Full wwPDB X-ray Structure Validation Report (i)

Aug 23, 2026 – 03:32 pm BST

PDB ID	:	9S6C / pdb_00009s6c
Title	:	B12 Binding protein - BtuK1
Authors	:	Clarke, C.; Banasik, M.; Pickersgill, R.W.
Deposited on	:	2025-07-31
Resolution	:	1.82 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:

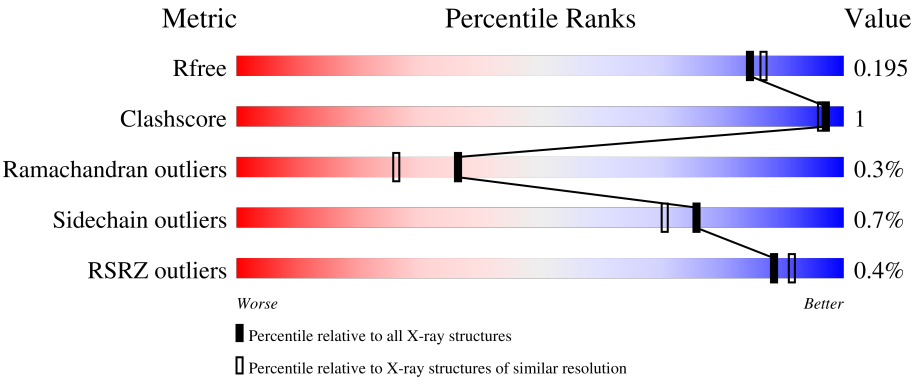
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.82 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}	180053	1112 (1.82-1.82)
Clashscore	190562	1148 (1.82-1.82)
Ramachandran outliers	187476	1140 (1.82-1.82)
Sidechain outliers	187428	1140 (1.82-1.82)
RSRZ outliers	180081	1112 (1.82-1.82)

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	C	337	95%
2	A	339	% 95% 5%
2	B	339	95%

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	CNC	A	401	X	-	-	-
3	CNC	B	401	X	-	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 16442 atoms, of which 7582 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 Quinoprotein amine dehydrogenase-like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	C	337	Total	C	H	N	O	S	0	0	0
			5086	1691	2447	423	515	10			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	15	GLY	-	expression tag	UNP Q8A7N8

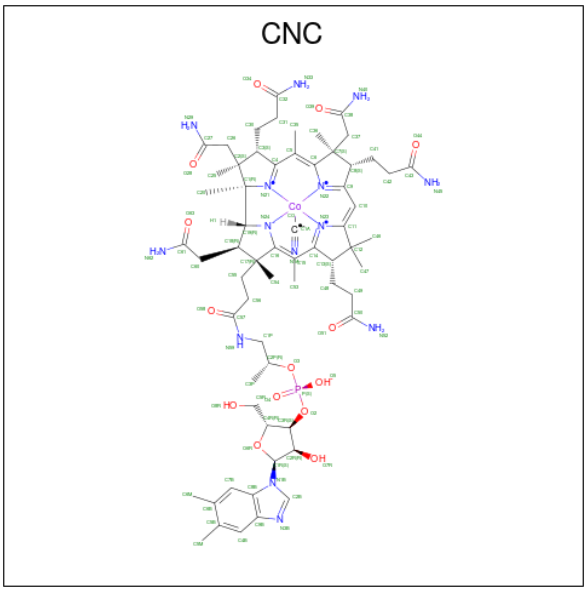
- Molecule 2 is a protein called Quinoprotein amine dehydrogenase-like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	339	Total	C	H	N	O	S	0	0	0
			5119	1702	2462	427	517	11			
2	B	337	Total	C	H	N	O	S	0	0	0
			5094	1694	2451	423	515	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	13	GLY	-	expression tag	UNP Q8A7N8
A	14	HIS	-	expression tag	UNP Q8A7N8
A	15	MET	-	expression tag	UNP Q8A7N8
B	13	GLY	-	expression tag	UNP Q8A7N8
B	14	HIS	-	expression tag	UNP Q8A7N8
B	15	MET	-	expression tag	UNP Q8A7N8

- Molecule 3 is CYANOCOBALAMIN (CCD ID: CNC) (formula: $C_{63}H_{89}CoN_{14}O_{14}P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	C	1	Total	C	Co	H	N	O	P	0	0
			167	63	1	74	14	14	1		
3	A	1	Total	C	Co	H	N	O	P	0	0
			167	63	1	74	14	14	1		
3	B	1	Total	C	Co	H	N	O	P	0	0
			167	63	1	74	14	14	1		

- Molecule 4 is water.

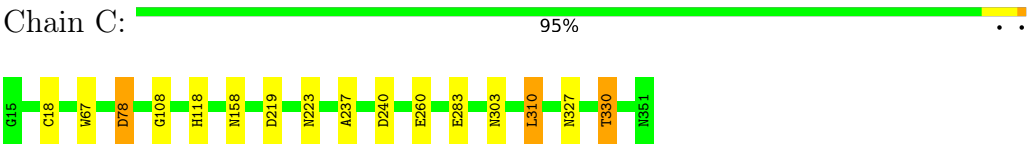
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	192	Total	O	0	0
			192	192		
4	A	253	Total	O	0	0
			253	253		
4	B	197	Total	O	0	0
			197	197		

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.

