



wwPDB X-ray Structure Validation Summary Report ⓘ

May 27, 2024 – 12:45 PM JST

PDB ID : 8YU9
Title : Tubulin-RB3-TTL in complex with compound SI10
Authors : Wu, C.Y.; Wang, Y.X.
Deposited on : 2024-03-27
Resolution : 3.25 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 : 2.36.2
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) : 2.36.2

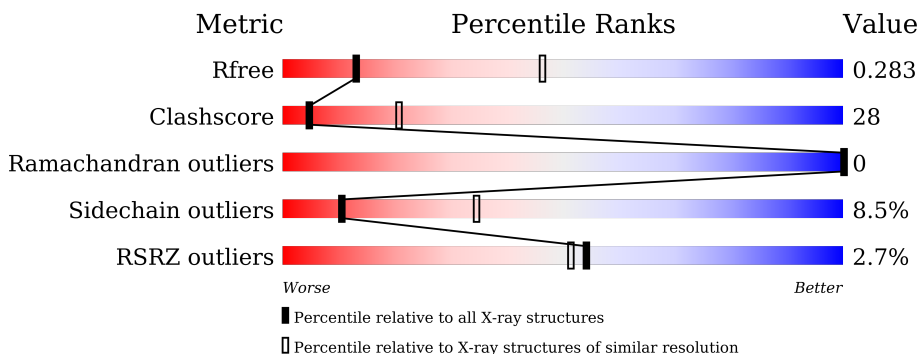
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 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	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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	440	 2% 56% 41% ..
1	C	440	 55% 41% .
2	B	431	 51% 46% ..
2	D	431	 2% 43% 48% 6% .
3	E	143	 48% 31% 5% 16%
4	F	380	 11% 35% 38% 5% 22%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	A1D7A	D	501	-	X	-	-

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 17095 atoms, of which 36 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	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	437	Total	C	N	O	S	0	0	0
			3394	2145	579	648	22			
1	C	440	Total	C	N	O	S	0	0	0
			3429	2169	582	656	22			

- 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	0	0
			3351	2104	572	649	26			
2	D	418	Total	C	N	O	S	0	0	0
			3275	2062	552	634	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	120	Total	C	N	O	S	0	0	0
			988	611	180	192	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	initiating methionine	UNP P63043
E	4	ALA	-	expression tag	UNP P63043

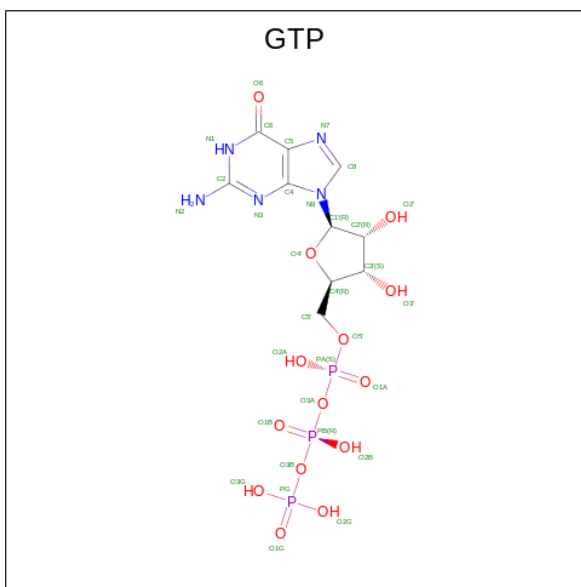
- Molecule 4 is a protein called Tubulin-tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	F	298	Total	C	N	O	S	0	0	0
			2396	1547	398	438	13			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	?	-	ALA	deletion	UNP A0A8V0Z8P0
F	?	-	GLU	deletion	UNP A0A8V0Z8P0
F	?	-	MET	deletion	UNP A0A8V0Z8P0
F	?	-	GLN	deletion	UNP A0A8V0Z8P0
F	?	-	GLN	deletion	UNP A0A8V0Z8P0
F	?	-	GLN	deletion	UNP A0A8V0Z8P0
F	?	-	LEU	deletion	UNP A0A8V0Z8P0
F	?	-	LEU	deletion	UNP A0A8V0Z8P0
F	?	-	GLU	deletion	UNP A0A8V0Z8P0
F	?	-	GLY	deletion	UNP A0A8V0Z8P0
F	?	-	ASP	deletion	UNP A0A8V0Z8P0
F	?	-	GLN	deletion	UNP A0A8V0Z8P0
F	?	-	THR	deletion	UNP A0A8V0Z8P0
F	?	-	LEU	deletion	UNP A0A8V0Z8P0
F	?	-	VAL	deletion	UNP A0A8V0Z8P0
F	?	-	LEU	deletion	UNP A0A8V0Z8P0
F	?	-	ALA	deletion	UNP A0A8V0Z8P0
F	?	-	SER	deletion	UNP A0A8V0Z8P0
F	?	-	SER	deletion	UNP A0A8V0Z8P0
F	?	-	THR	deletion	UNP A0A8V0Z8P0
F	?	-	HIS	deletion	UNP A0A8V0Z8P0
F	?	-	PRO	deletion	UNP A0A8V0Z8P0
F	?	-	GLU	deletion	UNP A0A8V0Z8P0
F	?	-	SER	deletion	UNP A0A8V0Z8P0
F	?	-	VAL	deletion	UNP A0A8V0Z8P0
F	?	-	ASP	deletion	UNP A0A8V0Z8P0
F	?	-	SER	deletion	UNP A0A8V0Z8P0
F	?	-	ASP	deletion	UNP A0A8V0Z8P0
F	?	-	LYS	deletion	UNP A0A8V0Z8P0
F	?	-	ASN	deletion	UNP A0A8V0Z8P0
F	?	-	HIS	deletion	UNP A0A8V0Z8P0
F	?	-	GLY	deletion	UNP A0A8V0Z8P0
F	?	-	PHE	deletion	UNP A0A8V0Z8P0
F	379	HIS	-	expression tag	UNP A0A8V0Z8P0
F	380	HIS	-	expression tag	UNP A0A8V0Z8P0

