

wwPDB X-ray Structure Validation Summary Report (i)

Dec 9, 2023 - 08:58 am GMT

PDB ID	:	8CLD
Title	:	Ansamitocin P3 bound to tubulin (T2R-TTL) complex
Authors	:	Wranik, M.; Kepa, M.W.; Bertrand, Q.; Weinert, T.; Steinmetz, M.; Standfuss,
		J.
Deposited on		
Resolution	:	3.20 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 (i) 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 (1)) were used in the production of this report:

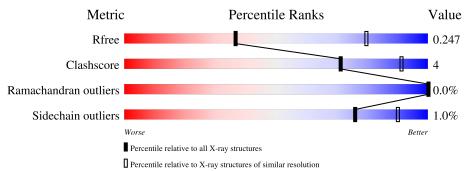
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7(2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.20 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	$\begin{array}{l} {\rm Similar\ resolution} \\ (\# {\rm Entries,\ resolution\ range}({\rm \AA})) \end{array}$		
R_{free}	130704	1133 (3.20-3.20)		
Clashscore	141614	1253 (3.20-3.20)		
Ramachandran outliers	138981	1234 (3.20-3.20)		
Sidechain outliers	138945	1233 (3.20-3.20)		

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%

Mol	Chain	Length	Quality of chain	
1	А	451	90%	7% •
1	С	451	92%	6% •
2	В	445	90%	6% •
2	D	445	85%	9% 5%
3	Е	189	61% • 36%	
4	F	384	74% 12%	• 12%



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 17497 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 Detyrosinated tubulin alpha-1B chain.

Mol	Chain	Residues		At	oms		ZeroOcc	AltConf	Trace	
1	А	437	Total 3416	C 2163	N 581	O 650	S 22	0	0	0
1	С	440	Total 3437	C 2175	N 584	O 656	S 22	0	0	0

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

Mol	Chain	Residues		At	oms		ZeroOcc	AltConf	Trace	
2	Р	427	Total	С	Ν	0	\mathbf{S}	0	0	0
	D	421	3361	2110	576	649	26	0	0	
0	П	421	Total	С	Ν	0	S	0	0	0
	D	421	3309	2080	562	640	27	0	0	0

• Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	Е	121	Total 1010	C 623	N 184	0 198	${ m S}{ m 5}$	0	1	0

• Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
4	F	336	Total 2761	C 1773	N 473	O 501	S 14	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP A0A8C9FGJ1
F	380	HIS	-	expression tag	UNP A0A8C9FGJ1
F	381	HIS	-	expression tag	UNP A0A8C9FGJ1
F	382	HIS	-	expression tag	UNP A0A8C9FGJ1

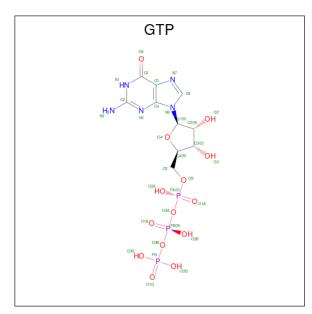
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Chain	Residue	Modelled	Actual	Comment	Reference
F	383	HIS	-	expression tag	UNP A0A8C9FGJ1
F	384	HIS	-	expression tag	UNP A0A8C9FGJ1

• 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	
5	Δ	1	Total	С	Ν	Ο	Р	0	0	
0	J A	L	32	10	5	14	3	0	0	
5	С	1	Total	С	Ν	Ο	Р	0	0	
5	U	1	32	10	5	14	3	0		

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

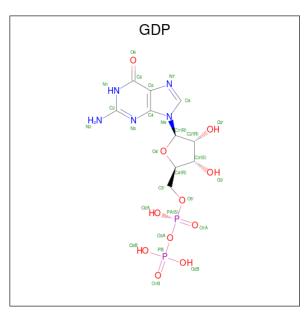
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total Mg 1 1	0	0
6	В	1	Total Mg 1 1	0	0
6	С	1	Total Mg 1 1	0	0

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



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	А	1	Total Ca 1 1	0	0
7	С	1	Total Ca 1 1	0	0

