



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 12:23 pm BST

PDB ID : 3DU7
Title : Tubulin-colchicine-phomopsin A: Stathmin-like domain complex
Authors : Cormier, A.; Marchand, M.; Ravelli, R.B.; Knossow, M.; Gigant, B.
Deposited on : 2008-07-17
Resolution : 4.10 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 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 : 2.11
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) : 2.11

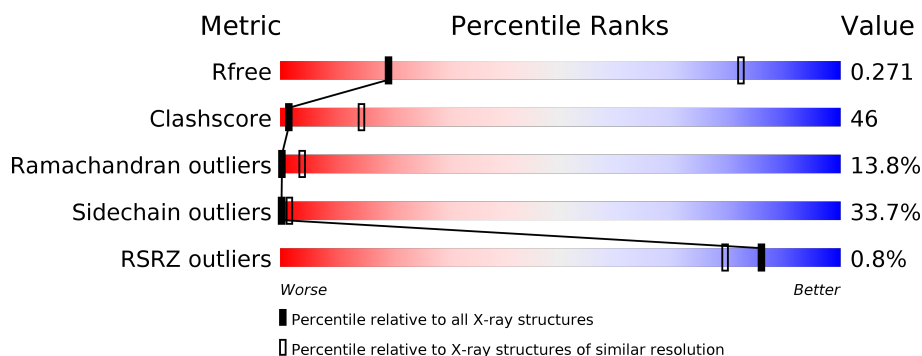
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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	1193 (4.50-3.70)
Clashscore	141614	1003 (4.44-3.76)
Ramachandran outliers	138981	1005 (4.48-3.72)
Sidechain outliers	138945	1199 (4.50-3.70)
RSRZ outliers	127900	1034 (4.50-3.70)

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 on 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	449	
1	C	449	
2	B	445	
2	D	445	
3	E	142	

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
5	CN2	B	700	-	-	X	-
5	CN2	D	701	-	-	X	-
6	HOS	B	800	-	-	X	-
6	HOS	D	801	-	-	X	-

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14258 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-1C chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3265	2070	554	620	21			
1	C	438	Total	C	N	O	S	0	0	0
			3317	2098	564	634	21			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	440	TYR	ALA	SEE REMARK 999	UNP Q3ZCJ7
A	442	ASP	GLY	SEE REMARK 999	UNP Q3ZCJ7
A	443	GLU	ASP	SEE REMARK 999	UNP Q3ZCJ7
A	447	GLU	ASP	SEE REMARK 999	UNP Q3ZCJ7
C	440	TYR	ALA	SEE REMARK 999	UNP Q3ZCJ7
C	442	ASP	GLY	SEE REMARK 999	UNP Q3ZCJ7
C	443	GLU	ASP	SEE REMARK 999	UNP Q3ZCJ7
C	447	GLU	ASP	SEE REMARK 999	UNP Q3ZCJ7

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	426	Total	C	N	O	S	0	0	0
			3282	2061	556	641	24			
2	D	426	Total	C	N	O	S	0	0	0
			3272	2056	551	641	24			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	203	SER	CYS	SEE REMARK 999	UNP Q6B856
B	318	VAL	ILE	SEE REMARK 999	UNP Q6B856
D	203	SER	CYS	SEE REMARK 999	UNP Q6B856
D	318	VAL	ILE	SEE REMARK 999	UNP Q6B856

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	121	Total	C	N	O	S	0	0	0
			830	504	158	163	5			

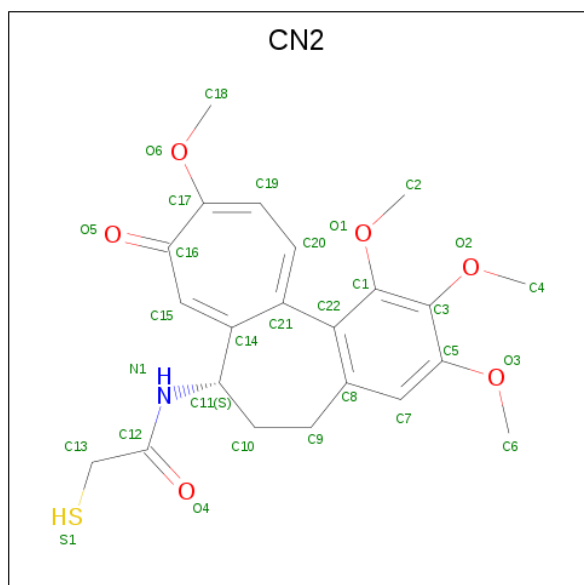
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	4	ALA	-	EXPRESSION TAG	UNP P63043

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

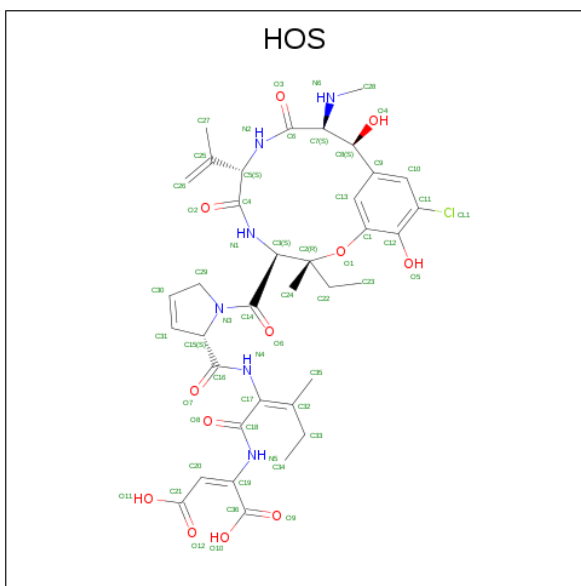
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		

- Molecule 5 is 2-MERCAPTO-N-[1,2,3,10-TETRAMETHOXY-9-OXO-5,6,7,9-TETRAHYDRO-BENZO[A]HEPTALEN-7-YL]ACETAMIDE (three-letter code: CN2) (formula: C₂₂H₂₅NO₆S).



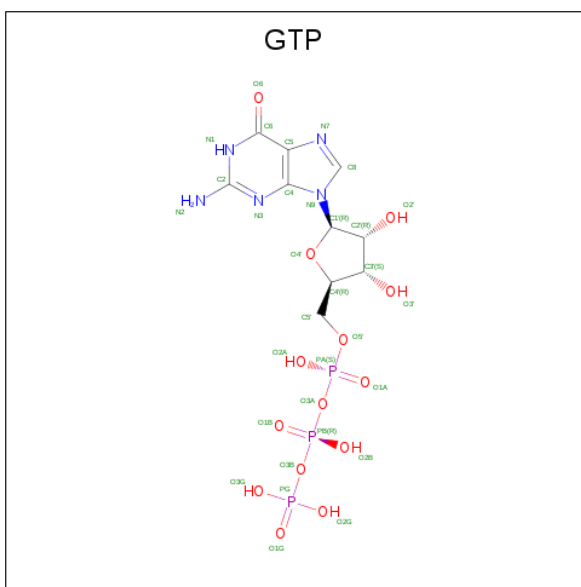
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	S	0	0
			30	22	1	6	1		
5	D	1	Total	C	N	O	S	0	0
			30	22	1	6	1		

- Molecule 6 is Phomopsin A (three-letter code: HOS) (formula: $C_{36}H_{45}ClN_6O_{12}$).



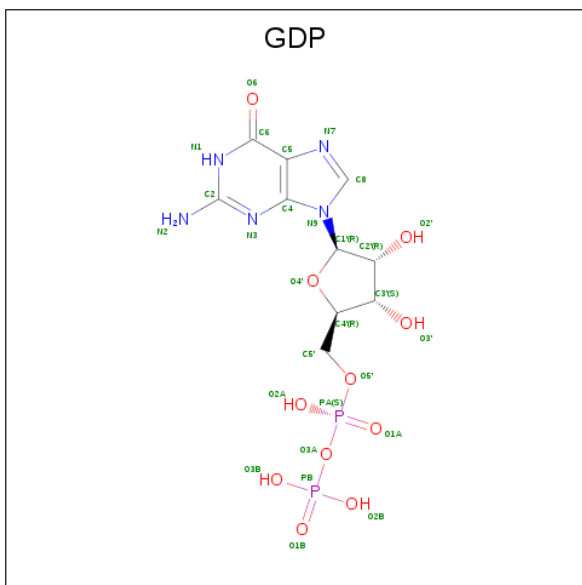
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	B	1	Total	C	Cl	N	O	0	0
			55	36	1	6	12		
6	D	1	Total	C	Cl	N	O	0	0
			55	36	1	6	12		