- 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	A	1	Total	C	N	O	P	32	0
				32	10	5	14		
5	C	1	Total	C	N	O	P	32	0
				32	10	5	14		

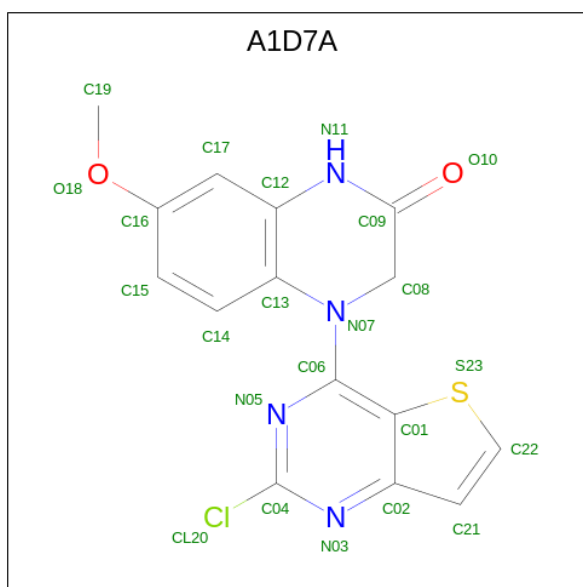
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	1	0
				1		
6	C	1	Total	Ca	1	0
				1		

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

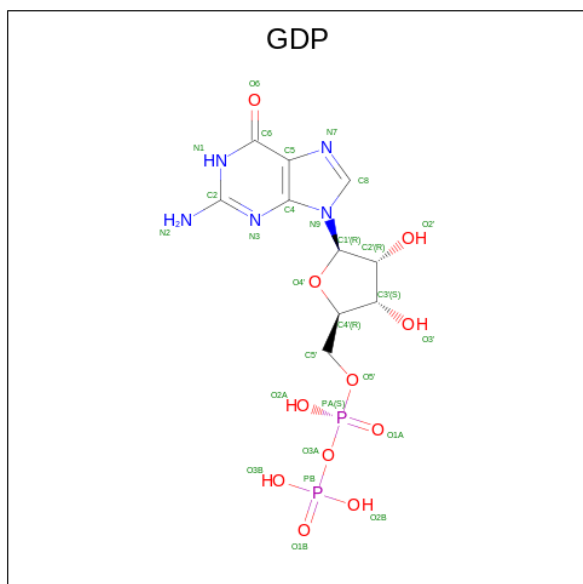
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mg	1	0
				1		
7	B	1	Total	Mg	1	0
				1		
7	C	1	Total	Mg	1	0
				1		

- Molecule 8 is 4-(2-chloranylthieno[3,2-d]pyrimidin-4-yl)-7-methoxy-1,3-dihydroquinoxalin-2-one (three-letter code: A1D7A) (formula: C₁₅H₁₁ClN₄O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf		
			Total	C	Cl	H	N	O			S	
8	B	1	Total	34	15	1	11	4	2	1	0	0
8	D	1	Total	34	15	1	11	4	2	1	0	0

- Molecule 9 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



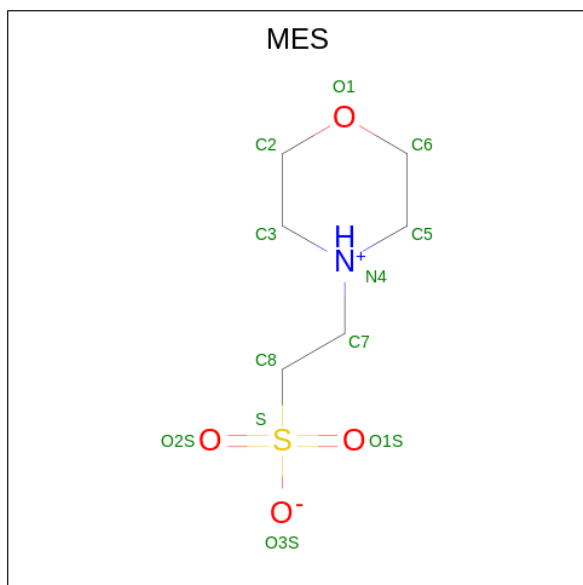
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			
9	B	1	Total	28	10	5	11	2	28	0

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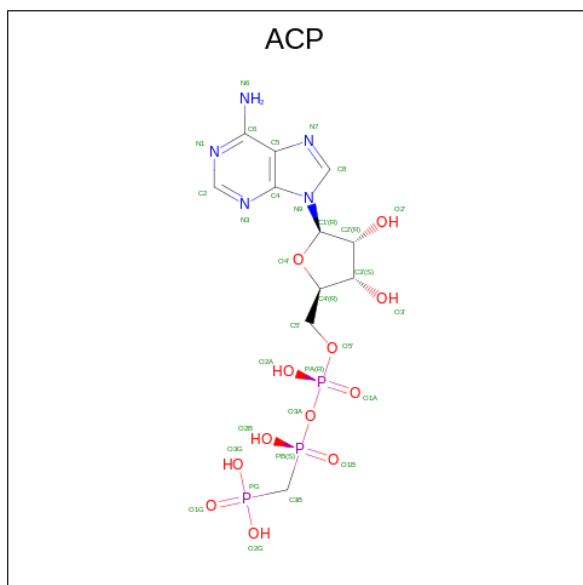
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
9	D	1	28	10	5	11	2	28	0

- 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	12	0
10	B	1	12	6	1	4	1	12	0

- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).

