



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 09:33 PM UTC

PDB ID : 4W9M / pdb_00004w9m
Title : AMPPNP bound Rad50 in complex with dsDNA
Authors : Rojowska, A.; Lammens, K.
Deposited on : 2014-08-27
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

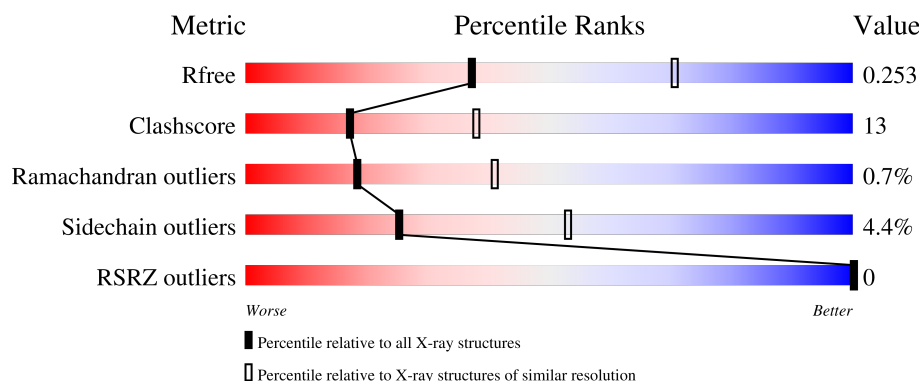
1 Overall quality at a glance

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	Y	15	67% 33%
1	Z	15	100%
2	A	15	47% 53%
2	G	15	53% 47%
3	C	365	67% 27% ••

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Mol	Chain	Length	Quality of chain
3	E	365	70%24%
3	I	365	74%20%
3	K	365	73%22%
4	D	37	89%8%
4	F	37	70%24%
4	J	37	70%24%
4	L	37	62%32%5%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 14169 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 DNA chain called DNA (5'-D(*GP*GP*TP*CP*GP*GP*TP*GP*AP*CP*CP*GP*AP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Y	15	Total	C	N	O	P	0	0	0
			306	145	59	88	14			
1	Z	15	Total	C	N	O	P	0	0	0
			306	145	59	88	14			

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*GP*TP*CP*GP*GP*TP*CP*AP*CP*CP*GP*AP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	15	Total	C	N	O	P	0	0	0
			303	144	57	88	14			
2	G	15	Total	C	N	O	P	0	0	0
			303	144	57	88	14			

- Molecule 3 is a protein called Probable DNA double-strand break repair Rad50 ATPase, Probable DNA double-strand break repair Rad50 ATPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	352	Total	C	N	O	S	256	0	0
			2824	1799	490	531	4			
3	E	351	Total	C	N	O	S	215	0	0
			2815	1794	489	528	4			
3	I	352	Total	C	N	O	S	211	0	0
			2824	1799	490	531	4			
3	K	352	Total	C	N	O	S	239	0	0
			2821	1797	490	530	4			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	676	SER	-	linker	UNP Q9X1X1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	677	SER	-	linker	UNP Q9X1X1
C	678	GLY	-	linker	UNP Q9X1X1
C	679	GLY	-	linker	UNP Q9X1X1
C	680	ALA	-	linker	UNP Q9X1X1
C	681	GLY	-	linker	UNP Q9X1X1
C	682	GLY	-	linker	UNP Q9X1X1
C	683	ALA	-	linker	UNP Q9X1X1
C	684	GLY	-	linker	UNP Q9X1X1
C	685	GLY	-	linker	UNP Q9X1X1
C	686	SER	-	linker	UNP Q9X1X1
E	676	SER	-	linker	UNP Q9X1X1
E	677	SER	-	linker	UNP Q9X1X1
E	678	GLY	-	linker	UNP Q9X1X1
E	679	GLY	-	linker	UNP Q9X1X1
E	680	ALA	-	linker	UNP Q9X1X1
E	681	GLY	-	linker	UNP Q9X1X1
E	682	GLY	-	linker	UNP Q9X1X1
E	683	ALA	-	linker	UNP Q9X1X1
E	684	GLY	-	linker	UNP Q9X1X1
E	685	GLY	-	linker	UNP Q9X1X1
E	686	SER	-	linker	UNP Q9X1X1
I	676	SER	-	linker	UNP Q9X1X1
I	677	SER	-	linker	UNP Q9X1X1
I	678	GLY	-	linker	UNP Q9X1X1
I	679	GLY	-	linker	UNP Q9X1X1
I	680	ALA	-	linker	UNP Q9X1X1
I	681	GLY	-	linker	UNP Q9X1X1
I	682	GLY	-	linker	UNP Q9X1X1
I	683	ALA	-	linker	UNP Q9X1X1
I	684	GLY	-	linker	UNP Q9X1X1
I	685	GLY	-	linker	UNP Q9X1X1
I	686	SER	-	linker	UNP Q9X1X1
K	189	SER	-	linker	UNP Q9X1X1
K	677	SER	-	linker	UNP Q9X1X1
K	678	GLY	-	linker	UNP Q9X1X1
K	679	GLY	-	linker	UNP Q9X1X1
K	680	ALA	-	linker	UNP Q9X1X1
K	681	GLY	-	linker	UNP Q9X1X1
K	682	GLY	-	linker	UNP Q9X1X1
K	683	ALA	-	linker	UNP Q9X1X1
K	684	GLY	-	linker	UNP Q9X1X1
K	685	GLY	-	linker	UNP Q9X1X1

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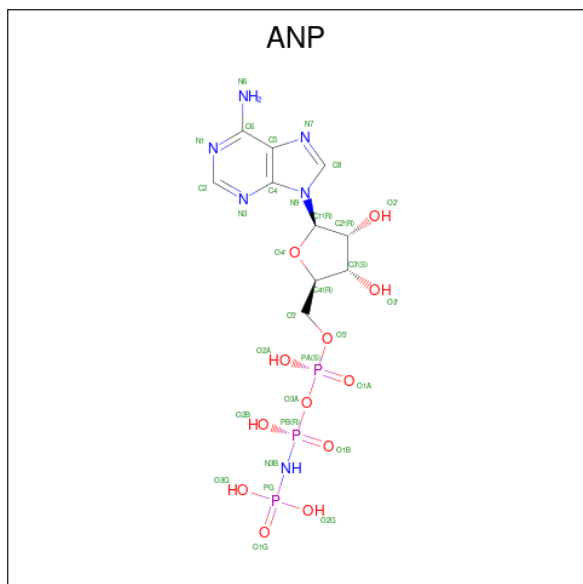
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Chain	Residue	Modelled	Actual	Comment	Reference
K	686	SER	-	linker	UNP Q9X1X1

