



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 22, 2020 – 02:12 AM BST

PDB ID : 3B60
Title : Crystal Structure of MsbA from Salmonella typhimurium with AMPPNP, higher resolution form
Authors : Ward, A.; Reyes, C.L.; Yu, J.; Roth, C.B.; Chang, G.
Deposited on : 2007-10-26
Resolution : 3.70 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

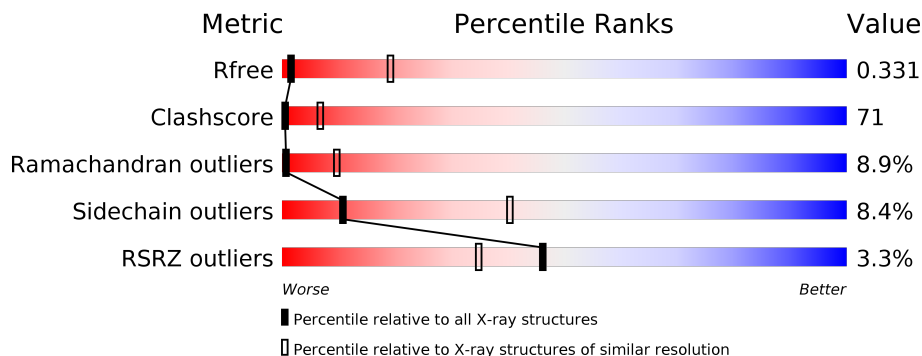
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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}	130704	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)

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 on 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	582	 5% 24% 61% 12% ..
1	B	582	 3% 25% 61% 11% ..
1	C	582	 3% 25% 61% 11% ..
1	D	582	 2% 25% 60% 12% ..

2 Entry composition [i](#)

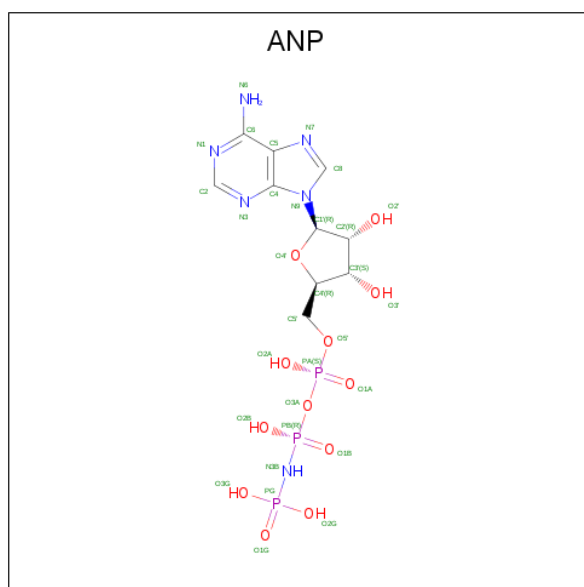
There are 2 unique types of molecules in this entry. The entry contains 17844 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Lipid A export ATP-binding/permease protein msbA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	572	Total 4430	C 2813	N 768	O 822	S 27	0	0	0
1	B	572	Total 4430	C 2813	N 768	O 822	S 27	0	0	0
1	C	572	Total 4430	C 2813	N 768	O 822	S 27	0	0	0
1	D	572	Total 4430	C 2813	N 768	O 822	S 27	0	0	0

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 31	C 10	N 6	O 12	P 3	0	0
2	B	1	Total 31	C 10	N 6	O 12	P 3	0	0

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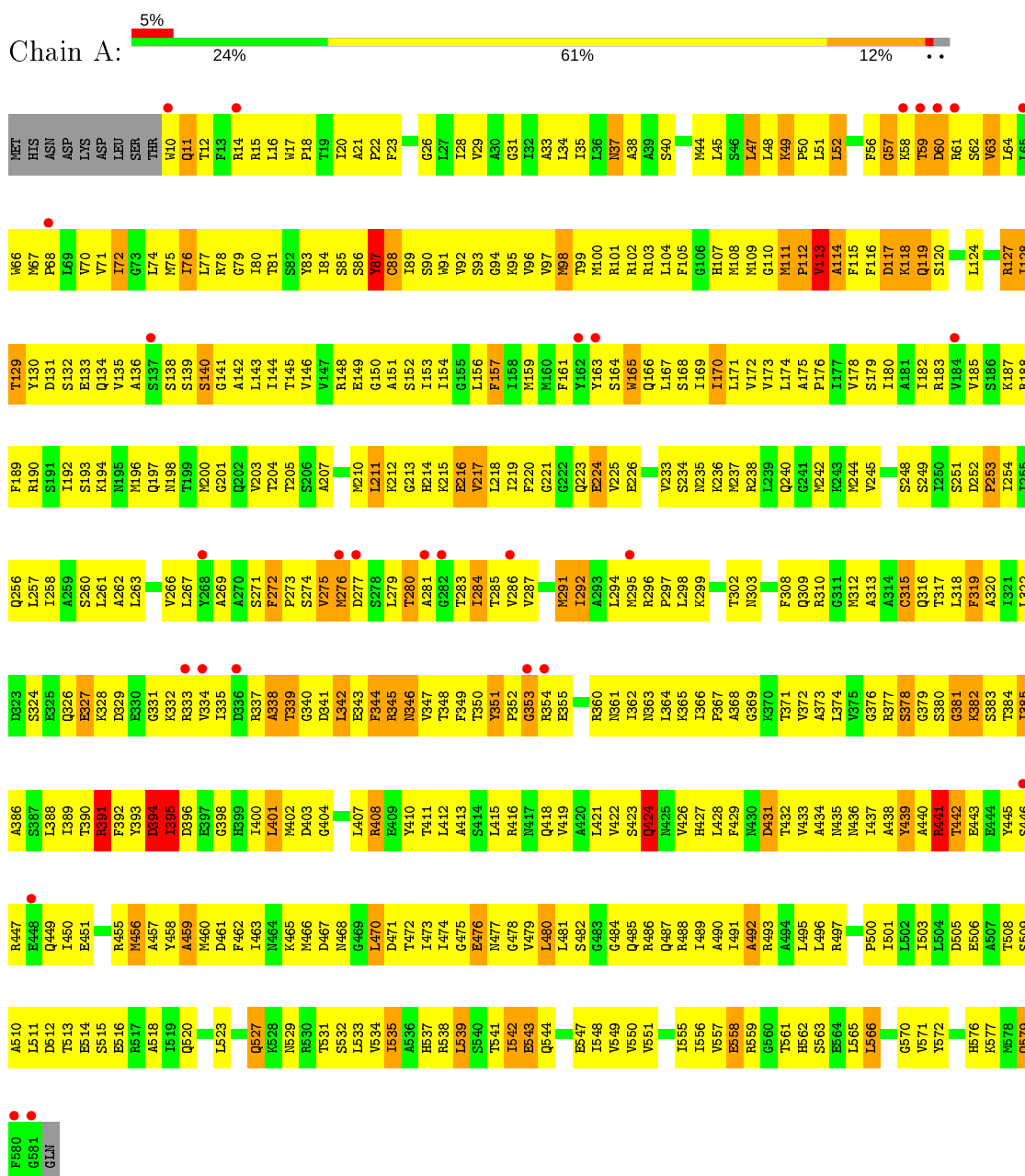
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