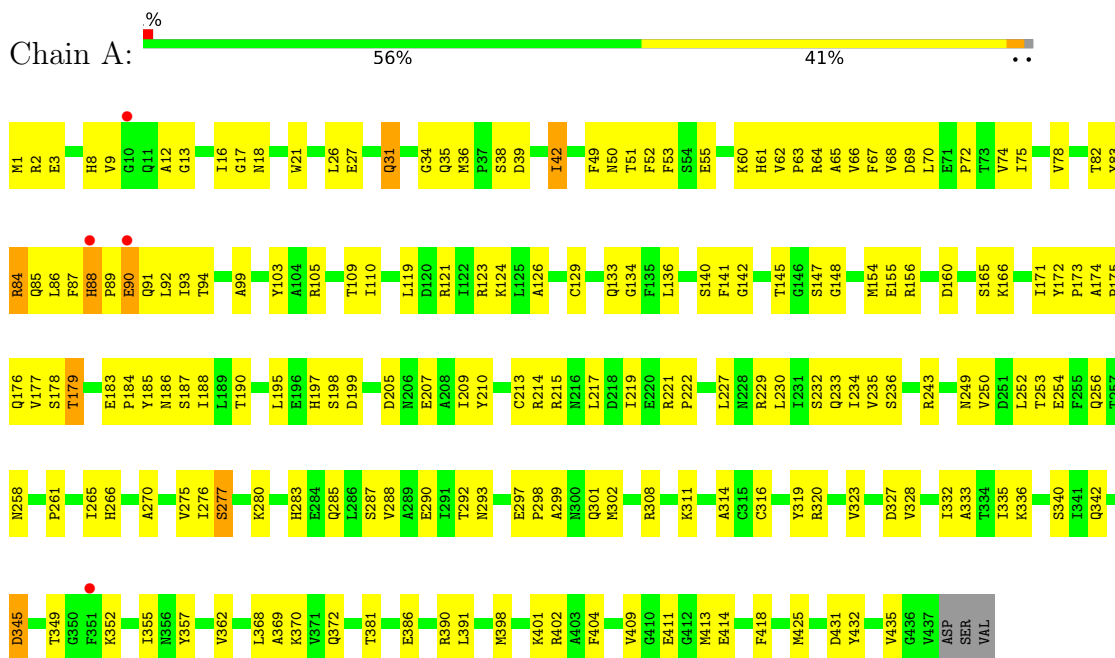


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	H	N	O			P
11	F	1	45	11	14	5	12	3	45	0

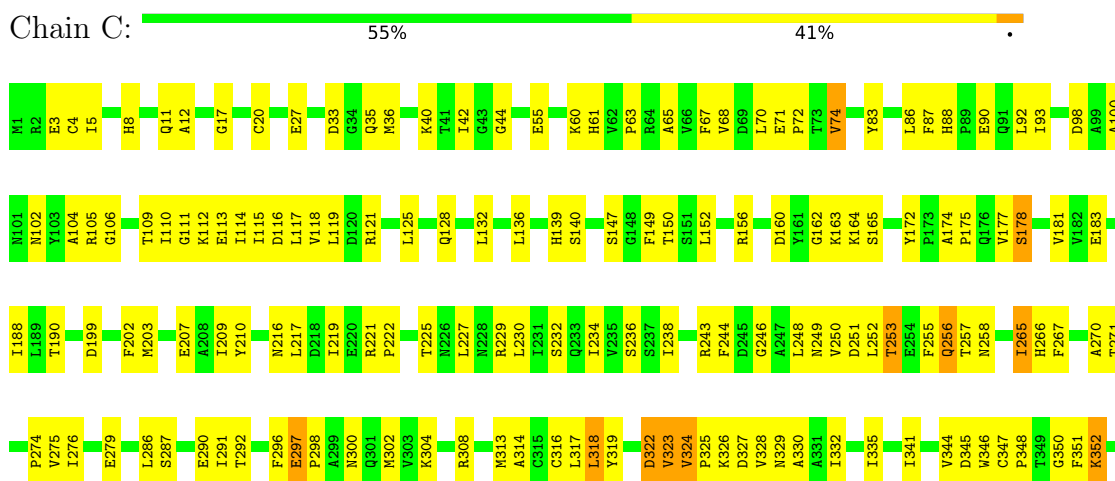
3 Residue-property plots [i](#)

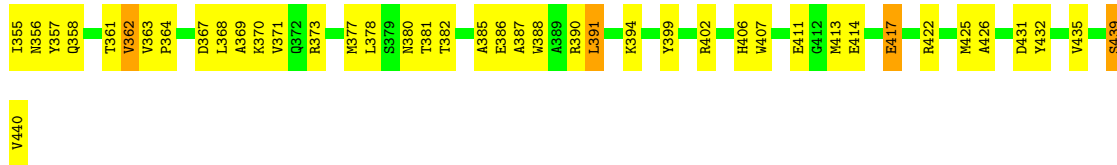
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Detyrosinated tubulin alpha-1B chain

