Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2023 – 09:29 AM EDT

PDB ID	:	6V9T
Title	:	Tudor domain of TDRD3 in complex with a small molecule
Authors	:	Li, W.; Tempel, W.; Arrowsmith, C.H.; Bountra, C.; Edwards, A.M.; Min, J.; Structural Genomics Consortium (SGC)
Deposited on	:	2019-12-16
Resolution	:	2.15 Å(reported)

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

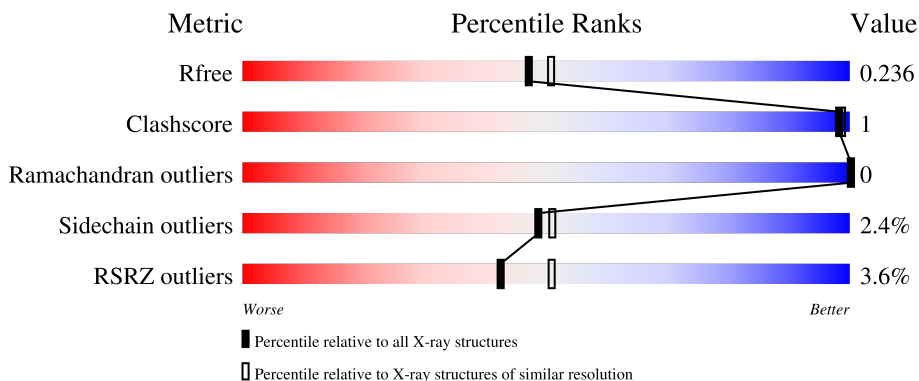|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1   Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	Percentile Ranks	Value
Rfree		0.236
Clashscore		1
Ramachandran outliers		0
Sidechain outliers		2.4%
RSRZ outliers		3.6%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

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	AAA	76	% / 66% 7% · 26%
1	BBB	76	4% / 70% · 28%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 959 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 Tudor domain-containing protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	56	Total 447	C 295	N 68	O 81	S 3	0	1	1
1	BBB	55	Total 428	C 282	N 63	O 81	S 2	0	0	1

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	536	MET	-	initiating methionine	UNP Q9H7E2
AAA	537	HIS	-	expression tag	UNP Q9H7E2
AAA	538	HIS	-	expression tag	UNP Q9H7E2
AAA	539	HIS	-	expression tag	UNP Q9H7E2
AAA	540	HIS	-	expression tag	UNP Q9H7E2
AAA	541	HIS	-	expression tag	UNP Q9H7E2
AAA	542	HIS	-	expression tag	UNP Q9H7E2
AAA	543	SER	-	expression tag	UNP Q9H7E2
AAA	544	SER	-	expression tag	UNP Q9H7E2
AAA	545	GLY	-	expression tag	UNP Q9H7E2
AAA	546	ARG	-	expression tag	UNP Q9H7E2
AAA	547	GLU	-	expression tag	UNP Q9H7E2
AAA	548	ASN	-	expression tag	UNP Q9H7E2
AAA	549	LEU	-	expression tag	UNP Q9H7E2
AAA	550	TYR	-	expression tag	UNP Q9H7E2
AAA	551	PHE	-	expression tag	UNP Q9H7E2
AAA	552	GLN	-	expression tag	UNP Q9H7E2
AAA	553	GLY	-	expression tag	UNP Q9H7E2
BBB	536	MET	-	initiating methionine	UNP Q9H7E2
BBB	537	HIS	-	expression tag	UNP Q9H7E2
BBB	538	HIS	-	expression tag	UNP Q9H7E2
BBB	539	HIS	-	expression tag	UNP Q9H7E2
BBB	540	HIS	-	expression tag	UNP Q9H7E2
BBB	541	HIS	-	expression tag	UNP Q9H7E2
BBB	542	HIS	-	expression tag	UNP Q9H7E2

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Chain	Residue	Modelled	Actual	Comment	Reference
BBB	543	SER	-	expression tag	UNP Q9H7E2
BBB	544	SER	-	expression tag	UNP Q9H7E2
BBB	545	GLY	-	expression tag	UNP Q9H7E2
BBB	546	ARG	-	expression tag	UNP Q9H7E2
BBB	547	GLU	-	expression tag	UNP Q9H7E2
BBB	548	ASN	-	expression tag	UNP Q9H7E2
BBB	549	LEU	-	expression tag	UNP Q9H7E2
BBB	550	TYR	-	expression tag	UNP Q9H7E2
BBB	551	PHE	-	expression tag	UNP Q9H7E2
BBB	552	GLN	-	expression tag	UNP Q9H7E2
BBB	553	GLY	-	expression tag	UNP Q9H7E2

- Molecule 2 is 4-methyl-2,3,4,5,6,7-hexahydrodicyclopenta[b,e]pyridin-8(1H)-imine (three-letter code: 36X) (formula: $C_{12}H_{16}N_2$) (labeled as "Ligand of Interest" by depositor).
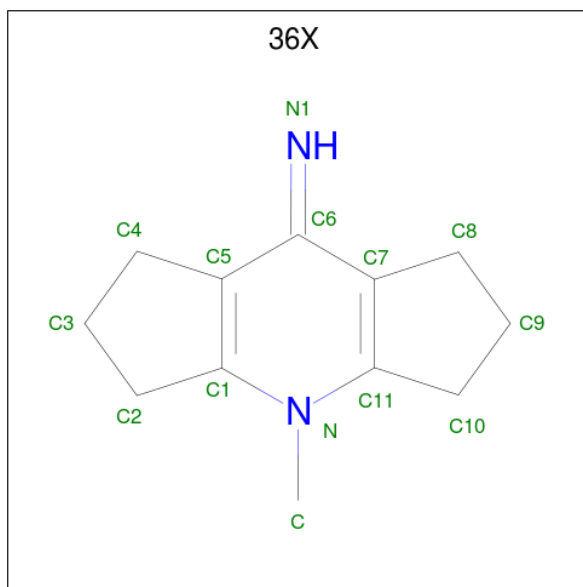
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total 28	C 24	N 4	0	1
2	AAA	1	Total 28	C 24	N 4	0	1
2	BBB	1	Total 14	C 12	N 2	0	0