- Molecule 7 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

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

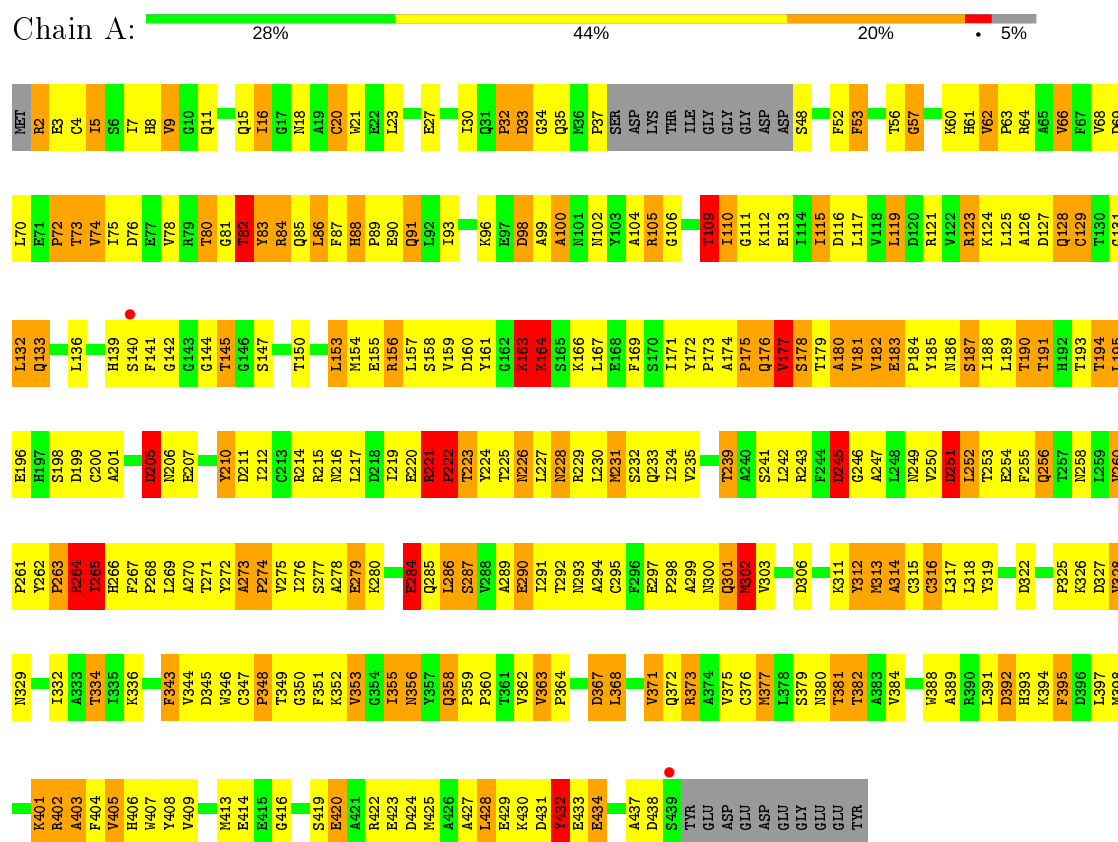


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
8	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

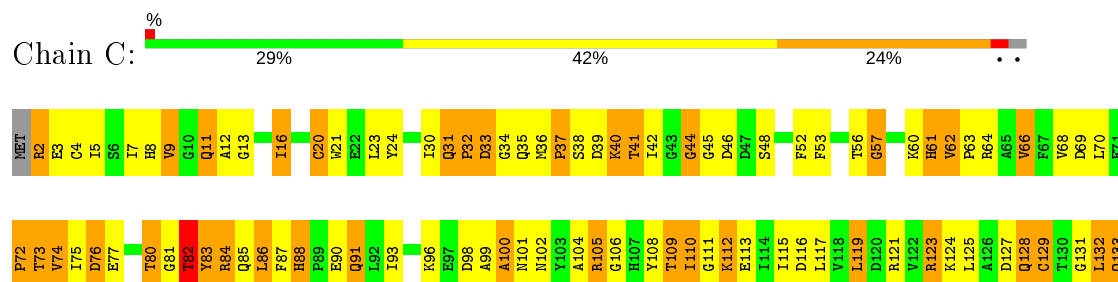
3 Residue-property plots [i](#)

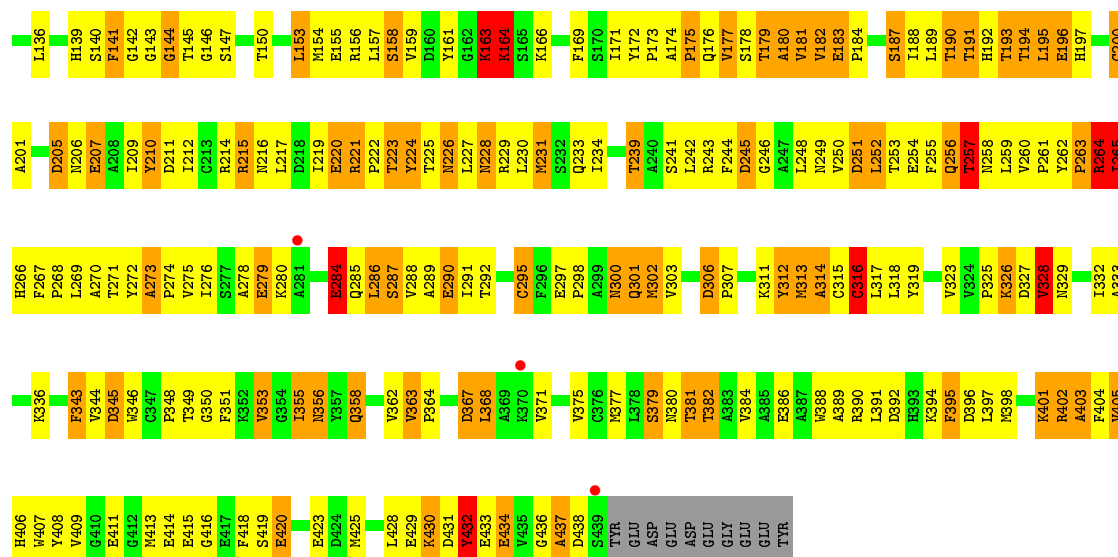
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