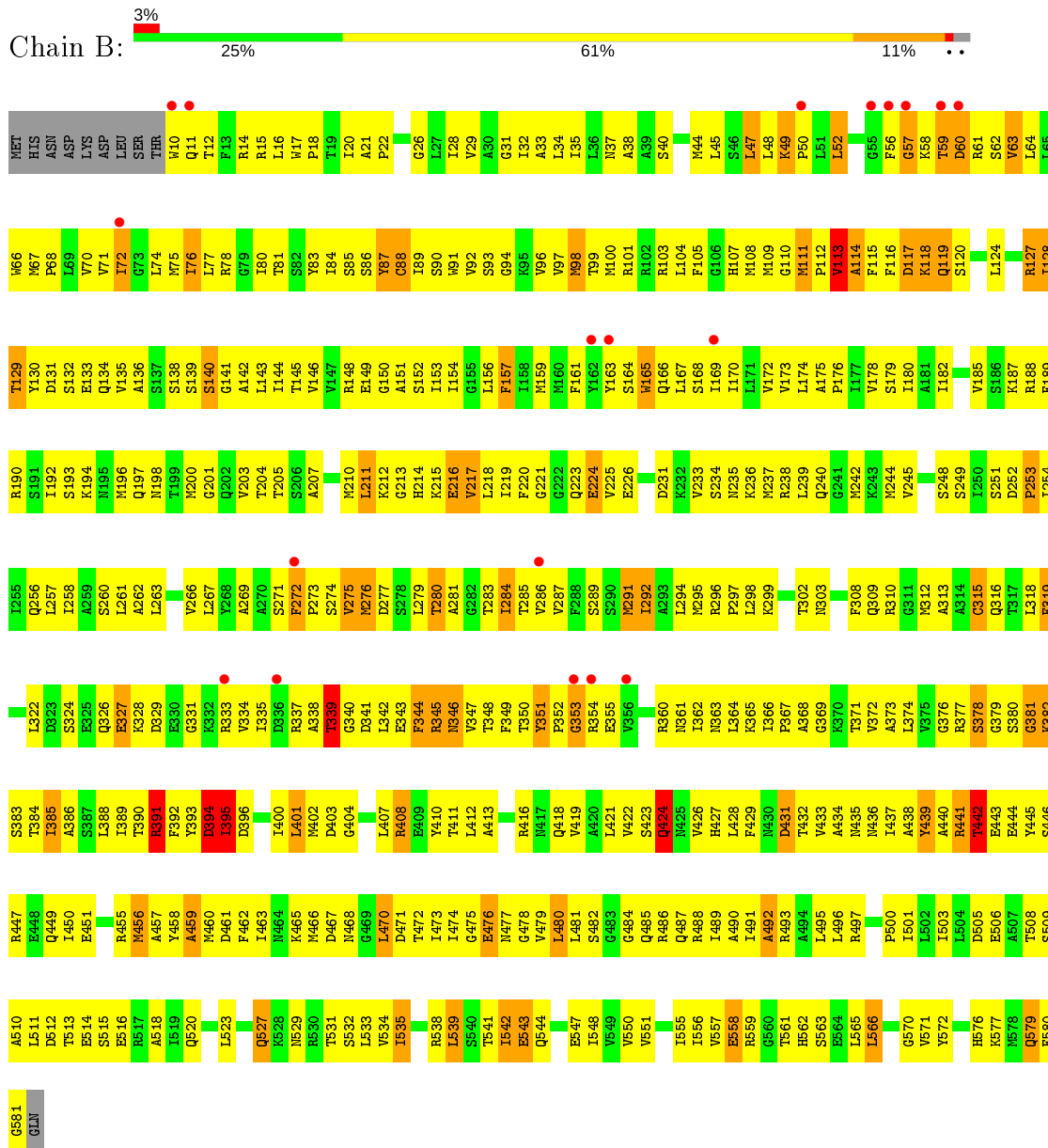
3 Residue-property plots

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.

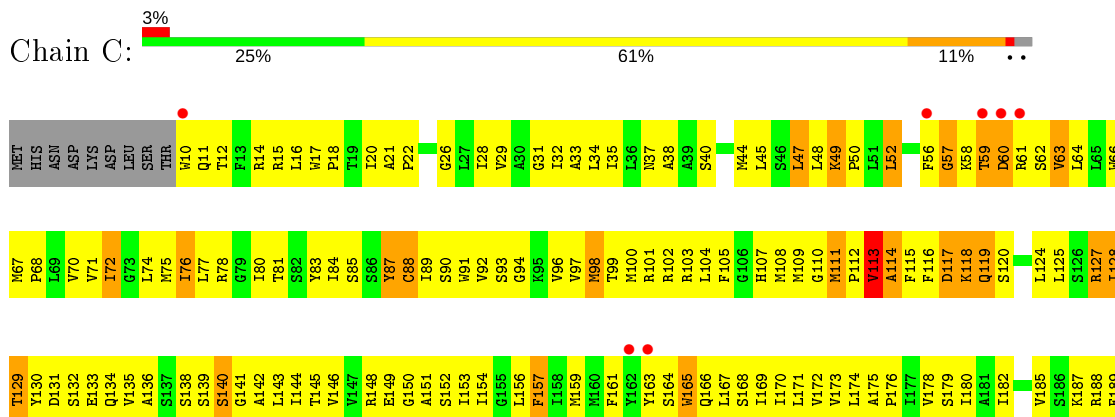
- Molecule 1: Lipid A export ATP-binding/permease protein msbA

