



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:46 PM UTC

PDB ID : 8HRZ / pdb_00008hrz
Title : Crystal structure of the p97-N/D1 hexamer in complex with six p47-UBX domains
Authors : Nguyen, T.Q.; Kang, W.
Deposited on : 2022-12-16
Resolution : 2.70 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

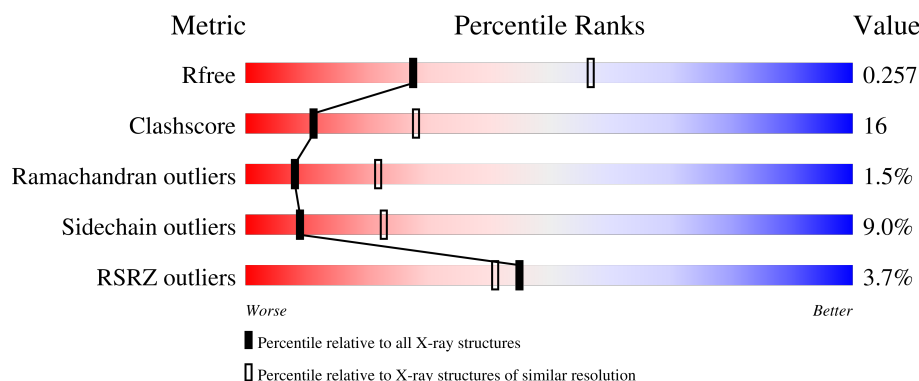
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	438	3% 72% 23% .
1	B	438	3% 70% 26% ..
1	C	438	3% 71% 24% ..
1	D	438	5% 67% 26% 6%
1	E	438	5% 67% 25% 6% .

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Mol	Chain	Length	Quality of chain
1	F	438	
1	G	438	
1	H	438	
1	I	438	
1	J	438	
1	K	438	
1	L	438	
2	M	85	
2	N	85	
2	O	85	
2	P	85	
2	Q	85	
2	R	85	
2	S	85	
2	T	85	
2	U	85	
2	V	85	
2	W	85	
2	X	85	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 49084 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 Transitional endoplasmic reticulum ATPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	436	Total	C	N	O	S	0	0	0
			3404	2139	605	642	18			
1	B	436	Total	C	N	O	S	0	0	0
			3404	2139	605	642	18			
1	C	436	Total	C	N	O	S	0	0	0
			3394	2133	601	642	18			
1	D	436	Total	C	N	O	S	0	0	0
			3398	2136	602	642	18			
1	E	436	Total	C	N	O	S	0	0	0
			3360	2116	585	641	18			
1	F	436	Total	C	N	O	S	0	0	0
			3404	2139	605	642	18			
1	G	436	Total	C	N	O	S	0	0	0
			3380	2125	596	641	18			
1	H	436	Total	C	N	O	S	0	0	0
			3404	2139	605	642	18			
1	I	436	Total	C	N	O	S	0	0	0
			3404	2139	605	642	18			
1	J	436	Total	C	N	O	S	0	0	0
			3398	2136	602	642	18			
1	K	436	Total	C	N	O	S	0	0	0
			3404	2139	605	642	18			
1	L	436	Total	C	N	O	S	0	0	0
			3384	2128	597	641	18			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	294	ALA	GLU	engineered mutation	UNP P55072
A	295	ALA	LYS	engineered mutation	UNP P55072
B	294	ALA	GLU	engineered mutation	UNP P55072
B	295	ALA	LYS	engineered mutation	UNP P55072
C	294	ALA	GLU	engineered mutation	UNP P55072

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Chain	Residue	Modelled	Actual	Comment	Reference
C	295	ALA	LYS	engineered mutation	UNP P55072
D	294	ALA	GLU	engineered mutation	UNP P55072
D	295	ALA	LYS	engineered mutation	UNP P55072
E	294	ALA	GLU	engineered mutation	UNP P55072
E	295	ALA	LYS	engineered mutation	UNP P55072
F	294	ALA	GLU	engineered mutation	UNP P55072
F	295	ALA	LYS	engineered mutation	UNP P55072
G	294	ALA	GLU	engineered mutation	UNP P55072
G	295	ALA	LYS	engineered mutation	UNP P55072
H	294	ALA	GLU	engineered mutation	UNP P55072
H	295	ALA	LYS	engineered mutation	UNP P55072
I	294	ALA	GLU	engineered mutation	UNP P55072
I	295	ALA	LYS	engineered mutation	UNP P55072
J	294	ALA	GLU	engineered mutation	UNP P55072
J	295	ALA	LYS	engineered mutation	UNP P55072
K	294	ALA	GLU	engineered mutation	UNP P55072
K	295	ALA	LYS	engineered mutation	UNP P55072
L	294	ALA	GLU	engineered mutation	UNP P55072
L	295	ALA	LYS	engineered mutation	UNP P55072

- Molecule 2 is a protein called NSFL1 cofactor p47.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	M	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	N	85	Total	C	N	O	S	0	0	0
			664	419	116	126	3			
2	O	85	Total	C	N	O	S	0	0	0
			664	419	116	126	3			
2	P	85	Total	C	N	O	S	0	0	0
			664	419	116	126	3			
2	Q	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	R	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	S	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	T	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	U	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	V	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			

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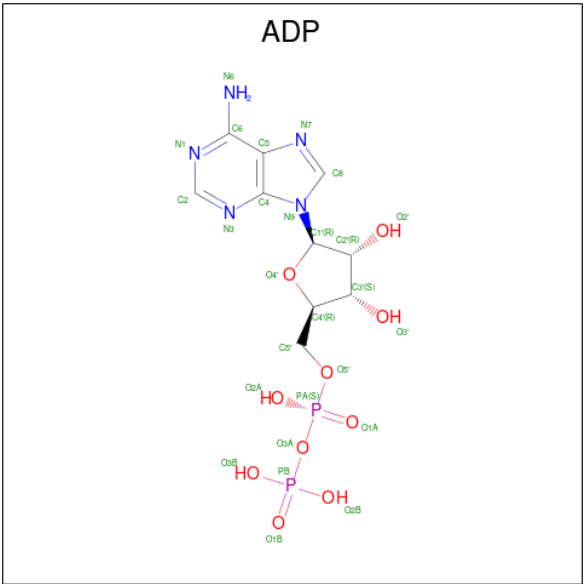
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	W	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			
2	X	85	Total	C	N	O	S	0	0	0
			670	422	119	126	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	286	MET	-	initiating methionine	UNP Q9UNZ2
N	286	MET	-	initiating methionine	UNP Q9UNZ2
O	286	MET	-	initiating methionine	UNP Q9UNZ2
P	286	MET	-	initiating methionine	UNP Q9UNZ2
Q	286	MET	-	initiating methionine	UNP Q9UNZ2
R	286	MET	-	initiating methionine	UNP Q9UNZ2
S	286	MET	-	initiating methionine	UNP Q9UNZ2
T	286	MET	-	initiating methionine	UNP Q9UNZ2
U	286	MET	-	initiating methionine	UNP Q9UNZ2
V	286	MET	-	initiating methionine	UNP Q9UNZ2
W	286	MET	-	initiating methionine	UNP Q9UNZ2
X	286	MET	-	initiating methionine	UNP Q9UNZ2

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (labeled as "Ligand of Interest" by depositor).

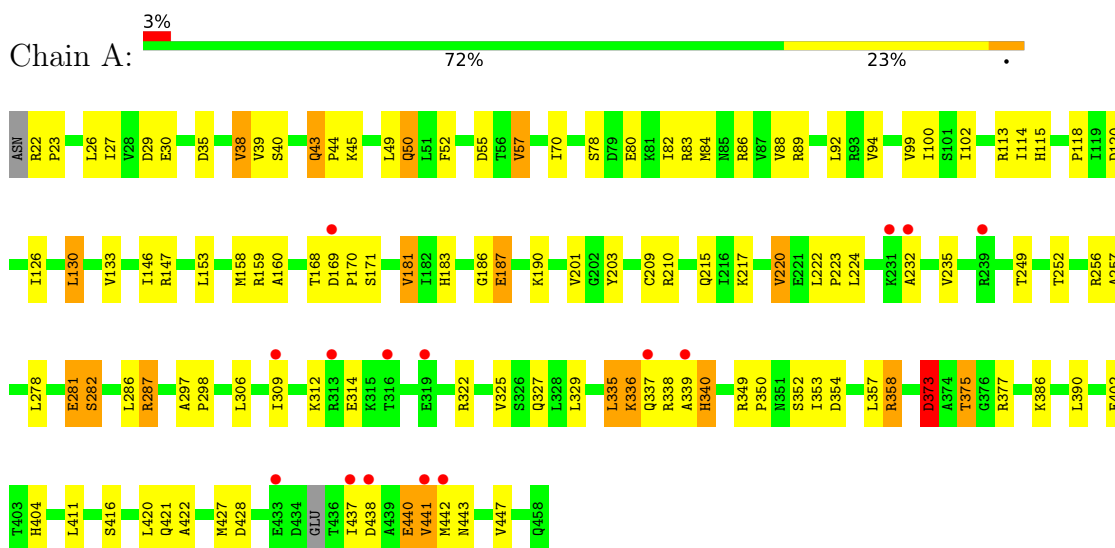


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	B	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	C	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	D	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	E	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	F	1	Total 27	C 10	N 5	O 10	P 2	0	0
3	G	1	Total 27	C 10	N 5	O 10	P 2	0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

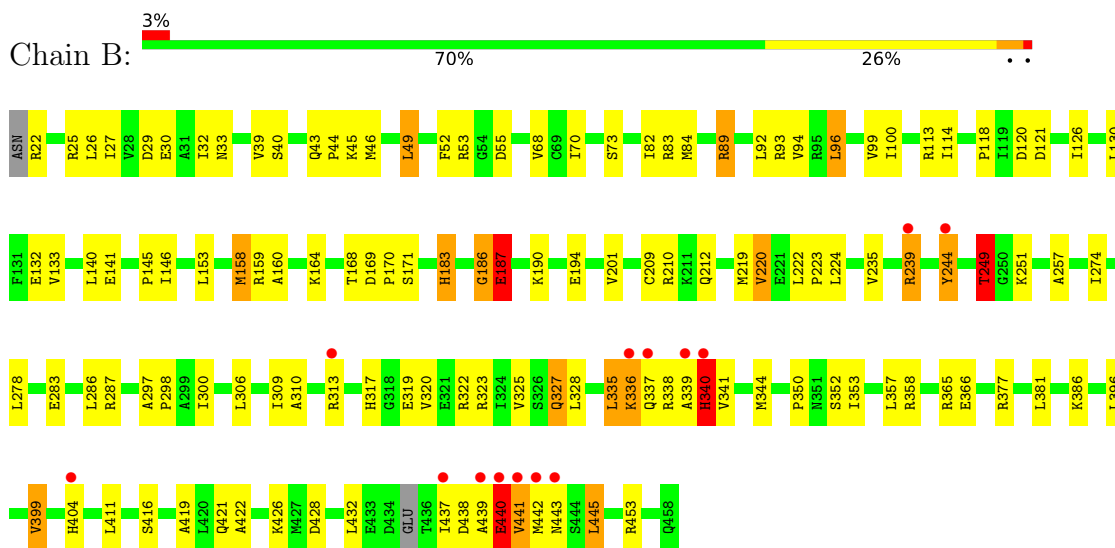
3 Residue-property plots [i](#)

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: Transitional endoplasmic reticulum ATPase

