WORLDWIDE wwPDB

PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Sep 13, 2023 – 11:30 am BST

PDB ID	:	8OKV
Title	:	lipoprotein BT2095 from Bacteroides thetaiotamicron bound to cyanocobalamin CnCbl
Authors	:	Javier Abellon-Ruiz, J.; van den Berg, B.; Jana, K.; Kleinekathofer, U.; Silale, A.; Frey, A.M.; Basle, A.; Trost, M.
Deposited on	:	2023-03-29
Resolution	:	2.60 Å(reported)

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

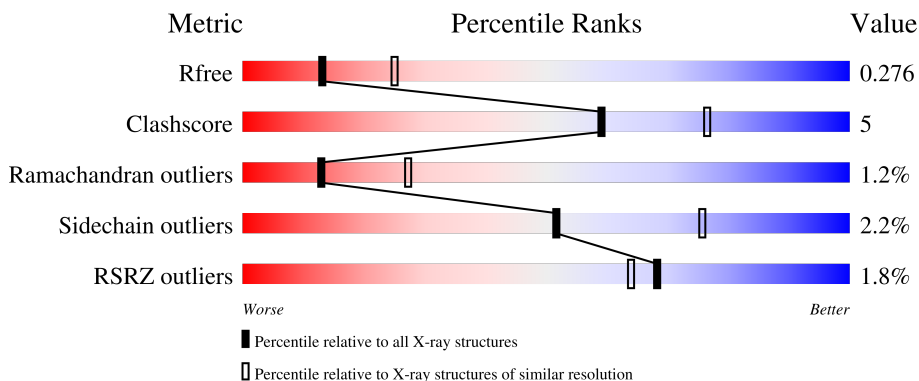|		
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (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 2.60 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		0.276
Clashscore		5
Ramachandran outliers		1.2%
Sidechain outliers		2.2%
RSRZ outliers		1.8%

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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	333	85% ... 11% ..
1	B	333	87% ... 10% ...
1	C	333	5% ... 84% ... 13% ..
1	D	333	.% ... 83% ... 12% ..

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
2	CNC	A	401	X	-	-	-
2	CNC	B	401	X	-	-	-
2	CNC	C	401	X	-	-	-
2	CNC	D	401	X	-	-	-

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 21033 atoms, of which 9944 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 Putative surface layer protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	330	Total	C	H	N	O	S	0	0	0
			5138	1739	2435	440	511	13			
1	A	321	Total	C	H	N	O	S	0	0	0
			4992	1686	2373	418	502	13			
1	C	327	Total	C	H	N	O	S	0	0	0
			5090	1721	2417	431	508	13			
1	D	322	Total	C	H	N	O	S	0	0	0
			5003	1689	2379	419	503	13			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	23	MET	-	initiating methionine	UNP Q8A5Z1
B	24	GLY	-	expression tag	UNP Q8A5Z1
B	25	HIS	-	expression tag	UNP Q8A5Z1
B	26	HIS	-	expression tag	UNP Q8A5Z1
B	27	HIS	-	expression tag	UNP Q8A5Z1
B	28	HIS	-	expression tag	UNP Q8A5Z1
B	29	HIS	-	expression tag	UNP Q8A5Z1
B	30	HIS	-	expression tag	UNP Q8A5Z1
A	23	MET	-	initiating methionine	UNP Q8A5Z1
A	24	GLY	-	expression tag	UNP Q8A5Z1
A	25	HIS	-	expression tag	UNP Q8A5Z1
A	26	HIS	-	expression tag	UNP Q8A5Z1
A	27	HIS	-	expression tag	UNP Q8A5Z1
A	28	HIS	-	expression tag	UNP Q8A5Z1
A	29	HIS	-	expression tag	UNP Q8A5Z1
A	30	HIS	-	expression tag	UNP Q8A5Z1
C	23	MET	-	initiating methionine	UNP Q8A5Z1
C	24	GLY	-	expression tag	UNP Q8A5Z1
C	25	HIS	-	expression tag	UNP Q8A5Z1
C	26	HIS	-	expression tag	UNP Q8A5Z1
C	27	HIS	-	expression tag	UNP Q8A5Z1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	28	HIS	-	expression tag	UNP Q8A5Z1
C	29	HIS	-	expression tag	UNP Q8A5Z1
C	30	HIS	-	expression tag	UNP Q8A5Z1
D	23	MET	-	initiating methionine	UNP Q8A5Z1
D	24	GLY	-	expression tag	UNP Q8A5Z1
D	25	HIS	-	expression tag	UNP Q8A5Z1
D	26	HIS	-	expression tag	UNP Q8A5Z1
D	27	HIS	-	expression tag	UNP Q8A5Z1
D	28	HIS	-	expression tag	UNP Q8A5Z1
D	29	HIS	-	expression tag	UNP Q8A5Z1
D	30	HIS	-	expression tag	UNP Q8A5Z1

