wwPDB X-ray Structure Validation Summary Report (i)

Nov 6, 2023 – 11:59 AM JST

PDB ID	:	8IGW
Title	:	Hexameric Ring Complex of Engineered V1-ATPase bound to 4 ADPs: A3(De)3_(ADP)3cat,1non-cat, Hexameric Ring Complex of Engineered V1-ATPase bound to 5 ADPs: A3(De)3_(ADP)3cat,2non-cat
Authors	:	Kosugi, T.; Tanabe, M.; Koga, N.
Deposited on	:	2023-02-21
Resolution	:	4.20 Å(reported)

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

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

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

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

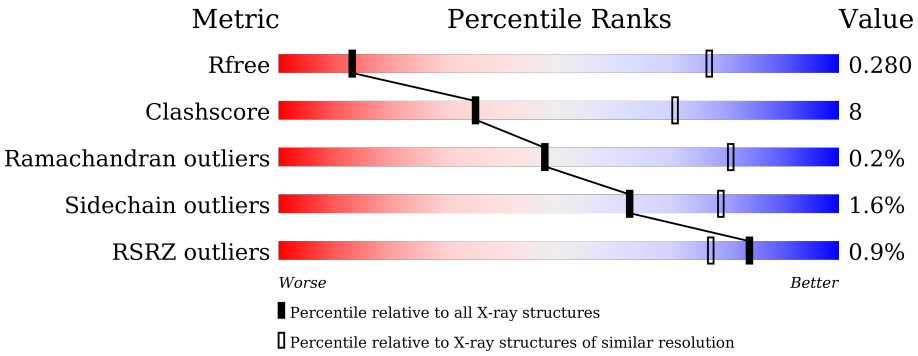
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 4.20 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	1005 (4.62-3.78)
Clashscore	141614	1044 (4.60-3.80)
Ramachandran outliers	138981	1000 (4.60-3.80)
Sidechain outliers	138945	1007 (4.62-3.78)
RSRZ outliers	127900	1063 (4.70-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	596	77% 21%
1	B	596	3% 66% 22% 11%
1	C	596	78% 20%
1	G	596	2% 76% 22%
1	H	596	% 77% 20%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	I	596	77% 20%
2	D	458	81% 15%
2	E	458	83% 14%
2	F	458	3% 76% 20%
2	J	458	75% 20%
2	K	458	80% 18%
2	L	458	% 80% 18%

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
4	MG	B	602	-	-	-	X
4	MG	H	602	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 47792 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 V-type sodium ATPase catalytic subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	586	Total	C	N	O	S	0	0	0
			4562	2866	766	904	26			
1	B	530	Total	C	N	O	S	0	0	0
			4113	2584	691	813	25			
1	C	585	Total	C	N	O	S	0	0	0
			4525	2844	761	895	25			
1	G	586	Total	C	N	O	S	0	0	0
			4562	2866	766	904	26			
1	H	586	Total	C	N	O	S	0	0	0
			4562	2866	766	904	26			
1	I	583	Total	C	N	O	S	0	0	0
			4509	2833	758	893	25			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q08636
A	-1	SER	-	expression tag	UNP Q08636
A	0	GLY	-	expression tag	UNP Q08636
B	-2	SER	-	expression tag	UNP Q08636
B	-1	SER	-	expression tag	UNP Q08636
B	0	GLY	-	expression tag	UNP Q08636
C	-2	SER	-	expression tag	UNP Q08636
C	-1	SER	-	expression tag	UNP Q08636
C	0	GLY	-	expression tag	UNP Q08636
G	-2	SER	-	expression tag	UNP Q08636
G	-1	SER	-	expression tag	UNP Q08636
G	0	GLY	-	expression tag	UNP Q08636
H	-2	SER	-	expression tag	UNP Q08636
H	-1	SER	-	expression tag	UNP Q08636
H	0	GLY	-	expression tag	UNP Q08636
I	-2	SER	-	expression tag	UNP Q08636
I	-1	SER	-	expression tag	UNP Q08636

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	0	GLY	-	expression tag	UNP Q08636

- Molecule 2 is a protein called V-type sodium ATPase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	444	Total	C	N	O	S	0	0	0
			3461	2191	596	660	14			
2	E	446	Total	C	N	O	S	0	0	0
			3444	2180	595	655	14			
2	F	442	Total	C	N	O	S	0	0	0
			3412	2160	583	655	14			
2	J	438	Total	C	N	O	S	0	0	0
			3396	2145	587	650	14			
2	K	450	Total	C	N	O	S	0	0	0
			3485	2205	598	668	14			
2	L	452	Total	C	N	O	S	0	0	0
			3509	2221	604	670	14			

There are 60 discrepancies between the modelled and reference sequences:

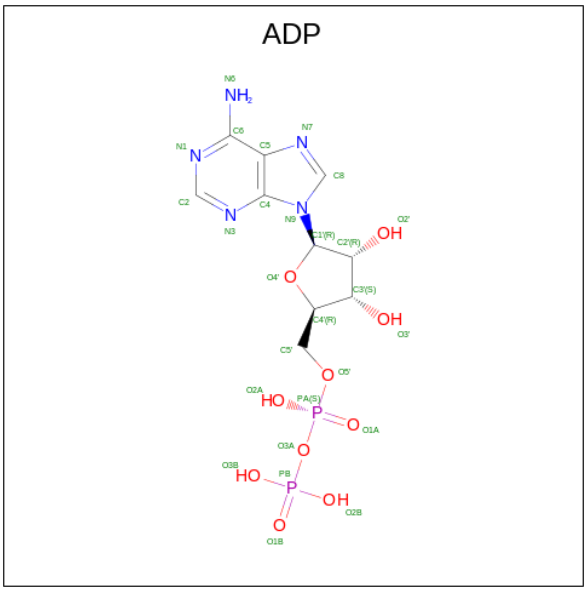
Chain	Residue	Modelled	Actual	Comment	Reference
D	151	GLY	SER	engineered mutation	UNP Q08637
D	152	PRO	GLY	engineered mutation	UNP Q08637
D	153	PRO	SER	engineered mutation	UNP Q08637
D	155	ALA	LEU	engineered mutation	UNP Q08637
D	156	GLY	PRO	engineered mutation	UNP Q08637
D	157	LYS	HIS	engineered mutation	UNP Q08637
D	158	SER	LYS	engineered mutation	UNP Q08637
D	159	ALA	GLU	engineered mutation	UNP Q08637
D	248	GLU	THR	engineered mutation	UNP Q08637
D	339	SER	GLN	engineered mutation	UNP Q08637
E	151	GLY	SER	engineered mutation	UNP Q08637
E	152	PRO	GLY	engineered mutation	UNP Q08637
E	153	PRO	SER	engineered mutation	UNP Q08637
E	155	ALA	LEU	engineered mutation	UNP Q08637
E	156	GLY	PRO	engineered mutation	UNP Q08637
E	157	LYS	HIS	engineered mutation	UNP Q08637
E	158	SER	LYS	engineered mutation	UNP Q08637
E	159	ALA	GLU	engineered mutation	UNP Q08637
E	248	GLU	THR	engineered mutation	UNP Q08637
E	339	SER	GLN	engineered mutation	UNP Q08637
F	151	GLY	SER	engineered mutation	UNP Q08637

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	152	PRO	GLY	engineered mutation	UNP Q08637
F	153	PRO	SER	engineered mutation	UNP Q08637
F	155	ALA	LEU	engineered mutation	UNP Q08637
F	156	GLY	PRO	engineered mutation	UNP Q08637
F	157	LYS	HIS	engineered mutation	UNP Q08637
F	158	SER	LYS	engineered mutation	UNP Q08637
F	159	ALA	GLU	engineered mutation	UNP Q08637
F	248	GLU	THR	engineered mutation	UNP Q08637
F	339	SER	GLN	engineered mutation	UNP Q08637
J	151	GLY	SER	engineered mutation	UNP Q08637
J	152	PRO	GLY	engineered mutation	UNP Q08637
J	153	PRO	SER	engineered mutation	UNP Q08637
J	155	ALA	LEU	engineered mutation	UNP Q08637
J	156	GLY	PRO	engineered mutation	UNP Q08637
J	157	LYS	HIS	engineered mutation	UNP Q08637
J	158	SER	LYS	engineered mutation	UNP Q08637
J	159	ALA	GLU	engineered mutation	UNP Q08637
J	248	GLU	THR	engineered mutation	UNP Q08637
J	339	SER	GLN	engineered mutation	UNP Q08637
K	151	GLY	SER	engineered mutation	UNP Q08637
K	152	PRO	GLY	engineered mutation	UNP Q08637
K	153	PRO	SER	engineered mutation	UNP Q08637
K	155	ALA	LEU	engineered mutation	UNP Q08637
K	156	GLY	PRO	engineered mutation	UNP Q08637
K	157	LYS	HIS	engineered mutation	UNP Q08637
K	158	SER	LYS	engineered mutation	UNP Q08637
K	159	ALA	GLU	engineered mutation	UNP Q08637
K	248	GLU	THR	engineered mutation	UNP Q08637
K	339	SER	GLN	engineered mutation	UNP Q08637
L	151	GLY	SER	engineered mutation	UNP Q08637
L	152	PRO	GLY	engineered mutation	UNP Q08637
L	153	PRO	SER	engineered mutation	UNP Q08637
L	155	ALA	LEU	engineered mutation	UNP Q08637
L	156	GLY	PRO	engineered mutation	UNP Q08637
L	157	LYS	HIS	engineered mutation	UNP Q08637
L	158	SER	LYS	engineered mutation	UNP Q08637
L	159	ALA	GLU	engineered mutation	UNP Q08637
L	248	GLU	THR	engineered mutation	UNP Q08637
L	339	SER	GLN	engineered mutation	UNP Q08637

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	G	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	L	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	B	1	Total	Mg	0	0
			1	1		

Continued on next page...

Continued from previous page...

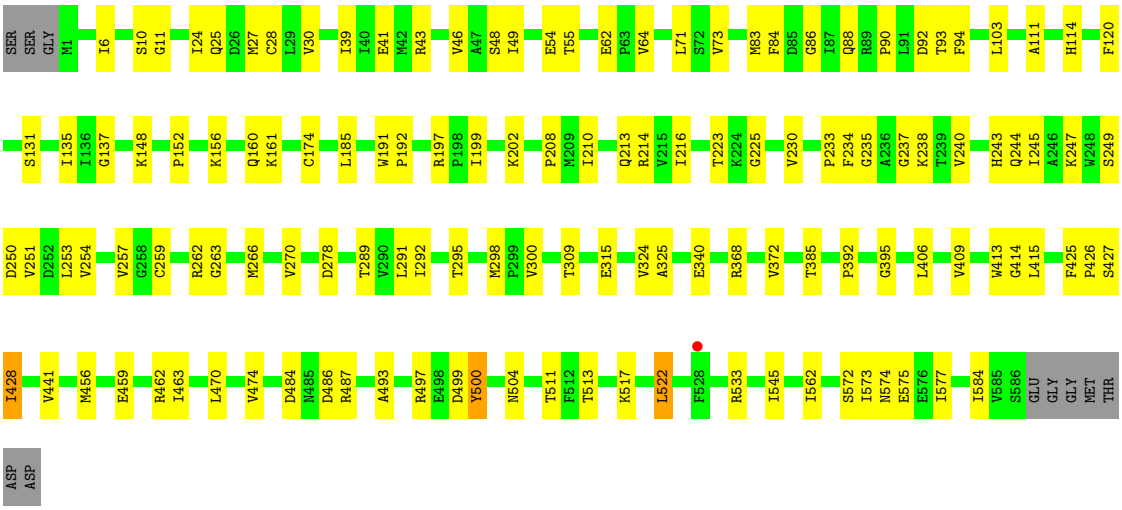
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0
4	G	1	Total Mg 1 1	0	0
4	H	1	Total Mg 1 1	0	0
4	I	1	Total Mg 1 1	0	0
4	J	1	Total Mg 1 1	0	0
4	L	1	Total Mg 1 1	0	0

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.

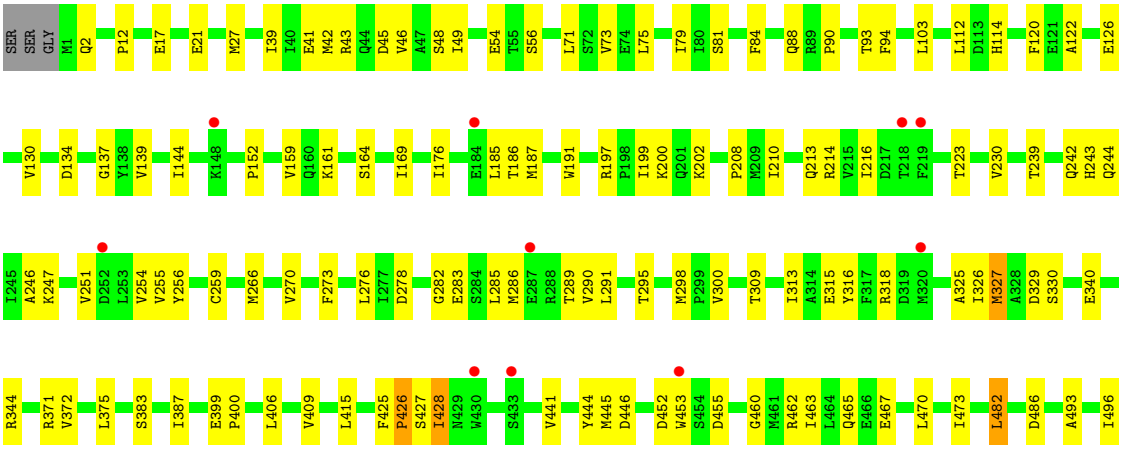
• Molecule 1: V-type sodium ATPase catalytic subunit A

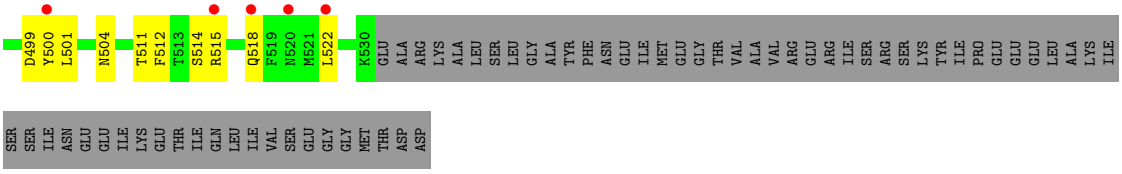
Chain A:



• Molecule 1: V-type sodium ATPase catalytic subunit A

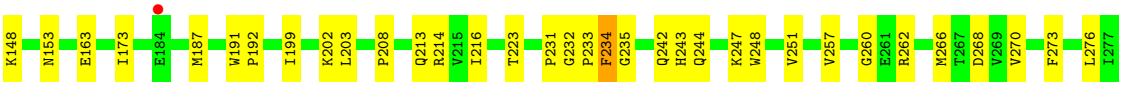
Chain B:





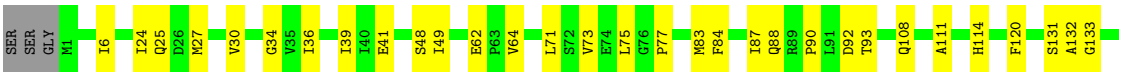
• Molecule 1: V-type sodium ATPase catalytic subunit A

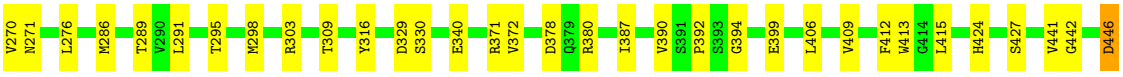
Chain C:

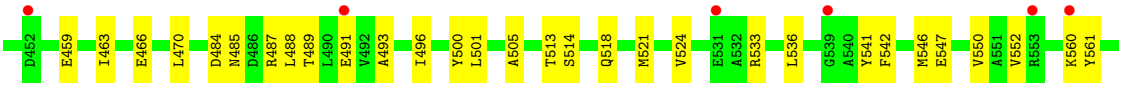


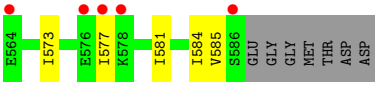
• Molecule 1: V-type sodium ATPase catalytic subunit A

Chain G:



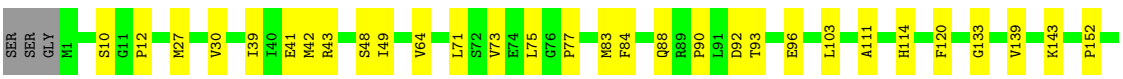


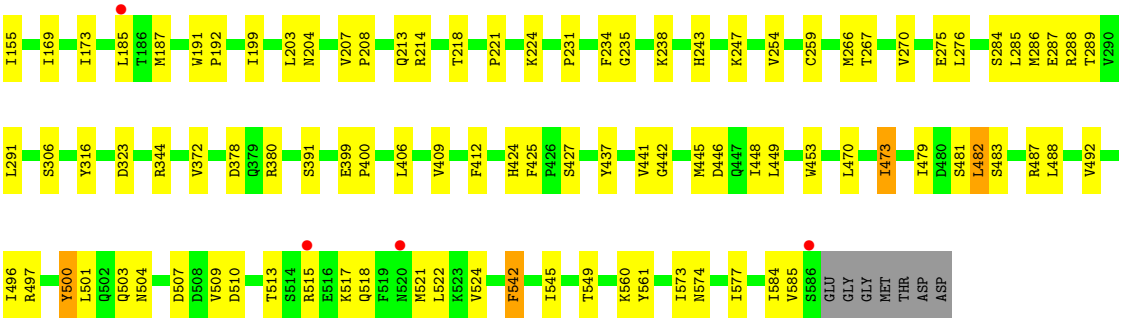




• Molecule 1: V-type sodium ATPase catalytic subunit A

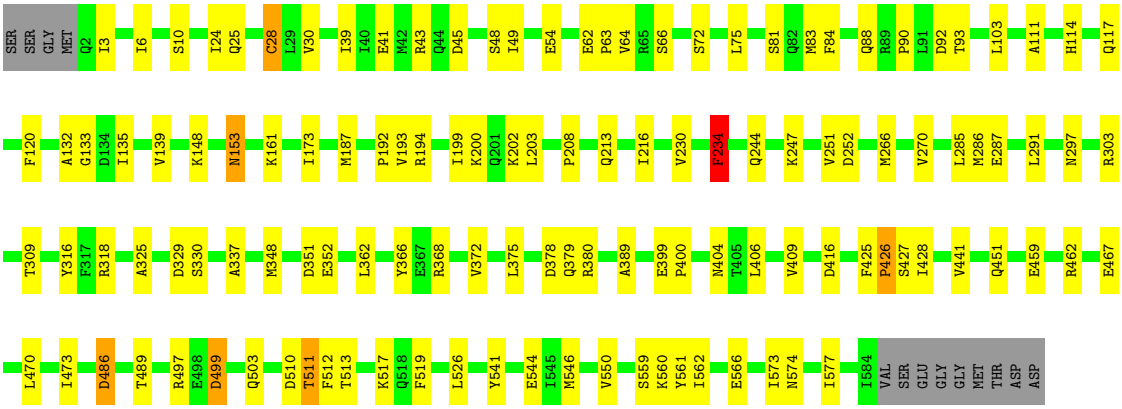
Chain H:





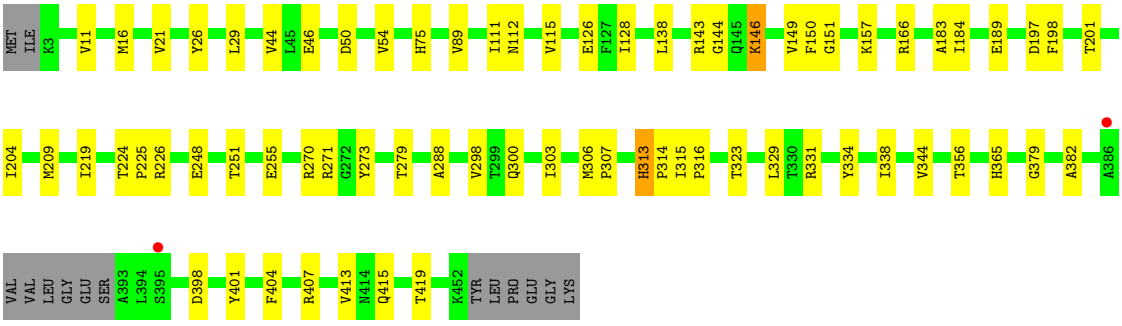
• Molecule 1: V-type sodium ATPase catalytic subunit A

Chain I: 77% 20%



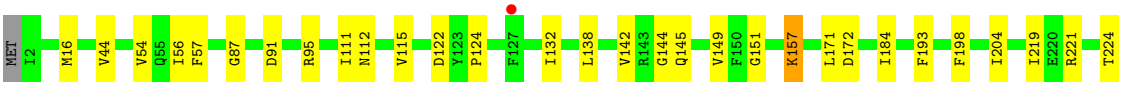
• Molecule 2: V-type sodium ATPase subunit B

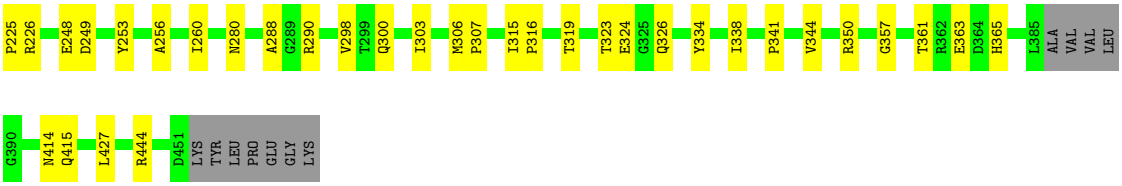
Chain D: 81% 15%



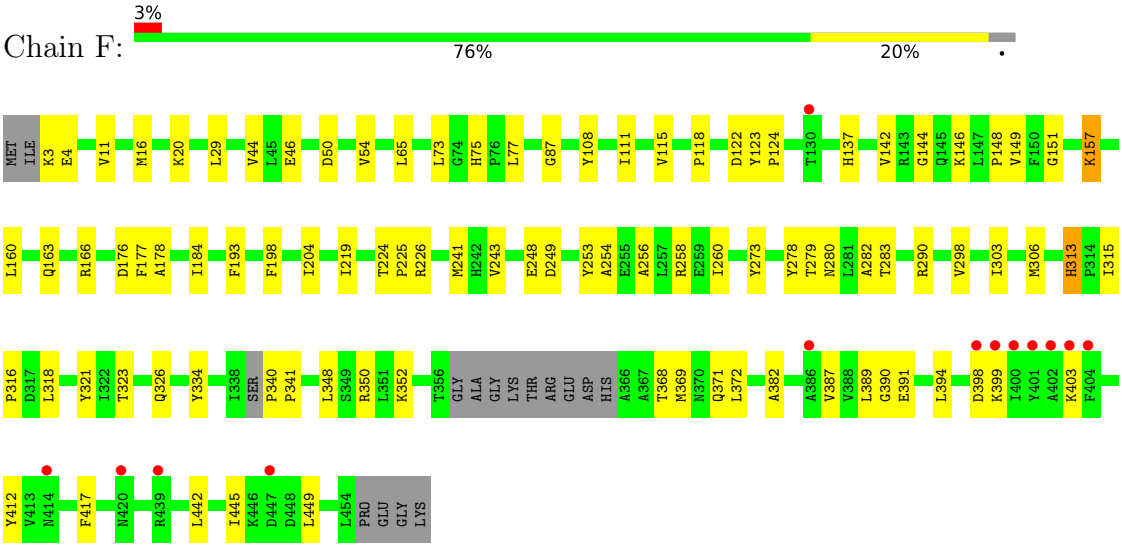
• Molecule 2: V-type sodium ATPase subunit B

Chain E: 83% 14%

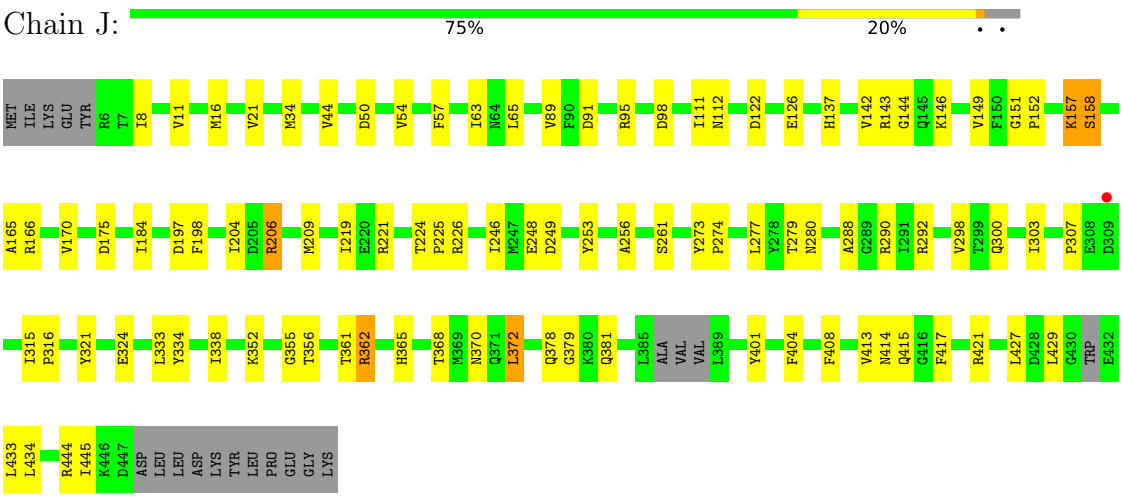




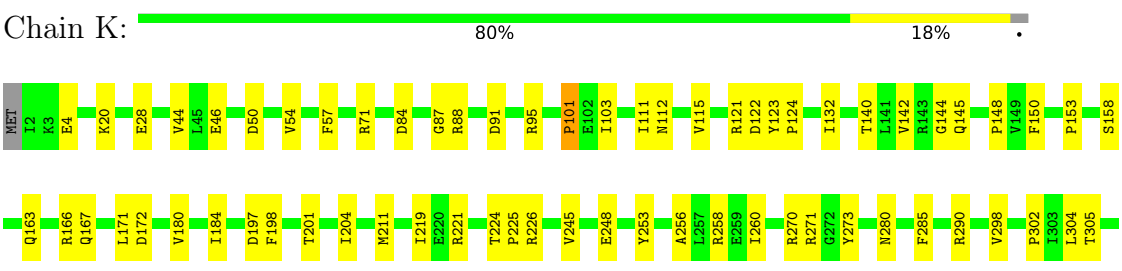
• Molecule 2: V-type sodium ATPase subunit B

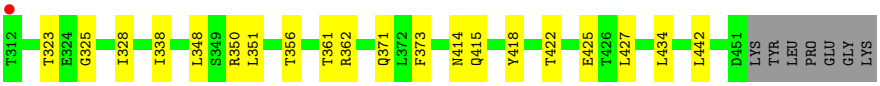


• Molecule 2: V-type sodium ATPase subunit B

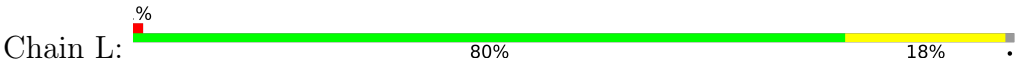


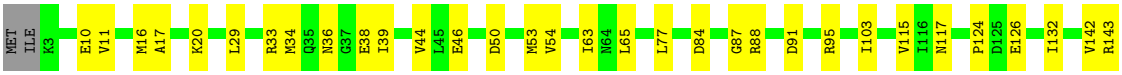
• Molecule 2: V-type sodium ATPase subunit B

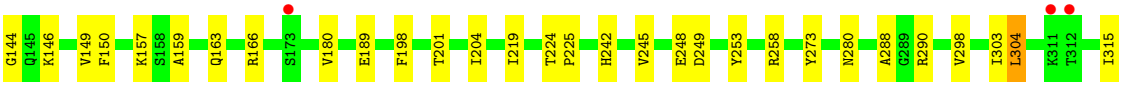




• Molecule 2: V-type sodium ATPase subunit B







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	179.41Å 125.08Å 180.91Å 90.00° 93.83° 90.00°	Depositor
Resolution (Å)	48.92 – 4.20 48.92 – 4.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.92-4.20) 99.9 (48.92-4.20)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.12 (at 4.14Å)	Xtriage
Refinement program	PHENIX 1.18_3845	Depositor
R, R_{free}	0.242 , 0.281 0.242 , 0.280	Depositor DCC
R_{free} test set	2921 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	116.2	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.24 , 76.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o,F_c correlation	0.87	EDS
Total number of atoms	47792	wwPDB-VP
Average B, all atoms (Å^2)	153.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.13% 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: MG, ADP