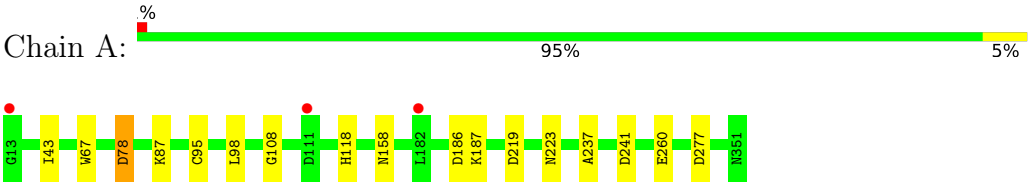
• Molecule 1: Quinoprotein amine dehydrogenase-like protein

Chain C:



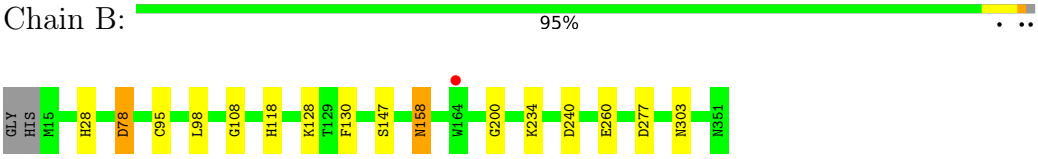
• Molecule 2: Quinoprotein amine dehydrogenase-like protein

Chain A:



• Molecule 2: Quinoprotein amine dehydrogenase-like protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	52.74Å 129.98Å 164.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.29 – 1.82 14.29 – 1.82	Depositor EDS
% Data completeness (in resolution range)	96.3 (14.29-1.82) 96.3 (14.29-1.82)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.27 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0430 (refmacat 0.4.105)	Depositor
R, R_{free}	0.163 , 0.192 0.164 , 0.195	Depositor DCC
R_{free} test set	6550 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å^2)	27.6	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 48.0	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	0.97	EDS
Total number of atoms	16442	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% of the height of the origin peak. No significant pseudotranslation is detected.*

[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	C	0.79	0/2704	1.35	8/3665 (0.2%)
2	A	0.80	0/2723	1.36	9/3690 (0.2%)
2	B	0.79	0/2708	1.34	11/3670 (0.3%)
All	All	0.79	0/8135	1.35	28/11025 (0.3%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	158	ASN	CA-CB-CG	9.30	121.90	112.60
1	C	283	GLU	CB-CG-CD	9.02	127.94	112.60
1	C	158	ASN	CA-CB-CG	8.64	121.25	112.60
2	A	118	HIS	CA-CB-CG	8.15	121.95	113.80
2	B	158	ASN	CA-CB-CG	7.11	119.71	112.60
2	B	28	HIS	CB-CG-CD2	-7.05	122.04	131.20
2	A	277	ASP	CA-CB-CG	7.01	119.61	112.60
1	C	118	HIS	CA-CB-CG	6.74	120.54	113.80
2	A	219	ASP	CA-CB-CG	6.74	119.33	112.60
1	C	260	GLU	CB-CG-CD	6.38	123.44	112.60
1	C	219	ASP	CA-CB-CG	6.22	118.82	112.60
2	B	78	ASP	CB-CA-C	6.09	122.54	110.42
2	A	78	ASP	CB-CA-C	6.04	122.43	110.42
1	C	78	ASP	CB-CA-C	5.86	122.09	110.42
2	B	260	GLU	CB-CG-CD	5.65	122.20	112.60
2	B	118	HIS	CA-CB-CG	5.60	119.40	113.80
2	B	277	ASP	CA-CB-CG	5.47	118.08	112.60
2	B	28	HIS	CB-CG-ND1	5.44	130.87	122.70
2	B	108	GLY	CA-C-O	-5.44	116.68	121.58
2	A	186	ASP	CA-CB-CG	5.42	118.02	112.60
1	C	240	ASP	CA-CB-CG	5.37	117.97	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	241	ASP	CA-CB-CG	5.32	117.92	112.60
1	C	303	ASN	CB-CA-C	5.29	115.20	110.44
2	B	240	ASP	CA-CB-CG	5.24	117.84	112.60
2	B	130	PHE	CA-CB-CG	-5.10	108.70	113.80
2	A	187	LYS	N-CA-CB	5.07	117.42	110.57
2	A	260	GLU	CB-CG-CD	5.05	121.19	112.60
2	B	303	ASN	CB-CA-C	5.04	114.98	110.44

