1
3	F	138	ASP	2.1
1	A	247	ALA	2.1
2	B	221	THR	2.1
2	B	277	SER	2.0
2	B	282	GLN	2.0
1	A	281	ALA	2.0
1	A	349	THR	2.0

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 ⓘ

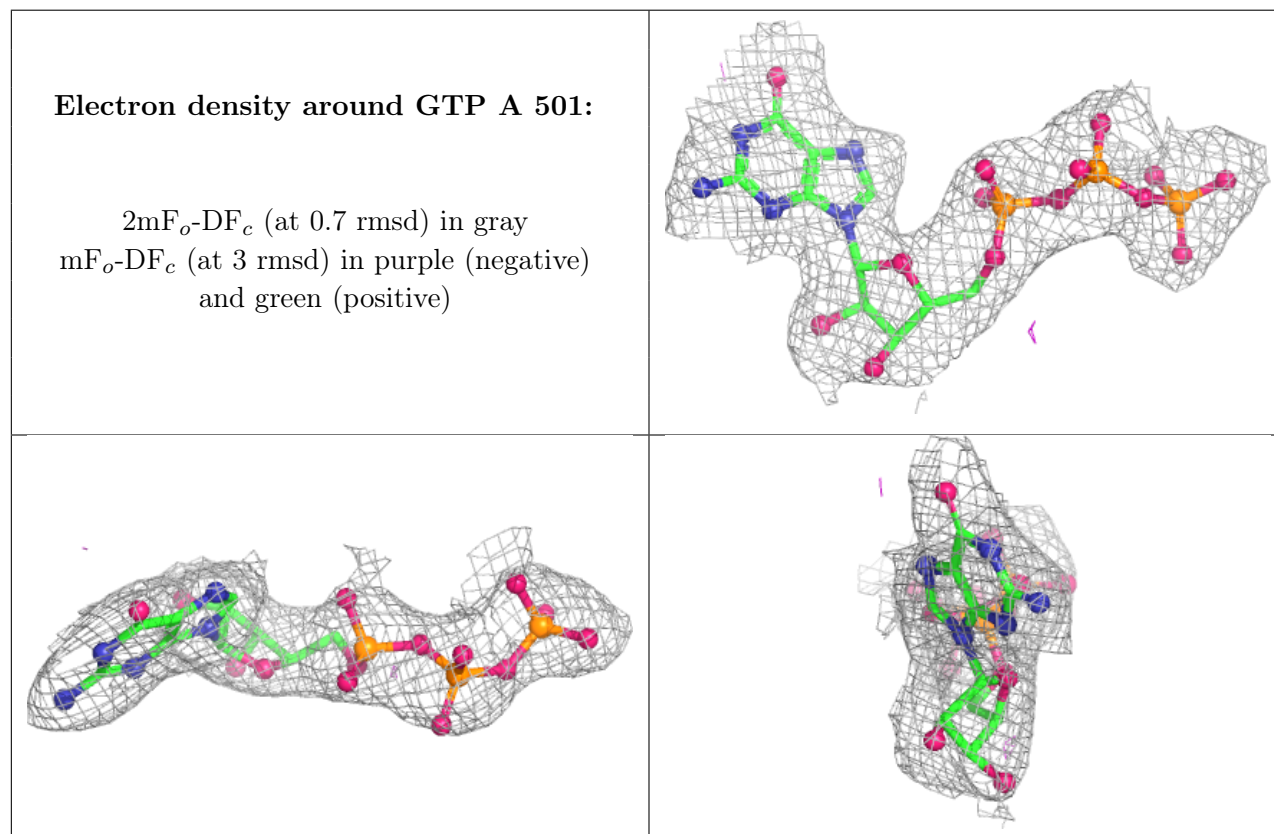
There are no oligosaccharides in this entry.