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	0.26	0/4638	0.46	0/6275
1	B	0.26	0/4185	0.47	1/5667 (0.0%)
1	C	0.26	0/4601	0.44	0/6230
1	G	0.26	0/4638	0.46	0/6275
1	H	0.26	0/4638	0.48	2/6275 (0.0%)
1	I	0.27	0/4585	0.46	1/6208 (0.0%)
2	D	0.26	0/3521	0.46	0/4757
2	E	0.26	0/3504	0.45	0/4734
2	F	0.26	0/3470	0.48	0/4685
2	J	0.27	0/3452	0.46	0/4663
2	K	0.26	0/3546	0.46	0/4798
2	L	0.25	0/3571	0.46	0/4824
All	All	0.26	0/48349	0.46	4/65391 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	482	LEU	CA-CB-CG	6.20	129.55	115.30
1	H	473	ILE	CG1-CB-CG2	-5.85	98.54	111.40
1	B	428	ILE	N-CA-C	-5.79	95.37	111.00
1	I	511	THR	CA-CB-CG2	-5.25	105.05	112.40

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	A	4562	0	4527	85	0
1	B	4113	0	4062	88	0
1	C	4525	0	4469	75	0
1	G	4562	0	4528	80	0
1	H	4562	0	4528	84	0
1	I	4509	0	4444	71	0
2	D	3461	0	3470	49	0
2	E	3444	0	3423	39	0
2	F	3412	0	3394	69	0
2	J	3396	0	3399	59	0
2	K	3485	0	3468	50	0
2	L	3509	0	3508	61	0
3	A	27	0	12	6	0
3	B	27	0	12	2	0
3	C	27	0	12	0	0
3	D	27	0	12	2	0
3	G	27	0	12	6	0
3	H	27	0	12	0	0
3	I	27	0	12	1	0
3	J	27	0	12	2	0
3	L	27	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	L	1	0	0	0	0
All	All	47792	0	47328	777	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 8.

The worst 5 of 777 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:F:137:HIS:CE1	2:F:372:LEU:HD12	1.83	1.13
2:F:137:HIS:HE1	2:F:372:LEU:HD12	1.27	0.94
1:A:55:THR:HG23	2:D:26:TYR:CD2	2.11	0.86
1:H:470:LEU:O	1:H:473:ILE:HG22	1.81	0.80
2:K:158:SER:OG	2:K:248:GLU:OE2	2.00	0.78

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	A	584/596 (98%)	563 (96%)	18 (3%)	3 (0%)	29 68
1	B	528/596 (89%)	503 (95%)	24 (4%)	1 (0%)	47 80
1	C	583/596 (98%)	562 (96%)	20 (3%)	1 (0%)	47 80
1	G	584/596 (98%)	550 (94%)	34 (6%)	0	100 100
1	H	584/596 (98%)	553 (95%)	31 (5%)	0	100 100
1	I	581/596 (98%)	559 (96%)	20 (3%)	2 (0%)	41 76
2	D	440/458 (96%)	424 (96%)	16 (4%)	0	100 100
2	E	442/458 (96%)	424 (96%)	18 (4%)	0	100 100
2	F	436/458 (95%)	417 (96%)	16 (4%)	3 (1%)	22 62
2	J	432/458 (94%)	417 (96%)	15 (4%)	0	100 100
2	K	448/458 (98%)	430 (96%)	17 (4%)	1 (0%)	47 80
2	L	450/458 (98%)	431 (96%)	19 (4%)	0	100 100
All	All	6092/6324 (96%)	5833 (96%)	248 (4%)	11 (0%)	47 80

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	234	PHE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	428	ILE
1	C	234	PHE
1	I	234	PHE
2	F	387	VAL

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	A	502/509 (99%)	495 (99%)	7 (1%)	67	80
1	B	452/509 (89%)	445 (98%)	7 (2%)	65	80
1	C	494/509 (97%)	485 (98%)	9 (2%)	59	76
1	G	502/509 (99%)	496 (99%)	6 (1%)	71	83
1	H	502/509 (99%)	497 (99%)	5 (1%)	76	86
1	I	491/509 (96%)	474 (96%)	17 (4%)	36	60
2	D	364/380 (96%)	360 (99%)	4 (1%)	73	84
2	E	356/380 (94%)	352 (99%)	4 (1%)	73	84
2	F	356/380 (94%)	350 (98%)	6 (2%)	60	78
2	J	357/380 (94%)	346 (97%)	11 (3%)	40	62
2	K	364/380 (96%)	361 (99%)	3 (1%)	81	89
2	L	367/380 (97%)	365 (100%)	2 (0%)	88	93
All	All	5107/5334 (96%)	5026 (98%)	81 (2%)	62	79

5 of 81 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	252	ASP
2	J	362	ARG
1	I	348	MET
2	J	146	LYS
2	J	417	PHE

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

Mol	Chain	Res	Type
2	F	163	GLN
1	G	424	HIS
2	J	381	GLN
1	H	518	GLN
1	I	153	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 9 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	ADP	A	601	4	24,29,29	0.97	1 (4%)	29,45,45	1.45	4 (13%)
3	ADP	H	601	4	24,29,29	0.95	1 (4%)	29,45,45	1.44	5 (17%)
3	ADP	D	601	-	24,29,29	0.96	1 (4%)	29,45,45	1.45	4 (13%)
3	ADP	C	601	4	24,29,29	0.96	1 (4%)	29,45,45	1.40	4 (13%)
3	ADP	G	601	4	24,29,29	0.96	1 (4%)	29,45,45	1.31	3 (10%)
3	ADP	I	601	4	24,29,29	0.96	1 (4%)	29,45,45	1.46	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	ADP	J	601	4	24,29,29	0.95	1 (4%)	29,45,45	1.42	4 (13%)
3	ADP	B	601	4	24,29,29	0.97	1 (4%)	29,45,45	1.39	4 (13%)
3	ADP	L	601	4	24,29,29	0.95	1 (4%)	29,45,45	1.40	4 (13%)

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	ADP	A	601	4	-	4/12/32/32	0/3/3/3
3	ADP	H	601	4	-	2/12/32/32	0/3/3/3
3	ADP	D	601	-	-	2/12/32/32	0/3/3/3
3	ADP	C	601	4	-	0/12/32/32	0/3/3/3
3	ADP	G	601	4	-	3/12/32/32	0/3/3/3
3	ADP	I	601	4	-	4/12/32/32	0/3/3/3
3	ADP	J	601	4	-	2/12/32/32	0/3/3/3
3	ADP	B	601	4	-	5/12/32/32	0/3/3/3
3	ADP	L	601	4	-	3/12/32/32	0/3/3/3

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	601	ADP	C5-C4	2.54	1.47	1.40
3	B	601	ADP	C5-C4	2.53	1.47	1.40
3	C	601	ADP	C5-C4	2.52	1.47	1.40
3	H	601	ADP	C5-C4	2.52	1.47	1.40
3	A	601	ADP	C5-C4	2.51	1.47	1.40

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	I	601	ADP	PA-O3A-PB	-3.55	120.64	132.83
3	H	601	ADP	PA-O3A-PB	-3.46	120.95	132.83
3	A	601	ADP	PA-O3A-PB	-3.46	120.97	132.83
3	C	601	ADP	PA-O3A-PB	-3.36	121.29	132.83
3	D	601	ADP	N3-C2-N1	-3.31	123.50	128.68

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	ADP	C5'-O5'-PA-O1A
3	B	601	ADP	O4'-C4'-C5'-O5'
3	B	601	ADP	C3'-C4'-C5'-O5'
3	D	601	ADP	C5'-O5'-PA-O1A
3	H	601	ADP	C5'-O5'-PA-O1A

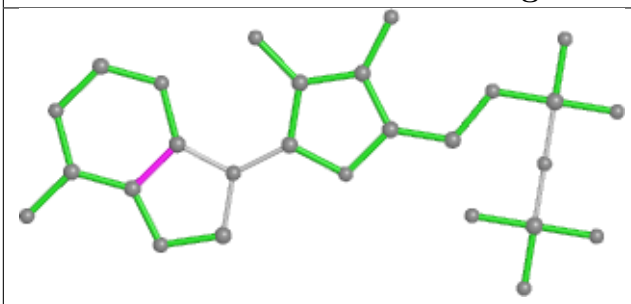
There are no ring outliers.

6 monomers are involved in 19 short contacts:

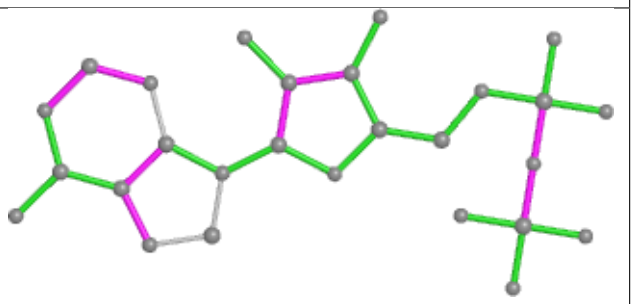
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	ADP	6	0
3	D	601	ADP	2	0
3	G	601	ADP	6	0
3	I	601	ADP	1	0
3	J	601	ADP	2	0
3	B	601	ADP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