- Molecule 2 is CYANOCOBALAMIN (three-letter code: CNC) (formula: $C_{63}H_{89}CoN_{14}O_{14}P$) (labeled as "Ligand of Interest" by depositor).
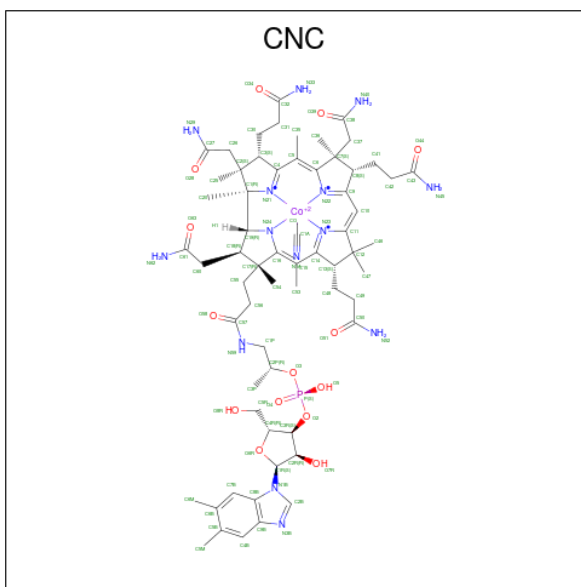
Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	B	1	Total	C	Co	H	N	O	P	0	0
			178	63	1	85	14	14	1		
2	A	1	Total	C	Co	H	N	O	P	0	0
			178	63	1	85	14	14	1		
2	C	1	Total	C	Co	H	N	O	P	0	0
			178	63	1	85	14	14	1		
2	D	1	Total	C	Co	H	N	O	P	0	0
			178	63	1	85	14	14	1		

- Molecule 3 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	28	Total 28	O 28	0	0
3	A	28	Total 28	O 28	0	0
3	C	24	Total 24	O 24	0	0
3	D	18	Total 18	O 18	0	0

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.
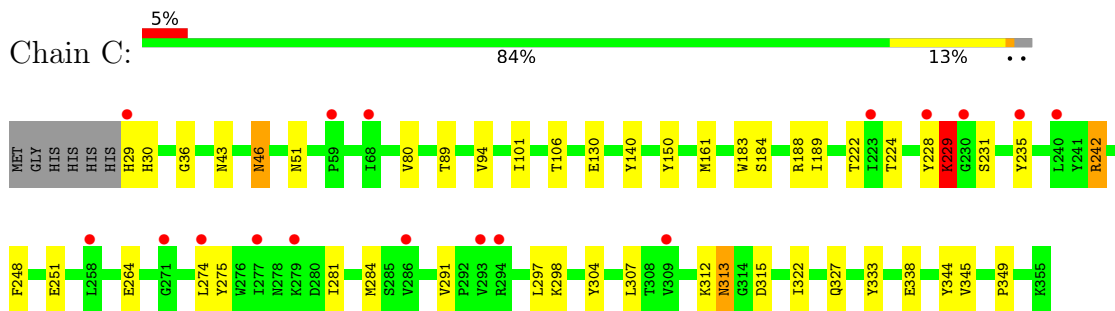
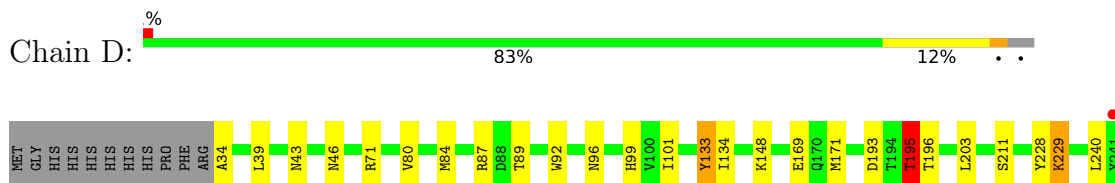• Molecule 1: Putative surface layer protein
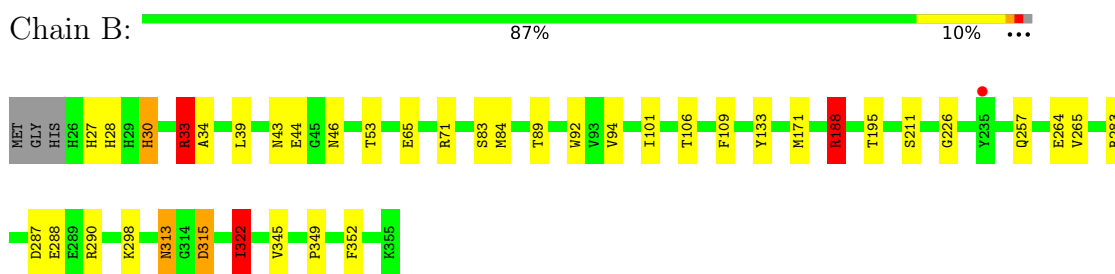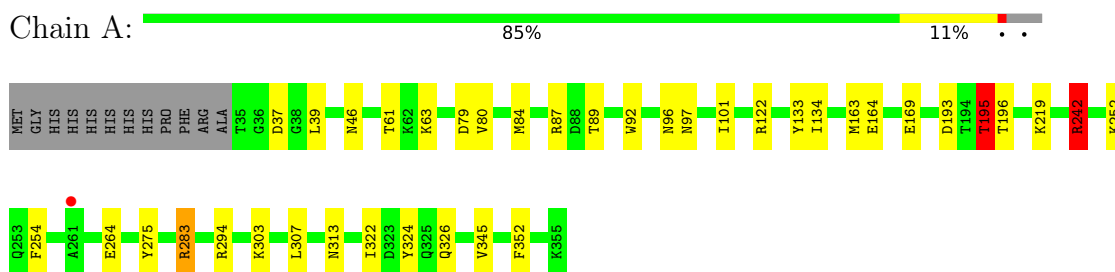
Chain B:

• Molecule 1: Putative surface layer protein

Chain A:

• Molecule 1: Putative surface layer protein

Chain C:

• Molecule 1: Putative surface layer protein

Chain D:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	74.77Å 131.04Å 179.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.12 – 2.60 74.01 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.3 (74.12-2.60) 99.3 (74.01-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.75 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.218 , 0.276 0.225 , 0.276	Depositor DCC
R_{free} test set	2675 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å^2)	56.5	Xtriage
Anisotropy	0.615	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 53.4	EDS
L-test for twinning[2]	$<|L|> = 0.52$, $<L^2> = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	21033	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CNC