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	C	2639	2447	2528	4	0
2	A	2657	2462	2544	3	0
2	B	2643	2451	2534	3	0
3	A	93	74	87	2	0
3	B	93	74	87	1	0
3	C	93	74	87	1	0
4	A	253	0	0	0	0
4	B	197	0	0	0	0
4	C	192	0	0	0	0
All	All	8860	7582	7867	14	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 (14) 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)
3:C:401:CNC:H351	3:C:401:CNC:H362	1.72	0.71
3:B:401:CNC:H351	3:B:401:CNC:H362	1.73	0.70
3:A:401:CNC:H351	3:A:401:CNC:H362	1.74	0.69
2:B:147:SER:H	2:B:158:ASN:HD22	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:95:CYS:HB3	2:A:98:LEU:HD21	1.89	0.55
2:B:158:ASN:HD21	2:B:200:GLY:HA2	1.75	0.52
2:B:95:CYS:HB3	2:B:98:LEU:HD21	1.98	0.45
3:A:401:CNC:N3B	3:A:401:CNC:H202	2.33	0.42
2:A:67:TRP:CD2	2:A:108:GLY:HA3	2.55	0.42
1:C:18:CYS:SG	1:C:310:LEU:HD22	2.60	0.41
1:C:327:ASN:CG	1:C:330:THR:HG22	2.46	0.41
1:C:223:ASN:HD22	1:C:237:ALA:HA	1.86	0.40
1:C:67:TRP:CD2	1:C:108:GLY:HA3	2.57	0.40
2:A:223:ASN:HD22	2:A:237:ALA:HA	1.85	0.40

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	C	335/337 (99%)	327 (98%)	7 (2%)	1 (0%)	36	26
2	A	337/339 (99%)	328 (97%)	8 (2%)	1 (0%)	36	26
2	B	335/339 (99%)	326 (97%)	8 (2%)	1 (0%)	36	26
All	All	1007/1015 (99%)	981 (97%)	23 (2%)	3 (0%)	36	26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	78	ASP
2	B	78	ASP
1	C	78	ASP

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	C	279/279 (100%)	277 (99%)	2 (1%)	76	70
2	A	281/281 (100%)	279 (99%)	2 (1%)	76	70
2	B	280/281 (100%)	278 (99%)	2 (1%)	76	70
All	All	840/841 (100%)	834 (99%)	6 (1%)	76	70

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	310	LEU
1	C	330	THR
2	A	43	ILE
2	A	87	LYS
2	B	128	LYS
2	B	234	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	102	GLN
1	C	210	ASN
1	C	223	ASN
2	A	102	GLN
2	A	140	ASN
2	A	210	ASN
2	A	222	ASN
2	A	223	ASN
2	B	140	ASN
2	B	158	ASN
2	B	210	ASN
2	B	223	ASN
2	B	228	ASN
2	B	319	GLN
2	B	351	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 oligosaccharides in this entry.

5.6 Ligand geometry

3 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	$\#\|Z\| > 2$
3	CNC	A	401	-	93,103,103	0.85	5 (5%)	148,171,171	1.23	15 (10%)
3	CNC	C	401	-	93,103,103	0.93	6 (6%)	148,171,171	1.38	18 (12%)
3	CNC	B	401	-	93,103,103	0.84	5 (5%)	148,171,171	1.27	17 (11%)

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
3	CNC	A	401	-	1/1/38/38	0/56/235/235	0/3/11/11
3	CNC	C	401	-	-	2/56/235/235	0/3/11/11
3	CNC	B	401	-	1/1/38/38	3/56/235/235	0/3/11/11

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	401	CNC	C14-N23	3.34	1.40	1.30
3	A	401	CNC	C14-N23	3.32	1.40	1.30
3	B	401	CNC	C14-N23	3.27	1.40	1.30
3	C	401	CNC	C1A-N1A	3.27	1.28	1.14
3	A	401	CNC	C1A-N1A	2.77	1.26	1.14
3	C	401	CNC	C6-C5	2.72	1.44	1.36
3	B	401	CNC	C19-N24	-2.44	1.44	1.49
3	B	401	CNC	C35-C5	2.38	1.55	1.50
3	C	401	CNC	C6B-C5B	2.23	1.46	1.40
3	C	401	CNC	C7B-C6B	2.12	1.42	1.39
3	A	401	CNC	C53-C15	2.10	1.55	1.50
3	A	401	CNC	C35-C5	2.09	1.55	1.50
3	B	401	CNC	C7B-C6B	2.09	1.42	1.39
3	C	401	CNC	C53-C15	2.05	1.55	1.50
3	A	401	CNC	C19-N24	-2.03	1.44	1.49
3	B	401	CNC	C53-C15	2.02	1.55	1.50