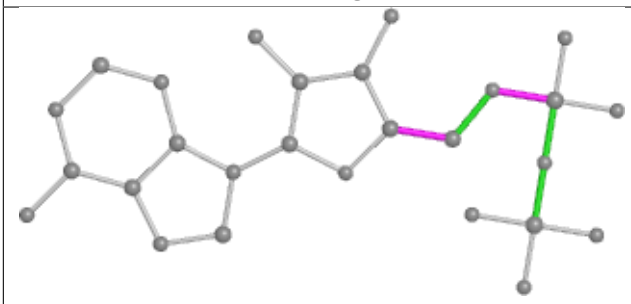
Ligand ADP A 601



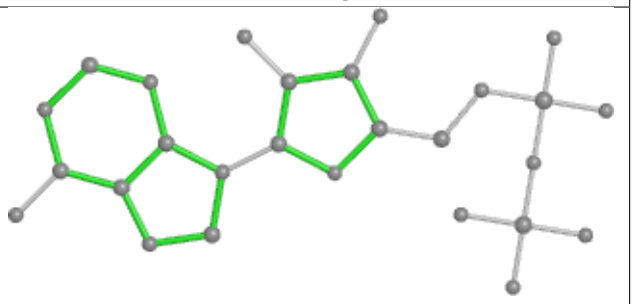
Bond lengths



Bond angles

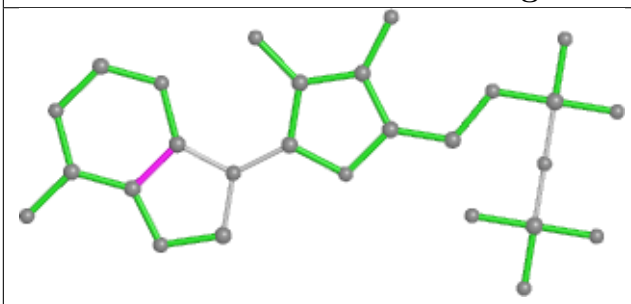


Torsions

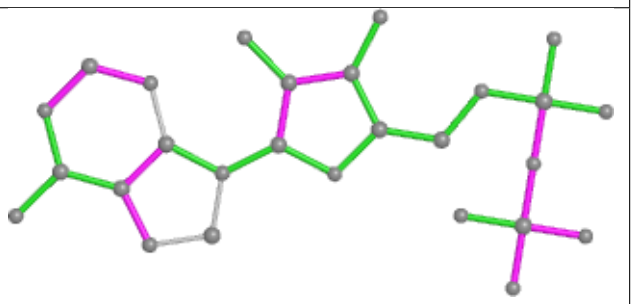


Rings

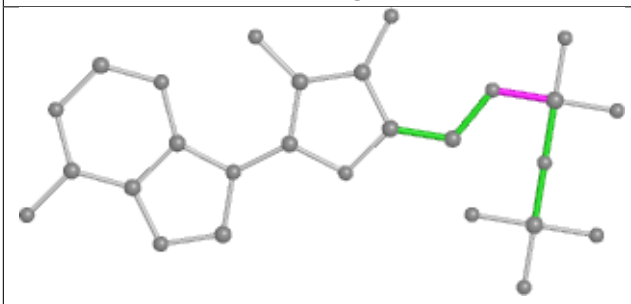
Ligand ADP H 601



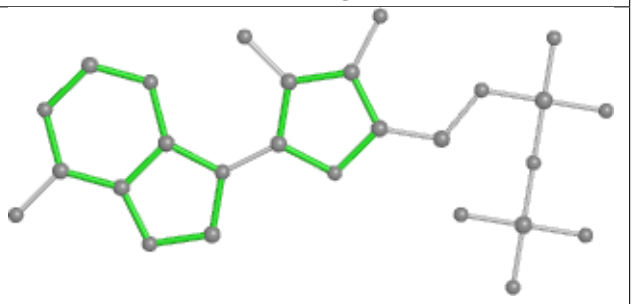
Bond lengths



Bond angles

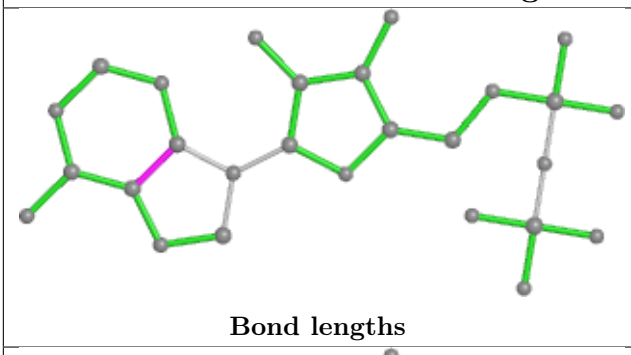


Torsions

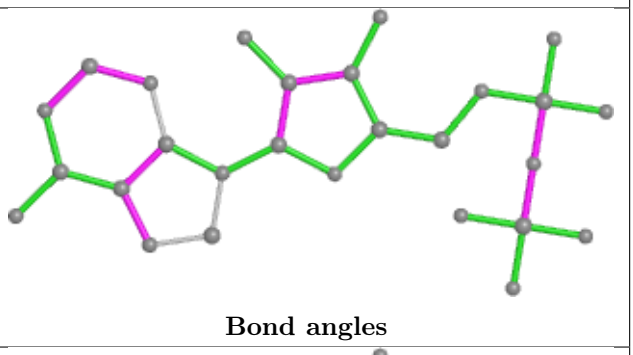


Rings

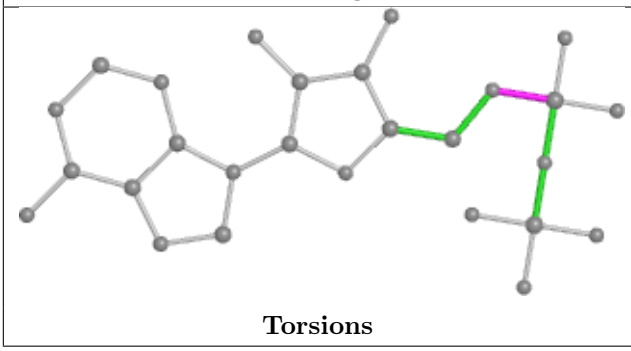
Ligand ADP D 601



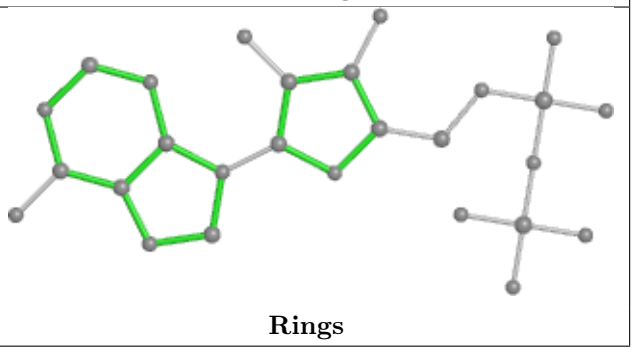
Bond lengths



Bond angles

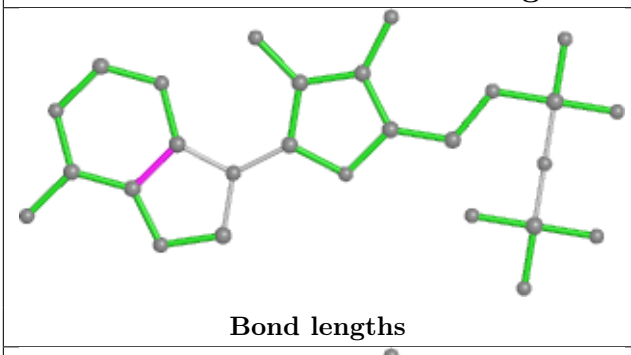


Torsions

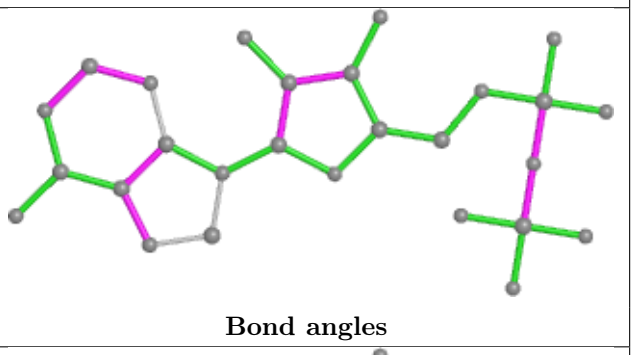


Rings

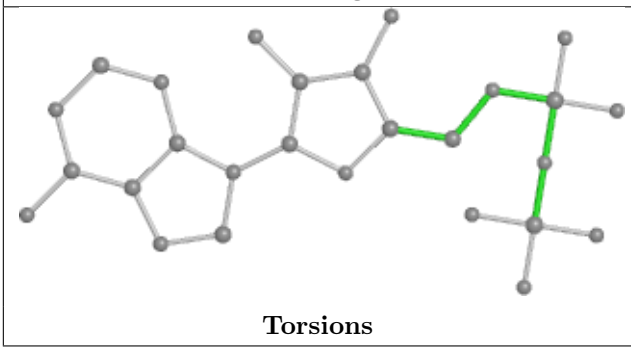
Ligand ADP C 601



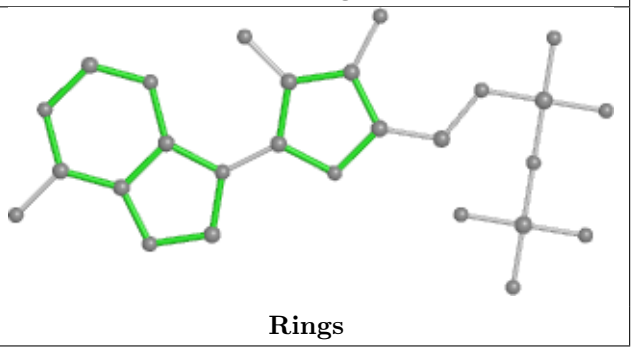
Bond lengths



Bond angles

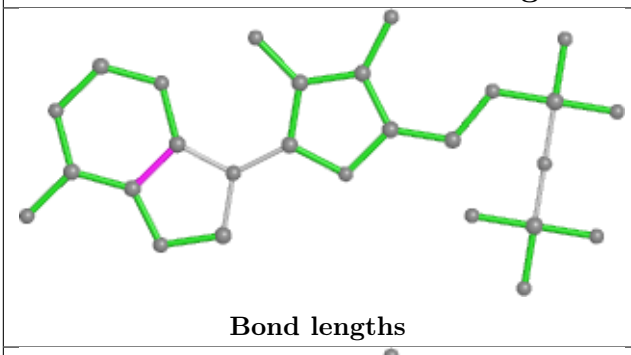


Torsions

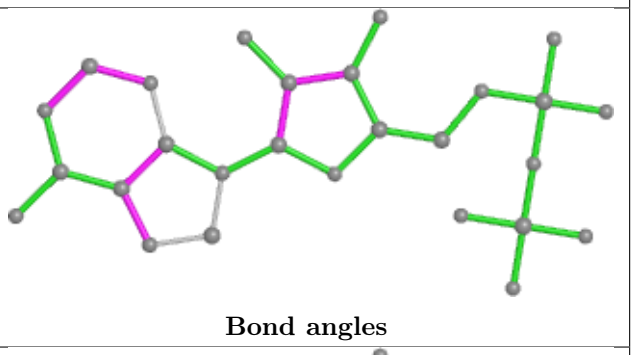


Rings

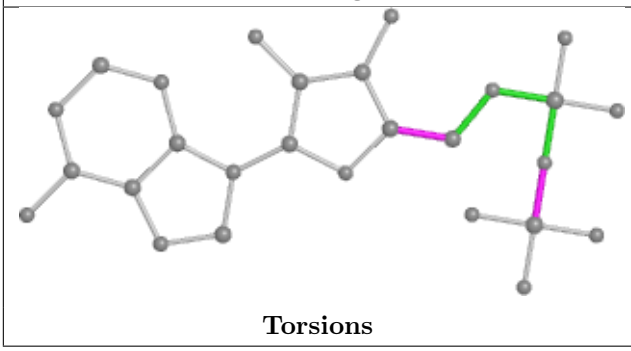
Ligand ADP G 601



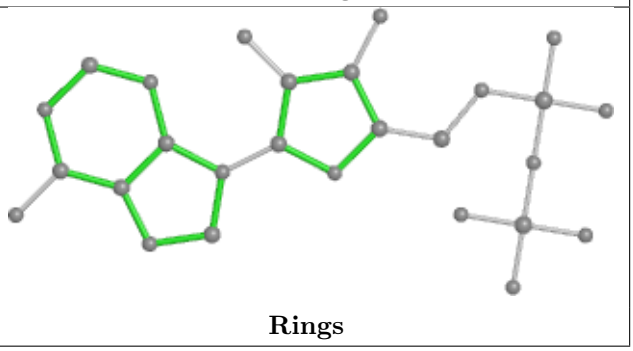
Bond lengths



Bond angles

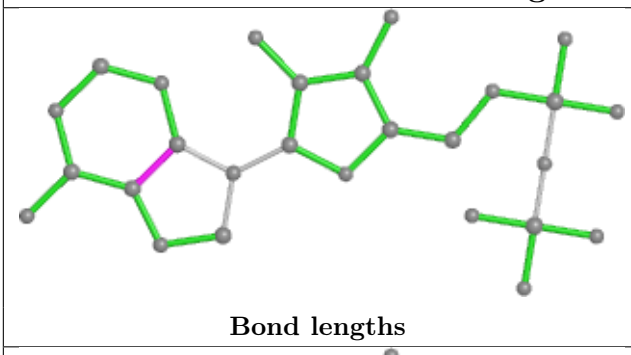


Torsions

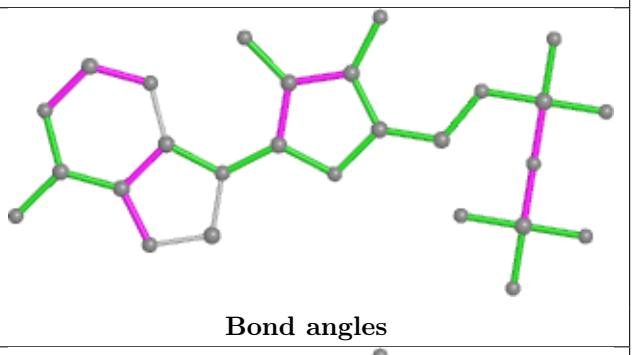


Rings

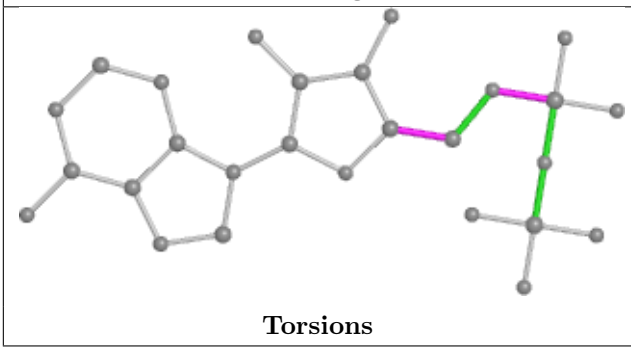
Ligand ADP I 601



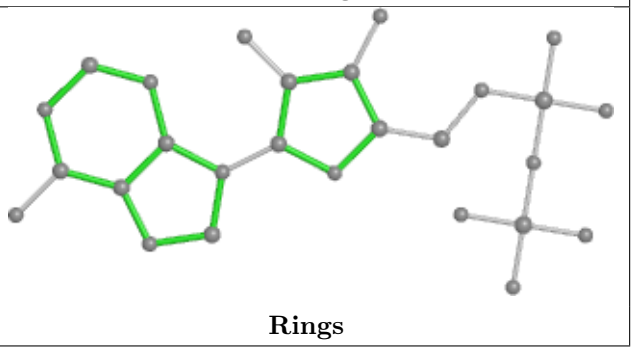
Bond lengths



Bond angles

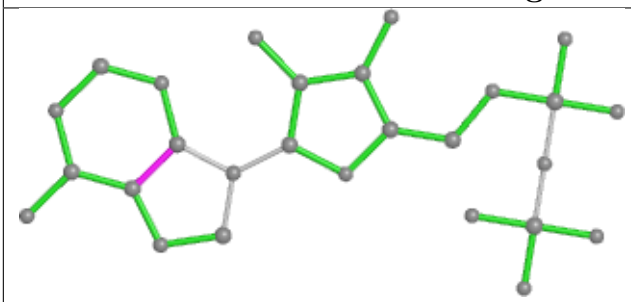


Torsions

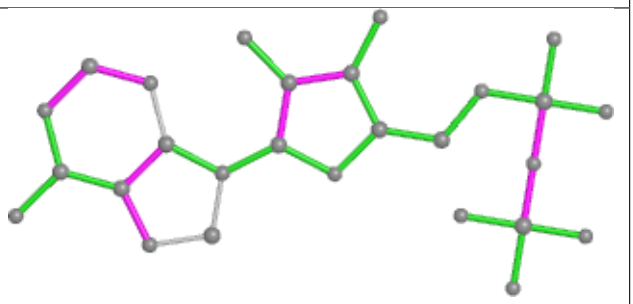


Rings

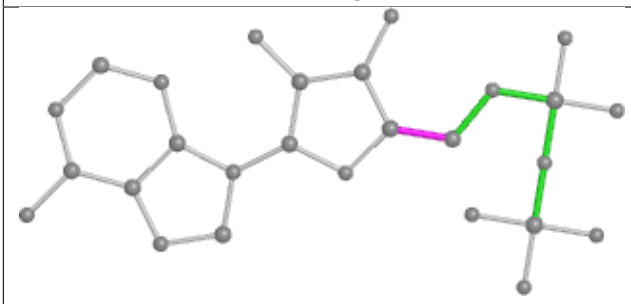
Ligand ADP J 601



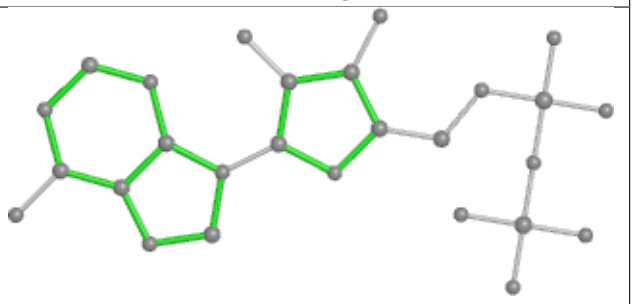
Bond lengths



Bond angles

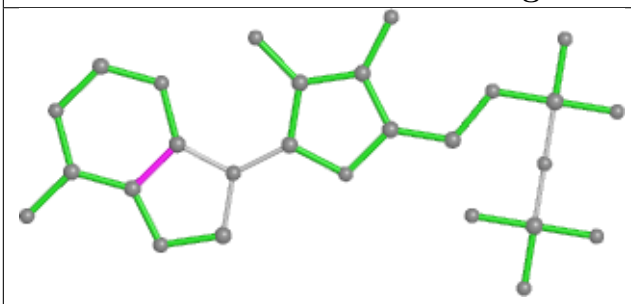


Torsions

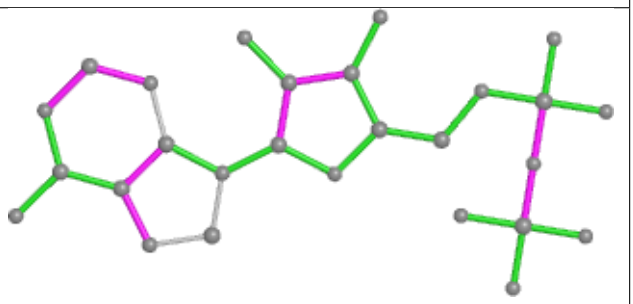


Rings

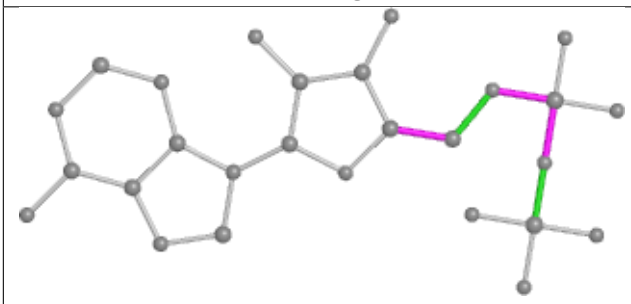
Ligand ADP B 601



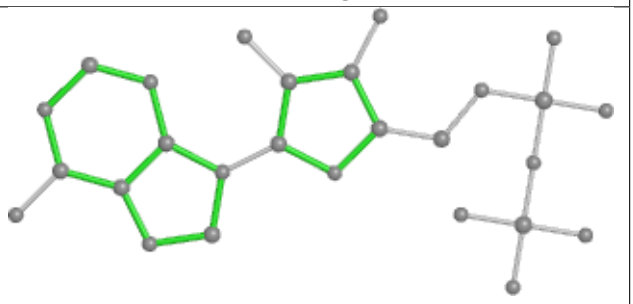
Bond lengths



Bond angles

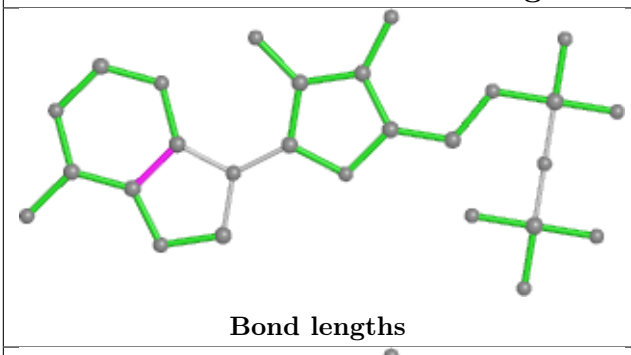


Torsions

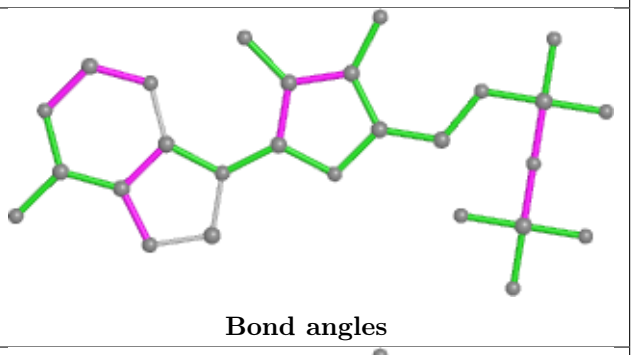


Rings

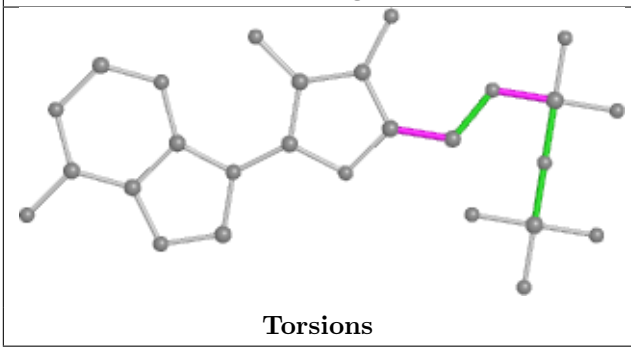
Ligand ADP L 601



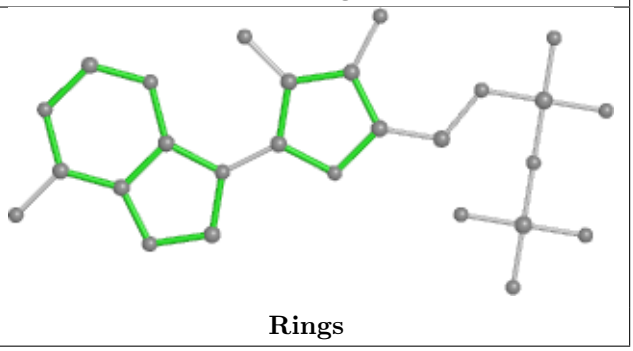
Bond lengths



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	A	586/596 (98%)	-0.33	1 (0%) 95 93	53, 110, 202, 240	0
1	B	530/596 (88%)	0.04	15 (2%) 53 42	91, 197, 290, 308	0