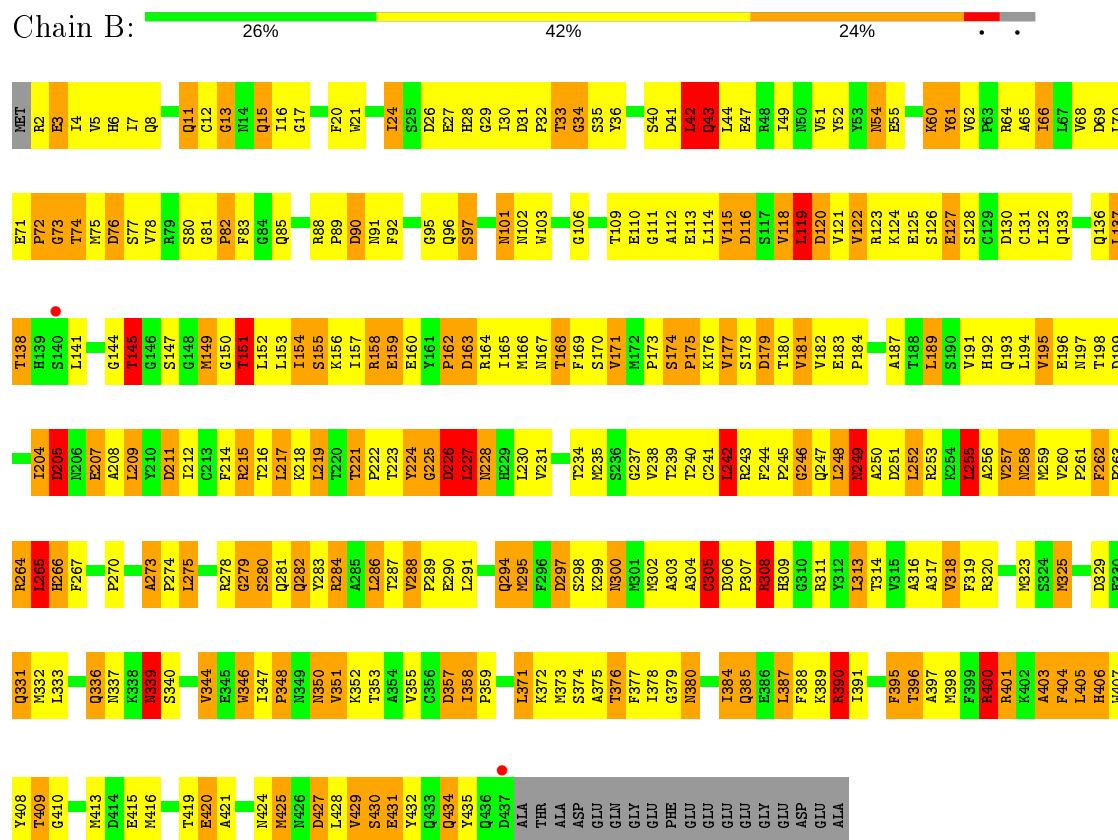


- Molecule 1: Tubulin alpha-1C chain

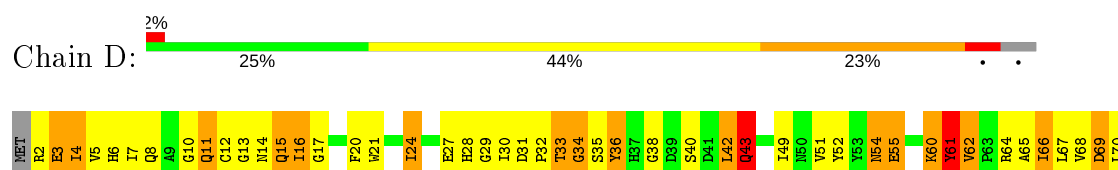


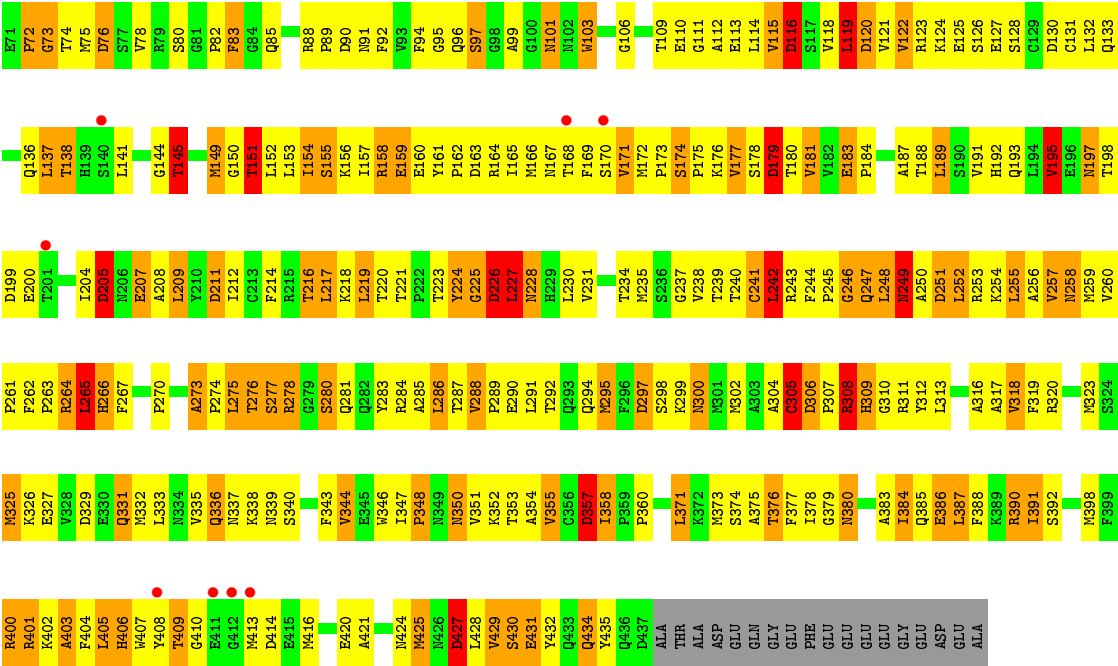


• Molecule 2: Tubulin beta-2B chain

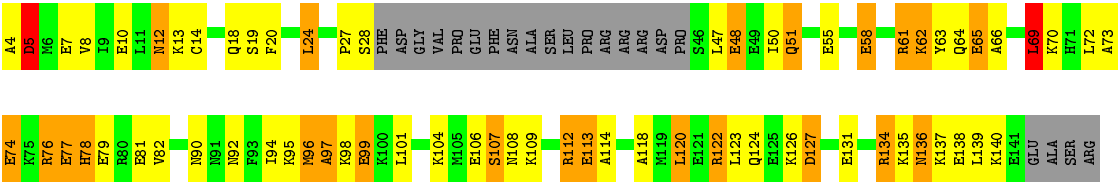


• Molecule 2: Tubulin beta-2B chain





● Molecule 3: Stathmin-4



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	327.13 Å 327.13 Å 53.67 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 4.10 38.97 – 4.09	Depositor EDS
% Data completeness (in resolution range)	96.4 (20.00-4.10) 95.9 (38.97-4.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 4.13 Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.215 , 0.265 0.216 , 0.271	Depositor DCC
R_{free} test set	1286 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	181.9	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 162.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.044 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14258	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.95% 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: GDP, GTP, MG, CN2, HOS

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	0.82	0/3340	1.02	17/4547 (0.4%)
1	C	0.79	1/3393 (0.0%)	0.99	10/4622 (0.2%)
2	B	0.77	0/3356	1.05	17/4561 (0.4%)
2	D	0.77	0/3346	1.02	15/4548 (0.3%)
3	E	0.74	0/836	0.91	4/1127 (0.4%)
All	All	0.78	1/14271 (0.0%)	1.02	63/19405 (0.3%)

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
1	A	0	2
1	C	0	2
2	B	0	5
2	D	0	6
3	E	0	1
All	All	0	16

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	231	MET	SD-CE	5.35	2.07	1.77

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	242	LEU	CA-CB-CG	9.96	138.20	115.30
2	D	242	LEU	CA-CB-CG	8.73	135.38	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	427	ASP	CB-CG-OD2	8.14	125.63	118.30
1	A	160	ASP	CB-CG-OD2	7.68	125.21	118.30
2	B	26	ASP	CB-CG-OD2	7.12	124.71	118.30

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	221	ARG	Peptide
1	A	284	GLU	Peptide
2	B	165	ILE	Peptide
2	B	246	GLY	Peptide
2	B	247	GLN	Peptide

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	3265	0	3102	280	0
1	C	3317	0	3128	299	0
2	B	3282	0	3072	318	0
2	D	3272	0	3054	327	0
3	E	830	0	672	56	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
5	B	30	0	23	12	0
5	D	30	0	23	12	0
6	B	55	0	43	26	0
6	D	55	0	43	24	0
7	D	64	0	24	6	0
8	D	56	0	24	8	0
All	All	14258	0	13208	1258	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 46.

The worst 5 of 1258 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:C:231:MET:CE	1:C:231:MET:SD	2.07	1.41
1:A:99:ALA:HB2	1:A:145:THR:HG22	1.23	1.14
1:C:99:ALA:HB2	1:C:145:THR:HG22	1.20	1.12
1:A:99:ALA:CB	1:A:145:THR:HG22	1.78	1.12
1:C:273:ALA:HB3	1:C:274:PRO:HD3	1.11	1.10

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	424/449 (94%)	297 (70%)	72 (17%)	55 (13%)	0	4
1	C	436/449 (97%)	303 (70%)	72 (16%)	61 (14%)	0	4
2	B	424/445 (95%)	276 (65%)	90 (21%)	58 (14%)	0	4
2	D	424/445 (95%)	274 (65%)	90 (21%)	60 (14%)	0	4
3	E	117/142 (82%)	72 (62%)	28 (24%)	17 (14%)	0	3
All	All	1825/1930 (95%)	1222 (67%)	352 (19%)	251 (14%)	0	4

5 of 251 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	ASP
1	A	62	VAL
1	A	72	PRO
1	A	112	LYS
1	A	124	LYS

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	338/378 (89%)	224 (66%)	114 (34%)	0	2
1	C	340/378 (90%)	232 (68%)	108 (32%)	0	2
2	B	349/383 (91%)	231 (66%)	118 (34%)	0	1
2	D	347/383 (91%)	226 (65%)	121 (35%)	0	1
3	E	60/126 (48%)	38 (63%)	22 (37%)	0	1
All	All	1434/1648 (87%)	951 (66%)	483 (34%)	0	2

5 of 483 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	400	ARG
1	C	176	GLN
2	D	390	ARG
2	B	415	GLU
1	C	75	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	350	ASN
1	C	88	HIS
2	D	380	ASN
1	C	8	HIS
1	C	101	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
7	GTP	D	601	-	26,34,34	1.14	2 (7%)	33,54,54	2.63	12 (36%)
5	CN2	B	700	-	28,32,32	3.30	7 (25%)	27,45,45	2.46	8 (29%)
5	CN2	D	701	-	28,32,32	3.15	6 (21%)	27,45,45	2.72	11 (40%)
7	GTP	D	600	-	26,34,34	0.99	2 (7%)	33,54,54	1.91	7 (21%)
8	GDP	D	602	-	24,30,30	1.01	2 (8%)	31,47,47	2.34	10 (32%)
6	HOS	B	800	-	45,57,57	1.55	6 (13%)	43,83,83	1.75	14 (32%)
8	GDP	D	603	-	24,30,30	1.14	2 (8%)	31,47,47	2.13	7 (22%)
6	HOS	D	801	-	45,57,57	1.57	9 (20%)	43,83,83	1.58	8 (18%)

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
7	GTP	D	601	-	-	5/18/38/38	0/3/3/3
5	CN2	B	700	-	-	3/10/27/27	0/3/3/3
5	CN2	D	701	-	-	3/10/27/27	0/3/3/3
7	GTP	D	600	-	-	5/18/38/38	0/3/3/3
8	GDP	D	602	-	-	4/12/32/32	0/3/3/3
6	HOS	B	800	-	-	16/76/92/92	0/2/3/3
8	GDP	D	603	-	-	6/12/32/32	0/3/3/3
6	HOS	D	801	-	-	23/76/92/92	0/2/3/3

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	700	CN2	C19-C17	-9.12	1.23	1.39
5	B	700	CN2	C19-C20	-7.98	1.17	1.40
5	D	701	CN2	C19-C17	-7.63	1.25	1.39
5	B	700	CN2	C20-C21	-7.57	1.21	1.40
5	D	701	CN2	C15-C16	7.39	1.54	1.39

The worst 5 of 77 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	701	CN2	C20-C19-C17	7.50	147.84	129.69
8	D	602	GDP	N3-C2-N1	-7.12	117.72	127.22
5	B	700	CN2	C20-C19-C17	7.05	146.76	129.69
8	D	603	GDP	N3-C2-N1	-6.91	118.01	127.22
7	D	601	GTP	PB-O3B-PG	-6.86	109.30	132.83

There are no chirality outliers.

