



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 26, 2021 – 04:08 PM JST

PDB ID : 7CMP
Title : parE in complex with AMPPNP
Authors : Jung, H.Y.; Heo, Y.-S.
Deposited on : 2020-07-28
Resolution : 2.89 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 : 2.22
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) : 2.22

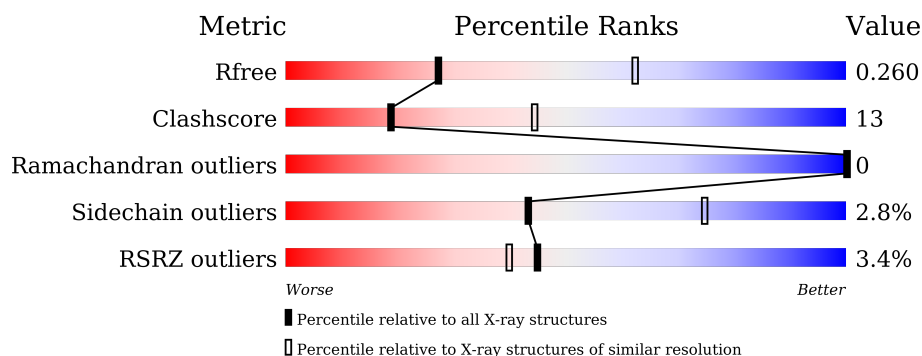
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.89 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	2691 (2.90-2.86)
Clashscore	141614	2947 (2.90-2.86)
Ramachandran outliers	138981	2868 (2.90-2.86)
Sidechain outliers	138945	2871 (2.90-2.86)
RSRZ outliers	127900	2629 (2.90-2.86)

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	408	 3% 69% 20% • 8%
1	B	408	 % 67% 22% •• 8%
1	C	408	 4% 69% 19% •• 8%
1	D	408	 3% 69% 21% • 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11878 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 DNA topoisomerase 4 subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	374	Total	C	N	O	S	0	0	0
			2923	1837	522	555	9			
1	B	374	Total	C	N	O	S	0	0	0
			2923	1837	522	555	9			
1	C	374	Total	C	N	O	S	0	0	0
			2923	1837	522	555	9			
1	D	374	Total	C	N	O	S	0	0	0
			2923	1837	522	555	9			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	MET	-	initiating methionine	UNP Q5GYJ8
A	27	GLY	-	expression tag	UNP Q5GYJ8
A	28	SER	-	expression tag	UNP Q5GYJ8
A	29	SER	-	expression tag	UNP Q5GYJ8
A	30	HIS	-	expression tag	UNP Q5GYJ8
A	31	HIS	-	expression tag	UNP Q5GYJ8
A	32	HIS	-	expression tag	UNP Q5GYJ8
A	33	HIS	-	expression tag	UNP Q5GYJ8
A	34	HIS	-	expression tag	UNP Q5GYJ8
A	35	HIS	-	expression tag	UNP Q5GYJ8
A	36	SER	-	expression tag	UNP Q5GYJ8
A	37	SER	-	expression tag	UNP Q5GYJ8
A	38	GLY	-	expression tag	UNP Q5GYJ8
A	39	LEU	-	expression tag	UNP Q5GYJ8
A	40	VAL	-	expression tag	UNP Q5GYJ8
A	41	PRO	-	expression tag	UNP Q5GYJ8
A	42	ARG	-	expression tag	UNP Q5GYJ8
A	43	GLY	-	expression tag	UNP Q5GYJ8
A	44	SER	-	expression tag	UNP Q5GYJ8
A	45	HIS	-	expression tag	UNP Q5GYJ8
B	26	MET	-	initiating methionine	UNP Q5GYJ8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	27	GLY	-	expression tag	UNP Q5GYJ8
B	28	SER	-	expression tag	UNP Q5GYJ8
B	29	SER	-	expression tag	UNP Q5GYJ8
B	30	HIS	-	expression tag	UNP Q5GYJ8
B	31	HIS	-	expression tag	UNP Q5GYJ8
B	32	HIS	-	expression tag	UNP Q5GYJ8
B	33	HIS	-	expression tag	UNP Q5GYJ8
B	34	HIS	-	expression tag	UNP Q5GYJ8
B	35	HIS	-	expression tag	UNP Q5GYJ8
B	36	SER	-	expression tag	UNP Q5GYJ8
B	37	SER	-	expression tag	UNP Q5GYJ8
B	38	GLY	-	expression tag	UNP Q5GYJ8
B	39	LEU	-	expression tag	UNP Q5GYJ8
B	40	VAL	-	expression tag	UNP Q5GYJ8
B	41	PRO	-	expression tag	UNP Q5GYJ8
B	42	ARG	-	expression tag	UNP Q5GYJ8
B	43	GLY	-	expression tag	UNP Q5GYJ8
B	44	SER	-	expression tag	UNP Q5GYJ8
B	45	HIS	-	expression tag	UNP Q5GYJ8
C	26	MET	-	initiating methionine	UNP Q5GYJ8
C	27	GLY	-	expression tag	UNP Q5GYJ8
C	28	SER	-	expression tag	UNP Q5GYJ8
C	29	SER	-	expression tag	UNP Q5GYJ8
C	30	HIS	-	expression tag	UNP Q5GYJ8
C	31	HIS	-	expression tag	UNP Q5GYJ8
C	32	HIS	-	expression tag	UNP Q5GYJ8
C	33	HIS	-	expression tag	UNP Q5GYJ8
C	34	HIS	-	expression tag	UNP Q5GYJ8
C	35	HIS	-	expression tag	UNP Q5GYJ8
C	36	SER	-	expression tag	UNP Q5GYJ8
C	37	SER	-	expression tag	UNP Q5GYJ8
C	38	GLY	-	expression tag	UNP Q5GYJ8
C	39	LEU	-	expression tag	UNP Q5GYJ8
C	40	VAL	-	expression tag	UNP Q5GYJ8
C	41	PRO	-	expression tag	UNP Q5GYJ8
C	42	ARG	-	expression tag	UNP Q5GYJ8
C	43	GLY	-	expression tag	UNP Q5GYJ8
C	44	SER	-	expression tag	UNP Q5GYJ8
C	45	HIS	-	expression tag	UNP Q5GYJ8
D	26	MET	-	initiating methionine	UNP Q5GYJ8
D	27	GLY	-	expression tag	UNP Q5GYJ8
D	28	SER	-	expression tag	UNP Q5GYJ8

Continued on next page...

