Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 07:06 PM EDT

PDB ID	:	1DDY
Title	:	MOLECULAR RECOGNITION BY THE VITAMIN B12 RNA APTAMER
Authors	:	Sussman, D.; Nix, J.C.; Wilson, C.
Deposited on	:	1999-11-12
Resolution	:	3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

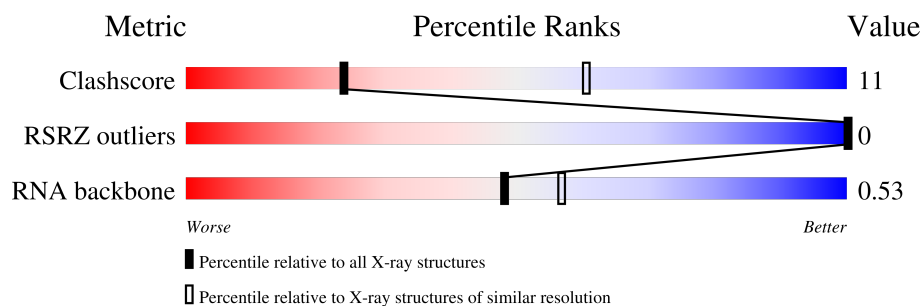|		
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 3.00 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
Clashscore		11
RSRZ outliers		0
RNA backbone		0.53

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))
Clashscore	141614	2416 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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 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	A	35	51% 29% 17% •
1	C	35	34% 46% 14% 6%
1	E	35	49% 40% 9% •
1	G	35	54% 34% 9% •

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
3	NME	A	102	-	X	-	-
3	NME	C	302	-	X	-	-
3	NME	E	502	-	X	-	-
3	NME	G	702	-	X	-	-

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 3376 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 RNA chain called VITAMIN B12 BINDING RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	35	Total	C	N	O	P	0	0	0
			751	335	141	240	35			
1	C	35	Total	C	N	O	P	0	0	0
			751	335	141	240	35			
1	E	35	Total	C	N	O	P	0	0	0
			751	335	141	240	35			
1	G	35	Total	C	N	O	P	0	0	0
			751	335	141	240	35			

- Molecule 2 is COBALAMIN (three-letter code: B12) (formula: $C_{62}H_{89}CoN_{13}O_{14}P$).
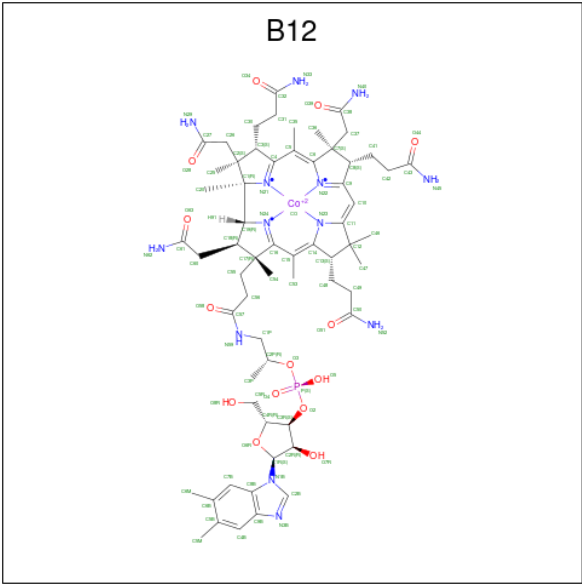
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		
2	C	1	Total	C	Co	N	O	P	0	0
			91	62	1	13	14	1		

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Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	E	1	Total	C	Co	N	O	P		0	0
			91	62	1	13	14	1			
2	G	1	Total	C	Co	N	O	P		0	0
			91	62	1	13	14	1			

- Molecule 3 is METHYLAMINE (three-letter code: NME) (formula: CH_5N).
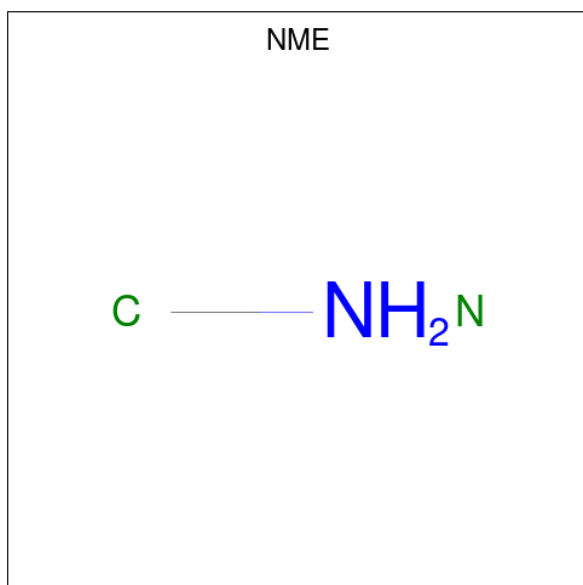
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			2	1	1		
3	C	1	Total	C	N	0	0
			2	1	1		
3	E	1	Total	C	N	0	0
			2	1	1		
3	G	1	Total	C	N	0	0
			2	1	1		

3 Residue-property plots ⓘ

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.
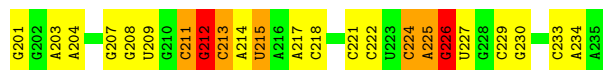
- Molecule 1: VITAMIN B12 BINDING RNA

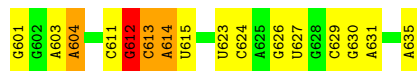Chain A:
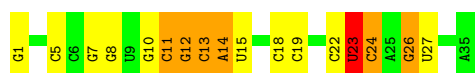
- Molecule 1: VITAMIN B12 BINDING RNA

Chain C:

- Molecule 1: VITAMIN B12 BINDING RNA

Chain E:

- Molecule 1: VITAMIN B12 BINDING RNA

Chain G:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	91.33Å 161.88Å 100.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 3.00 19.89 – 3.00	Depositor EDS
% Data completeness (in resolution range)	87.9 (12.00-3.00) 88.1 (19.89-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	1089.77 (at 2.98Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.204 , 0.246 0.192 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	20.3	Xtriage
Anisotropy	1.079	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , -13.1	EDS
L-test for twinning[2]	$< |L| > = 0.29, < L^2 > = 0.13$	Xtriage
Estimated twinning fraction	0.207 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.208 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o,F_c correlation	0.82	EDS
Total number of atoms	3376	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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: NME, B12

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	0.57	1/840 (0.1%)	0.83	5/1306 (0.4%)
1	C	0.59	1/840 (0.1%)	0.79	2/1306 (0.2%)
1	E	0.57	1/840 (0.1%)	0.78	1/1306 (0.1%)
1	G	0.56	1/840 (0.1%)	0.76	1/1306 (0.1%)
All	All	0.57	4/3360 (0.1%)	0.79	9/5224 (0.2%)

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	2	0
1	C	1	2
1	E	1	1
1	G	2	1
All	All	6	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	401	G	OP3-P	-7.04	1.52	1.61
1	G	601	G	OP3-P	-7.00	1.52	1.61
1	C	201	G	OP3-P	-6.92	1.52	1.61
1	A	1	G	OP3-P	-6.91	1.52	1.61

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	23	U	C2'-C3'-O3'	9.45	130.29	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	212	G	C2'-C3'-O3'	8.04	127.20	109.50
1	E	412	G	C2'-C3'-O3'	7.39	125.77	109.50
1	G	612	G	C2'-C3'-O3'	7.32	125.59	109.50
1	A	12	G	C2'-C3'-O3'	6.57	124.21	113.70
1	A	23	U	C4'-C3'-O3'	5.34	123.68	113.00
1	A	1	G	OP1-P-OP2	-5.30	111.65	119.60
1	A	11	C	N1-C1'-C2'	5.13	120.67	114.00
1	C	215	U	N1-C1'-C2'	5.04	120.55	114.00

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	12	G	C3'
1	A	23	U	C3'
1	C	212	G	C3'
1	E	412	G	C3'
1	G	612	G	C3'
1	G	623	U	C3'

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	214	A	Sidechain
1	C	226	G	Sidechain
1	E	414	A	Sidechain
1	G	614	A	Sidechain

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	751	0	382	7	0
1	C	751	0	382	14	0
1	E	751	0	382	11	0
1	G	751	0	382	11	0
2	A	91	0	86	3	0
2	C	91	0	86	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	91	0	86	3	0
2	G	91	0	86	5	0
3	A	2	0	0	0	0
3	C	2	0	0	0	0
3	E	2	0	0	0	0
3	G	2	0	0	0	0
All	All	3376	0	1872	55	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 11.

All (55) 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)
2:C:301:B12:H362	2:C:301:B12:H351	1.69	0.74
2:A:101:B12:H351	2:A:101:B12:H362	1.70	0.72
2:G:701:B12:H351	2:G:701:B12:H362	1.71	0.71
2:E:501:B12:H362	2:E:501:B12:H351	1.74	0.69
1:C:221:C:O2'	1:C:222:C:H5'	1.95	0.67
1:G:613:C:H2'	1:G:614:A:C8	2.31	0.65
1:G:603:A:H5'	1:G:604:A:OP2	1.97	0.65
2:E:501:B12:H531	2:E:501:B12:H552	1.82	0.60
2:A:101:B12:H552	2:A:101:B12:H531	1.85	0.59
2:G:701:B12:H552	2:G:701:B12:H531	1.85	0.58
1:C:217:A:H2'	1:C:218:C:O4'	2.08	0.54
1:G:612:G:C2'	1:G:613:C:H5'	2.39	0.53
1:C:229:C:O2'	1:E:418:C:H4'	2.09	0.53
1:C:211:C:C6	1:C:215:U:C6	2.98	0.52
2:C:301:B12:H552	2:C:301:B12:H531	1.91	0.52
1:E:411:C:H5'	1:E:412:G:OP2	2.10	0.51
1:C:229:C:H3'	1:C:230:G:H2'	1.93	0.51
1:G:611:C:C2	1:G:615:U:C5	2.99	0.50
1:E:407:G:C6	1:E:408:G:C5	3.00	0.50
2:A:101:B12:O63	2:A:101:B12:H551	2.12	0.50
1:E:413:C:H2'	1:E:414:A:C8	2.47	0.50
1:G:613:C:H2'	1:G:614:A:H8	1.76	0.50
1:G:613:C:OP2	1:G:614:A:H3'	2.11	0.50
1:C:208:G:H2'	1:C:209:U:H6	1.78	0.49
1:E:411:C:H2'	1:E:414:A:O2'	2.13	0.48
1:C:203:A:O2'	1:C:204:A:H5'	2.13	0.48
1:G:611:C:C6	1:G:615:U:C6	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:411:C:C6	1:E:415:U:C6	3.01	0.47
1:E:418:C:H2'	1:E:419:C:C6	2.49	0.47
1:E:421:C:O2'	1:E:422:C:H5'	2.13	0.47
1:G:635:A:H8	1:G:635:A:O5'	1.98	0.47
1:E:419:C:O2	1:E:428:G:C2	2.68	0.47
2:E:501:B12:H601	2:E:501:B12:H252	1.96	0.47
1:C:208:G:O2'	1:C:209:U:H5'	2.15	0.47
1:C:207:G:C6	1:C:208:G:C5	3.04	0.46
2:G:701:B12:H301	2:G:701:B12:H203	1.97	0.46
1:A:18:C:H2'	1:A:19:C:O4'	2.16	0.46
1:E:408:G:O2'	1:E:425:A:N1	2.46	0.46
1:G:603:A:H2'	1:G:604:A:H1'	1.98	0.45
1:A:13:C:H2'	1:A:14:A:C8	2.51	0.45
1:A:7:G:O2'	1:A:8:G:H5'	2.15	0.45
1:C:224:C:H5"	1:C:225:A:OP2	2.17	0.44
1:G:603:A:H2'	1:G:604:A:C1'	2.46	0.44
1:C:208:G:H2'	1:C:209:U:C6	2.53	0.44
1:A:13:C:H5"	1:A:14:A:OP2	2.18	0.43
1:A:11:C:C2	1:A:15:U:C5	3.07	0.43
1:A:23:U:O2'	1:A:24:C:OP2	2.28	0.42
1:E:407:G:H2'	1:E:408:G:O4'	2.19	0.41
2:G:701:B12:H601	2:G:701:B12:H252	2.02	0.41
1:C:212:G:O2'	1:C:213:C:H5'	2.20	0.41
1:A:10:G:O4'	1:A:26:G:H8	2.03	0.40
2:G:701:B12:H531	2:G:701:B12:C55	2.51	0.40
1:G:629:C:H3'	1:G:630:G:H2'	2.03	0.40
1:C:225:A:H5"	1:C:226:G:OP1	2.22	0.40
1:C:233:C:H2'	1:C:234:A:O4'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

There are no protein molecules in this entry.