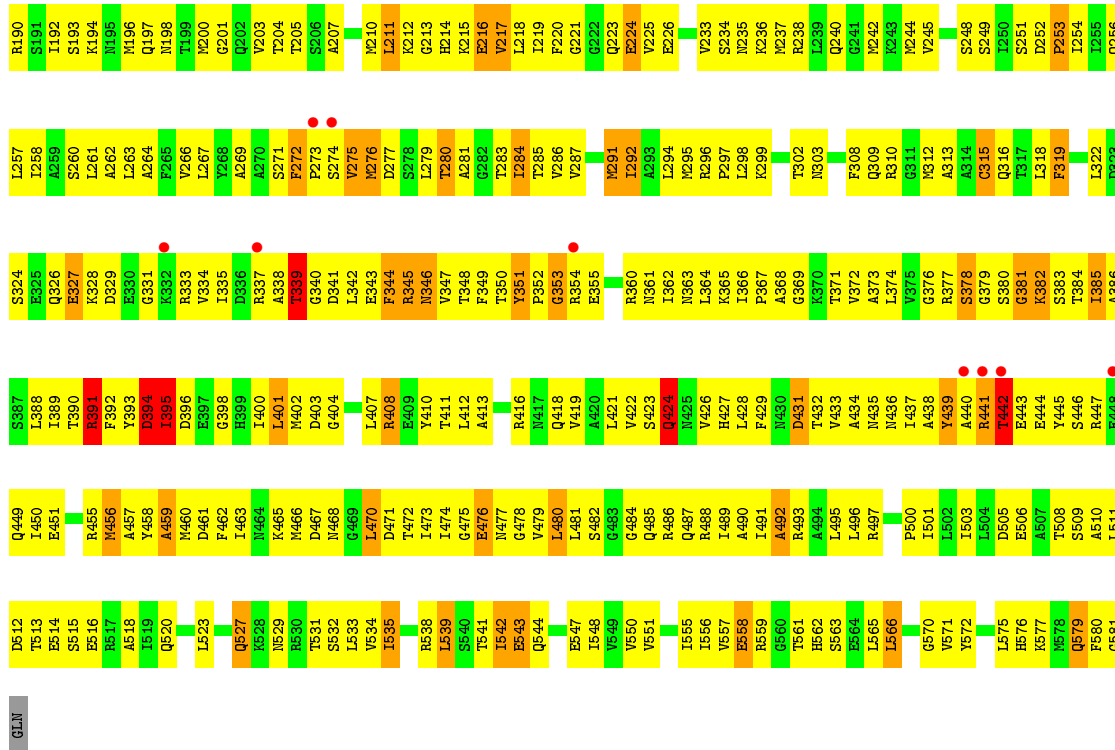


• Molecule 1: Lipid A export ATP-binding/permease protein msbA

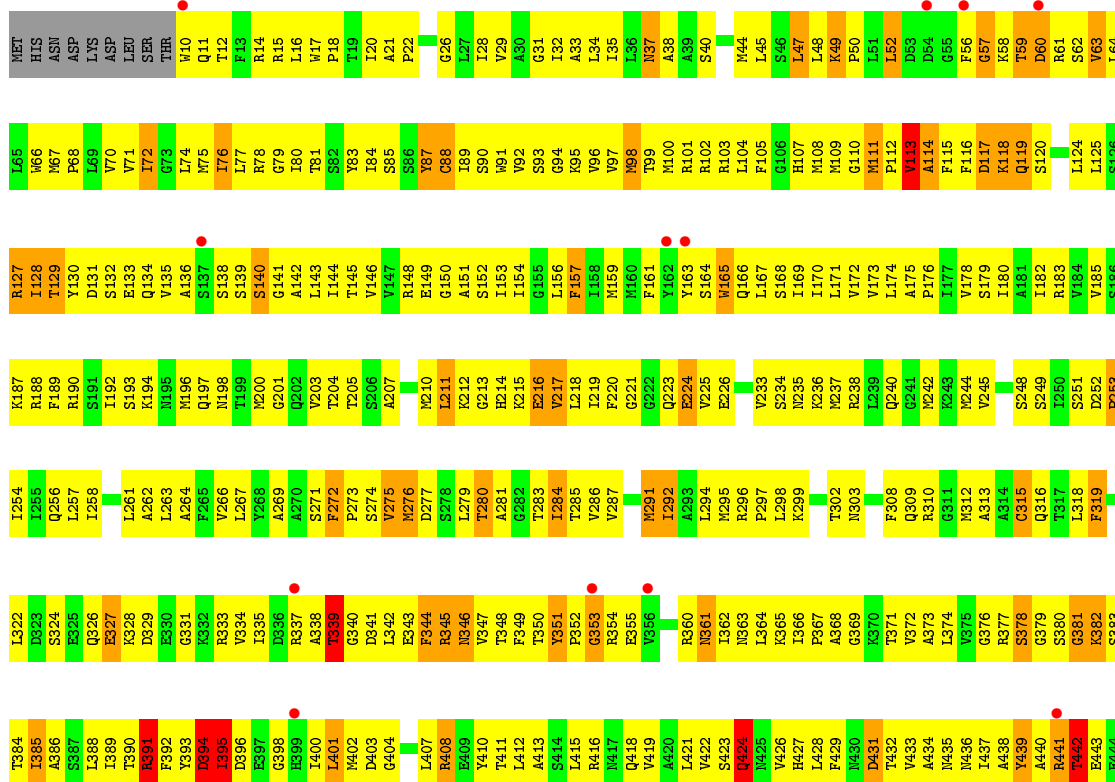


• Molecule 1: Lipid A export ATP-binding/permease protein msbA





• Molecule 1: Lipid A export ATP-binding/permease protein msbA



Y445	T608	K578
S446	S509	Q579
R447	A510	F580
E448	L511	G581
Q449	D512	GLN
I450	T513	
E451	E514	
	S515	
R455	E516	
M456	R517	
A457	A518	
Y458	I519	
A459	Q520	
M460	I523	
D461		
F462	Q527	
I463	K528	
M464	N529	
K465	R530	
M466	T531	
D467	S532	
N468	L533	
G469	V534	
L470	I535	
D471		
T472	R538	
I473	L539	
I474	S540	
G475	T541	
E476	I542	
W477	E543	
G478	Q544	
V479		
L480	E547	
L481	I548	
S482	V549	
G483	V550	
G484	V551	
Q485	I555	
R486	I556	
Q487	V557	
R488	E558	
I489	R559	
A490	G560	
I491	T561	
A492	H562	
R493	S563	
A494	E564	
L495	L565	
L496	L566	
R497		
	P500	
	I501	
	L502	
	I503	
	L504	
	D505	
	E506	
	A507	
	T570	
	V571	
	Y572	
	L575	
	H576	
	K577	