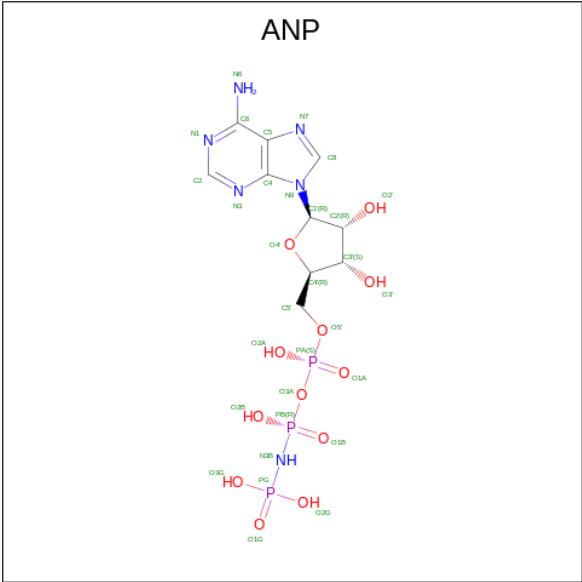
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	29	SER	-	expression tag	UNP Q5GYJ8
D	30	HIS	-	expression tag	UNP Q5GYJ8
D	31	HIS	-	expression tag	UNP Q5GYJ8
D	32	HIS	-	expression tag	UNP Q5GYJ8
D	33	HIS	-	expression tag	UNP Q5GYJ8
D	34	HIS	-	expression tag	UNP Q5GYJ8
D	35	HIS	-	expression tag	UNP Q5GYJ8
D	36	SER	-	expression tag	UNP Q5GYJ8
D	37	SER	-	expression tag	UNP Q5GYJ8
D	38	GLY	-	expression tag	UNP Q5GYJ8
D	39	LEU	-	expression tag	UNP Q5GYJ8
D	40	VAL	-	expression tag	UNP Q5GYJ8
D	41	PRO	-	expression tag	UNP Q5GYJ8
D	42	ARG	-	expression tag	UNP Q5GYJ8
D	43	GLY	-	expression tag	UNP Q5GYJ8
D	44	SER	-	expression tag	UNP Q5GYJ8
D	45	HIS	-	expression tag	UNP Q5GYJ8

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃) (labeled as "Ligand of Interest" by depositor).



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

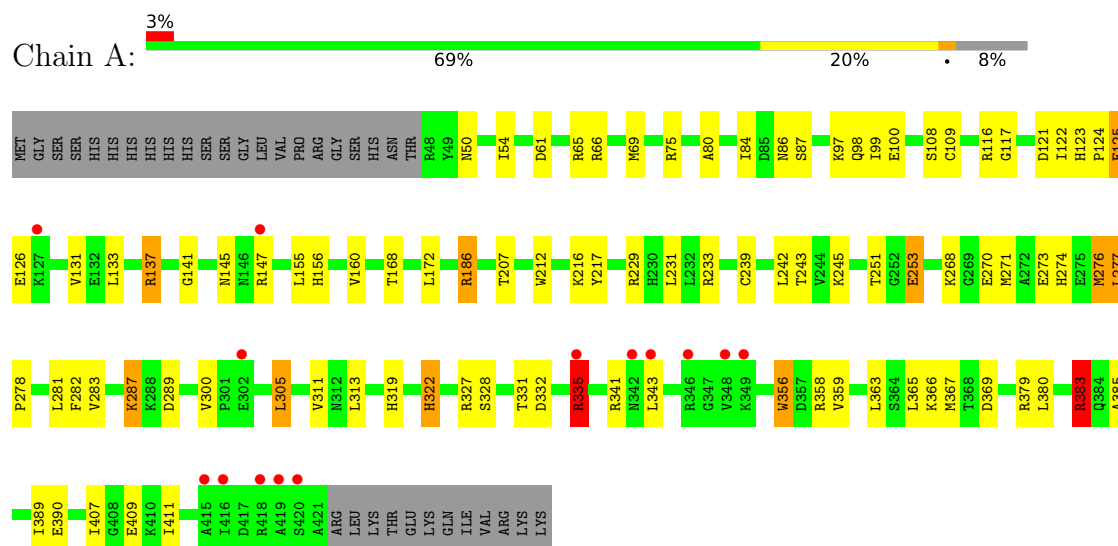
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	28	Total	O	0	0
			28	28		
4	B	7	Total	O	0	0
			7	7		
4	C	16	Total	O	0	0
			16	16		
4	D	7	Total	O	0	0
			7	7		

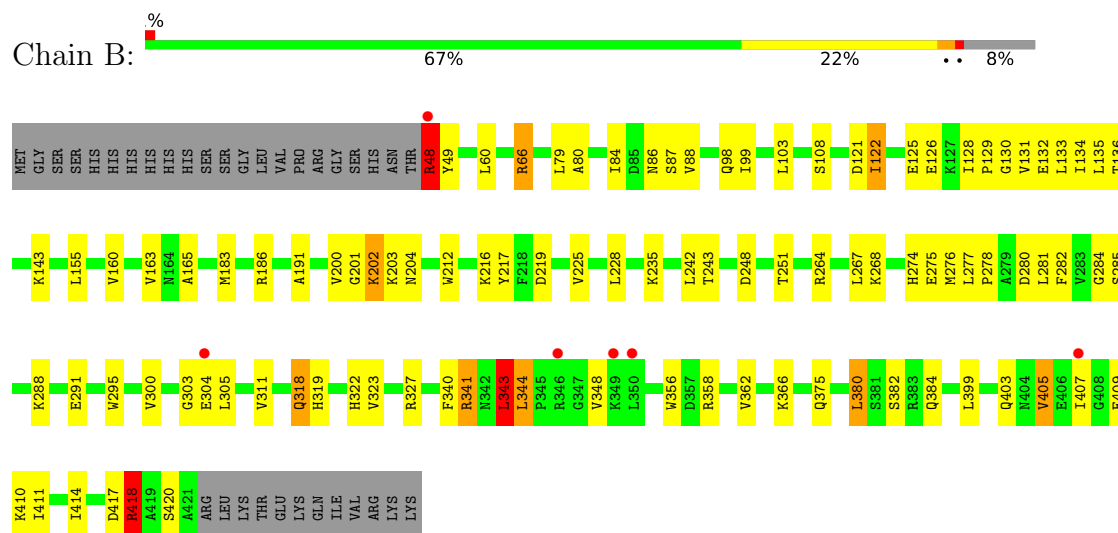
3 Residue-property plots [i](#)