5.3.2 Protein sidechains ⓘ

There are no protein molecules in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	34/35 (97%)	8 (23%)	2 (5%)
1	C	34/35 (97%)	5 (14%)	3 (8%)
1	E	34/35 (97%)	6 (17%)	2 (5%)
1	G	34/35 (97%)	8 (23%)	2 (5%)
All	All	136/140 (97%)	27 (19%)	9 (6%)

All (27) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	C
1	A	12	G
1	A	13	C
1	A	14	A
1	A	22	C
1	A	24	C
1	A	26	G
1	A	27	U
1	C	212	G
1	C	213	C
1	C	225	A
1	C	226	G
1	C	227	U
1	E	410	G
1	E	412	G
1	E	413	C
1	E	416	A
1	E	424	C
1	E	427	U
1	G	604	A
1	G	612	G
1	G	613	C
1	G	623	U
1	G	624	C
1	G	626	G
1	G	627	U
1	G	631	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	12	G

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Mol	Chain	Res	Type
1	A	23	U
1	C	211	C
1	C	212	G
1	C	224	C
1	E	411	C
1	E	412	G
1	G	612	G
1	G	623	U

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)

8 ligands are modelled in this entry.

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	B12	G	701	3	91,101,101	1.13	8 (8%)	140,166,166	1.26	11 (7%)
2	B12	A	101	3	91,101,101	1.21	10 (10%)	140,166,166	1.21	11 (7%)
3	NME	E	502	2	1,1,1	2.60	1 (100%)	-		
2	B12	E	501	3	91,101,101	1.13	9 (9%)	140,166,166	1.13	10 (7%)
3	NME	A	102	2	1,1,1	2.63	1 (100%)	-		
3	NME	G	702	2	1,1,1	2.57	1 (100%)	-		
3	NME	C	302	2	1,1,1	2.64	1 (100%)	-		
2	B12	C	301	3	91,101,101	1.14	8 (8%)	140,166,166	1.27	11 (7%)

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	B12	G	701	3	-	6/52/223/223	0/3/11/11
2	B12	C	301	3	-	9/52/223/223	0/3/11/11
2	B12	E	501	3	-	3/52/223/223	0/3/11/11
2	B12	A	101	3	-	6/52/223/223	0/3/11/11

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	101	B12	C1-C2	3.41	1.66	1.58
2	A	101	B12	C61-N62	-3.28	1.22	1.32
2	E	501	B12	C61-N62	-3.24	1.22	1.32
2	G	701	B12	O63-C61	3.20	1.33	1.23
2	C	301	B12	C61-N62	-3.17	1.22	1.32
2	G	701	B12	C61-N62	-3.12	1.22	1.32
2	E	501	B12	O63-C61	2.84	1.32	1.23
2	C	301	B12	C1-C2	2.76	1.65	1.58
2	A	101	B12	O63-C61	2.65	1.32	1.23
3	C	302	NME	C-N	-2.64	1.14	1.43
3	A	102	NME	C-N	-2.63	1.15	1.43
3	E	502	NME	C-N	-2.60	1.15	1.43
2	E	501	B12	C1-C2	2.60	1.65	1.58
3	G	702	NME	C-N	-2.57	1.15	1.43
2	G	701	B12	C1-C2	2.49	1.64	1.58
2	C	301	B12	O63-C61	2.48	1.31	1.23
2	C	301	B12	C7B-C6B	2.42	1.43	1.37
2	G	701	B12	C53-C15	2.38	1.55	1.50
2	C	301	B12	C53-C15	2.37	1.55	1.50
2	A	101	B12	C53-C15	2.36	1.55	1.50
2	G	701	B12	C48-C49	2.34	1.59	1.52
2	E	501	B12	C7B-C6B	2.31	1.43	1.37
2	E	501	B12	C12-C11	2.29	1.56	1.52
2	G	701	B12	C17-C18	2.23	1.58	1.54
2	C	301	B12	C12-C11	2.17	1.55	1.52
2	C	301	B12	C1R-N1B	-2.17	1.44	1.49
2	A	101	B12	C12-C11	2.14	1.55	1.52
2	G	701	B12	C35-C5	2.13	1.55	1.50
2	G	701	B12	C4B-C9B	2.12	1.45	1.41
2	A	101	B12	C13-C14	2.11	1.56	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	501	B12	C53-C15	2.11	1.55	1.50
2	A	101	B12	C17-C18	2.10	1.58	1.54
2	E	501	B12	C7-C6	2.10	1.59	1.54
2	A	101	B12	C48-C49	2.10	1.59	1.52
2	A	101	B12	C7B-C6B	2.09	1.42	1.37
2	C	301	B12	C5M-C5B	2.07	1.54	1.51
2	A	101	B12	C2R-C3R	-2.06	1.48	1.53
2	E	501	B12	O6R-C1R	2.05	1.43	1.40
2	E	501	B12	C48-C49	2.03	1.59	1.52