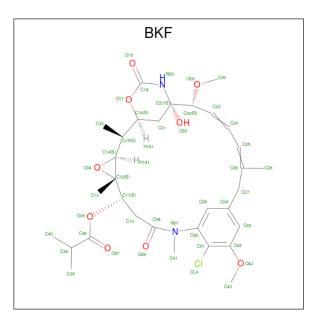
• Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
0	В	1	Total	С	Ν	Ο	Р	0	0
0	D	1	28	10	5	11	2	0	0
0	Л	1	Total	С	Ν	Ο	Р	0	0
0	D	1	28	10	5	11	2	0	U

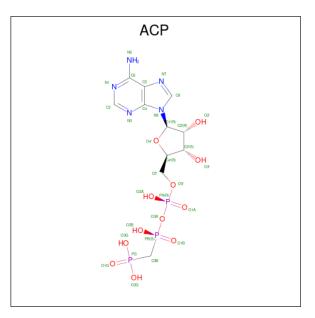
• Molecule 9 is (1S,2S,3S,5S,6S,16Z,18Z,20R,21S)-11-chloro-21-hydroxy-12,20-dimethoxy-2, 5,9,16-tetramethyl-8,23-dioxo-4,24-dioxa-9,22-diazatetracyclo[19.3.1.1 10,14 .0 3,5]hexac osa-10(26),11,13,16,18-pentaen-6-yl 2-methylpropanoate (three-letter code: BKF) (formula: $C_{32}H_{43}ClN_2O_9$) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
0	Л	1	Total	С	Cl	Ν	0	0	0
9	D	1	44	32	1	2	9	0	0

• Molecule 10 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
10	F	1	Total 31		N 5		Р 3	0	0

• Molecule 11 is water.



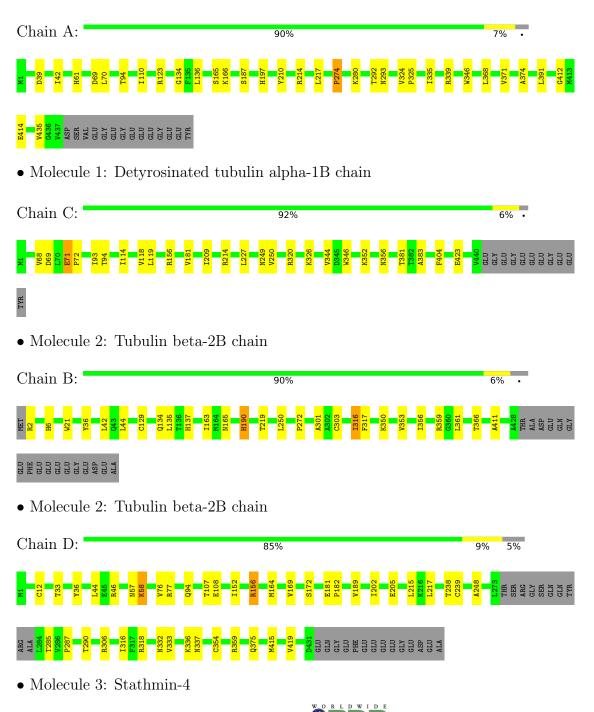
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	А	1	Total O 1 1	0	0
11	С	1	Total O 1 1	0	0
11	Е	1	Total O 1 1	0	0



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. 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. 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: Detyrosinated tubulin alpha-1B chain