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	0.66	2/2686 (0.1%)	1.07	7/3646 (0.2%)
1	B	0.68	3/2777 (0.1%)	1.13	12/3770 (0.3%)
1	C	0.64	2/2744 (0.1%)	1.07	7/3725 (0.2%)
1	D	0.74	4/2691 (0.1%)	1.14	10/3653 (0.3%)
All	All	0.68	11/10898 (0.1%)	1.10	36/14794 (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	0	3
1	B	0	6
1	C	0	2
1	D	0	7
All	All	0	18

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	264	GLU	CD-OE2	14.63	1.41	1.25
1	A	164	GLU	CD-OE1	8.77	1.35	1.25
1	C	264	GLU	CD-OE1	8.47	1.34	1.25
1	B	264	GLU	CD-OE2	7.81	1.34	1.25
1	A	169	GLU	CD-OE2	7.27	1.33	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	313	ASN	CB-CA-C	-7.96	94.48	110.40
1	D	99	HIS	CB-CA-C	7.80	126.00	110.40
1	C	29	HIS	CA-CB-CG	7.52	126.38	113.60
1	C	313	ASN	CB-CA-C	-7.47	95.46	110.40
1	B	33	ARG	NE-CZ-NH2	-7.41	116.59	120.30

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	188	ARG	Sidechain
1	B	226	GLY	Peptide
1	B	283	ARG	Sidechain
1	B	33	ARG	Sidechain
1	B	71	ARG	Sidechain

5.2   Too-close contacts   (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2619	2373	2526	19	0
1	B	2703	2435	2595	13	0
1	C	2673	2417	2574	26	0
1	D	2624	2379	2531	18	0
2	A	93	85	86	9	0
2	B	93	85	86	6	0
2	C	93	85	87	9	0
2	D	93	85	87	8	0
3	A	28	0	0	3	0
3	B	28	0	0	1	0
3	C	24	0	0	1	0
3	D	18	0	0	0	0
All	All	11089	9944	10572	101	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 5.

The worst 5 of 101 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:401:CNC:H362	2:C:401:CNC:H351	1.55	0.88
2:D:401:CNC:H362	2:D:401:CNC:H351	1.55	0.88
1:A:264:GLU:OE1	3:A:501:HOH:O	1.93	0.87
2:B:401:CNC:H351	2:B:401:CNC:H362	1.58	0.85
1:D:96:ASN:HD21	2:D:401:CNC:H331	1.22	0.84

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	A	319/333 (96%)	292 (92%)	23 (7%)	4 (1%)	12	24
1	B	328/333 (98%)	299 (91%)	26 (8%)	3 (1%)	17	35
1	C	325/333 (98%)	301 (93%)	20 (6%)	4 (1%)	13	27
1	D	320/333 (96%)	297 (93%)	19 (6%)	4 (1%)	12	24
All	All	1292/1332 (97%)	1189 (92%)	88 (7%)	15 (1%)	13	27

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	229	LYS
1	D	229	LYS
1	A	322	ILE
1	C	322	ILE
1	D	322	ILE

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	A	284/294 (97%)	280 (99%)	4 (1%)	67	85
1	B	292/294 (99%)	284 (97%)	8 (3%)	44	71
1	C	289/294 (98%)	281 (97%)	8 (3%)	43	69
1	D	284/294 (97%)	279 (98%)	5 (2%)	59	80
All	All	1149/1176 (98%)	1124 (98%)	25 (2%)	52	76

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	184	SER
1	C	248	PHE
1	D	294	ARG
1	C	229	LYS
1	C	274	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	313	ASN
1	C	327	GLN
1	D	325	GLN
1	D	97	ASN
1	D	253	GLN

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 ⓘ

4 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	CNC	A	401	-	90,103,103	1.80	17 (18%)	139,171,171	2.10	44 (31%)
2	CNC	B	401	-	90,103,103	1.60	8 (8%)	139,171,171	2.05	37 (26%)
2	CNC	C	401	-	90,103,103	1.61	8 (8%)	139,171,171	2.36	41 (29%)
2	CNC	D	401	-	90,103,103	1.77	18 (20%)	139,171,171	2.34	46 (33%)

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	CNC	A	401	-	1/1/38/38	8/52/235/235	0/3/11/11
2	CNC	B	401	-	2/2/38/38	15/52/235/235	0/3/11/11
2	CNC	C	401	-	2/2/38/38	12/52/235/235	0/3/11/11
2	CNC	D	401	-	1/1/38/38	12/52/235/235	0/3/11/11

The worst 5 of 51 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	CNC	C19-N24	-11.15	1.25	1.49
2	C	401	CNC	C19-N24	-9.71	1.28	1.49
2	A	401	CNC	C19-N24	-8.55	1.31	1.49
2	D	401	CNC	C19-N24	-8.10	1.32	1.49
2	A	401	CNC	C8B-C9B	5.62	1.52	1.40

The worst 5 of 168 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	CNC	C13-C12-C11	-12.43	83.95	100.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	401	CNC	O3-C2P-C1P	7.55	121.98	106.92
2	A	401	CNC	C18-C19-N24	7.53	113.84	101.88
2	B	401	CNC	C20-C1-C19	-7.19	95.81	110.23
2	C	401	CNC	C1-C19-C18	6.98	132.13	121.81

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	401	CNC	C19
2	B	401	CNC	N24
2	A	401	CNC	N24
2	C	401	CNC	C19
2	C	401	CNC	N24

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	CNC	C3P-C2P-O3-P
2	B	401	CNC	C2P-O3-P-O5
2	A	401	CNC	C38-C37-C7-C6
2	A	401	CNC	C1P-C2P-O3-P
2	A	401	CNC	C3P-C2P-O3-P

There are no ring outliers.