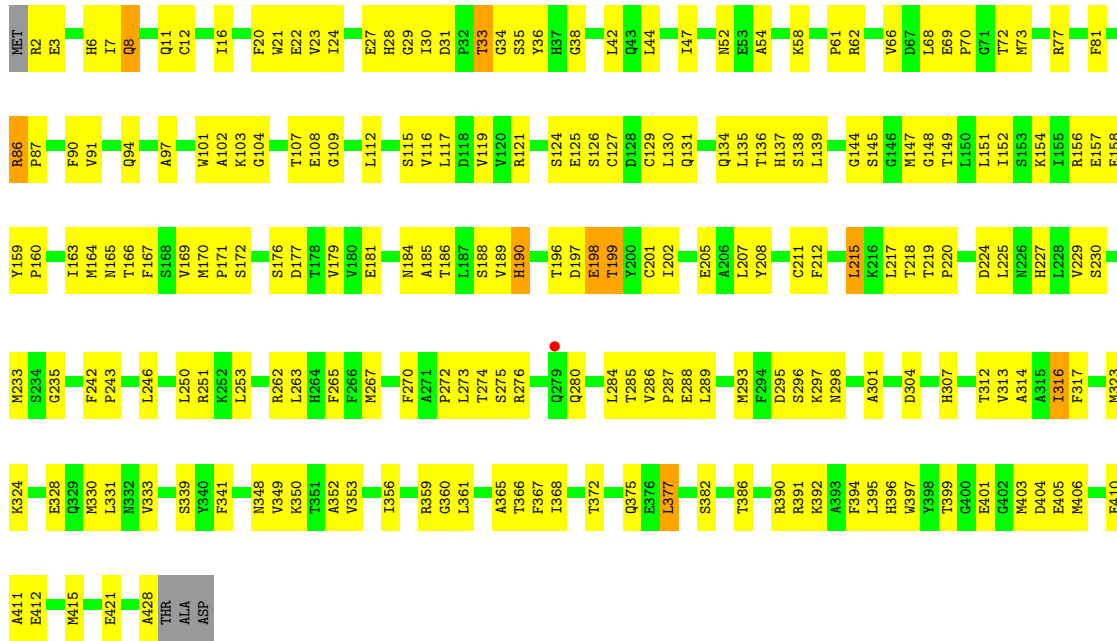


- Molecule 1: Detyrosinated tubulin alpha-1B chain

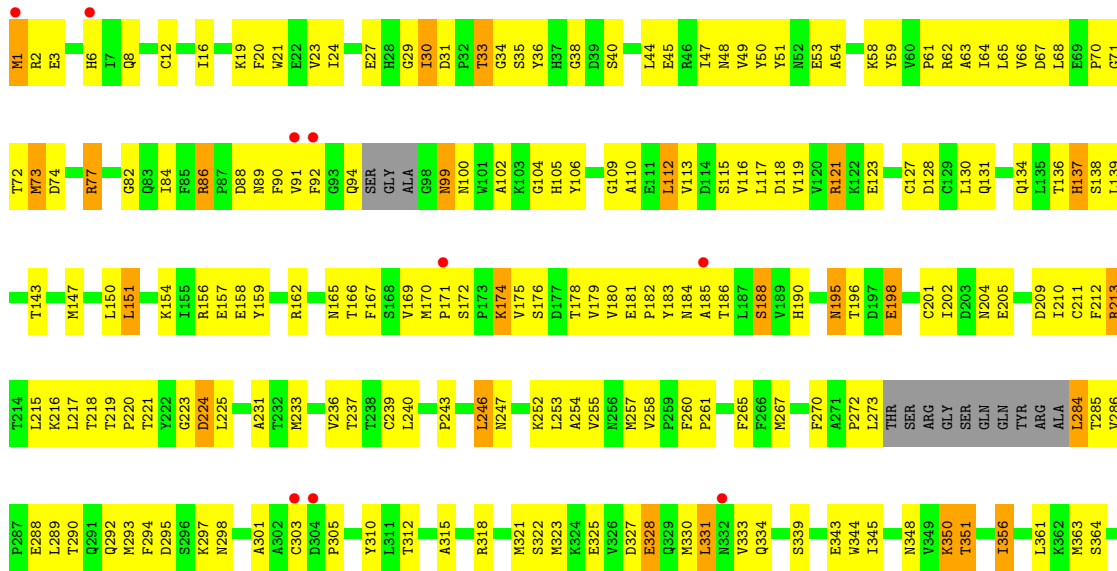


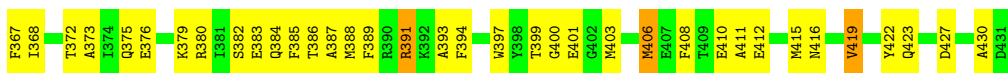


● Molecule 2: Tubulin beta chain



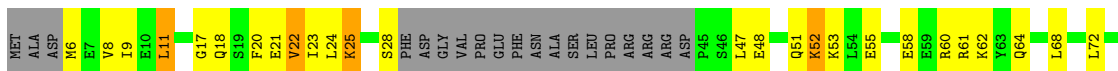
● Molecule 2: Tubulin beta chain





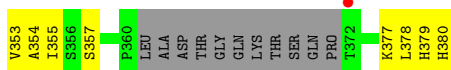
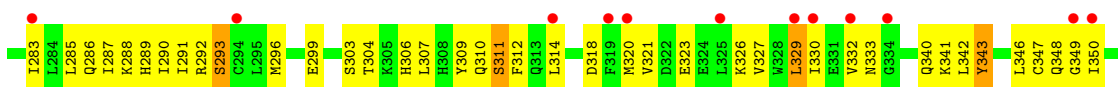
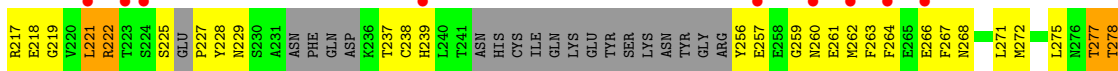
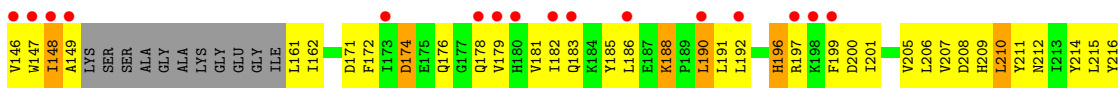
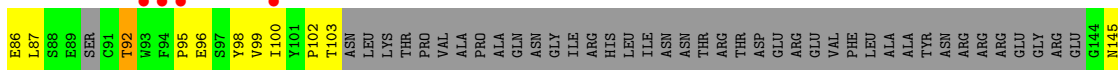
- Molecule 3: Stathmin-4