Chain E:	61%	•	36%	
MET THR LEU ALA ALA LYS GLU	MET LYS CLU CLU CLU CLU CLU CLU CLU CLU CYS SER CYS CYS CYS CYS CYS CYS CYS CYS CYS CYS	SER ASP PASP PASP PASP ASP TYR TYR TYR ASP ALA ASP ASP ASP ASP ASP ASP ASP ASP ASP	TRP CYS VAL ILE SER ASP M6	S28 PHE ASP GLY PRO GLU PHE ASN
ALA SER LEU PRO ARG ARG ARG ARG	K52 R60 M19 K123 K126 K126 GLU GLU SER ARG			
• Molecule	4: Tubulin tyrosine li	gase		
Chain F:	7	74%	12% •	12%
M1 E16 R19 R31	H40 L41 L41 K79 K79 T83 C90 C91 T92 H93 H93 Y101	P102 T103 T103 LEU LEU LEU LEU PRO AIA AIA GLY CLI CLI TIE LEU TIE	ASN ASN ARN ARG THR D126 D126	V130 R138 R142 V146 W147 I148
A149 SER SER ALA GLY CLYS LYS	0.1 0.1 0.1 0.1 0.1 1.160 1.160 1.160 1.160 1.173 1.17	L191 L192 L192 P194 P194 P194 P194 F199 F131 Y214 Y214 F226 F233 F233	L240 K247 GLU TYR SER LYS N252	Y256 E261 M262 L271 L275
M296 C297 I298 I302 W328	L346 A362 A362 C17 C17 C17 C17 C17 C17 C17 C17 C17 C17	2222 1222 1222 1222 1222 1222 1222 122		



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	106.06Å 159.61Å 180.61Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.10 - 3.20	Depositor
Resolution (A)	15.10 - 2.50	EDS
% Data completeness	99.9 (15.10-3.20)	Depositor
(in resolution range)	87.7 (15.10-2.50)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.95 (at 2.51 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.20_4487	Depositor
D D.	0.200 , 0.241	Depositor
R, R_{free}	0.208 , 0.247	DCC
R_{free} test set	2000 reflections $(2.15%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	62.5	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.34,52.3	EDS
L-test for twinning ²	$ \langle L \rangle = 0.48, \langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17497	wwPDB-VP
Average B, all atoms $(Å^2)$	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.57% 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: BKF, CA, MG, GDP, GTP, ACP

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
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.28	0/3494	0.51	0/4743
1	С	0.29	0/3515	0.51	0/4772
2	В	0.28	0/3436	0.51	0/4654
2	D	0.28	0/3382	0.51	0/4581
3	Ε	0.26	0/1019	0.48	0/1352
4	F	0.31	0/2823	0.54	0/3813
All	All	0.29	0/17669	0.51	0/23915

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	D	0	2
4	F	0	3
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	156	ARG	Sidechain
2	D	359	ARG	Sidechain
4	F	19	ARG	Sidechain
4	F	193	GLU	Peptide
4	F	197	ARG	Sidechain



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	3416	0	3330	22	0
1	С	3437	0	3348	14	0
2	В	3361	0	3238	16	0
2	D	3309	0	3189	24	0
3	Е	1010	0	1024	3	0
4	F	2761	0	2733	46	0
5	А	32	0	12	0	0
5	С	32	0	12	0	0
6	А	1	0	0	0	0
6	В	1	0	0	0	0
6	С	1	0	0	0	0
7	А	1	0	0	0	0
7	С	1	0	0	0	0
8	В	28	0	12	0	0
8	D	28	0	12	1	0
9	D	44	0	0	1	0
10	F	31	0	14	0	0
11	А	1	0	0	0	0
11	С	1	0	0	0	0
11	Е	1	0	0	0	0
All	All	17497	0	16924	122	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.

The worst 5 of 122 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)
4:F:100:ILE:HD12	4:F:173:ILE:HD13	1.55	0.89
1:A:42:ILE:HD12	1:A:42:ILE:O	1.86	0.75
4:F:192:LEU:HD23	4:F:193:GLU:N	2.05	0.72
4:F:192:LEU:HD22	4:F:197:ARG:NE	2.07	0.68
1:A:293:ASN:ND2	1:A:339:ARG:HH21	1.97	0.63

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	Perce	ntiles
1	А	435/451~(96%)	422 (97%)	13 (3%)	0	100	100
1	С	438/451~(97%)	426 (97%)	12 (3%)	0	100	100
2	В	425/445~(96%)	416 (98%)	9~(2%)	0	100	100
2	D	417/445 (94%)	407 (98%)	10 (2%)	0	100	100
3	Ε	118/189~(62%)	116 (98%)	2(2%)	0	100	100
4	F	326/384~(85%)	309~(95%)	16 (5%)	1 (0%)	41	74
All	All	2159/2365~(91%)	2096 (97%)	62 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	91	CYS