- Molecule 3 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total 1	X 1	0	0
3	BBB	2	Total 2	X 2	0	0

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AAA	8	Total 8	O 8	0	0
4	BBB	3	Total 3	O 3	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: Tudor domain-containing protein 3

Chain AAA:

• Molecule 1: Tudor domain-containing protein 3

Chain BBB:
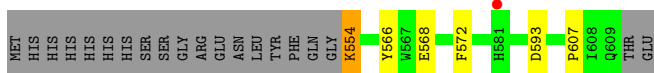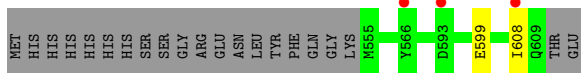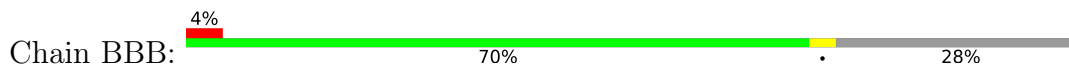
4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	83.86Å 83.86Å 114.05Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.85 – 2.15 44.85 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.85-2.15) 99.9 (44.85-2.15)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.39 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.196 , 0.229 0.201 , 0.236	Depositor DCC
R_{free} test set	699 reflections (8.17%)	wwPDB-VP
Wilson B-factor (Å^2)	40.8	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 49.4	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	0.96	EDS
Total number of atoms	959	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.96% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: UNX, 36X

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	AAA	1.11	3/464 (0.6%)	1.16	2/630 (0.3%)
1	BBB	1.01	1/441 (0.2%)	1.04	0/602
All	All	1.06	4/905 (0.4%)	1.10	2/1232 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	599	GLU	CD-OE2	9.77	1.36	1.25
1	AAA	554	LYS	C-O	5.53	1.33	1.23
1	AAA	607	PRO	CA-C	5.40	1.63	1.52
1	AAA	572	PHE	C-O	-5.03	1.13	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	593	ASP	CB-CG-OD1	-7.22	111.80	118.30
1	AAA	593	ASP	CB-CG-OD2	6.47	124.13	118.30

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	AAA	447	0	408	1	0
1	BBB	428	0	379	0	0
2	AAA	56	0	63	0	0
2	BBB	14	0	16	0	0
3	AAA	1	0	0	0	0
3	BBB	2	0	0	0	0
4	AAA	8	0	0	0	0
4	BBB	3	0	0	0	0
All	All	959	0	866	1	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 1.

All (1) 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:AAA:566:TYR:CE2	1:AAA:568:GLU:HB3	2.46	0.50

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	AAA	55/76 (72%)	54 (98%)	1 (2%)	0	100	100
1	BBB	53/76 (70%)	52 (98%)	1 (2%)	0	100	100
All	All	108/152 (71%)	106 (98%)	2 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AAA	43/67 (64%)	42 (98%)	1 (2%)	50	53
1	BBB	41/67 (61%)	40 (98%)	1 (2%)	49	51
All	All	84/134 (63%)	82 (98%)	2 (2%)	49	51

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	554	LYS
1	BBB	608	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 3 are unknown - leaving 5 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	$\#|Z| > 2$
2	36X	AAA	702[B]	-	13,16,16	1.21	1 (7%)	14,24,24	0.85	0
2	36X	AAA	701[B]	-	13,16,16	0.91	1 (7%)	14,24,24	0.72	0
2	36X	BBB	701	-	13,16,16	0.68	0	14,24,24	0.78	0
2	36X	AAA	702[A]	-	13,16,16	0.77	1 (7%)	14,24,24	0.76	0
2	36X	AAA	701[A]	-	13,16,16	1.00	1 (7%)	14,24,24	0.90	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
2	36X	AAA	702[B]	-	-	-	0/3/3/3
2	36X	AAA	701[B]	-	-	-	0/3/3/3
2	36X	BBB	701	-	-	-	0/3/3/3
2	36X	AAA	702[A]	-	-	-	0/3/3/3
2	36X	AAA	701[A]	-	-	-	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AAA	702[B]	36X	C1-N	-3.52	1.34	1.39
2	AAA	701[A]	36X	C1-N	-2.82	1.35	1.39
2	AAA	701[B]	36X	C11-N	-2.13	1.36	1.39
2	AAA	702[A]	36X	C11-N	-2.12	1.36	1.39