- Molecule 4 is a protein called Exonuclease, putative.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	36	Total	C	N	O	81	0	0
			319	209	50	60			
4	F	36	Total	C	N	O	82	0	0
			321	210	50	61			
4	J	36	Total	C	N	O	83	0	0
			319	209	50	60			
4	L	35	Total	C	N	O	102	0	0
			313	206	49	58			

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
5	E	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
5	I	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
5	K	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	1	Total 1	Mg 1	0	0
6	E	1	Total 1	Mg 1	0	0
6	I	1	Total 1	Mg 1	0	0
6	K	1	Total 1	Mg 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	Y	2	Total 2	O 2	0	0
7	C	64	Total 64	O 64	0	0
7	D	1	Total 1	O 1	0	0
7	E	63	Total 63	O 63	0	0
7	F	1	Total 1	O 1	0	0
7	G	1	Total 1	O 1	0	0
7	I	67	Total 67	O 67	0	0
7	J	2	Total 2	O 2	0	0
7	K	63	Total 63	O 63	0	0
7	L	3	Total 3	O 3	0	0

3 Residue-property plots [i](#)

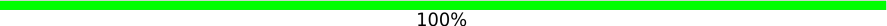
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DNA (5'-D(*GP*GP*TP*CP*GP*GP*TP*GP*AP*CP*CP*GP*AP*CP*C)-3')

Chain Y: 

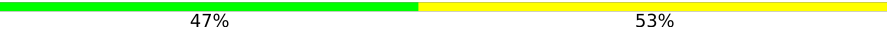


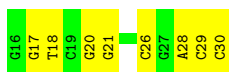
- Molecule 1: DNA (5'-D(*GP*GP*TP*CP*GP*GP*TP*GP*AP*CP*CP*GP*AP*CP*C)-3')

Chain Z: 

There are no outlier residues recorded for this chain.

- Molecule 2: DNA (5'-D(*GP*GP*TP*CP*GP*GP*TP*CP*AP*CP*CP*GP*AP*CP*C)-3')

Chain A: 



- Molecule 2: DNA (5'-D(*GP*GP*TP*CP*GP*GP*TP*CP*AP*CP*CP*GP*AP*CP*C)-3')

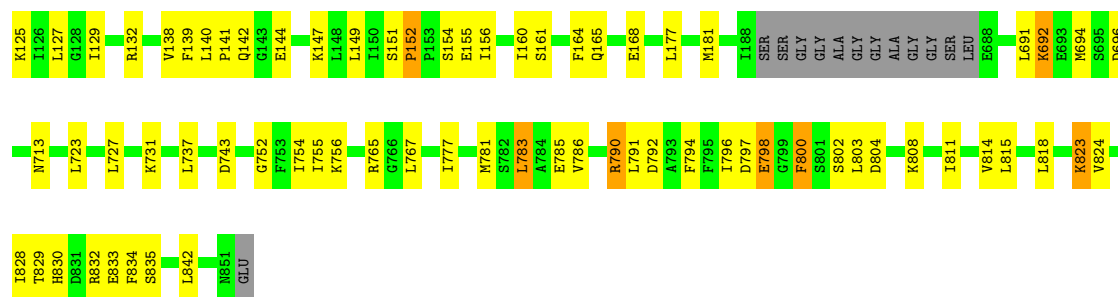
Chain G: 



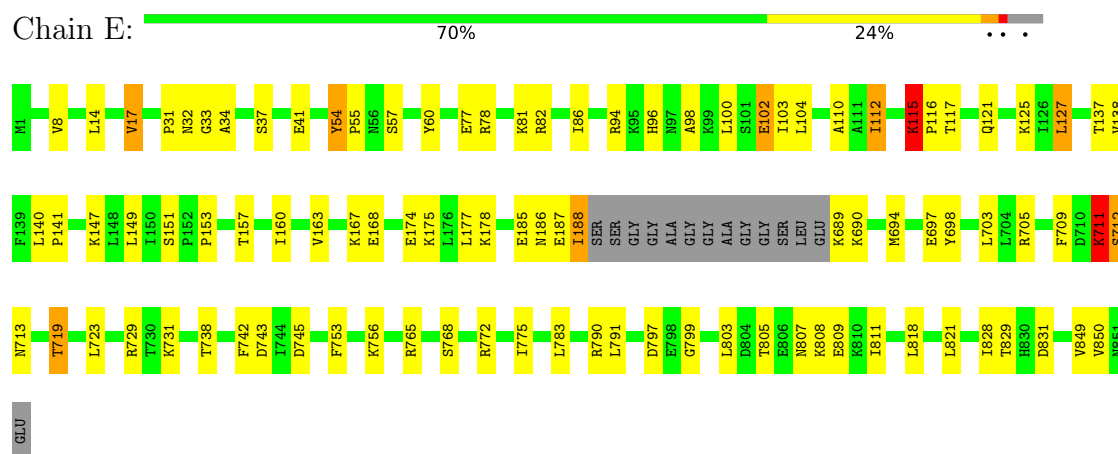
- Molecule 3: Probable DNA double-strand break repair Rad50 ATPase, Probable DNA double-strand break repair Rad50 ATPase

Chain C: 

