

Full wwPDB X-ray Structure Validation Report (i)

Mar 21, 2022 – 06:14 pm GMT

PDB ID	:	7Z02
Title	:	Z-SBTub2M photoswitch bound to tubulin-DARPin D1 complex
Authors	:	Wranik, M.; Weinert, T.; Standfuss, J.; Steinmetz, M.
Deposited on		
Resolution	:	2.36 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

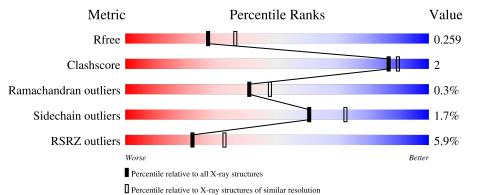
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as 541 be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.27
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 2.36 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	$1164 \ (2.36-2.36)$
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 <=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	А	451	<mark>6%</mark> 91%	6% •
2	В	445	88%	9% •
3	F	169	^{2%} 88%	• 8%



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 15764 atoms, of which 7735 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						AltConf	Trace
1	А	437	Total 6745	С	Н	Ν	0	S	9	8	0
-	11	101	2168	3324	581	648	24	0	Ũ	Ű	

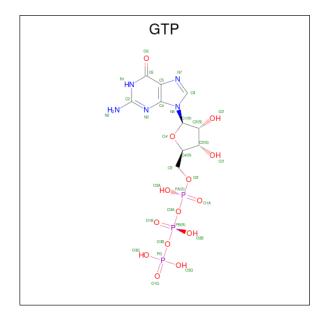
• Molecule 2 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	В	431	$\begin{array}{c} \text{Total} \\ 6569 \end{array}$	C 2110	Н 3215	N 569	O 647	S 28	0	3	0

• Molecule 3 is a protein called Designed Ankyrin Repeat Protein (DARPIN) D1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	F	155	Total 2317	C 731	Н 1158	N 196	0 229	${ m S} { m 3}$	0	2	0

• Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



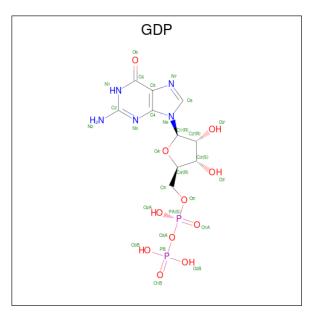


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	А	1	Total 41	C 10	Н 9	N 5	0 14	Р 3	0	0

• Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

\mathbf{N}	lol	Chain	Residues	Atoms	ZeroOcc	AltConf
	5	А	2	Total Mg 2 2	0	0

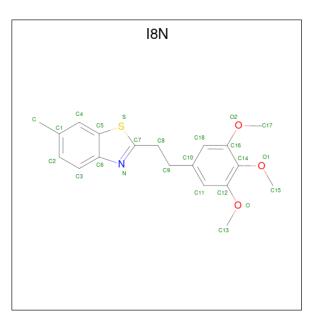
• Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
6	В	1	Total	С	Η	Ν	Ο	Р	0	0
0	D	1	38	10	10	5	11	2	0	0

• Molecule 7 is 6-methyl-2-[2-(3,4,5-trimethoxyphenyl)ethyl]-1,3-benzothiazole (three-letter code: I8N) (formula: C₁₉H₂₁NO₃S) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
7	В	1	Total	Ŭ	Н	Ν	0	S	0	0
	D	Ŧ	43	19	19	1	3	1	U U	, j

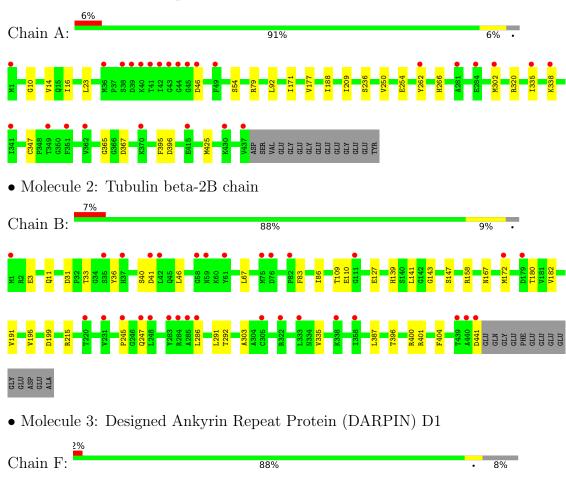
• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	3	Total O 3 3	0	0
8	В	6	Total O 6 6	0	0