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	249.64Å 119.90Å 168.80Å 90.00° 120.61° 90.00°	Depositor
Resolution (Å)	20.00 – 3.70 20.00 – 3.70	Depositor EDS
% Data completeness (in resolution range)	87.7 (20.00-3.70) 87.7 (20.00-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 3.71Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.307 , 0.343 0.294 , 0.331	Depositor DCC
R_{free} test set	2019 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	118.5	Xtrriage
Anisotropy	0.291	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 98.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	17844	wwPDB-VP
Average B, all atoms (Å ²)	144.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	A	0.45	0/4497	0.73	4/6076 (0.1%)
1	B	0.33	0/4497	0.68	4/6076 (0.1%)
1	C	0.33	0/4497	0.68	4/6076 (0.1%)
1	D	0.33	0/4497	0.68	4/6076 (0.1%)
All	All	0.37	0/17988	0.69	16/24304 (0.1%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	441	ARG	C-N-CA	12.51	152.96	121.70
1	D	441	ARG	C-N-CA	7.75	141.07	121.70
1	C	441	ARG	C-N-CA	7.72	141.01	121.70
1	B	441	ARG	C-N-CA	7.71	140.97	121.70
1	A	338	ALA	C-N-CA	-7.59	102.73	121.70

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	4430	0	4555	719	0
1	B	4430	0	4556	689	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4430	0	4556	714	0
1	D	4430	0	4556	711	0
2	A	31	0	13	5	0
2	B	31	0	13	6	0
2	C	31	0	13	3	0
2	D	31	0	13	5	0
All	All	17844	0	18275	2575	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 71.

The worst 5 of 2575 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:A:221:GLY:HA3	1:B:441:ARG:CD	1.57	1.35
1:A:221:GLY:CA	1:B:441:ARG:HD3	1.67	1.22
1:C:11:GLN:HG2	1:C:12:THR:H	1.10	1.17
1:C:281:ALA:HB2	1:D:56:PHE:HB3	1.24	1.17
1:C:441:ARG:CD	1:D:221:GLY:HA3	1.75	1.16

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	570/582 (98%)	414 (73%)	102 (18%)	54 (10%)	0	8
1	B	570/582 (98%)	413 (72%)	107 (19%)	50 (9%)	1	10
1	C	570/582 (98%)	413 (72%)	107 (19%)	50 (9%)	1	10
1	D	570/582 (98%)	414 (73%)	106 (19%)	50 (9%)	1	10
All	All	2280/2328 (98%)	1654 (72%)	422 (18%)	204 (9%)	1	10

5 of 204 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	ASP
1	A	113	VAL
1	A	161	PHE
1	A	217	VAL
1	A	351	TYR

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	483/493 (98%)	441 (91%)	42 (9%)	10	38
1	B	483/493 (98%)	443 (92%)	40 (8%)	11	40
1	C	483/493 (98%)	443 (92%)	40 (8%)	11	40
1	D	483/493 (98%)	443 (92%)	40 (8%)	11	40
All	All	1932/1972 (98%)	1770 (92%)	162 (8%)	11	40

5 of 162 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	408	ARG
1	C	117	ASP
1	D	385	ILE
1	B	431	ASP
1	C	34	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	520	GLN
1	C	134	GLN
1	D	464	ASN
1	B	537	HIS
1	C	37	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](#)

4 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
2	ANP	A	5001	-	29,33,33	2.23	11 (37%)	31,52,52	2.10	8 (25%)
2	ANP	C	5003	-	29,33,33	2.01	12 (41%)	31,52,52	1.99	7 (22%)
2	ANP	D	5004	-	29,33,33	1.96	9 (31%)	31,52,52	1.95	8 (25%)
2	ANP	B	5002	-	29,33,33	2.16	11 (37%)	31,52,52	1.95	8 (25%)

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
2	ANP	A	5001	-	-	4/14/38/38	0/3/3/3
2	ANP	C	5003	-	-	4/14/38/38	0/3/3/3
2	ANP	D	5004	-	-	4/14/38/38	0/3/3/3
2	ANP	B	5002	-	-	4/14/38/38	0/3/3/3

The worst 5 of 43 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	5002	ANP	PB-O3A	-6.64	1.50	1.59
2	A	5001	ANP	PB-O3A	-6.61	1.50	1.59
2	C	5003	ANP	PB-O3A	-5.64	1.52	1.59
2	D	5004	ANP	PB-O3A	-5.40	1.52	1.59
2	B	5002	ANP	PB-O2B	-3.81	1.46	1.56

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5001	ANP	O1G-PG-N3B	-6.08	102.82	111.77
2	B	5002	ANP	O1G-PG-N3B	-5.81	103.22	111.77
2	D	5004	ANP	O1G-PG-N3B	-5.58	103.56	111.77
2	C	5003	ANP	O1G-PG-N3B	-5.39	103.84	111.77
2	A	5001	ANP	O2B-PB-O1B	4.70	119.77	109.92

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	5001	ANP	PB-N3B-PG-O1G
2	A	5001	ANP	PG-N3B-PB-O1B
2	C	5003	ANP	PB-N3B-PG-O1G
2	C	5003	ANP	PG-N3B-PB-O1B
2	D	5004	ANP	PB-N3B-PG-O1G

