Full wwPDB X-ray Structure Validation Report (i)

Aug 7, 2023 – 06:24 pm BST

PDB ID	:	8AJS
Title	:	Crystal structure of the F324A mutant of S-adenosyl-L-homocysteine hydrolase from Pseudomonas aeruginosa cocrystallized with adenosine in the presence of K+ cations
Authors	:	Drozdzal, P.; Wozniak, K.; Malecki, P.; Gawel, M.; Komorowska, M.; Brzezinski, K.
Deposited on	:	2022-07-28
Resolution	:	1.68 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 (1)) were used in the production of this report:

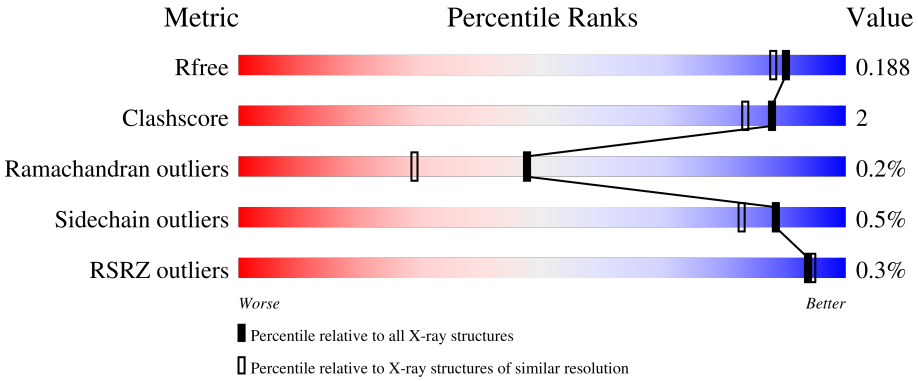
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.34
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.34

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 1.68 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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	472	93%
1	BBB	472	93% 5%
1	CCC	472	93% 5%
1	DDD	472	% 92% 6%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 16251 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.

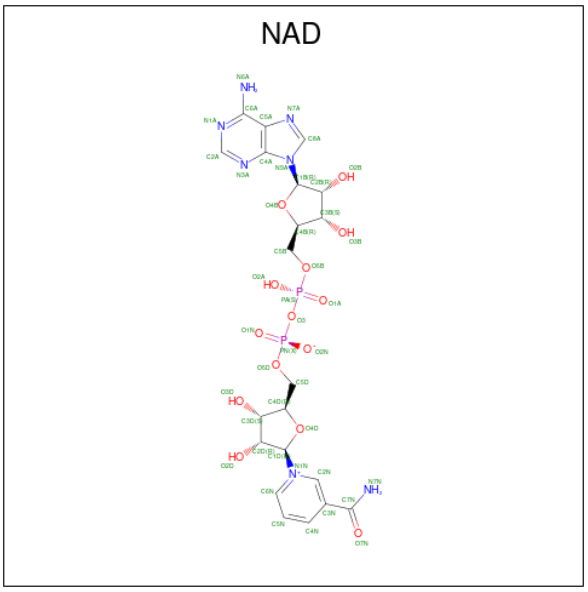
- Molecule 1 is a protein called Adenosylhomocysteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	461	Total	C	N	O	S	1	4	0
			3578	2252	622	681	23			
1	BBB	461	Total	C	N	O	S	9	4	0
			3571	2249	619	681	22			
1	CCC	461	Total	C	N	O	S	5	4	0
			3577	2254	619	682	22			
1	DDD	461	Total	C	N	O	S	24	4	0
			3571	2248	619	681	23			

There are 16 discrepancies between the modelled and reference sequences:

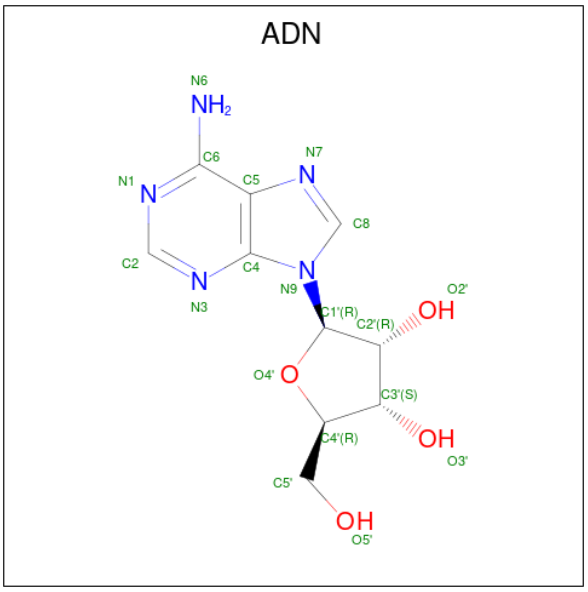
Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-2	SER	-	expression tag	UNP Q9I685
AAA	-1	ASN	-	expression tag	UNP Q9I685
AAA	0	ALA	-	expression tag	UNP Q9I685
AAA	324	ALA	PHE	engineered mutation	UNP Q9I685
BBB	-2	SER	-	expression tag	UNP Q9I685
BBB	-1	ASN	-	expression tag	UNP Q9I685
BBB	0	ALA	-	expression tag	UNP Q9I685
BBB	324	ALA	PHE	engineered mutation	UNP Q9I685
CCC	-2	SER	-	expression tag	UNP Q9I685
CCC	-1	ASN	-	expression tag	UNP Q9I685
CCC	0	ALA	-	expression tag	UNP Q9I685
CCC	324	ALA	PHE	engineered mutation	UNP Q9I685
DDD	-2	SER	-	expression tag	UNP Q9I685
DDD	-1	ASN	-	expression tag	UNP Q9I685
DDD	0	ALA	-	expression tag	UNP Q9I685
DDD	324	ALA	PHE	engineered mutation	UNP Q9I685

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	BBB	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	CCC	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	DDD	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is ADENOSINE (three-letter code: ADN) (formula: $C_{10}H_{13}N_5O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	AAA	1	Total C N O 19 10 5 4	0	0
3	BBB	1	Total C N O 19 10 5 4	0	0
3	CCC	1	Total C N O 19 10 5 4	0	0
3	DDD	1	Total C N O 19 10 5 4	0	0

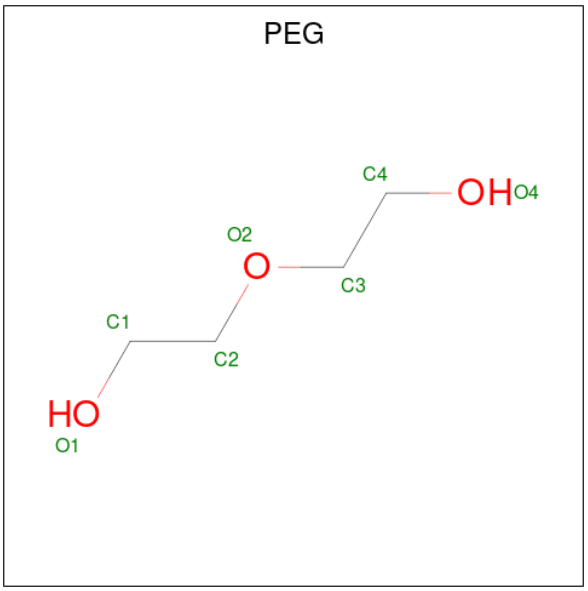
- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	1	Total K 1 1	0	0
4	BBB	1	Total K 1 1	0	0
4	CCC	1	Total K 1 1	0	0
4	DDD	1	Total K 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	BBB	1	Total Cl 1 1	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	CCC	1	Total C O 7 4 3	0	0

- Molecule 7 is water.

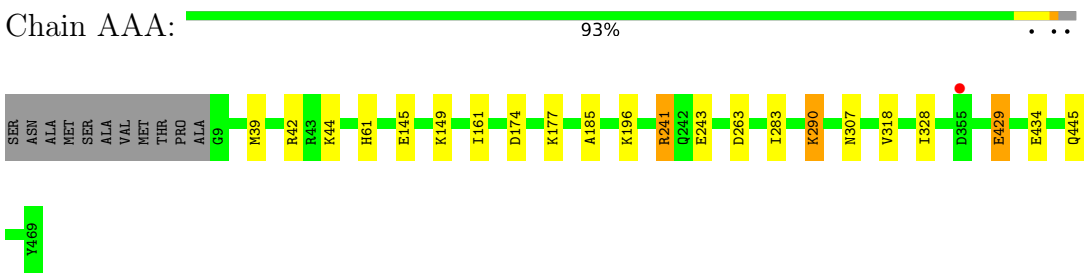
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	AAA	435	Total O 435 435	0	0
7	BBB	405	Total O 406 406	1	1
7	CCC	477	Total O 477 477	0	0
7	DDD	372	Total O 372 372	0	0

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.

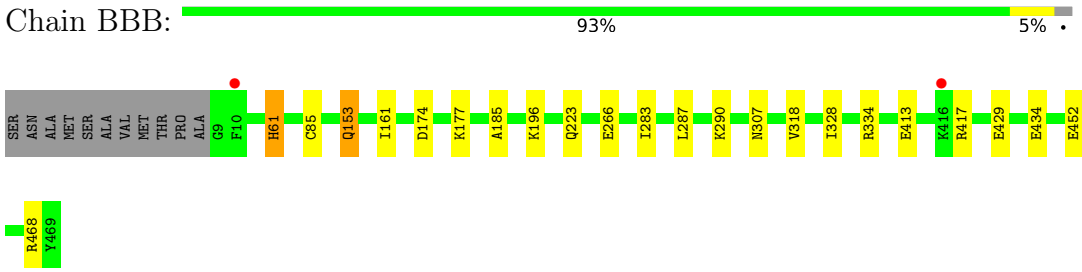
• Molecule 1: Adenosylhomocysteinase

Chain AAA:



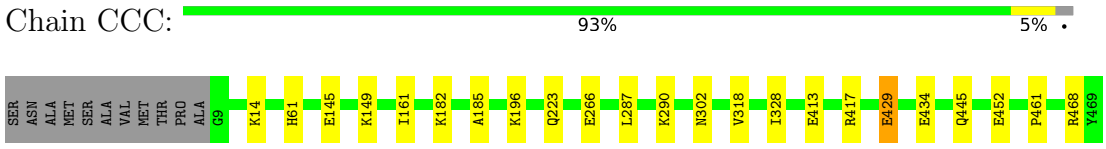
• Molecule 1: Adenosylhomocysteinase

Chain BBB:



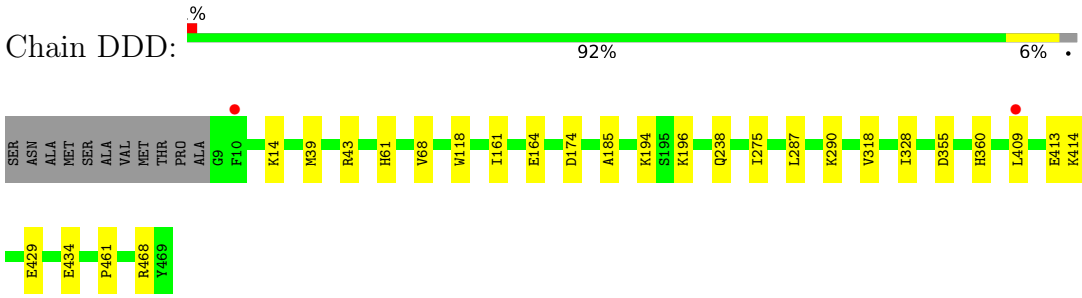
• Molecule 1: Adenosylhomocysteinase

Chain CCC:



• Molecule 1: Adenosylhomocysteinase

Chain DDD:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	177.84Å 134.96Å 109.39Å 90.00° 106.04° 90.00°	Depositor
Resolution (Å)	105.92 – 1.68 105.92 – 1.68	Depositor EDS
% Data completeness (in resolution range)	99.7 (105.92-1.68) 99.7 (105.92-1.68)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 1.68Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.151 , 0.178 0.163 , 0.188	Depositor DCC
R_{free} test set	1039 reflections (0.37%)	wwPDB-VP
Wilson B-factor (Å^2)	35.4	Xtriage
Anisotropy	0.075	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 48.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -1/2*h+1/2*k+l,1/2*h-1/2*k+l,1/2*h+1/2*k 0.000 for -1/2*h-1/2*k+l,-1/2*h-1/2*k-l,1/2*h-1/2*k	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	16251	wwPDB-VP
Average B, all atoms (Å^2)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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: NAD, PEG, ADN, K, CL

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	0.82	4/3643 (0.1%)	0.72	2/4924 (0.0%)
1	BBB	0.80	4/3642 (0.1%)	0.72	1/4924 (0.0%)
1	CCC	0.82	3/3646 (0.1%)	0.73	1/4930 (0.0%)
1	DDD	0.80	2/3636 (0.1%)	0.72	0/4915
All	All	0.81	13/14567 (0.1%)	0.72	4/19693 (0.0%)