Chain E: 48% 31% 5% 16%



- Molecule 4: Tubulin–tyrosine ligase

Chain F: 11% 35% 38% 5% 22%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.97Å 157.38Å 182.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	87.33 – 3.25 87.33 – 3.25	Depositor EDS
% Data completeness (in resolution range)	86.9 (87.33-3.25) 86.9 (87.33-3.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 3.26Å)	Xtrriage
Refinement program	PHENIX (1.21_5207: ???)	Depositor
R, R_{free}	0.205 , 0.286 0.203 , 0.283	Depositor DCC
R_{free} test set	1999 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	84.4	Xtrriage
Anisotropy	0.332	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 63.4	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	0.92	EDS
Total number of atoms	17095	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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: MG, CA, ACP, MES, A1D7A, GDP, GTP

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	0.51	0/3470	0.68	1/4713 (0.0%)
1	C	0.58	1/3507 (0.0%)	0.72	0/4764
2	B	0.54	0/3426	0.70	0/4643
2	D	0.45	0/3347	0.63	0/4536
3	E	0.51	0/996	0.61	0/1320
4	F	0.43	0/2450	0.62	0/3319
All	All	0.51	1/17196 (0.0%)	0.67	1/23295 (0.0%)

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

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	20	CYS	CB-SG	-5.42	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	261	PRO	C-N-CA	-5.61	107.68	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	280	GLN	Peptide

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	3394	0	3294	174	0
1	C	3429	0	3326	168	0
2	B	3351	0	3214	181	0
2	D	3275	0	3140	255	0
3	E	988	0	1011	54	0
4	F	2396	0	2323	144	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
6	A	1	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
8	B	23	11	0	2	0
8	D	23	11	0	2	0
9	B	28	0	12	0	0
9	D	28	0	12	0	0
10	B	24	0	26	0	0
11	F	31	14	14	0	0
All	All	17059	36	16396	926	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 28.

The worst 5 of 926 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:123:ARG:HH22	1:A:160:ASP:HB3	1.16	1.05
4:F:289:HIS:O	4:F:293:SER:OG	1.75	1.03
1:A:336:LYS:HD3	3:E:24:LEU:HD12	1.40	1.01
2:B:170:MET:HG3	2:B:377:LEU:HD11	1.42	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:253:THR:HA	1:C:256:GLN:HB2	1.43	0.96

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	435/440 (99%)	413 (95%)	22 (5%)	0	100	100
1	C	438/440 (100%)	417 (95%)	21 (5%)	0	100	100
2	B	425/431 (99%)	404 (95%)	21 (5%)	0	100	100
2	D	412/431 (96%)	389 (94%)	23 (6%)	0	100	100
3	E	116/143 (81%)	109 (94%)	7 (6%)	0	100	100
4	F	282/380 (74%)	269 (95%)	13 (5%)	0	100	100
All	All	2108/2265 (93%)	2001 (95%)	107 (5%)	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	364/371 (98%)	344 (94%)	20 (6%)	21	52
1	C	369/371 (100%)	344 (93%)	25 (7%)	16	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	367/372 (99%)	348 (95%)	19 (5%)	23	53
2	D	359/372 (96%)	324 (90%)	35 (10%)	8	29
3	E	107/127 (84%)	88 (82%)	19 (18%)	2	7
4	F	260/338 (77%)	222 (85%)	38 (15%)	3	13
All	All	1826/1951 (94%)	1670 (92%)	156 (8%)	10	34

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	128	LYS
4	F	222	ARG
4	F	11	SER
4	F	148	ILE
4	F	293	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	6	HIS
2	D	15	GLN
2	D	48	ASN
1	C	88	HIS
2	B	6	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 14 ligands modelled in this entry, 5 are monoatomic - leaving 9 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
11	ACP	F	401	-	27,33,33	2.17	3 (11%)	32,52,52	1.15	3 (9%)
8	A1D7A	D	501	-	24,26,26	3.35	15 (62%)	25,38,38	4.44	16 (64%)
5	GTP	C	501	7	26,34,34	1.11	2 (7%)	32,54,54	1.61	7 (21%)
5	GTP	A	501	7	26,34,34	1.10	2 (7%)	32,54,54	1.58	7 (21%)
10	MES	B	503	2	12,12,12	1.14	1 (8%)	14,16,16	0.85	0
9	GDP	B	502	7	24,30,30	0.94	1 (4%)	30,47,47	1.31	4 (13%)
9	GDP	D	502	-	24,30,30	0.94	1 (4%)	30,47,47	1.33	4 (13%)
8	A1D7A	B	501	-	24,26,26	4.07	12 (50%)	25,38,38	3.34	13 (52%)
10	MES	B	504	-	12,12,12	1.12	1 (8%)	14,16,16	0.85	0

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
11	ACP	F	401	-	-	2/15/38/38	0/3/3/3
8	A1D7A	D	501	-	-	4/5/18/18	0/3/4/4
5	GTP	C	501	7	-	6/18/38/38	0/3/3/3
5	GTP	A	501	7	-	9/18/38/38	0/3/3/3
10	MES	B	503	2	-	0/6/14/14	0/1/1/1
9	GDP	B	502	7	-	3/12/32/32	0/3/3/3
9	GDP	D	502	-	-	4/12/32/32	0/3/3/3
8	A1D7A	B	501	-	-	2/5/18/18	0/4/4/4
10	MES	B	504	-	-	3/6/14/14	0/1/1/1