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	А	368/379~(97%)	365~(99%)	3~(1%)	81 93
1	С	371/379~(98%)	368~(99%)	3~(1%)	81 93
2	В	369/383~(96%)	365~(99%)	4 (1%)	73 88
2	D	364/383~(95%)	363 (100%)	1 (0%)	92 96
3	Е	110/171~(64%)	107 (97%)	3(3%)	44 75
4	F	303/342~(89%)	298~(98%)	5(2%)	60 83

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Mol	Chain	Analysed	Analysed Rotameric		Percentiles	
All	All	1885/2037~(92%)	1866 (99%)	19 (1%)	76 90	

 $5~{\rm of}~19$ residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
4	F	31	ARG
4	F	161	LEU
4	F	197	ARG
4	F	160	ILE
1	С	214	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	134	GLN
2	D	14	ASN
2	В	426	GLN
2	В	375	GLN
1	С	101	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 5 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	В	Bond lengths			Bond angles		
MIOI	туре	Ullalli	1162	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	ACP	F	401	-	27,33,33	0.86	1 (3%)	$32,\!52,\!52$	1.57	2 (6%)	
8	GDP	В	501	6	24,30,30	1.04	3 (12%)	30,47,47	0.69	1 (3%)	
5	GTP	С	501	6	26,34,34	1.07	3 (11%)	32,54,54	0.77	0	
5	GTP	А	501	6	26,34,34	1.08	3 (11%)	32,54,54	0.75	0	
9	BKF	D	502	-	45,47,47	2.90	15 (33%)	53,71,71	<mark>3.64</mark>	26 (49%)	
8	GDP	D	501	-	24,30,30	1.08	3 (12%)	30,47,47	0.87	1 (3%)	

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	ACP	F	401	-	-	6/15/38/38	0/3/3/3
8	GDP	В	501	6	-	3/12/32/32	0/3/3/3
5	GTP	С	501	6	-	5/18/38/38	0/3/3/3
5	GTP	А	501	6	-	4/18/38/38	0/3/3/3
9	BKF	D	502	-	-	21/49/76/76	0/2/4/4
8	GDP	D	501	-	-	4/12/32/32	0/3/3/3

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	D	502	BKF	C08-N07	7.92	1.51	1.35
9	D	502	BKF	C12-C14	7.25	1.56	1.47
9	D	502	BKF	C10-C11	7.11	1.62	1.52
9	D	502	BKF	C06-N07	6.99	1.52	1.44
9	D	502	BKF	C15-C16	6.55	1.69	1.53

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^{o})$	$Ideal(^{o})$
9	D	502	BKF	C10-C08-N07	11.61	131.99	118.89
9	D	502	BKF	C01-C06-N07	8.78	129.71	120.71
9	D	502	BKF	C05-C06-C01	-8.27	111.98	122.53

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
9	D	502	BKF	C28-C26-C25	-7.61	102.95	122.59
10	F	401	ACP	PB-O3A-PA	-7.10	110.06	132.56

There are no chirality outliers.

5 of 43 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	А	501	GTP	C5'-O5'-PA-O3A
5	А	501	GTP	C5'-O5'-PA-O2A
5	С	501	GTP	C5'-O5'-PA-O3A
5	С	501	GTP	C5'-O5'-PA-O2A
8	В	501	GDP	PA-O3A-PB-O3B