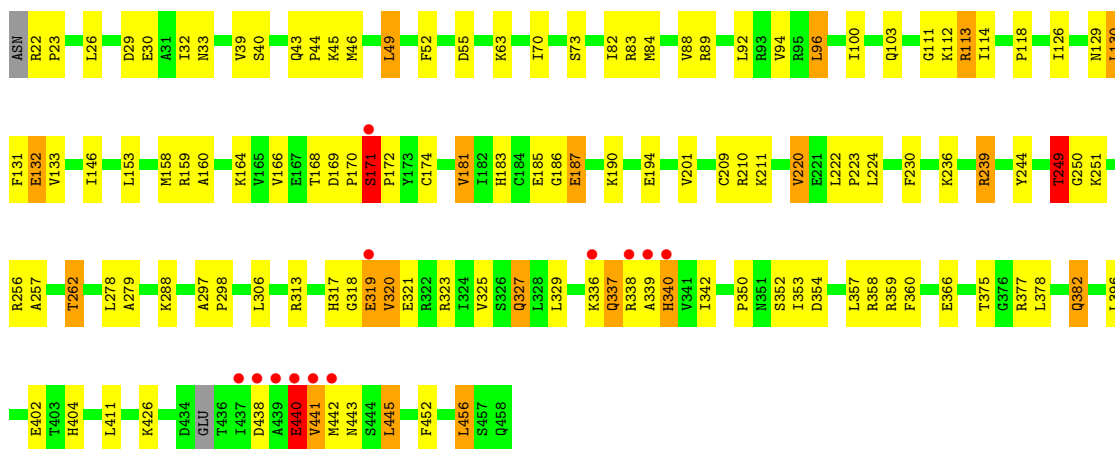


- Molecule 1: Transitional endoplasmic reticulum ATPase

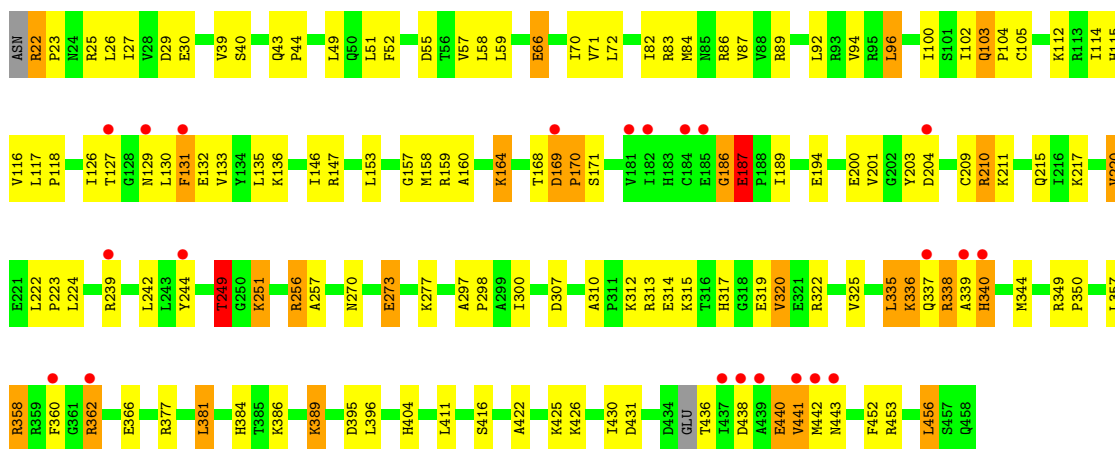


- Molecule 1: Transitional endoplasmic reticulum ATPase

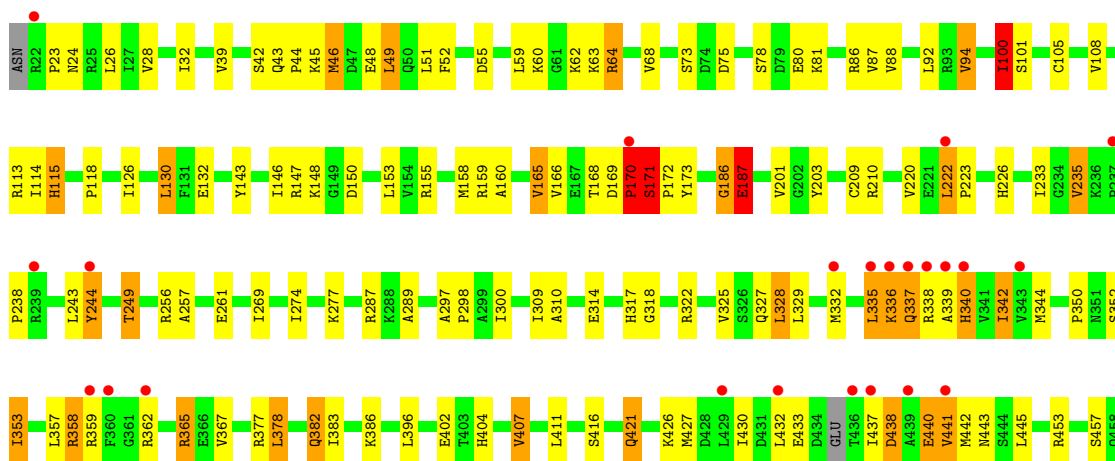




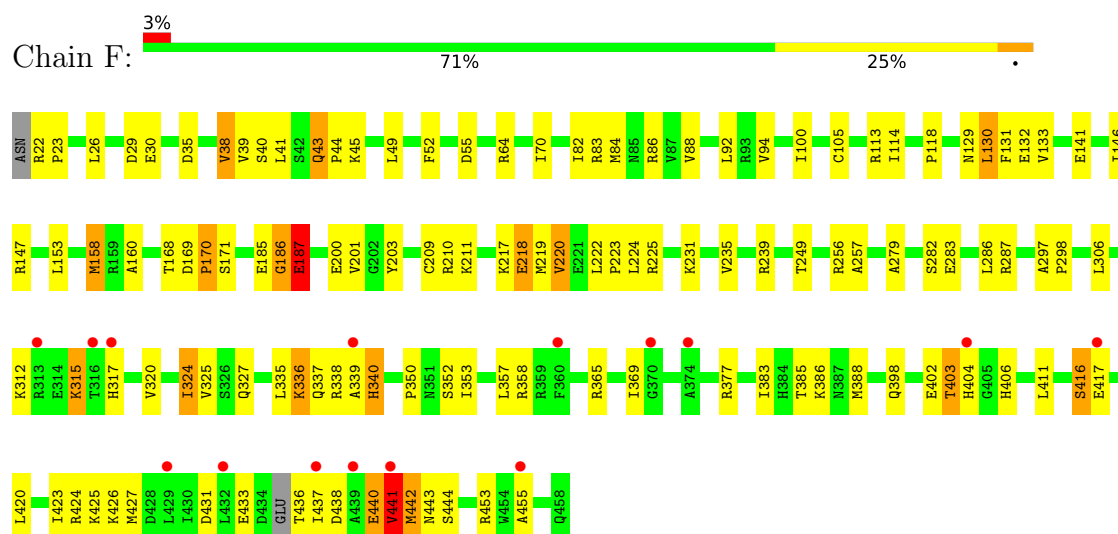
• Molecule 1: Transitional endoplasmic reticulum ATPase



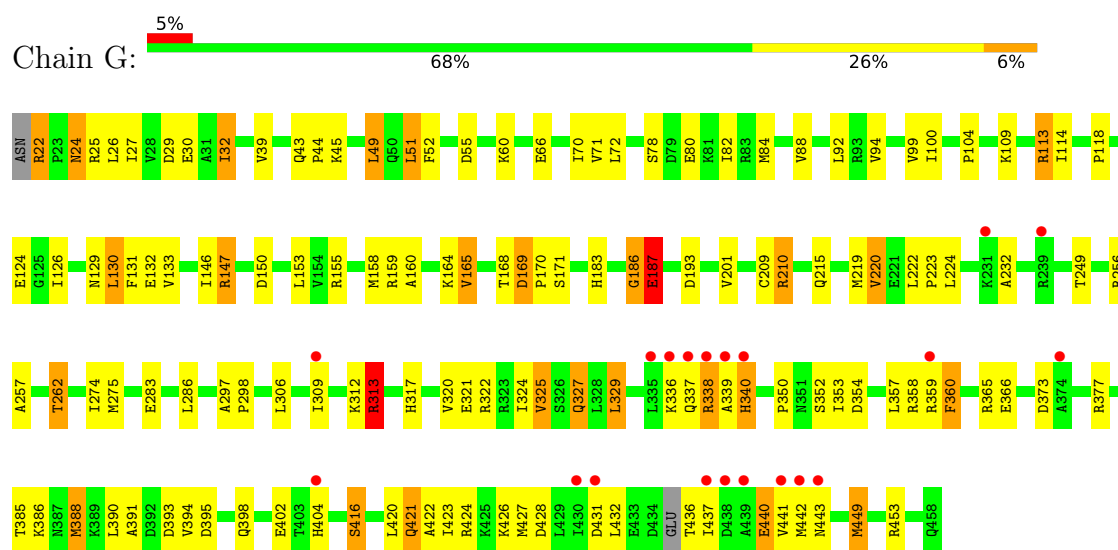
• Molecule 1: Transitional endoplasmic reticulum ATPase



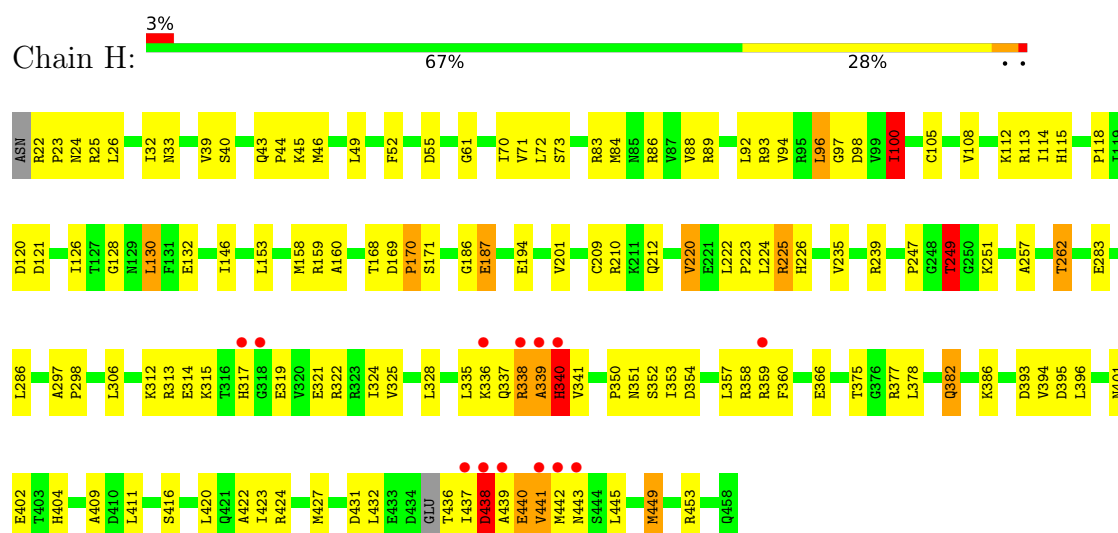
• Molecule 1: Transitional endoplasmic reticulum ATPase



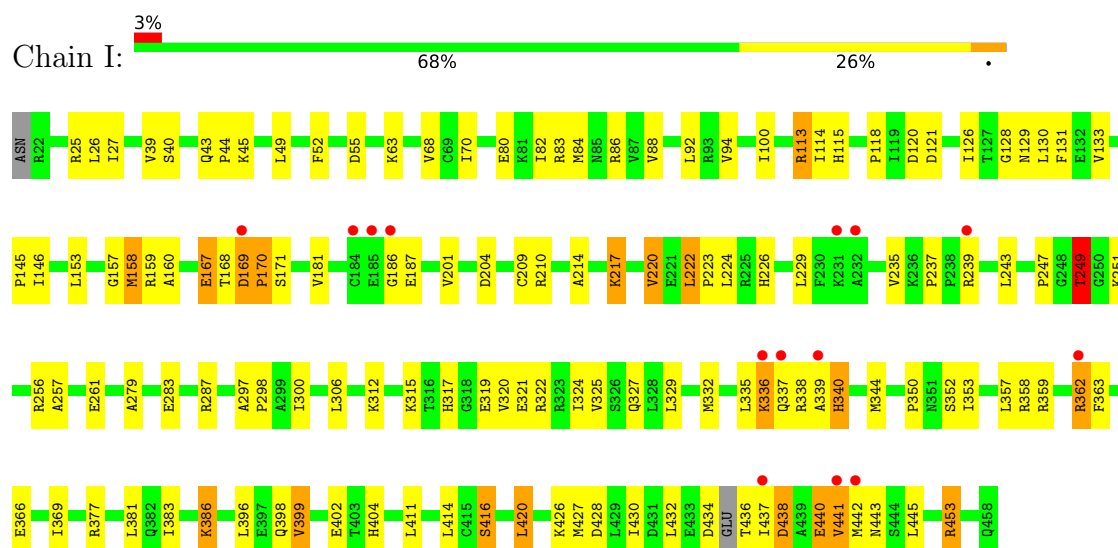
• Molecule 1: Transitional endoplasmic reticulum ATPase



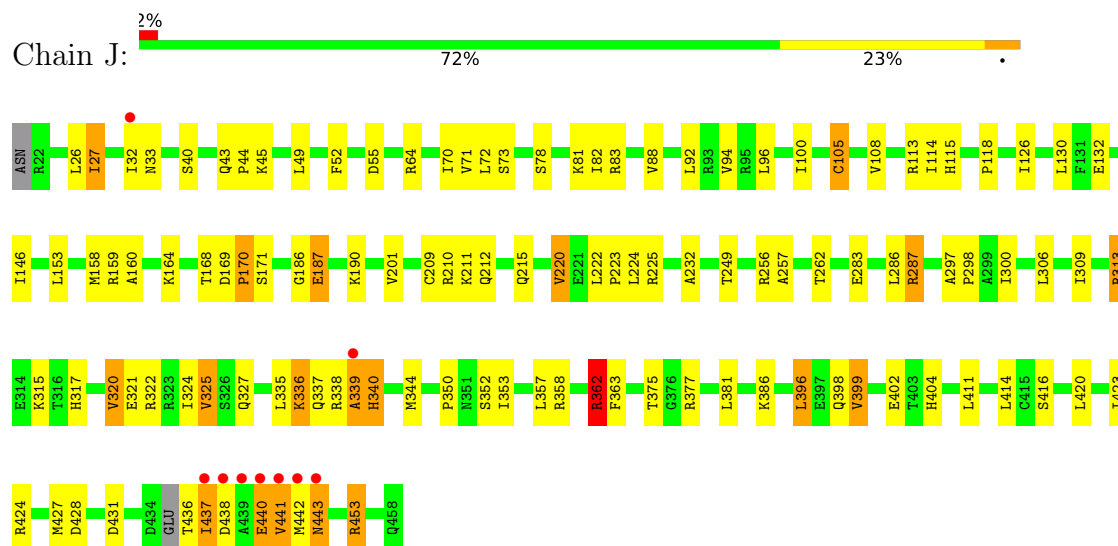
• Molecule 1: Transitional endoplasmic reticulum ATPase