4 monomers are involved in 32 short contacts:

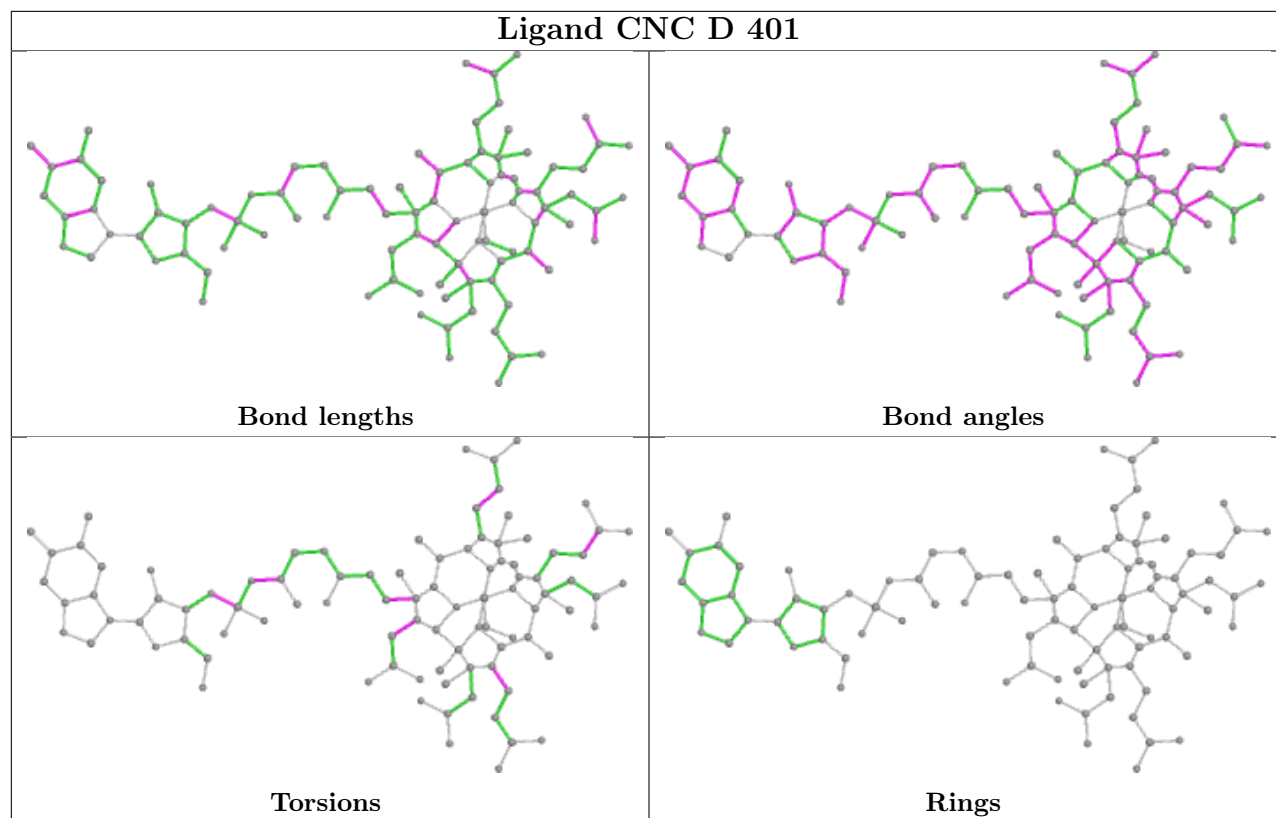| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	CNC	9	0
2	B	401	CNC	6	0
2	C	401	CNC	9	0
2	D	401	CNC	8	0