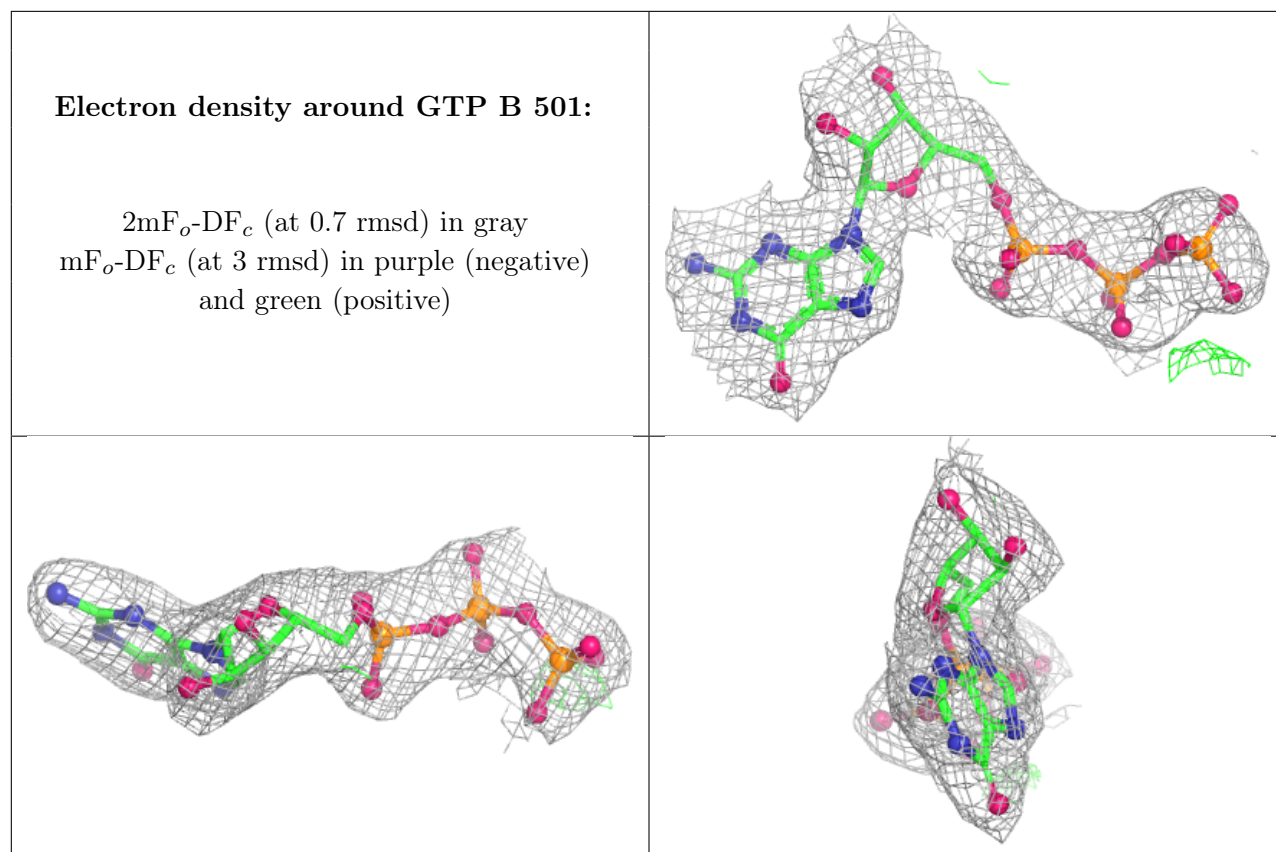
6.4 Ligands ⓘ

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
8	GOL	B	504	6/6	0.76	0.18	32,42,44,45	0
8	GOL	F	201	6/6	0.86	0.11	48,54,57,59	0
5	MG	B	502	1/1	0.88	0.21	50,50,50,50	0
7	MES	B	503	12/12	0.89	0.12	52,54,65,68	0
6	SO4	A	503	5/5	0.93	0.11	54,55,55,55	0
5	MG	A	502	1/1	0.94	0.09	30,30,30,30	0
4	GTP	A	501	32/32	0.97	0.07	26,36,43,45	0
4	GTP	B	501	32/32	0.97	0.07	35,43,64,67	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.