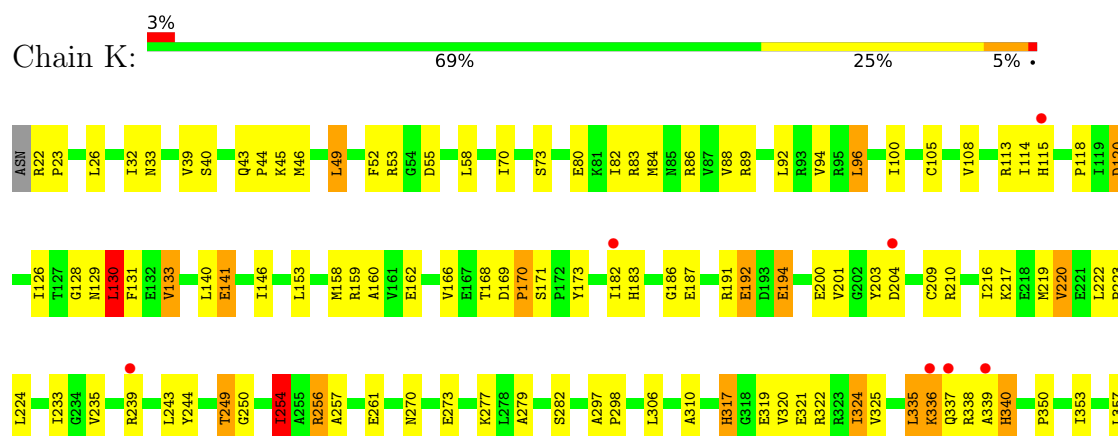
• Molecule 1: Transitional endoplasmic reticulum ATPase

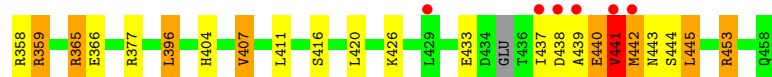


• Molecule 1: Transitional endoplasmic reticulum ATPase

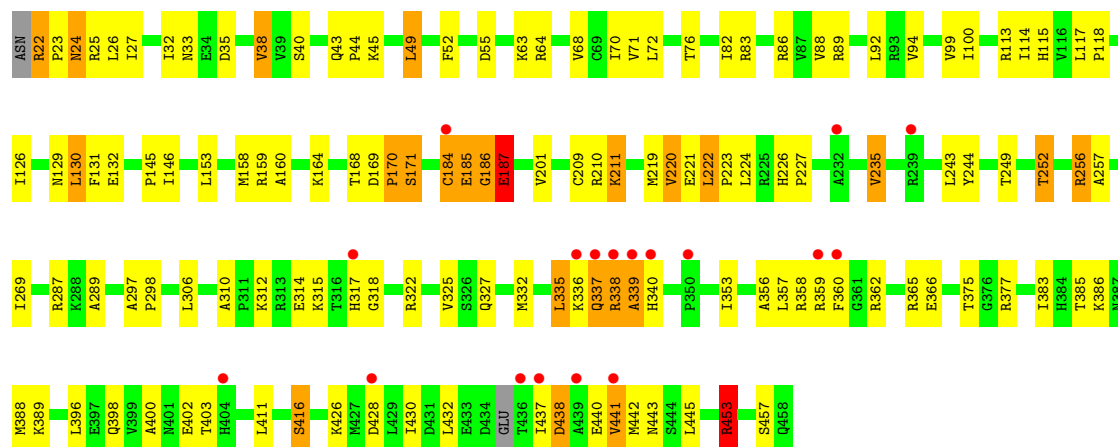


• Molecule 1: Transitional endoplasmic reticulum ATPase

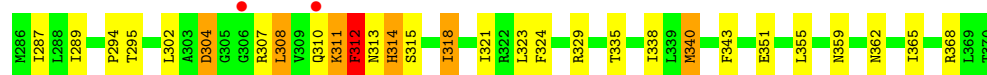




- Molecule 1: Transitional endoplasmic reticulum ATPase



- Molecule 2: NSFL1 cofactor p47



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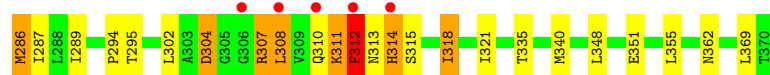
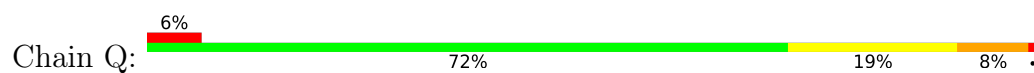
- Molecule 2: NSFL1 cofactor p47



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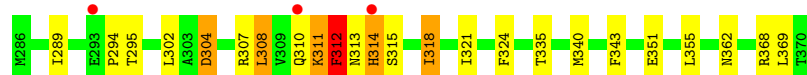
• Molecule 2: NSFL1 cofactor p47



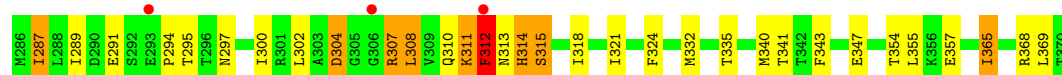
• Molecule 2: NSFL1 cofactor p47



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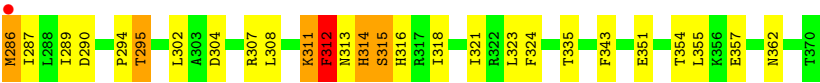


• Molecule 2: NSFL1 cofactor p47



• Molecule 2: NSFL1 cofactor p47





● Molecule 2: NSFL1 cofactor p47



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	170.78Å 178.85Å 171.33Å 90.00° 119.80° 90.00°	Depositor
Resolution (Å)	40.01 – 2.70 40.01 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.01-2.70) 99.3 (40.01-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.03 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0411	Depositor
R, R_{free}	0.213 , 0.256 0.214 , 0.257	Depositor DCC
R_{free} test set	11938 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	62.0	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.049 for -h-l,k,h 0.049 for l,k,-h-l 0.047 for h,-k,-h-l 0.049 for -h-l,-k,l 0.077 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	49084	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 33.48 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.9479e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: 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	0.59	0/3456	1.16	9/4670 (0.2%)
1	B	0.59	0/3456	1.17	11/4670 (0.2%)
1	C	0.60	0/3446	1.14	6/4659 (0.1%)
1	D	0.60	0/3450	1.18	12/4663 (0.3%)
1	E	0.64	0/3412	1.18	14/4619 (0.3%)
1	F	0.58	0/3456	1.16	10/4670 (0.2%)
1	G	0.58	0/3432	1.16	8/4643 (0.2%)
1	H	0.58	0/3456	1.16	10/4670 (0.2%)
1	I	0.58	0/3456	1.14	6/4670 (0.1%)
1	J	0.59	0/3450	1.13	5/4663 (0.1%)
1	K	0.59	0/3456	1.16	10/4670 (0.2%)
1	L	0.58	0/3436	1.16	14/4647 (0.3%)
2	M	0.64	0/678	1.24	3/917 (0.3%)
2	N	0.64	0/672	1.30	4/910 (0.4%)
2	O	0.67	0/672	1.29	4/910 (0.4%)
2	P	0.66	0/672	1.29	3/910 (0.3%)
2	Q	0.66	0/678	1.28	7/917 (0.8%)
2	R	0.64	0/678	1.29	6/917 (0.7%)
2	S	0.65	0/678	1.34	7/917 (0.8%)
2	T	0.69	0/678	1.27	3/917 (0.3%)
2	U	0.64	0/678	1.25	3/917 (0.3%)
2	V	0.65	0/678	1.29	4/917 (0.4%)
2	W	0.65	0/678	1.30	4/917 (0.4%)
2	X	0.69	0/678	1.28	5/917 (0.5%)
All	All	0.60	0/49480	1.18	168/66897 (0.3%)

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	F	0	1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	322	ARG	CG-CD-NE	-10.71	88.44	112.00
2	W	295	THR	CA-CB-OG1	10.60	125.50	109.60
2	N	312	PHE	CA-CB-CG	10.59	124.39	113.80
1	B	183	HIS	CA-CB-CG	10.24	124.04	113.80
2	V	312	PHE	CA-CB-CG	9.70	123.50	113.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	86	ARG	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3404	0	3461	96	0
1	B	3404	0	3461	106	0
1	C	3394	0	3439	106	0
1	D	3398	0	3450	119	0
1	E	3360	0	3378	132	0
1	F	3404	0	3461	115	0
1	G	3380	0	3411	132	0
1	H	3404	0	3461	119	0
1	I	3404	0	3461	135	0
1	J	3398	0	3450	98	0
1	K	3404	0	3461	119	0
1	L	3384	0	3422	109	0
2	M	670	0	691	23	0
2	N	664	0	680	23	0
2	O	664	0	680	26	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	P	664	0	680	31	0
2	Q	670	0	691	22	0
2	R	670	0	691	24	0
2	S	670	0	691	26	0
2	T	670	0	691	32	0
2	U	670	0	691	20	0
2	V	670	0	691	32	0
2	W	670	0	691	28	0
2	X	670	0	691	26	0
3	A	27	0	12	3	0
3	B	27	0	12	0	0
3	C	27	0	12	1	0
3	D	27	0	12	1	0
3	E	27	0	12	0	0
3	F	27	0	12	0	0
3	G	27	0	12	0	0
3	H	27	0	12	1	0
3	I	27	0	12	0	0
3	J	27	0	12	0	0
3	K	27	0	12	0	0
3	L	27	0	12	1	0
All	All	49084	0	49719	1606	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 16.

The worst 5 of 1606 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:E:238:PRO:HB3	1:E:365:ARG:NE	1.47	1.29
1:F:385:THR:HG22	1:F:388:MET:CE	1.73	1.18
1:L:385:THR:HG22	1:L:388:MET:CE	1.74	1.18
1:I:251:LYS:HG2	1:I:369:ILE:HD12	1.25	1.14
1:E:238:PRO:CB	1:E:365:ARG:HE	1.61	1.12

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	432/438 (99%)	400 (93%)	25 (6%)	7 (2%)	7	20
1	B	432/438 (99%)	404 (94%)	22 (5%)	6 (1%)	9	23
1	C	432/438 (99%)	403 (93%)	22 (5%)	7 (2%)	7	20
1	D	432/438 (99%)	396 (92%)	31 (7%)	5 (1%)	10	27
1	E	432/438 (99%)	397 (92%)	27 (6%)	8 (2%)	6	17
1	F	432/438 (99%)	403 (93%)	23 (5%)	6 (1%)	9	23
1	G	432/438 (99%)	404 (94%)	23 (5%)	5 (1%)	10	27
1	H	432/438 (99%)	403 (93%)	23 (5%)	6 (1%)	9	23
1	I	432/438 (99%)	404 (94%)	22 (5%)	6 (1%)	9	23
1	J	432/438 (99%)	403 (93%)	22 (5%)	7 (2%)	7	20
1	K	432/438 (99%)	403 (93%)	21 (5%)	8 (2%)	6	17
1	L	432/438 (99%)	400 (93%)	25 (6%)	7 (2%)	7	20
2	M	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	N	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	O	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	P	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	Q	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	R	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	S	83/85 (98%)	77 (93%)	4 (5%)	2 (2%)	4	12
2	T	83/85 (98%)	78 (94%)	3 (4%)	2 (2%)	4	12
2	U	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	V	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	W	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
2	X	83/85 (98%)	77 (93%)	5 (6%)	1 (1%)	10	27
All	All	6180/6276 (98%)	5745 (93%)	343 (6%)	92 (2%)	8	22

5 of 92 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	186	GLY
1	A	282	SER
1	A	340	HIS
1	B	340	HIS
1	B	441	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	370/373 (99%)	345 (93%)	25 (7%)	14	35
1	B	370/373 (99%)	345 (93%)	25 (7%)	14	35
1	C	368/373 (99%)	336 (91%)	32 (9%)	9	24
1	D	369/373 (99%)	329 (89%)	40 (11%)	6	16
1	E	362/373 (97%)	325 (90%)	37 (10%)	7	18
1	F	370/373 (99%)	342 (92%)	28 (8%)	12	30
1	G	365/373 (98%)	331 (91%)	34 (9%)	8	21
1	H	370/373 (99%)	341 (92%)	29 (8%)	11	29
1	I	370/373 (99%)	345 (93%)	25 (7%)	14	35
1	J	369/373 (99%)	338 (92%)	31 (8%)	10	26
1	K	370/373 (99%)	341 (92%)	29 (8%)	11	29
1	L	366/373 (98%)	341 (93%)	25 (7%)	14	35
2	M	75/75 (100%)	62 (83%)	13 (17%)	2	5
2	N	74/75 (99%)	64 (86%)	10 (14%)	4	9
2	O	74/75 (99%)	66 (89%)	8 (11%)	6	16
2	P	74/75 (99%)	64 (86%)	10 (14%)	4	9
2	Q	75/75 (100%)	67 (89%)	8 (11%)	6	16
2	R	75/75 (100%)	66 (88%)	9 (12%)	5	12
2	S	75/75 (100%)	62 (83%)	13 (17%)	2	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	T	75/75 (100%)	67 (89%)	8 (11%)	6	16
2	U	75/75 (100%)	67 (89%)	8 (11%)	6	16
2	V	75/75 (100%)	63 (84%)	12 (16%)	2	6
2	W	75/75 (100%)	66 (88%)	9 (12%)	5	12
2	X	75/75 (100%)	64 (85%)	11 (15%)	3	8
All	All	5316/5376 (99%)	4837 (91%)	479 (9%)	9	23

5 of 479 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	212	GLN
2	U	318	ILE
1	J	190	LYS
2	T	369	LEU
2	X	312	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 72 such sidechains are listed below:

Mol	Chain	Res	Type
2	M	362	ASN
2	W	362	ASN
2	N	362	ASN
2	U	299	GLN
1	E	327	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ADP	G	501	-	28,29,29	0.56	0	43,45,45	0.58	0
3	ADP	B	501	-	28,29,29	0.47	0	43,45,45	0.63	0
3	ADP	K	501	-	28,29,29	0.44	0	43,45,45	0.86	2 (4%)
3	ADP	E	501	-	28,29,29	0.57	0	43,45,45	0.63	0
3	ADP	L	501	-	28,29,29	0.55	0	43,45,45	0.76	1 (2%)
3	ADP	D	501	-	28,29,29	0.49	0	43,45,45	0.81	1 (2%)
3	ADP	C	501	-	28,29,29	0.42	0	43,45,45	0.90	2 (4%)
3	ADP	H	501	-	28,29,29	0.51	0	43,45,45	0.68	0
3	ADP	A	501	-	28,29,29	0.54	1 (3%)	43,45,45	0.80	1 (2%)
3	ADP	J	501	-	28,29,29	0.47	0	43,45,45	0.67	0
3	ADP	I	501	-	28,29,29	0.42	0	43,45,45	0.73	2 (4%)
3	ADP	F	501	-	28,29,29	0.73	1 (3%)	43,45,45	0.72	0

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	G	501	-	-	3/16/32/32	0/3/3/3
3	ADP	B	501	-	-	4/16/32/32	0/3/3/3
3	ADP	K	501	-	-	6/16/32/32	0/3/3/3
3	ADP	E	501	-	-	4/16/32/32	0/3/3/3
3	ADP	L	501	-	-	5/16/32/32	0/3/3/3
3	ADP	D	501	-	-	4/16/32/32	0/3/3/3
3	ADP	C	501	-	-	2/16/32/32	0/3/3/3
3	ADP	H	501	-	-	5/16/32/32	0/3/3/3
3	ADP	A	501	-	-	4/16/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	J	501	-	-	5/16/32/32	0/3/3/3
3	ADP	I	501	-	-	7/16/32/32	0/3/3/3
3	ADP	F	501	-	-	3/16/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	501	ADP	PA-O3A	3.06	1.62	1.59
3	A	501	ADP	PA-O3A	2.07	1.61	1.59

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	501	ADP	O2B-PB-O3A	3.35	115.86	104.64
3	C	501	ADP	O3A-PB-O1B	-2.76	96.51	111.04
3	D	501	ADP	O4'-C1'-N9	2.71	113.30	108.09
3	L	501	ADP	O2B-PB-O3A	2.31	112.37	104.64
3	A	501	ADP	O2A-PA-O3A	2.21	113.25	107.27

There are no chirality outliers.

5 of 52 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	ADP	C5'-O5'-PA-O3A
3	B	501	ADP	C5'-O5'-PA-O2A
3	B	501	ADP	C5'-O5'-PA-O3A
3	D	501	ADP	C5'-O5'-PA-O1A
3	D	501	ADP	C5'-O5'-PA-O2A

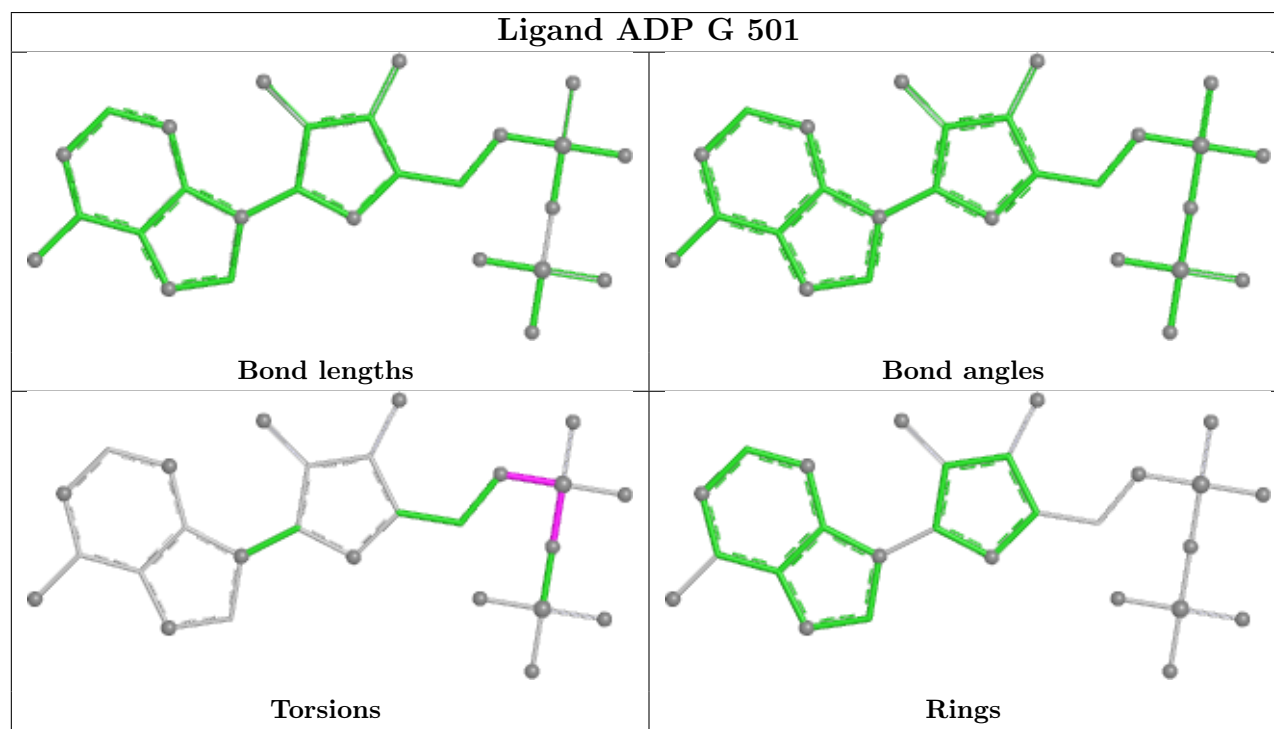
There are no ring outliers.

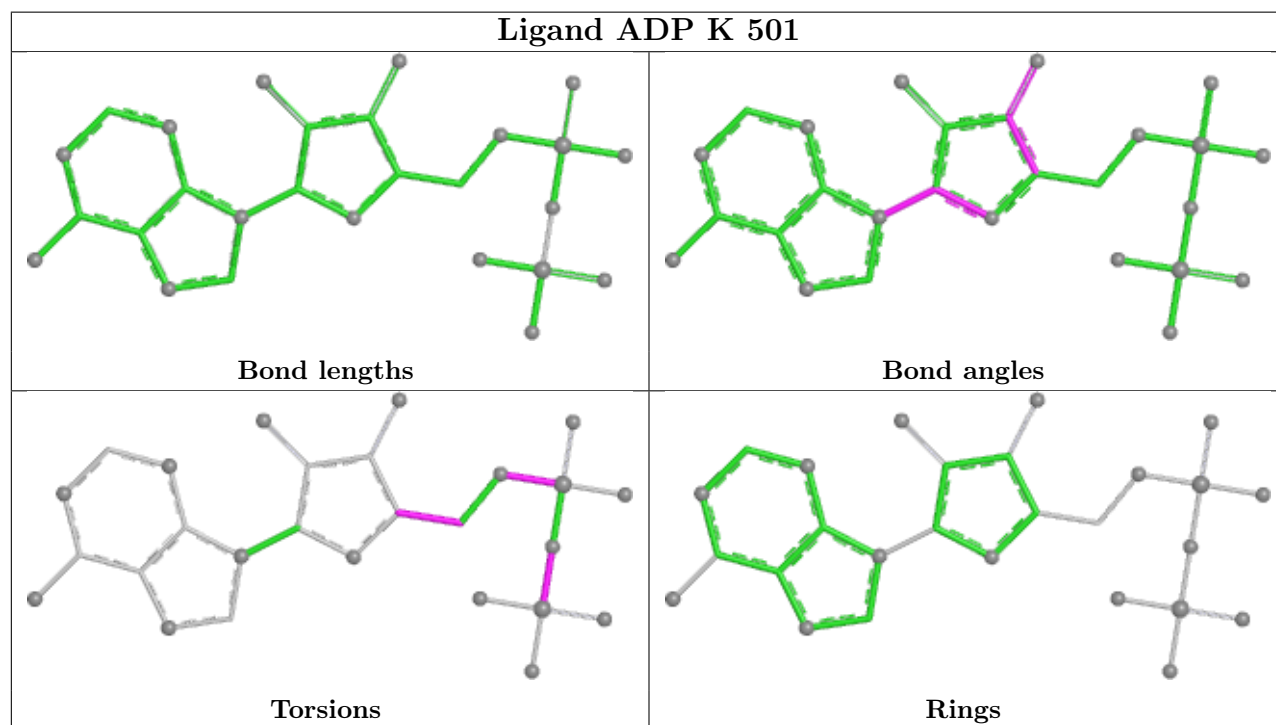
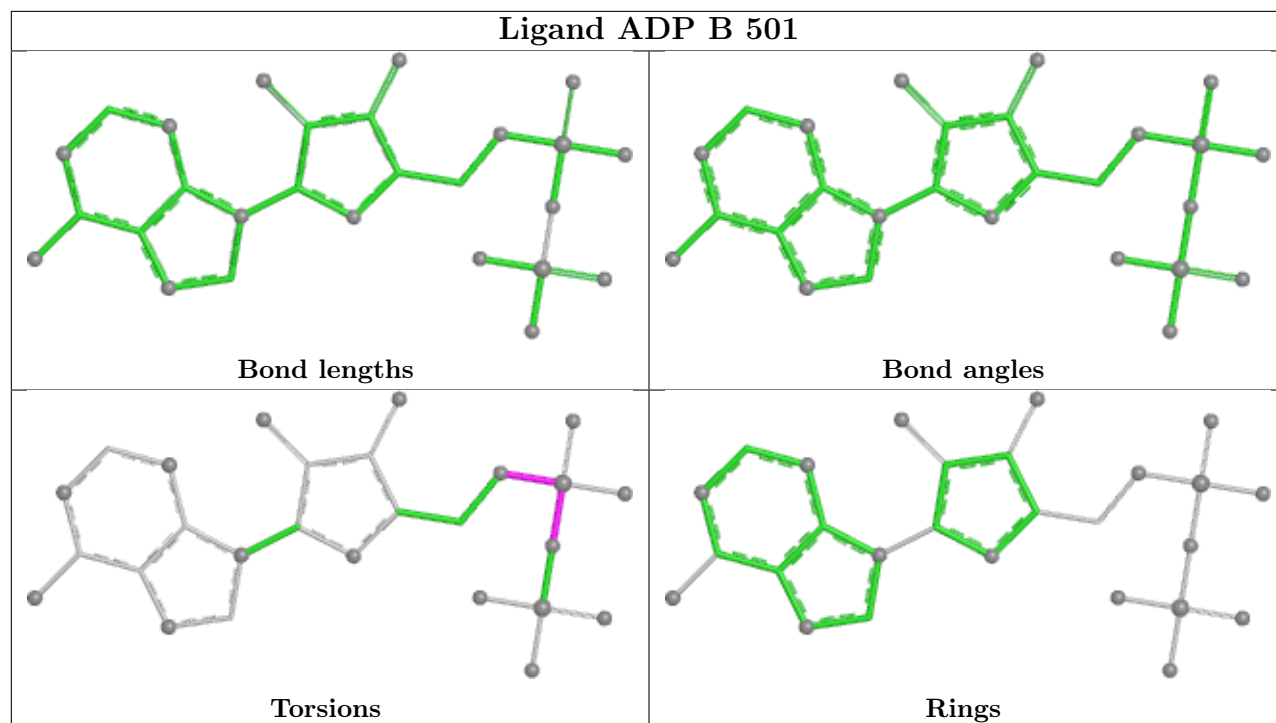
5 monomers are involved in 7 short contacts:

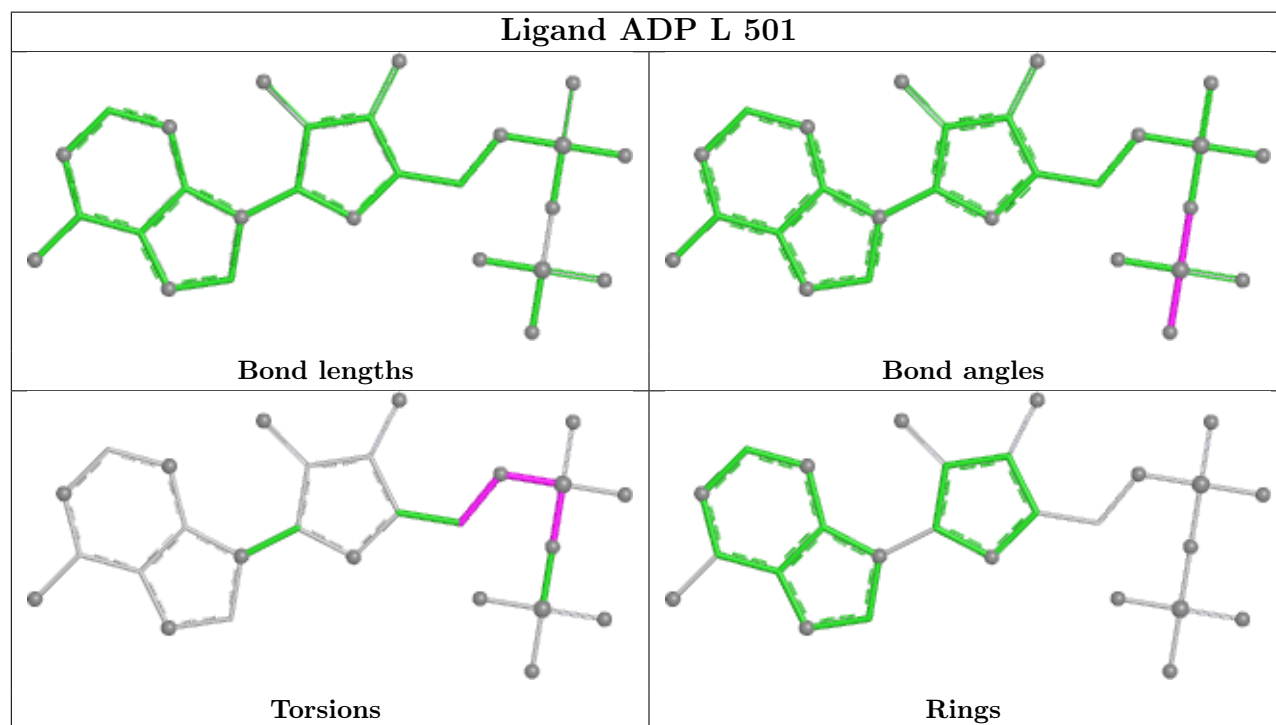
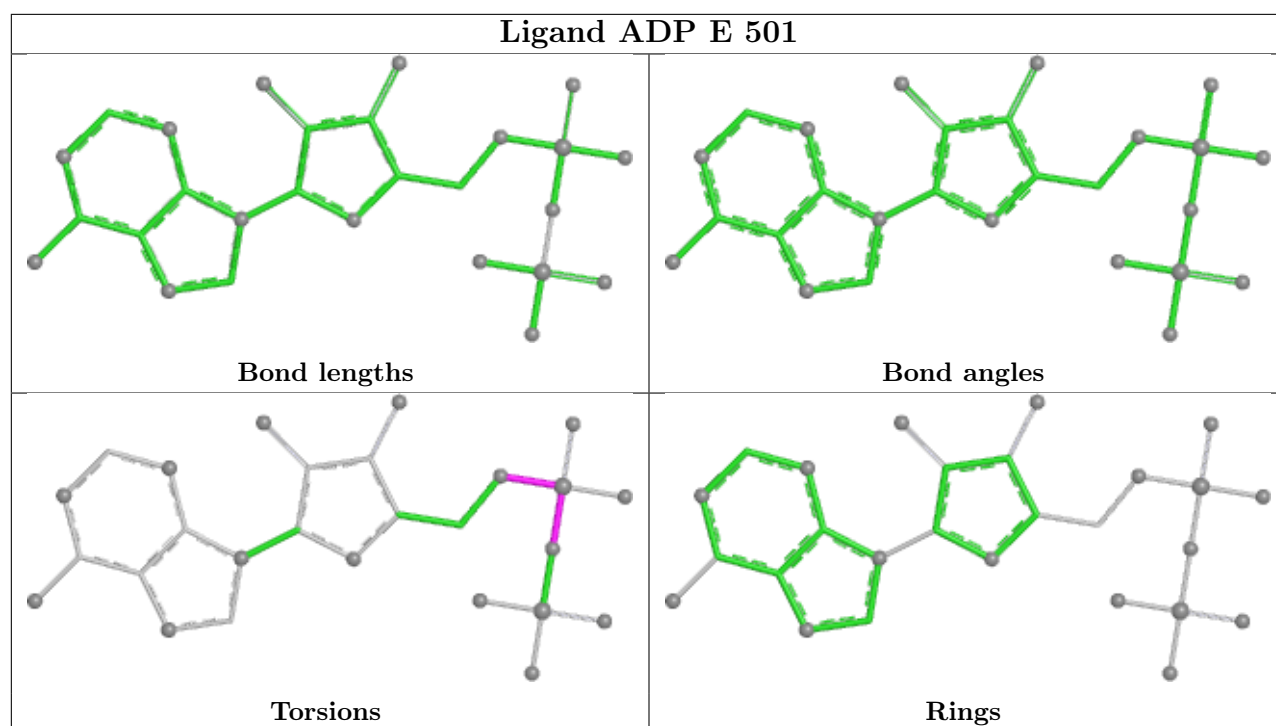
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	501	ADP	1	0
3	D	501	ADP	1	0
3	C	501	ADP	1	0
3	H	501	ADP	1	0
3	A	501	ADP	3	0

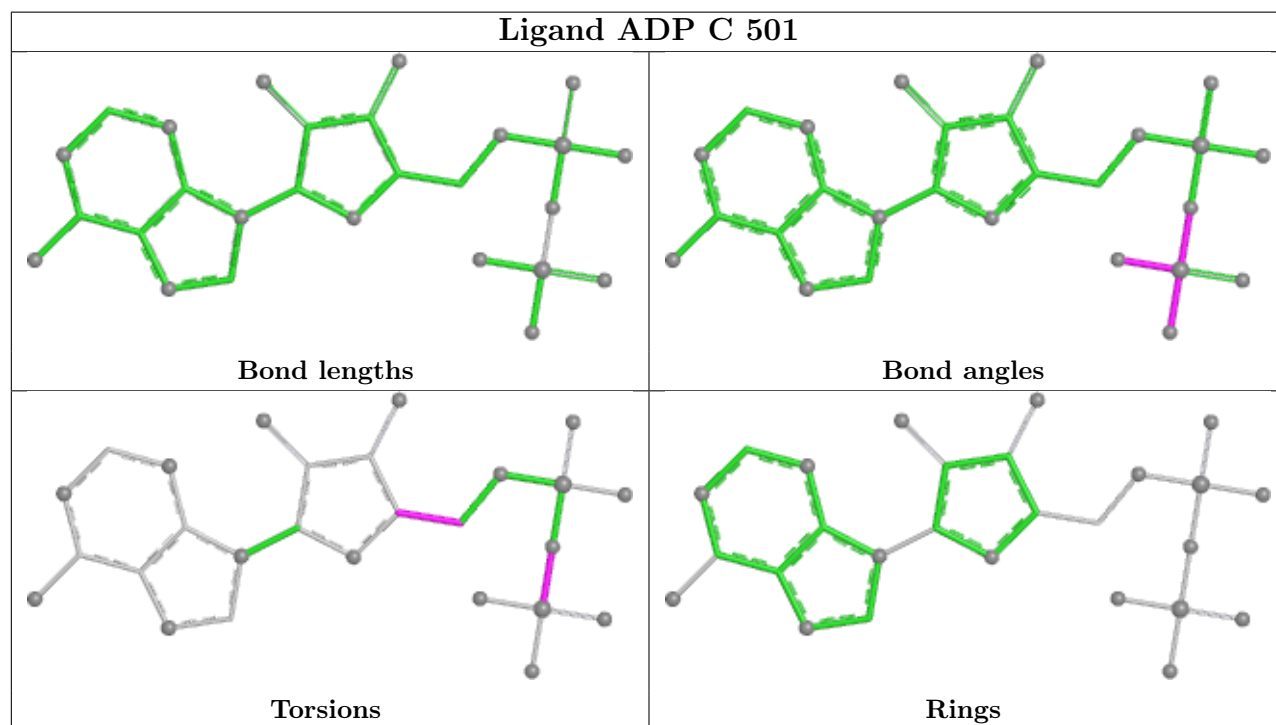
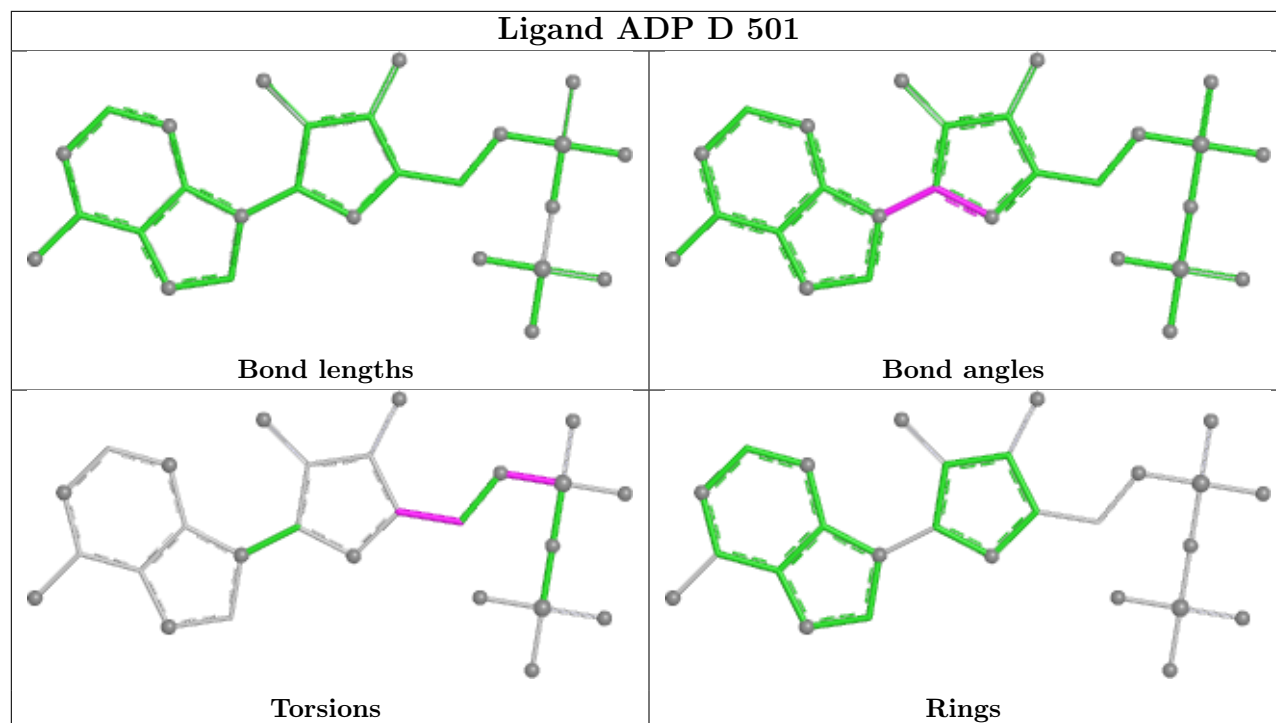
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

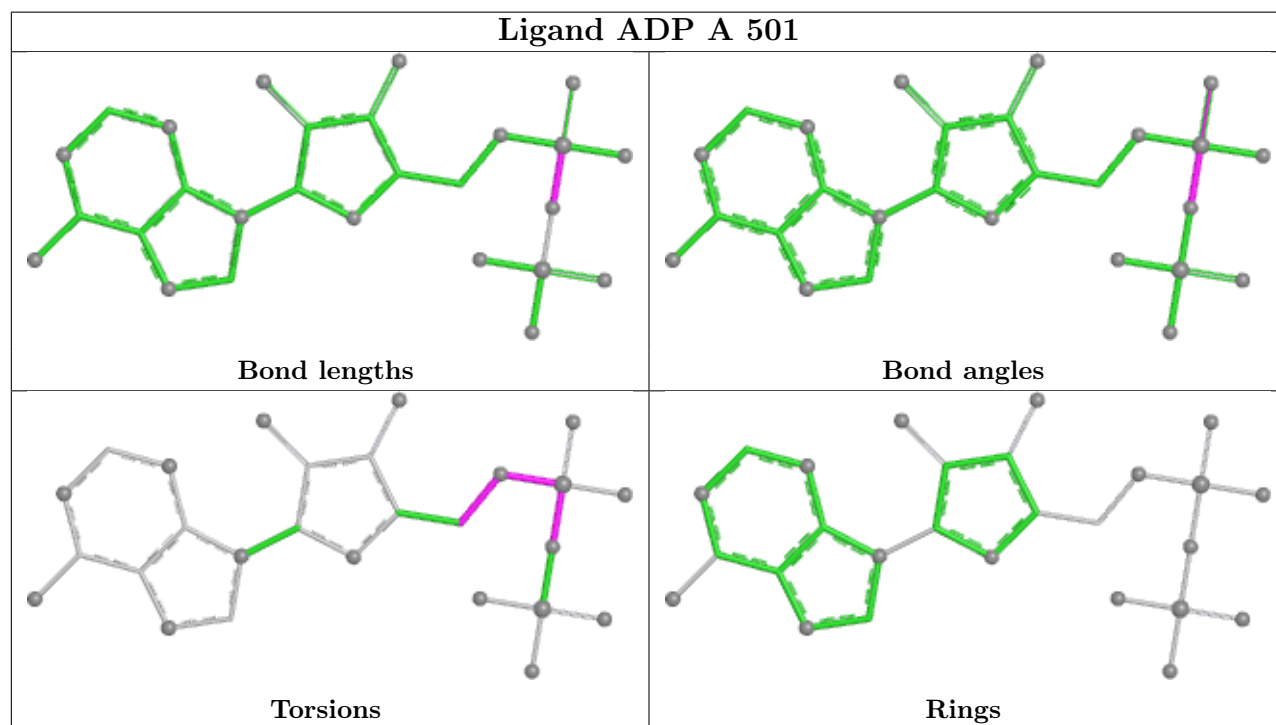
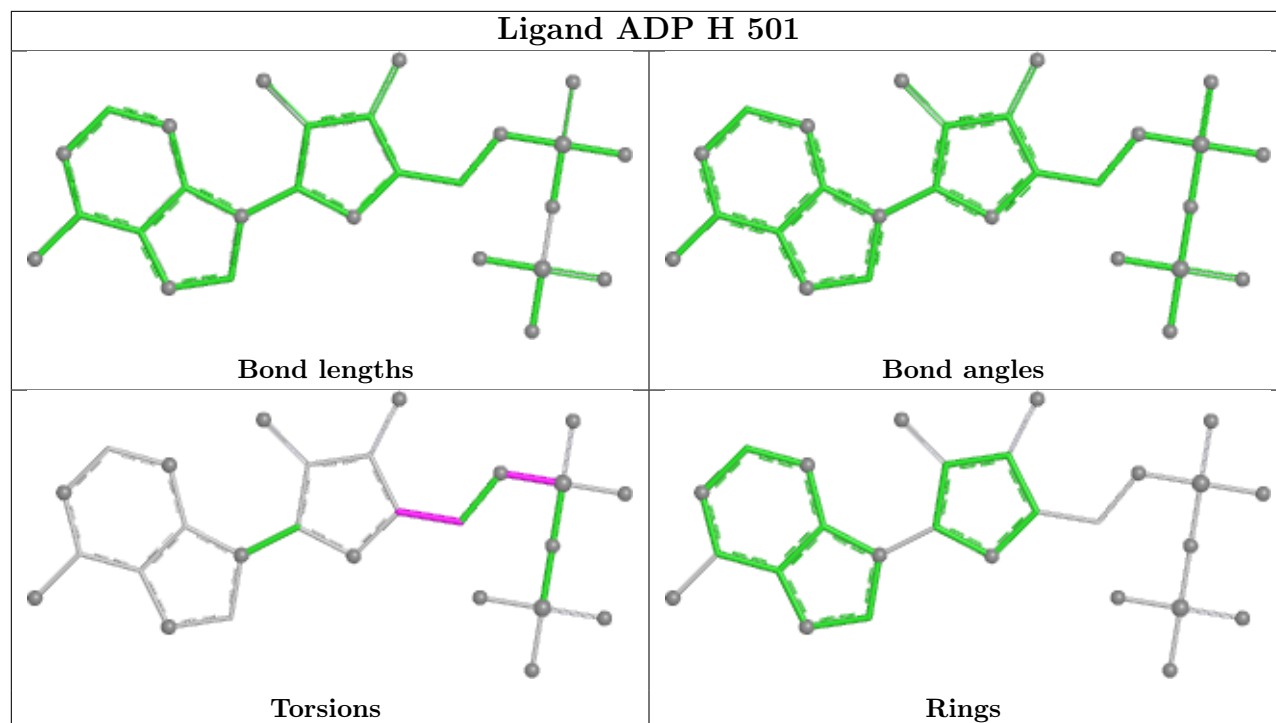
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.