1	C	585/596 (98%)	-0.29	1 (0%) 95 93	91, 143, 201, 235	0
1	G	586/596 (98%)	-0.15	11 (1%) 66 58	62, 137, 252, 279	0
1	H	586/596 (98%)	-0.14	4 (0%) 87 82	85, 166, 241, 266	0
1	I	583/596 (97%)	-0.38	0 100 100	75, 118, 195, 228	0
2	D	444/458 (96%)	-0.31	2 (0%) 91 86	80, 132, 230, 265	0
2	E	446/458 (97%)	-0.19	1 (0%) 95 93	72, 163, 226, 242	0
2	F	442/458 (96%)	0.03	13 (2%) 51 41	95, 164, 247, 276	0
2	J	438/458 (95%)	-0.35	1 (0%) 95 93	66, 113, 214, 252	0
2	K	450/458 (98%)	-0.30	1 (0%) 95 93	78, 150, 213, 253	0
2	L	452/458 (98%)	-0.21	5 (1%) 80 72	76, 158, 224, 245	0
All	All	6128/6324 (96%)	-0.22	55 (0%) 84 77	53, 147, 237, 308	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	522	LEU	3.7
1	B	520	ASN	3.5
2	J	309	ASP	3.4
1	B	218	THR	3.2
1	H	520	ASN	3.0

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 (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

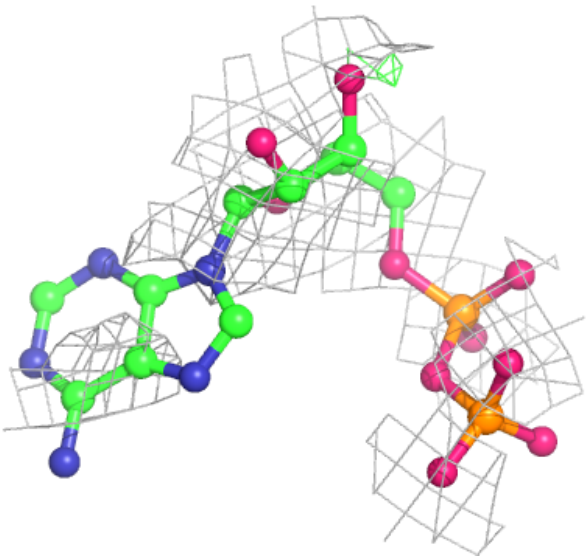
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

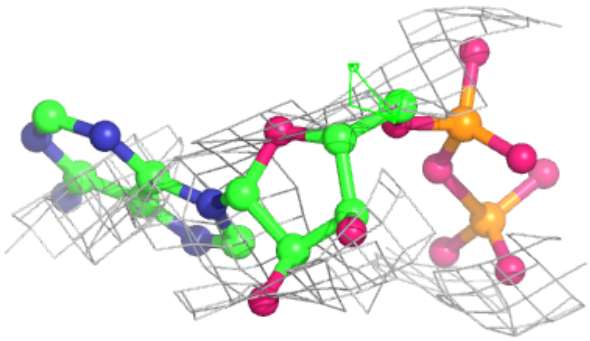
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ADP	L	601	27/27	0.76	0.33	173,195,203,211	0
4	MG	B	602	1/1	0.79	0.46	229,229,229,229	0
4	MG	H	602	1/1	0.80	0.49	156,156,156,156	0
3	ADP	B	601	27/27	0.81	0.30	213,233,249,253	0
3	ADP	D	601	27/27	0.83	0.31	144,167,172,174	0
4	MG	A	602	1/1	0.83	1.00	89,89,89,89	0
3	ADP	G	601	27/27	0.84	0.33	163,200,226,228	0
3	ADP	J	601	27/27	0.84	0.29	123,147,158,165	0
4	MG	G	602	1/1	0.86	0.71	145,145,145,145	0
3	ADP	C	601	27/27	0.87	0.26	139,156,168,170	0
4	MG	C	602	1/1	0.90	0.51	119,119,119,119	0
3	ADP	A	601	27/27	0.90	0.29	113,161,179,183	0
3	ADP	I	601	27/27	0.90	0.38	121,143,165,168	0
4	MG	I	602	1/1	0.90	1.02	85,85,85,85	0
3	ADP	H	601	27/27	0.91	0.30	161,182,203,204	0
4	MG	L	602	1/1	0.94	0.14	182,182,182,182	0
4	MG	D	602	1/1	0.95	0.30	129,129,129,129	0
4	MG	J	602	1/1	0.97	0.17	107,107,107,107	0

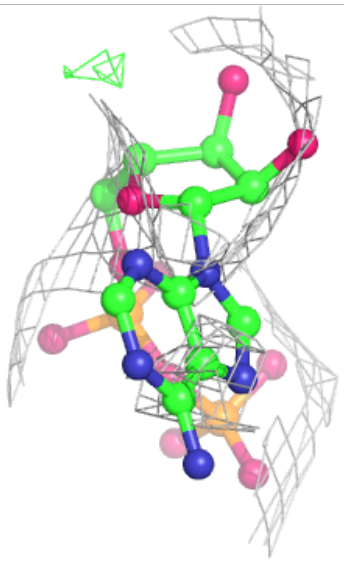
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP L 601:

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

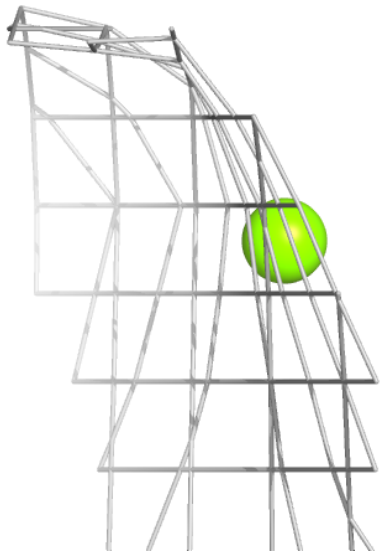


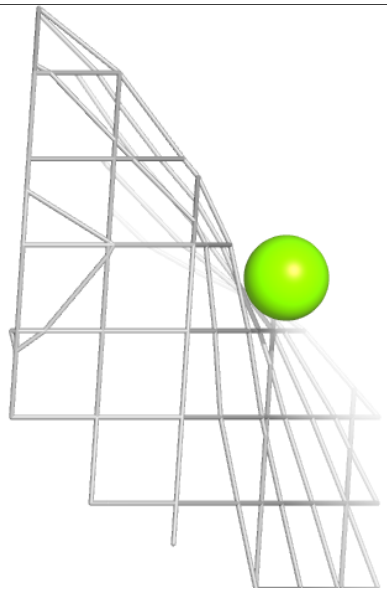


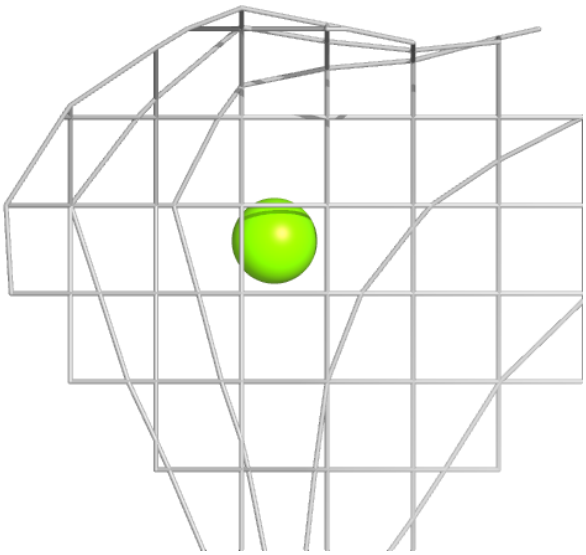


Electron density around MG B 602:

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

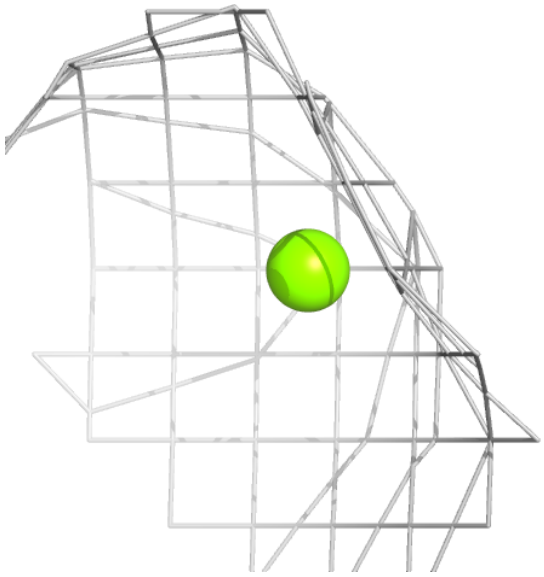


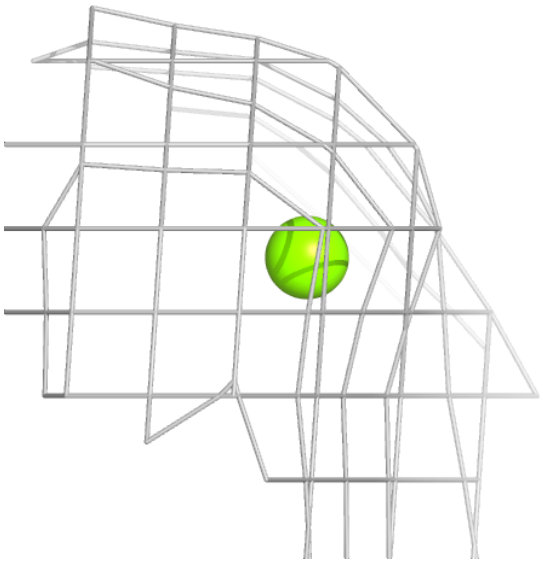


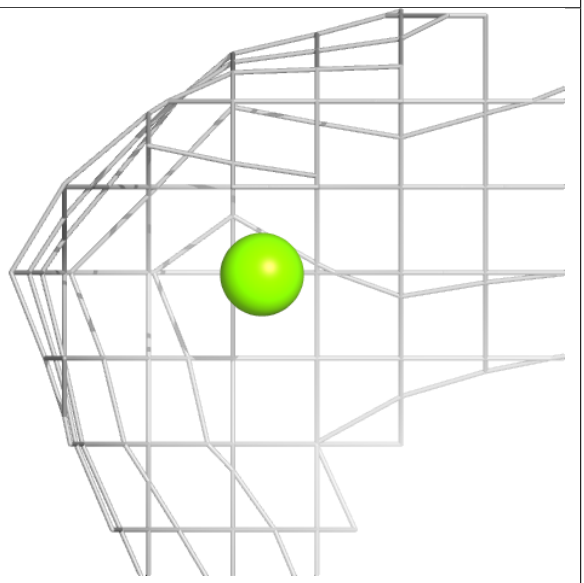


Electron density around MG H 602:

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

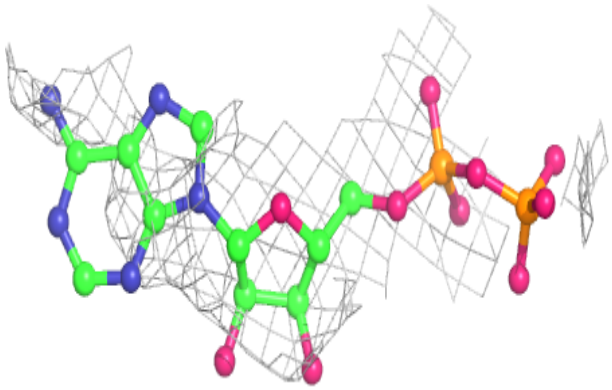


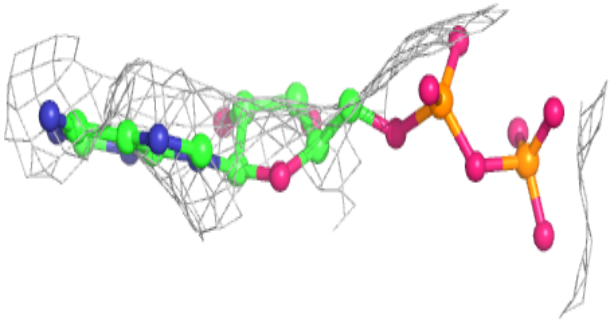


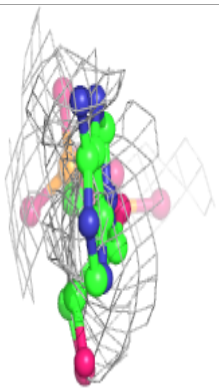


Electron density around ADP B 601:

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

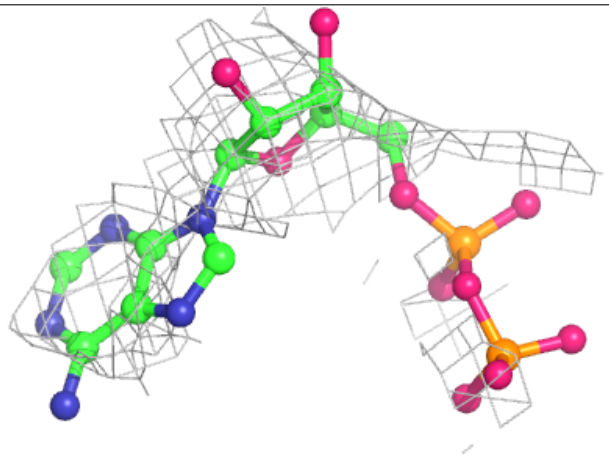


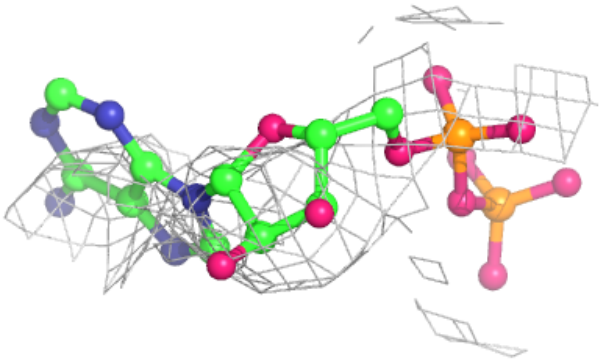


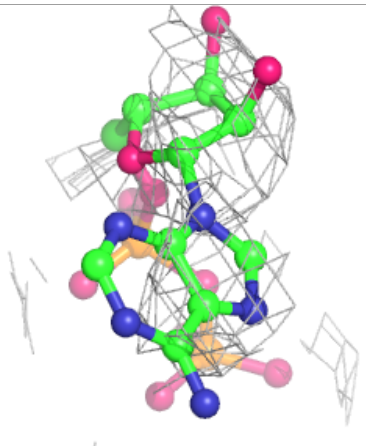


Electron density around ADP D 601:

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

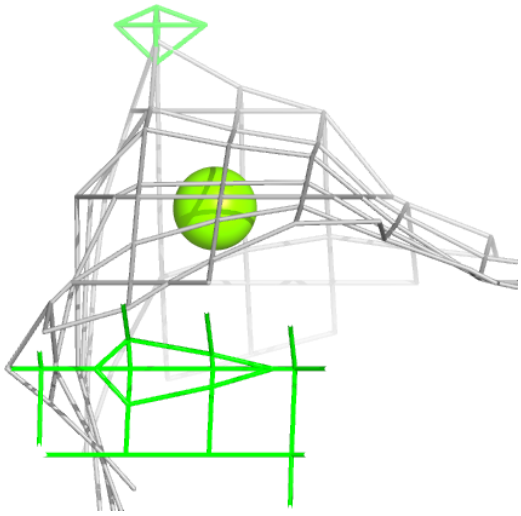


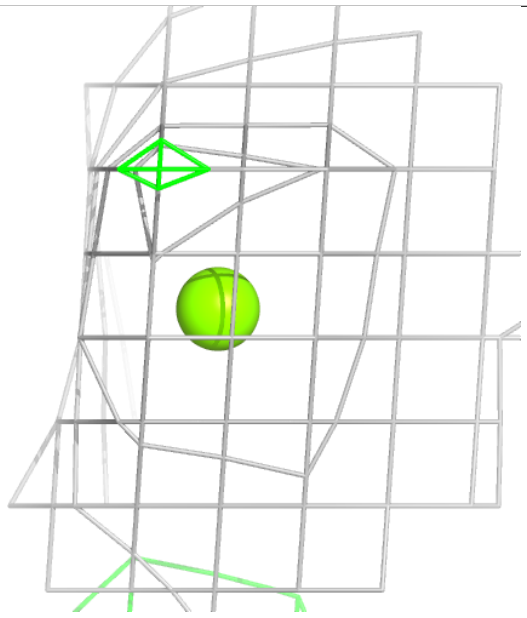


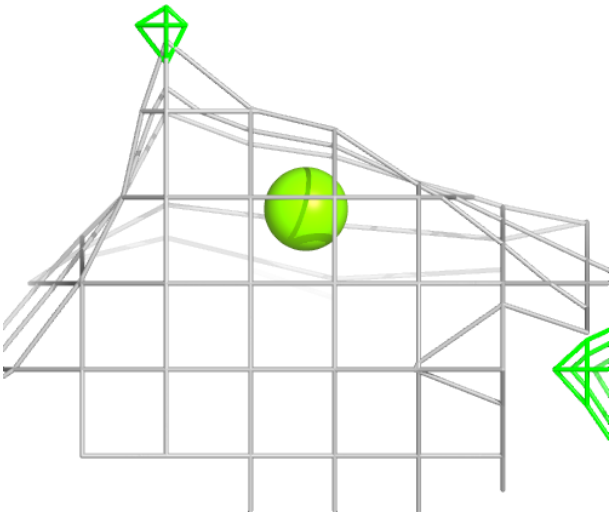


Electron density around MG A 602:

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

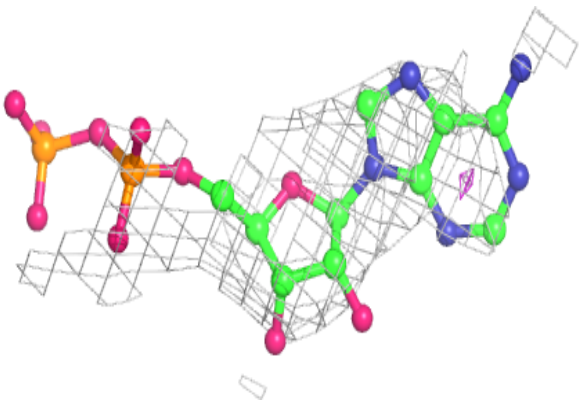


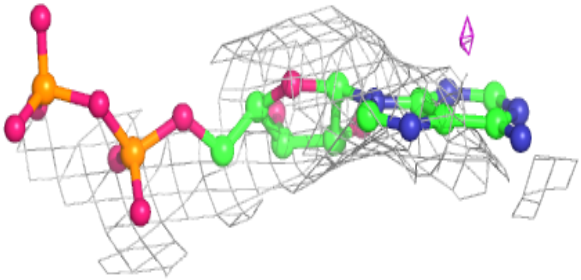


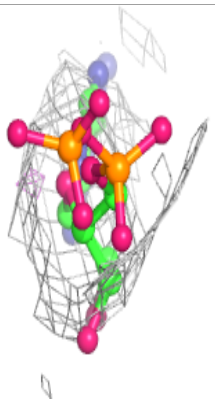


Electron density around ADP G 601:

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

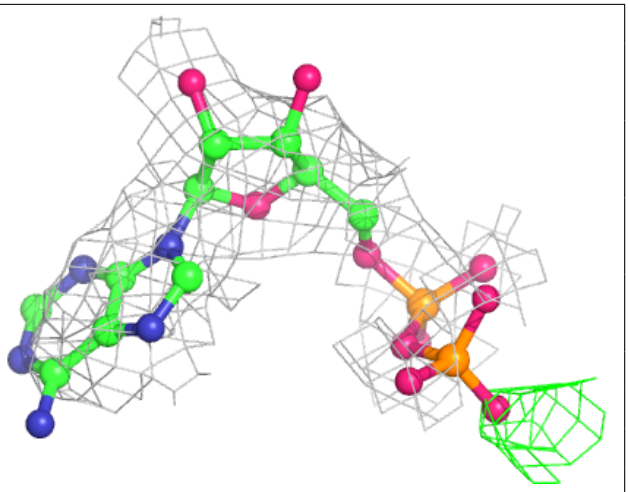


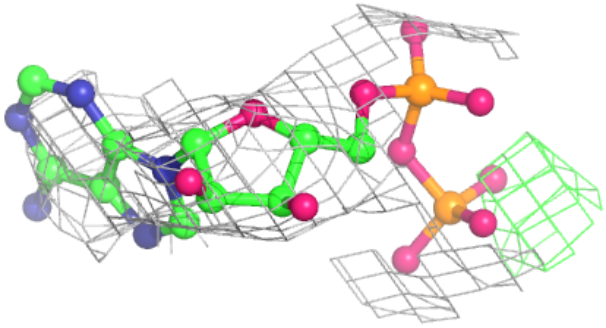


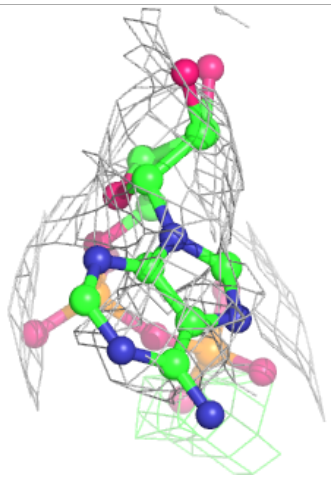


Electron density around ADP J 601:

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

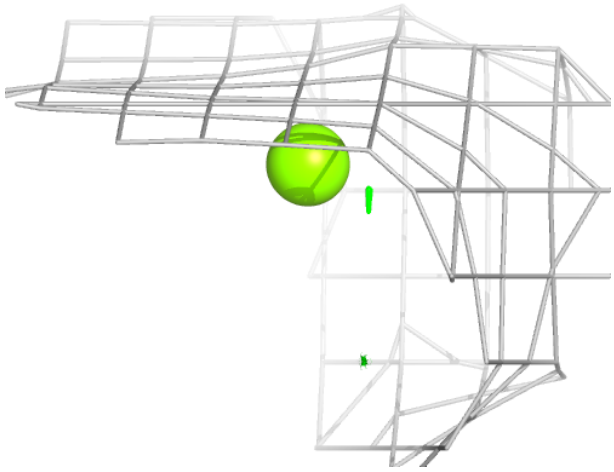


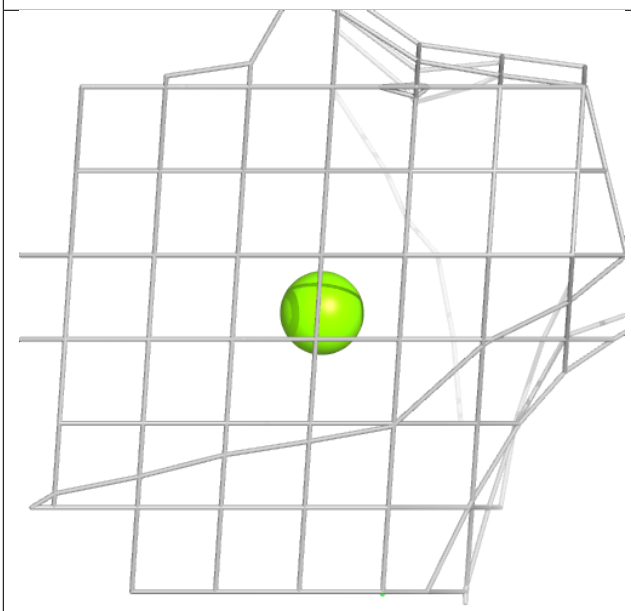


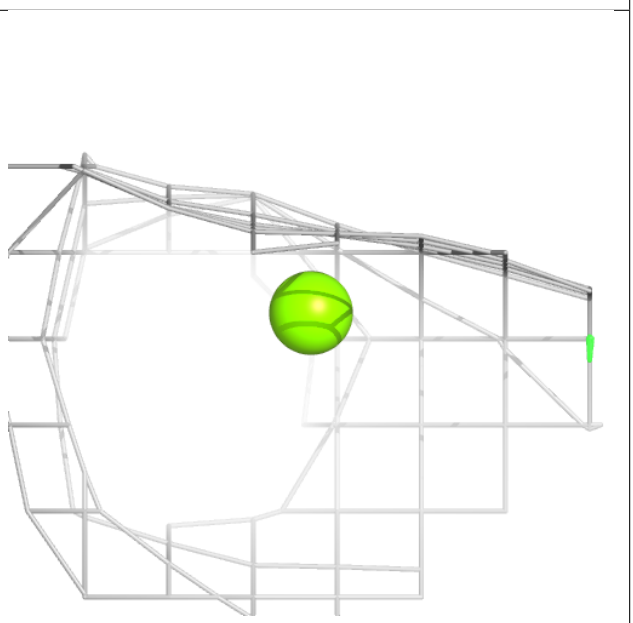


Electron density around MG G 602:

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

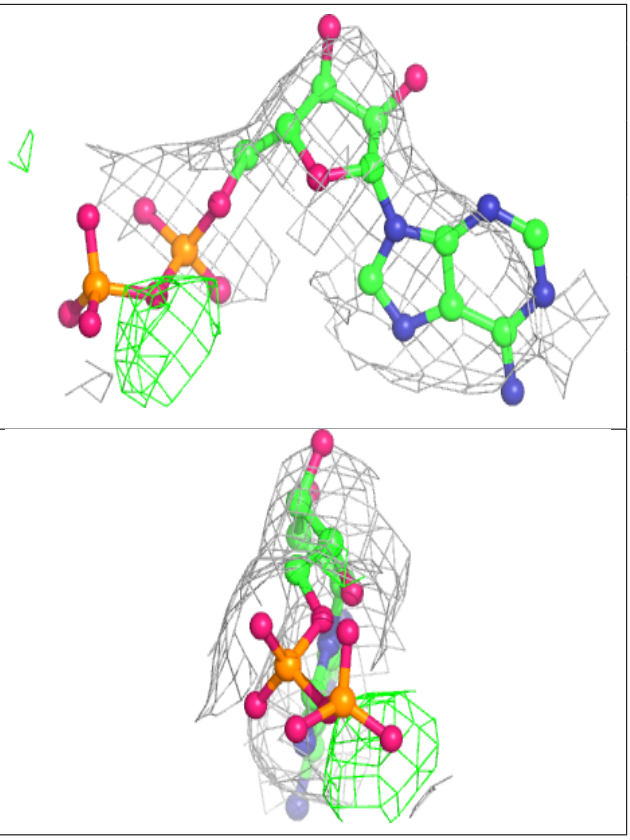


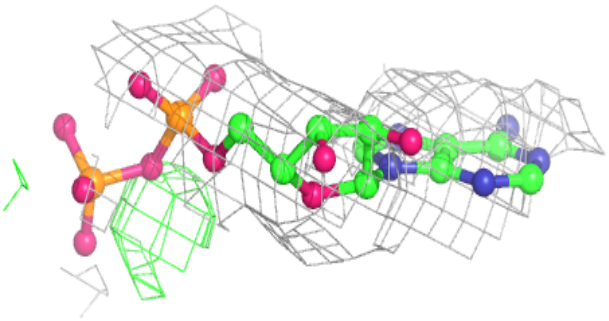




Electron density around ADP C 601:

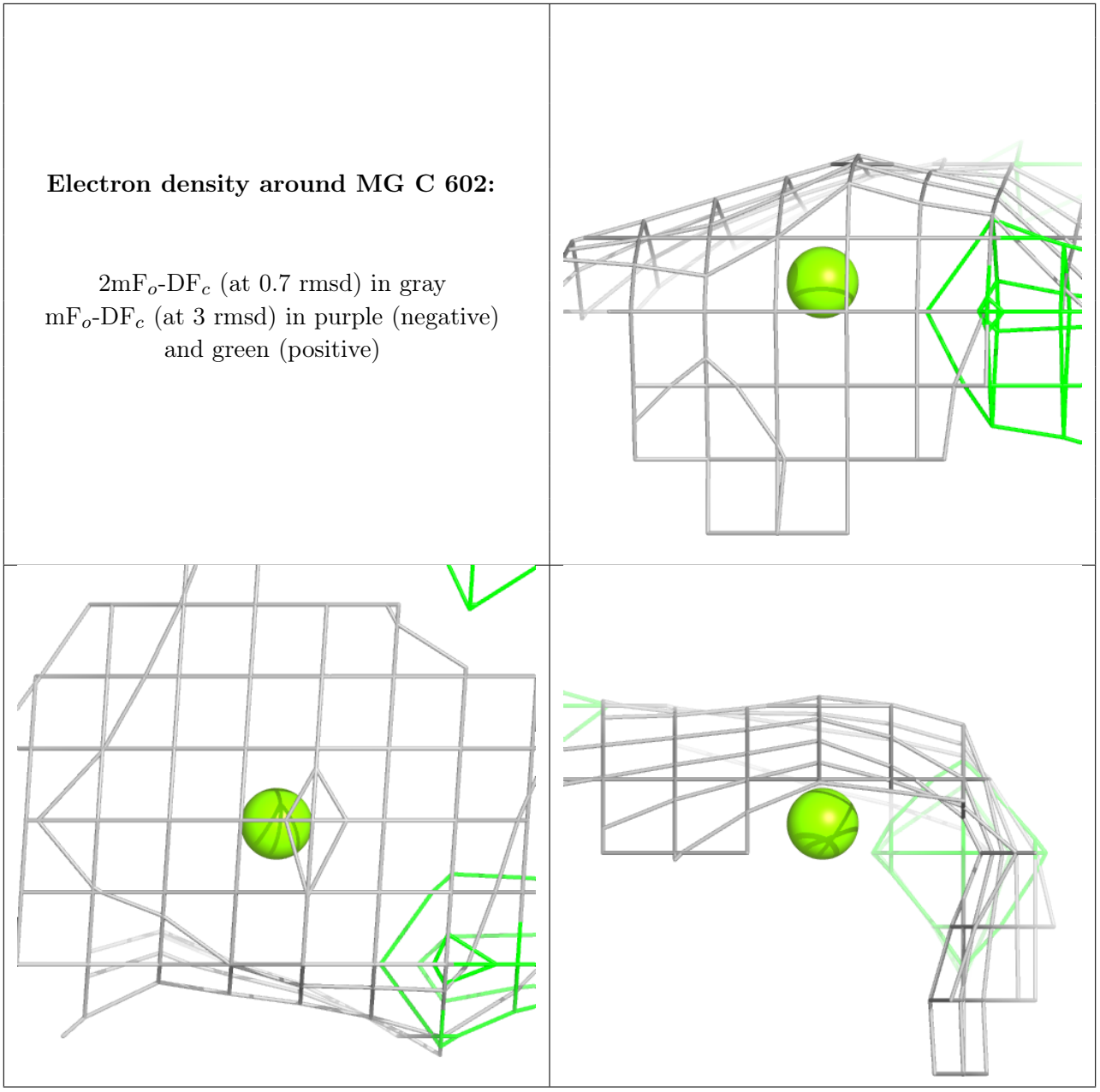
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





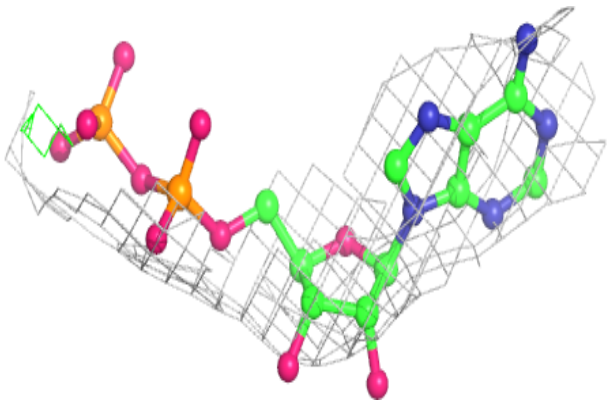
Electron density around MG C 602:

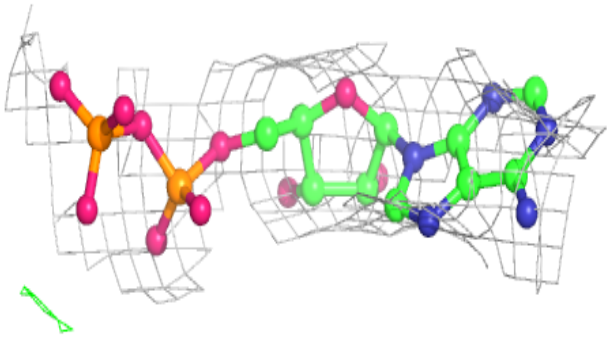
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

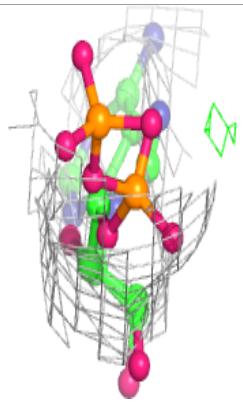


Electron density around ADP A 601:

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

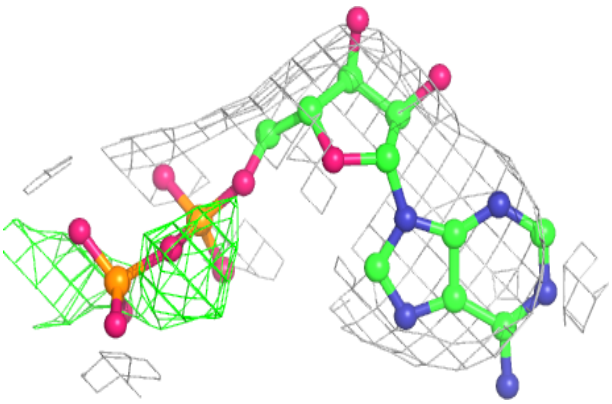


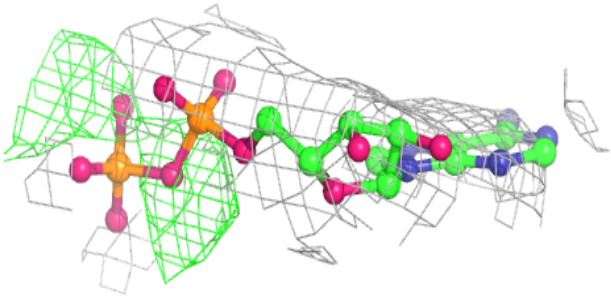


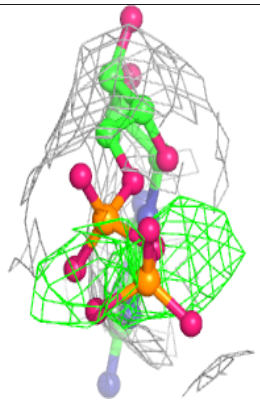


Electron density around ADP I 601:

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

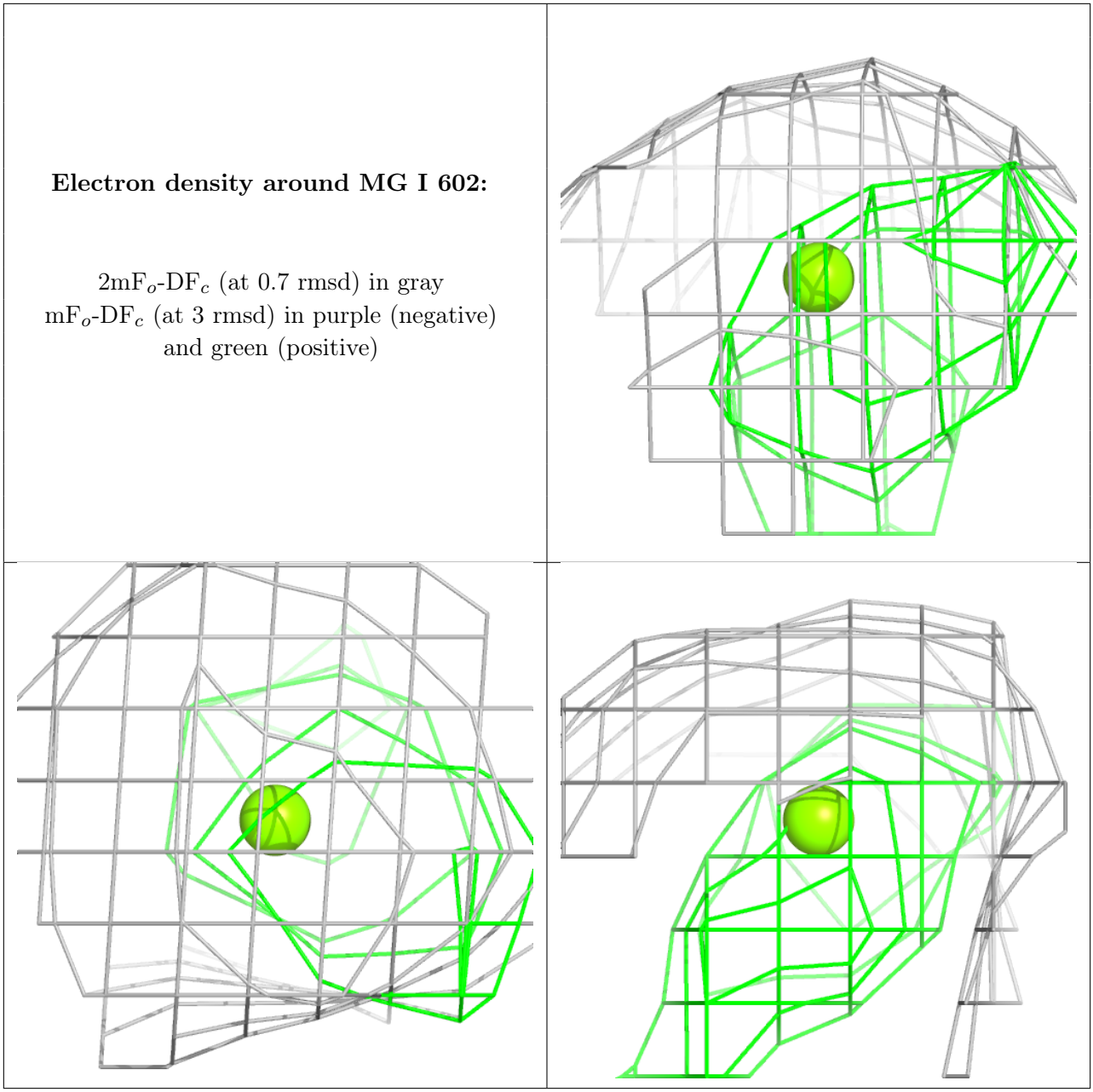






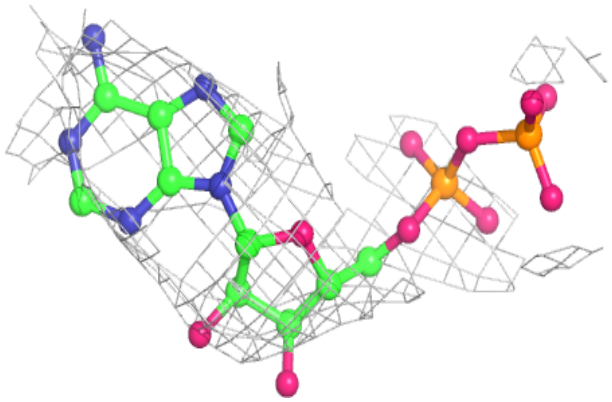
Electron density around MG I 602:

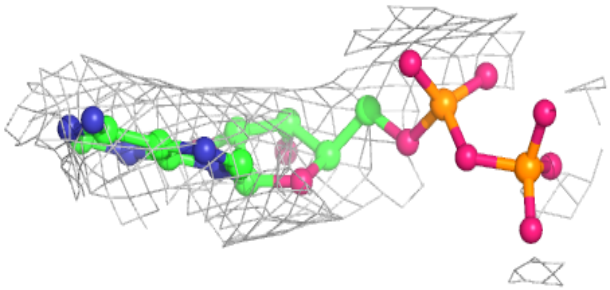
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

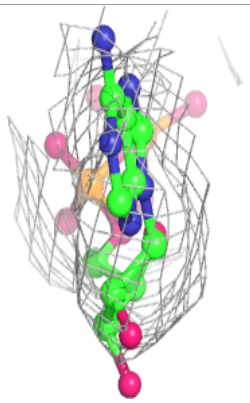


Electron density around ADP H 601:

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

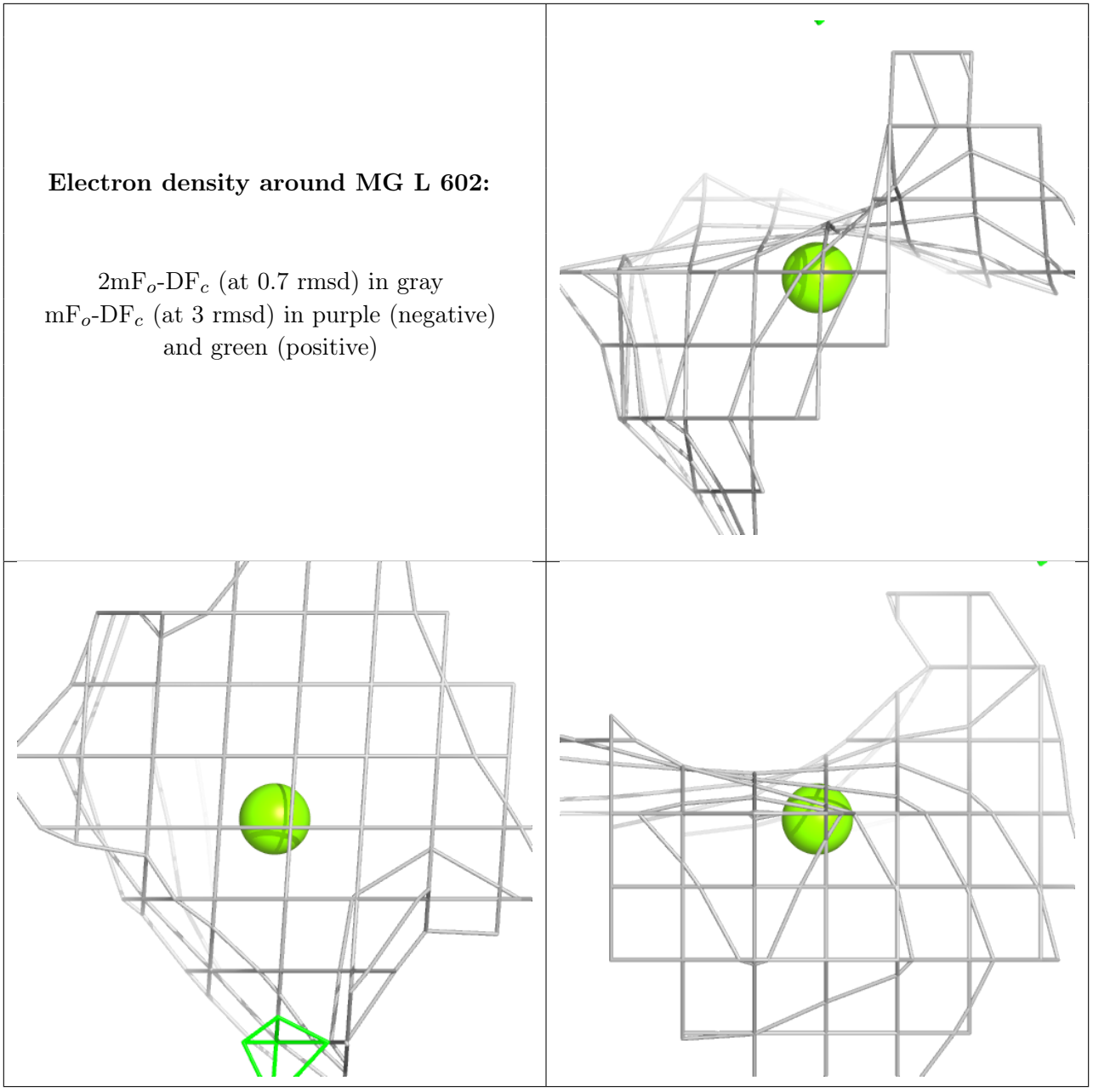






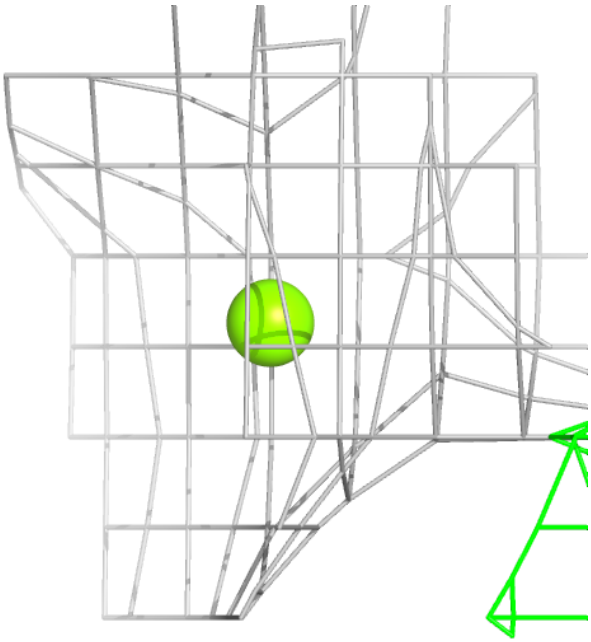
Electron density around MG L 602:

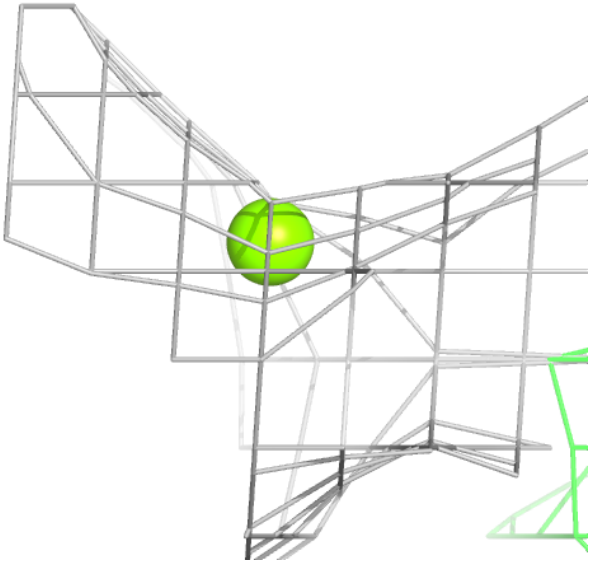
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

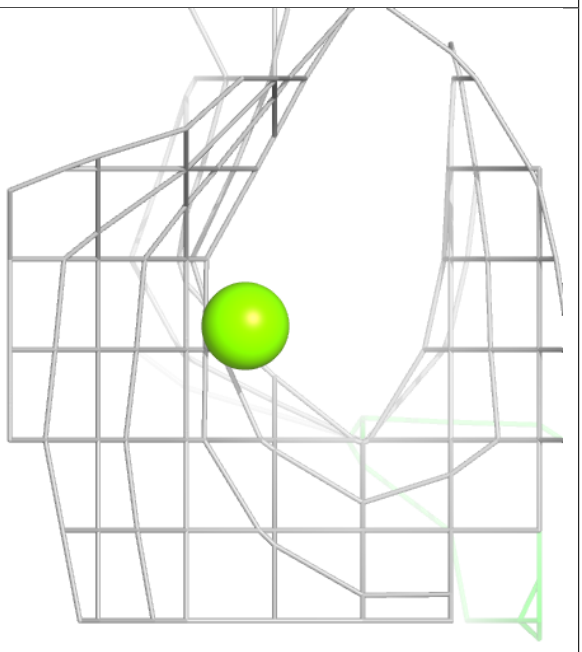


Electron density around MG D 602:

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

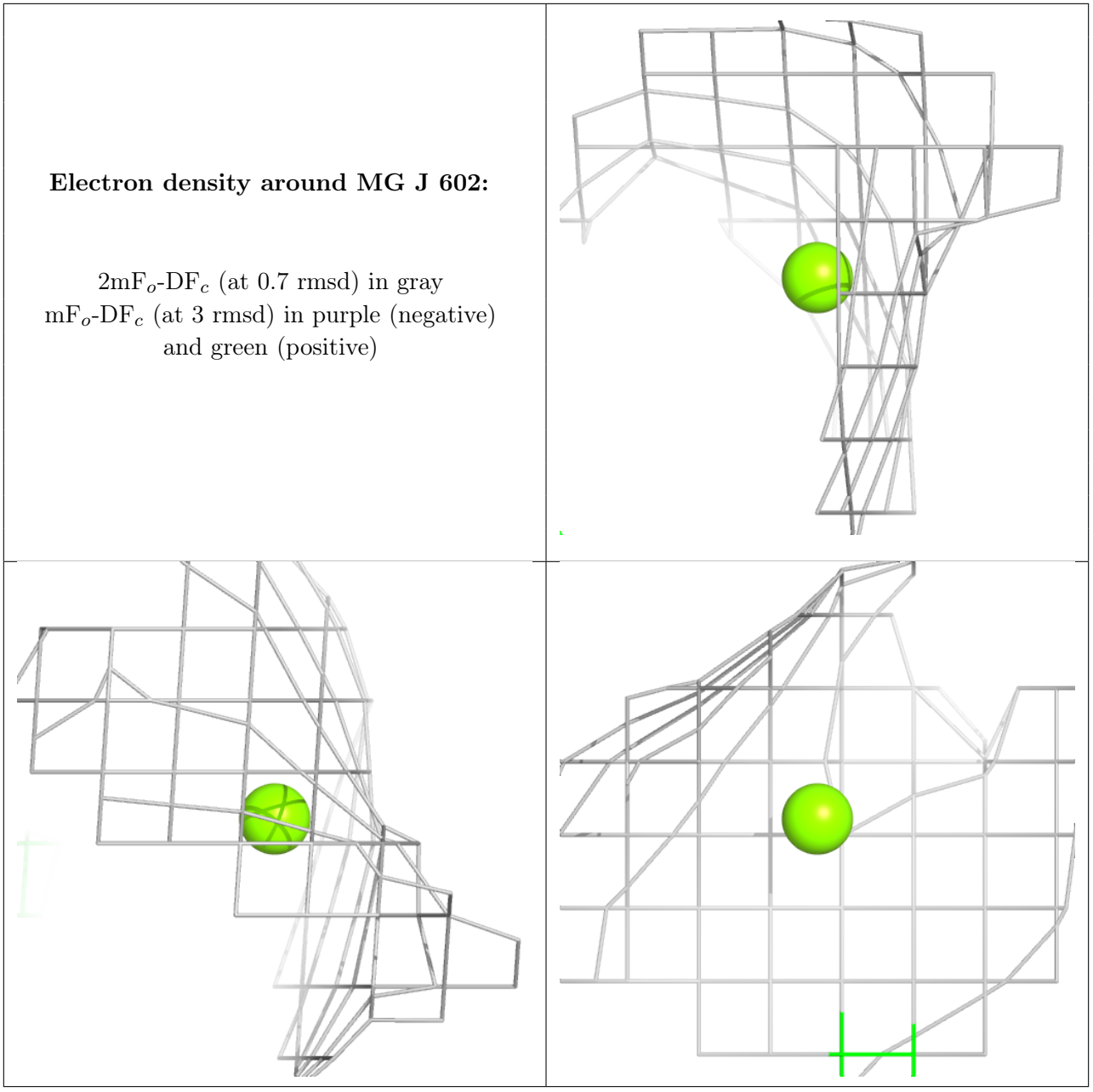






Electron density around MG J 602:

$2mF_o$-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.