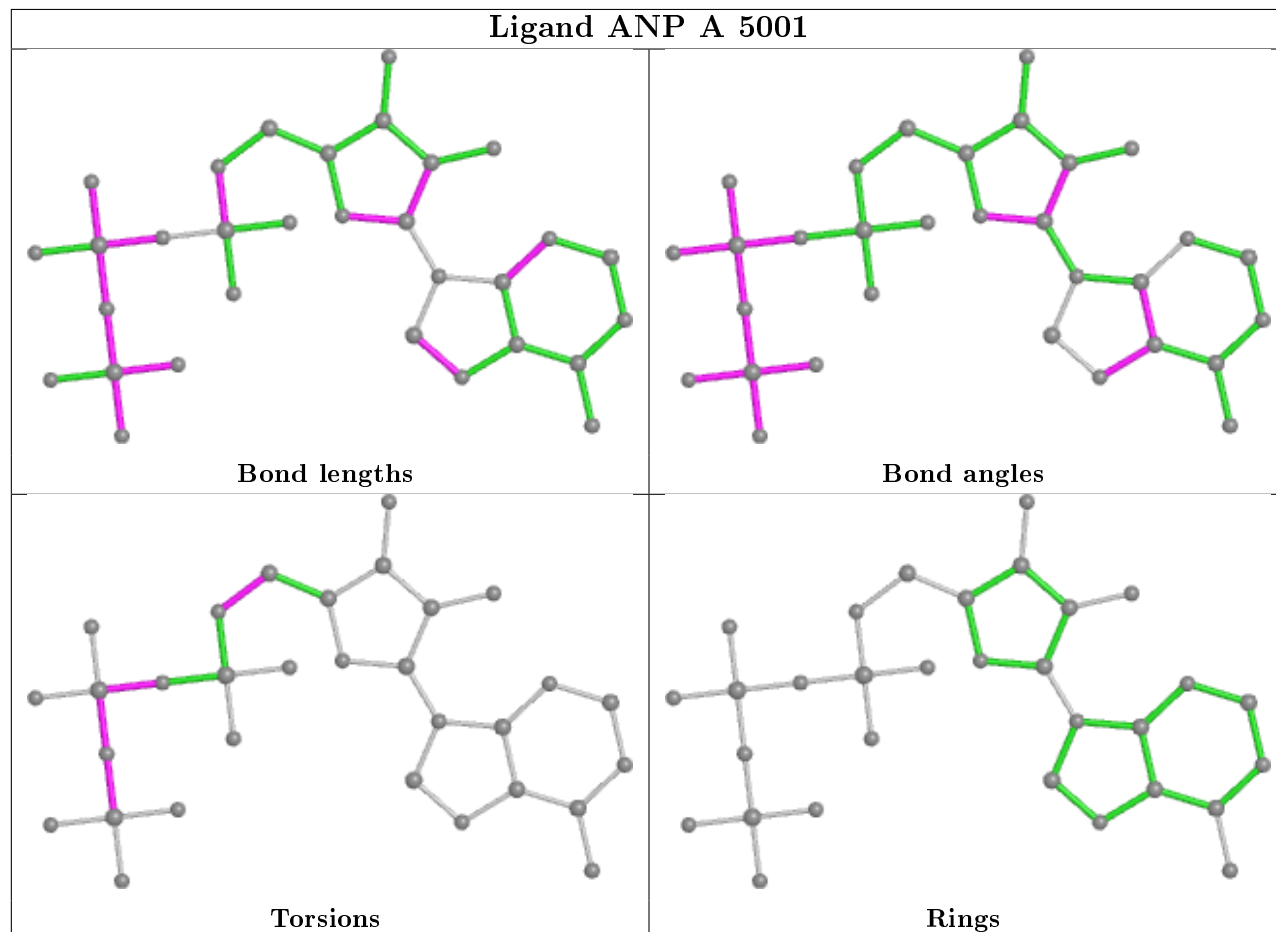
There are no ring outliers.

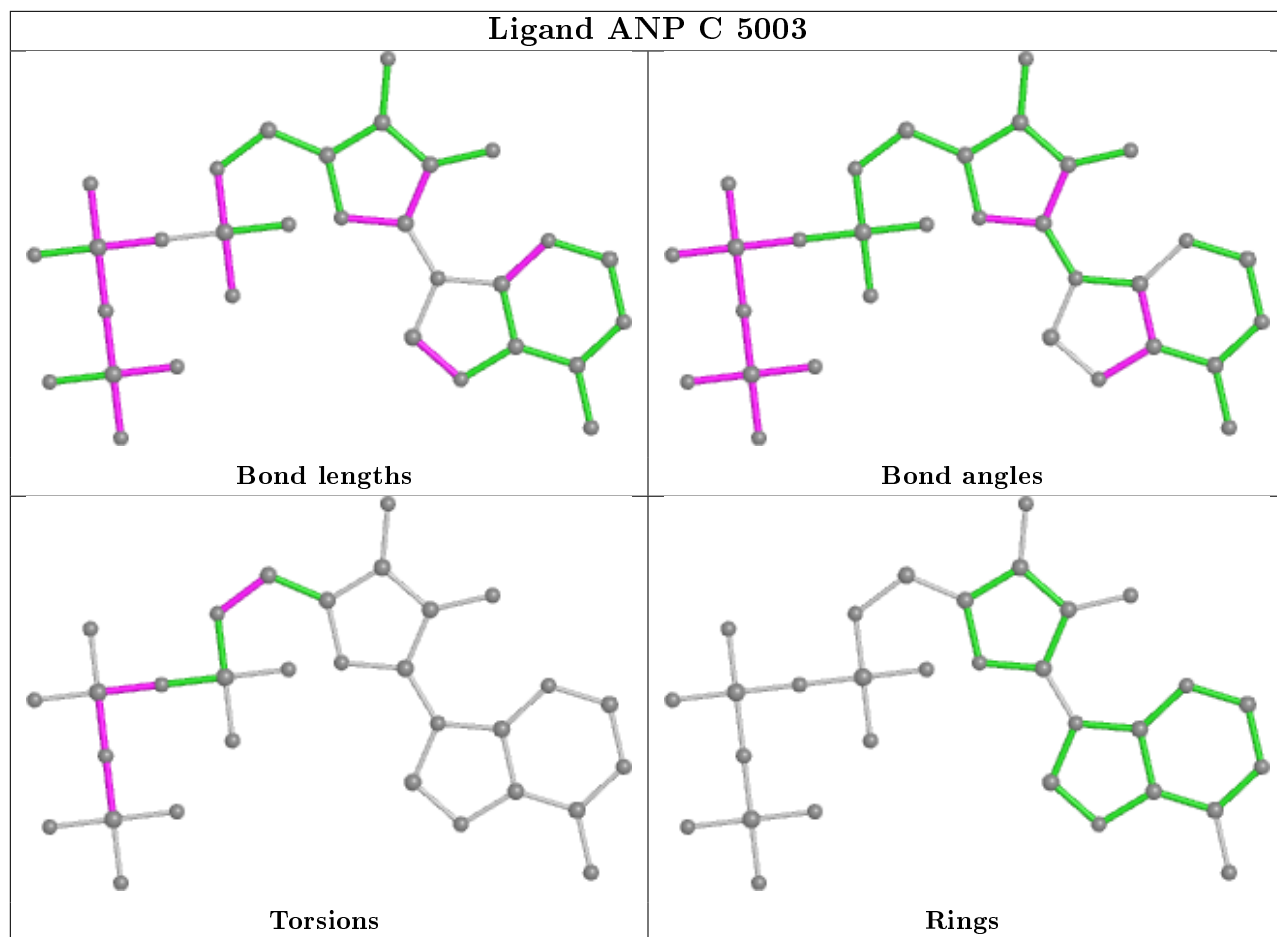
4 monomers are involved in 19 short contacts:

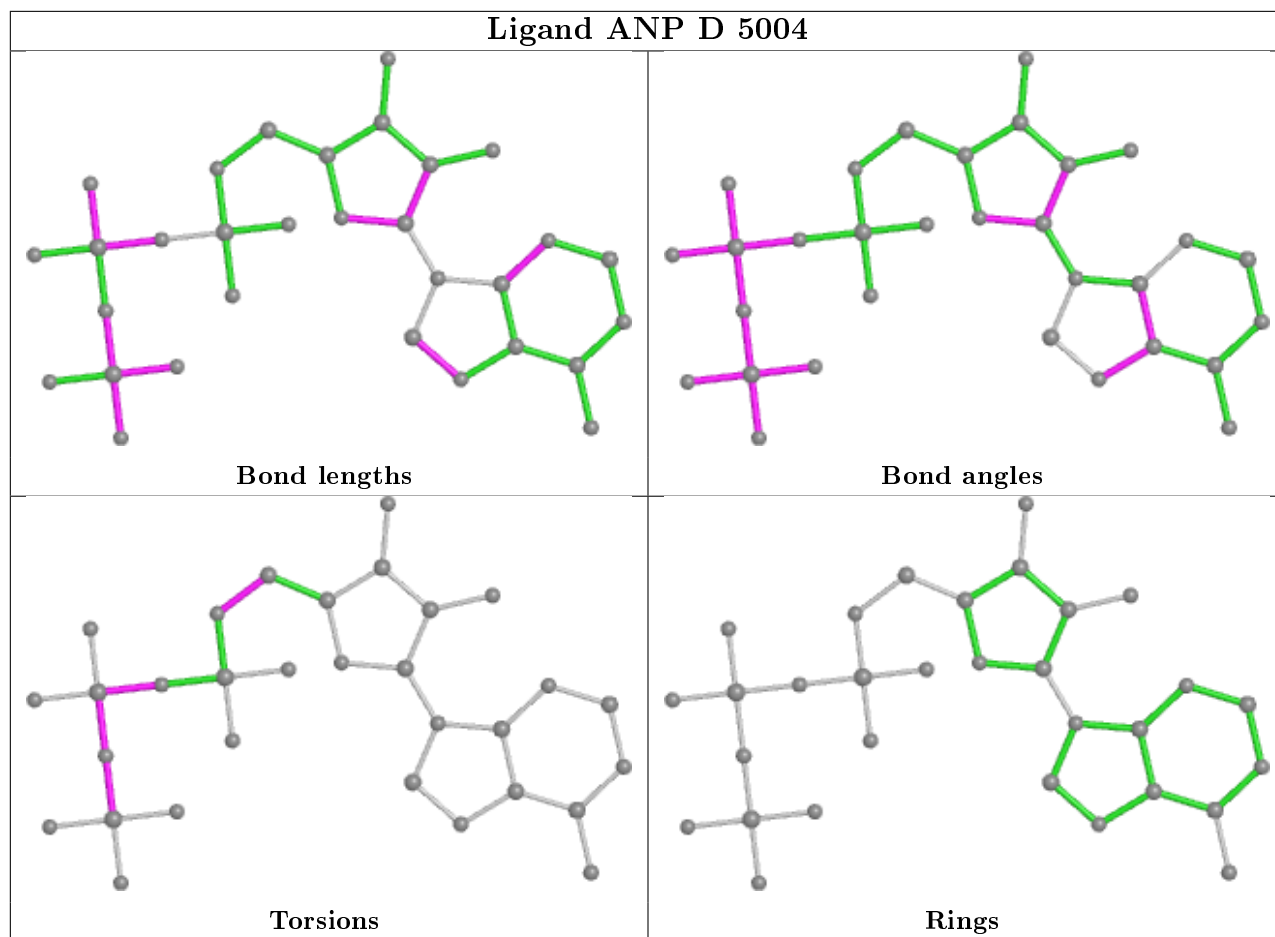
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5001	ANP	5	0
2	C	5003	ANP	3	0
2	D	5004	ANP	5	0
2	B	5002	ANP	6	0

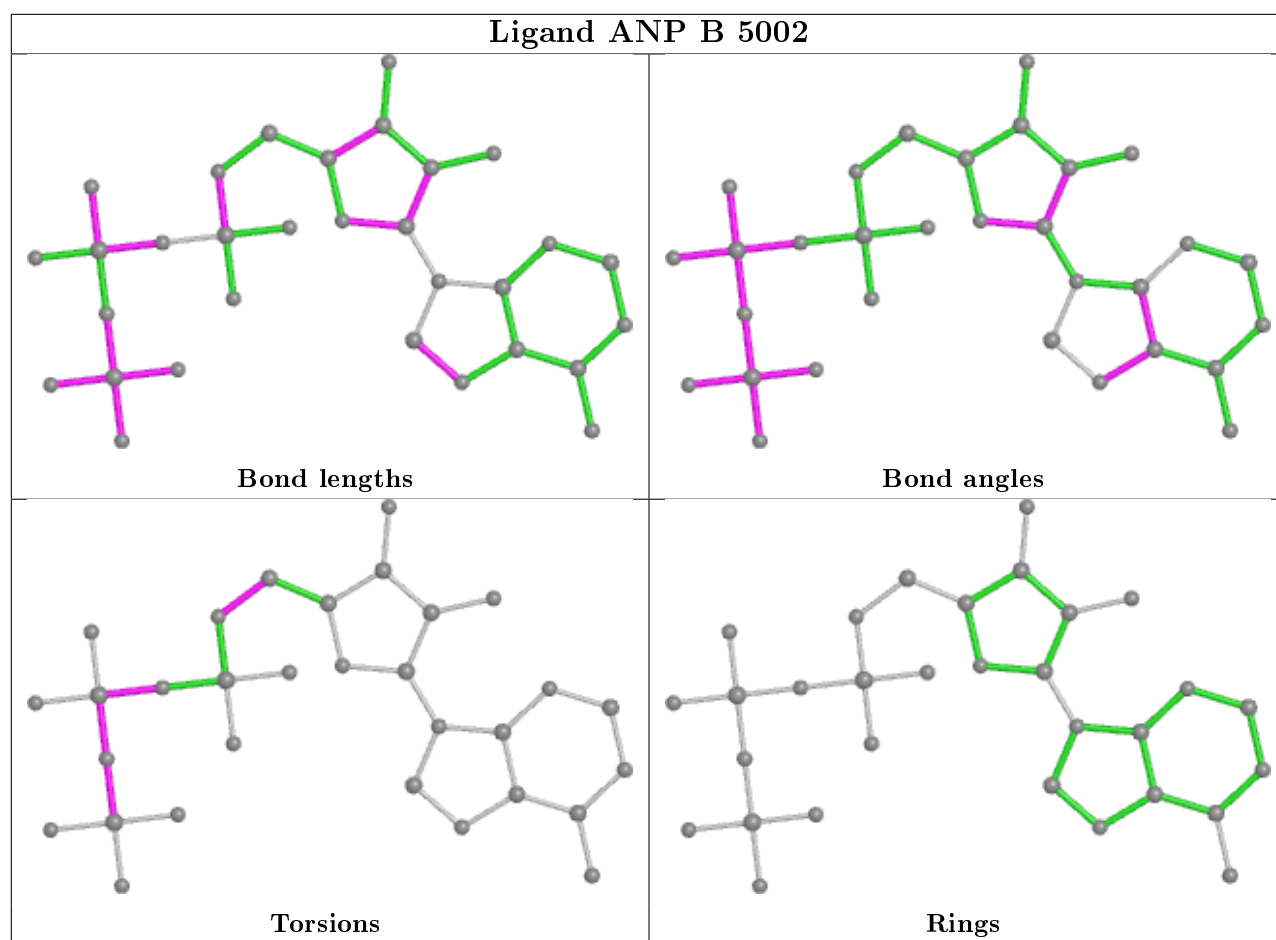
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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