5 of 65 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	701	CN2	C10-C11-N1-C12
7	D	600	GTP	C5'-O5'-PA-O1A
8	D	602	GDP	C5'-O5'-PA-O1A
8	D	602	GDP	C5'-O5'-PA-O2A
6	B	800	HOS	C24-C2-C22-C23

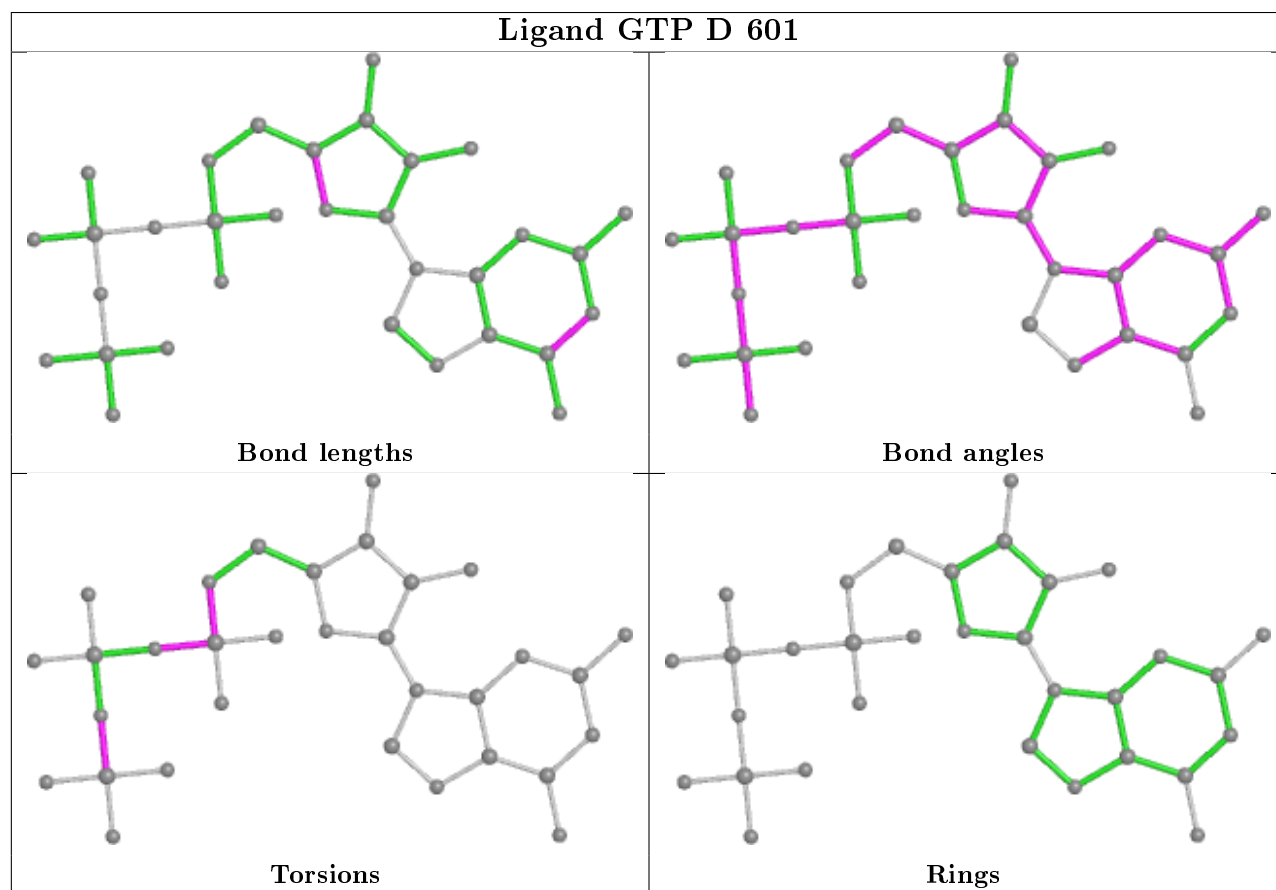
There are no ring outliers.

8 monomers are involved in 88 short contacts:

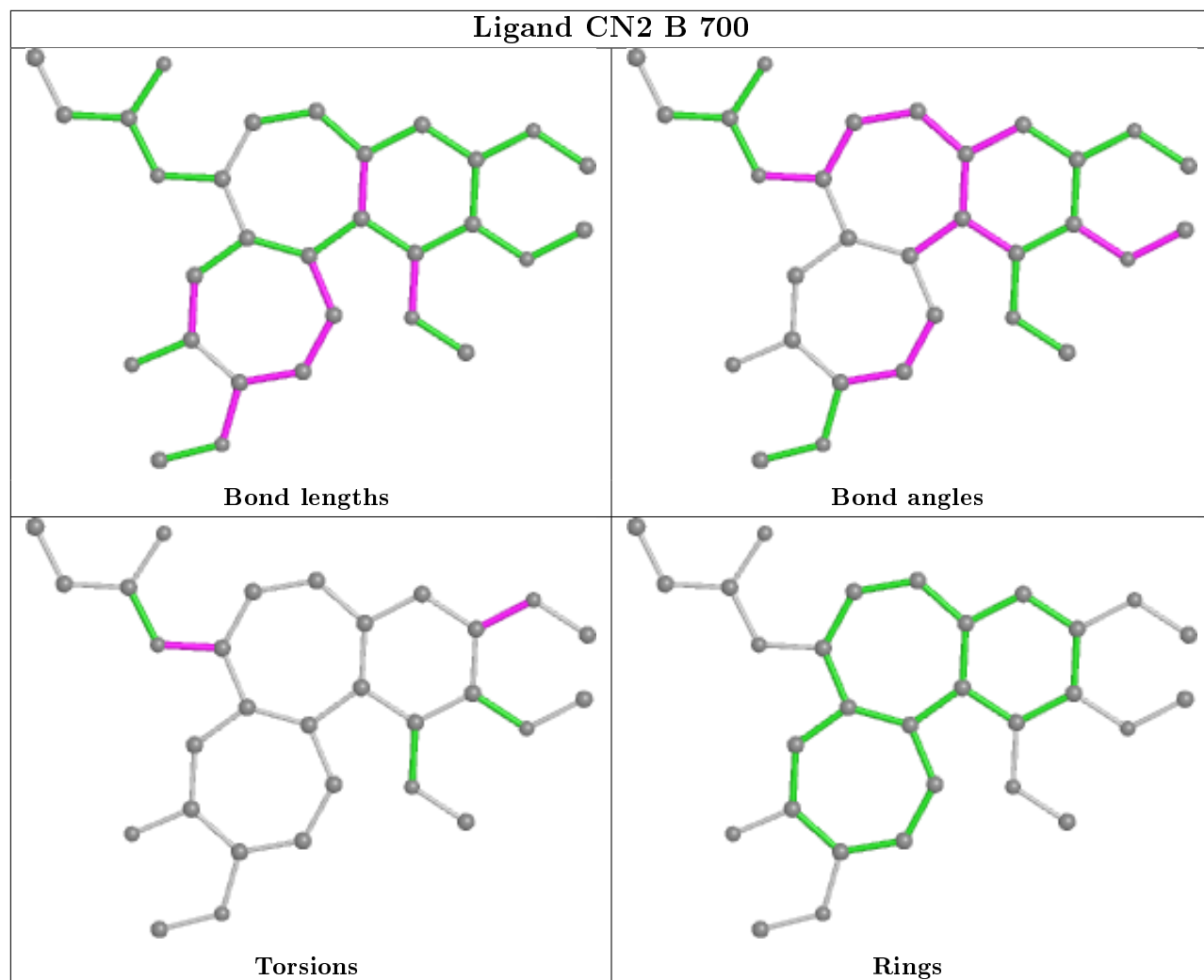
Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	D	601	GTP	4	0
5	B	700	CN2	12	0
5	D	701	CN2	12	0
7	D	600	GTP	2	0
8	D	602	GDP	4	0
6	B	800	HOS	26	0
8	D	603	GDP	4	0
6	D	801	HOS	24	0