The worst 5 of 38 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	B	501	A1D7A	C09-N11	12.94	1.49	1.35
11	F	401	ACP	PB-O3A	10.02	1.69	1.58
8	D	501	A1D7A	C09-N11	8.38	1.44	1.35
8	B	501	A1D7A	C04-N03	7.75	1.36	1.30
8	D	501	A1D7A	C04-N03	5.87	1.34	1.30

The worst 5 of 54 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	501	A1D7A	O10-C09-N11	-9.66	112.91	121.43
8	D	501	A1D7A	C19-O18-C16	8.66	136.30	117.51
8	D	501	A1D7A	C21-C02-C01	8.43	116.77	110.62
8	B	501	A1D7A	N03-C04-N05	-7.79	122.78	130.62
8	B	501	A1D7A	C21-C02-C01	7.39	116.01	110.62

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	PB-O3B-PG-O2G
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

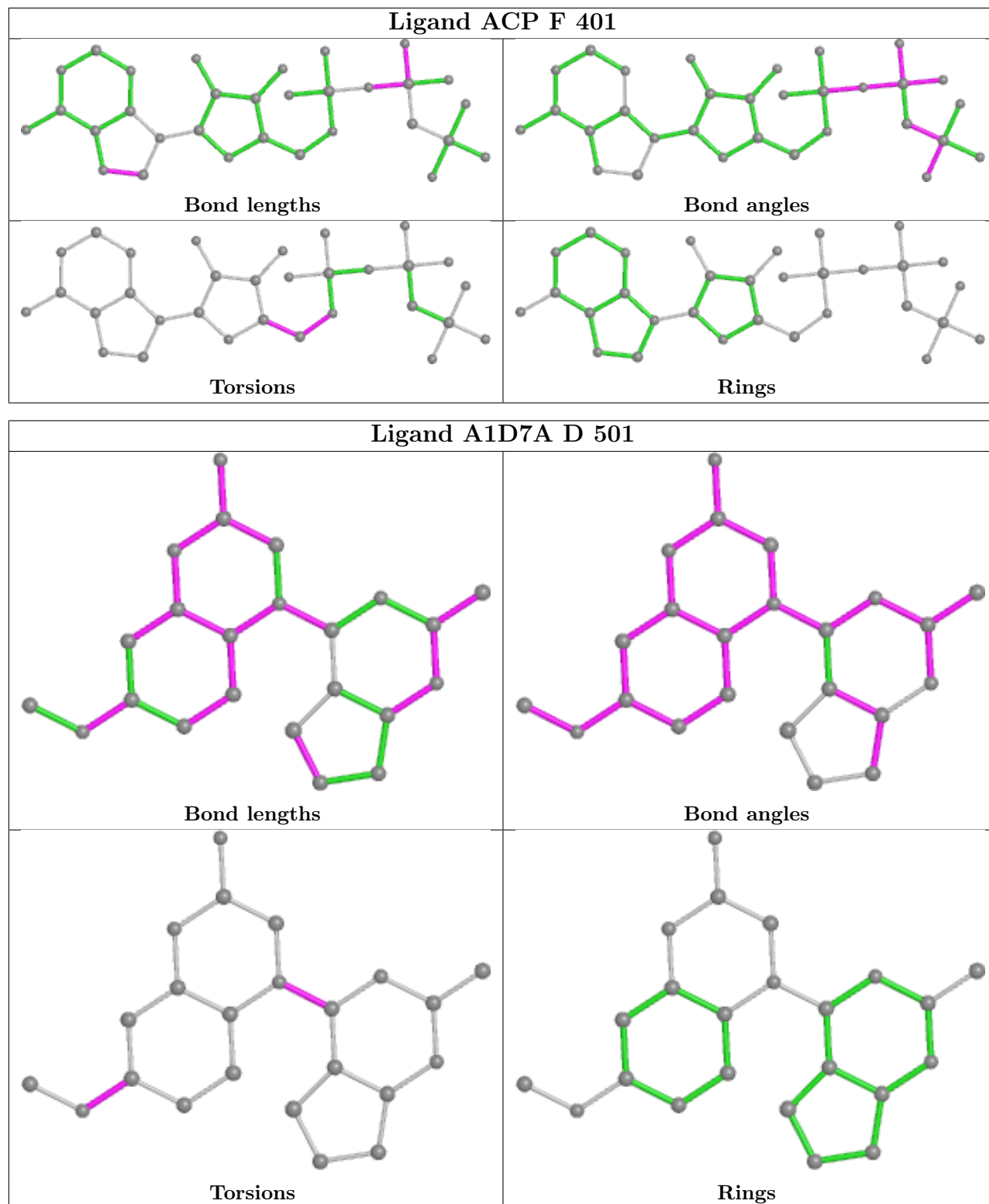
There are no ring outliers.