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 [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	A	572/582 (98%)	-0.12	28 (4%) 29 22	61, 154, 203, 205	0
1	B	572/582 (98%)	-0.27	19 (3%) 46 35	55, 135, 200, 205	0
1	C	572/582 (98%)	-0.32	16 (2%) 53 40	66, 137, 197, 205	0
1	D	572/582 (98%)	-0.30	12 (2%) 63 52	59, 146, 201, 205	0
All	All	2288/2328 (98%)	-0.26	75 (3%) 46 35	55, 143, 201, 205	0

The worst 5 of 75 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	60	ASP	6.0
1	A	61	ARG	5.6
1	B	163	TYR	4.6
1	D	60	ASP	4.3
1	B	353	GLY	4.1

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](#)

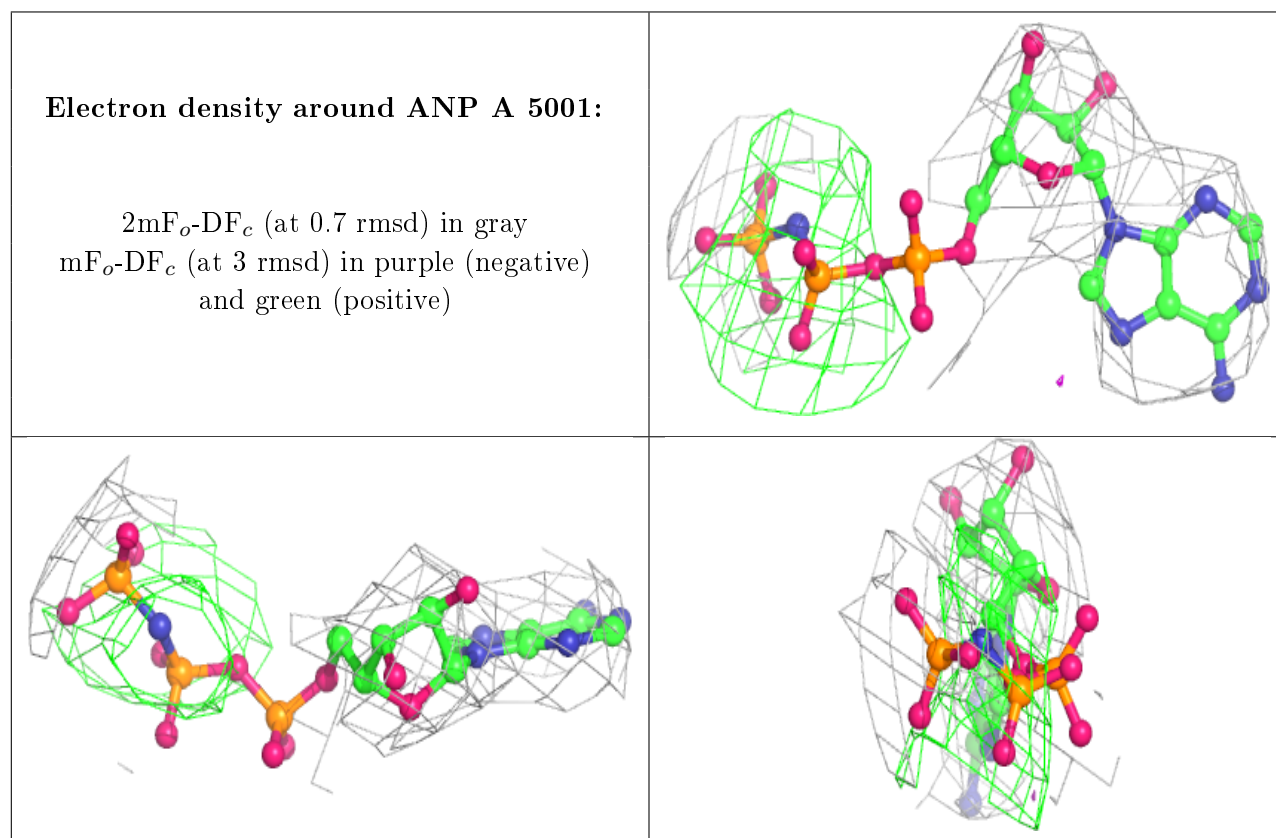
There are no monosaccharides in this entry.

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, 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.

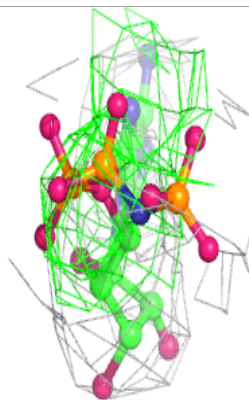
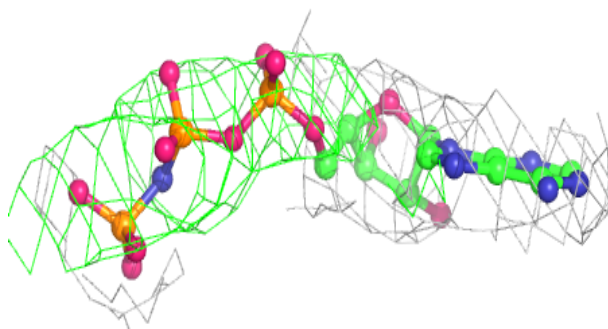
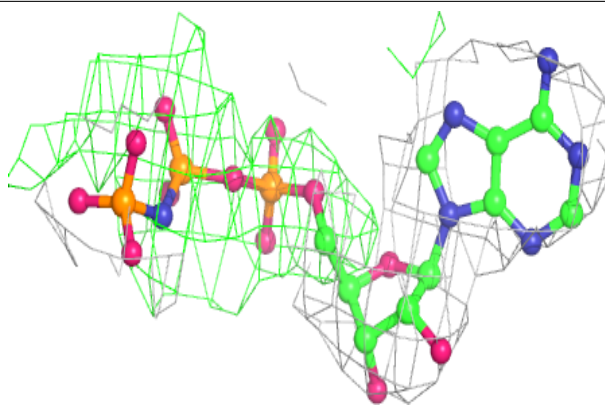
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ANP	A	5001	31/31	0.91	0.24	121,121,121,121	0
2	ANP	C	5003	31/31	0.92	0.26	111,111,111,111	0
2	ANP	D	5004	31/31	0.92	0.22	139,139,139,139	0
2	ANP	B	5002	31/31	0.93	0.22	124,124,124,124	0