There are no bond angle outliers.
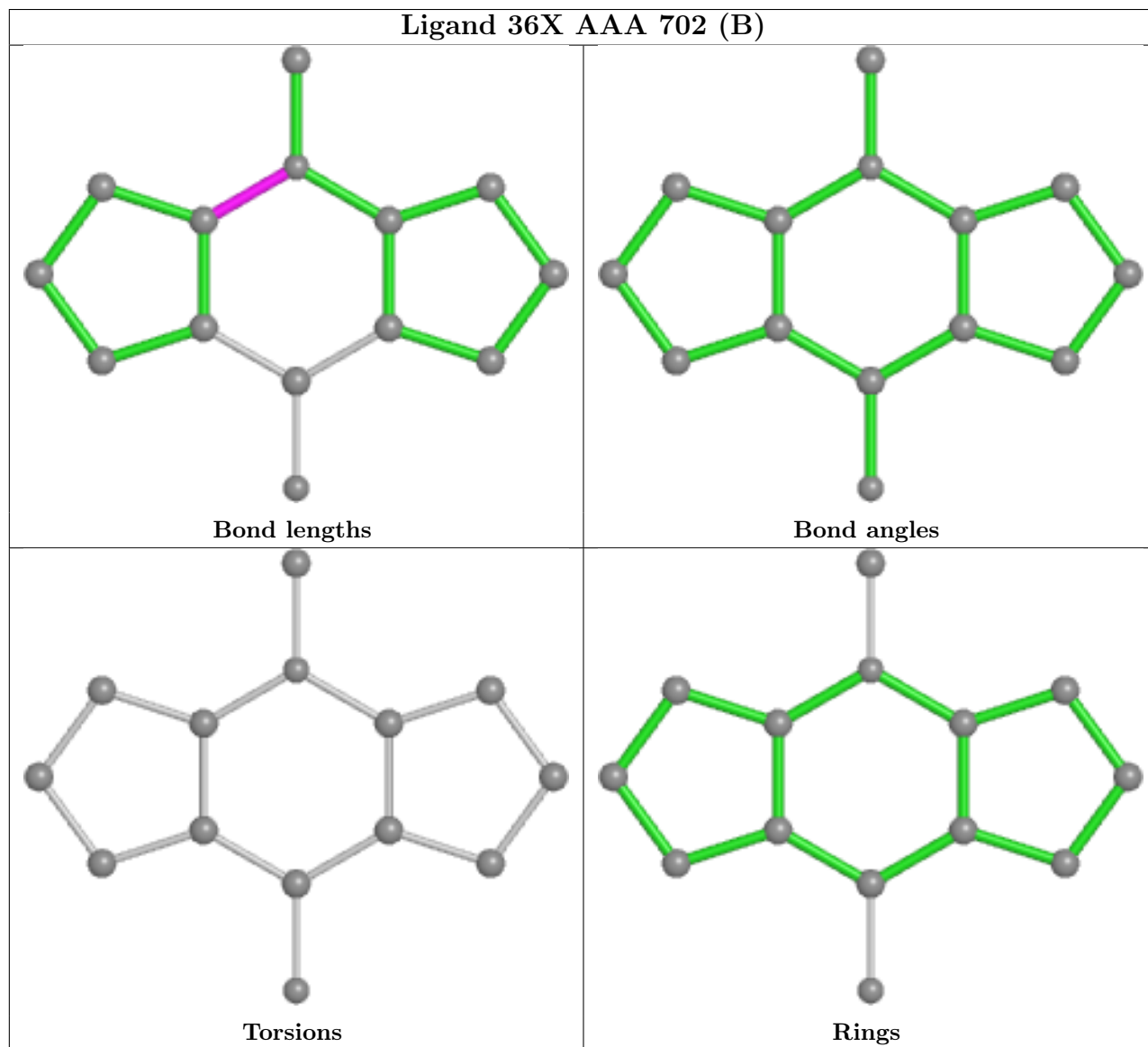
There are no chirality outliers.
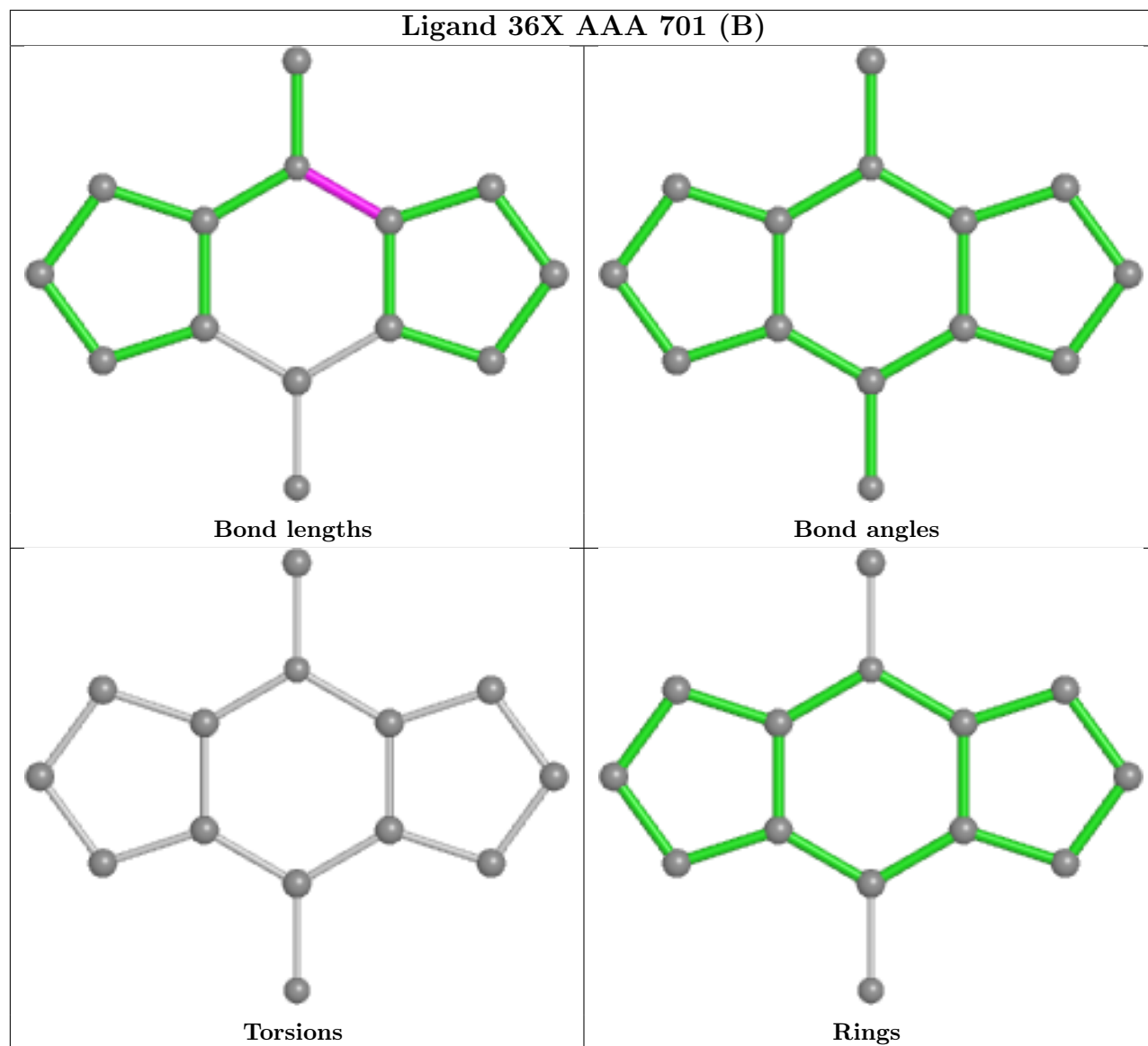
There are no torsion outliers.