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	G	701	B12	C9-N22-C6	5.20	111.54	105.28
2	A	101	B12	C9-N22-C6	5.05	111.36	105.28
2	C	301	B12	C9-N22-C6	5.03	111.33	105.28
2	E	501	B12	C9-N22-C6	4.87	111.14	105.28
2	G	701	B12	C20-C1-C19	-4.65	104.87	109.35
2	A	101	B12	C7B-C8B-C9B	4.32	124.82	120.54
2	G	701	B12	C7B-C8B-C9B	4.29	124.78	120.54
2	A	101	B12	C20-C1-C19	-4.20	105.30	109.35
2	C	301	B12	C7B-C8B-C9B	4.19	124.68	120.54
2	G	701	B12	C4B-C9B-C8B	-3.76	117.25	121.10
2	C	301	B12	C20-C1-C19	-3.53	105.95	109.35
2	E	501	B12	C7B-C8B-C9B	3.43	123.94	120.54
2	A	101	B12	C4B-C9B-C8B	-3.36	117.66	121.10
2	E	501	B12	C20-C1-C19	-3.16	106.31	109.35
2	E	501	B12	C4B-C9B-C8B	-3.06	117.97	121.10
2	C	301	B12	C47-C12-C46	-3.02	104.39	109.41
2	C	301	B12	C4B-C9B-C8B	-3.02	118.01	121.10
2	G	701	B12	C47-C12-C46	-2.95	104.53	109.41
2	C	301	B12	O63-C61-C60	-2.94	114.73	120.87
2	A	101	B12	C2R-C3R-C4R	2.93	108.37	103.24
2	E	501	B12	C2R-C3R-C4R	2.87	108.27	103.24
2	C	301	B12	C2R-C3R-C4R	2.85	108.23	103.24
2	G	701	B12	C2-C1-C19	2.79	122.96	118.61
2	E	501	B12	C47-C12-C46	-2.78	104.80	109.41
2	G	701	B12	C19-C1-N21	2.70	104.92	102.14
2	G	701	B12	C2R-C3R-C4R	2.55	107.70	103.24
2	C	301	B12	C19-N24-C16	2.52	110.05	107.29
2	E	501	B12	O63-C61-C60	-2.48	115.69	120.87
2	G	701	B12	C1-C2-C3	-2.46	98.50	101.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	101	B12	C47-C12-C46	-2.42	105.39	109.41
2	A	101	B12	O63-C61-C60	-2.39	115.88	120.87
2	A	101	B12	C19-N24-C16	2.39	109.90	107.29
2	C	301	B12	C49-C48-C13	2.34	121.27	114.65
2	A	101	B12	C15-C14-N23	-2.30	123.48	126.26
2	A	101	B12	C30-C3-C4	2.30	115.06	109.66
2	E	501	B12	C19-N24-C16	2.28	109.78	107.29
2	G	701	B12	O63-C61-C60	-2.25	116.17	120.87
2	A	101	B12	C2-C1-C19	2.24	122.09	118.61
2	G	701	B12	C19-N24-C16	2.21	109.71	107.29
2	E	501	B12	C15-C14-N23	-2.21	123.60	126.26
2	C	301	B12	C36-C7-C37	2.13	114.35	110.74
2	E	501	B12	C1-C19-N24	2.02	108.50	106.25
2	C	301	B12	C47-C12-C13	2.00	120.86	112.74

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	501	B12	C18-C60-C61-O63
2	E	501	B12	C18-C60-C61-N62
2	G	701	B12	C18-C60-C61-O63
2	G	701	B12	C18-C60-C61-N62
2	G	701	B12	O6R-C4R-C5R-O8R
2	G	701	B12	C3R-C4R-C5R-O8R
2	E	501	B12	C13-C48-C49-C50
2	C	301	B12	C13-C48-C49-C50
2	A	101	B12	O6R-C4R-C5R-O8R
2	C	301	B12	C18-C60-C61-O63
2	C	301	B12	C18-C60-C61-N62
2	C	301	B12	C4-C3-C30-C31
2	C	301	B12	O6R-C4R-C5R-O8R
2	C	301	B12	C30-C31-C32-O34
2	A	101	B12	C3R-C4R-C5R-O8R
2	A	101	B12	C48-C49-C50-O51
2	C	301	B12	C30-C31-C32-N33
2	C	301	B12	C2-C3-C30-C31
2	C	301	B12	C3R-C4R-C5R-O8R
2	A	101	B12	C48-C49-C50-N52
2	A	101	B12	C4-C3-C30-C31
2	A	101	B12	C13-C48-C49-C50
2	G	701	B12	C13-C48-C49-C50

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Mol	Chain	Res	Type	Atoms
2	G	701	B12	C48-C49-C50-N52