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 CNC A 401

Bond lengths

Bond angles

Torsions

Rings

Ligand CNC B 401

Bond lengths

Bond angles

Torsions

Rings

Ligand CNC C 401

Bond lengths

Bond angles

Torsions

Rings

Ligand CNC D 401

Bond lengths

Bond angles

Torsions

Rings
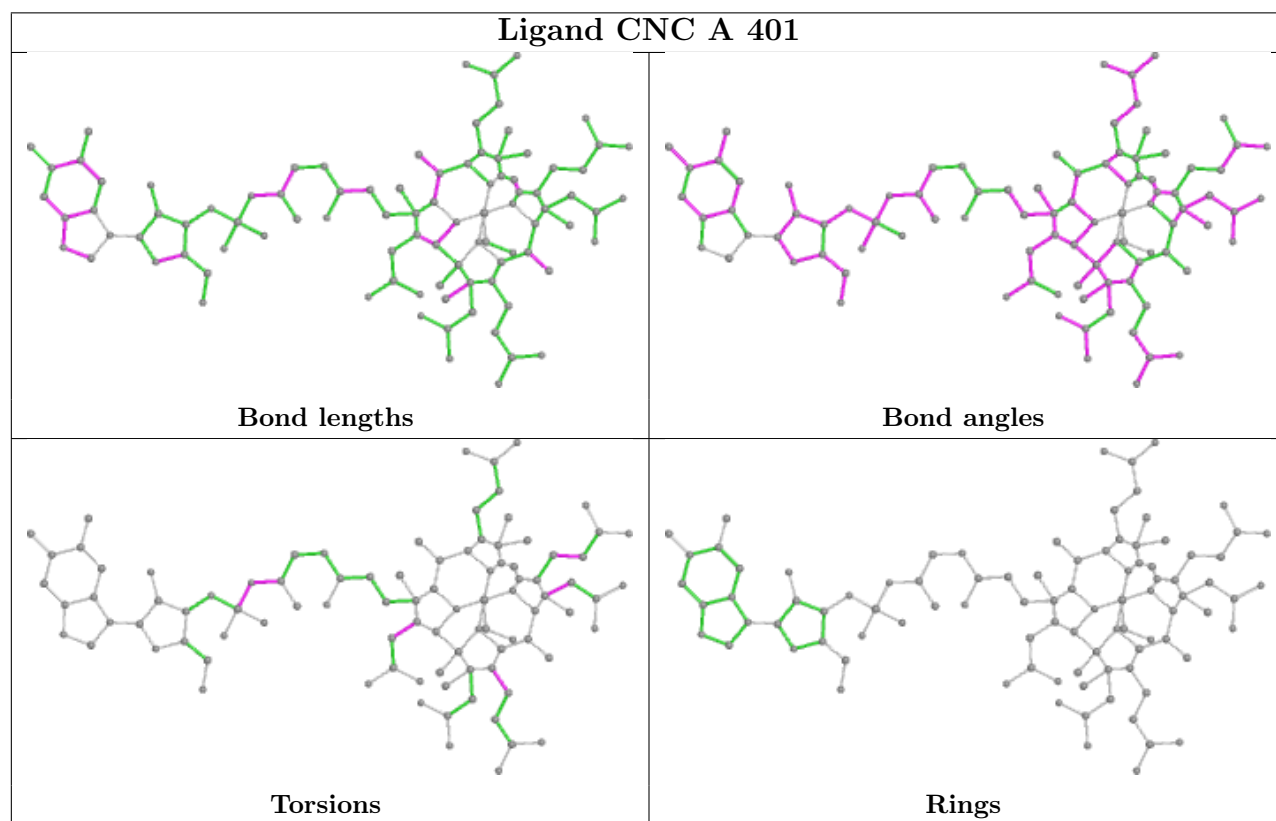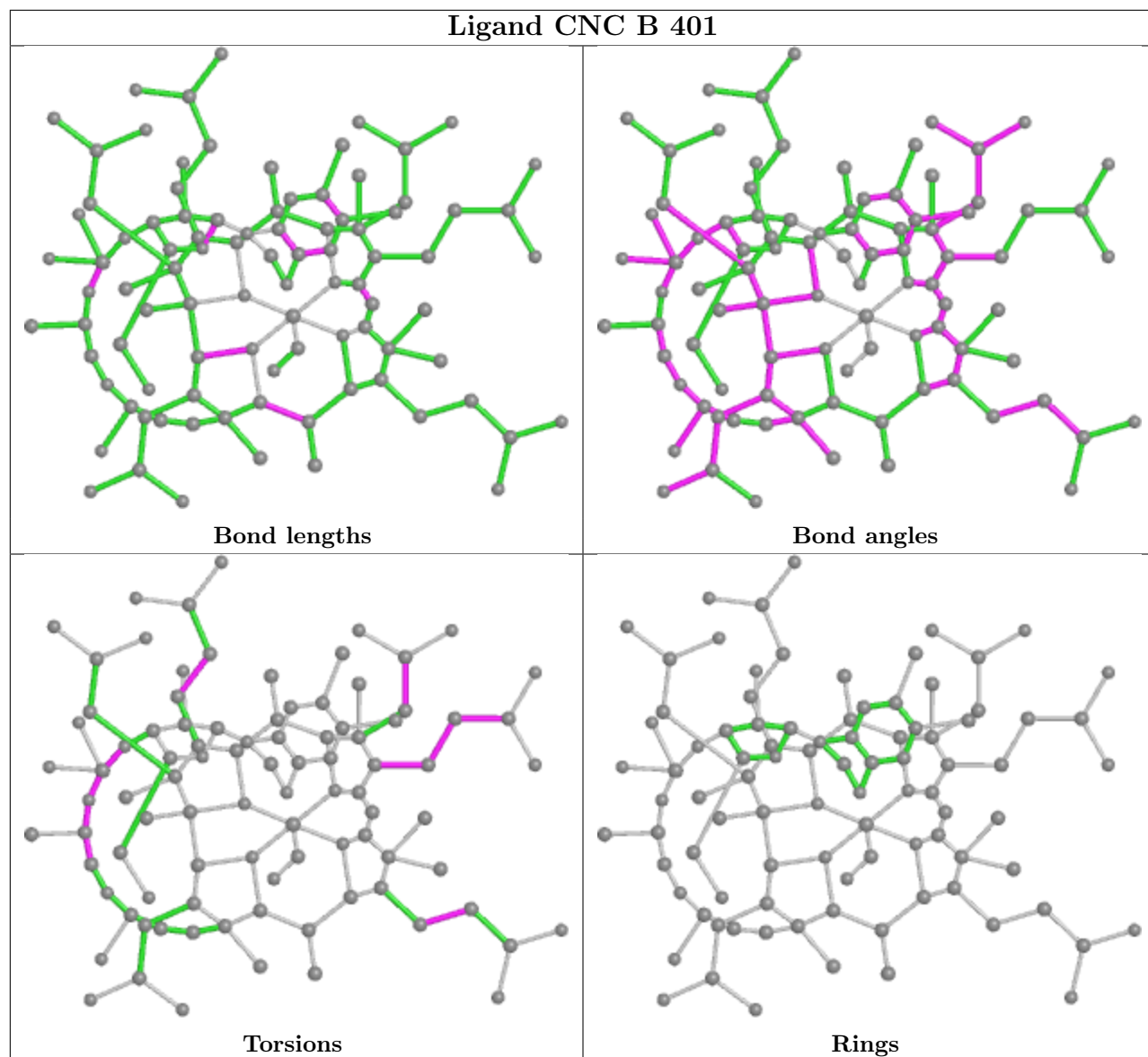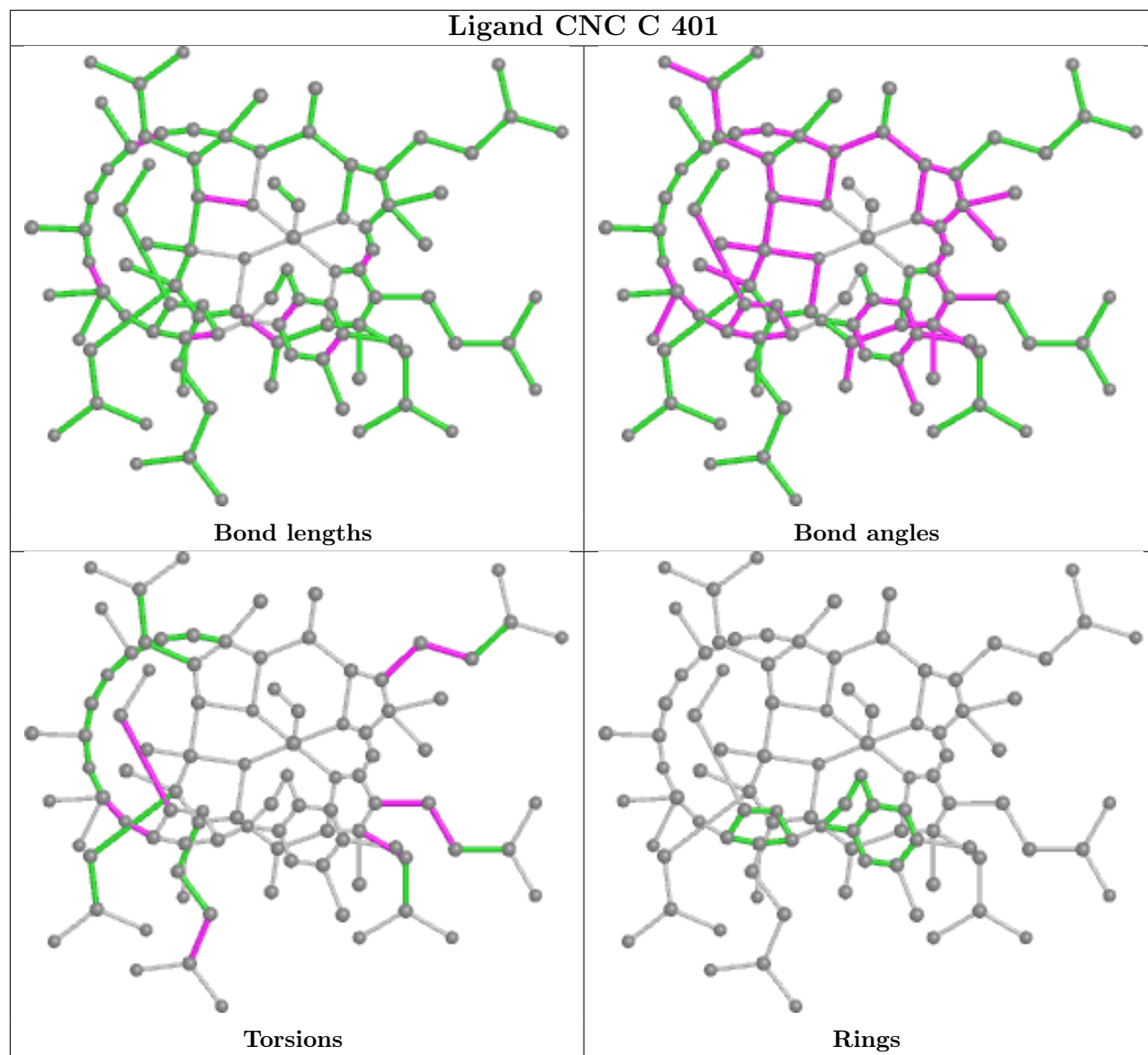
5.7 Other polymers ⓘ