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 topoisomerase 4 subunit B

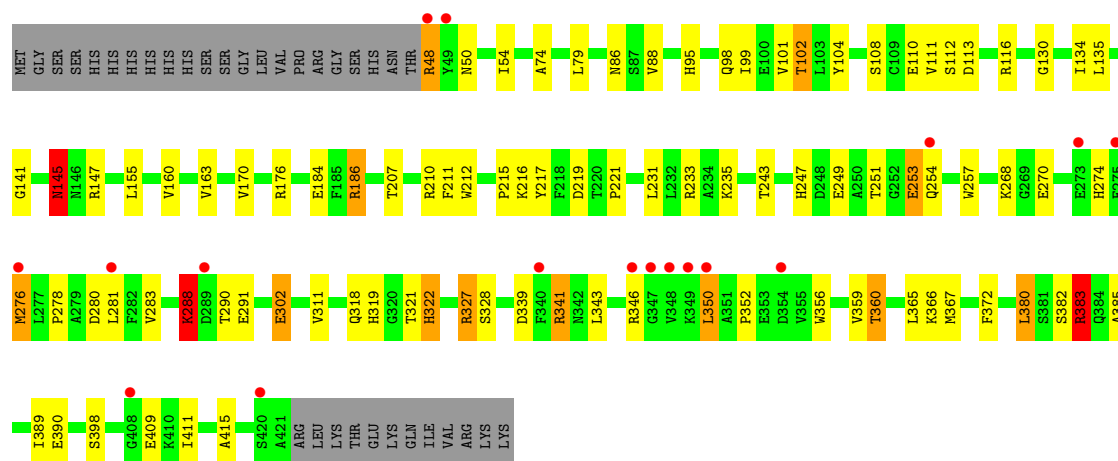


• Molecule 1: DNA topoisomerase 4 subunit B

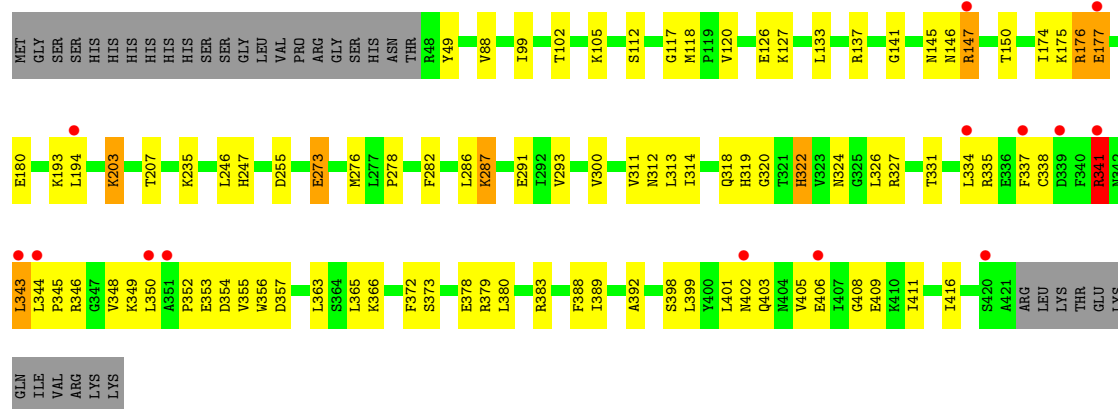


• Molecule 1: DNA topoisomerase 4 subunit B





• Molecule 1: DNA topoisomerase 4 subunit B



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	74.02Å 126.75Å 96.04Å 90.00° 109.61° 90.00°	Depositor
Resolution (Å)	46.10 – 2.89 46.10 – 2.89	Depositor EDS
% Data completeness (in resolution range)	98.5 (46.10-2.89) 98.5 (46.10-2.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.202 , 0.260 0.202 , 0.260	Depositor DCC
R_{free} test set	1847 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11878	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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, MG

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	0.46	2/2983 (0.1%)	0.99	23/4036 (0.6%)
1	B	0.54	6/2983 (0.2%)	0.89	23/4036 (0.6%)
1	C	0.43	1/2983 (0.0%)	0.81	15/4036 (0.4%)
1	D	0.56	6/2983 (0.2%)	0.89	22/4036 (0.5%)
All	All	0.50	15/11932 (0.1%)	0.90	83/16144 (0.5%)

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	B	0	3
1	C	0	1
1	D	0	1
All	All	0	5

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	273	GLU	CD-OE2	9.90	1.36	1.25
1	B	288	LYS	CD-CE	8.99	1.73	1.51
1	A	253	GLU	CD-OE2	8.91	1.35	1.25
1	B	125	GLU	CD-OE2	8.20	1.34	1.25
1	D	177	GLU	CD-OE2	7.38	1.33	1.25
1	B	125	GLU	CG-CD	-6.95	1.41	1.51
1	D	406	GLU	CD-OE2	6.91	1.33	1.25
1	B	275	GLU	CD-OE2	6.72	1.33	1.25
1	C	383	ARG	CG-CD	-6.50	1.35	1.51
1	D	177	GLU	CD-OE1	6.13	1.32	1.25
1	B	48	ARG	CD-NE	-6.13	1.36	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	273	GLU	CG-CD	-5.58	1.43	1.51
1	A	253	GLU	CG-CD	5.44	1.60	1.51
1	D	273	GLU	CB-CG	-5.32	1.42	1.52
1	B	409	GLU	CB-CG	-5.10	1.42	1.52