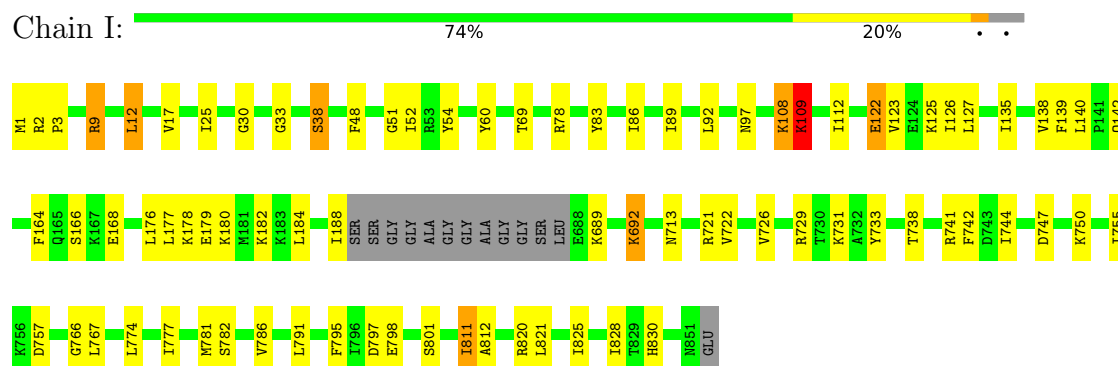




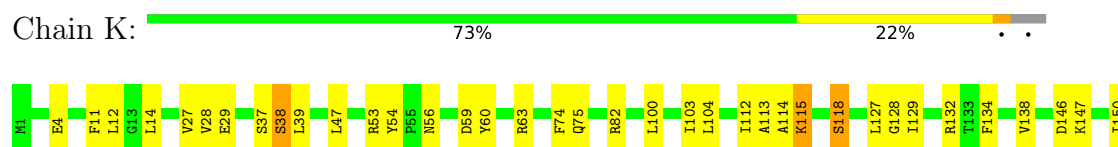
- Molecule 3: Probable DNA double-strand break repair Rad50 ATPase, Probable DNA double-strand break repair Rad50 ATPase

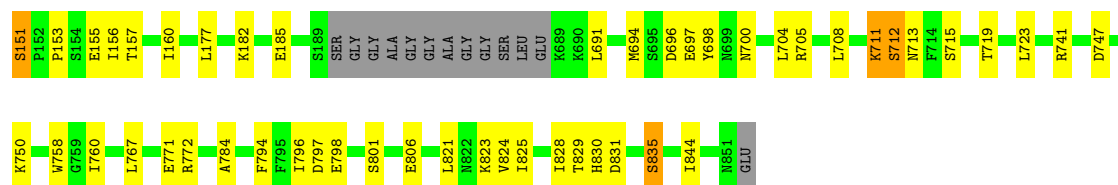


- Molecule 3: Probable DNA double-strand break repair Rad50 ATPase, Probable DNA double-strand break repair Rad50 ATPase



- Molecule 3: Probable DNA double-strand break repair Rad50 ATPase, Probable DNA double-strand break repair Rad50 ATPase





- Molecule 4: Exonuclease, putative

Chain D: 89% 8% .



- Molecule 4: Exonuclease, putative

Chain F: 70% 24% . .



- Molecule 4: Exonuclease, putative

Chain J: 70% 24% . .



- Molecule 4: Exonuclease, putative

Chain L: 62% 32% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.71Å 96.39Å 105.93Å 90.01° 89.22° 81.67°	Depositor
Resolution (Å)	47.69 – 2.70 47.69 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.3 (47.69-2.70) 92.4 (47.69-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.69Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.215 , 0.270 (Not available) , 0.253	Depositor DCC
R_{free} test set	2573 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	43.5	Xtriage
Anisotropy	0.357	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.368 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14169	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% of the height of the origin peak. No significant pseudotranslation is detected.*

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: MG, ANP

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	Y	0.16	0/343	0.64	0/528
1	Z	0.19	0/343	0.69	0/528
2	A	0.18	0/339	0.68	0/521
2	G	0.22	0/339	0.75	0/521
3	C	0.64	1/2865 (0.0%)	0.98	14/3840 (0.4%)
3	E	0.78	6/2856 (0.2%)	1.13	15/3828 (0.4%)
3	I	1.03	3/2865 (0.1%)	1.27	16/3840 (0.4%)
3	K	0.70	1/2862 (0.0%)	1.05	10/3836 (0.3%)
4	D	0.34	0/323	0.72	0/427
4	F	0.37	0/325	0.82	1/430 (0.2%)
4	J	0.35	0/323	0.72	0/427
4	L	0.35	0/317	0.87	0/419
All	All	0.73	11/14100 (0.1%)	1.05	56/19145 (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
3	E	0	3
3	I	0	1
All	All	0	4

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	108	LYS	C-N	-41.48	0.86	1.33
3	I	109	LYS	C-N	-11.30	1.17	1.33
3	E	711	LYS	C-N	-8.77	1.21	1.33
3	C	28	VAL	C-N	-8.49	1.21	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	712	SER	C-N	-6.72	1.24	1.33

The worst 5 of 56 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	109	LYS	O-C-N	-38.20	75.29	122.65
3	I	109	LYS	CA-C-N	21.87	153.38	121.02
3	I	109	LYS	C-N-CA	21.87	153.38	121.02
3	E	711	LYS	O-C-N	-18.39	102.91	122.03
3	E	712	SER	O-C-N	-16.42	101.28	121.97

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	E	711	LYS	Peptide,Mainchain
3	E	799	GLY	Peptide
3	I	109	LYS	Mainchain

5.2 Too-close contacts

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	Y	306	0	169	5	0
1	Z	306	0	169	0	0
2	A	303	0	169	4	1
2	G	303	0	169	5	0
3	C	2824	0	2891	86	5
3	E	2815	0	2886	62	4
3	I	2824	0	2891	62	0
3	K	2821	0	2891	62	0
4	D	319	0	332	1	0
4	F	321	0	331	5	0
4	J	319	0	332	7	0
4	L	313	0	327	7	0
5	C	31	0	13	2	0
5	E	31	0	13	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	I	31	0	13	3	0
5	K	31	0	13	2	0
6	C	1	0	0	0	0
6	E	1	0	0	0	0
6	I	1	0	0	0	0
6	K	1	0	0	0	0
7	C	64	0	0	7	0
7	D	1	0	0	0	0
7	E	63	0	0	8	0
7	F	1	0	0	0	0
7	G	1	0	0	0	0
7	I	67	0	0	8	0
7	J	2	0	0	0	0
7	K	63	0	0	10	0
7	L	3	0	0	0	0
7	Y	2	0	0	0	0
All	All	14169	0	13609	301	5

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 13.