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	DDD	0	1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AAA	434	GLU	CD-OE2	8.55	1.35	1.25
1	BBB	434	GLU	CD-OE2	8.17	1.34	1.25
1	AAA	429	GLU	CD-OE1	6.44	1.32	1.25
1	AAA	243	GLU	CD-OE1	6.43	1.32	1.25
1	BBB	452	GLU	CG-CD	6.22	1.61	1.51
1	BBB	266	GLU	CD-OE1	6.17	1.32	1.25
1	DDD	413	GLU	CB-CG	-5.95	1.40	1.52
1	CCC	434	GLU	CD-OE2	5.72	1.31	1.25
1	AAA	44	LYS	CE-NZ	5.67	1.63	1.49
1	BBB	452	GLU	CD-OE1	5.11	1.31	1.25
1	DDD	434	GLU	CD-OE2	5.11	1.31	1.25
1	CCC	266	GLU	CD-OE2	-5.04	1.20	1.25
1	CCC	429	GLU	CD-OE1	5.03	1.31	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	CCC	182	LYS	CD-CE-NZ	-7.41	94.67	111.70
1	AAA	241[A]	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	AAA	241[B]	ARG	NE-CZ-NH1	-5.08	117.76	120.30
1	BBB	153	GLN	CA-CB-CG	-5.02	102.35	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	DDD	355	ASP	Mainchain

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	3578	0	3587	11	0
1	BBB	3571	0	3583	14	0
1	CCC	3577	0	3583	15	0
1	DDD	3571	0	3577	18	0
2	AAA	44	0	26	1	0
2	BBB	44	0	26	1	0
2	CCC	44	0	26	1	0
2	DDD	44	0	26	1	0
3	AAA	19	0	13	1	0
3	BBB	19	0	13	1	0
3	CCC	19	0	13	1	0
3	DDD	19	0	13	1	0
4	AAA	1	0	0	0	0
4	BBB	1	0	0	0	0
4	CCC	1	0	0	0	0
4	DDD	1	0	0	0	0
5	BBB	1	0	0	0	0
6	CCC	7	0	10	0	0
7	AAA	435	0	0	1	0
7	BBB	406	0	0	1	0
7	CCC	477	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	DDD	372	0	0	6	0
All	All	16251	0	14496	58	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 2.

All (58) 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:CCC:145:GLU:OE1	1:CCC:149:LYS:HE2	1.35	1.25
1:BBB:413:GLU:OE2	1:BBB:417:ARG:NH1	2.04	0.91
1:CCC:413:GLU:OE1	1:CCC:417:ARG:NH2	2.07	0.87
1:DDD:238:GLN:HG2	7:DDD:911:HOH:O	1.74	0.86
1:AAA:241[A]:ARG:NH1	1:AAA:263:ASP:O	2.10	0.80
2:CCC:501:NAD:C4N	3:CCC:502:ADN:H3'	2.19	0.72
2:AAA:501:NAD:C4N	3:AAA:502:ADN:H3'	2.20	0.71
1:BBB:287:LEU:HD12	7:BBB:747:HOH:O	1.92	0.69
2:DDD:501:NAD:C4N	3:DDD:502:ADN:H3'	2.23	0.68
1:DDD:287:LEU:HD12	7:DDD:849:HOH:O	1.96	0.66
1:CCC:318:VAL:HG12	1:CCC:328:ILE:HD13	1.79	0.65
1:CCC:223[B]:GLN:HE22	1:CCC:290:LYS:NZ	1.95	0.64
1:CCC:287:LEU:HD12	7:CCC:858:HOH:O	1.98	0.63
1:AAA:445:GLN:HG3	1:DDD:275:ILE:CD1	2.30	0.62
1:AAA:318:VAL:HG12	1:AAA:328:ILE:HD13	1.81	0.61
1:BBB:223[B]:GLN:HE22	1:BBB:290:LYS:HE2	1.65	0.61
1:BBB:318:VAL:HG12	1:BBB:328:ILE:HD13	1.81	0.61
1:CCC:14:LYS:NZ	7:CCC:601:HOH:O	2.33	0.60
1:DDD:43:ARG:HD3	7:DDD:601:HOH:O	2.04	0.58
1:AAA:145:GLU:OE1	1:AAA:149:LYS:HE2	2.04	0.57
1:DDD:318:VAL:HG12	1:DDD:328:ILE:HD13	1.85	0.57
1:BBB:223[B]:GLN:HE22	1:BBB:290:LYS:CE	2.18	0.56
1:AAA:290:LYS:HD2	7:AAA:913:HOH:O	2.05	0.55
1:CCC:145:GLU:OE1	1:CCC:149:LYS:CE	2.30	0.55
1:CCC:445:GLN:HG3	7:CCC:706:HOH:O	2.07	0.54
1:BBB:174:ASP:OD1	1:BBB:177:LYS:HE3	2.07	0.54
1:AAA:174:ASP:OD1	1:AAA:177:LYS:HE3	2.09	0.53
1:CCC:223[B]:GLN:HE22	1:CCC:290:LYS:CE	2.21	0.53
1:BBB:223[B]:GLN:NE2	1:BBB:290:LYS:HE2	2.23	0.52
2:BBB:501:NAD:C4N	3:BBB:502:ADN:H3'	2.39	0.52
1:BBB:223[B]:GLN:HE22	1:BBB:290:LYS:NZ	2.07	0.52
1:AAA:196:LYS:HE3	1:DDD:468:ARG:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CCC:223[B]:GLN:HE22	1:CCC:290:LYS:HE2	1.75	0.50
1:BBB:196:LYS:HE3	1:CCC:468:ARG:HB2	1.94	0.48
1:BBB:468:ARG:HB2	1:CCC:196:LYS:HE3	1.94	0.48
1:DDD:14:LYS:HD3	1:DDD:118:TRP:CH2	2.49	0.48
1:BBB:429:GLU:OE1	1:BBB:461:PRO:HA	2.13	0.48
1:DDD:360:HIS:HE1	7:DDD:890:HOH:O	1.98	0.46
1:CCC:445:GLN:CG	7:CCC:706:HOH:O	2.63	0.46
1:AAA:161:ILE:O	1:AAA:185:ALA:HA	2.16	0.46
1:DDD:161:ILE:O	1:DDD:185:ALA:HA	2.16	0.46
1:DDD:429:GLU:OE1	1:DDD:461:PRO:HA	2.16	0.46
1:AAA:429:GLU:OE1	1:AAA:461:PRO:HA	2.17	0.45
1:DDD:409:LEU:O	1:DDD:414:LYS:HE2	2.15	0.45
1:BBB:161:ILE:O	1:BBB:185:ALA:HA	2.17	0.45
1:CCC:161:ILE:O	1:CCC:185:ALA:HA	2.17	0.44
1:CCC:429:GLU:OE1	1:CCC:461:PRO:HA	2.17	0.44
1:DDD:360:HIS:CE1	7:DDD:890:HOH:O	2.69	0.43
1:DDD:409:LEU:CD1	1:DDD:417:ARG:HD2	2.49	0.42
1:DDD:196:LYS:HD3	7:DDD:737:HOH:O	2.19	0.42
1:AAA:283:ILE:HG13	1:AAA:307:ASN:HB3	2.02	0.42
1:DDD:318:VAL:HG12	1:DDD:328:ILE:CD1	2.51	0.41
1:AAA:39[A]:MET:HE1	1:AAA:42:ARG:NH2	2.36	0.41
1:BBB:61:HIS:CE1	1:BBB:85:CYS:SG	3.14	0.41
1:DDD:39[A]:MET:HE1	1:DDD:68:VAL:CG1	2.50	0.40
1:BBB:283:ILE:HG13	1:BBB:307:ASN:HB3	2.02	0.40
1:DDD:39[A]:MET:HE1	1:DDD:68:VAL:HG13	2.03	0.40
1:DDD:164:GLU:O	1:DDD:194:LYS:HE3	2.21	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	AAA	463/472 (98%)	450 (97%)	12 (3%)	1 (0%)	47 29
1	BBB	463/472 (98%)	451 (97%)	11 (2%)	1 (0%)	47 29
1	CCC	463/472 (98%)	450 (97%)	12 (3%)	1 (0%)	47 29
1	DDD	463/472 (98%)	450 (97%)	12 (3%)	1 (0%)	47 29
All	All	1852/1888 (98%)	1801 (97%)	47 (2%)	4 (0%)	47 29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	AAA	61	HIS
1	CCC	61	HIS
1	BBB	61	HIS
1	DDD	61	HIS

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	AAA	380/384 (99%)	379 (100%)	1 (0%)	92 89
1	BBB	380/384 (99%)	378 (100%)	2 (0%)	88 83
1	CCC	380/384 (99%)	378 (100%)	2 (0%)	88 83
1	DDD	379/384 (99%)	377 (100%)	2 (0%)	88 83
All	All	1519/1536 (99%)	1512 (100%)	7 (0%)	88 83

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	290	LYS
1	BBB	153	GLN
1	BBB	334	ARG
1	CCC	302	ASN
1	CCC	452	GLU
1	DDD	174	ASP
1	DDD	290	LYS

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 14 ligands modelled in this entry, 5 are monoatomic - leaving 9 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	$\#\|Z\| > 2$
3	ADN	BBB	502	-	18,21,21	0.60	0	18,31,31	0.91	1 (5%)
3	ADN	CCC	502	-	18,21,21	0.57	0	18,31,31	0.94	1 (5%)
2	NAD	AAA	501	-	42,48,48	0.76	1 (2%)	50,73,73	0.76	2 (4%)
3	ADN	DDD	502	-	18,21,21	0.59	0	18,31,31	0.89	0
2	NAD	DDD	501	-	42,48,48	0.88	2 (4%)	50,73,73	0.92	5 (10%)
2	NAD	CCC	501	-	42,48,48	0.85	1 (2%)	50,73,73	0.79	1 (2%)
3	ADN	AAA	502	-	18,21,21	0.48	0	18,31,31	1.03	1 (5%)
6	PEG	CCC	503	-	6,6,6	0.21	0	5,5,5	0.13	0
2	NAD	BBB	501	-	42,48,48	0.92	2 (4%)	50,73,73	0.96	5 (10%)

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	ADN	BBB	502	-	-	2/2/22/22	0/3/3/3
3	ADN	CCC	502	-	-	0/2/22/22	0/3/3/3
2	NAD	AAA	501	-	-	5/26/62/62	0/5/5/5
3	ADN	DDD	502	-	-	1/2/22/22	0/3/3/3
2	NAD	DDD	501	-	-	5/26/62/62	0/5/5/5
2	NAD	CCC	501	-	-	5/26/62/62	0/5/5/5
3	ADN	AAA	502	-	-	0/2/22/22	0/3/3/3
6	PEG	CCC	503	-	-	2/4/4/4	-
2	NAD	BBB	501	-	-	5/26/62/62	0/5/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	DDD	501	NAD	C2N-N1N	3.34	1.39	1.35
2	BBB	501	NAD	O4D-C1D	3.04	1.45	1.41
2	AAA	501	NAD	C2N-N1N	2.93	1.38	1.35
2	CCC	501	NAD	C2N-N1N	2.82	1.38	1.35
2	BBB	501	NAD	C2N-N1N	2.73	1.38	1.35
2	DDD	501	NAD	C8A-N7A	-2.01	1.31	1.34

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	BBB	501	NAD	C6N-N1N-C2N	-3.18	119.08	121.97
3	AAA	502	ADN	C5-C6-N6	2.70	124.46	120.35
2	DDD	501	NAD	C5A-C6A-N6A	2.49	124.14	120.35
2	AAA	501	NAD	C6N-N1N-C2N	-2.48	119.72	121.97
3	BBB	502	ADN	C5-C6-N6	2.47	124.10	120.35
2	CCC	501	NAD	O2N-PN-O1N	2.41	124.14	112.24
2	BBB	501	NAD	O2A-PA-O1A	2.31	123.66	112.24
2	DDD	501	NAD	PN-O3-PA	-2.30	124.93	132.83
3	CCC	502	ADN	C5-C6-N6	2.25	123.77	120.35
2	BBB	501	NAD	O4D-C1D-C2D	-2.15	103.78	106.93
2	AAA	501	NAD	C5A-C6A-N6A	2.12	123.58	120.35
2	DDD	501	NAD	O4B-C1B-C2B	-2.12	103.83	106.93
2	DDD	501	NAD	O2N-PN-O1N	2.10	122.64	112.24
2	DDD	501	NAD	C6N-N1N-C2N	-2.07	120.08	121.97
2	BBB	501	NAD	O4B-C1B-C2B	-2.06	103.92	106.93
2	BBB	501	NAD	PN-O3-PA	-2.01	125.92	132.83

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	501	NAD	O4D-C1D-N1N-C2N
2	AAA	501	NAD	O4D-C1D-N1N-C6N
2	AAA	501	NAD	C2D-C1D-N1N-C2N
2	AAA	501	NAD	C2D-C1D-N1N-C6N
2	BBB	501	NAD	O4D-C1D-N1N-C2N
2	BBB	501	NAD	O4D-C1D-N1N-C6N
2	BBB	501	NAD	C2D-C1D-N1N-C2N
2	BBB	501	NAD	C2D-C1D-N1N-C6N
2	CCC	501	NAD	O4D-C1D-N1N-C2N
2	CCC	501	NAD	O4D-C1D-N1N-C6N
2	CCC	501	NAD	C2D-C1D-N1N-C2N
2	CCC	501	NAD	C2D-C1D-N1N-C6N
2	DDD	501	NAD	O4D-C1D-N1N-C2N
2	DDD	501	NAD	O4D-C1D-N1N-C6N
2	DDD	501	NAD	C2D-C1D-N1N-C2N
2	DDD	501	NAD	C2D-C1D-N1N-C6N
3	BBB	502	ADN	C3'-C4'-C5'-O5'
6	CCC	503	PEG	O1-C1-C2-O2
3	BBB	502	ADN	O4'-C4'-C5'-O5'
6	CCC	503	PEG	O2-C3-C4-O4
3	DDD	502	ADN	C3'-C4'-C5'-O5'
2	AAA	501	NAD	O4B-C4B-C5B-O5B
2	BBB	501	NAD	O4B-C4B-C5B-O5B
2	CCC	501	NAD	O4B-C4B-C5B-O5B
2	DDD	501	NAD	O4B-C4B-C5B-O5B

There are no ring outliers.