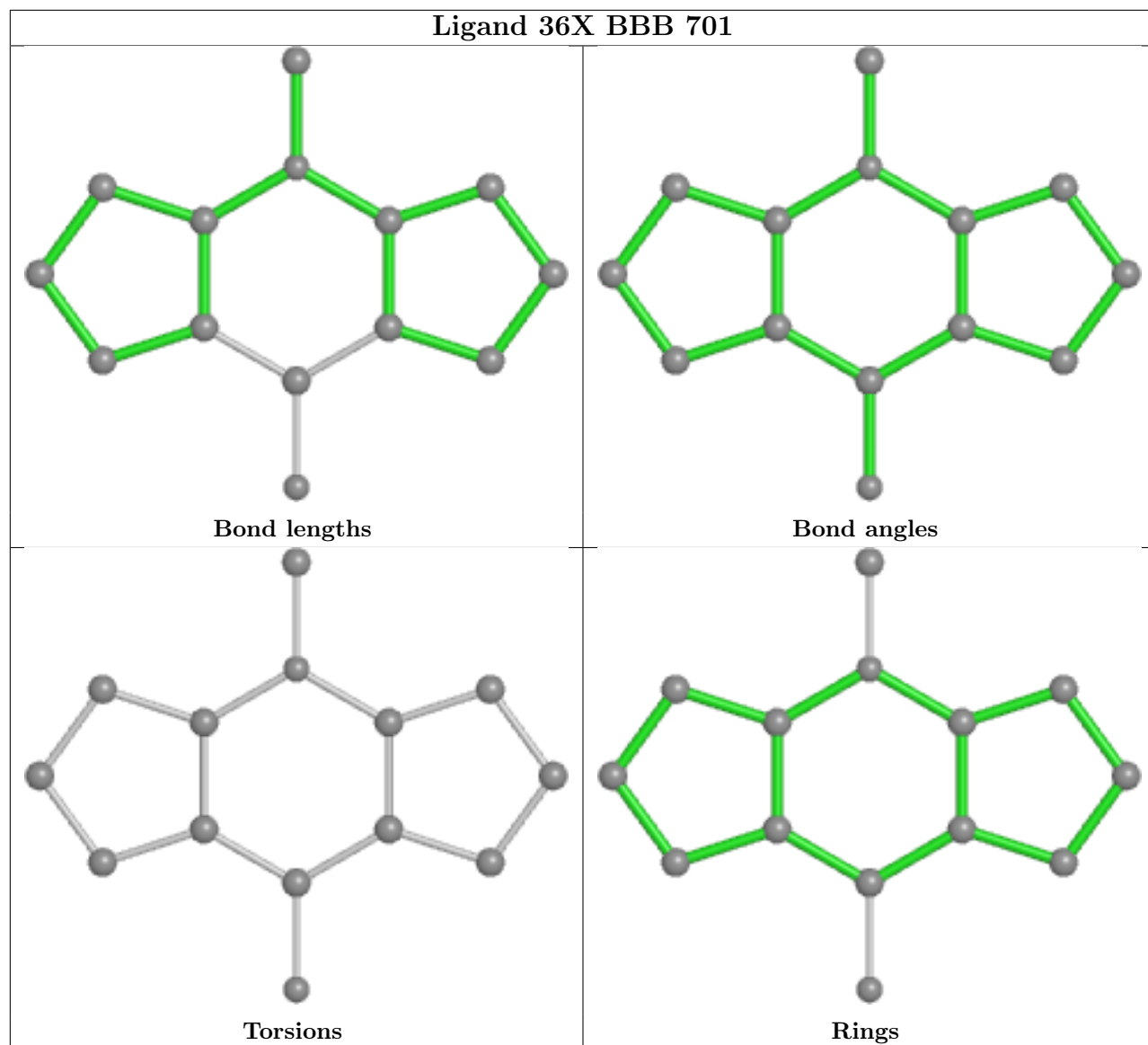
There are no ring outliers.
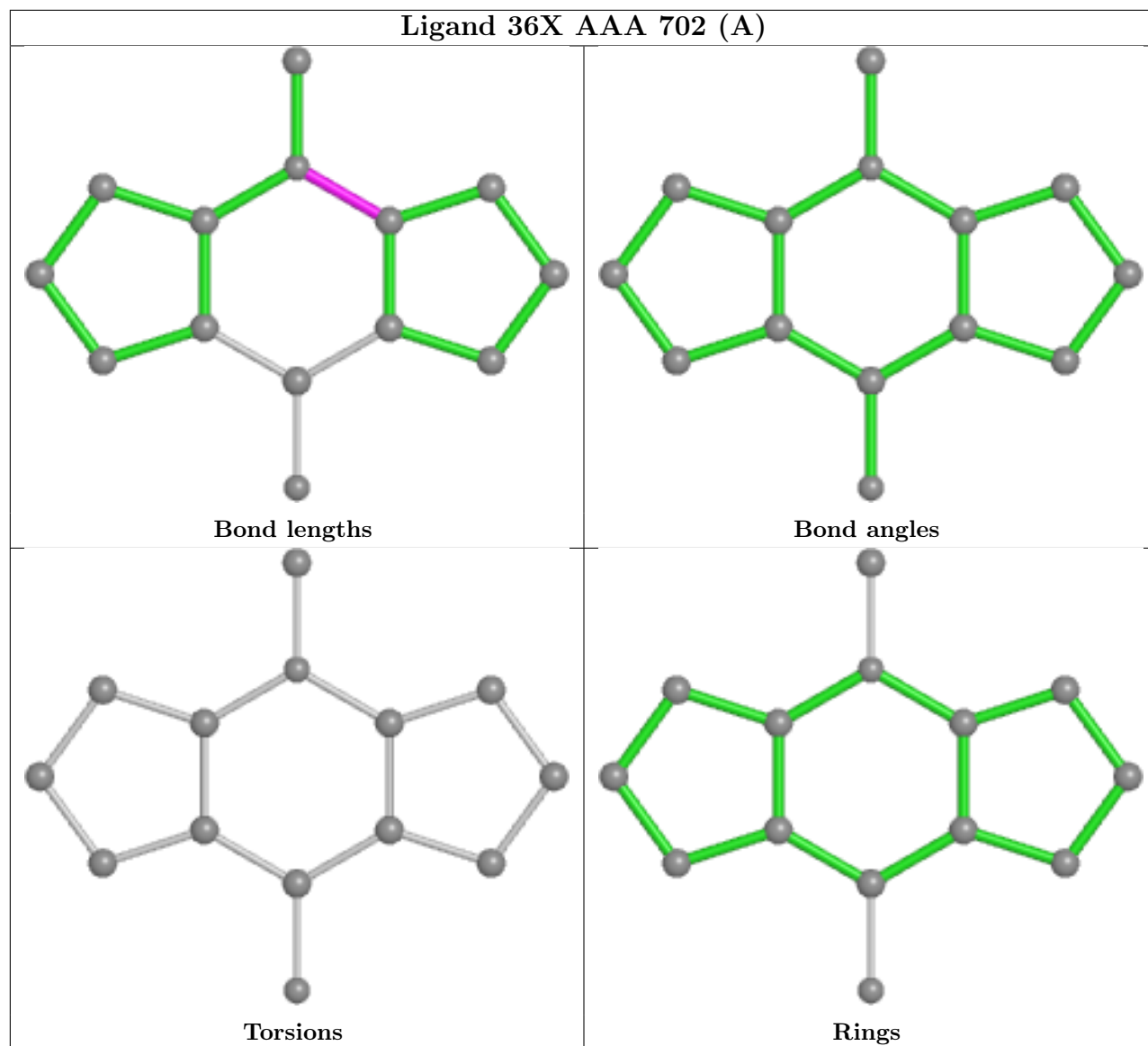
No monomer is involved in short contacts.