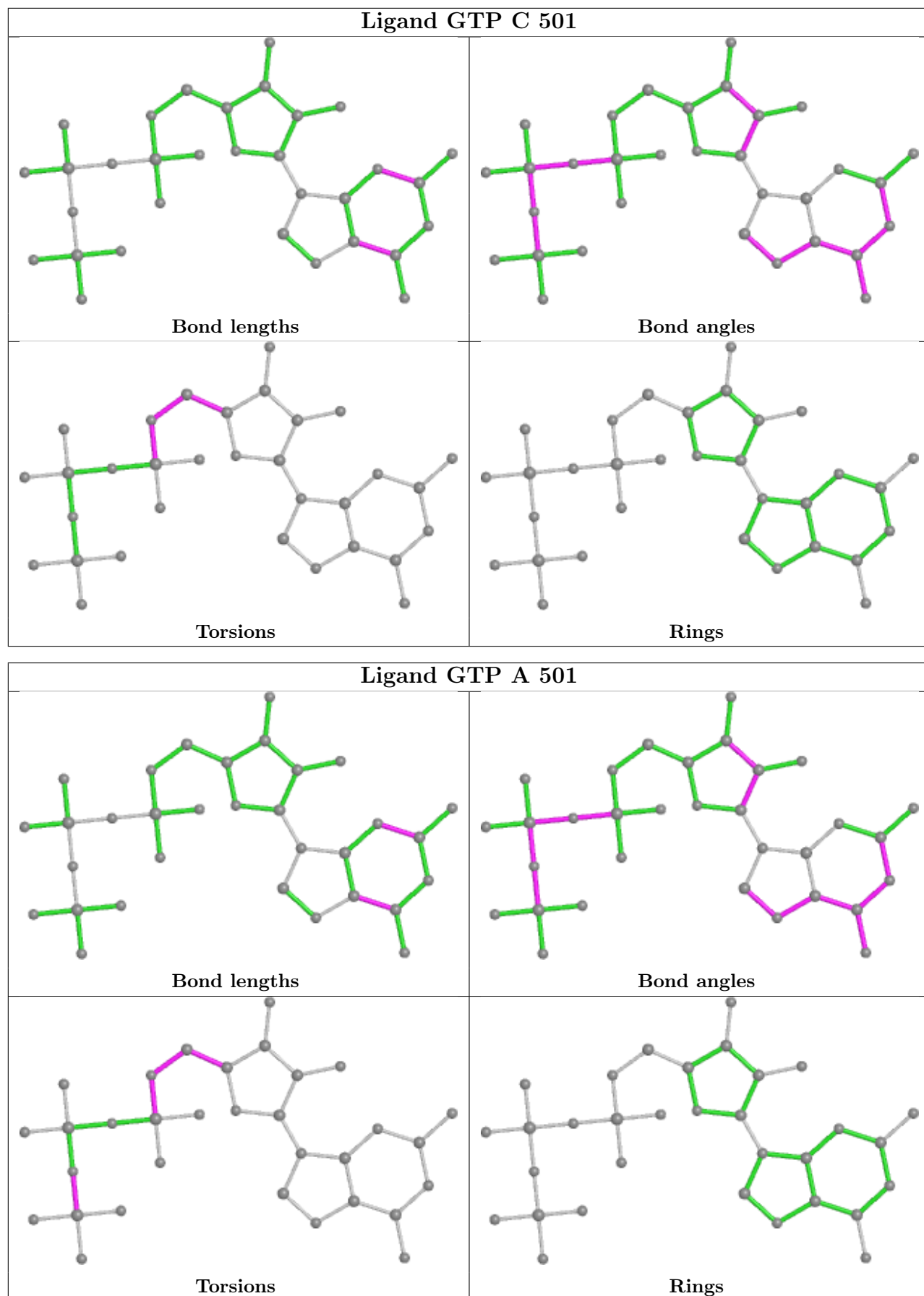
2 monomers are involved in 4 short contacts:

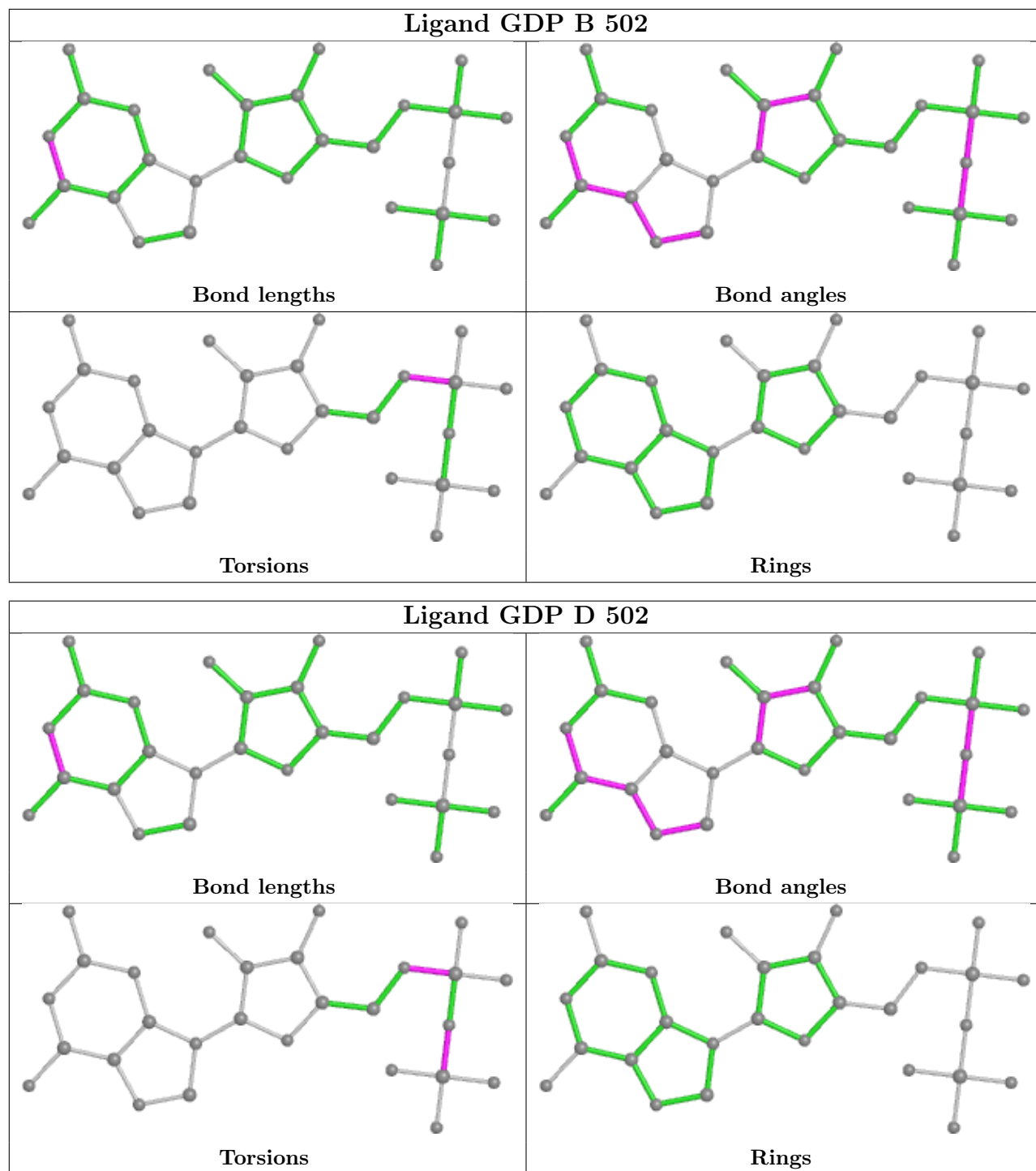
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	D	501	A1D7A	2	0
8	B	501	A1D7A	2	0