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

MET ARG GLY GLY SER HIS HIS HIS HIS HIS HIS GLY SER



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	73.68Å 91.61Å 83.11Å	Depositor
a, b, c, α , β , γ	90.00° 97.39° 90.00°	Depositor
Resolution (Å)	45.81 - 2.36	Depositor
Resolution (A)	45.81 - 2.29	EDS
% Data completeness	61.8(45.81-2.36)	Depositor
(in resolution range)	52.8 (45.81 - 2.29)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.72 (at 2.29 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
D D	0.205 , 0.258	Depositor
R, R_{free}	0.205 , 0.259	DCC
R_{free} test set	2000 reflections $(7.15%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	41.3	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ L > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	15764	wwPDB-VP
Average B, all atoms $(Å^2)$	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.78% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: GTP, MG, GDP, I8N

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	l Chain Bond lengths		Bond	angles	
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.26	0/3526	0.48	0/4789
2	В	0.25	0/3440	0.47	0/4663
3	F	0.24	0/1181	0.40	0/1606
All	All	0.25	0/8147	0.46	0/11058

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 (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	А	3421	3324	3307	9	1
2	В	3354	3215	3215	23	0
3	F	1159	1158	1157	4	0
4	А	32	9	12	0	0
5	А	2	0	0	0	0
6	В	28	10	12	0	0
7	В	24	19	0	0	0
8	А	3	0	0	0	0
8	В	6	0	0	0	0
All	All	8029	7735	7703	33	1



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 2.

All (33) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

$\begin{array}{c c c c c c c c c c c c c c c c c c c $	Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	2.E.191.AI A.UD1	2.F.161.I FU.UD91	· · ·	- ()
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2:B:387:LEU:HD232:B:387:LEU:O2.150.471:A:79:ARG:NH21:A:92:LEU:O2.460.472:B:46:LEU:N2:B:46:LEU:HD222.300.471:A:16:ILE:HD131:A:171:ILE:HD111.950.461:A:17:VAL:HG221:A:177:VAL:O2.160.452:B:31:ASP:OD22:B:33:THR:OG12.340.441:A:250:VAL:HG221:A:254:GLU:OE12.170.442:B:109:THR:OG12:B:110:GLU:N2.500.442:B:11:GLN:N2:B:11:GLN:OE12.510.442:B:67:LEU:HD131:A:338:LYS:NZ2.320.442:B:396:THR:O2:B:67:LEU:N2.320.431:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	2:B:143:GLY:O	2:B:147:SER:OG	2.19	0.51
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2:B:11:GLN:N2:B:11:GLN:OE12.510.441:A:335:ILE:HD131:A:338:LYS:NZ2.320.442:B:67:LEU:HD122:B:67:LEU:N2.320.432:B:396:THR:O2:B:400:ARG:HG32.180.431:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	1:A:250:VAL:HG22	1:A:254:GLU:OE1	2.17	0.44
1:A:335:ILE:HD131:A:338:LYS:NZ2.320.442:B:67:LEU:HD122:B:67:LEU:N2.320.432:B:396:THR:O2:B:400:ARG:HG32.180.431:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	2:B:109:THR:OG1	2:B:110:GLU:N	2.50	0.44
2:B:67:LEU:HD122:B:67:LEU:N2.320.432:B:396:THR:O2:B:400:ARG:HG32.180.431:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	2:B:11:GLN:N	2:B:11:GLN:OE1	2.51	0.44
2:B:396:THR:O2:B:400:ARG:HG32.180.431:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	1:A:335:ILE:HD13	1:A:338:LYS:NZ	2.32	0.44
1:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	2:B:67:LEU:HD12	2:B:67:LEU:N	2.32	0.43
1:A:23:LEU:HD231:A:236:SER:HB22.020.422:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41	2:B:396:THR:O	2:B:400:ARG:HG3	2.18	0.43
2:B:286:LEU:HD232:B:291:LEU:HD232.010.422:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41				
2:B:404:PHE:HE23:F:90:ILE:HD121.850.412:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41				
2:B:36:TYR:OH2:B:40:SER:O2.380.412:B:141:LEU:HD122:B:172:MET:SD2.600.41				
2:B:141:LEU:HD12 2:B:172:MET:SD 2.60 0.41				
	2:B:387:LEU:HD23	2:B:387:LEU:C	2.42	0.40

All (1) 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)
1:A:262:TYR:OH	1:A:365:GLY:H[2_556]	1.55	0.05