The worst 5 of 301 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:I:108:LYS:C	3:I:109:LYS:CA	2.11	1.21
3:I:108:LYS:O	3:I:109:LYS:N	1.77	1.16
3:C:142:GLN:HG3	3:C:798:GLU:CB	1.79	1.13
3:I:108:LYS:CA	3:I:109:LYS:N	2.14	1.08
3:I:142:GLN:HG3	3:I:798:GLU:HB3	1.34	1.08

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:833:GLU:CA	3:E:94:ARG:NH1[1_455]	1.33	0.87
3:C:833:GLU:N	3:E:94:ARG:NH2[1_455]	1.87	0.33
3:C:833:GLU:N	3:E:94:ARG:NH1[1_455]	1.93	0.27
2:A:26:DC:OP2	3:C:108:LYS:NZ[1_655]	2.00	0.20
3:C:833:GLU:N	3:E:94:ARG:CZ[1_455]	2.10	0.10

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	
3	C	348/365 (95%)	327 (94%)	17 (5%)	4 (1%)	11	29
3	E	347/365 (95%)	331 (95%)	14 (4%)	2 (1%)	21	44
3	I	348/365 (95%)	329 (94%)	18 (5%)	1 (0%)	36	60
3	K	348/365 (95%)	325 (93%)	19 (6%)	4 (1%)	11	29
4	D	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
4	F	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
4	J	34/37 (92%)	32 (94%)	2 (6%)	0	100	100
4	L	33/37 (89%)	29 (88%)	4 (12%)	0	100	100
All	All	1526/1608 (95%)	1437 (94%)	78 (5%)	11 (1%)	18	41

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	E	713	ASN
3	K	712	SER
3	C	51	GLY
3	C	713	ASN
3	K	713	ASN

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	306/311 (98%)	293 (96%)	13 (4%)	26	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	305/311 (98%)	289 (95%)	16 (5%)	21	47
3	I	306/311 (98%)	293 (96%)	13 (4%)	26	55
3	K	306/311 (98%)	296 (97%)	10 (3%)	33	63
4	D	36/37 (97%)	34 (94%)	2 (6%)	19	44
4	F	36/37 (97%)	34 (94%)	2 (6%)	19	44
4	J	36/37 (97%)	34 (94%)	2 (6%)	19	44
4	L	35/37 (95%)	33 (94%)	2 (6%)	18	43
All	All	1366/1392 (98%)	1306 (96%)	60 (4%)	25	53

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	729	ARG
3	K	821	LEU
3	I	38	SER
3	K	806	GLU
4	L	367	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	I	16	ASN
3	I	822	ASN
3	C	699	ASN
3	E	75	GLN
3	E	106	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
5	ANP	K	901	6	33,33,33	1.62	6 (18%)	45,52,52	1.00	4 (8%)
5	ANP	E	901	6	33,33,33	1.49	5 (15%)	45,52,52	1.00	4 (8%)
5	ANP	I	901	6	33,33,33	1.77	2 (6%)	45,52,52	1.18	4 (8%)
5	ANP	C	901	6	33,33,33	2.21	6 (18%)	45,52,52	0.71	1 (2%)

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
5	ANP	K	901	6	-	7/18/38/38	0/3/3/3
5	ANP	E	901	6	-	4/18/38/38	0/3/3/3
5	ANP	I	901	6	-	4/18/38/38	0/3/3/3
5	ANP	C	901	6	-	4/18/38/38	0/3/3/3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	901	ANP	PG-O1G	9.13	1.60	1.46
5	C	901	ANP	PG-O1G	8.32	1.58	1.46
5	C	901	ANP	PB-O1B	6.65	1.56	1.46
5	K	901	ANP	PB-O1B	6.11	1.55	1.46
5	E	901	ANP	PB-O1B	6.04	1.55	1.46

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	901	ANP	O1B-PB-N3B	-4.60	105.00	111.77
5	I	901	ANP	O1G-PG-N3B	3.42	116.81	111.77
5	K	901	ANP	O3G-PG-O1G	-3.25	105.29	113.45
5	E	901	ANP	O2G-PG-O1G	-3.20	105.43	113.45
5	E	901	ANP	O3G-PG-O1G	-3.14	105.57	113.45

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

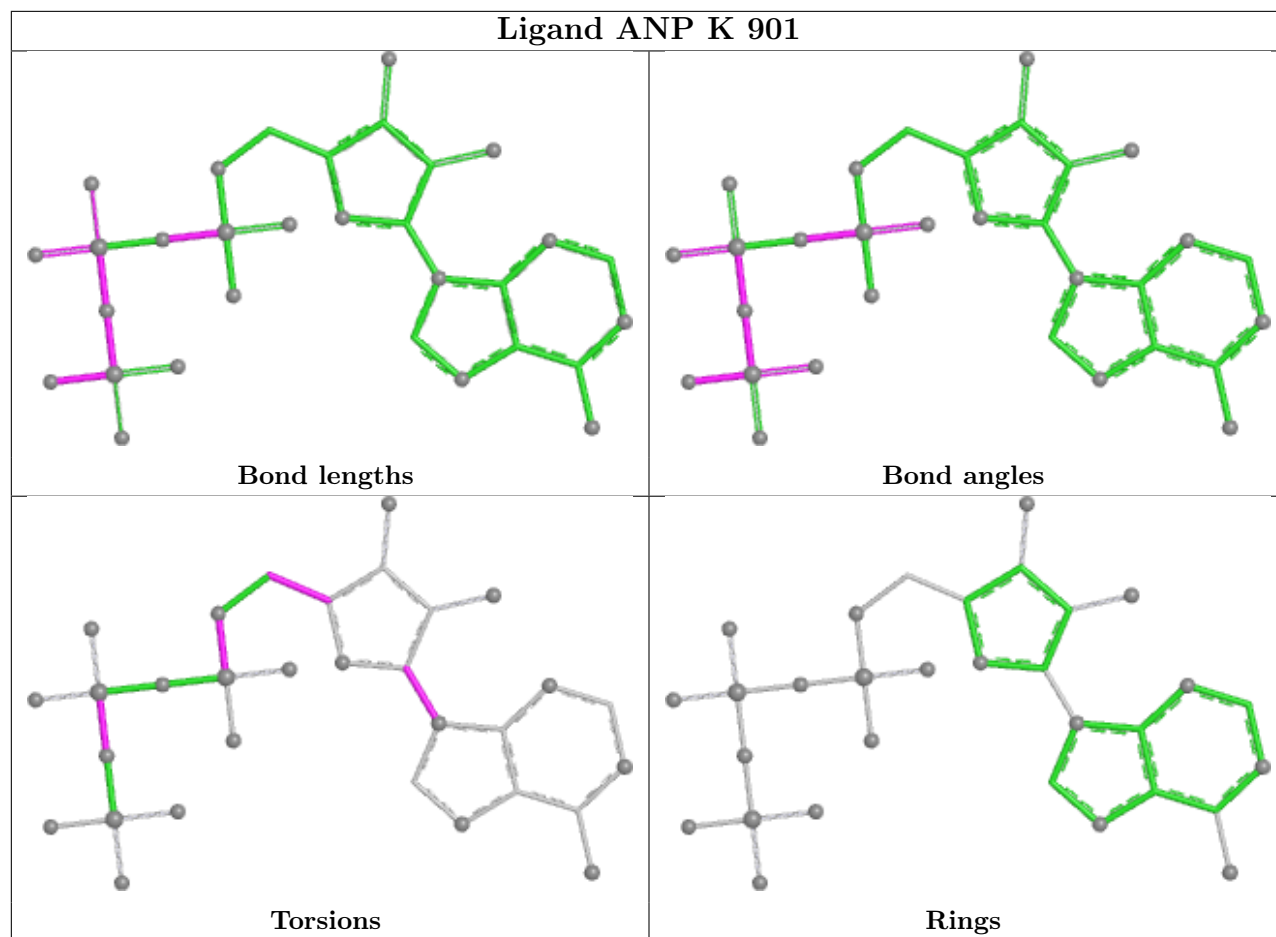
Mol	Chain	Res	Type	Atoms
5	C	901	ANP	PA-O3A-PB-O1B
5	E	901	ANP	PB-N3B-PG-O1G
5	I	901	ANP	PG-N3B-PB-O1B
5	K	901	ANP	PG-N3B-PB-O3A
5	K	901	ANP	C3'-C4'-C5'-O5'