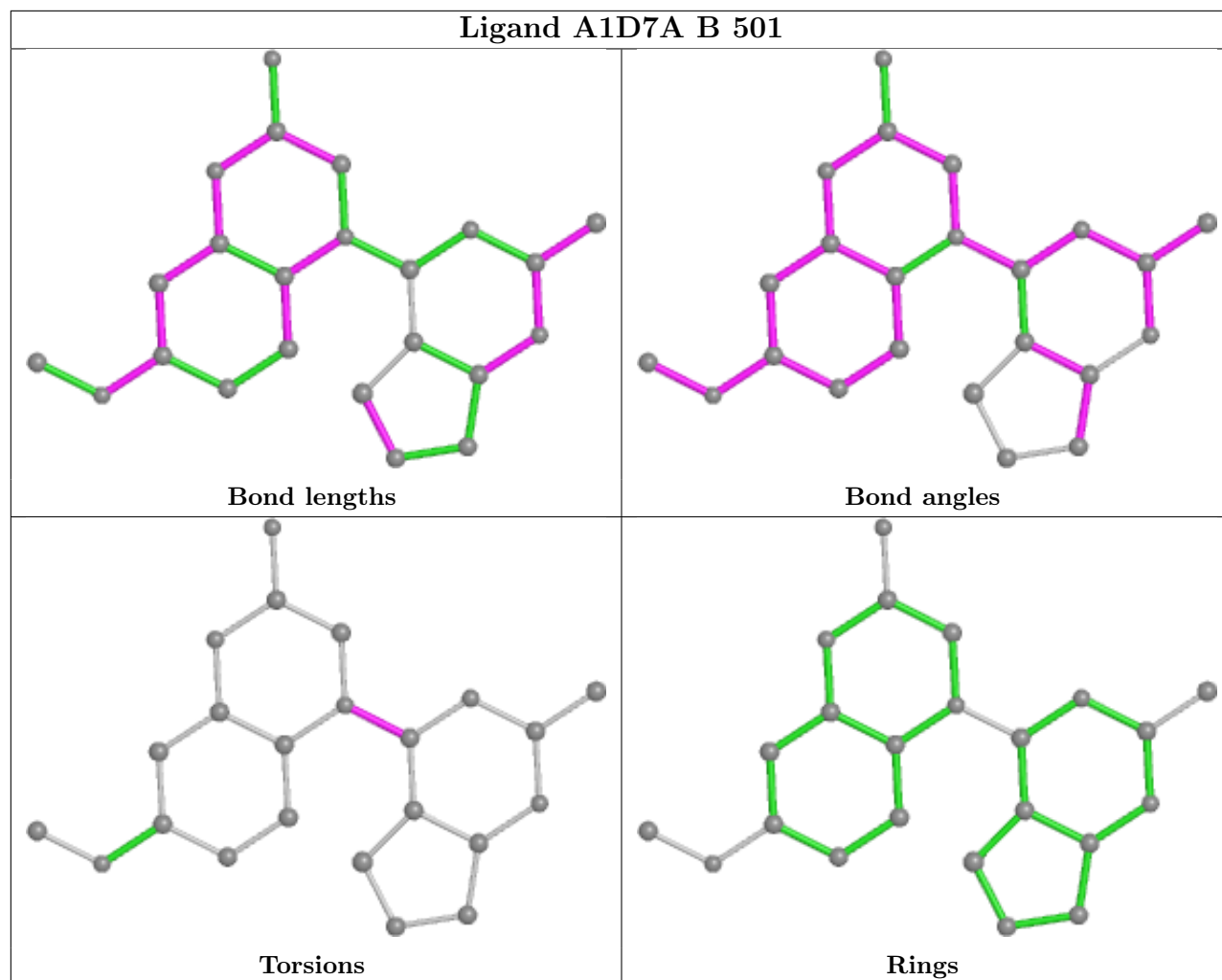
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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 [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	437/440 (99%)	0.28	4 (0%) 84 84	48, 73, 103, 150	0
1	C	440/440 (100%)	0.03	0 100 100	41, 61, 90, 123	0
2	B	427/431 (99%)	0.19	1 (0%) 95 95	47, 68, 103, 165	0
2	D	418/431 (96%)	0.42	9 (2%) 62 59	53, 92, 130, 175	0
3	E	120/143 (83%)	0.07	0 100 100	59, 84, 124, 158	0
4	F	298/380 (78%)	0.95	43 (14%) 2 2	63, 96, 155, 234	0
All	All	2140/2265 (94%)	0.32	57 (2%) 54 51	41, 76, 122, 234	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	239	HIS	3.8
4	F	320	MET	3.6
4	F	173	ILE	3.5
4	F	149	ALA	3.4
4	F	186	LEU	3.3

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](#)

LIGAND-RSR INFOmissingINFO

6.5 Other polymers [i](#)

There are no such residues in this entry.