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	186	ARG	NE-CZ-NH2	-22.77	108.92	120.30
1	B	48	ARG	NE-CZ-NH2	-19.69	110.45	120.30
1	D	343	LEU	CB-CG-CD2	-17.33	81.53	111.00
1	B	343	LEU	CA-CB-CG	-12.95	85.52	115.30
1	A	186	ARG	NE-CZ-NH1	12.86	126.73	120.30
1	A	186	ARG	CG-CD-NE	12.19	137.40	111.80
1	A	97	LYS	CD-CE-NZ	12.07	139.47	111.70
1	A	186	ARG	CB-CG-CD	-11.66	81.29	111.60
1	A	335	ARG	NE-CZ-NH2	-11.12	114.74	120.30
1	A	186	ARG	CD-NE-CZ	10.64	138.50	123.60
1	D	273	GLU	CA-CB-CG	-10.62	90.02	113.40
1	A	287	LYS	CB-CG-CD	-10.16	85.17	111.60
1	A	277	LEU	CB-CG-CD2	10.10	128.17	111.00
1	C	383	ARG	CB-CG-CD	-9.92	85.80	111.60
1	A	335	ARG	NE-CZ-NH1	9.76	125.18	120.30
1	C	253	GLU	CA-CB-CG	-9.61	92.26	113.40
1	A	383	ARG	NE-CZ-NH1	-9.41	115.59	120.30
1	B	125	GLU	CG-CD-OE1	-8.86	100.58	118.30
1	D	147	ARG	NE-CZ-NH1	8.54	124.57	120.30
1	D	105	LYS	CB-CA-C	-8.31	93.77	110.40
1	B	122	ILE	CG1-CB-CG2	-8.30	93.15	111.40
1	B	409	GLU	CA-CB-CG	-8.29	95.16	113.40
1	A	287	LYS	CA-CB-CG	8.28	131.61	113.40
1	C	341	ARG	NE-CZ-NH1	-8.06	116.27	120.30
1	C	327	ARG	NE-CZ-NH1	-8.05	116.28	120.30
1	D	147	ARG	CA-CB-CG	8.00	130.99	113.40
1	D	343	LEU	CB-CG-CD1	7.81	124.28	111.00
1	D	273	GLU	CB-CA-C	-7.63	95.14	110.40
1	D	341	ARG	CA-CB-CG	-7.59	96.71	113.40
1	B	203	LYS	CD-CE-NZ	7.52	129.00	111.70
1	B	48	ARG	CG-CD-NE	7.41	127.36	111.80
1	B	288	LYS	CG-CD-CE	-7.38	89.76	111.90
1	C	341	ARG	CG-CD-NE	-7.19	96.71	111.80
1	B	125	GLU	CA-CB-CG	-7.13	97.72	113.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	287	LYS	CB-CG-CD	-7.08	93.18	111.60
1	D	147	ARG	CG-CD-NE	-7.05	97.00	111.80
1	C	350	LEU	CB-CG-CD2	-7.01	99.08	111.00
1	D	341	ARG	CG-CD-NE	-6.95	97.21	111.80
1	B	48	ARG	CD-NE-CZ	6.87	133.21	123.60
1	B	48	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	D	273	GLU	CG-CD-OE1	-6.76	104.77	118.30
1	A	50	ASN	CB-CA-C	-6.69	97.02	110.40
1	C	288	LYS	CD-CE-NZ	6.69	127.08	111.70
1	C	48	ARG	N-CA-C	-6.59	93.21	111.00
1	A	383	ARG	NE-CZ-NH2	6.57	123.59	120.30
1	D	147	ARG	CD-NE-CZ	6.45	132.63	123.60
1	C	145	ASN	CB-CA-C	-6.21	97.99	110.40
1	D	177	GLU	CA-CB-CG	-6.16	99.84	113.40
1	B	418	ARG	N-CA-CB	-6.11	99.60	110.60
1	D	341	ARG	NE-CZ-NH1	-6.09	117.26	120.30
1	B	203	LYS	CG-CD-CE	-6.06	93.72	111.90
1	B	341	ARG	CA-CB-CG	6.03	126.67	113.40
1	B	304	GLU	CA-CB-CG	-6.03	100.14	113.40
1	B	341	ARG	CB-CG-CD	-6.02	95.95	111.60
1	C	48	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	287	LYS	CG-CD-CE	5.85	129.44	111.90
1	B	48	ARG	N-CA-C	5.75	126.52	111.00
1	C	383	ARG	CG-CD-NE	5.71	123.78	111.80
1	B	48	ARG	CA-CB-CG	-5.63	101.02	113.40
1	B	125	GLU	CG-CD-OE2	5.60	129.50	118.30
1	D	409	GLU	N-CA-CB	-5.52	100.66	110.60
1	B	341	ARG	CG-CD-NE	5.48	123.31	111.80
1	B	405	VAL	CA-CB-CG2	-5.45	102.72	110.90
1	A	287	LYS	N-CA-CB	5.44	120.40	110.60
1	A	335	ARG	CD-NE-CZ	5.39	131.14	123.60
1	D	147	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	D	273	GLU	OE1-CD-OE2	5.38	129.75	123.30
1	D	406	GLU	CB-CA-C	5.31	121.02	110.40
1	C	383	ARG	NE-CZ-NH2	-5.30	117.65	120.30
1	D	203	LYS	CA-CB-CG	5.30	125.07	113.40
1	A	287	LYS	CB-CA-C	-5.24	99.92	110.40
1	C	360	THR	CA-CB-CG2	-5.23	105.08	112.40
1	A	335	ARG	CB-CG-CD	-5.22	98.03	111.60
1	C	48	ARG	NE-CZ-NH2	-5.21	117.70	120.30
1	A	305	LEU	CB-CG-CD2	-5.18	102.19	111.00
1	A	253	GLU	CG-CD-OE1	-5.17	107.97	118.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	125	GLU	OE1-CD-OE2	5.11	129.43	123.30
1	D	105	LYS	N-CA-CB	5.06	119.71	110.60
1	A	276	MET	CB-CG-SD	-5.04	97.27	112.40
1	C	380	LEU	CA-CB-CG	5.04	126.89	115.30
1	A	125	GLU	CA-CB-CG	-5.01	102.38	113.40
1	D	341	ARG	CB-CG-CD	5.00	124.61	111.60
1	B	344	LEU	CA-CB-CG	5.00	126.80	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	318	GLN	Peptide
1	B	48	ARG	Sidechain,Peptide
1	C	302	GLU	Peptide
1	D	341	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	2923	0	2875	76	0
1	B	2923	0	2874	84	0
1	C	2923	0	2875	72	0
1	D	2923	0	2874	94	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	31	0	12	2	0
3	B	31	0	13	1	0
3	C	31	0	12	3	0
3	D	31	0	12	2	0
4	A	28	0	0	5	0
4	B	7	0	0	0	0
4	C	16	0	0	0	0
4	D	7	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11878	0	11547	307	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 13.