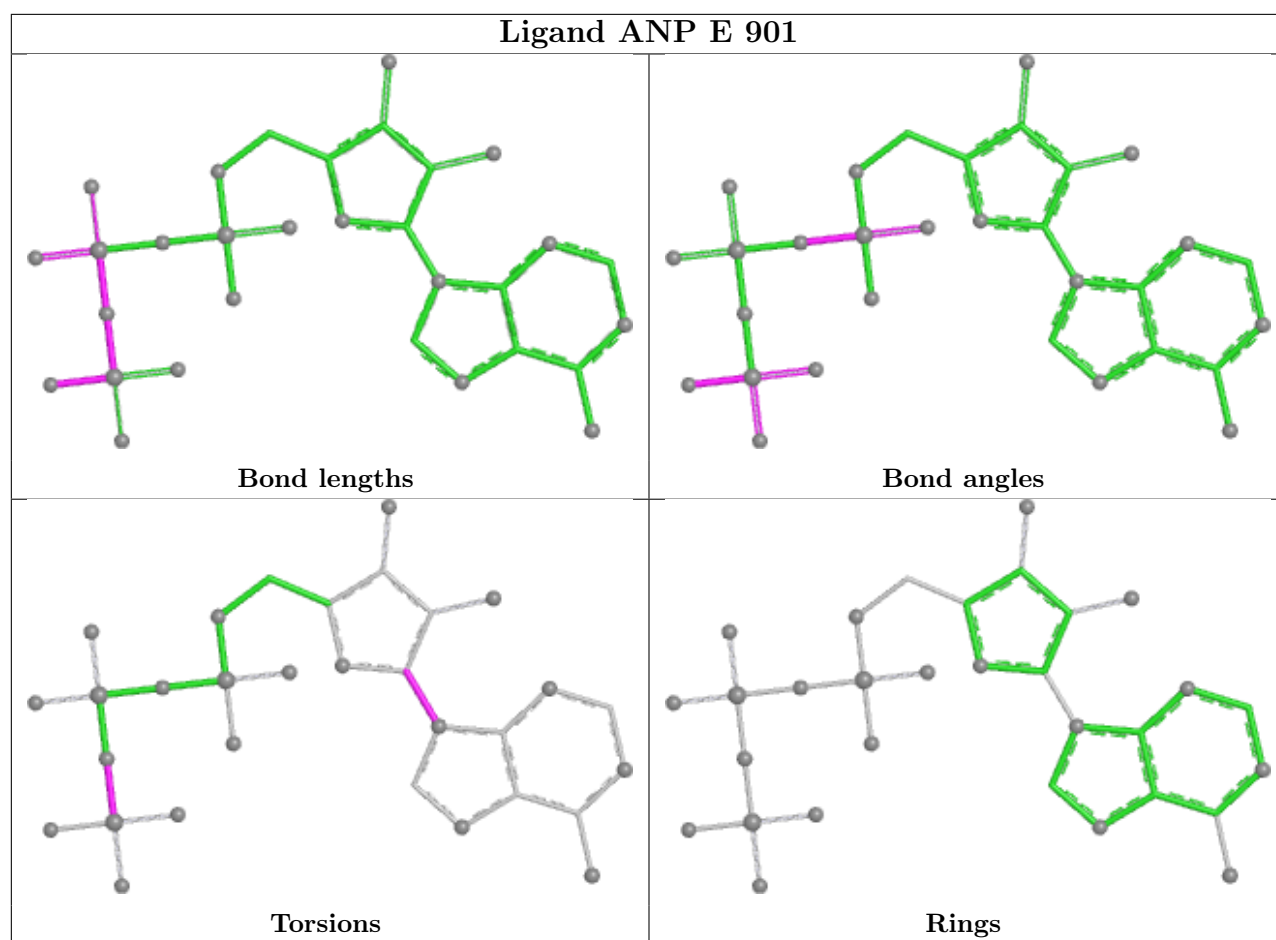
There are no ring outliers.

4 monomers are involved in 10 short contacts:

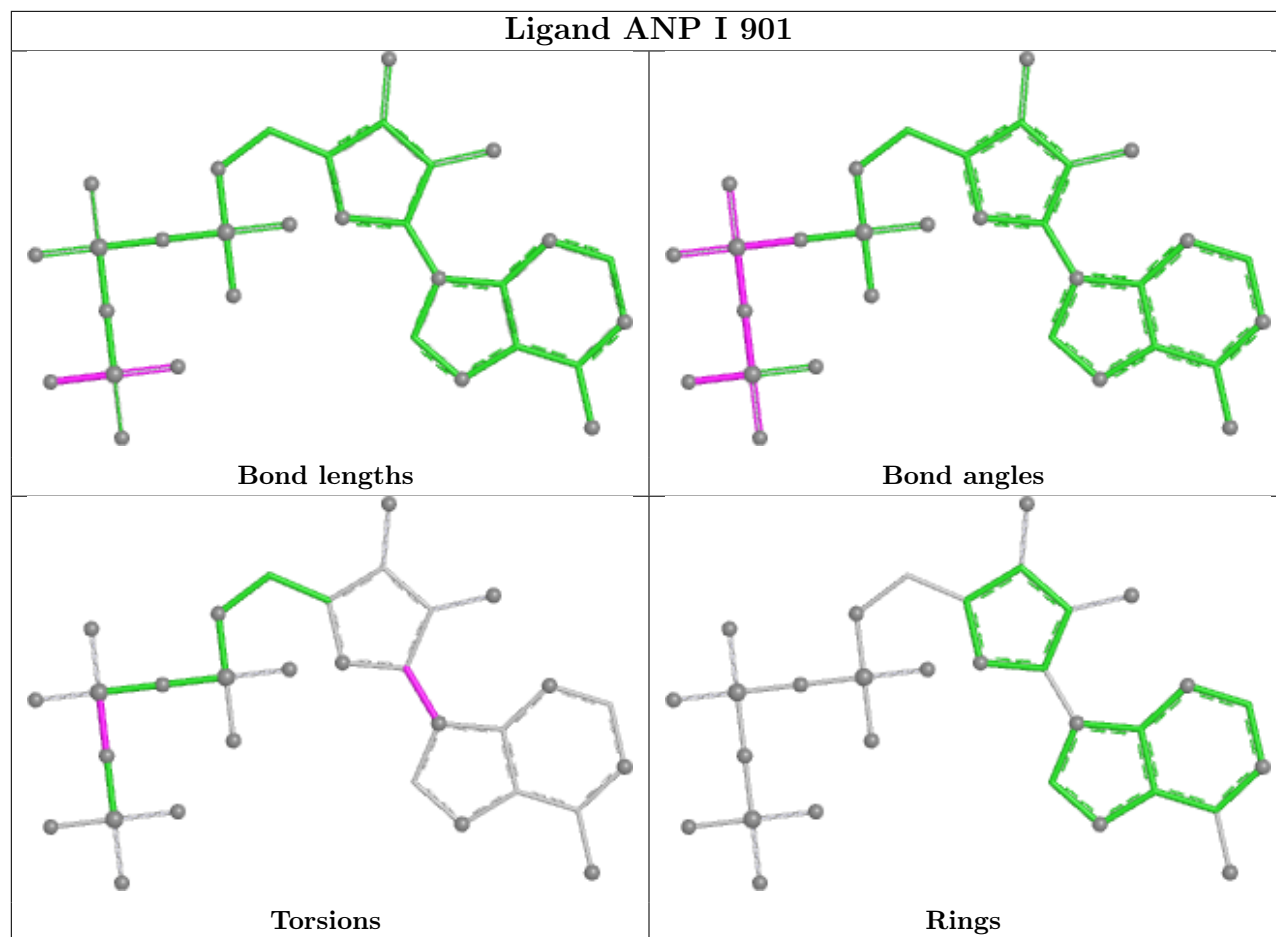
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	K	901	ANP	2	0
5	E	901	ANP	3	0
5	I	901	ANP	3	0
5	C	901	ANP	2	0

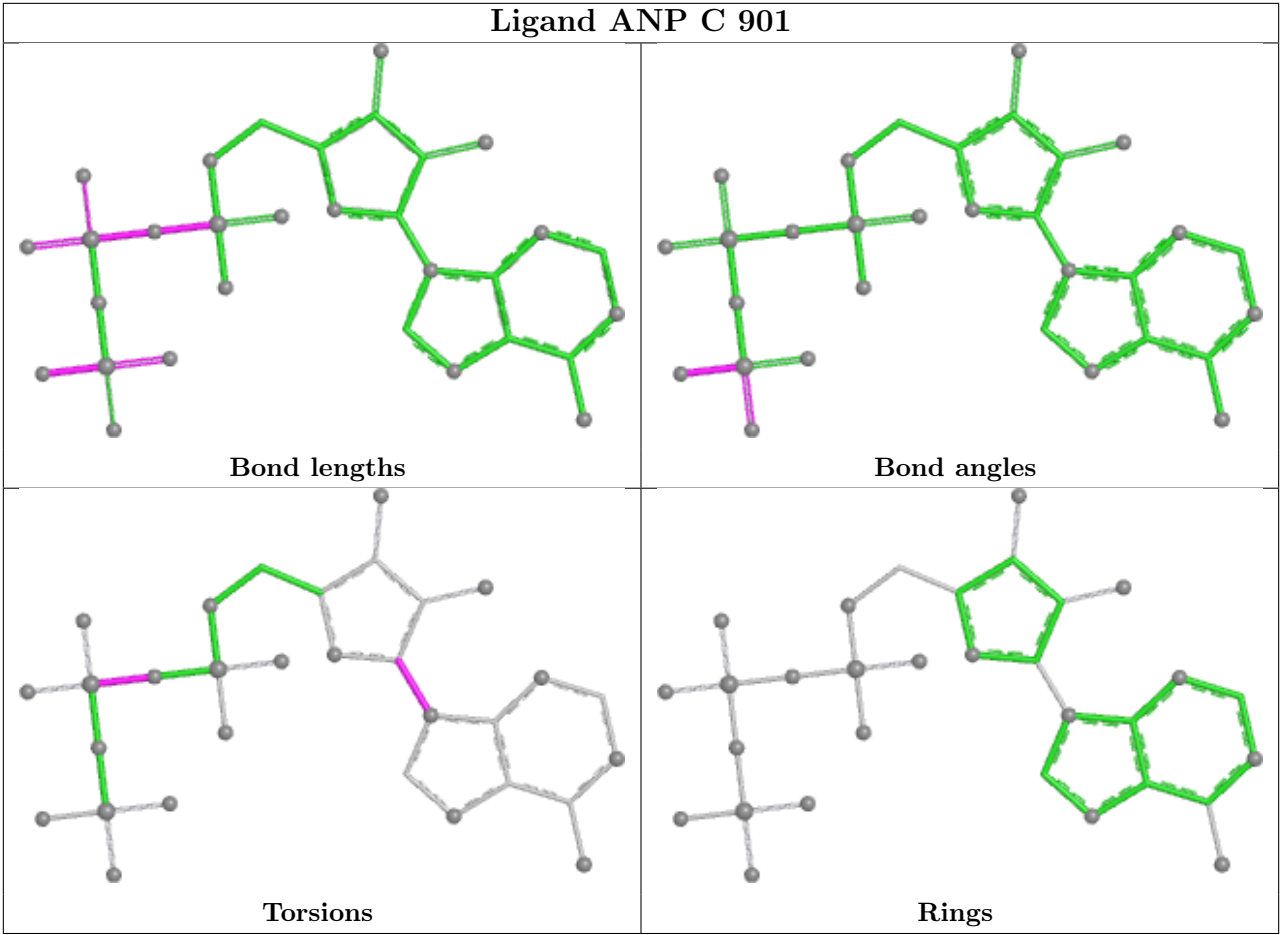
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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 ANP I 901