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	A	321/333 (96%)	0.10	1 (0%)	94	93	43, 66, 96, 123	0
1	B	330/333 (99%)	0.21	1 (0%)	94	93	39, 69, 109, 130	0
1	C	327/333 (98%)	0.50	17 (5%)	27	21	34, 75, 118, 146	0
1	D	322/333 (96%)	0.23	4 (1%)	79	76	44, 72, 104, 124	0
All	All	1300/1332 (97%)	0.26	23 (1%)	68	64	34, 70, 109, 146	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	293	VAL	3.7
1	C	294	ARG	3.6
1	C	235	TYR	3.0
1	A	261	ALA	2.9
1	C	29	HIS	2.9

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

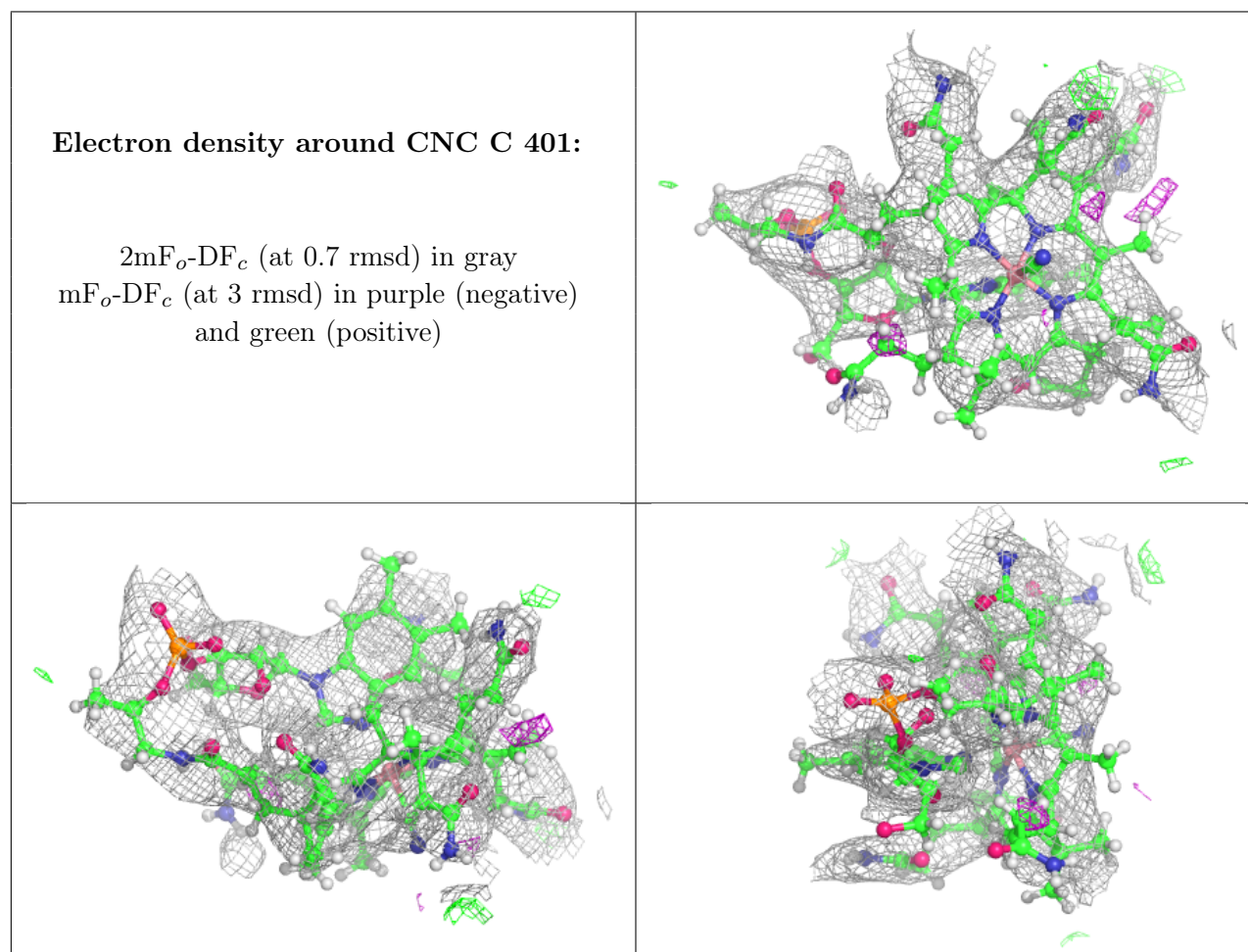There are no non-standard protein/DNA/RNA residues in this entry.