All (307) 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:B:122:ILE:CD1	1:B:122:ILE:CG1	1.75	1.54
1:A:155:LEU:HD12	1:B:66:ARG:NE	1.51	1.22
1:D:176:ARG:HB2	1:D:177:GLU:OE1	1.43	1.16
1:A:379:ARG:NH2	1:B:318:GLN:OE1	1.83	1.12
1:A:155:LEU:HD12	1:B:66:ARG:HE	1.13	1.01
1:A:383:ARG:CD	4:A:602:HOH:O	2.12	0.98
1:A:66:ARG:HE	1:B:155:LEU:HB2	1.30	0.96
1:D:176:ARG:CB	1:D:177:GLU:OE1	2.18	0.91
1:A:383:ARG:HD3	4:A:602:HOH:O	1.68	0.91
1:B:341:ARG:NH2	1:B:405:VAL:HG21	1.85	0.91
1:B:186:ARG:HD2	1:B:191:ALA:CB	2.04	0.88
1:B:276:MET:HE1	1:B:281:LEU:HG	1.53	0.87
1:D:337:PHE:O	1:D:341:ARG:HB2	1.76	0.86
1:D:353:GLU:HG2	1:D:354:ASP:N	1.92	0.85
1:C:276:MET:CE	1:C:360:THR:HG21	2.08	0.84
1:B:186:ARG:HD2	1:B:191:ALA:HB1	1.60	0.82
1:B:264:ARG:NH1	1:B:280:ASP:O	2.12	0.82
1:A:327:ARG:HD3	1:A:356:TRP:CG	2.13	0.82
1:C:383:ARG:HD2	1:C:383:ARG:C	2.00	0.82
1:D:276:MET:HG2	1:D:300:VAL:HG22	1.61	0.81
1:C:341:ARG:HB3	1:C:343:LEU:HD13	1.62	0.81
1:A:87:SER:HB3	1:A:99:ILE:HD12	1.63	0.80
1:C:268:LYS:NZ	1:C:280:ASP:OD2	2.13	0.80
1:A:332:ASP:OD1	1:A:335:ARG:NH2	2.15	0.80
1:A:379:ARG:HH22	1:B:318:GLN:CD	1.84	0.79
1:A:168:THR:O	1:A:186:ARG:HD2	1.82	0.79
1:B:87:SER:HB3	1:B:99:ILE:HD12	1.65	0.78
1:A:366:LYS:NZ	4:A:601:HOH:O	2.16	0.78
1:C:184:GLU:OE1	1:C:186:ARG:NH1	2.16	0.78
1:D:193:LYS:HG2	1:D:194:LEU:H	1.48	0.77
1:C:276:MET:HE2	1:C:360:THR:HG21	1.65	0.77
1:D:176:ARG:HD3	1:D:177:GLU:OE2	1.85	0.76
1:D:343:LEU:HD21	1:D:416:ILE:CD1	2.15	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:327:ARG:HG3	1:C:356:TRP:CD2	2.22	0.75
1:B:341:ARG:HB2	1:B:343:LEU:CD1	2.17	0.75
1:B:341:ARG:HB2	1:B:343:LEU:HD12	1.68	0.75
1:D:399:LEU:O	1:D:403:GLN:HG2	1.88	0.74
1:C:346:ARG:HG2	1:C:346:ARG:HH11	1.53	0.73
1:D:335:ARG:NH1	1:D:350:LEU:O	2.21	0.73
1:D:327:ARG:HD3	1:D:352:PRO:HB3	1.71	0.72
1:B:88:VAL:HG21	1:B:235:LYS:HD2	1.71	0.72
1:D:88:VAL:HG21	1:D:235:LYS:HD2	1.71	0.72
1:A:383:ARG:HD2	4:A:602:HOH:O	1.83	0.72
1:B:274:HIS:CD2	1:B:303:GLY:HA3	2.25	0.71
1:D:353:GLU:HG2	1:D:354:ASP:H	1.56	0.71
1:D:326:LEU:HD12	1:D:363:LEU:HD13	1.74	0.70
1:A:277:LEU:CD2	1:A:411:ILE:HG12	2.22	0.70
1:D:326:LEU:HD22	1:D:356:TRP:HH2	1.57	0.70
1:D:327:ARG:O	1:D:331:THR:HG23	1.92	0.70
1:A:80:ALA:O	1:A:84:ILE:HG12	1.92	0.70
1:A:121:ASP:OD2	1:A:122:ILE:N	2.26	0.69
1:D:193:LYS:HZ2	1:D:194:LEU:HB3	1.57	0.69
1:B:86:ASN:ND2	1:B:160:VAL:HG23	2.08	0.68
1:D:343:LEU:HD21	1:D:416:ILE:HD11	1.75	0.68
1:C:290:THR:O	1:C:291:GLU:HG3	1.94	0.68
1:D:176:ARG:HD3	1:D:177:GLU:CD	2.15	0.67
1:D:120:VAL:HG22	1:D:176:ARG:HD2	1.78	0.66
1:C:319:HIS:O	1:C:322:HIS:NE2	2.29	0.65
1:D:312:ASN:OD1	1:D:366:LYS:HA	1.96	0.65
1:C:50:ASN:OD1	1:D:176:ARG:NH1	2.30	0.65
1:A:383:ARG:HD2	1:B:219:ASP:OD1	1.96	0.65
1:A:98:GLN:HG2	1:A:243:THR:HB	1.77	0.64
1:B:380:LEU:HD22	1:B:382:SER:H	1.60	0.64
1:B:80:ALA:O	1:B:84:ILE:HG12	1.97	0.64
1:D:338:CYS:HB3	1:D:344:LEU:HB2	1.78	0.64
1:A:277:LEU:HD22	1:A:411:ILE:HG12	1.79	0.64
1:B:186:ARG:HD2	1:B:191:ALA:HB2	1.78	0.62
1:A:66:ARG:NE	1:B:155:LEU:HB2	2.08	0.61
1:C:339:ASP:C	1:C:341:ARG:H	2.03	0.61
1:A:86:ASN:ND2	1:A:160:VAL:HG23	2.15	0.61
1:D:175:LYS:HG2	1:D:180:GLU:HB2	1.82	0.61
1:D:126:GLU:CD	1:D:137:ARG:HH22	2.04	0.61
1:D:341:ARG:CZ	1:D:405:VAL:HG11	2.29	0.61
1:C:54:ILE:HD11	1:D:133:LEU:HD23	1.81	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:343:LEU:HD21	1:C:409:GLU:HG2	1.83	0.61
1:D:319:HIS:O	1:D:322:HIS:NE2	2.34	0.61
1:D:383:ARG:O	1:D:383:ARG:HG2	1.99	0.60
1:A:216:LYS:HE3	1:A:217:TYR:CZ	2.36	0.60
1:A:131:VAL:HG21	1:A:172:LEU:HD11	1.82	0.60
1:B:264:ARG:NH1	1:B:281:LEU:O	2.35	0.60
1:D:146:ASN:ND2	1:D:150:THR:O	2.35	0.59
1:D:141:GLY:HA2	3:D:502:ANP:H4'	1.84	0.59
1:D:319:HIS:O	1:D:322:HIS:CD2	2.56	0.59
1:D:278:PRO:HG2	1:D:282:PHE:H	1.68	0.59
1:B:305:LEU:HD11	1:B:358:ARG:HA	1.85	0.58
1:B:278:PRO:HD3	1:B:411:ILE:HD11	1.85	0.58
1:A:117:GLY:HA2	1:A:207:THR:OG1	2.02	0.58
1:B:414:ILE:O	1:B:418:ARG:HG2	2.04	0.58
1:D:278:PRO:HD3	1:D:411:ILE:HD11	1.86	0.58
1:B:202:LYS:HD2	1:B:202:LYS:H	1.68	0.58
1:C:346:ARG:HG2	1:C:346:ARG:NH1	2.17	0.58
1:D:193:LYS:NZ	1:D:194:LEU:HB3	2.18	0.58
1:A:343:LEU:HD11	1:A:409:GLU:HG2	1.86	0.57
1:C:276:MET:HE3	1:C:360:THR:HG21	1.87	0.57
1:D:343:LEU:HD23	1:D:343:LEU:C	2.24	0.57
1:B:132:GLU:O	1:B:136:THR:OG1	2.17	0.57
1:A:145:ASN:ND2	1:A:147:ARG:HB2	2.19	0.57
1:B:399:LEU:O	1:B:403:GLN:HG3	2.04	0.57
1:D:341:ARG:NH2	1:D:405:VAL:HG11	2.19	0.57
1:C:319:HIS:O	1:C:322:HIS:CD2	2.57	0.57
1:B:126:GLU:HG2	1:B:133:LEU:HD13	1.85	0.57
1:C:88:VAL:HG21	1:C:235:LYS:HE3	1.87	0.56
1:A:99:ILE:HG12	1:A:242:LEU:HD11	1.87	0.56
1:A:327:ARG:HD3	1:A:356:TRP:CD2	2.40	0.56
1:C:79:LEU:HD22	1:C:163:VAL:HA	1.87	0.56
1:C:86:ASN:ND2	1:C:160:VAL:HG23	2.21	0.56
1:C:276:MET:CE	1:C:360:THR:CG2	2.83	0.56
1:B:319:HIS:O	1:B:322:HIS:HE1	1.89	0.55
1:D:341:ARG:HH22	1:D:405:VAL:HG21	1.71	0.55
1:D:337:PHE:CD1	1:D:401:LEU:HB3	2.41	0.55
1:B:131:VAL:HG13	1:B:183:MET:HE1	1.89	0.55
1:B:276:MET:CE	1:B:281:LEU:HG	2.32	0.55
1:C:290:THR:C	1:C:291:GLU:HG3	2.26	0.54
1:B:130:GLY:O	1:B:134:ILE:HG12	2.07	0.54
1:C:281:LEU:O	1:C:283:VAL:HG23	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:193:LYS:HG2	1:D:194:LEU:N	2.21	0.54
1:B:341:ARG:HH22	1:B:405:VAL:HG21	1.69	0.54
1:D:343:LEU:CD2	1:D:416:ILE:HD11	2.37	0.54
1:A:155:LEU:HD12	1:B:66:ARG:CD	2.36	0.54
1:A:233:ARG:NH2	1:A:270:GLU:OE2	2.40	0.54
1:A:108:SER:HB3	1:A:212:TRP:CD1	2.43	0.54
1:A:278:PRO:HG2	1:A:282:PHE:H	1.73	0.54
1:B:200:VAL:HG12	1:B:204:ASN:HB3	1.90	0.54
1:B:340:PHE:HE2	1:B:341:ARG:HE	1.55	0.54
1:C:311:VAL:HG21	1:C:380:LEU:HG	1.89	0.53
1:D:401:LEU:O	1:D:405:VAL:HA	2.07	0.53
1:A:61:ASP:O	1:A:65:ARG:HG2	2.08	0.53
1:A:271:MET:HB2	1:A:276:MET:CE	2.38	0.53
1:C:98:GLN:HG3	1:C:243:THR:HB	1.91	0.53
1:B:268:LYS:HG3	1:B:281:LEU:HD12	1.91	0.53
1:D:126:GLU:OE2	1:D:137:ARG:NH2	2.38	0.53
1:B:79:LEU:HG	1:B:163:VAL:HA	1.91	0.53
1:D:345:PRO:O	1:D:348:VAL:HG22	2.09	0.52
1:A:155:LEU:HD12	1:B:66:ARG:CZ	2.34	0.52
1:C:274:HIS:CE1	1:C:302:GLU:OE1	2.62	0.52
1:D:314:ILE:HD11	1:D:372:PHE:CE1	2.44	0.52
1:C:101:VAL:HG22	1:C:111:VAL:HG22	1.91	0.52
1:B:48:ARG:HG3	1:B:49:TYR:N	2.25	0.52
1:D:126:GLU:O	1:D:127:LYS:HB2	2.09	0.52
1:A:311:VAL:HG21	1:A:380:LEU:HG	1.92	0.52
1:D:338:CYS:SG	1:D:343:LEU:HD22	2.49	0.52
1:C:104:TYR:HA	1:C:249:GLU:HG2	1.91	0.51
1:C:276:MET:HE2	1:C:360:THR:CG2	2.39	0.51
1:C:274:HIS:ND1	1:C:302:GLU:OE1	2.43	0.51
1:A:123:HIS:ND1	1:A:126:GLU:HB2	2.25	0.51
1:A:319:HIS:O	1:A:322:HIS:CD2	2.63	0.51
1:A:281:LEU:O	1:A:283:VAL:HG23	2.10	0.51
1:A:331:THR:HG22	1:A:335:ARG:NE	2.25	0.51
1:D:378:GLU:HA	1:D:378:GLU:OE2	2.10	0.51
1:D:322:HIS:HB2	1:D:389:ILE:HD12	1.92	0.51
1:D:365:LEU:HD13	1:D:389:ILE:HD11	1.93	0.51
1:A:268:LYS:HG3	1:A:281:LEU:HD12	1.93	0.50
1:B:248:ASP:HB3	1:B:251:THR:OG1	2.11	0.50
1:A:229:ARG:NH2	1:A:253:GLU:OE1	2.43	0.50
1:D:399:LEU:O	1:D:403:GLN:CG	2.56	0.50
1:D:401:LEU:HD22	1:D:408:GLY:HA3	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:338:CYS:O	1:D:343:LEU:N	2.44	0.50
1:B:200:VAL:CG1	1:B:204:ASN:HB3	2.42	0.50
1:D:341:ARG:NH1	1:D:405:VAL:HG11	2.27	0.49