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	Perce	ntiles
1	А	443/451~(98%)	413 (93%)	29~(6%)	1 (0%)	47	56
2	В	432/445~(97%)	406 (94%)	25~(6%)	1 (0%)	47	56
3	F	155/169~(92%)	151 (97%)	3~(2%)	1 (1%)	25	27
All	All	1030/1065~(97%)	970 (94%)	57~(6%)	3~(0%)	41	47

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	396	ASP
2	В	245	PRO
3	F	26	GLN

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	367/379~(97%)	360~(98%)	7~(2%)	57 68
2	В	364/383~(95%)	358~(98%)	6 (2%)	62 75
3	F	121/132~(92%)	119~(98%)	2(2%)	60 72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	852/894~(95%)	837~(98%)	15~(2%)	60 70

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	46	ASP
1	А	54	SER
1	А	266	HIS
1	А	320	ARG
1	А	347	CYS
1	А	367	ASP
1	А	395	PHE
2	В	41	ASP
2	В	127	GLU
2	В	139	HIS
2	В	167	ASN
2	В	247	GLN
2	В	441	ASP
3	F	64[A]	GLU
3	F	64[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	8	HIS

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 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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		Chain	Link	Bo	ond leng	\mathbf{ths}	В	ond ang	les
IVIOI	туре	Unam	ries	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
4	GTP	А	501	5	26,34,34	0.99	1 (3%)	$33,\!54,\!54$	1.84	6 (18%)	
6	GDP	В	501	-	24,30,30	1.16	2 (8%)	31,47,47	1.90	8 (25%)	
7	I8N	В	502	-	24,26,26	1.56	2 (8%)	30,36,36	1.73	3 (10%)	

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	А	501	5	-	5/18/38/38	0/3/3/3
6	GDP	В	501	-	-	4/12/32/32	0/3/3/3
7	I8N	В	502	-	-	3/10/11/11	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms		Observed(Å)	Ideal(Å)
7	В	502	I8N	C8-C7	-6.35	1.45	1.49
6	В	501	GDP	C5-C6	4.07	1.48	1.41
4	А	501	GTP	C6-N1	3.19	1.38	1.33
7	В	502	I8N	C9-C8	-2.91	1.33	1.53
6	В	501	GDP	C5-C4	2.40	1.47	1.40

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
7	В	502	I8N	C9-C8-C7	7.26	124.85	112.67
4	А	501	GTP	N3-C2-N1	-5.37	120.06	127.22
6	В	501	GDP	C2-N3-C4	4.61	120.62	115.36

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	А	501	GTP	C2-N3-C4	4.42	120.41	115.36
6	В	501	GDP	C2-N1-C6	4.06	122.39	115.93
4	А	501	GTP	PB-O3B-PG	-4.04	118.97	132.83
6	В	501	GDP	C5-C6-N1	-4.00	117.96	123.43
7	В	502	I8N	C8-C9-C10	3.84	126.76	113.28
6	В	501	GDP	C4-C5-C6	-3.84	117.14	120.80
4	А	501	GTP	PA-O3A-PB	-3.49	120.85	132.83
6	В	501	GDP	PA-O3A-PB	-3.32	121.45	132.83
6	В	501	GDP	N3-C2-N1	-3.22	122.92	127.22
7	В	502	I8N	C5-C6-N	2.98	114.98	108.04
4	А	501	GTP	C5-C6-N1	-2.73	119.70	123.43
6	В	501	GDP	C4-C5-N7	-2.73	106.56	109.40
4	А	501	GTP	C2-N1-C6	2.43	119.80	115.93
6	В	501	GDP	C3'-C2'-C1'	2.15	104.22	100.98

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There are no chirality outliers.

Mol	Chain	Res	Type	Atoms
4	А	501	GTP	C5'-O5'-PA-O1A
4	А	501	GTP	C5'-O5'-PA-O2A
6	В	501	GDP	C5'-O5'-PA-O1A
6	В	501	GDP	C5'-O5'-PA-O2A
7	В	502	I8N	N-C7-C8-C9
4	А	501	GTP	C5'-O5'-PA-O3A
4	А	501	GTP	PB-O3A-PA-O1A
6	В	501	GDP	PA-O3A-PB-O1B
4	А	501	GTP	C4'-C5'-O5'-PA
7	В	502	I8N	C18-C10-C9-C8
7	В	502	I8N	С11-С10-С9-С8
6	В	501	GDP	C5'-O5'-PA-O3A

All (12) torsion outliers are listed below:

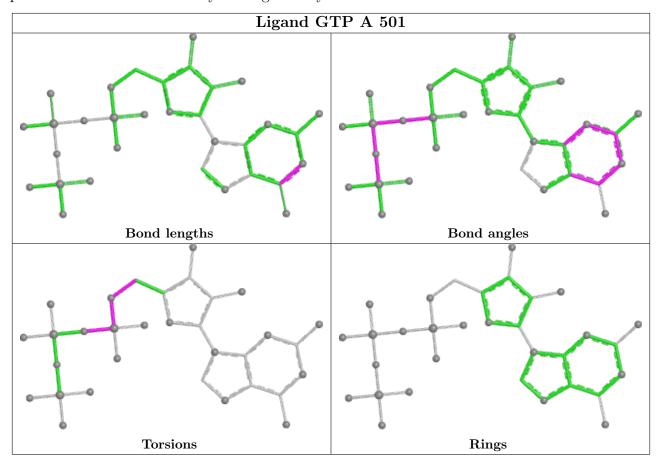
There are no ring outliers.

No monomer is involved in short contacts.

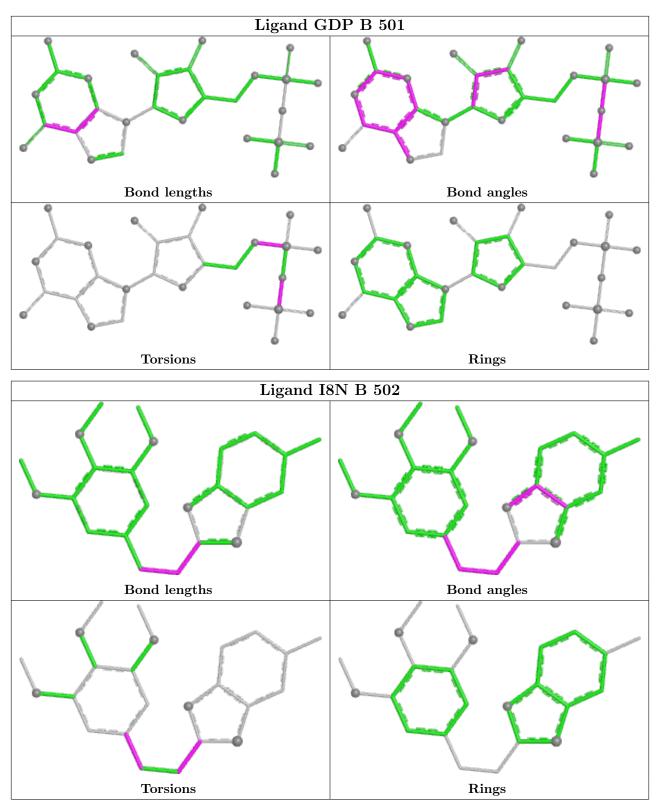
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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 (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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	А	437/451~(96%)	0.51	26 (5%) 22 33	21, 39, 78, 190	1 (0%)
2	В	431/445~(96%)	0.60	31 (7%) 15 23	23, 50, 91, 130	0
3	F	155/169~(91%)	0.25	3 (1%) 66 76	19, 36, 60, 73	0
All	All	1023/1065~(96%)	0.51	60 (5%) 22 33	19, 43, 84, 190	1 (0%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	43	GLY	11.5
1	А	42	ILE	11.4
1	А	41	THR	10.7
1	А	44	GLY	10.6
1	А	39	ASP	6.6
1	А	46	ASP	6.3
1	А	38	SER	5.6
2	В	440	ALA	5.5
1	А	45	GLY	5.3
2	В	285	ALA	4.9
1	А	338	LYS	4.6
1	А	40	LYS	4.5
2	В	220	THR	4.0
2	В	284	ARG	3.8
2	В	441	ASP	3.6
2	В	283	TYR	3.6
1	А	262	TYR	3.2
1	А	351	PHE	3.1
2	В	179	ASP	3.0
2	В	59	ASN	3.0
2	В	41	ASP	2.9
1	А	1	MET	2.9
2	В	172	MET	2.9