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	401	CNC	C3-C4-N21	-5.75	104.76	111.97
3	C	401	CNC	C1-N21-C4	4.90	117.12	109.37
3	A	401	CNC	C1-N21-C4	4.64	116.71	109.37
3	C	401	CNC	C2-C3-C4	4.42	106.66	101.63
3	A	401	CNC	C3-C4-N21	-4.12	106.80	111.97
3	C	401	CNC	C1-C2-C3	-3.99	96.51	101.60
3	B	401	CNC	C1-C19-N24	3.90	112.50	106.33
3	B	401	CNC	C3-C4-N21	-3.74	107.28	111.97
3	B	401	CNC	C1-N21-C4	3.59	115.05	109.37
3	A	401	CNC	C1-C19-N24	3.59	112.01	106.33
3	C	401	CNC	C1-C19-N24	3.32	111.59	106.33
3	C	401	CNC	C60-C18-C19	3.15	121.59	114.09
3	A	401	CNC	C2-C3-C4	3.10	105.15	101.63
3	C	401	CNC	C30-C3-C4	3.02	116.66	109.63
3	A	401	CNC	C18-C60-C61	2.86	121.11	113.97
3	B	401	CNC	C55-C17-C18	-2.81	105.72	111.15
3	C	401	CNC	C18-C60-C61	2.77	120.89	113.97
3	B	401	CNC	C2-C3-C4	2.74	104.75	101.63
3	A	401	CNC	C10-C9-N22	2.74	128.87	125.73
3	A	401	CNC	C60-C18-C19	2.66	120.44	114.09
3	A	401	CNC	O58-C57-C56	-2.57	117.31	122.02
3	C	401	CNC	C25-C2-C1	2.51	117.56	113.78
3	B	401	CNC	C30-C3-C4	2.46	115.35	109.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	401	CNC	C41-C8-C7	2.45	120.88	114.14
3	B	401	CNC	O2-P-O4	-2.42	100.40	109.47
3	C	401	CNC	O58-C57-C56	-2.41	117.61	122.02
3	C	401	CNC	C3-C4-C5	2.38	127.81	123.81
3	C	401	CNC	C17-C16-C15	2.33	130.27	126.73
3	A	401	CNC	C9B-N3B-C2B	2.28	107.16	104.44
3	C	401	CNC	C5-C6-N22	-2.26	120.42	123.88
3	B	401	CNC	C1-C2-C3	-2.24	98.73	101.60
3	A	401	CNC	C1-C2-C3	-2.24	98.74	101.60
3	B	401	CNC	C36-C7-C37	2.22	114.47	110.80
3	B	401	CNC	C42-C41-C8	2.22	121.13	114.73
3	A	401	CNC	C17-C16-C15	2.22	130.10	126.73
3	B	401	CNC	O58-C57-C56	-2.20	118.00	122.02
3	C	401	CNC	C9B-N3B-C2B	2.20	107.06	104.44
3	C	401	CNC	C48-C13-C12	2.15	122.64	116.63
3	A	401	CNC	C49-C48-C13	2.14	120.91	114.73
3	A	401	CNC	C8B-C9B-N3B	-2.14	107.61	109.97
3	C	401	CNC	C13-C14-C15	2.12	127.39	123.81
3	B	401	CNC	C18-C60-C61	2.12	119.26	113.97
3	A	401	CNC	C7B-C8B-C9B	-2.11	120.02	122.52
3	B	401	CNC	C2R-C1R-N1B	-2.10	107.99	113.30
3	C	401	CNC	C55-C17-C18	-2.06	107.18	111.15
3	A	401	CNC	C55-C17-C18	-2.04	107.21	111.15
3	B	401	CNC	O7R-C2R-C1R	2.04	116.83	110.02
3	C	401	CNC	C8B-C9B-N3B	-2.03	107.73	109.97
3	B	401	CNC	C5-C4-N21	2.02	127.47	124.19
3	B	401	CNC	C19-N24-C16	2.01	115.22	111.96

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	401	CNC	N24
3	B	401	CNC	N24

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	401	CNC	O6R-C4R-C5R-O8R
3	C	401	CNC	C3R-C4R-C5R-O8R
3	B	401	CNC	C13-C48-C49-C50
3	B	401	CNC	C41-C42-C43-N45
3	B	401	CNC	C41-C42-C43-O44

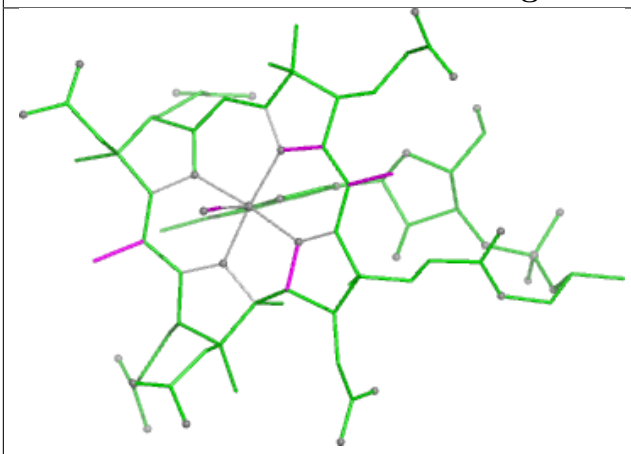
There are no ring outliers.

3 monomers are involved in 4 short contacts:

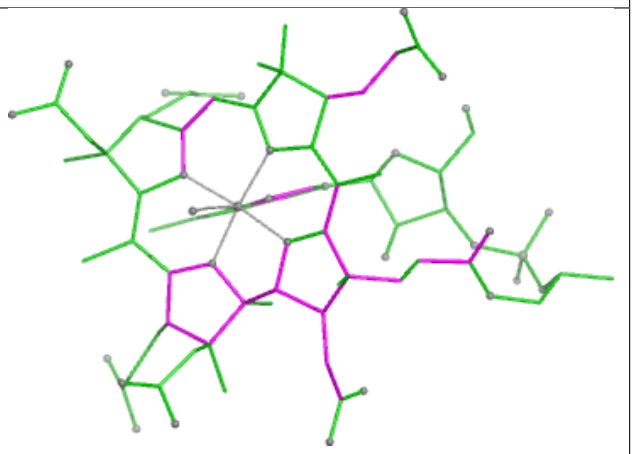
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	CNC	2	0
3	C	401	CNC	1	0
3	B	401	CNC	1	0

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.