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	I	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	I	109:LYS	C	110:ALA	N	1.17
1	I	108:LYS	C	109:LYS	N	0.86

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	Y	15/15 (100%)	-0.46	0 100 100	136, 158, 186, 194	0
1	Z	15/15 (100%)	-0.72	0 100 100	122, 146, 183, 183	0
2	A	15/15 (100%)	-1.08	0 100 100	75, 140, 176, 177	0
2	G	15/15 (100%)	-1.13	0 100 100	64, 132, 167, 167	0
3	C	352/365 (96%)	-1.44	0 100 100	11, 27, 44, 63	94 (26%)
3	E	351/365 (96%)	-1.48	0 100 100	14, 26, 48, 67	78 (22%)
3	I	352/365 (96%)	-1.43	0 100 100	12, 27, 45, 62	67 (19%)
3	K	352/365 (96%)	-1.44	0 100 100	10, 25, 47, 73	78 (22%)
4	D	36/37 (97%)	-1.47	0 100 100	22, 39, 59, 72	23 (63%)
4	F	36/37 (97%)	-1.40	0 100 100	24, 44, 64, 74	22 (61%)
4	J	36/37 (97%)	-1.43	0 100 100	22, 35, 56, 65	20 (55%)
4	L	35/37 (94%)	-1.33	0 100 100	18, 38, 66, 71	27 (77%)
All	All	1610/1668 (96%)	-1.42	0 100 100	10, 28, 61, 194	409 (25%)

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

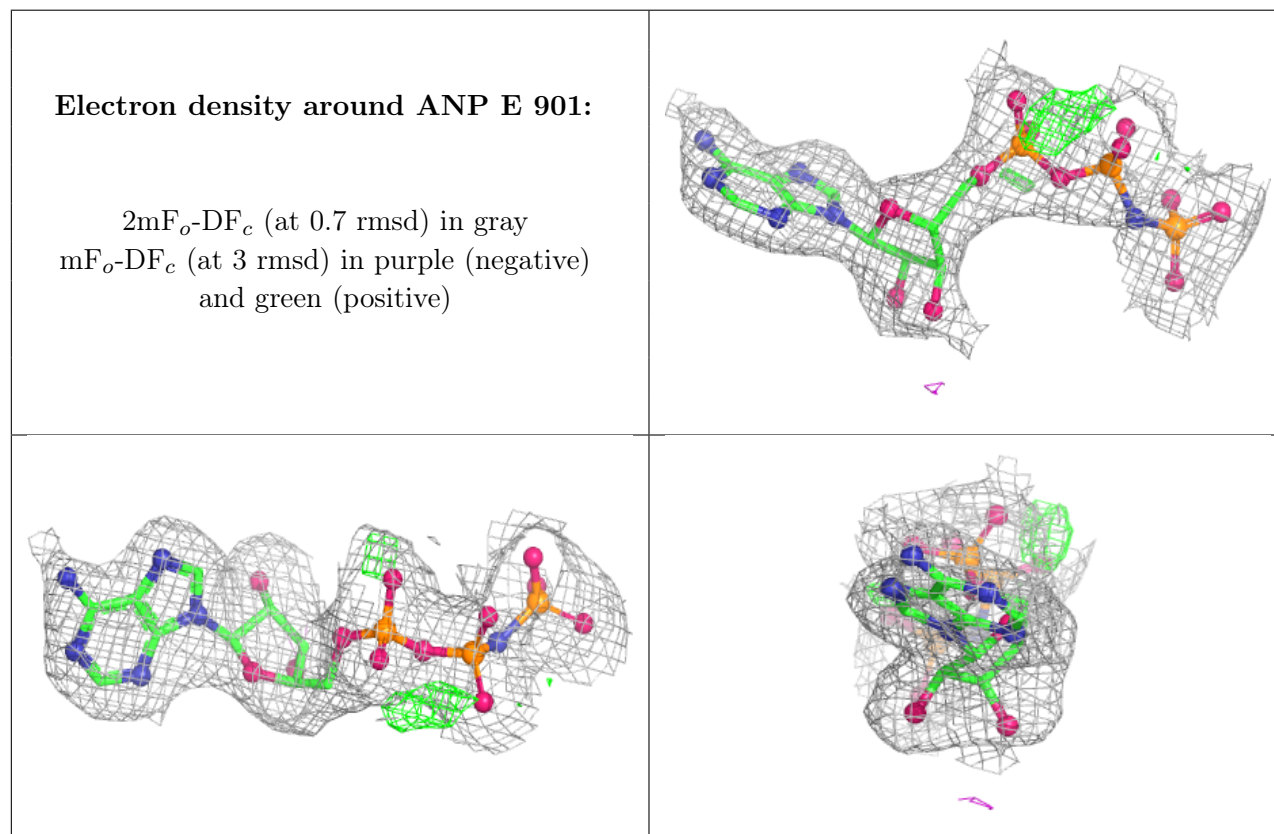
There are no oligosaccharides in this entry.

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.