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	701	B12	5	0
2	A	101	B12	3	0
2	E	501	B12	3	0
2	C	301	B12	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 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 B12 G 701
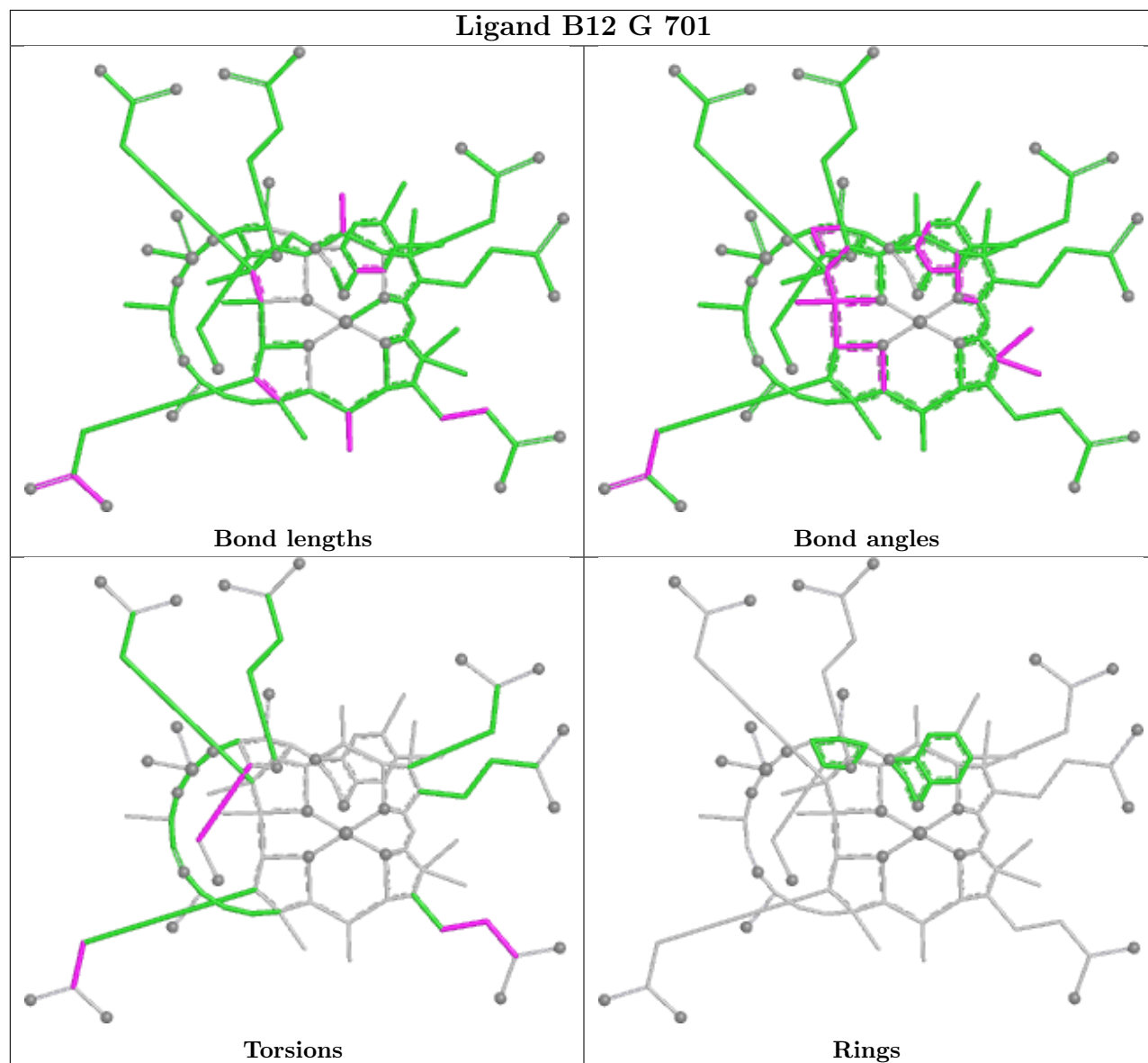
Bond lengths