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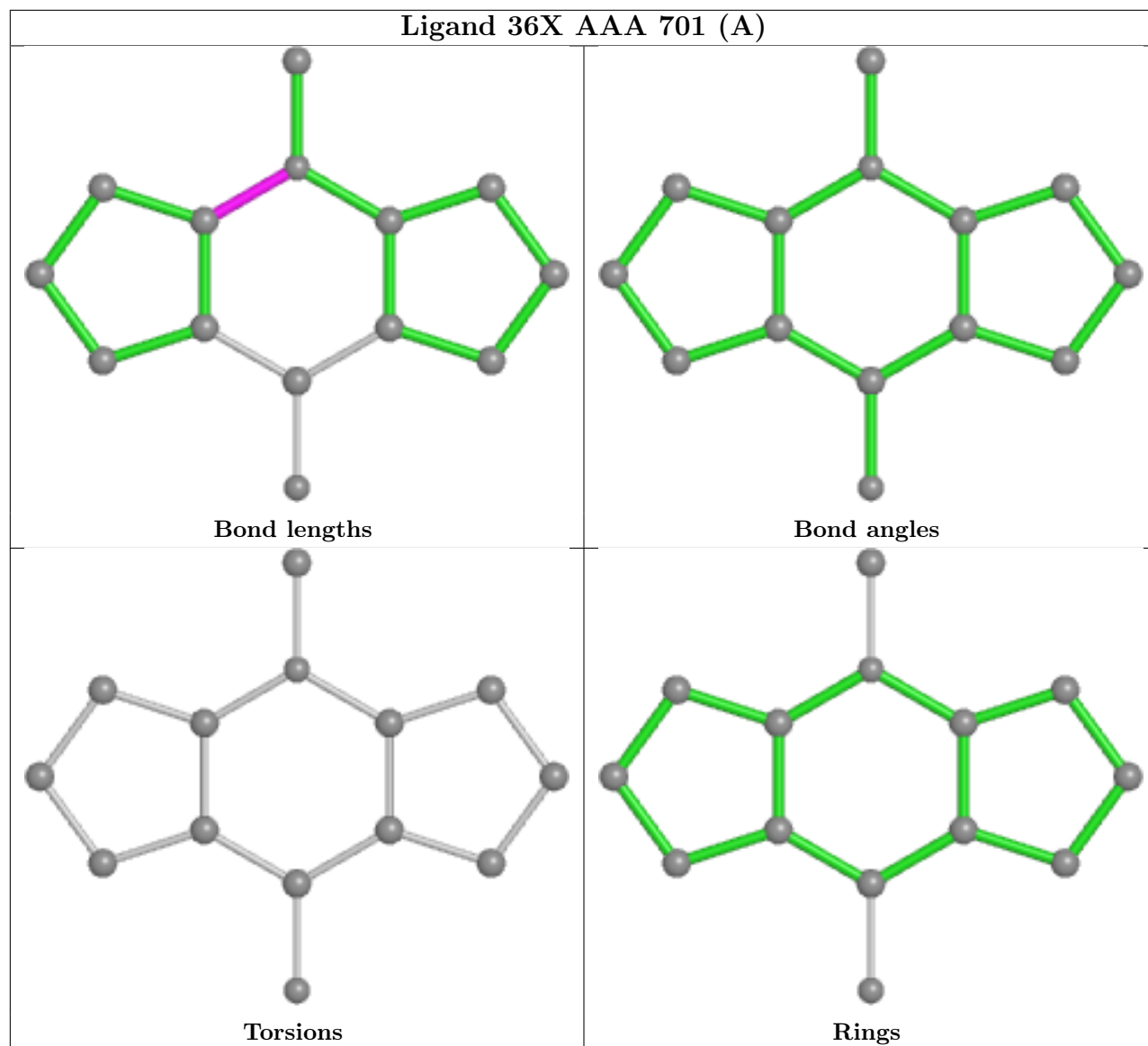
also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted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