1:D:353:GLU:O	1:D:357:ASP:N	2.45	0.49
1:A:328:SER:HB2	1:A:390:GLU:HG3	1.94	0.49
1:D:343:LEU:HD23	1:D:343:LEU:O	2.12	0.49
1:A:251:THR:HA	1:D:383:ARG:HH12	1.77	0.49
1:B:327:ARG:HG3	1:B:356:TRP:CD2	2.48	0.49
1:C:278:PRO:HD3	1:C:411:ILE:HD11	1.95	0.49
1:C:141:GLY:HA2	3:C:502:ANP:H4'	1.94	0.49
1:D:373:SER:OG	1:D:379:ARG:HG2	2.12	0.49
1:A:305:LEU:HD22	1:A:359:VAL:O	2.12	0.49
1:D:349:LYS:HB2	1:D:349:LYS:HE3	1.58	0.49
1:D:193:LYS:CG	1:D:194:LEU:H	2.21	0.49
1:D:291:GLU:HB3	1:D:388:PHE:CE2	2.47	0.49
1:A:86:ASN:HD22	1:A:160:VAL:HG23	1.78	0.48
1:B:216:LYS:HE2	1:B:217:TYR:CZ	2.49	0.48
1:C:365:LEU:HD13	1:C:389:ILE:HD11	1.95	0.48
1:A:273:GLU:HG2	1:A:274:HIS:N	2.27	0.48
3:C:502:ANP:O2'	1:D:49:TYR:OH	2.16	0.48
1:D:102:THR:HG23	1:D:247:HIS:HB3	1.94	0.48
1:D:327:ARG:CD	1:D:352:PRO:HB3	2.40	0.48
1:B:128:ILE:HD12	1:B:132:GLU:HG2	1.96	0.48
1:C:360:THR:HG23	1:C:360:THR:O	2.14	0.48
1:A:124:PRO:C	1:A:125:GLU:HG3	2.34	0.48
1:C:291:GLU:HA	1:C:366:LYS:O	2.14	0.48
1:A:407:ILE:O	1:A:411:ILE:HG13	2.14	0.48
1:C:102:THR:HG23	1:C:247:HIS:HB3	1.96	0.48
1:C:318:GLN:OE1	1:D:318:GLN:NE2	2.32	0.48
1:D:145:ASN:OD1	1:D:147:ARG:HB2	2.14	0.48
1:A:126:GLU:HG2	1:A:133:LEU:HD13	1.96	0.47
1:A:300:VAL:HG22	1:A:305:LEU:HD21	1.96	0.47
1:B:48:ARG:CG	1:B:49:TYR:N	2.78	0.47
1:D:117:GLY:HA2	1:D:207:THR:OG1	2.14	0.47
1:A:86:ASN:HB3	3:A:502:ANP:N7	2.29	0.47
1:B:103:LEU:HD11	1:B:228:LEU:HD23	1.96	0.47
1:C:210:ARG:HG2	1:C:212:TRP:CH2	2.50	0.47
1:D:324:ASN:HD22	1:D:327:ARG:HH12	1.61	0.47
1:D:341:ARG:NH2	1:D:405:VAL:CG1	2.77	0.47
1:A:239:CYS:HB2	1:A:313:LEU:HD21	1.96	0.47
1:B:225:VAL:HG21	1:B:248:ASP:OD1	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:GLU:HA	1:B:366:LYS:O	2.14	0.47
1:B:417:ASP:O	1:B:420:SER:HB2	2.15	0.47
1:D:341:ARG:CZ	1:D:405:VAL:CG1	2.92	0.47
1:B:277:LEU:HD23	1:B:411:ILE:HG12	1.98	0.46
1:D:286:LEU:HD22	1:D:392:ALA:HB2	1.97	0.46
1:B:99:ILE:HG12	1:B:242:LEU:HD11	1.96	0.46
1:B:284:GLY:HA3	1:B:295:TRP:CZ2	2.49	0.46
1:A:369:ASP:HA	1:B:66:ARG:HH22	1.81	0.46
1:D:175:LYS:HG2	1:D:180:GLU:CB	2.46	0.46
1:B:122:ILE:CD1	1:B:122:ILE:CB	2.79	0.46
1:C:350:LEU:HD11	1:C:415:ALA:HB1	1.98	0.46
1:A:341:ARG:NH1	1:A:409:GLU:OE1	2.48	0.46
1:B:98:GLN:HA	1:B:243:THR:O	2.15	0.46
1:C:145:ASN:CG	1:C:147:ARG:H	2.19	0.46
1:C:328:SER:OG	1:C:390:GLU:HG3	2.16	0.46
1:C:135:LEU:HD22	1:C:160:VAL:HG11	1.99	0.45
1:C:327:ARG:HG3	1:C:356:TRP:CE3	2.50	0.45
1:A:271:MET:HB2	1:A:276:MET:HE2	1.98	0.45
1:B:86:ASN:HD21	1:B:160:VAL:HG23	1.80	0.45
1:D:334:LEU:HD23	1:D:350:LEU:HD13	1.98	0.45
1:C:134:ILE:HD12	3:C:502:ANP:H4'	1.99	0.45
1:B:276:MET:HG2	1:B:300:VAL:HG22	1.98	0.45
1:A:300:VAL:CG2	1:A:305:LEU:HD21	2.46	0.45
1:A:156:HIS:CD2	1:B:66:ARG:HD3	2.52	0.45
1:C:130:GLY:O	1:C:134:ILE:HG12	2.17	0.45
1:C:251:THR:HG23	1:C:253:GLU:HB2	1.99	0.45
1:C:322:HIS:CD2	1:C:322:HIS:H	2.34	0.45
1:A:277:LEU:HD23	1:A:411:ILE:HG12	1.98	0.45
1:B:341:ARG:CZ	1:B:405:VAL:HG21	2.44	0.45
1:D:176:ARG:CD	1:D:177:GLU:OE1	2.65	0.45
1:D:401:LEU:HD23	1:D:401:LEU:HA	1.72	0.44
1:C:327:ARG:NH1	1:C:352:PRO:HB2	2.33	0.44
1:D:345:PRO:HG2	1:D:348:VAL:HG11	2.00	0.44
1:A:66:ARG:NH1	4:A:604:HOH:O	2.32	0.44
1:B:276:MET:HE2	1:B:276:MET:HB2	1.76	0.44
1:C:291:GLU:HG2	1:C:367:MET:HB2	2.00	0.44
1:D:177:GLU:OE1	1:D:177:GLU:N	2.51	0.44
1:B:277:LEU:HD21	1:B:410:LYS:HB2	1.99	0.44
1:C:170:VAL:HG22	1:C:211:PHE:CB	2.47	0.44
1:C:216:LYS:HE3	1:C:217:TYR:CZ	2.53	0.44
1:A:300:VAL:HG23	1:A:358:ARG:NH2	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:LEU:HD13	1:B:165:ALA:HB2	1.99	0.44
1:B:278:PRO:HG2	1:B:282:PHE:H	1.81	0.44
1:C:327:ARG:HA	1:C:356:TRP:CZ3	2.53	0.44
1:B:134:ILE:HG23	3:B:502:ANP:H5'1	2.00	0.44
1:C:95:HIS:CE1	1:C:116:ARG:HD3	2.53	0.44
1:C:233:ARG:NH2	1:C:270:GLU:OE2	2.51	0.43
1:A:271:MET:HB2	1:A:276:MET:HE3	1.99	0.43
1:A:273:GLU:HG3	1:A:274:HIS:CE1	2.54	0.43
1:B:135:LEU:HD22	1:B:160:VAL:HG11	2.01	0.43
1:C:99:ILE:HA	1:C:112:SER:O	2.18	0.43
1:D:193:LYS:CG	1:D:194:LEU:N	2.81	0.43
1:A:343:LEU:CD1	1:A:409:GLU:HG2	2.47	0.43
1:B:267:LEU:HB3	1:B:281:LEU:HD11	2.01	0.43
1:C:98:GLN:HA	1:C:243:THR:O	2.19	0.43
1:A:141:GLY:HA2	3:A:502:ANP:H4'	1.99	0.43
1:C:86:ASN:HD21	1:C:160:VAL:HG23	1.84	0.43
1:D:311:VAL:O	1:D:314:ILE:HG13	2.19	0.43
1:A:319:HIS:O	1:A:322:HIS:NE2	2.52	0.43
1:A:365:LEU:HD21	1:A:367:MET:CE	2.49	0.43
1:C:233:ARG:HB2	1:C:257:TRP:CE2	2.53	0.43
1:D:146:ASN:HB3	1:D:150:THR:HA	2.01	0.43
1:B:278:PRO:HB3	1:B:407:ILE:HG21	2.00	0.42
1:C:108:SER:HB2	1:C:212:TRP:CD1	2.54	0.42
1:B:248:ASP:HB3	1:B:251:THR:HG1	1.83	0.42
1:B:267:LEU:HD13	1:B:362:VAL:HG23	2.01	0.42
1:D:320:GLY:HA3	1:D:380:LEU:H	1.84	0.42
1:A:367:MET:CE	1:A:385:ALA:HB2	2.50	0.42
1:B:200:VAL:HG12	1:B:201:GLY:N	2.34	0.42
1:D:341:ARG:HH22	1:D:405:VAL:HG11	1.84	0.42
1:B:300:VAL:O	1:B:358:ARG:NH1	2.53	0.42
1:A:69:MET:CE	1:B:375:GLN:HG2	2.49	0.42
1:A:363:LEU:HD11	1:A:389:ILE:HD13	2.02	0.42
1:C:155:LEU:HD21	1:C:372:PHE:HD2	1.85	0.42
1:C:356:TRP:HA	1:C:359:VAL:HG23	2.00	0.42
1:C:155:LEU:HD21	1:C:372:PHE:CD2	2.54	0.42
1:C:215:PRO:HB3	1:C:221:PRO:HG3	2.01	0.42
1:A:116:ARG:NH1	1:B:49:TYR:HB2	2.35	0.42
1:A:156:HIS:HD2	1:B:66:ARG:HD3	1.85	0.42
1:C:176:ARG:NH2	1:D:49:TYR:O	2.52	0.42
1:D:278:PRO:CG	1:D:282:PHE:H	2.31	0.41
1:B:319:HIS:HB3	1:B:323:VAL:HG21	2.03	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:113:ASP:OD2	1:C:207:THR:N	2.44	0.41
1:A:100:GLU:HG3	1:A:245:LYS:HB2	2.03	0.41
1:C:104:TYR:HE1	1:C:110:GLU:HB3	1.85	0.41
1:C:288:LYS:C	1:C:290:THR:H	2.22	0.41
1:D:118:MET:HB2	1:D:174:ILE:HD13	2.01	0.41
1:A:126:GLU:HG3	1:A:137:ARG:NH2	2.35	0.41
1:D:331:THR:HG22	1:D:355:VAL:HB	2.02	0.41
1:B:344:LEU:HD12	1:B:348:VAL:HG13	2.03	0.41
1:C:48:ARG:HH11	1:C:48:ARG:HG2	1.85	0.41
1:D:176:ARG:CG	1:D:177:GLU:OE1	2.66	0.41
1:A:287:LYS:HE3	1:A:289:ASP:OD2	2.21	0.41
1:B:108:SER:HB3	1:B:212:TRP:CD1	2.55	0.41
1:C:74:ALA:HA	1:C:219:ASP:OD2	2.21	0.41
1:D:99:ILE:HA	1:D:112:SER:O	2.21	0.41
1:D:235:LYS:NZ	1:D:313:LEU:O	2.38	0.41
1:C:321:THR:OG1	1:C:382:SER:O	2.25	0.41
1:C:356:TRP:HA	1:C:359:VAL:CG2	2.51	0.41
1:C:367:MET:HE2	1:C:385:ALA:HB2	2.03	0.41
1:D:246:LEU:HB3	1:D:255:ASP:HB2	2.03	0.41
1:D:286:LEU:HB3	1:D:293:VAL:HG12	2.03	0.40
1:D:337:PHE:HE1	1:D:402:ASN:HD22	1.70	0.40
1:A:54:ILE:HD12	1:B:134:ILE:HD11	2.03	0.40
1:D:343:LEU:CD2	1:D:416:ILE:CD1	2.94	0.40
1:B:121:ASP:OD1	1:B:121:ASP:N	2.53	0.40
1:B:129:PRO:HD2	1:B:132:GLU:OE2	2.22	0.40
1:B:311:VAL:HG21	1:B:380:LEU:HG	2.03	0.40
3:D:502:ANP:O1A	3:D:502:ANP:O2B	2.39	0.40
1:D:176:ARG:NH1	1:D:177:GLU:OE2	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	372/408 (91%)	354 (95%)	18 (5%)	0	100	100
1	B	372/408 (91%)	355 (95%)	17 (5%)	0	100	100
1	C	372/408 (91%)	354 (95%)	18 (5%)	0	100	100
1	D	372/408 (91%)	352 (95%)	20 (5%)	0	100	100
All	All	1488/1632 (91%)	1415 (95%)	73 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	309/340 (91%)	301 (97%)	8 (3%)	46	76
1	B	309/340 (91%)	300 (97%)	9 (3%)	42	74
1	C	309/340 (91%)	299 (97%)	10 (3%)	39	71
1	D	309/340 (91%)	302 (98%)	7 (2%)	50	79
All	All	1236/1360 (91%)	1202 (97%)	34 (3%)	43	75