Bond angles

Torsions

Rings

Ligand B12 A 101

Bond lengths

Bond angles

Torsions

Rings

Ligand B12 E 501

Bond lengths

Bond angles

Torsions

Rings

Ligand B12 C 301

Bond lengths

Bond angles

Torsions

Rings
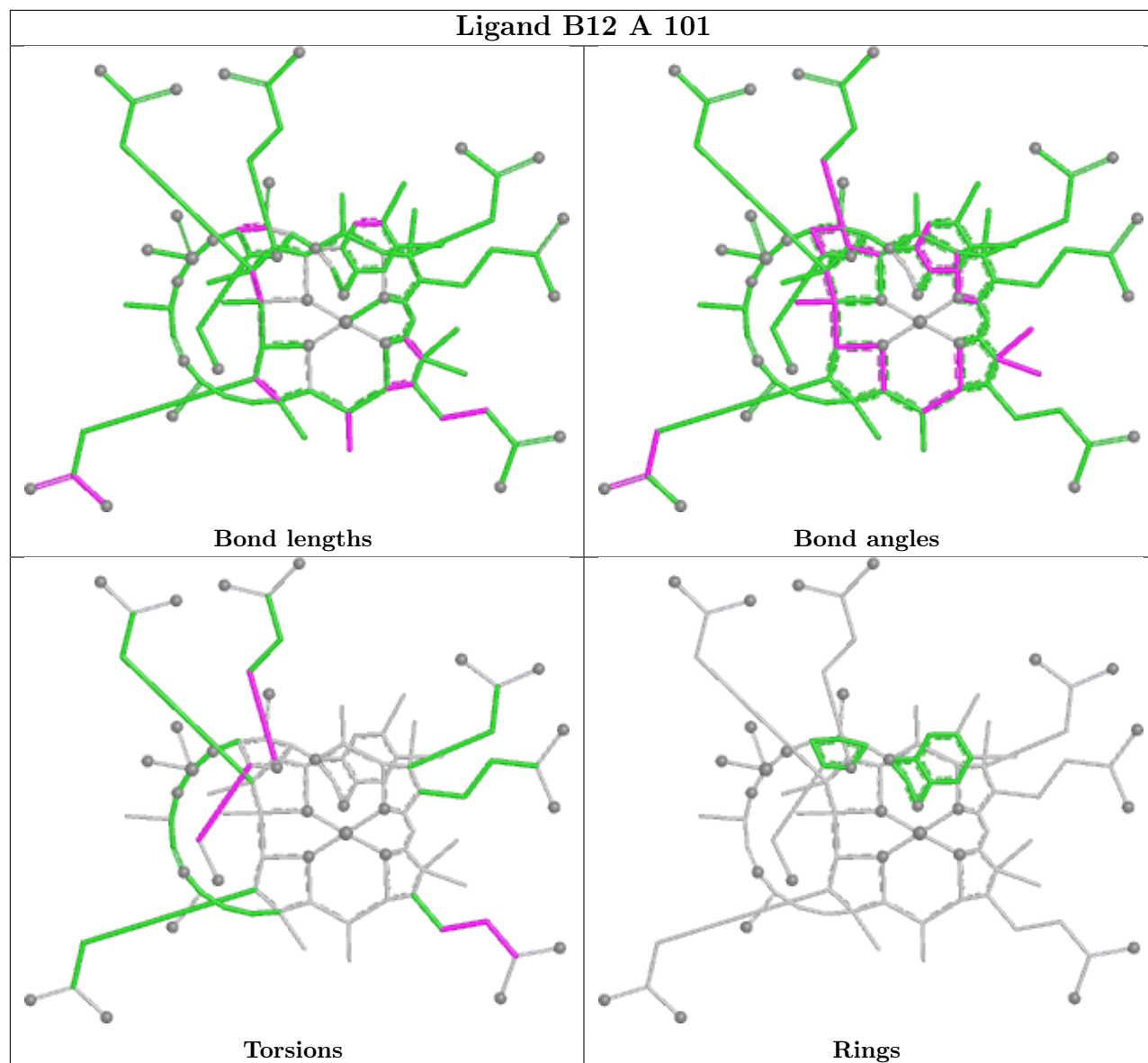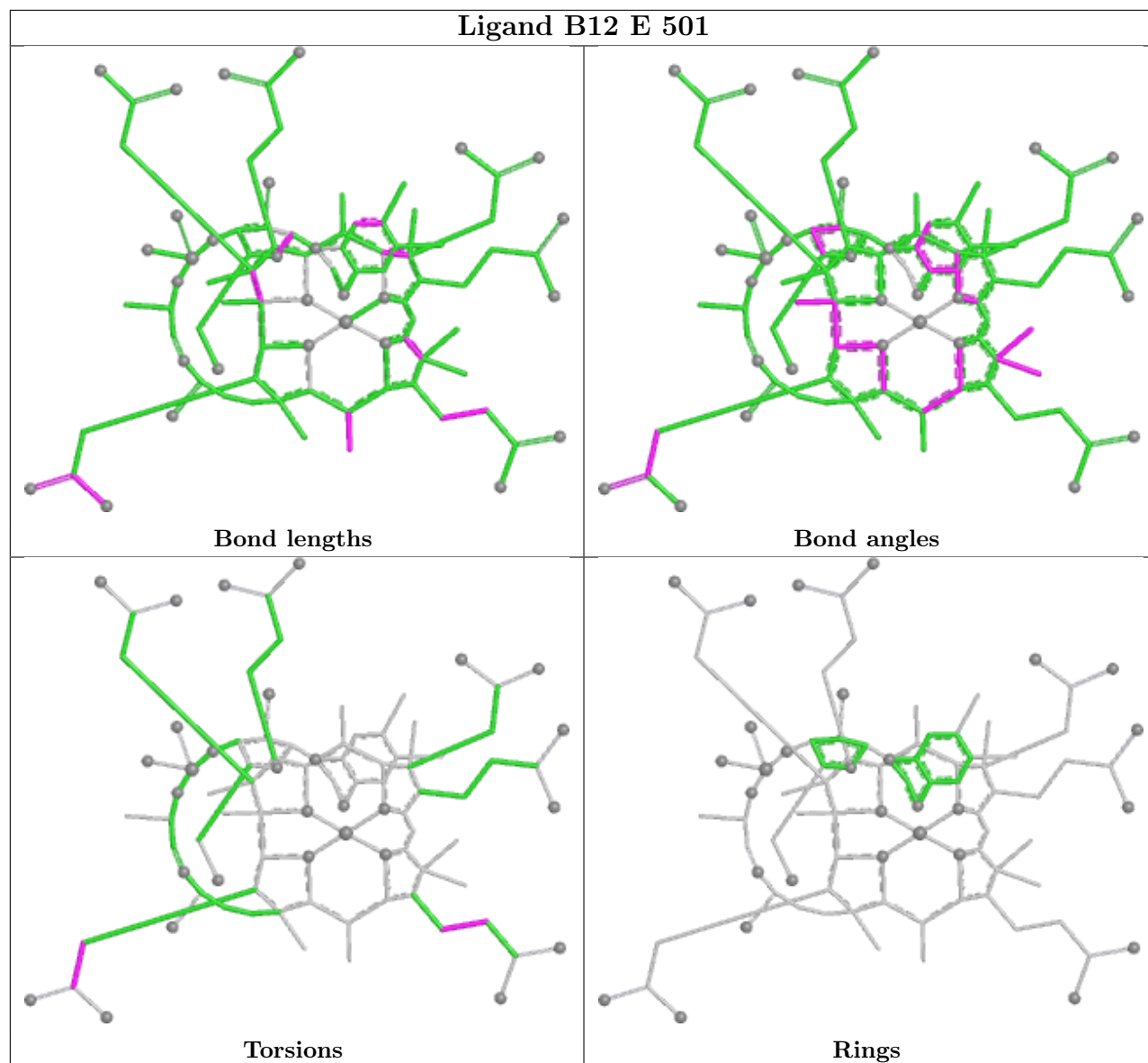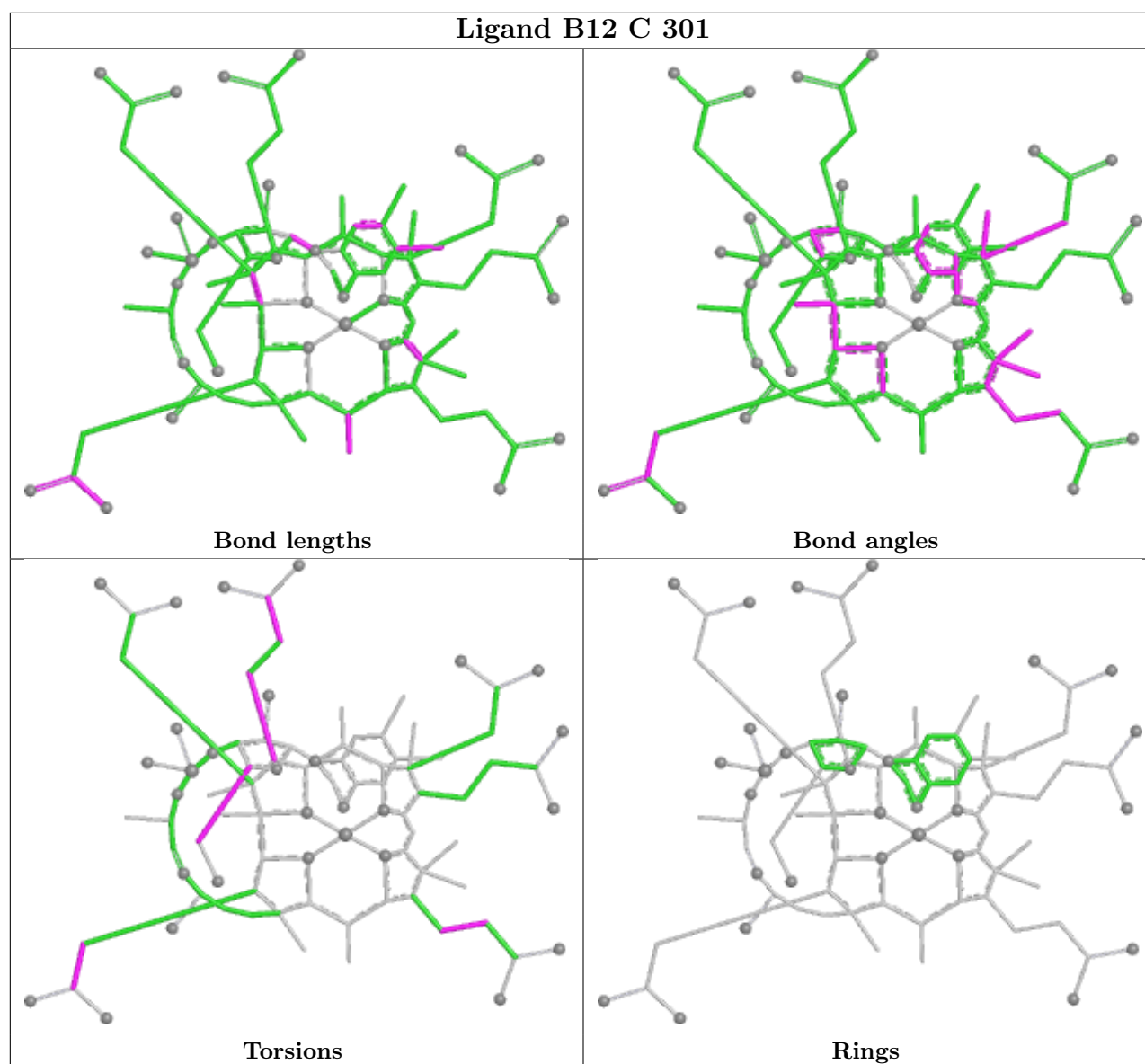
5.7 Other polymers ⓘ