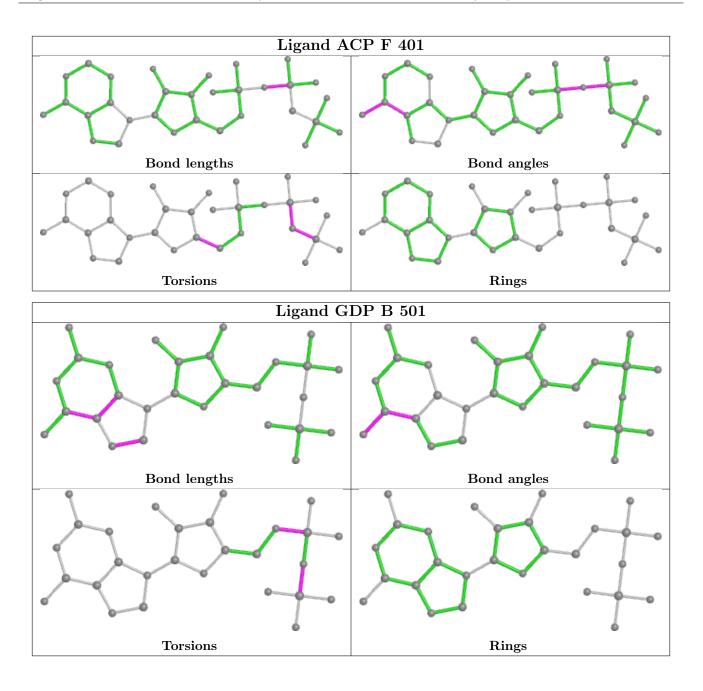
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	D	502	BKF	1	0
8	D	501	GDP	1	0

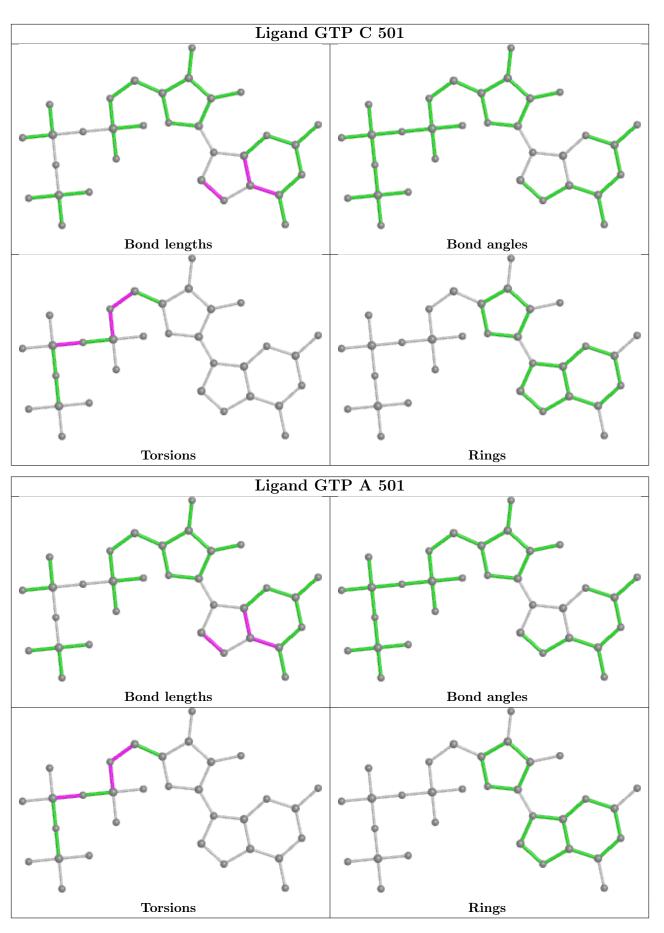
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.