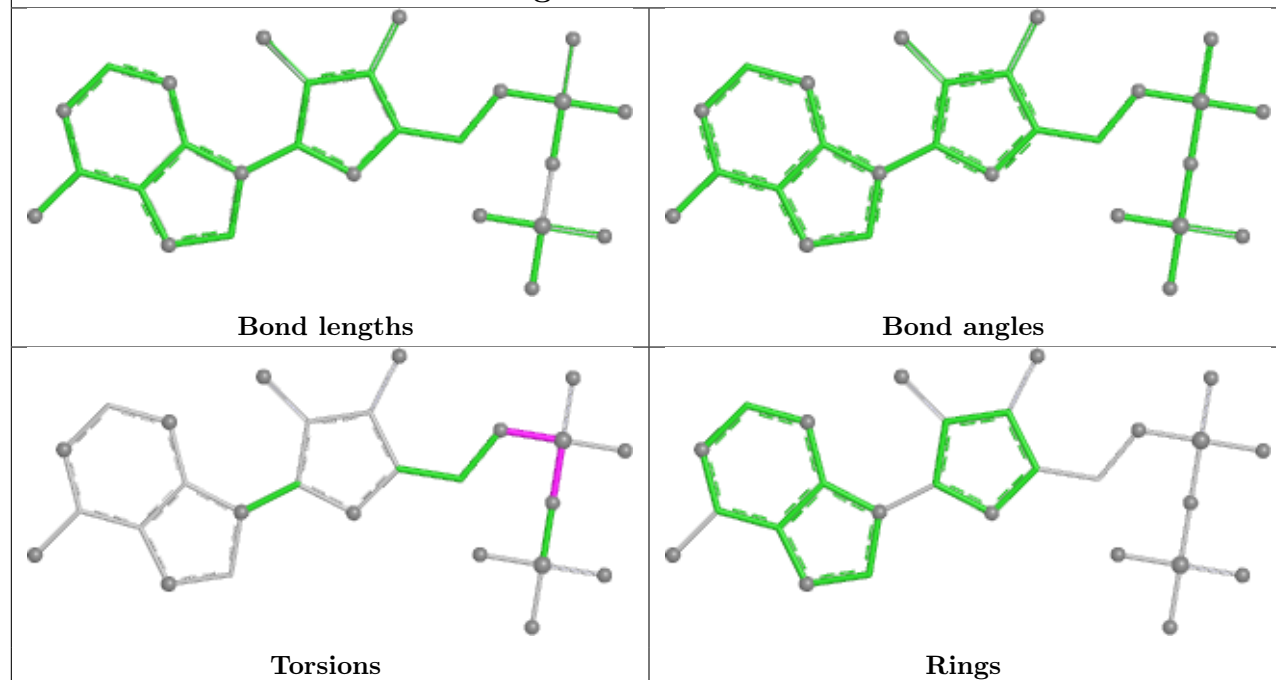




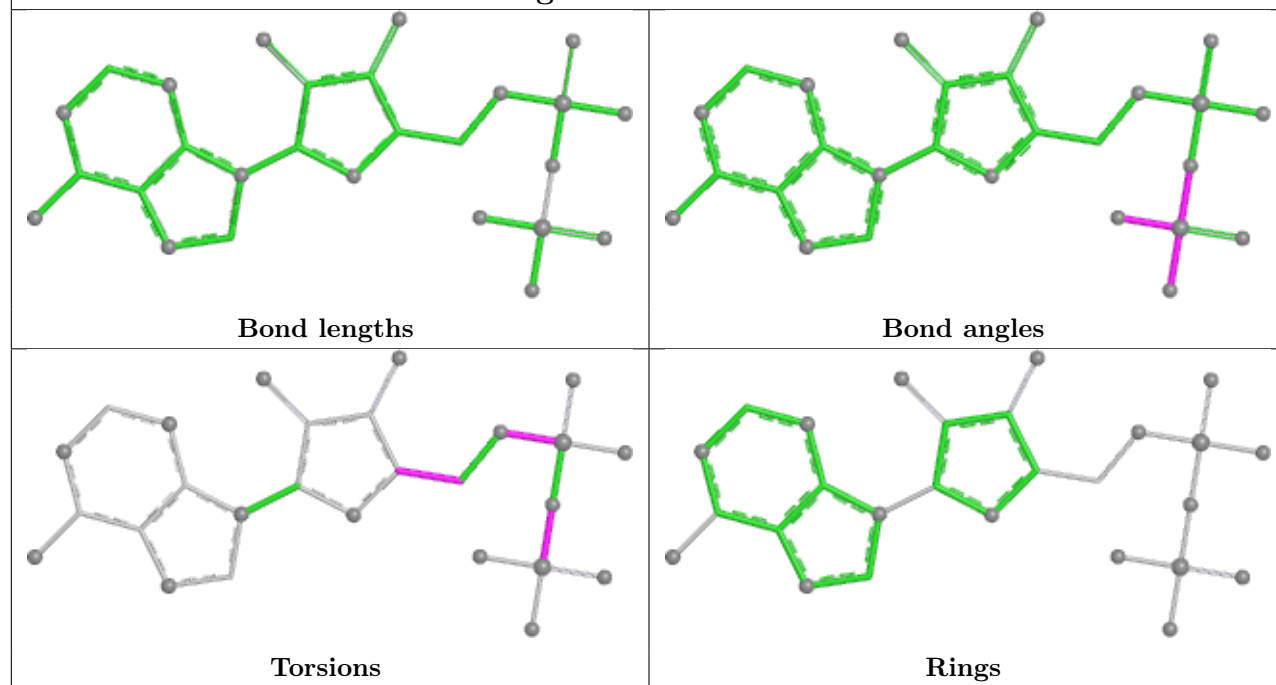


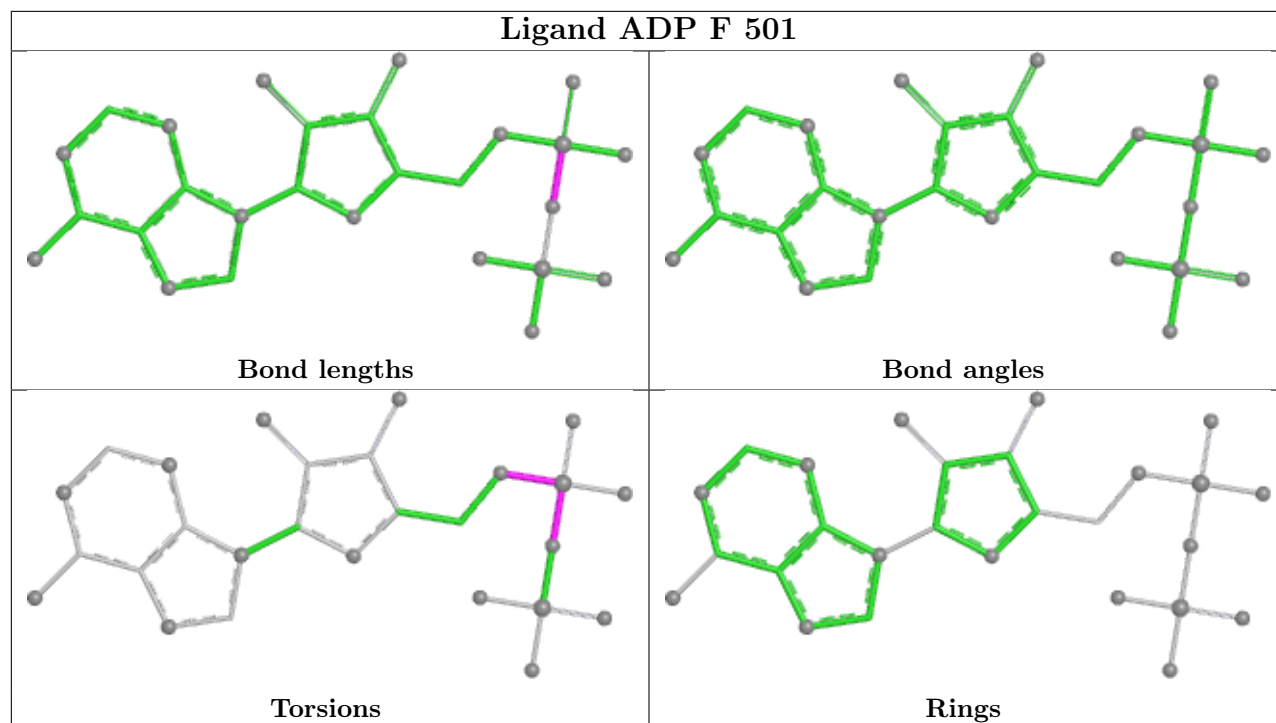


Ligand ADP J 501



Ligand ADP I 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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	436/438 (99%)	0.08	15 (3%)	48	44	35, 66, 127, 193	0
1	B	436/438 (99%)	-0.12	14 (3%)	50	46	33, 58, 121, 219	0
1	C	436/438 (99%)	-0.08	12 (2%)	55	51	35, 58, 116, 196	0
1	D	436/438 (99%)	0.22	22 (5%)	34	30	39, 67, 133, 224	0
1	E	436/438 (99%)	0.57	23 (5%)	32	28	30, 77, 132, 206	0
1	F	436/438 (99%)	0.15	15 (3%)	48	44	35, 66, 133, 211	0
1	G	436/438 (99%)	0.23	20 (4%)	37	34	46, 71, 132, 203	0
1	H	436/438 (99%)	-0.02	13 (2%)	52	49	40, 63, 126, 202	0
1	I	436/438 (99%)	0.07	14 (3%)	50	46	36, 66, 125, 186	0
1	J	436/438 (99%)	-0.05	9 (2%)	63	61	34, 61, 119, 197	0
1	K	436/438 (99%)	0.03	13 (2%)	52	49	35, 61, 117, 182	0
1	L	436/438 (99%)	0.16	18 (4%)	41	37	36, 67, 124, 207	0
2	M	85/85 (100%)	-0.02	2 (2%)	59	56	37, 60, 99, 119	0
2	N	85/85 (100%)	0.17	5 (5%)	28	25	42, 63, 104, 138	0
2	O	85/85 (100%)	-0.01	4 (4%)	36	33	40, 57, 93, 119	0
2	P	85/85 (100%)	0.10	4 (4%)	36	33	37, 60, 102, 136	0
2	Q	85/85 (100%)	0.11	5 (5%)	28	25	44, 63, 99, 137	0
2	R	85/85 (100%)	-0.11	5 (5%)	28	25	35, 53, 88, 124	0
2	S	85/85 (100%)	0.26	3 (3%)	47	43	50, 69, 107, 130	0
2	T	85/85 (100%)	-0.00	6 (7%)	22	19	36, 56, 92, 123	0
2	U	85/85 (100%)	-0.00	3 (3%)	47	43	37, 59, 100, 131	0
2	V	85/85 (100%)	0.13	3 (3%)	47	43	39, 64, 101, 132	0
2	W	85/85 (100%)	-0.07	1 (1%)	76	75	38, 59, 92, 129	0
2	X	85/85 (100%)	-0.05	3 (3%)	47	43	38, 56, 98, 118	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
All	All	6252/6276 (99%)	0.09	232 (3%)	45	41	30, 64, 122, 224	0

The worst 5 of 232 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	339	ALA	7.5
1	E	337	GLN	6.6
1	B	439	ALA	6.3
1	C	441	VAL	5.4
1	G	337	GLN	4.8