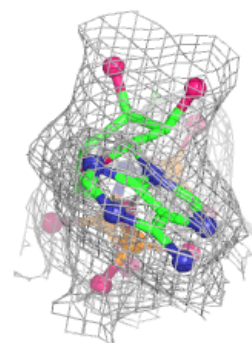
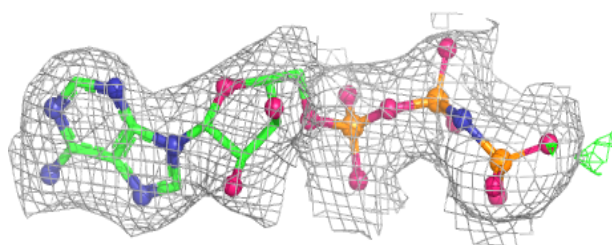
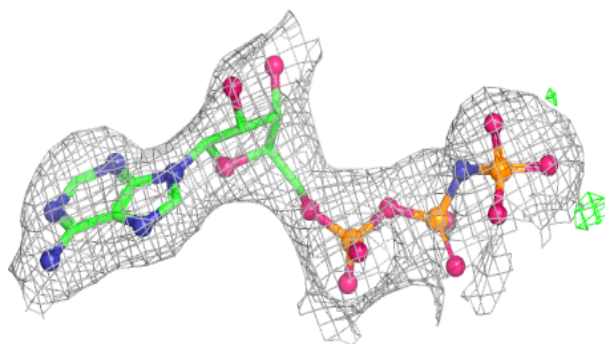
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	ANP	E	901	31/31	0.99	0.03	11,19,23,24	0
5	ANP	C	901	31/31	1.00	0.03	14,19,22,23	0
5	ANP	I	901	31/31	1.00	0.03	15,19,24,24	0
5	ANP	K	901	31/31	1.00	0.03	11,19,23,26	0
6	MG	C	902	1/1	1.00	0.03	15,15,15,15	0
6	MG	E	902	1/1	1.00	0.04	14,14,14,14	0
6	MG	I	902	1/1	1.00	0.03	16,16,16,16	0
6	MG	K	902	1/1	1.00	0.04	13,13,13,13	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.

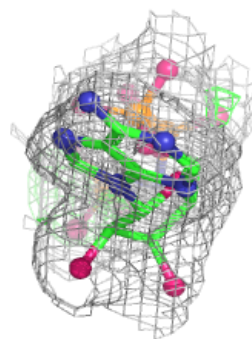
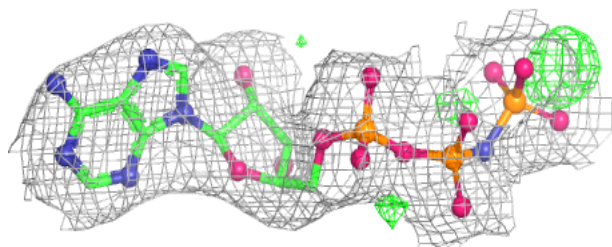
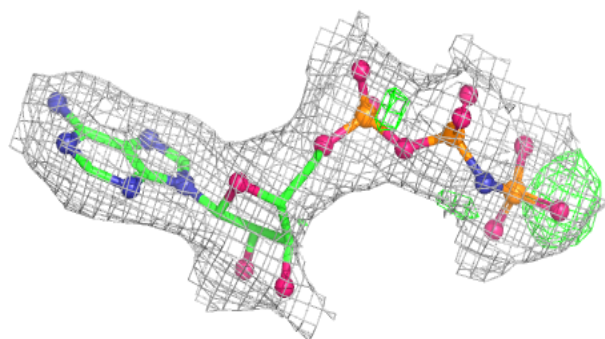


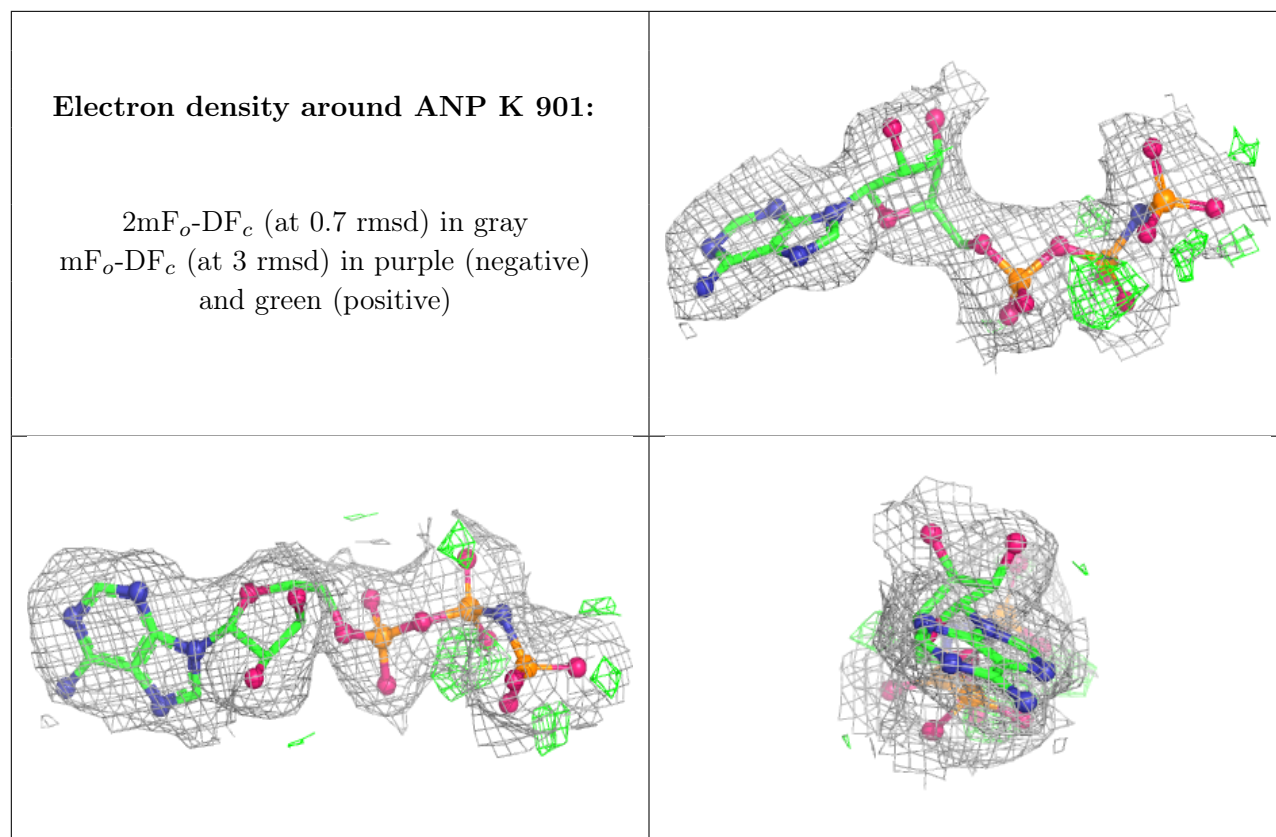
Electron density around ANP C 901:

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

**Electron density around ANP I 901:**

$2mF_o-DF_c$ (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.