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.

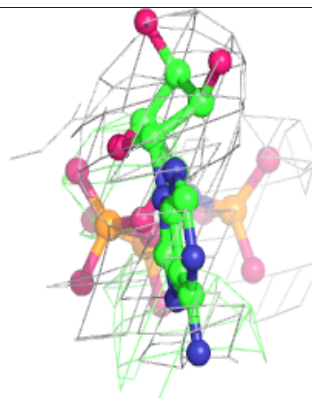
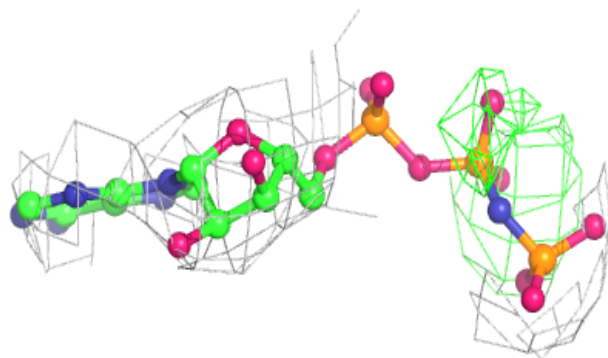
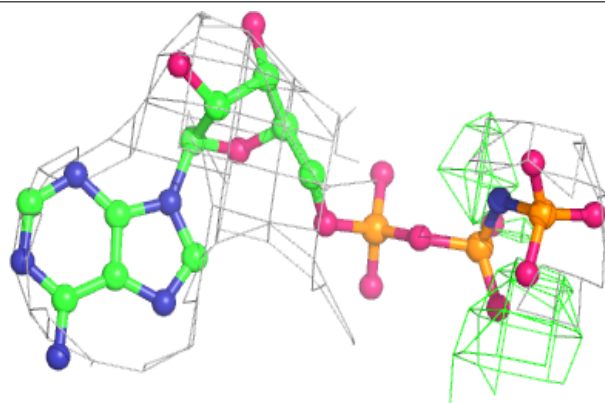


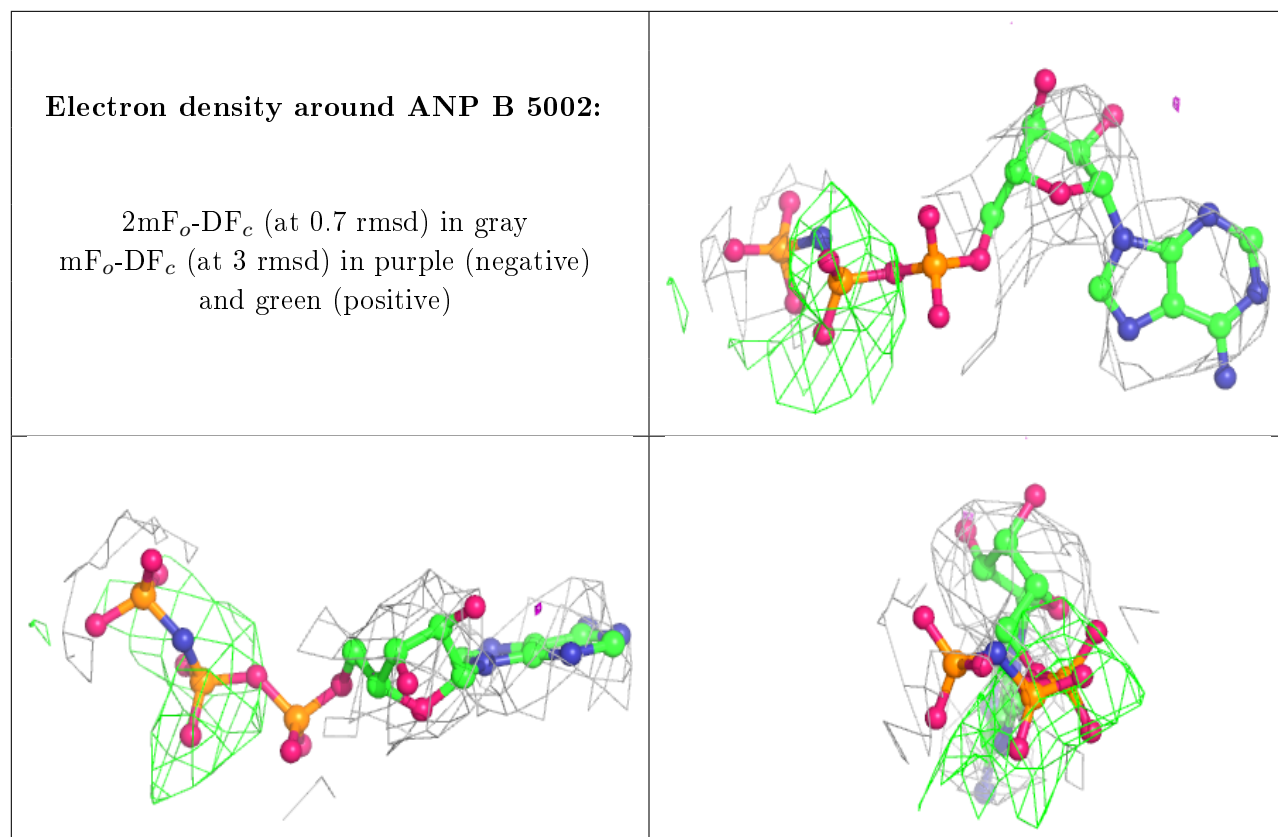
Electron density around ANP C 5003:

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

**Electron density around ANP D 5004:**

$2mF_o-DF_c$ (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.