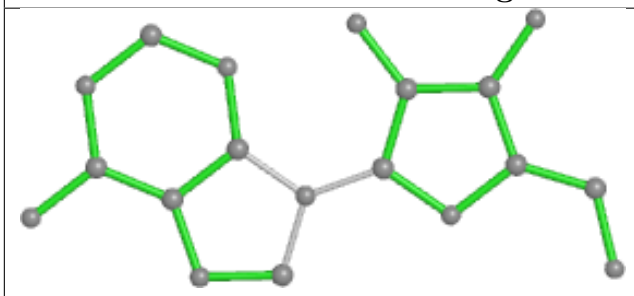
8 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	BBB	502	ADN	1	0
3	CCC	502	ADN	1	0
2	AAA	501	NAD	1	0
3	DDD	502	ADN	1	0
2	DDD	501	NAD	1	0
2	CCC	501	NAD	1	0
3	AAA	502	ADN	1	0
2	BBB	501	NAD	1	0

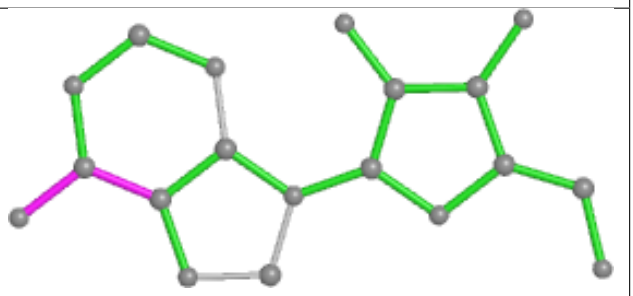
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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.