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ARG
1	A	109	CYS
1	A	137	ARG
1	A	231	LEU
1	A	322	HIS
1	A	335	ARG
1	A	356	TRP
1	A	383	ARG
1	B	48	ARG
1	B	66	ARG
1	B	143	LYS
1	B	202	LYS
1	B	285	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	343	LEU
1	B	380	LEU
1	B	384	GLN
1	B	418	ARG
1	C	102	THR
1	C	145	ASN
1	C	186	ARG
1	C	231	LEU
1	C	254	GLN
1	C	276	MET
1	C	288	LYS
1	C	322	HIS
1	C	383	ARG
1	C	398	SER
1	D	176	ARG
1	D	203	LYS
1	D	273	GLU
1	D	287	LYS
1	D	322	HIS
1	D	346	ARG
1	D	398	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	156	HIS
1	A	322	HIS
1	A	371	GLN
1	B	78	HIS
1	B	274	HIS
1	C	394	HIS
1	D	402	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 monosaccharides 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$
3	ANP	C	502	1,2	29,33,33	1.08	3 (10%)	31,52,52	1.19	2 (6%)
3	ANP	B	502	1,2	29,33,33	1.17	4 (13%)	31,52,52	1.08	4 (12%)
3	ANP	D	502	1,2	29,33,33	1.08	5 (17%)	31,52,52	1.31	3 (9%)
3	ANP	A	502	1,2	29,33,33	1.15	5 (17%)	31,52,52	1.25	2 (6%)