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Mol	Chain	Res	Type	RSRZ
2	В	333	LEU	2.9
2	В	439	THR	2.9
2	В	37	HIS	2.9
2	В	247	247 GLN	
2	В	286	LEU	2.8
2	В	338	LYS	2.7
1	А	49	PHE	2.7
2	В	1	MET	2.6
1	А	335	ILE	2.6
2	В	111	GLY	2.6
1	А	349	THR	2.6
2	В	75	MET	2.6
1	А	437	VAL	2.5
1	А	362	VAL	2.5
1	А	284	GLU	2.5
2	В	61	TYR	2.4
1	А	302	MET	2.4
2	В	305[A]	CYS	2.3
2	В	82	PRO	2.3
1	А	430	LYS	2.3
3	F	134	LYS	2.3
2	В	248	LEU	2.3
2	В	358	ILE	2.3
3	F	167	LYS	2.2
2	В	76	ASP	2.1
1	А	370	LYS	2.1
2	В	322	ARG	2.1
1	А	415	GLU	2.1
1	А	281	ALA	2.1
2	В	58	GLY	2.1
2	В	231	VAL	2.1
1	А	341	ILE	2.1
2	В	35	SER	2.1
2	В	42	LEU	2.1
2	В	245	PRO	2.1
3	F	14	LEU	2.0
1	А	36	MET	2.0

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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)

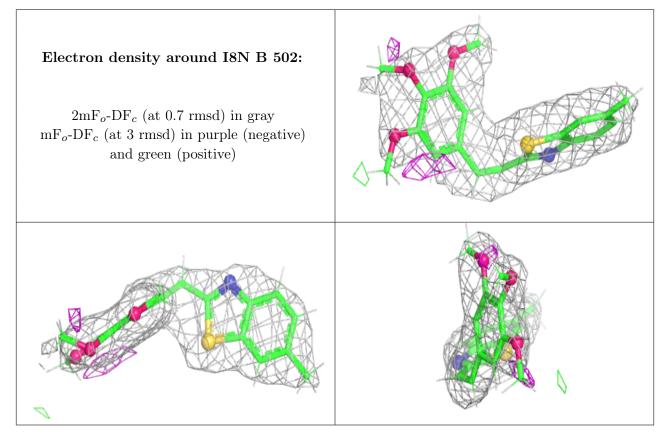
There are no monosaccharides in this entry.

6.4 Ligands (i)

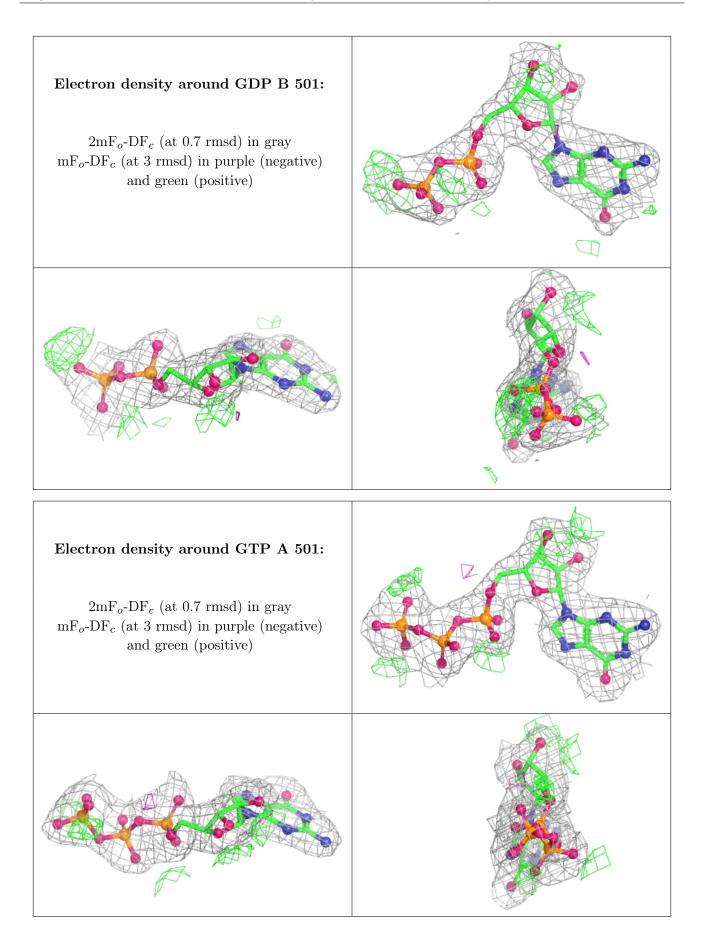
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
7	I8N	В	502	24/24	0.90	0.20	$56,\!61,\!75,\!76$	0
6	GDP	В	501	28/28	0.94	0.14	46,50,74,76	0
4	GTP	А	501	32/32	0.97	0.16	30,33,74,77	0
5	MG	А	503	1/1	0.97	0.18	28,28,28,28	0
5	MG	А	502	1/1	0.98	0.21	40,40,40,40	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.