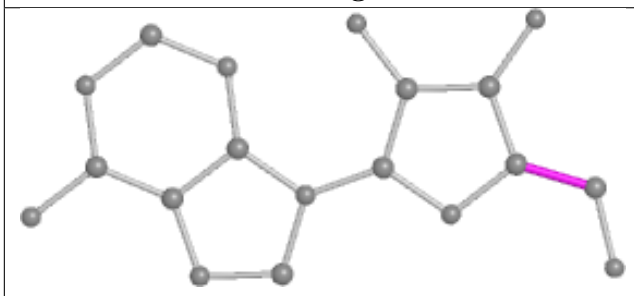
Ligand ADN BBB 502



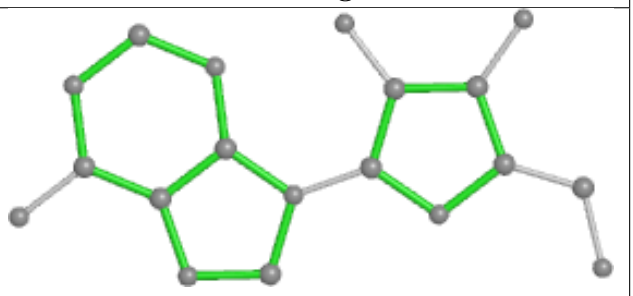
Bond lengths



Bond angles

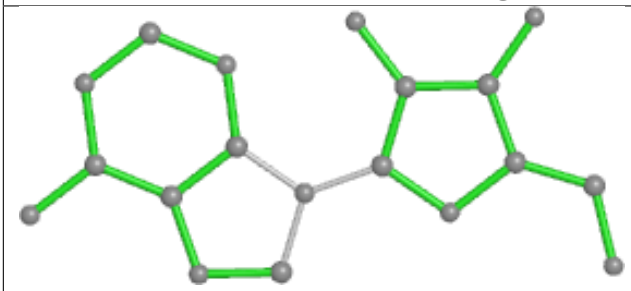


Torsions

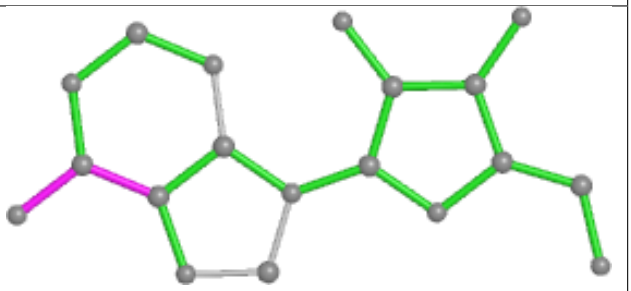


Rings

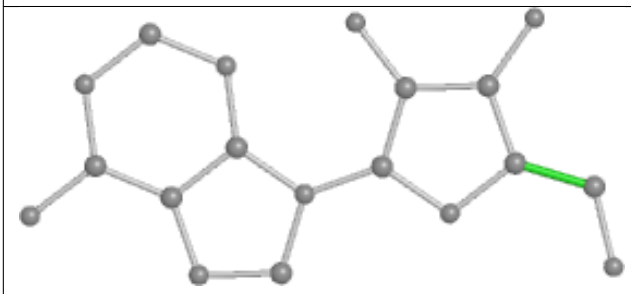
Ligand ADN CCC 502



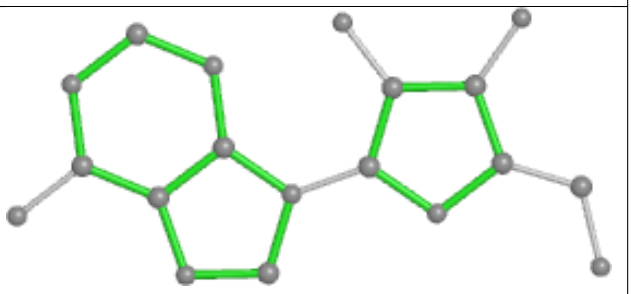
Bond lengths



Bond angles

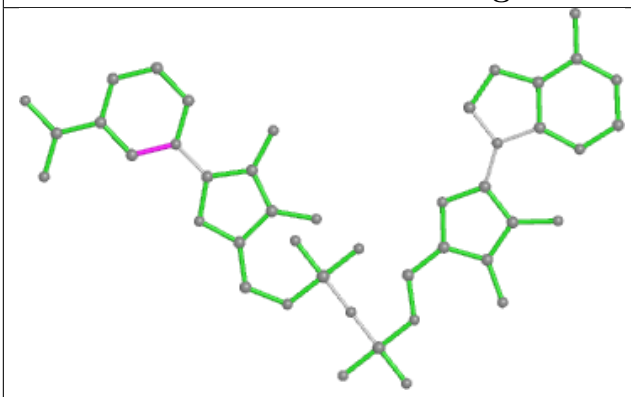


Torsions

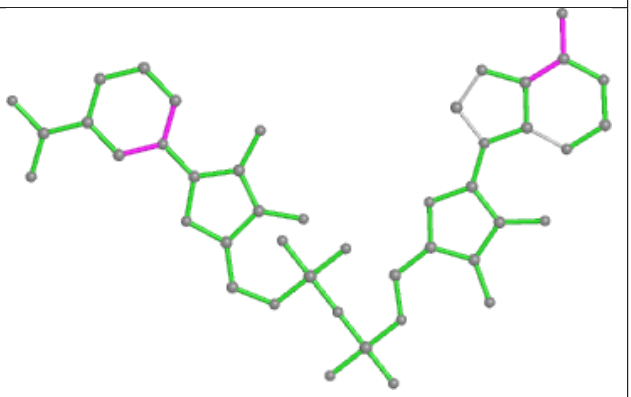


Rings

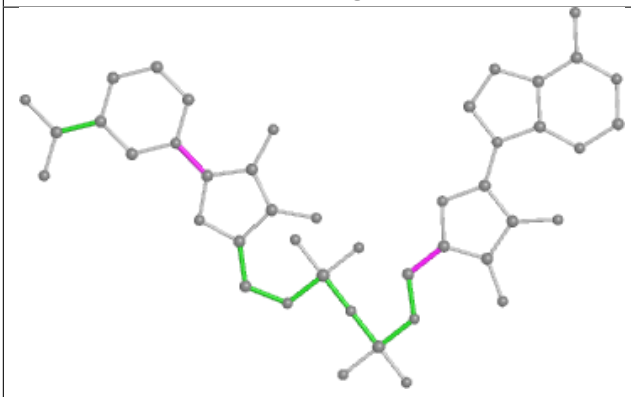
Ligand NAD AAA 501



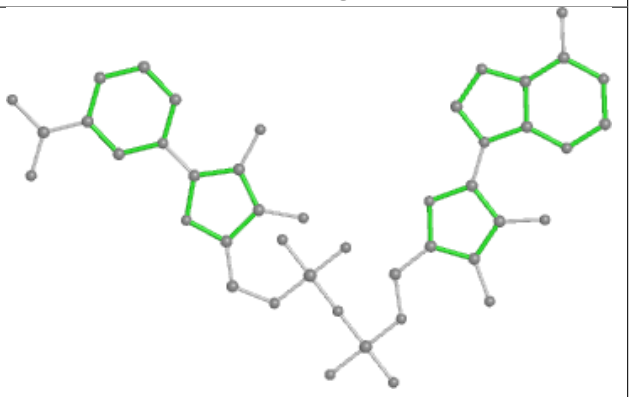
Bond lengths



Bond angles

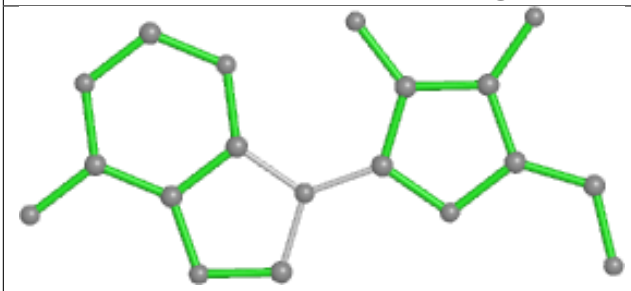


Torsions

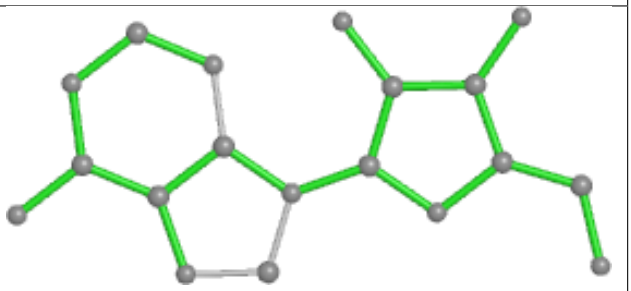


Rings

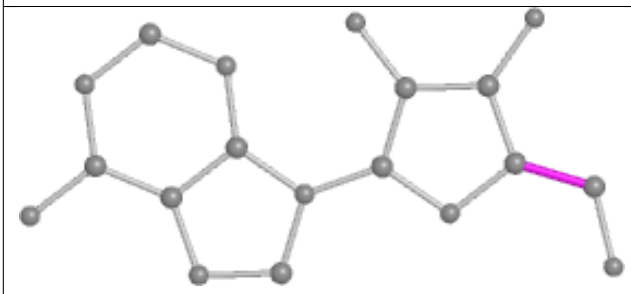
Ligand ADN DDD 502



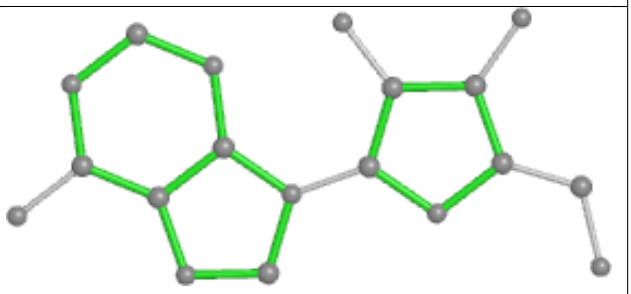
Bond lengths



Bond angles

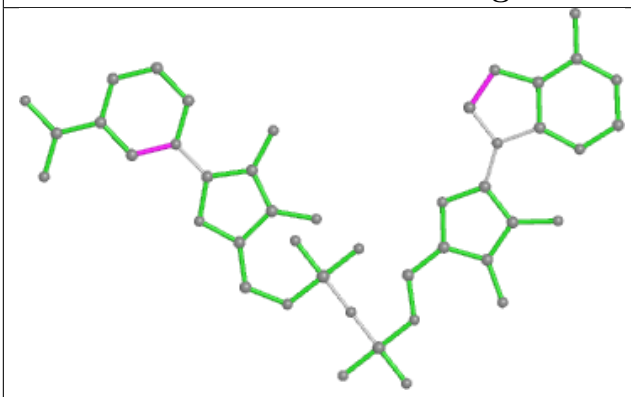


Torsions

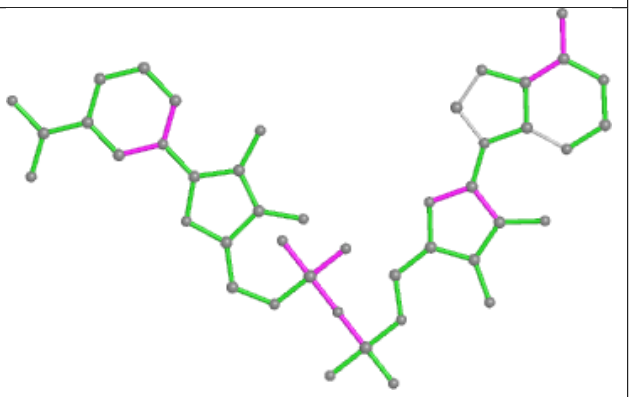


Rings

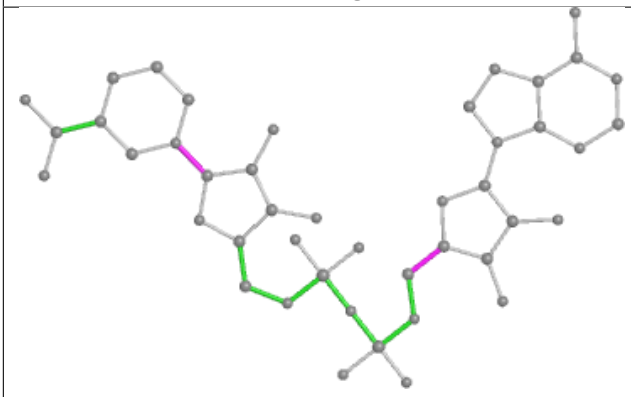
Ligand NAD DDD 501



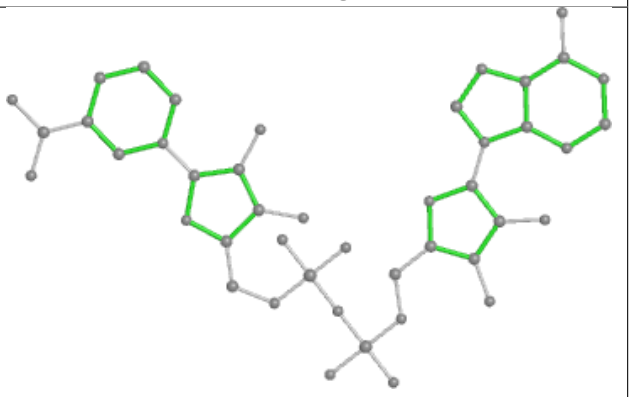
Bond lengths



Bond angles

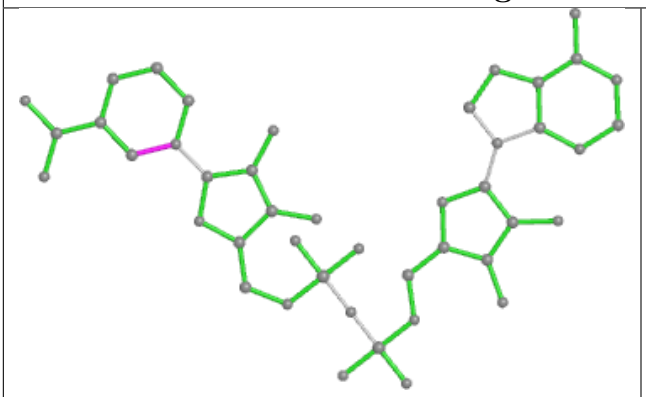


Torsions

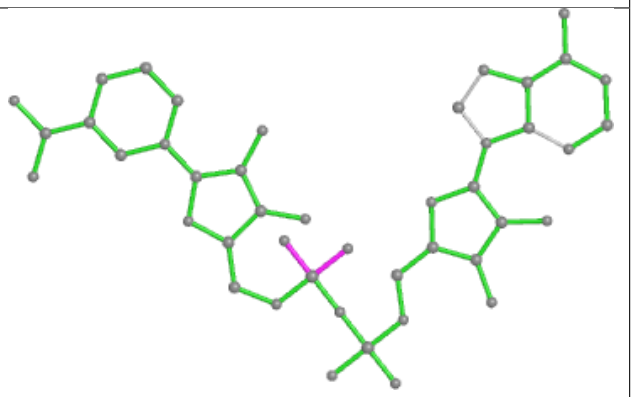


Rings

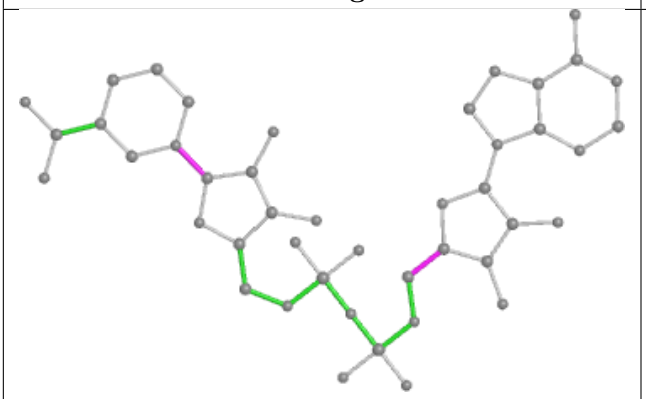
Ligand NAD CCC 501



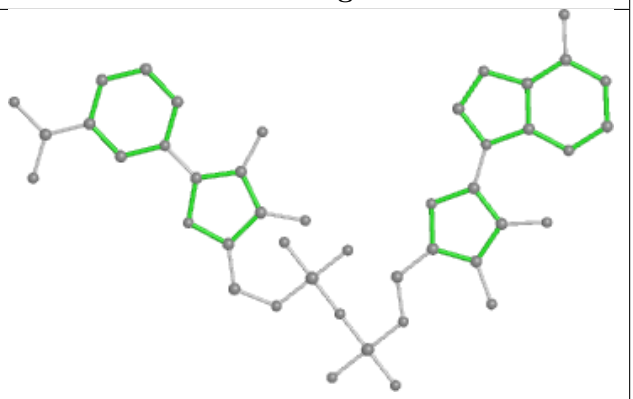
Bond lengths



Bond angles

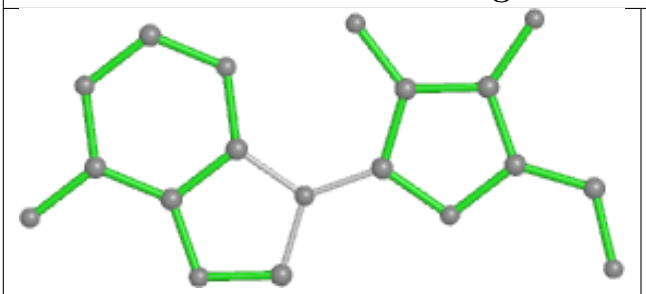


Torsions

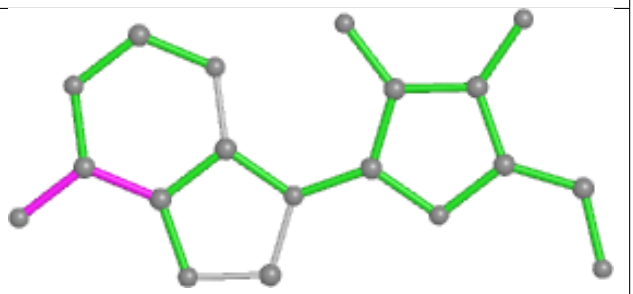


Rings

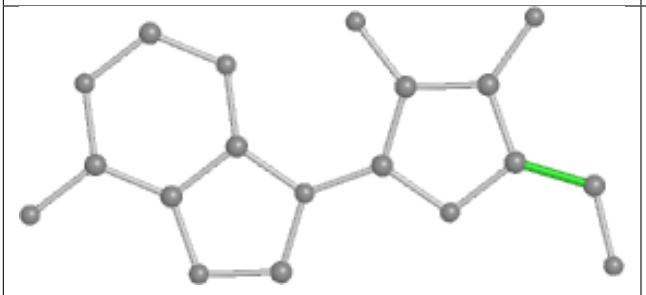
Ligand ADN AAA 502



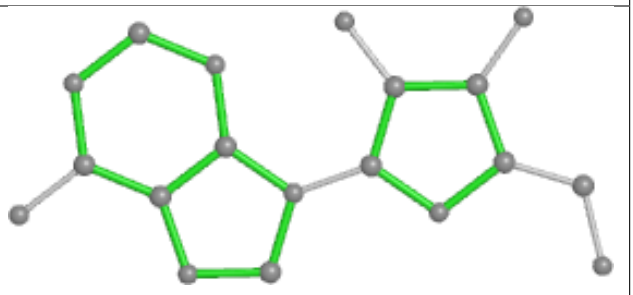
Bond lengths



Bond angles