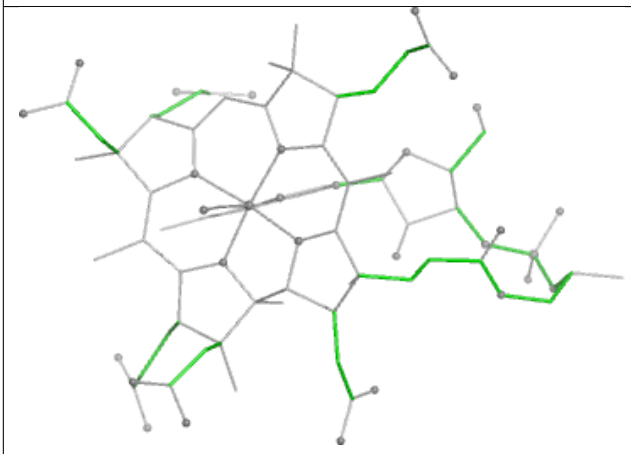
Ligand CNC A 401



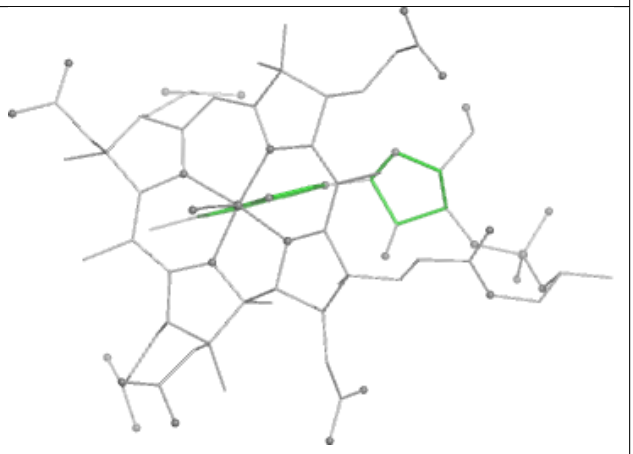
Bond lengths



Bond angles

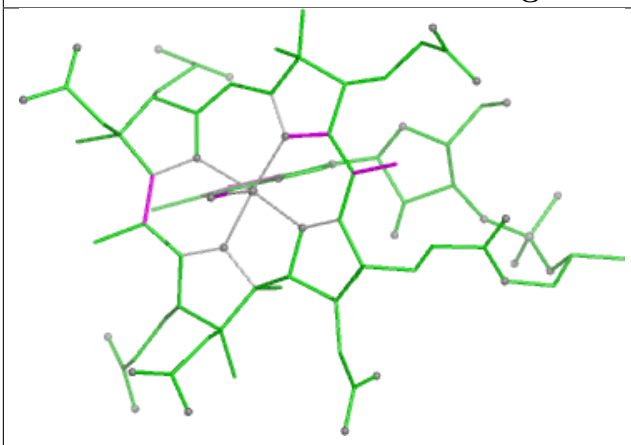


Torsions

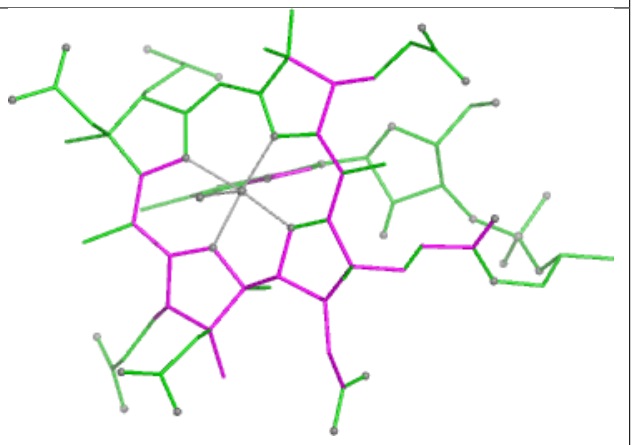


Rings

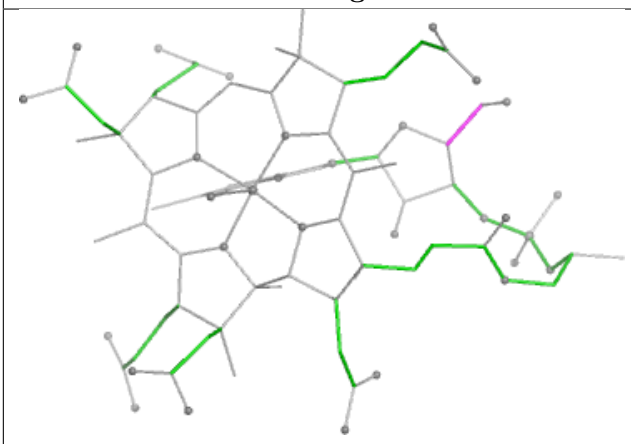
Ligand CNC C 401



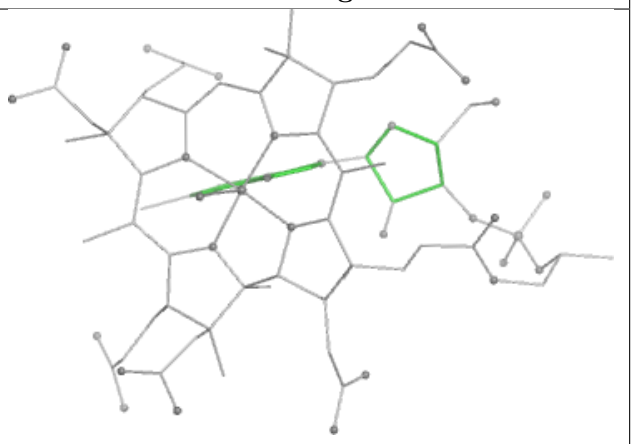
Bond lengths



Bond angles

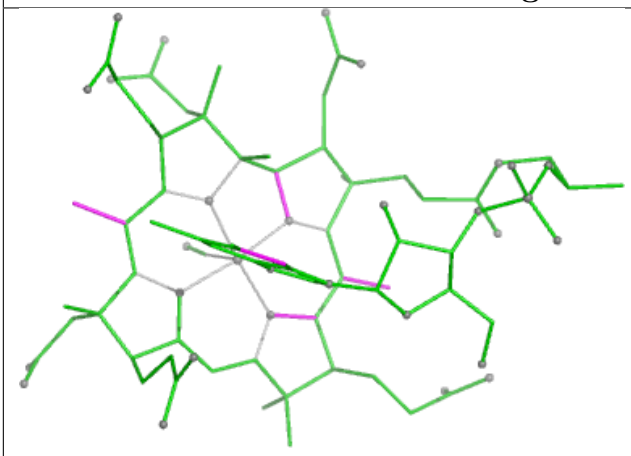


Torsions

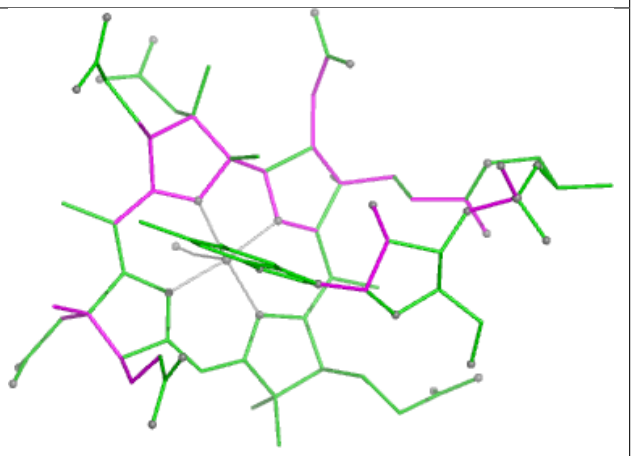


Rings

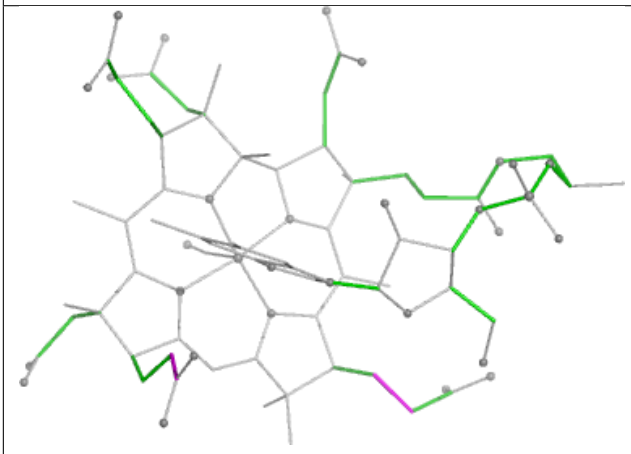
Ligand CNC B 401



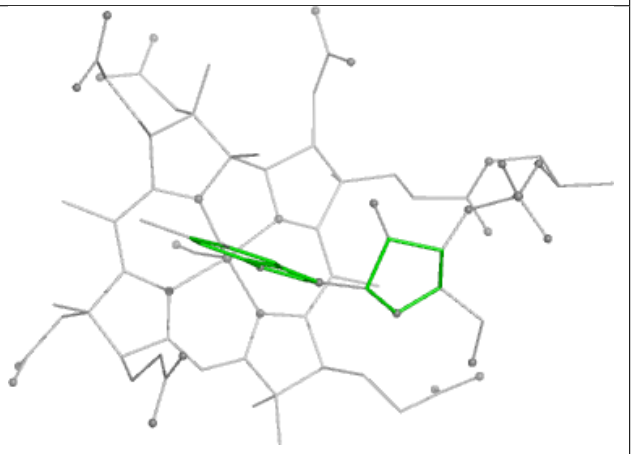
Bond lengths



Bond angles



Torsions



Rings

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

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, 95^{th} 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	C	337/337 (100%)	-0.57	0 100 100	20, 33, 58, 72	0
2	A	339/339 (100%)	-0.66	3 (0%) 81 85	18, 29, 50, 72	0
2	B	337/339 (99%)	-0.56	1 (0%) 90 93	20, 34, 53, 87	0
All	All	1013/1015 (99%)	-0.60	4 (0%) 88 91	18, 32, 54, 87	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	13	GLY	2.3
2	B	164	TRP	2.2
2	A	182	LEU	2.2
2	A	111	ASP	2.1

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 oligosaccharides in this entry.