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
2	CNC	C	401	93/93	0.94	0.22	60,87,130,153	0
2	CNC	A	401	93/93	0.96	0.23	34,59,78,107	0
2	CNC	D	401	93/93	0.96	0.23	37,59,87,95	0
2	CNC	B	401	93/93	0.97	0.21	49,77,123,138	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.
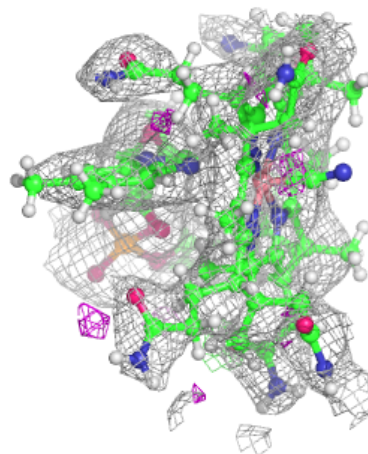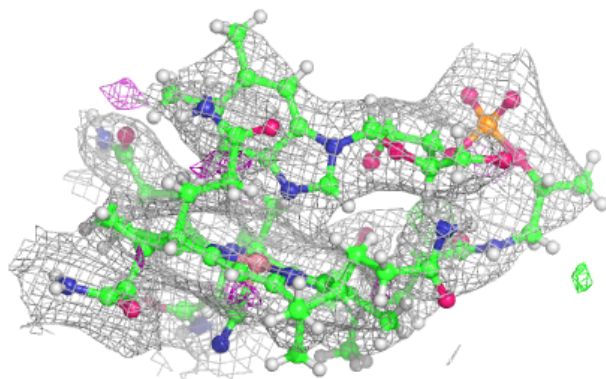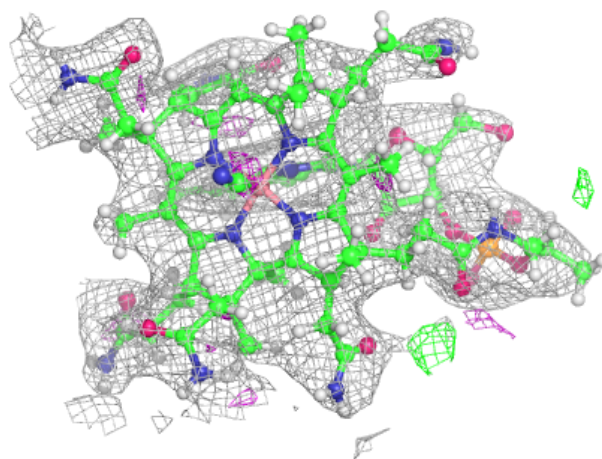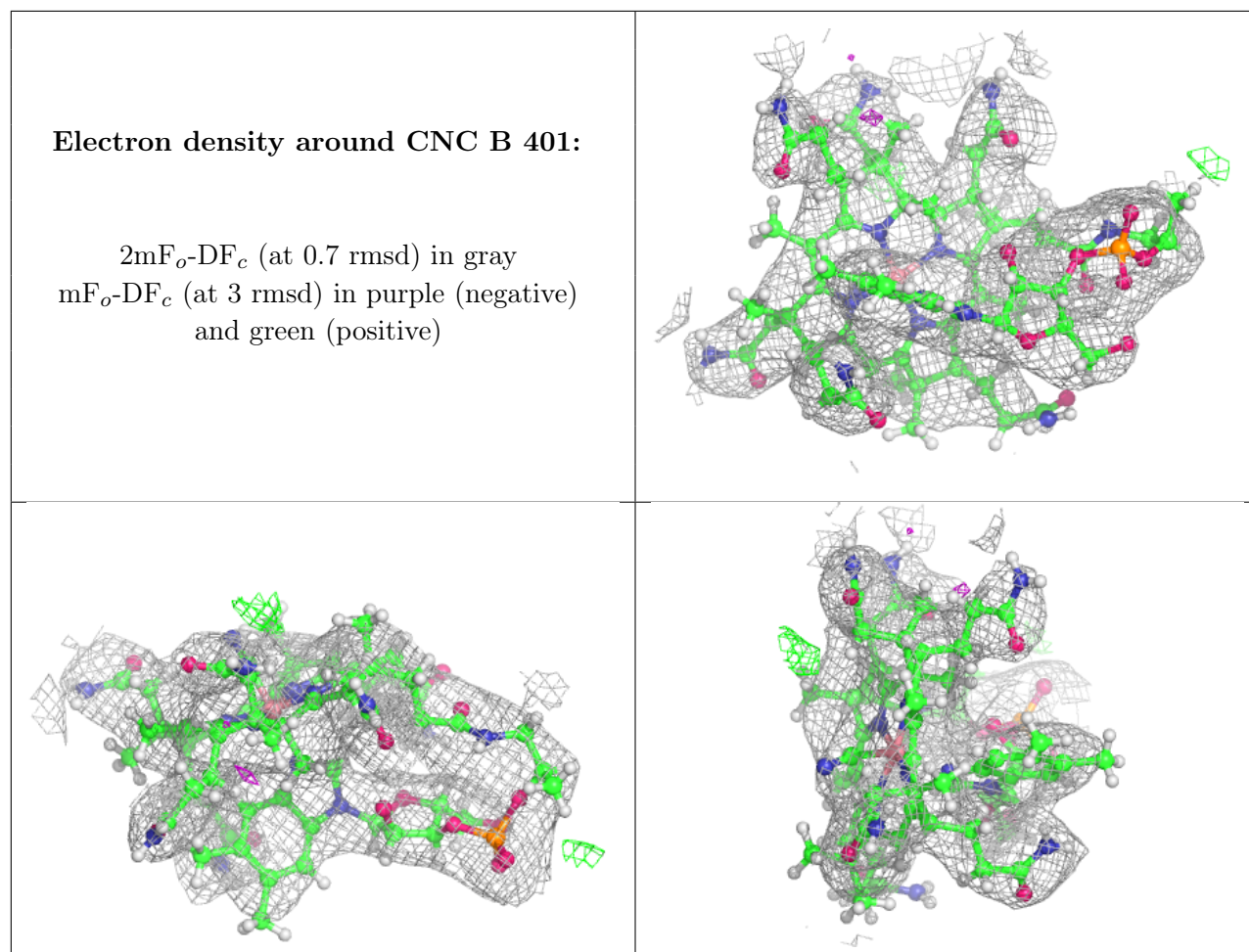

Electron density around CNC C 401:

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

Electron density around CNC A 401:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
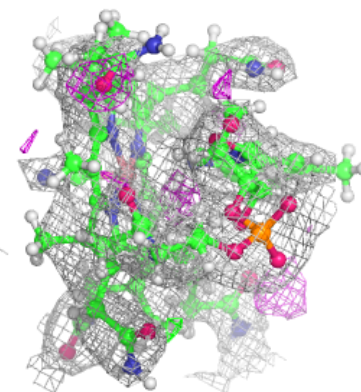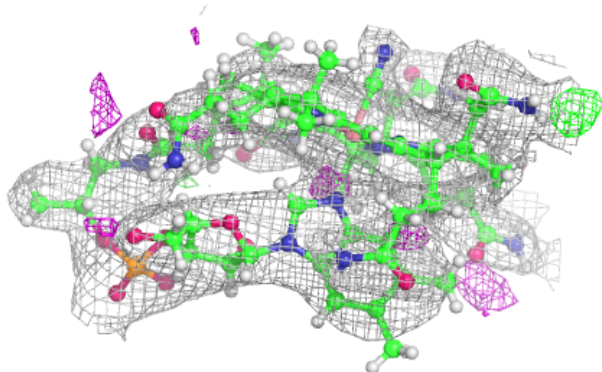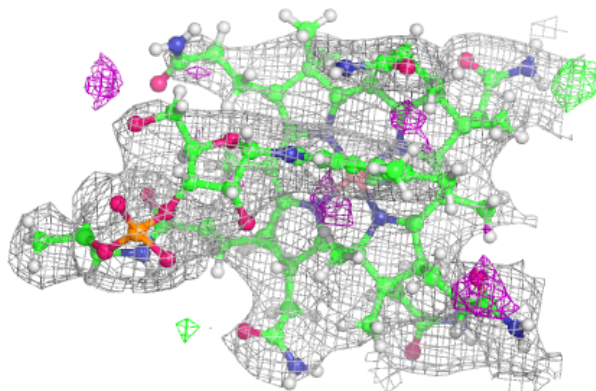
Electron density around CNC D 401:

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

Electron density around CNC B 401:

$2mF_o$-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.