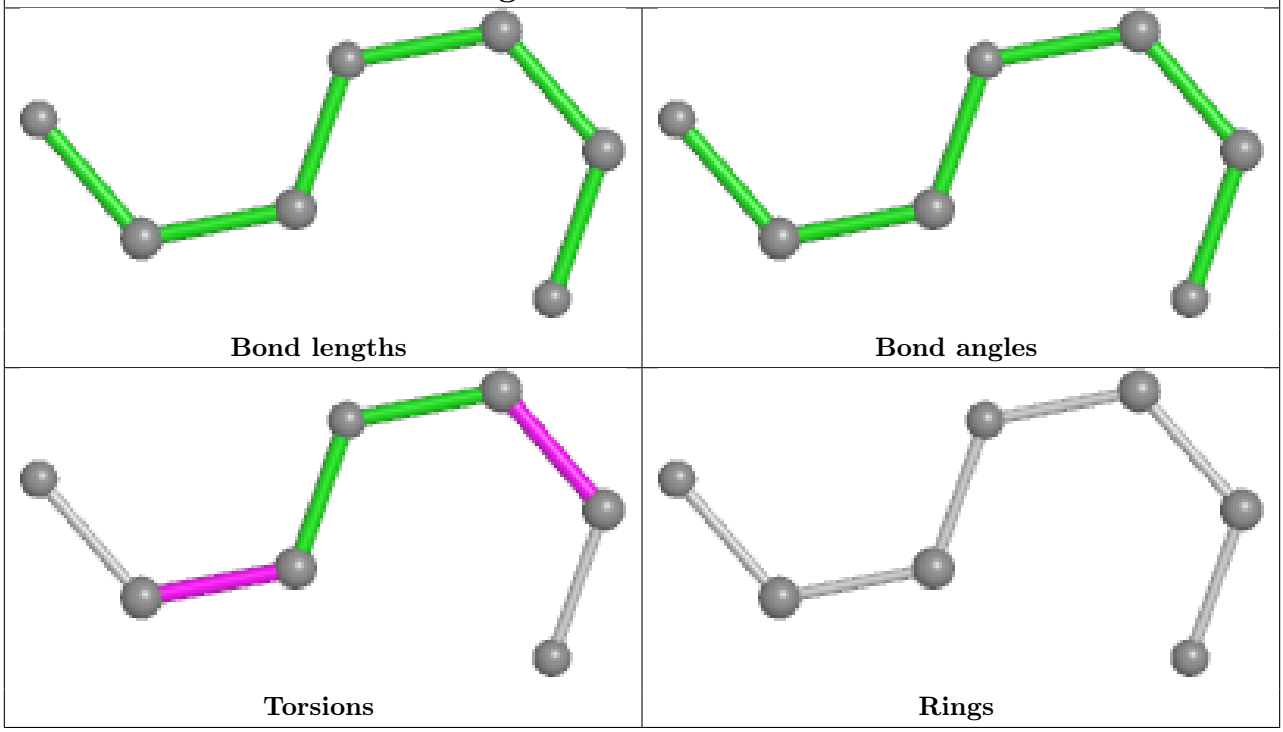


Torsions

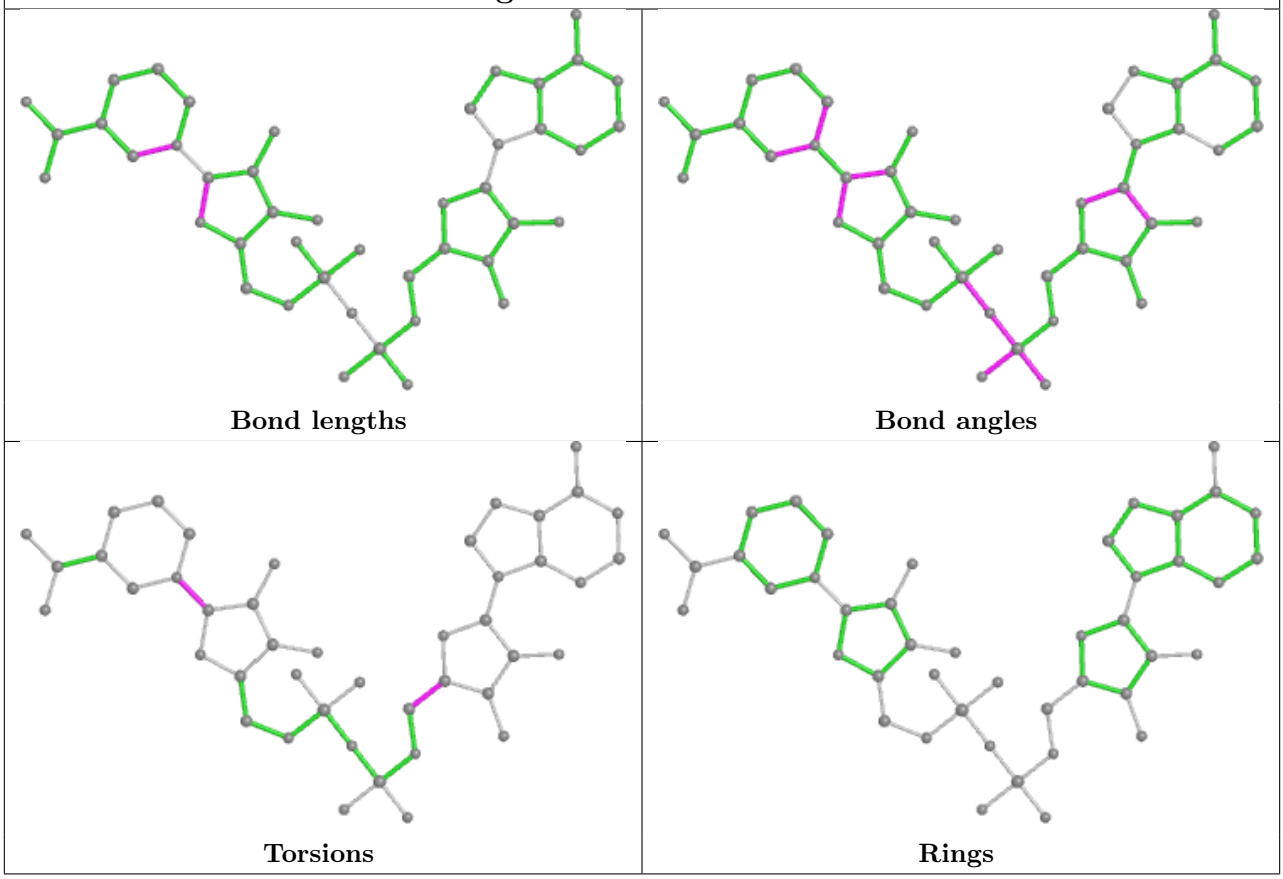


Rings

Ligand PEG CCC 503



Ligand NAD BBB 501



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	AAA	461/472 (97%)	-0.37	1 (0%)	95	95	28, 39, 61, 86	9 (1%)
1	BBB	461/472 (97%)	-0.29	2 (0%)	92	93	26, 39, 69, 104	10 (2%)
1	CCC	461/472 (97%)	-0.39	0	100	100	27, 36, 55, 76	9 (1%)
1	DDD	461/472 (97%)	-0.29	3 (0%)	87	89	25, 40, 71, 100	12 (2%)
All	All	1844/1888 (97%)	-0.34	6 (0%)	94	94	25, 38, 66, 104	40 (2%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	10	PHE	3.5
1	AAA	355	ASP	3.2
1	DDD	10	PHE	2.8
1	BBB	416	LYS	2.5
1	DDD	409	LEU	2.2
1	DDD	417	ARG	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,

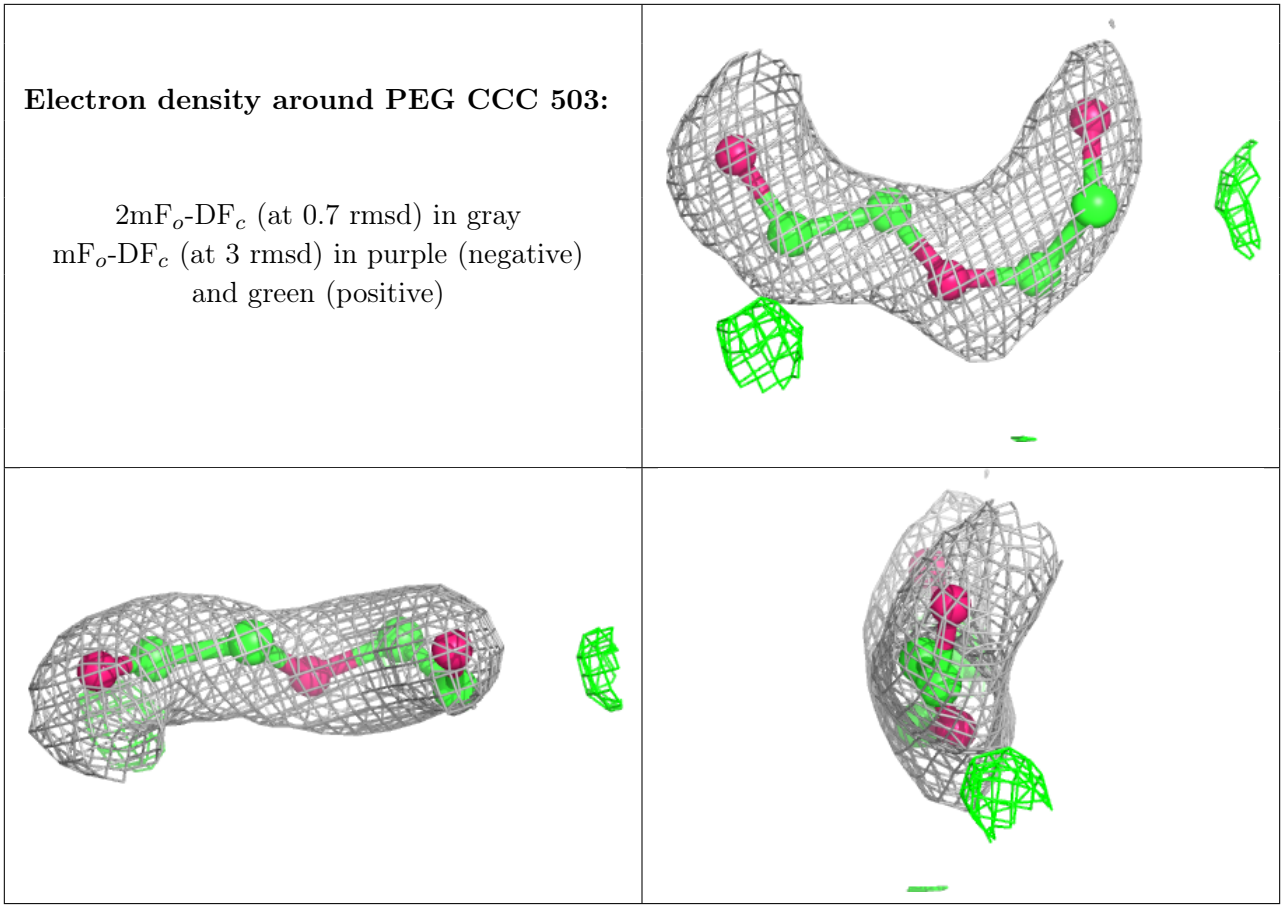
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
6	PEG	CCC	503	7/7	0.78	0.17	73,74,82,82	0
5	CL	BBB	504	1/1	0.95	0.07	36,36,36,36	1
3	ADN	CCC	502	19/19	0.96	0.10	27,30,42,44	0
3	ADN	AAA	502	19/19	0.96	0.10	27,31,46,48	0
3	ADN	BBB	502	19/19	0.96	0.09	30,32,45,49	0
3	ADN	DDD	502	19/19	0.97	0.08	29,34,45,49	0
2	NAD	CCC	501	44/44	0.98	0.07	26,30,34,36	0
2	NAD	DDD	501	44/44	0.98	0.07	27,31,35,38	0
2	NAD	AAA	501	44/44	0.98	0.07	31,33,38,40	0
2	NAD	BBB	501	44/44	0.98	0.08	26,31,35,36	0
4	K	CCC	504	1/1	0.99	0.10	29,29,29,29	0
4	K	DDD	503	1/1	0.99	0.15	30,30,30,30	0
4	K	AAA	503	1/1	0.99	0.10	30,30,30,30	0
4	K	BBB	503	1/1	0.99	0.11	31,31,31,31	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.

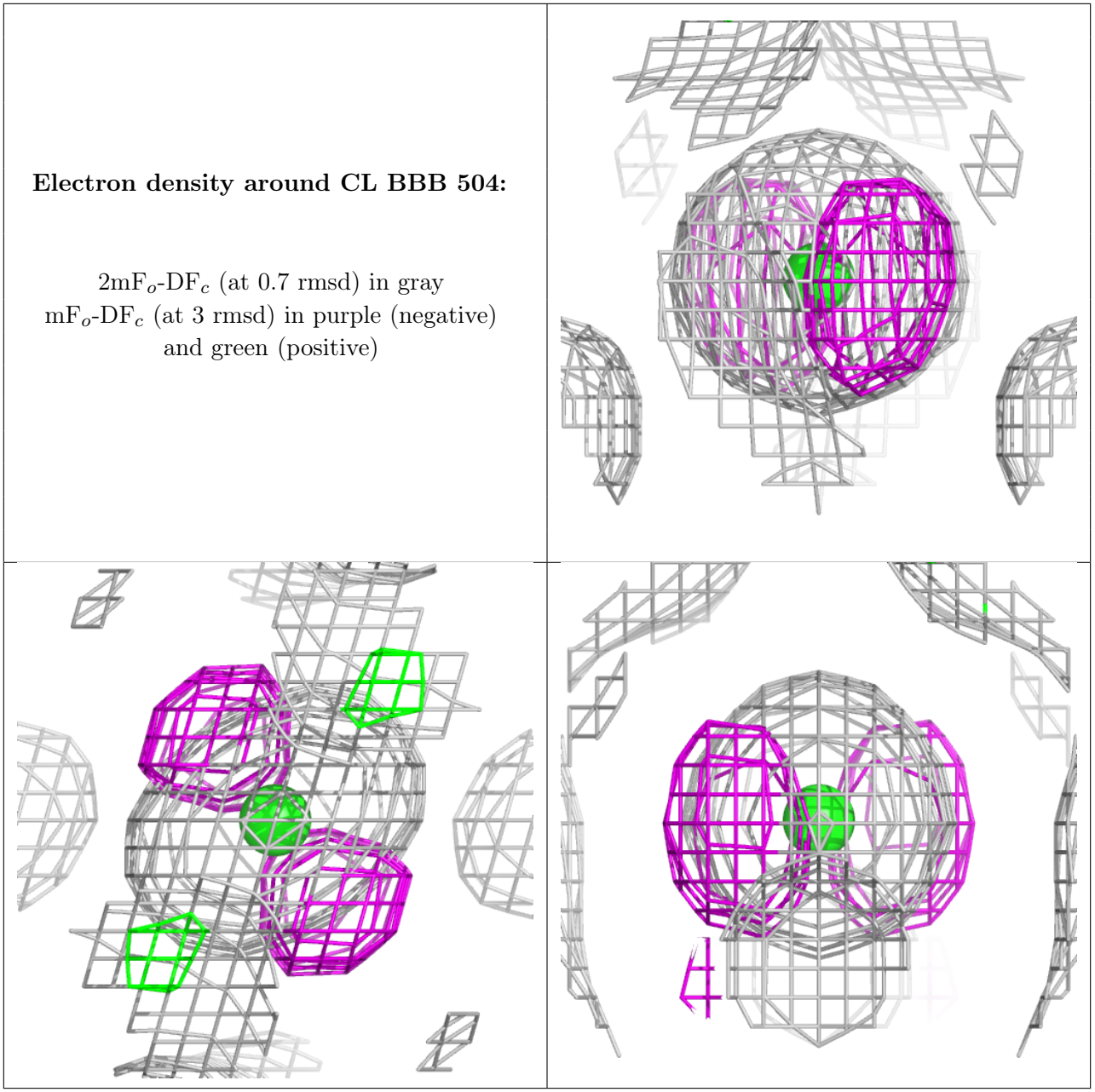
Electron density around PEG CCC 503:

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



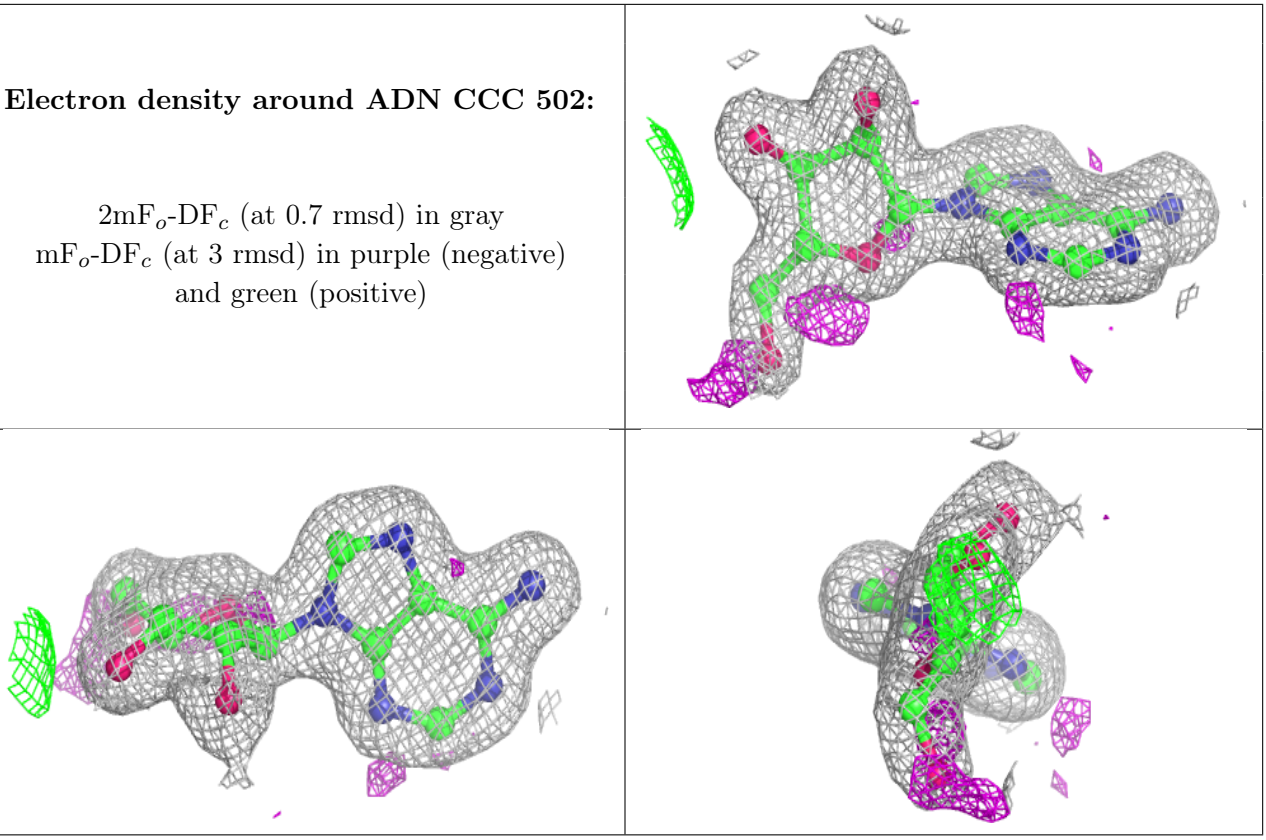
Electron density around CL BBB 504:

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



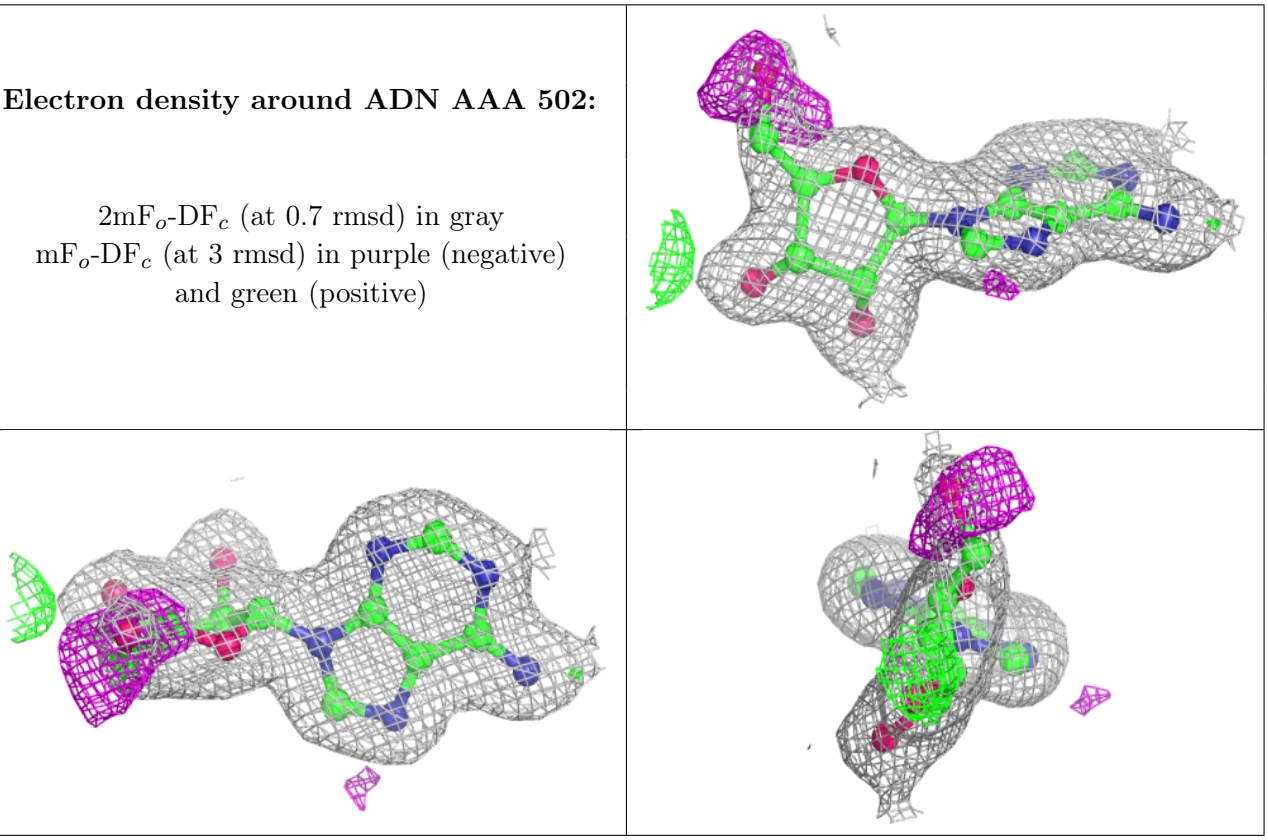
Electron density around ADN CCC 502:

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



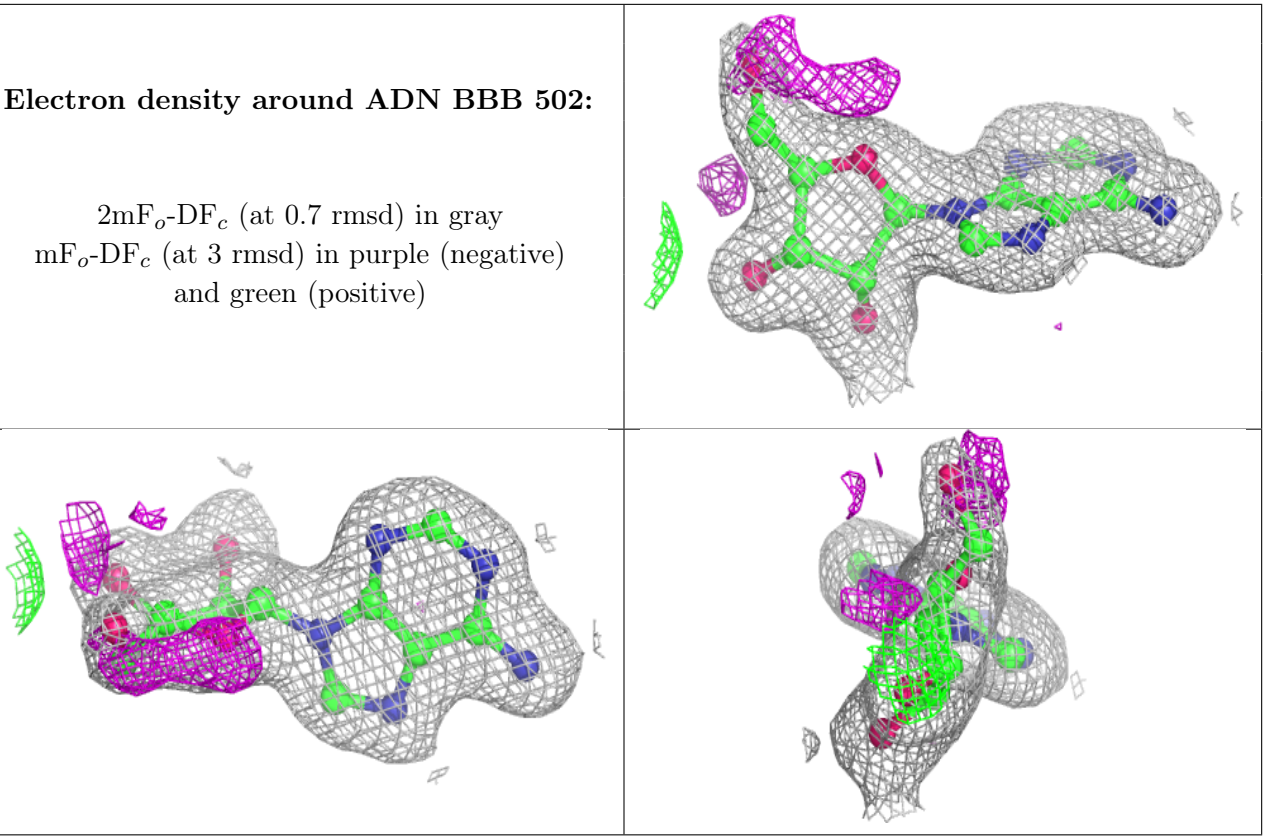
Electron density around ADN AAA 502:

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



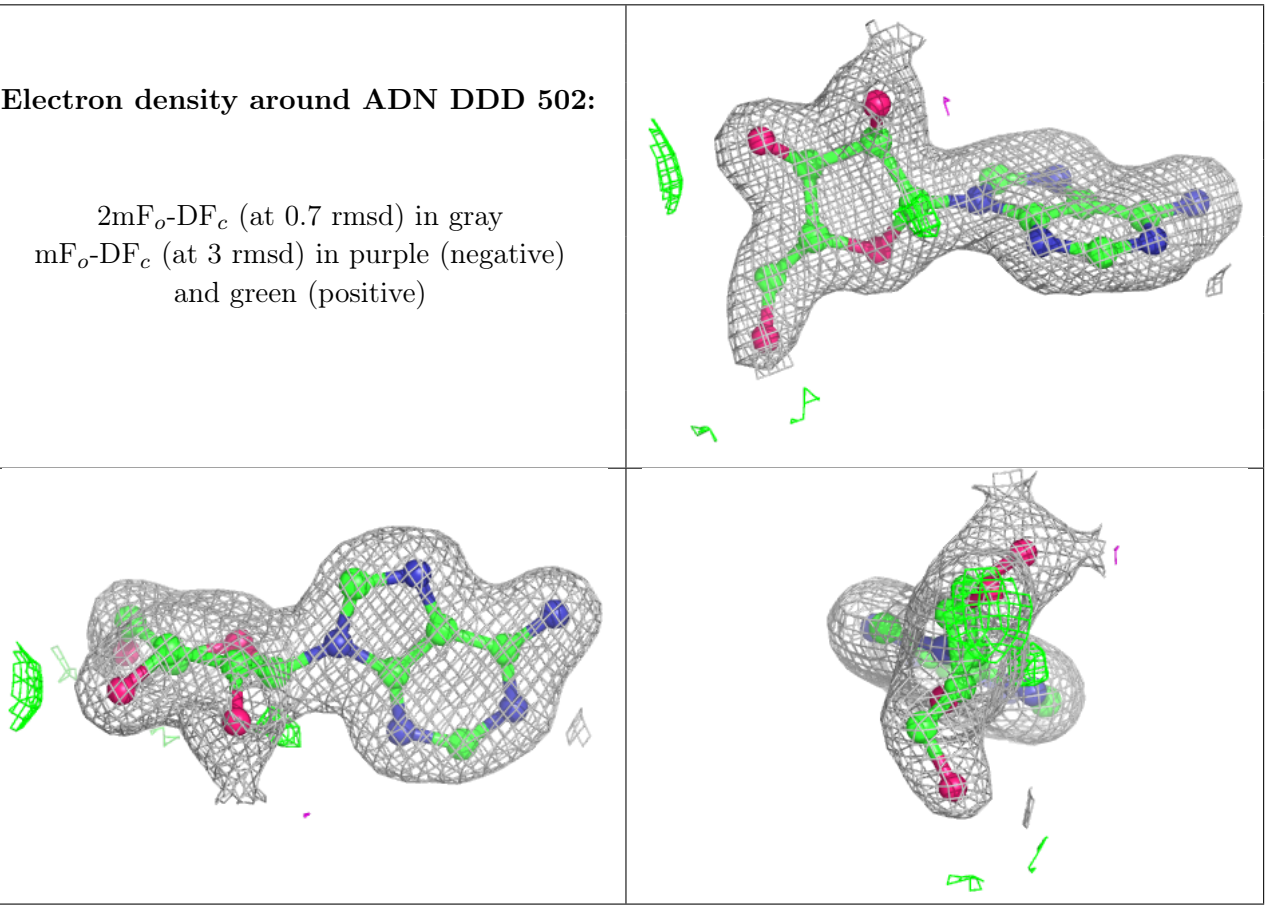
Electron density around ADN BBB 502:

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



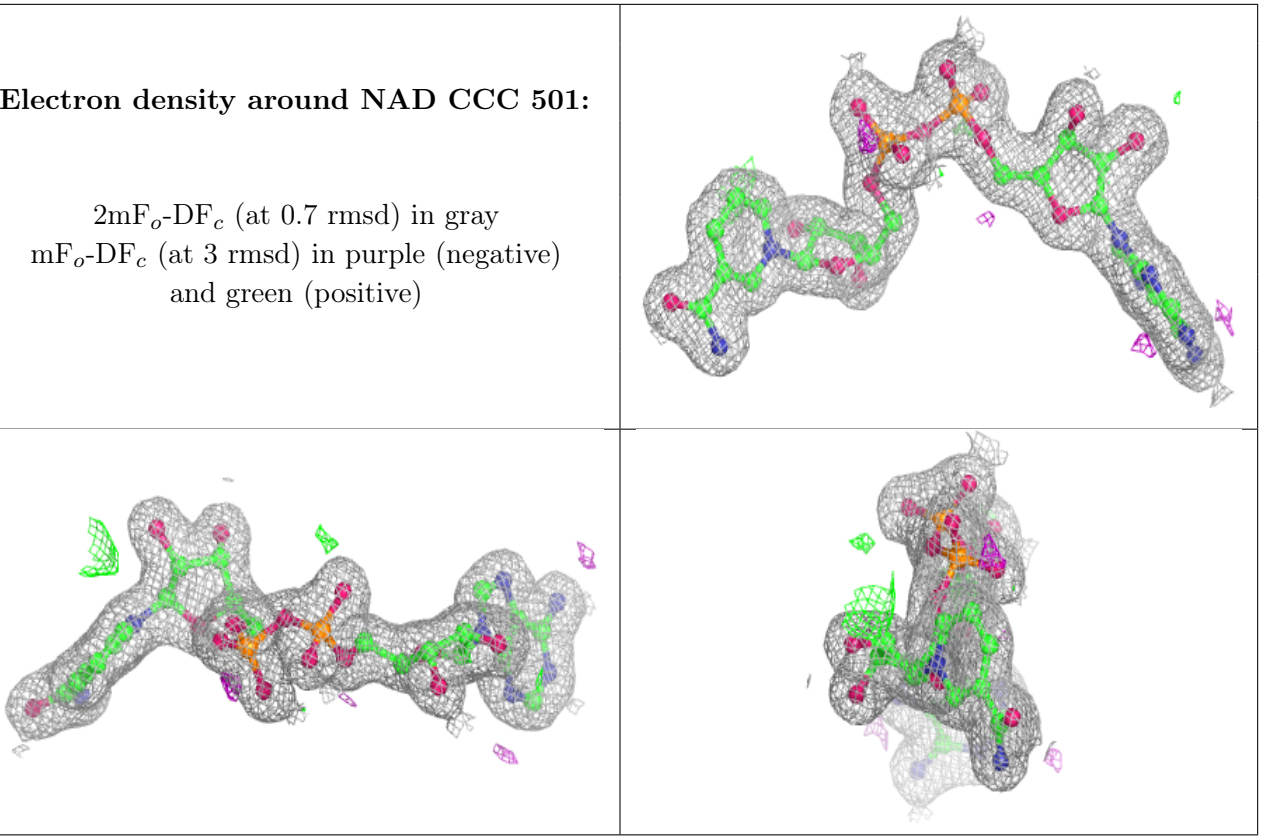
Electron density around ADN DDD 502:

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



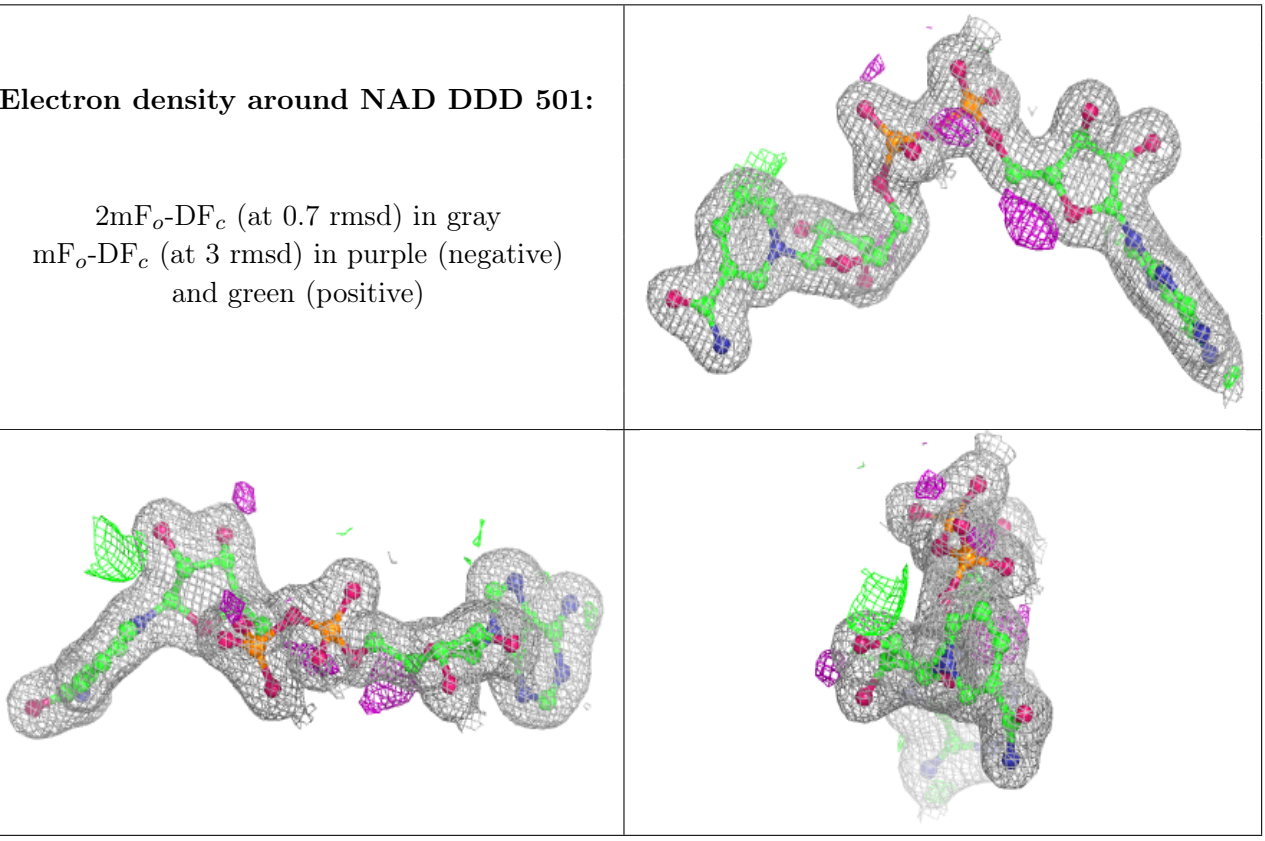
Electron density around NAD CCC 501:

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



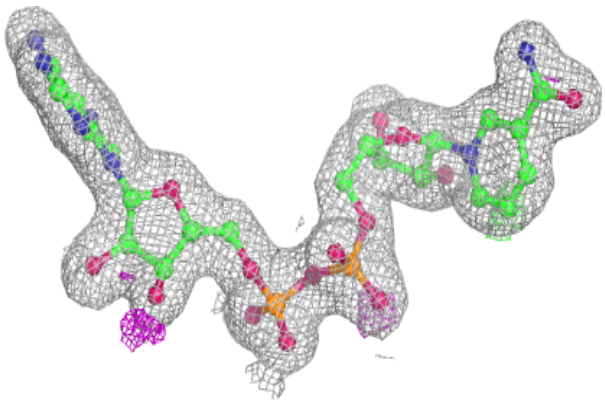
Electron density around NAD DDD 501:

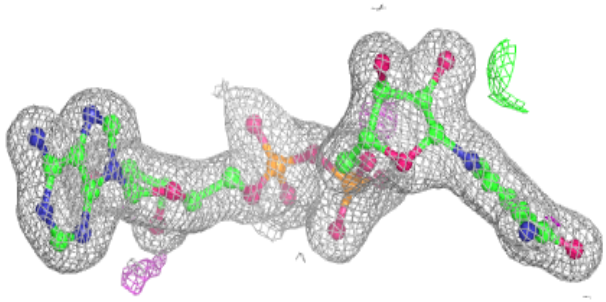
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

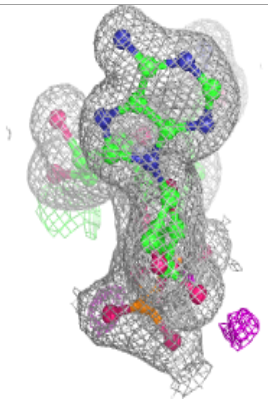


Electron density around NAD AAA 501:

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

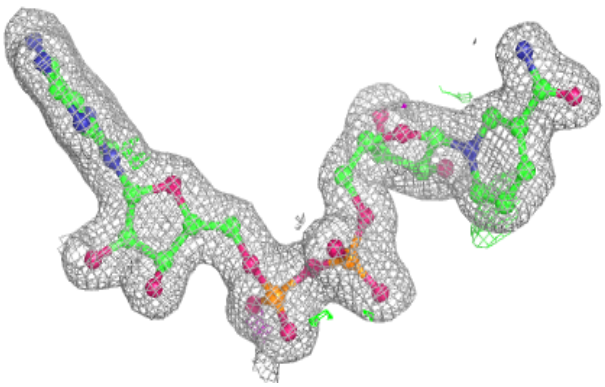


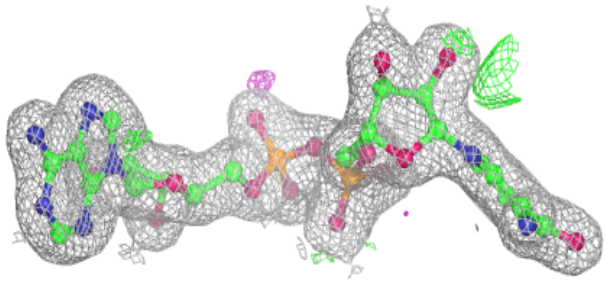


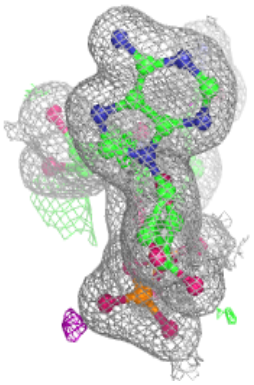


Electron density around NAD BBB 501:

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

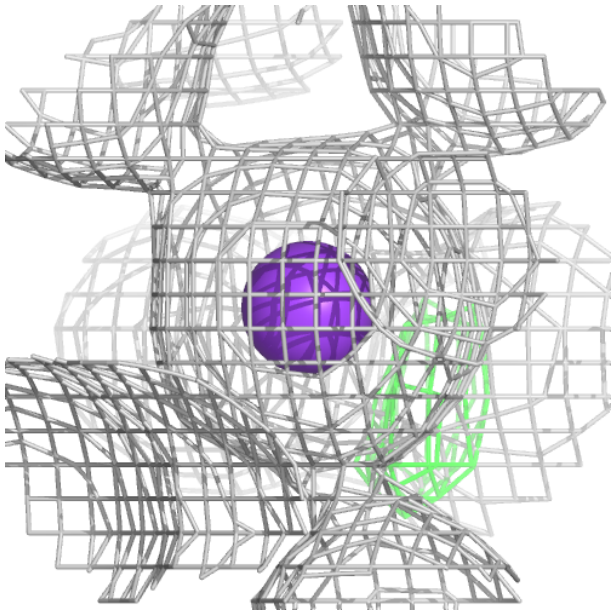


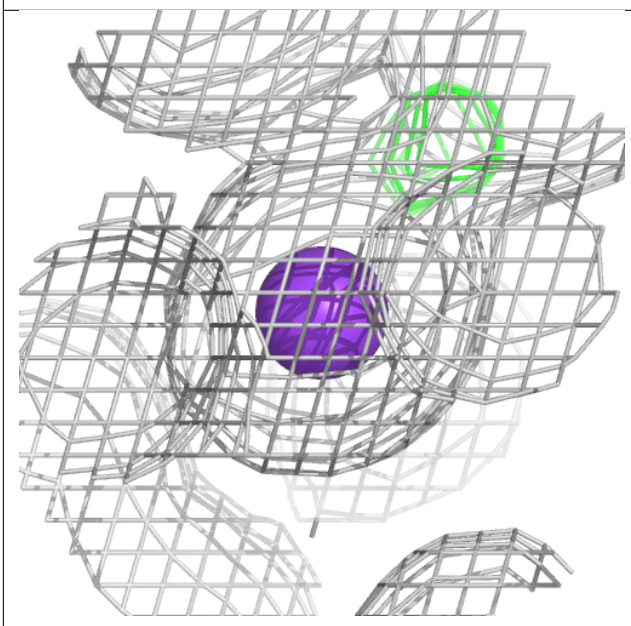


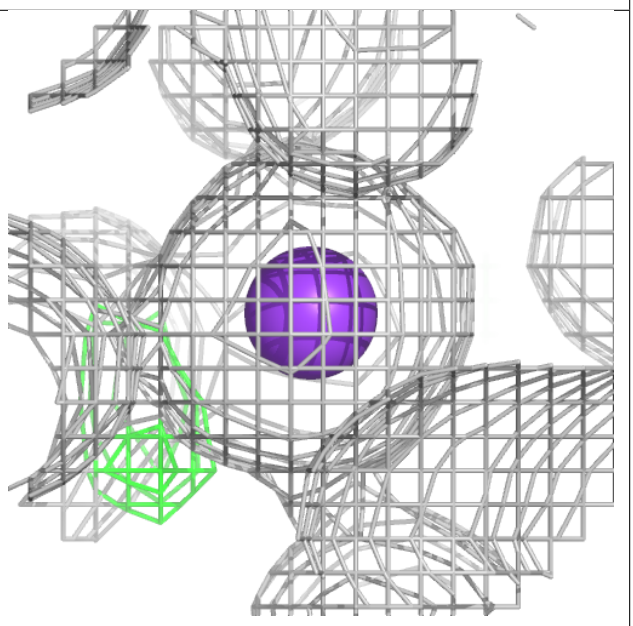


Electron density around K CCC 504:

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

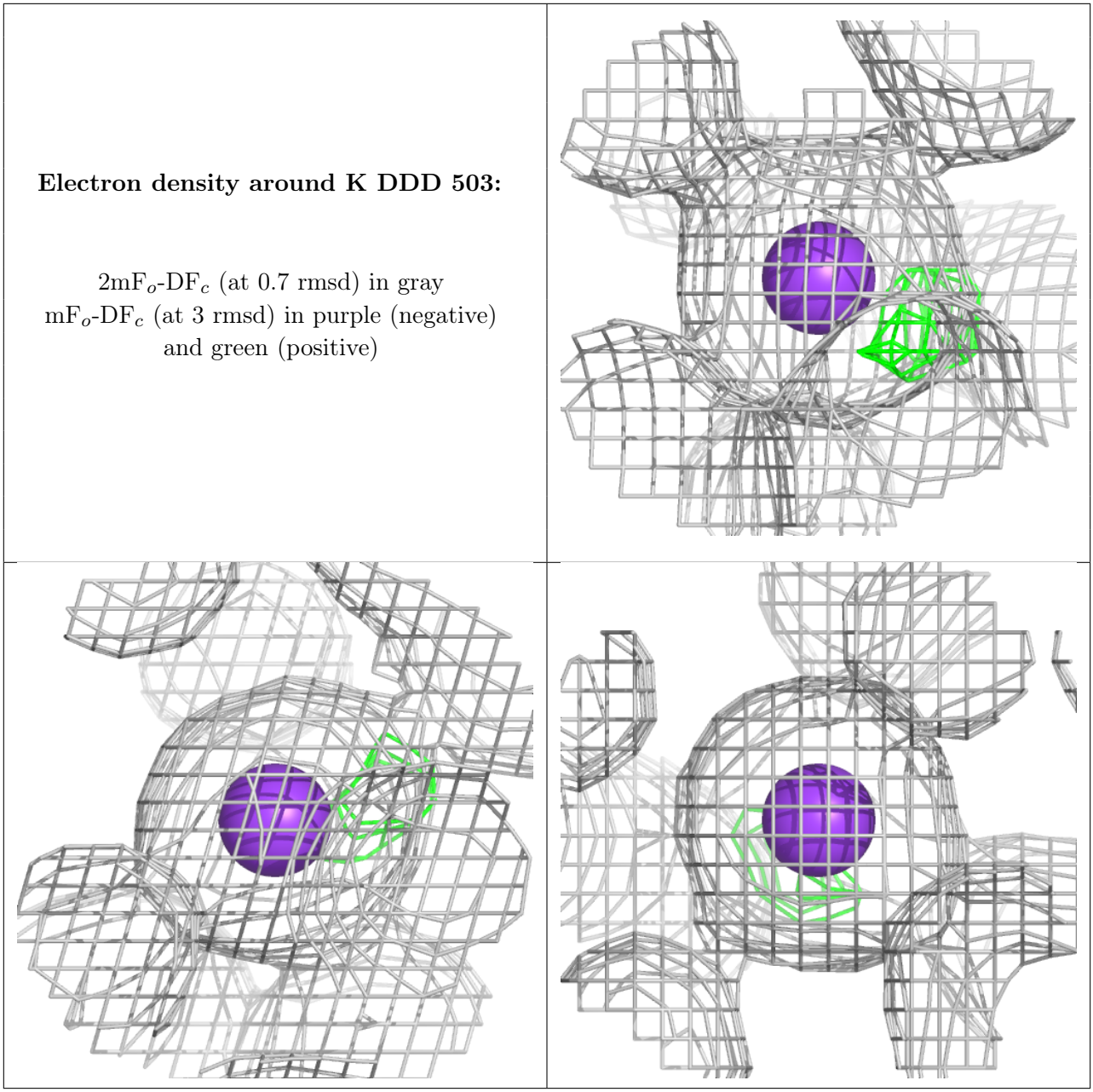






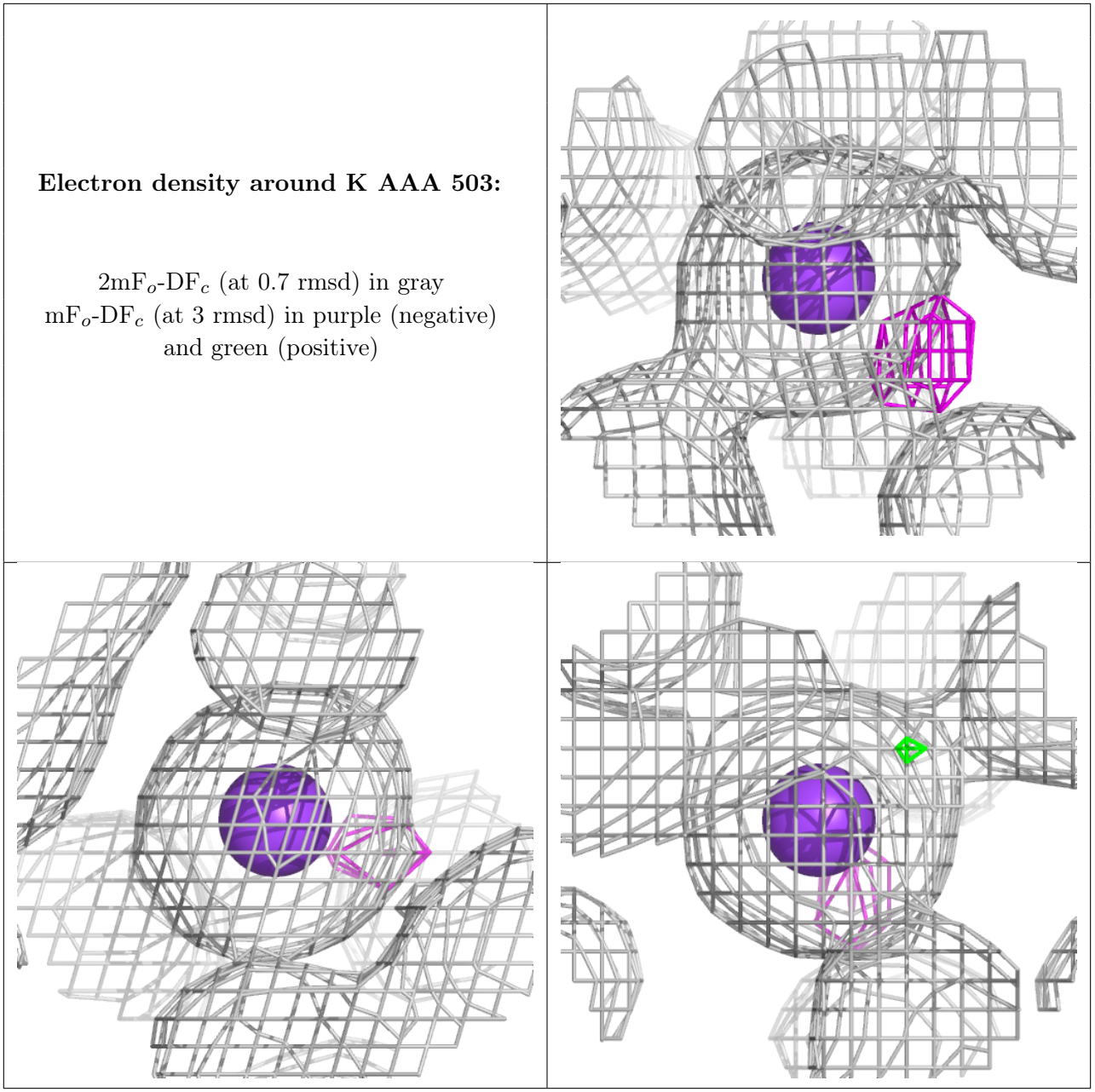
Electron density around K DDD 503:

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



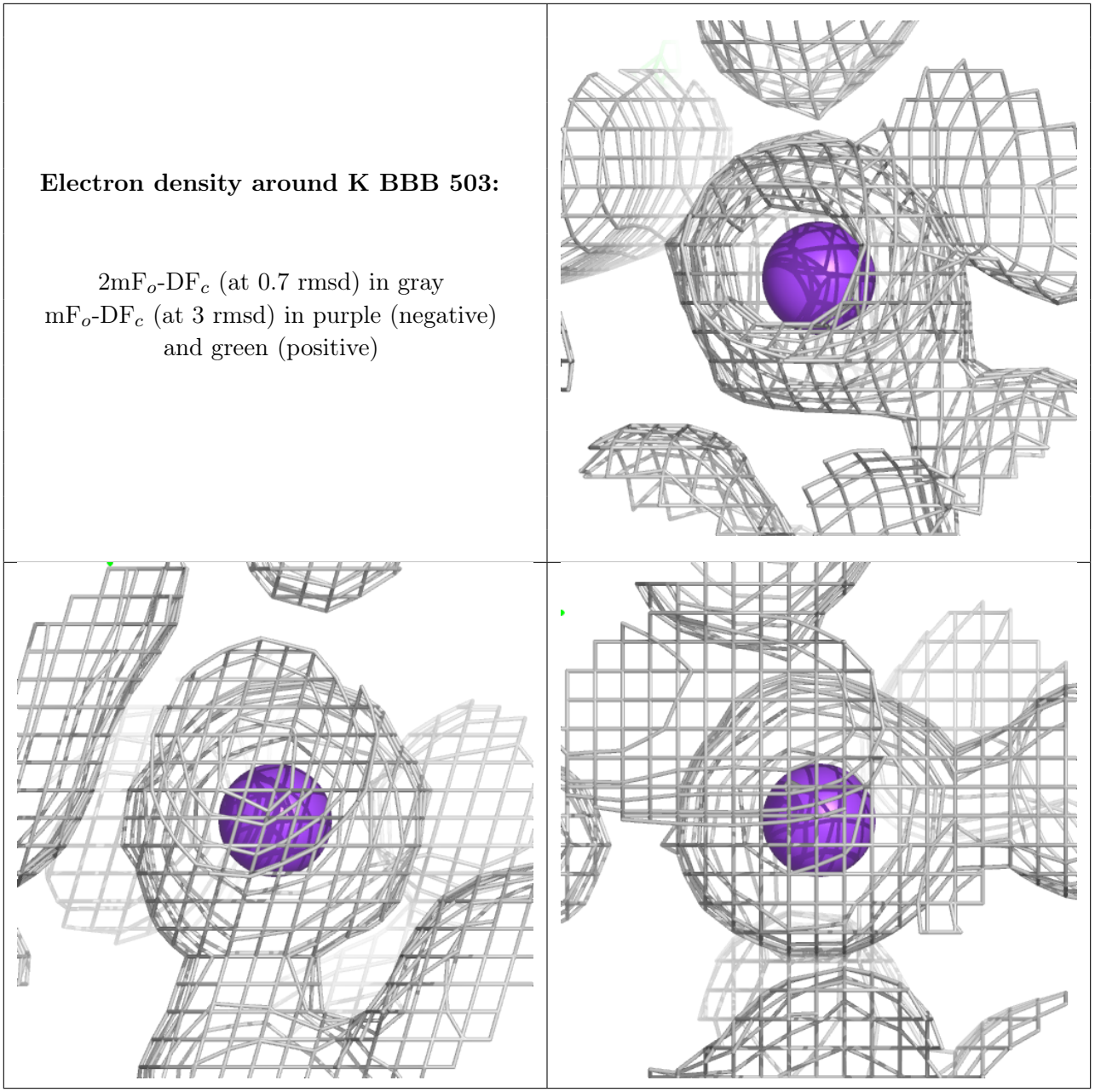
Electron density around K AAA 503:

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



Electron density around K BBB 503:

$2mF_o$-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.