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

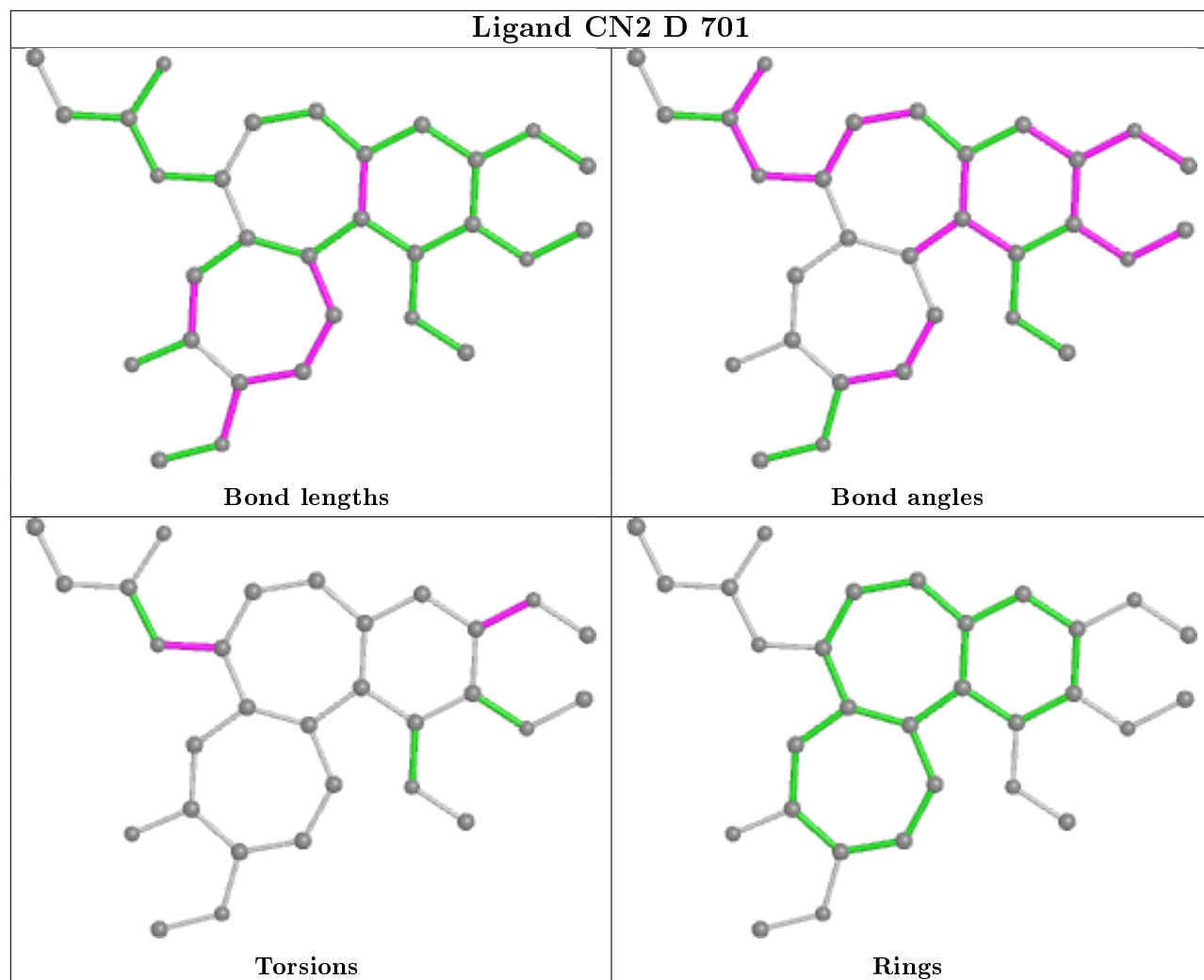
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.

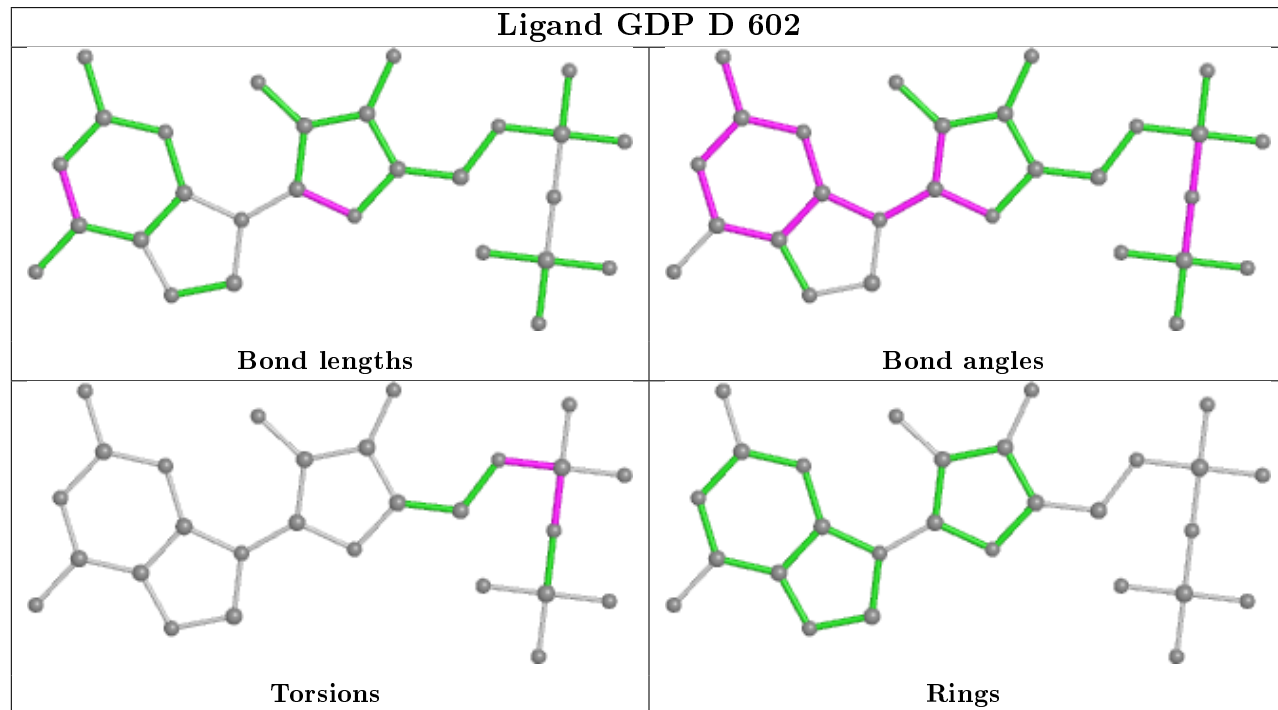
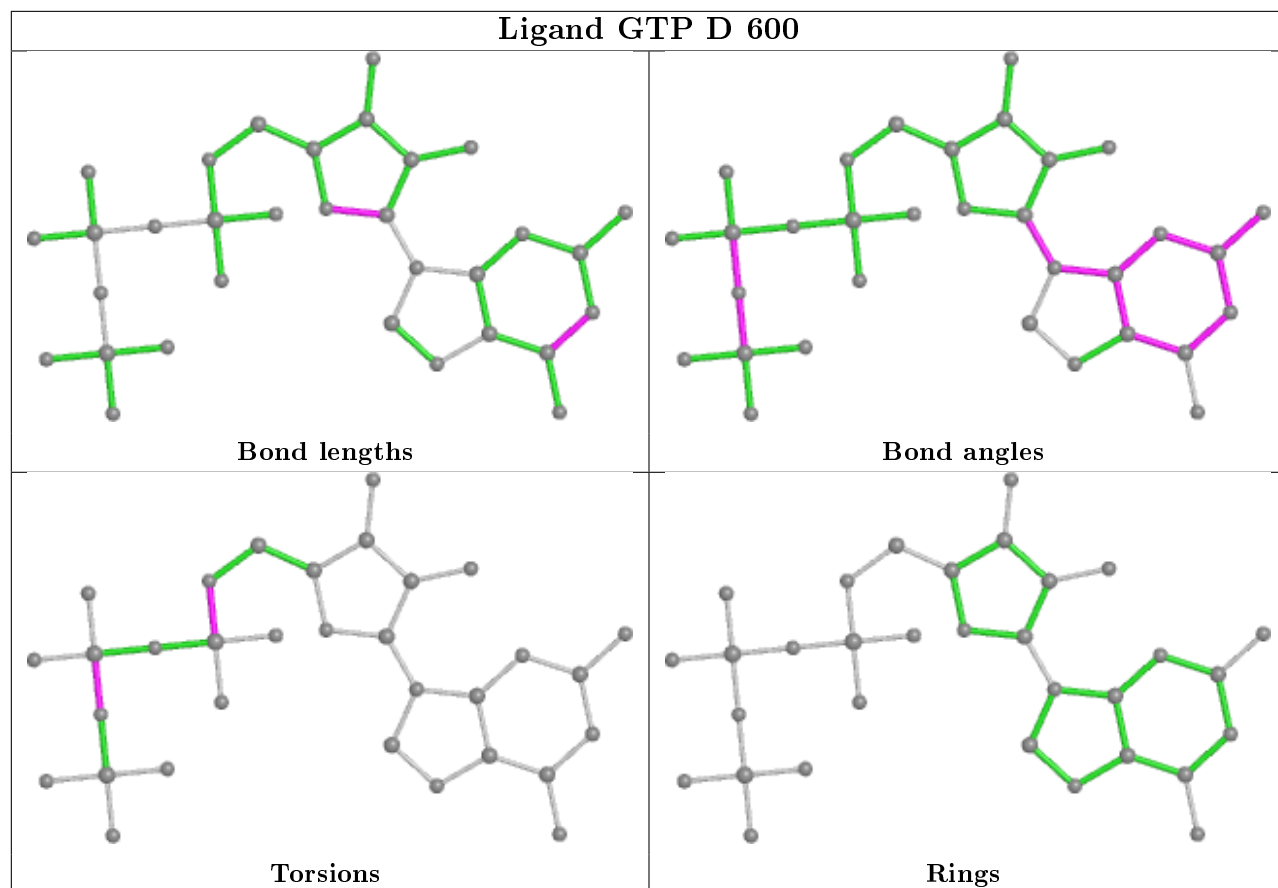