Ligand 36X AAA 702 (B)

Bond lengths

Bond angles

Torsions

Rings

Ligand 36X AAA 701 (B)

Bond lengths

Bond angles

Torsions

Rings

Ligand 36X BBB 701

Bond lengths

Bond angles

Torsions

Rings

Ligand 36X AAA 702 (A)

Bond lengths

Bond angles

Torsions

Rings

Ligand 36X AAA 701 (A)

Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	AAA	56/76 (73%)	0.16	1 (1%)	68	75	32, 46, 70, 80	0
1	BBB	55/76 (72%)	0.33	3 (5%)	25	34	31, 45, 62, 74	0
All	All	111/152 (73%)	0.25	4 (3%)	42	51	31, 46, 70, 80	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	581[A]	HIS	2.3
1	BBB	608	ILE	2.3
1	BBB	593	ASP	2.3
1	BBB	566	TYR	2.2

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.
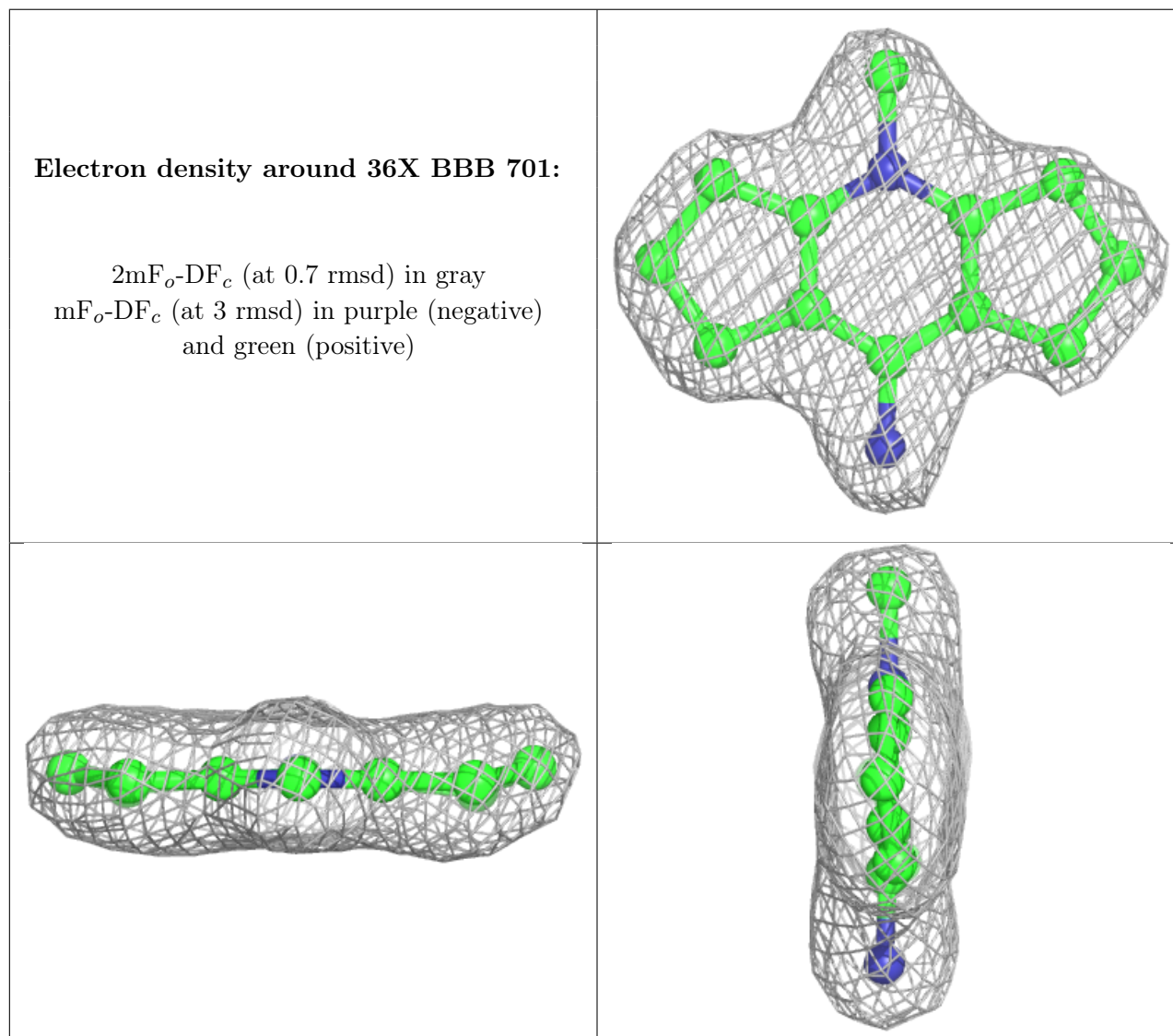
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	UNX	BBB	703	1/1	0.65	0.16	50,50,50,50	1

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WORLDWIDE wwPDB PROTEIN DATA BANK

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| Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\mathrm{\mathring{A}}^2$)	Q<0.9
3	UNX	BBB	702	1/1	0.88	0.36	34,34,34,34	0
2	36X	BBB	701	14/14	0.94	0.23	38,45,56,56	0
2	36X	AAA	702[B]	14/14	0.95	0.14	36,39,43,44	14
2	36X	AAA	701[A]	14/14	0.95	0.18	56,57,64,67	14
3	UNX	AAA	703	1/1	0.95	0.18	29,29,29,29	0
2	36X	AAA	701[B]	14/14	0.95	0.18	55,57,62,65	14
2	36X	AAA	702[A]	14/14	0.95	0.14	31,33,37,37	14

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 36X BBB 701:

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

Electron density around 36X AAA 702 (B):