6.4 Ligands

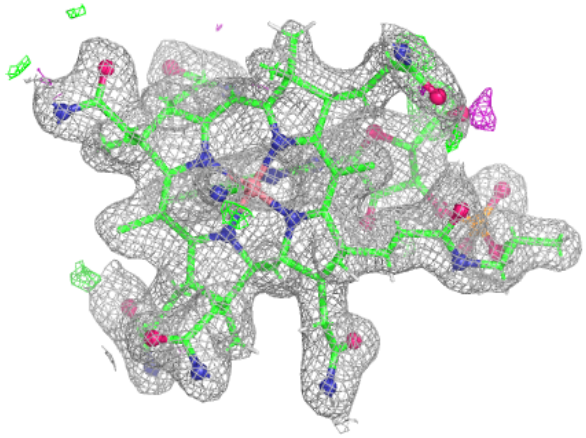
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

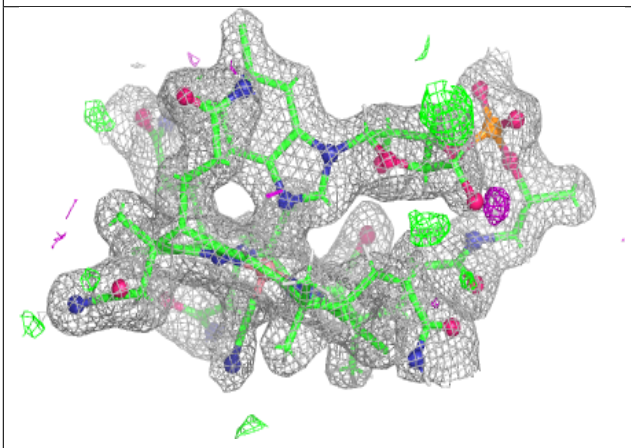
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	CNC	C	401	93/93	0.98	0.06	23,33,48,57	0
3	CNC	A	401	93/93	0.98	0.05	20,27,37,57	0
3	CNC	B	401	93/93	0.98	0.05	22,25,36,46	0

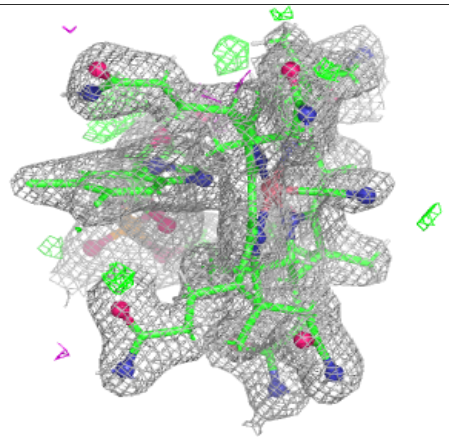
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