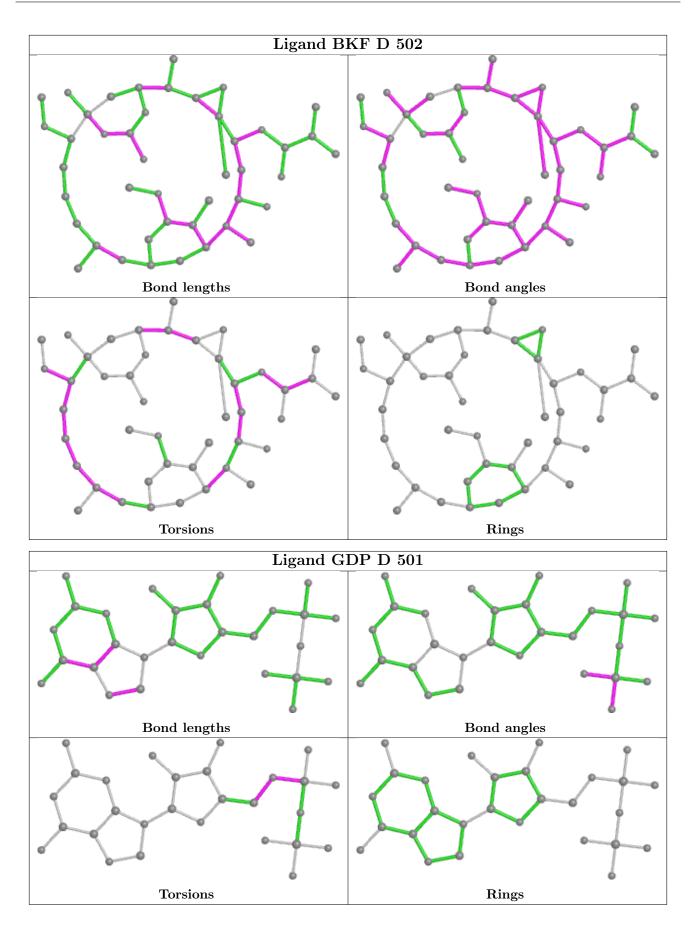














5.7 Other polymers (i)

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

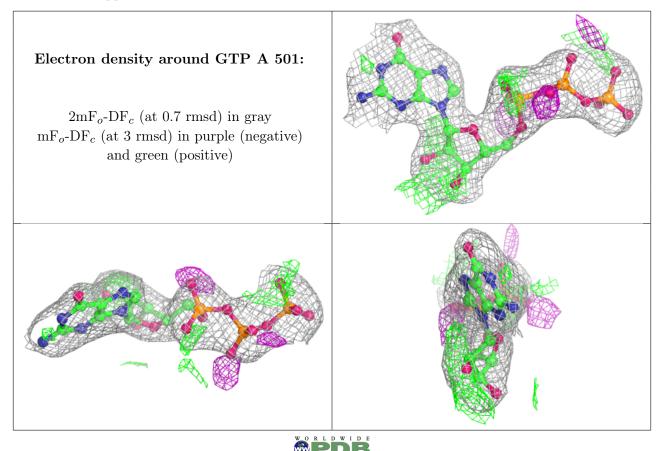
6.3 Carbohydrates (i)

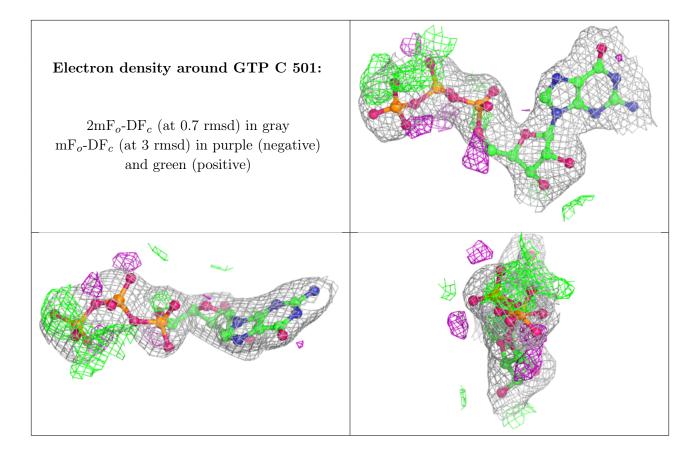
Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

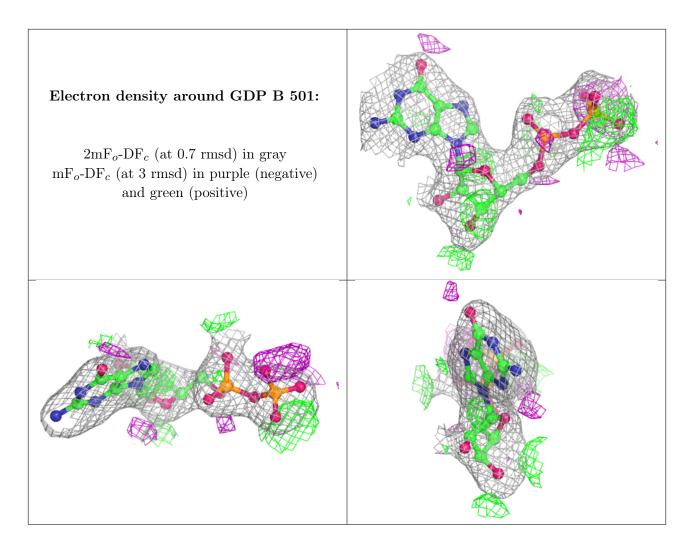
Unable to reproduce the depositors R factor - this section is therefore empty.