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)
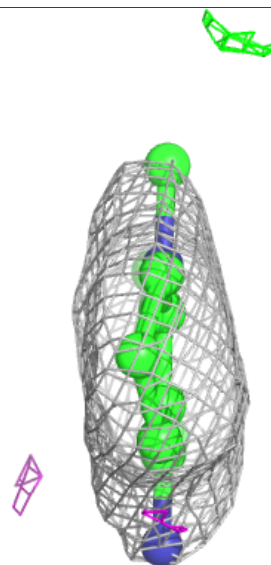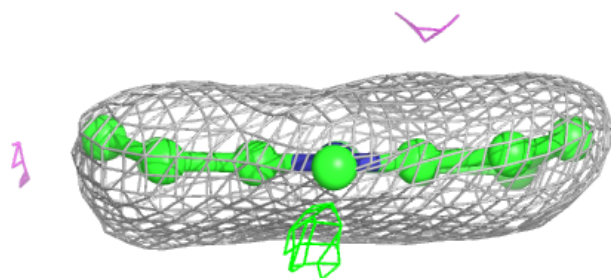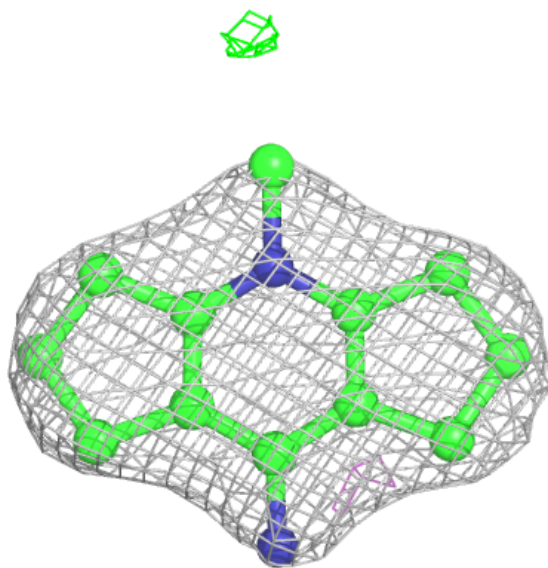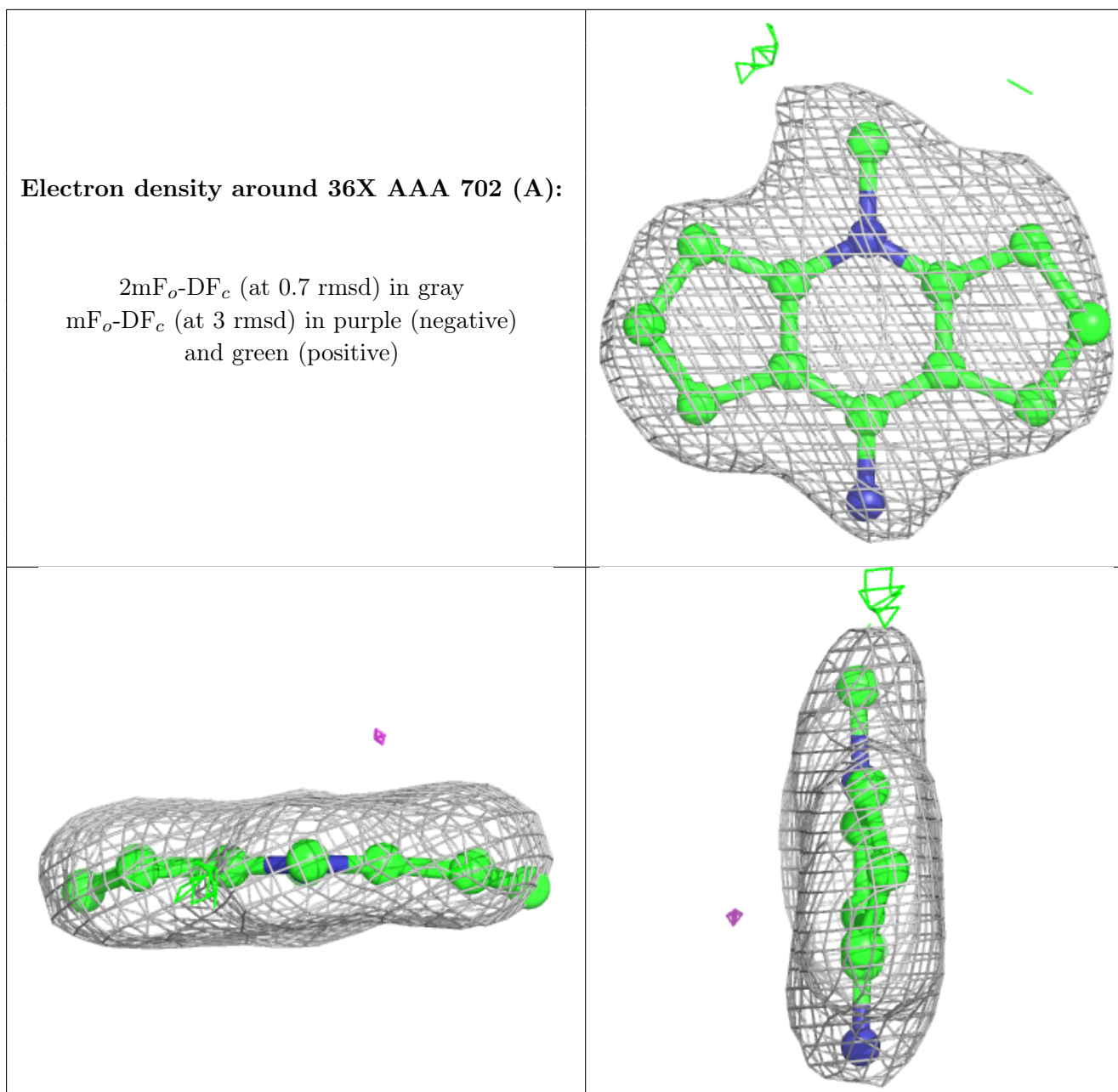
Electron density around 36X AAA 701 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