Ligand CN2 B 700

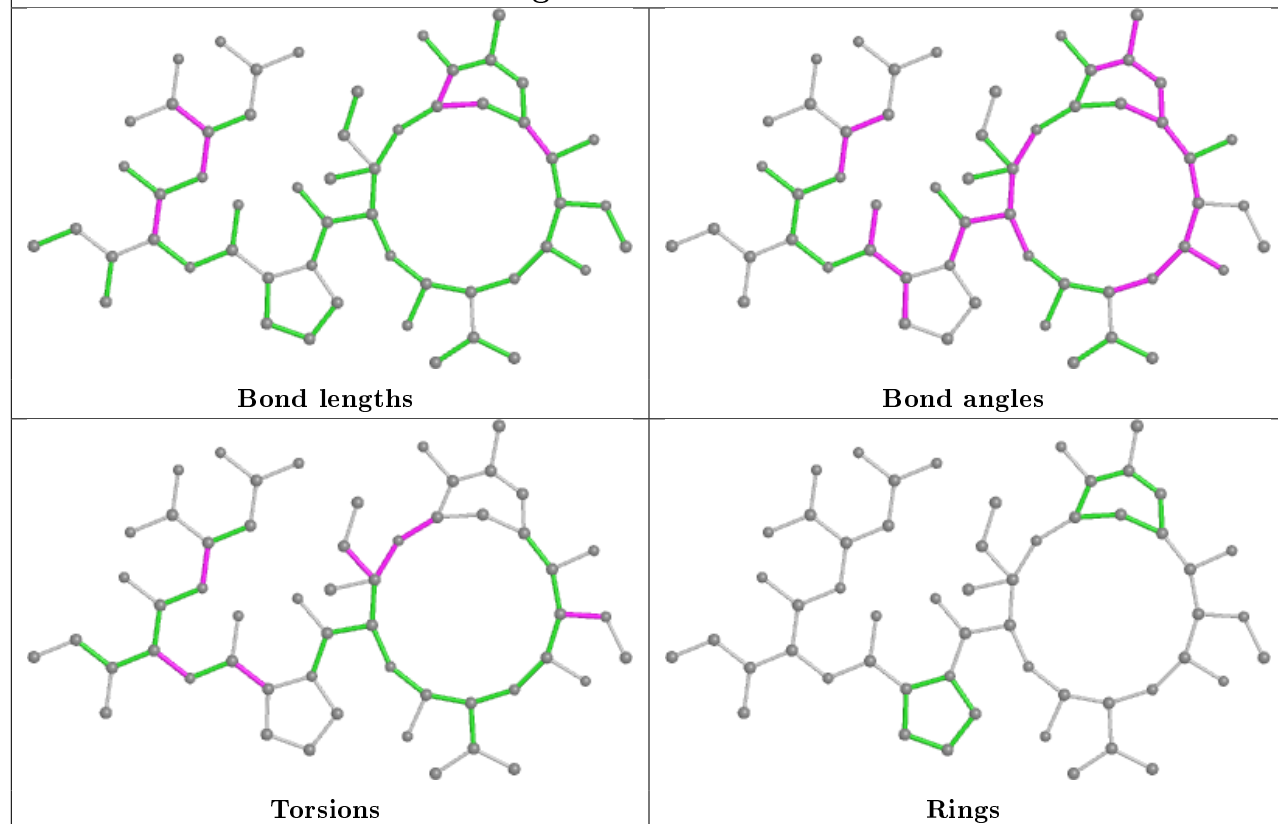


Ligand CN2 D 701

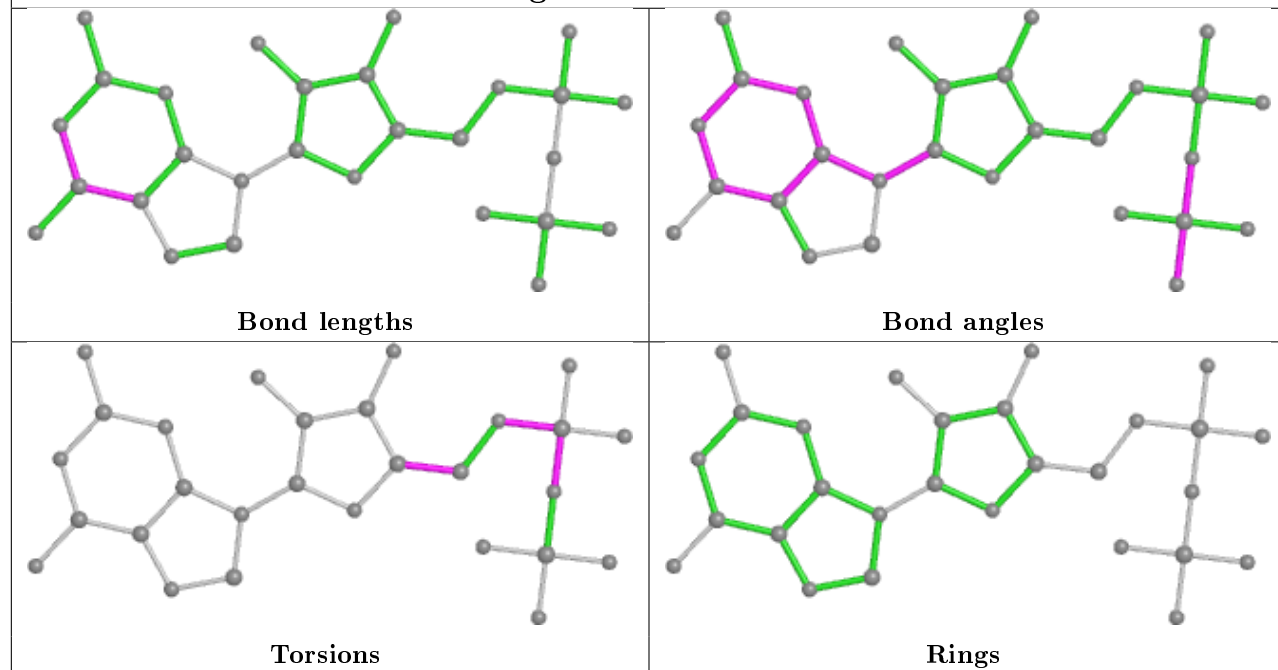


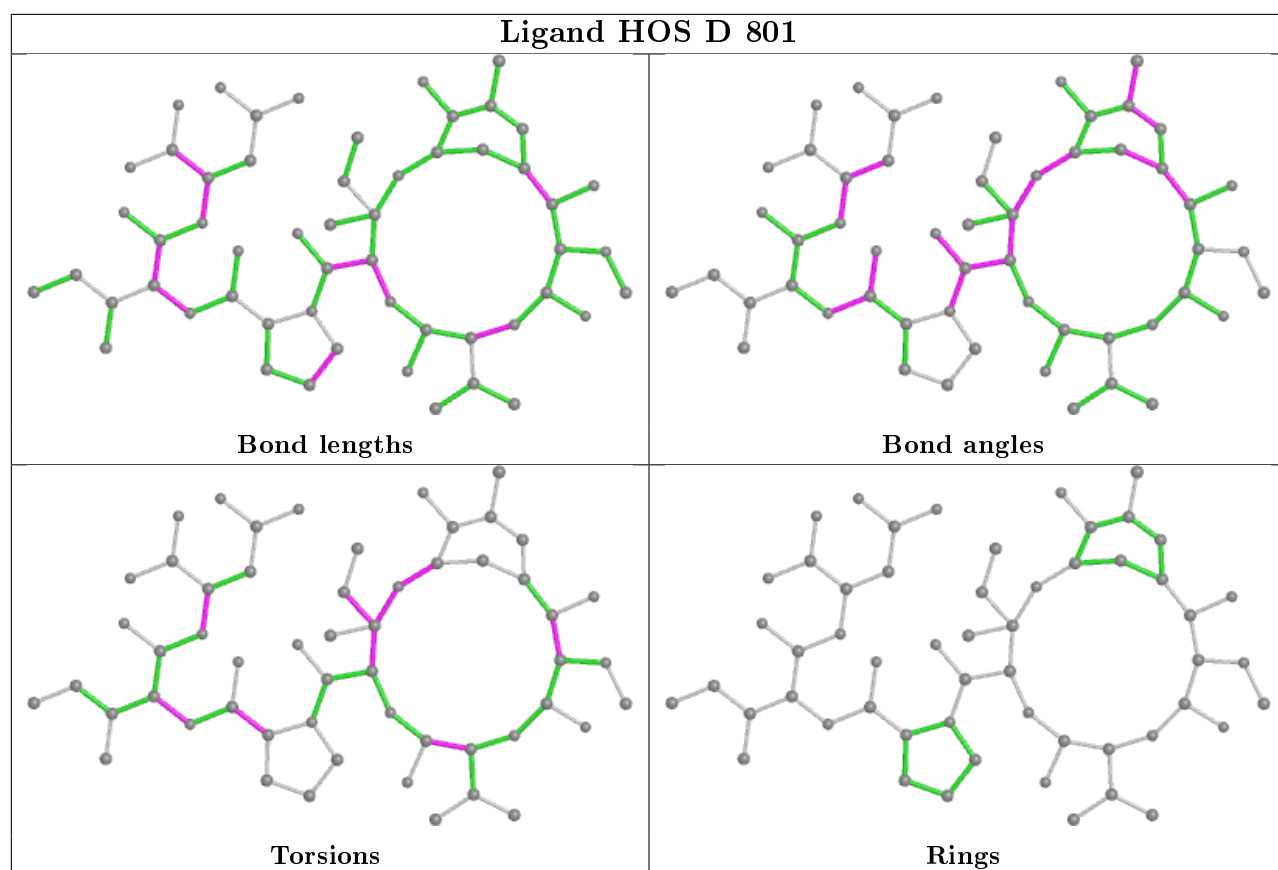


Ligand HOS B 800



Ligand GDP D 603





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	428/449 (95%)	-0.42	2 (0%) 91 85	96, 96, 96, 96	0
1	C	438/449 (97%)	-0.26	3 (0%) 87 82	96, 96, 96, 96	0
2	B	426/445 (95%)	-0.35	2 (0%) 91 85	96, 96, 96, 96	0
2	D	426/445 (95%)	-0.22	8 (1%) 66 58	96, 96, 96, 96	0
3	E	121/142 (85%)	-0.27	0 100 100	96, 96, 96, 96	0
All	All	1839/1930 (95%)	-0.31	15 (0%) 86 79	96, 96, 96, 96	0

The worst 5 of 15 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	281	ALA	4.0
1	C	370	LYS	3.5
2	D	412	GLY	3.0
2	D	201	THR	3.0
2	D	413	MET	2.8

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 carbohydrates in this entry.