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.

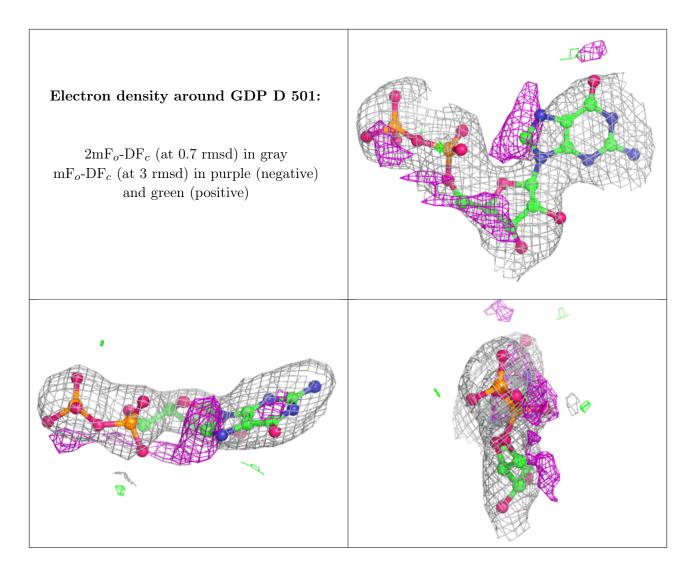




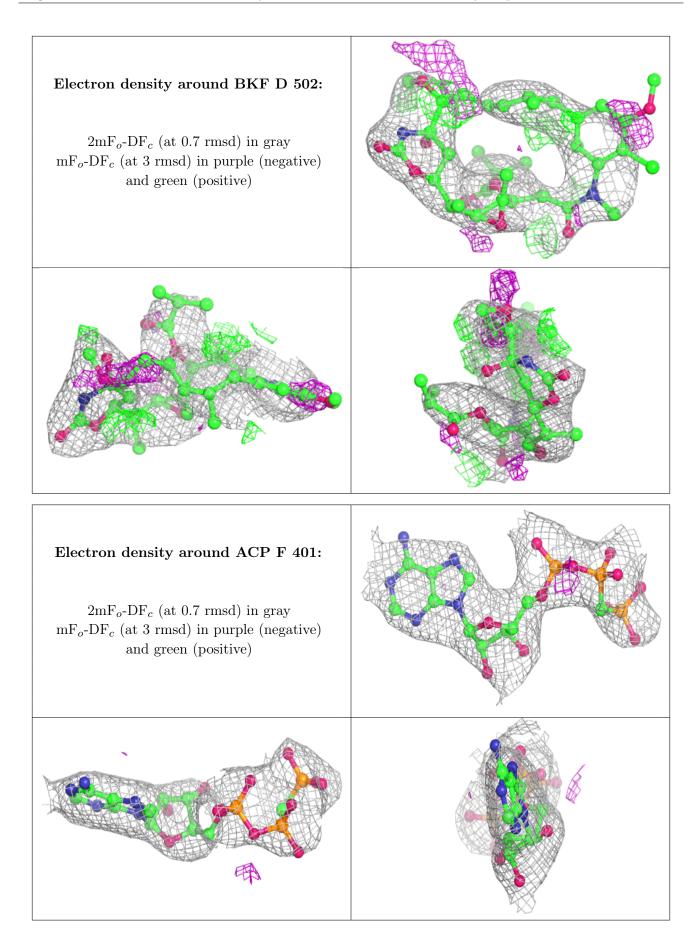














6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