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

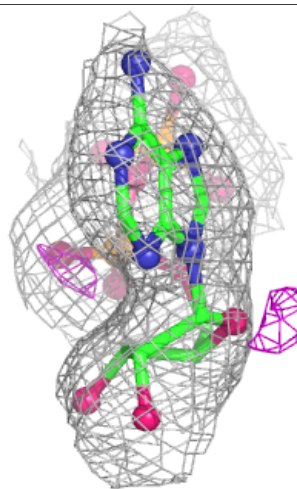
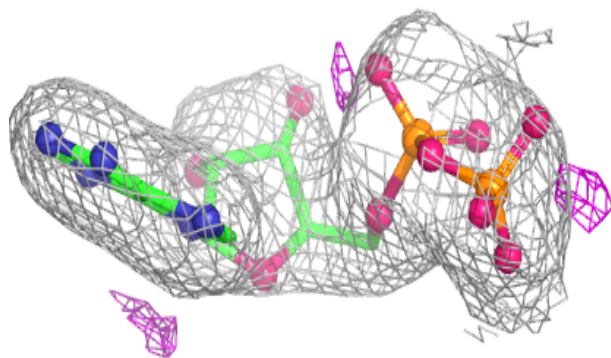
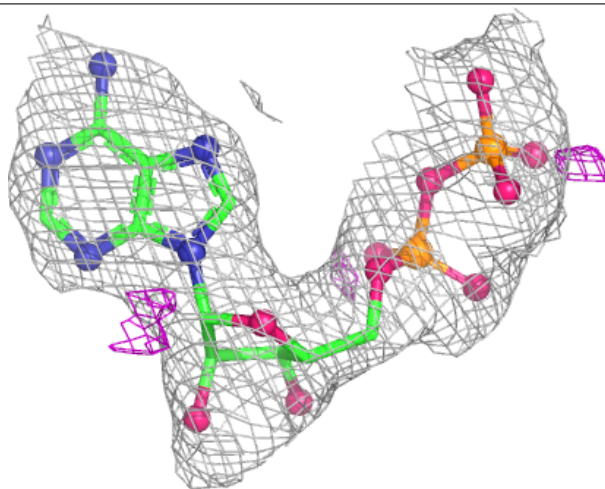
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ADP	L	501	27/27	0.94	0.08	60,71,87,96	0
3	ADP	D	501	27/27	0.95	0.07	53,64,78,88	0
3	ADP	E	501	27/27	0.95	0.07	65,75,88,100	0
3	ADP	G	501	27/27	0.95	0.06	62,72,89,90	0
3	ADP	H	501	27/27	0.95	0.07	58,68,75,82	0
3	ADP	J	501	27/27	0.95	0.07	53,65,79,81	0
3	ADP	A	501	27/27	0.95	0.07	49,68,85,87	0
3	ADP	I	501	27/27	0.96	0.06	55,67,78,80	0
3	ADP	C	501	27/27	0.96	0.07	52,61,71,87	0
3	ADP	K	501	27/27	0.96	0.07	49,62,76,86	0
3	ADP	F	501	27/27	0.96	0.06	56,68,87,89	0
3	ADP	B	501	27/27	0.97	0.06	40,57,69,73	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.

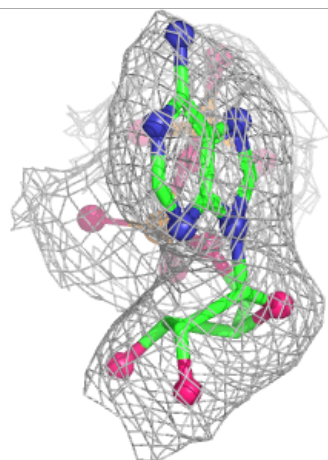
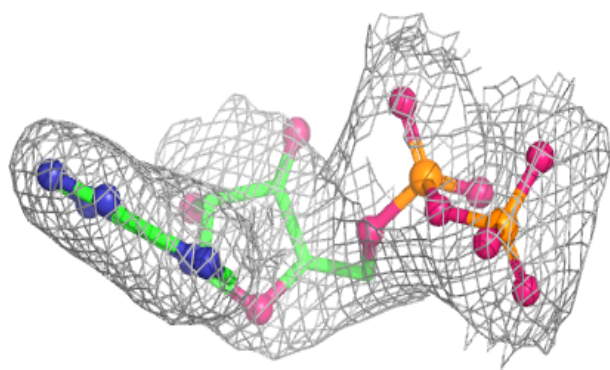
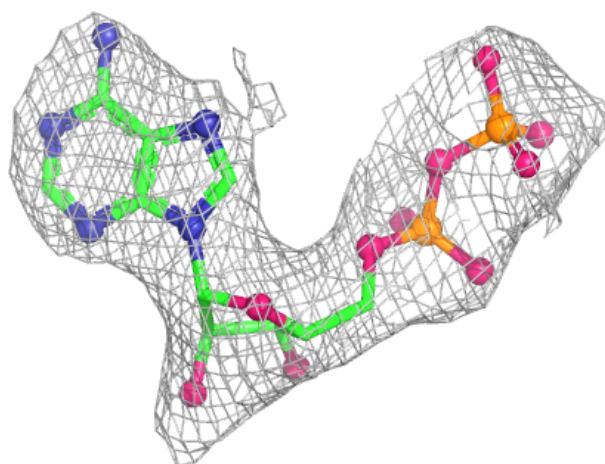
Electron density around ADP L 501:

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



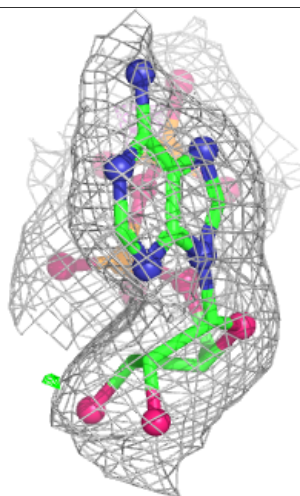
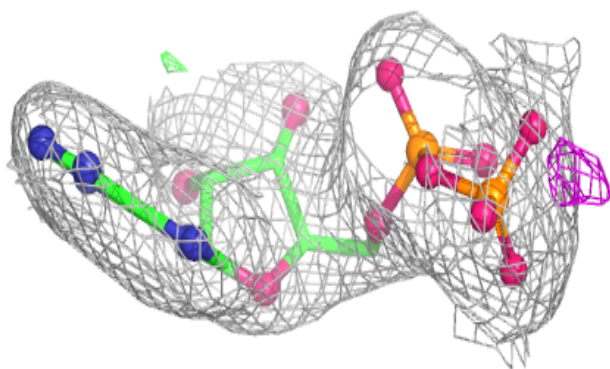
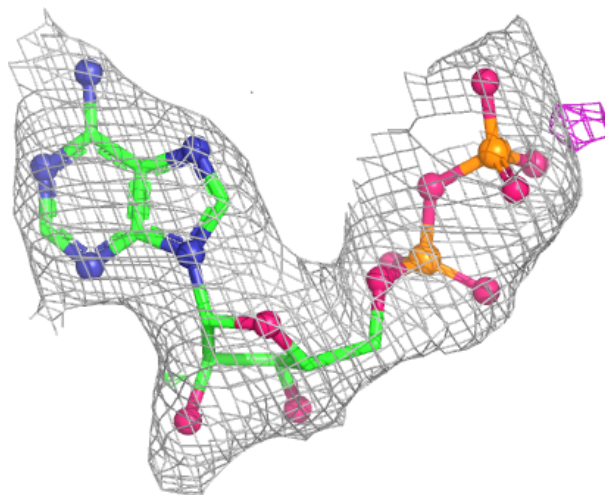
Electron density around ADP D 501:

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



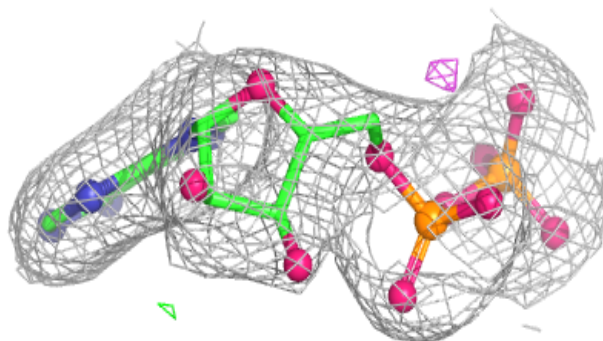
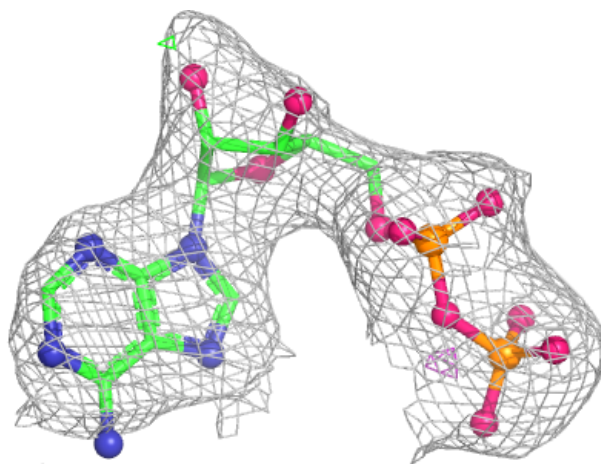
Electron density around ADP E 501:

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



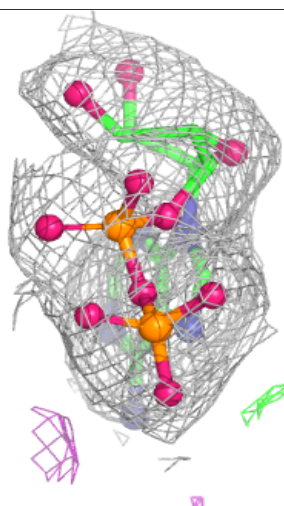
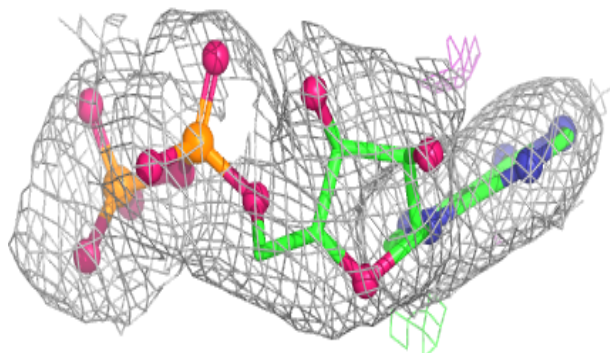
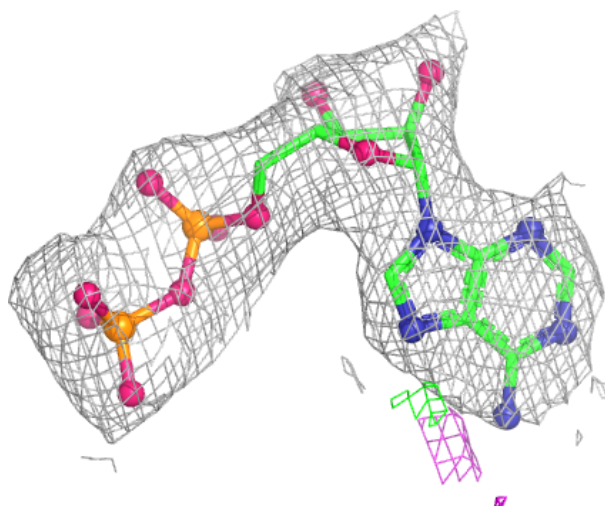
Electron density around ADP G 501:

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



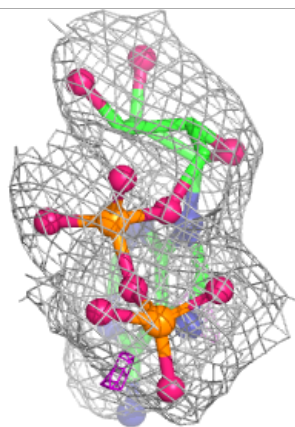
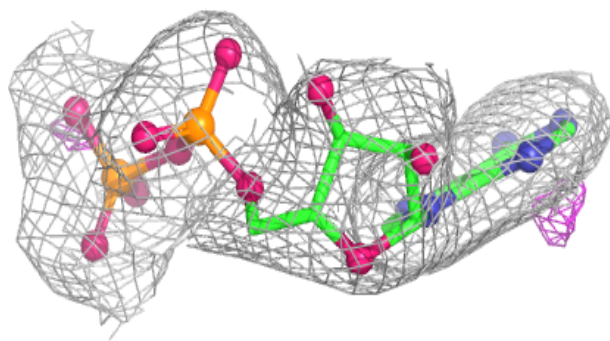
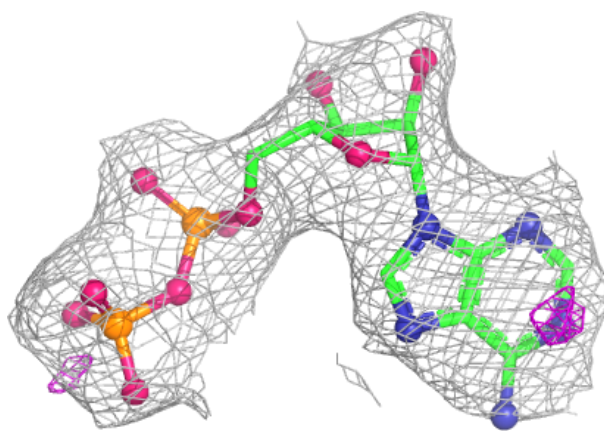
Electron density around ADP H 501:

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



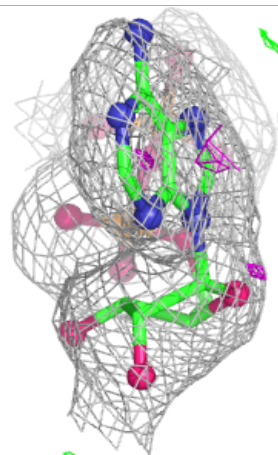
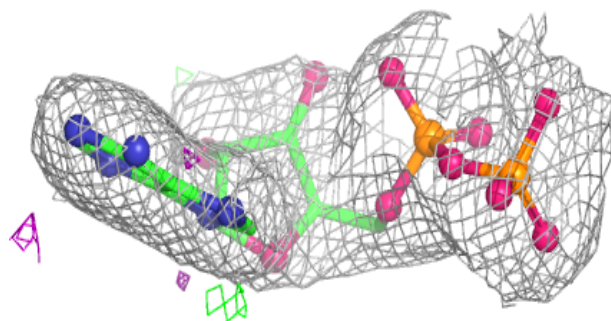
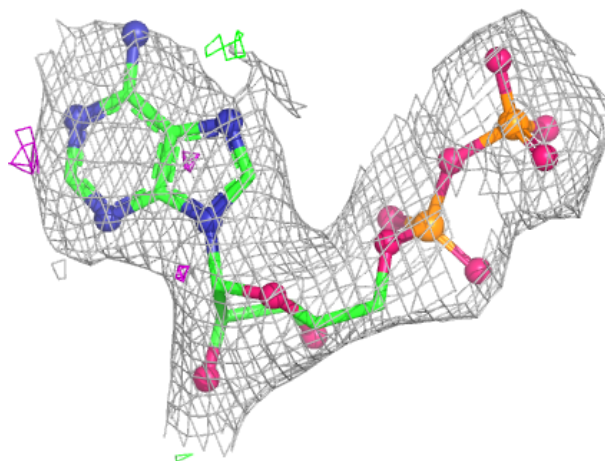
Electron density around ADP J 501:

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



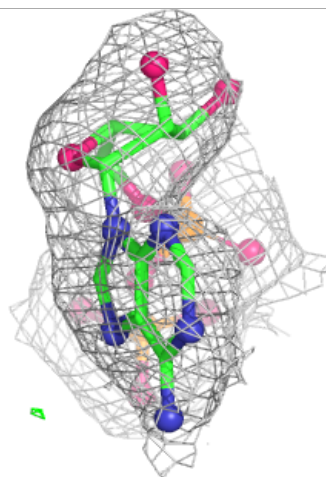
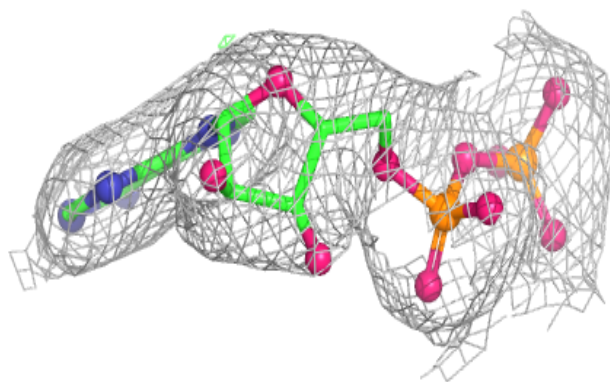
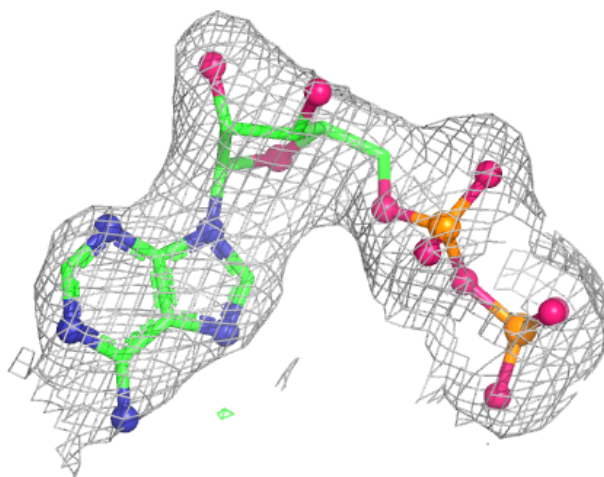
Electron density around ADP A 501:

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



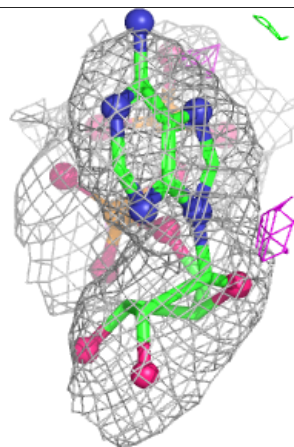
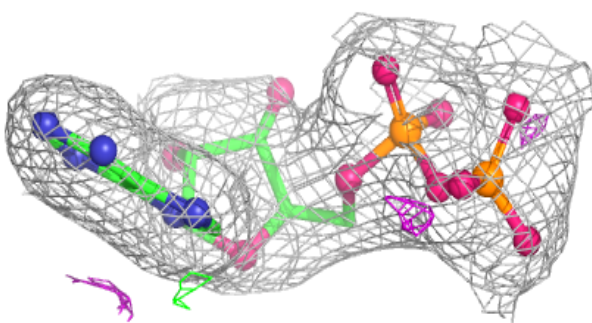
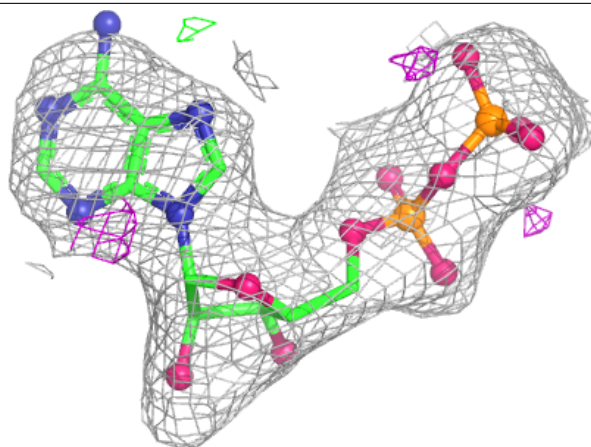
Electron density around ADP I 501:

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



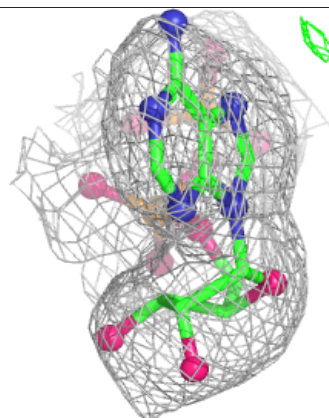
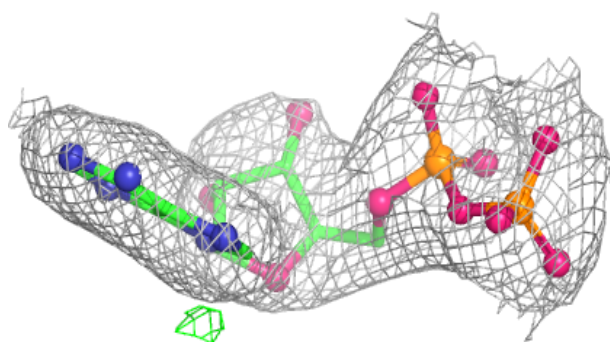
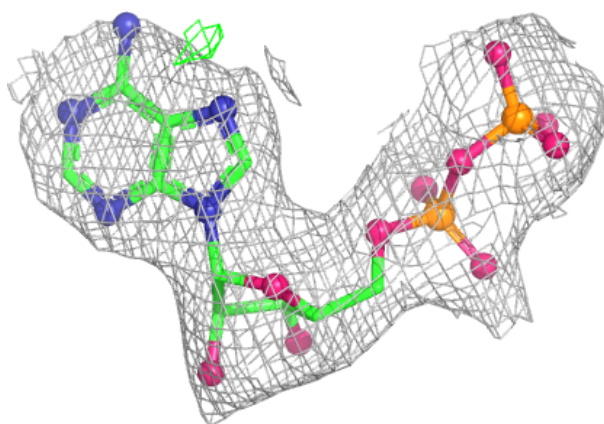
Electron density around ADP C 501:

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



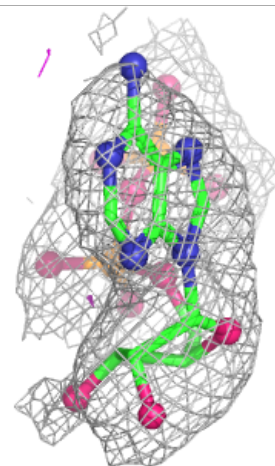
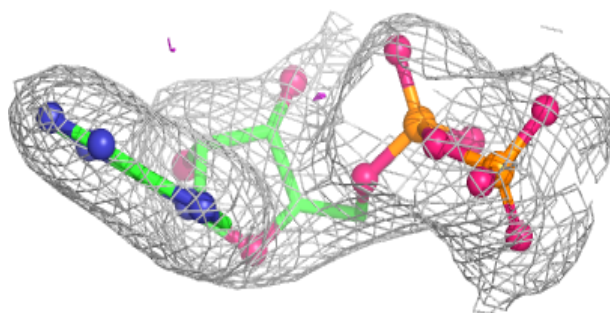
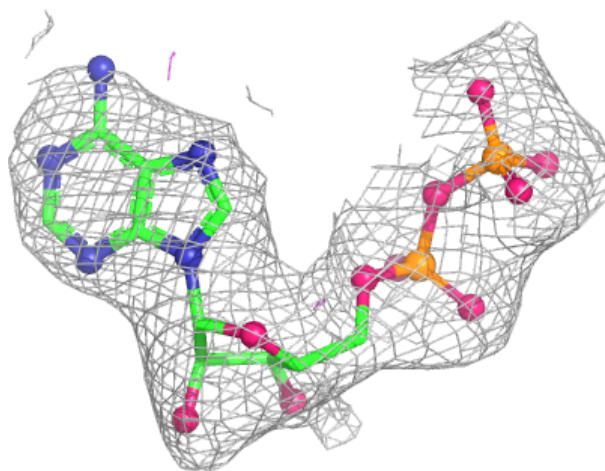
Electron density around ADP K 501:

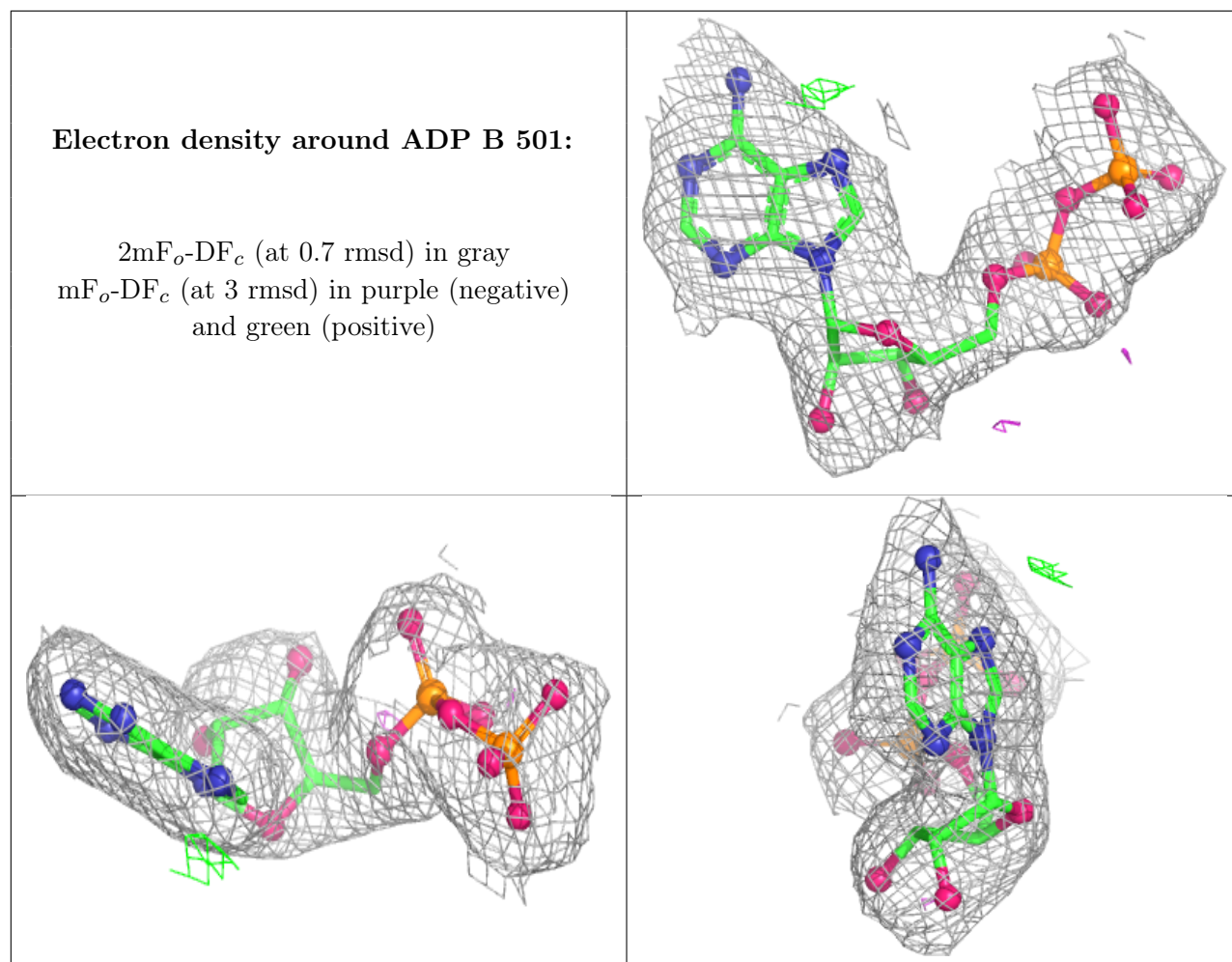
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ADP F 501:

$2mF_o-DF_c$ (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.