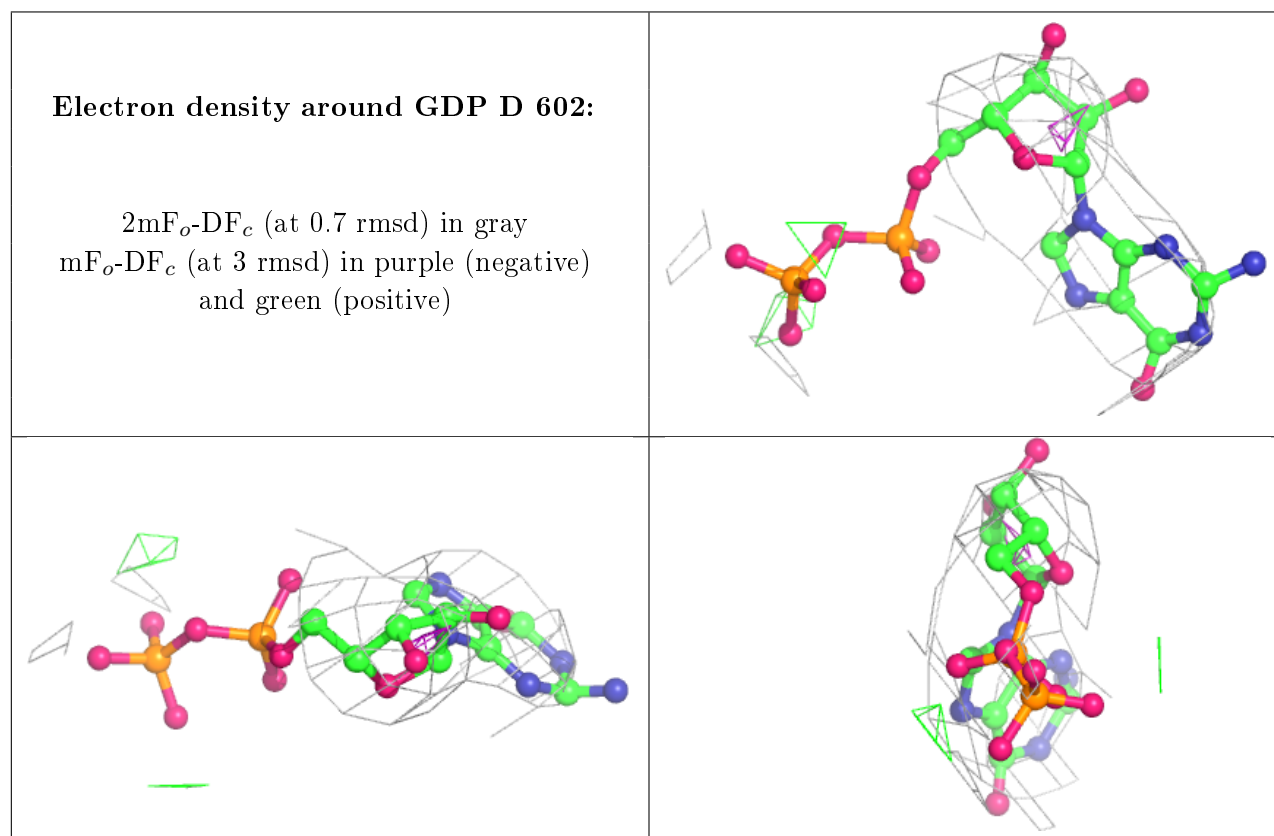
6.4 Ligands [i](#)

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, 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.

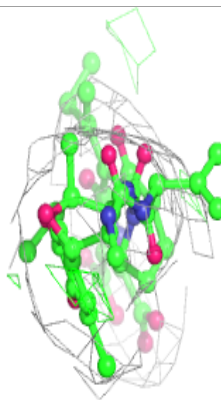
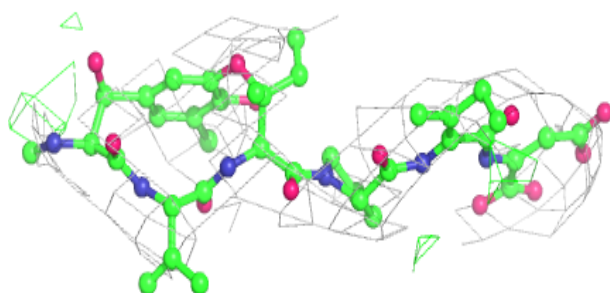
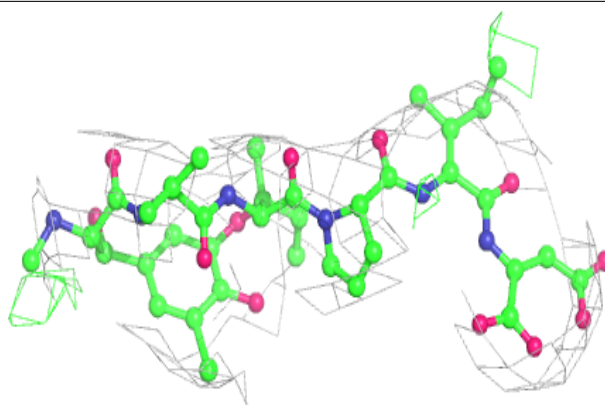
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
8	GDP	D	602	28/28	0.87	0.37	98,98,98,98	0
6	HOS	B	800	55/55	0.89	0.21	98,98,98,98	0
8	GDP	D	603	28/28	0.90	0.33	98,98,98,98	0
5	CN2	B	700	30/30	0.92	0.24	98,98,98,98	0
6	HOS	D	801	55/55	0.93	0.21	98,98,98,98	0
7	GTP	D	600	32/32	0.94	0.36	98,98,98,98	0
5	CN2	D	701	30/30	0.94	0.25	98,98,98,98	0
4	MG	A	500	1/1	0.96	0.55	98,98,98,98	0
7	GTP	D	601	32/32	0.96	0.33	98,98,98,98	0
4	MG	C	501	1/1	0.98	0.32	98,98,98,98	0

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

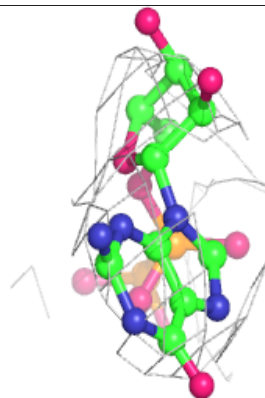
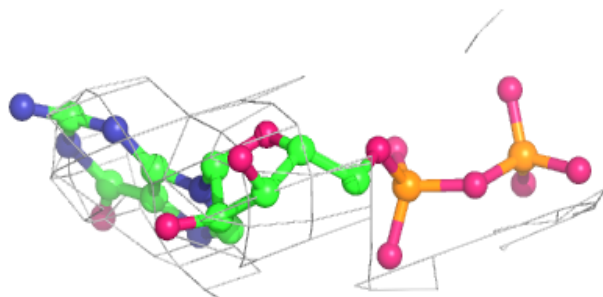
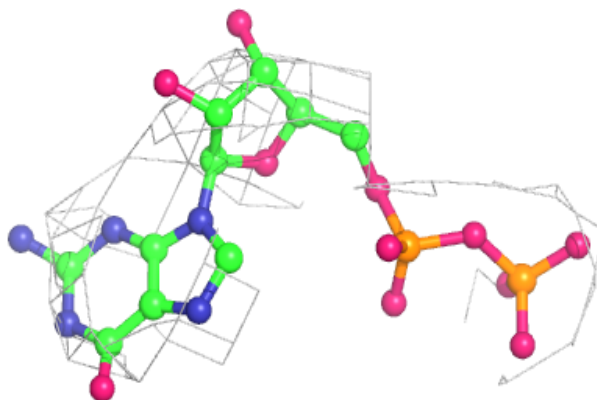


Electron density around HOS B 800:

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

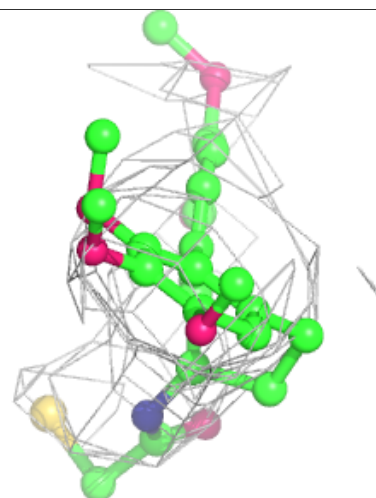
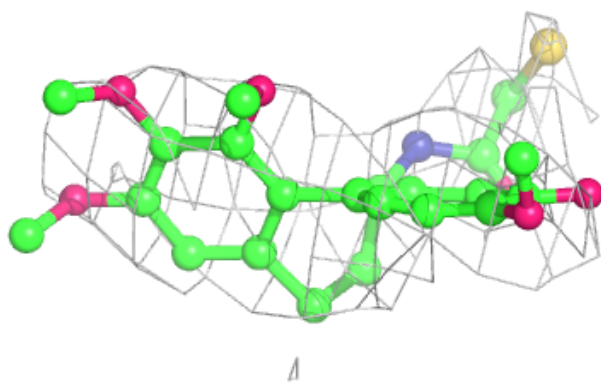
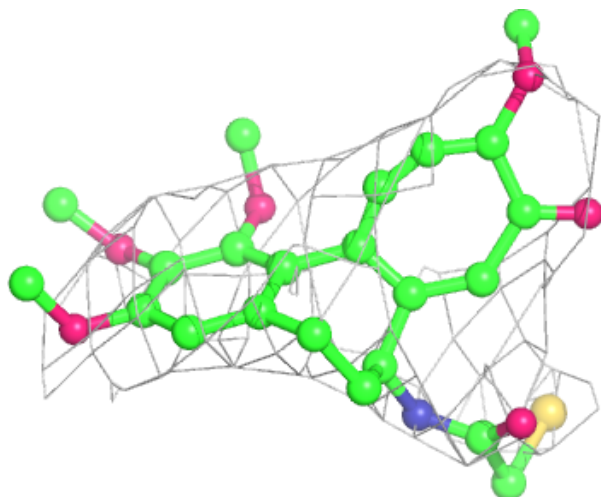
**Electron density around GDP D 603:**

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



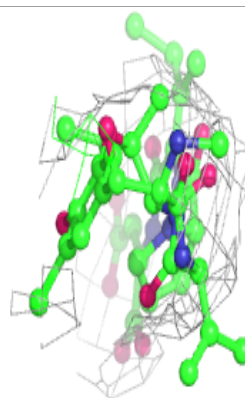
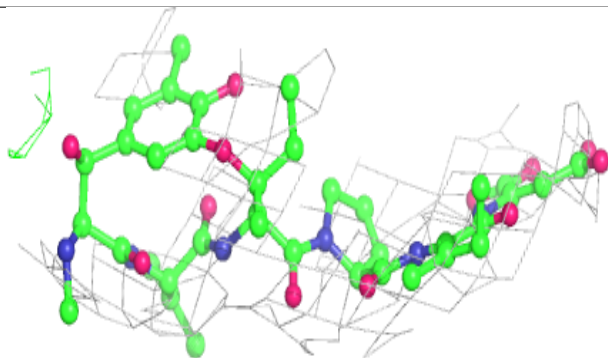
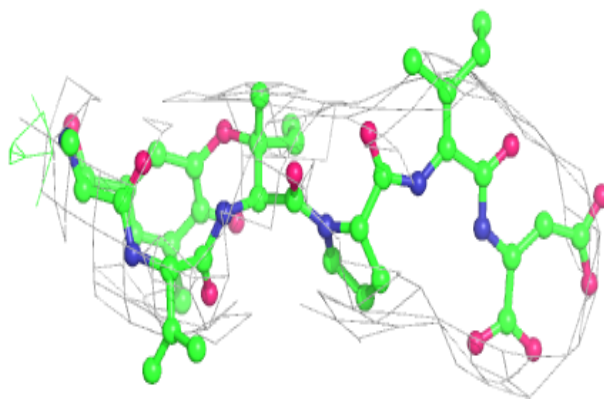
Electron density around CN2 B 700:

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

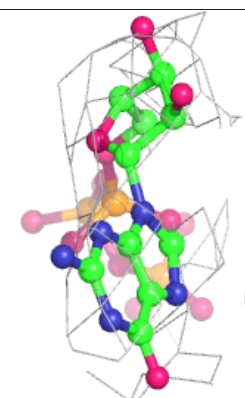
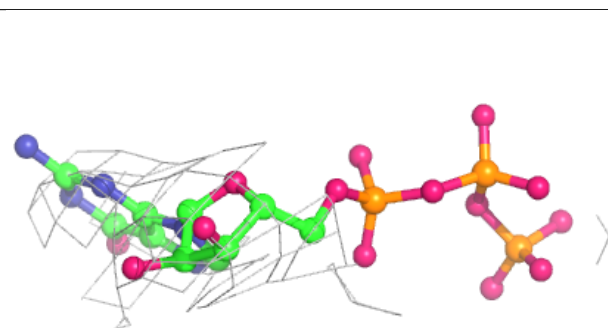
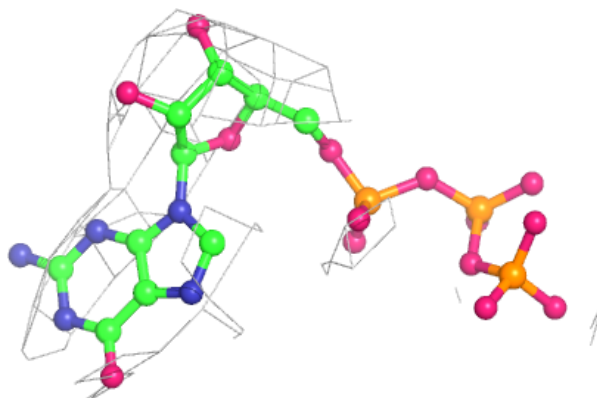


Electron density around HOS D 801:

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

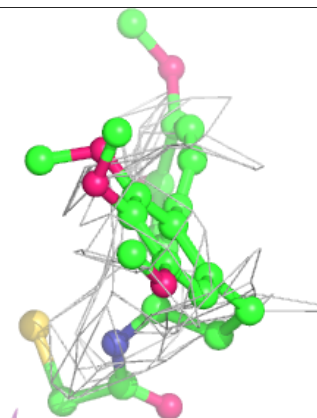
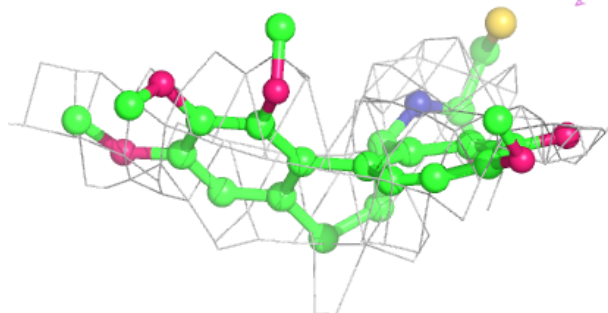
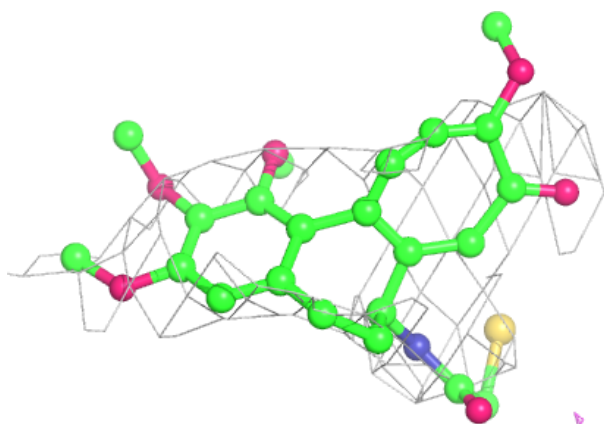
**Electron density around GTP D 600:**

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

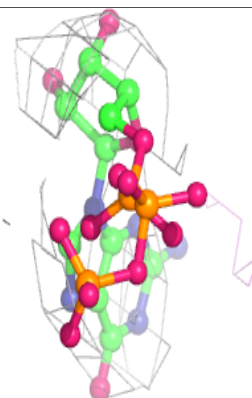
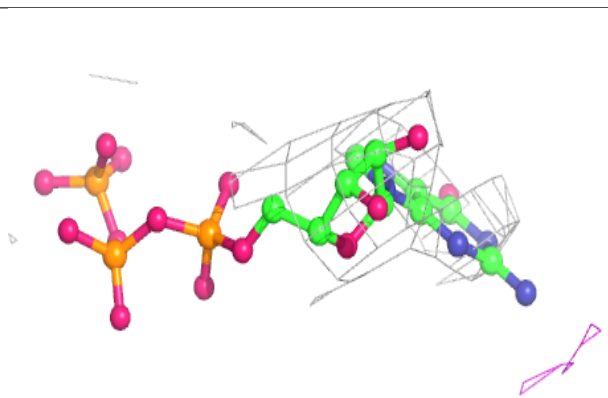
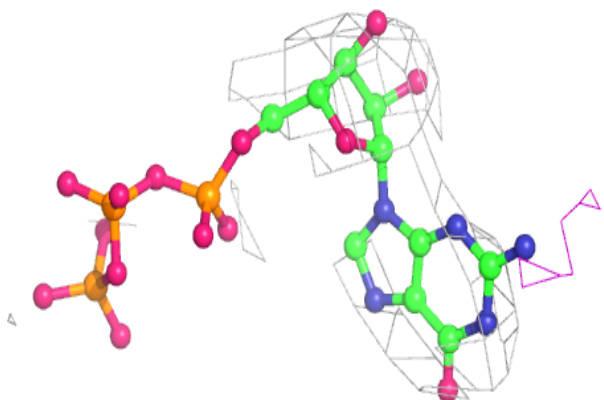


Electron density around CN2 D 701:

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

**Electron density around GTP D 601:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.