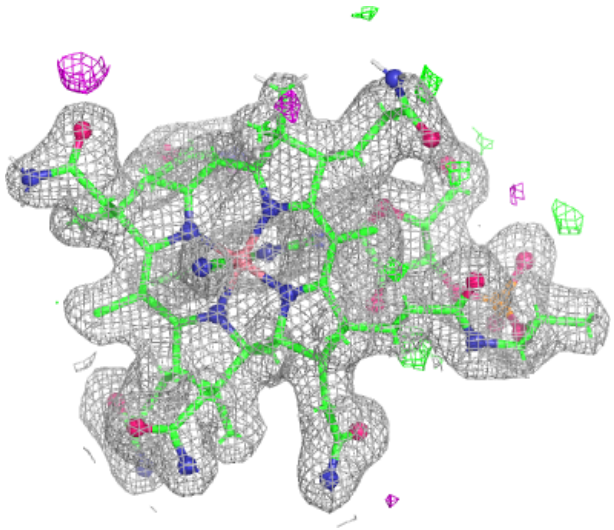


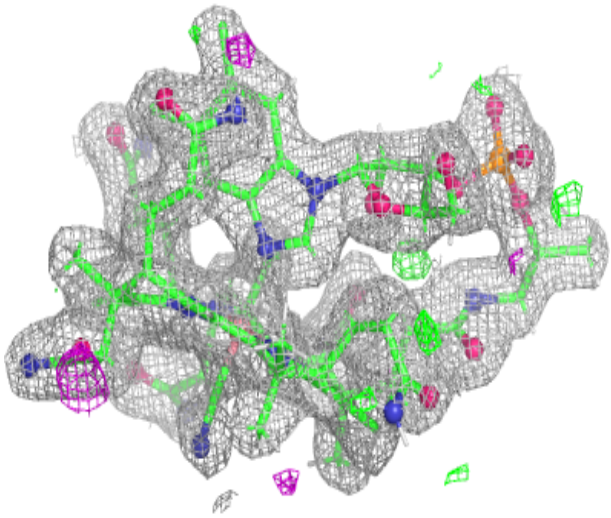


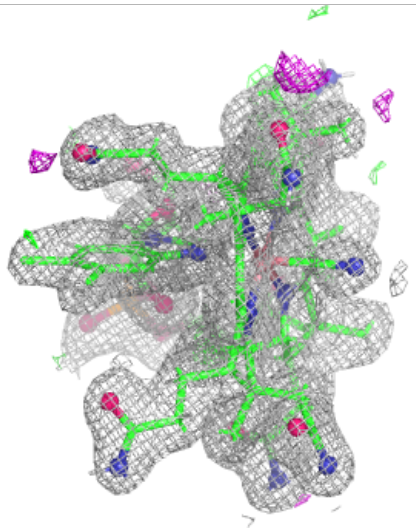


Electron density around CNC A 401:

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

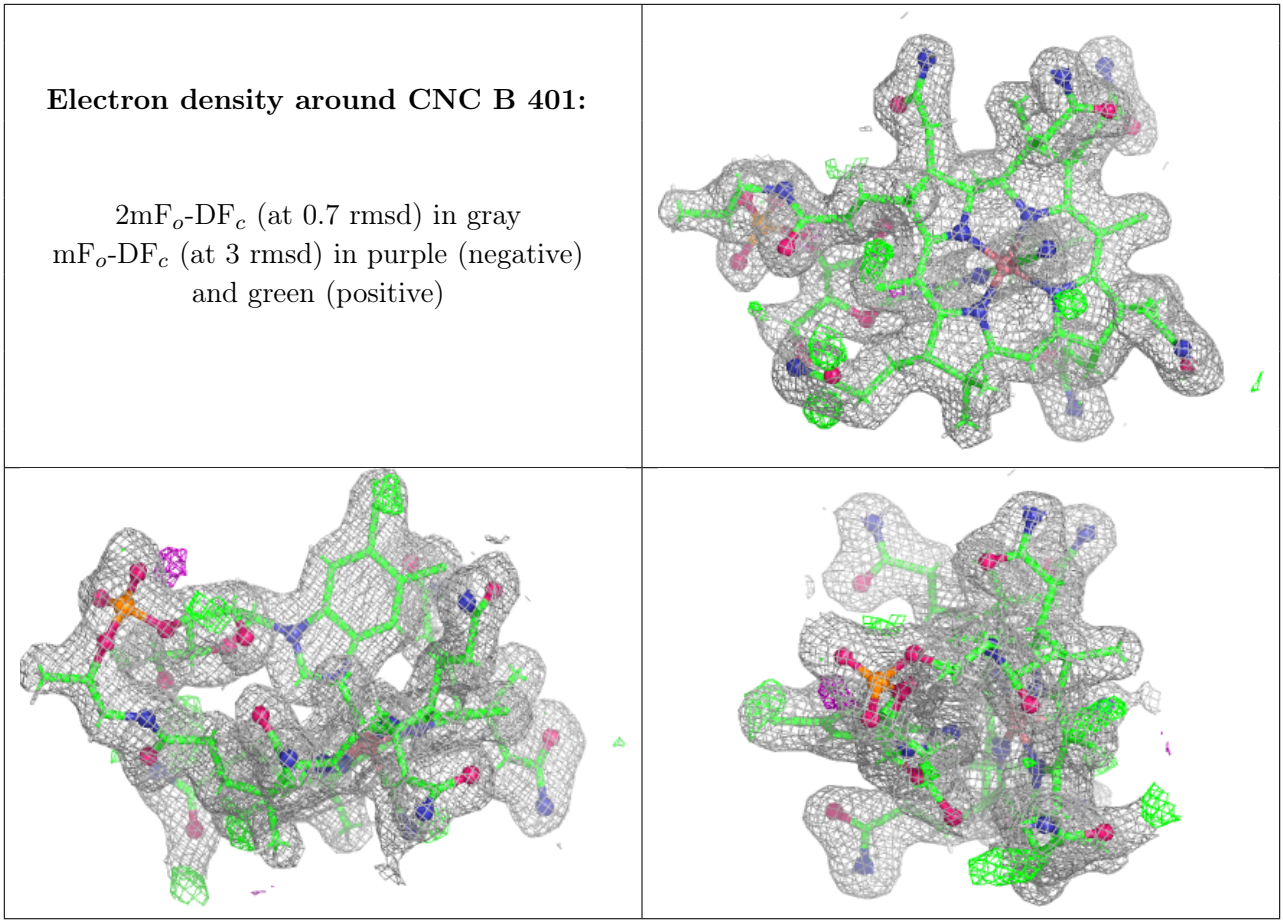






Electron density around CNC B 401:

$2mF_o$-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 (i)

There are no such residues in this entry.