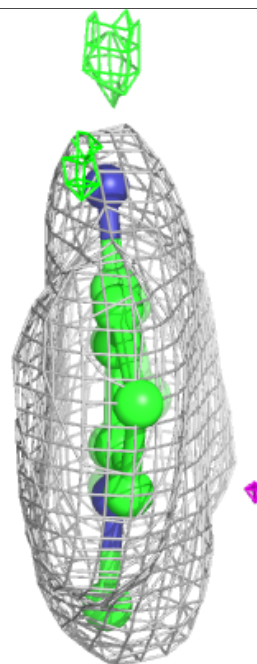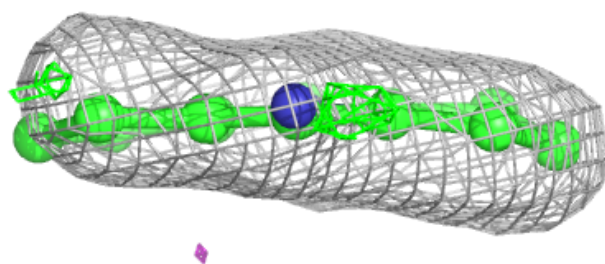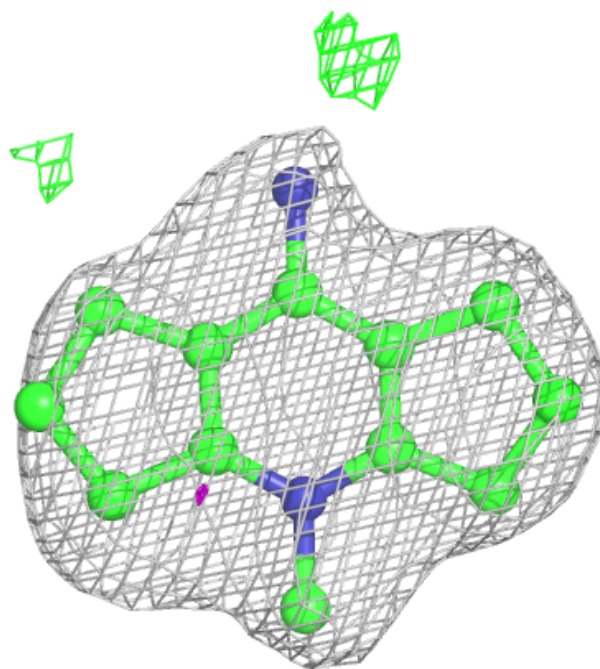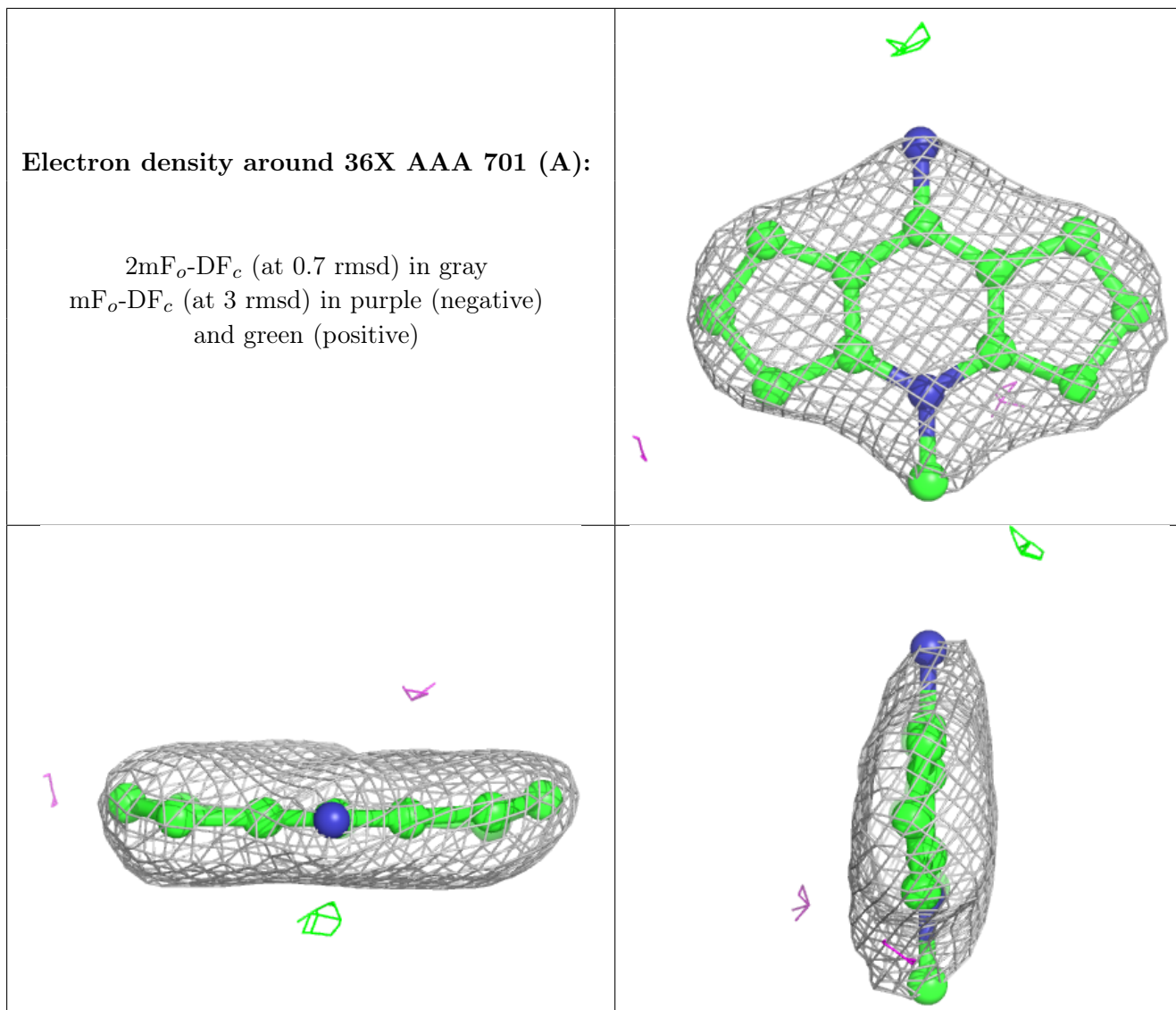
Electron density around 36X AAA 701 (B):

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

Electron density around 36X AAA 702 (A):

$2mF_o$-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 ⓘ

There are no such residues in this entry.