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(Å²)	Q<0.9
1	A	35/35 (100%)	-0.04	0	100	100	18, 26, 47, 57	0
1	C	35/35 (100%)	-0.14	0	100	100	13, 24, 36, 39	0
1	E	35/35 (100%)	-0.10	0	100	100	14, 20, 44, 50	0
1	G	35/35 (100%)	-0.14	0	100	100	10, 23, 43, 56	0
All	All	140/140 (100%)	-0.10	0	100	100	10, 24, 44, 57	0

There are no RSRZ outliers to report.

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(Å²)	Q<0.9
2	B12	A	101	91/91	0.91	0.25	17,33,51,56	0
2	B12	C	301	91/91	0.92	0.22	10,29,41,52	0
2	B12	E	501	91/91	0.92	0.23	15,22,36,41	0
2	B12	G	701	91/91	0.92	0.23	12,22,32,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NME	C	302	2/2	0.97	0.17	27,27,27,32	0
3	NME	E	502	2/2	0.97	0.16	23,23,23,26	0
3	NME	A	102	2/2	0.98	0.15	33,33,33,36	0
3	NME	G	702	2/2	0.98	0.15	22,22,22,30	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 B12 A 101:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
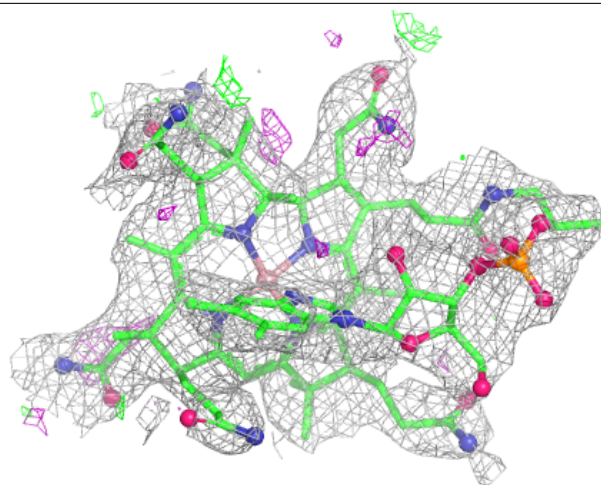$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative) and green (positive)
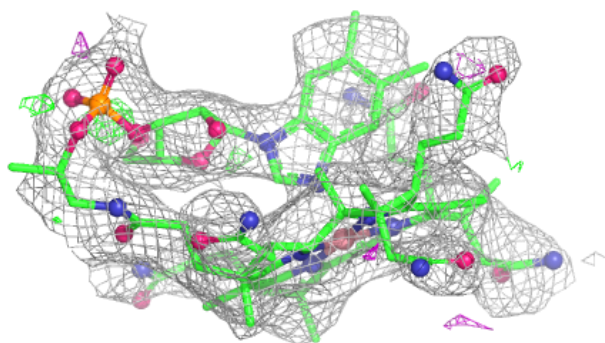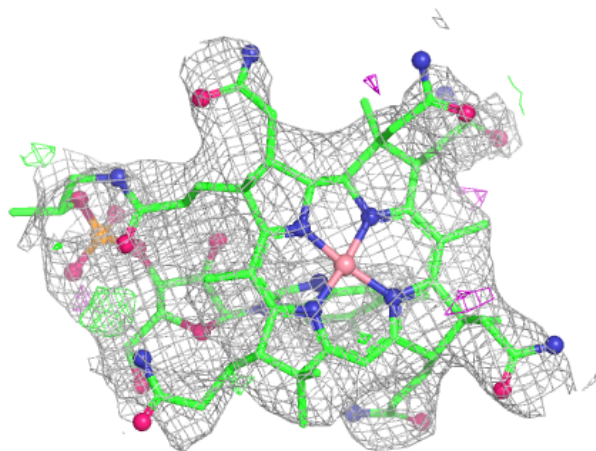
Electron density around B12 C 301:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
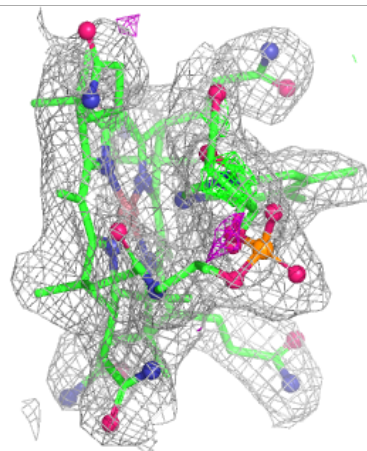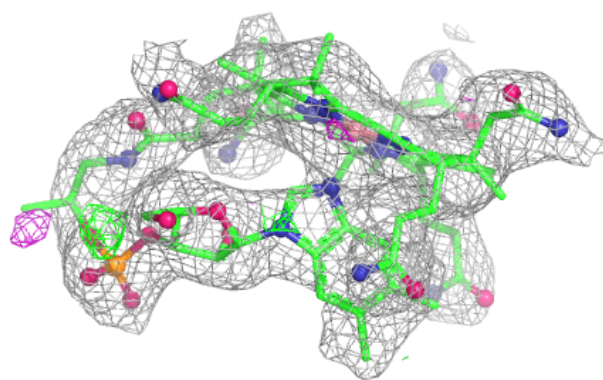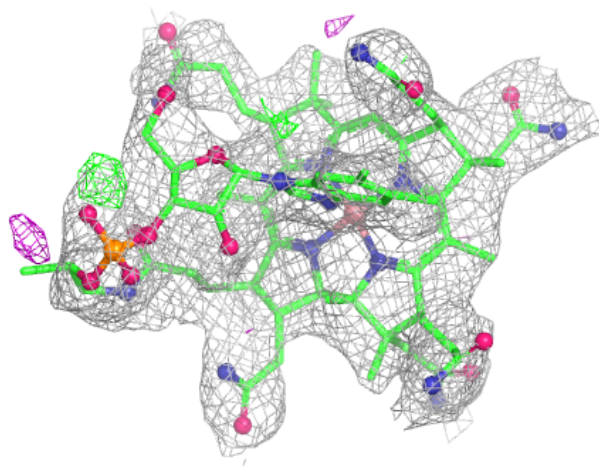and green (positive)
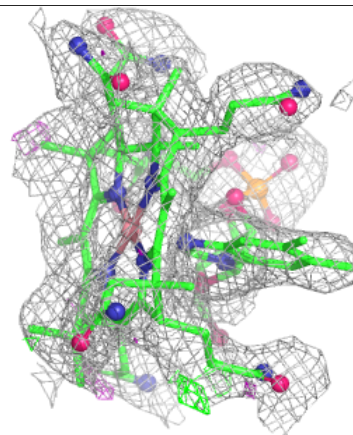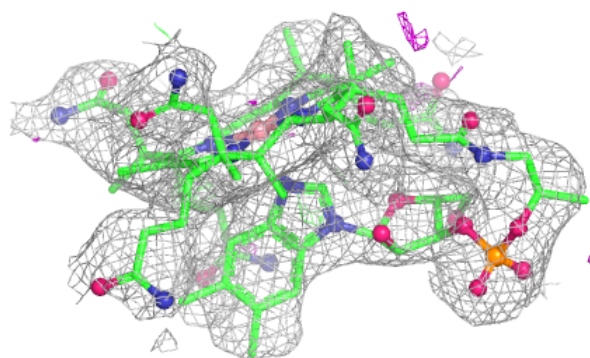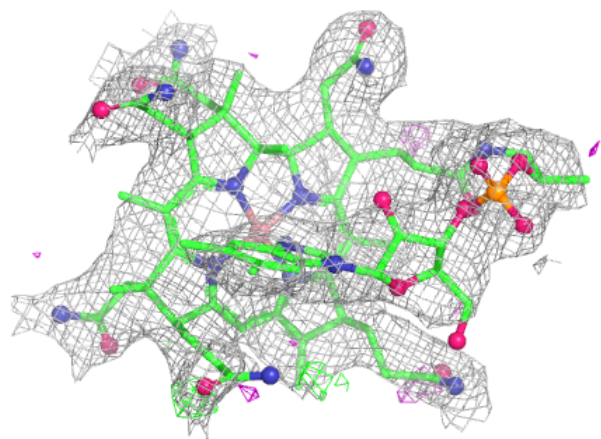
Electron density around B12 E 501:

2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray
mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative)
and green (positive)
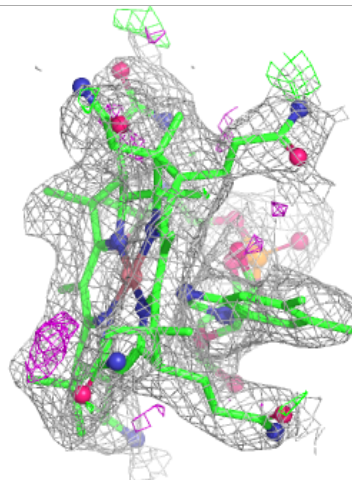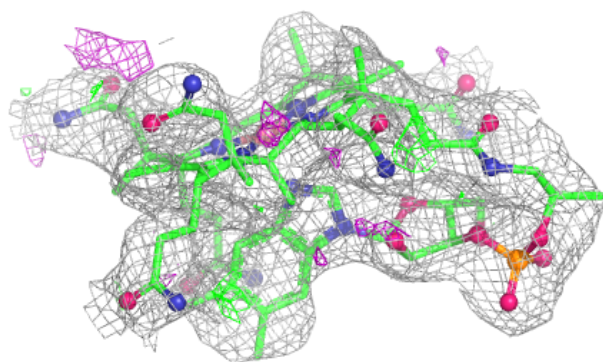
Electron density around B12 G 701:

$2mF_o$-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.