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	ANP	C	502	1,2	-	4/14/38/38	0/3/3/3
3	ANP	B	502	1,2	-	3/14/38/38	0/3/3/3
3	ANP	D	502	1,2	-	4/14/38/38	0/3/3/3
3	ANP	A	502	1,2	-	2/14/38/38	0/3/3/3

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	ANP	PG-N3B	2.94	1.71	1.63
3	B	502	ANP	PG-O1G	2.57	1.50	1.46
3	B	502	ANP	PB-O1B	2.55	1.50	1.46
3	A	502	ANP	PG-N3B	2.49	1.69	1.63
3	C	502	ANP	PG-N3B	2.46	1.69	1.63
3	A	502	ANP	PG-O1G	2.45	1.50	1.46

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	502	ANP	PG-O1G	2.43	1.50	1.46
3	A	502	ANP	PB-O1B	2.36	1.49	1.46
3	B	502	ANP	PB-O3A	-2.33	1.56	1.59
3	D	502	ANP	PG-O1G	2.32	1.49	1.46
3	C	502	ANP	PB-O1B	2.30	1.49	1.46
3	A	502	ANP	PB-O3A	-2.30	1.56	1.59
3	D	502	ANP	PB-O1B	2.29	1.49	1.46
3	D	502	ANP	PG-N3B	2.28	1.69	1.63
3	A	502	ANP	C4-N3	-2.27	1.32	1.35
3	D	502	ANP	PB-O3A	-2.13	1.56	1.59
3	D	502	ANP	C8-N7	-2.12	1.30	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	502	ANP	PA-O3A-PB	-4.13	118.06	132.62
3	A	502	ANP	PA-O3A-PB	-4.01	118.51	132.62
3	C	502	ANP	PA-O3A-PB	-3.39	120.69	132.62
3	C	502	ANP	C3'-C2'-C1'	2.68	105.02	100.98
3	D	502	ANP	O1B-PB-N3B	-2.61	107.92	111.77
3	B	502	ANP	PA-O3A-PB	-2.61	123.41	132.62
3	A	502	ANP	C3'-C2'-C1'	2.61	104.91	100.98
3	D	502	ANP	C3'-C2'-C1'	2.48	104.71	100.98
3	B	502	ANP	O2B-PB-O3A	2.39	112.62	104.64
3	B	502	ANP	C5-C6-N6	2.34	123.90	120.35
3	B	502	ANP	O1B-PB-N3B	-2.01	108.81	111.77

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	ANP	PB-N3B-PG-O1G
3	B	502	ANP	PB-N3B-PG-O1G
3	B	502	ANP	PG-N3B-PB-O1B
3	B	502	ANP	PB-O3A-PA-O5'
3	C	502	ANP	PA-O3A-PB-O2B
3	D	502	ANP	O4'-C4'-C5'-O5'
3	C	502	ANP	O4'-C4'-C5'-O5'
3	C	502	ANP	C3'-C4'-C5'-O5'
3	D	502	ANP	C3'-C4'-C5'-O5'
3	C	502	ANP	C5'-O5'-PA-O3A
3	D	502	ANP	C5'-O5'-PA-O3A

Continued on next page...

Continued from previous page...

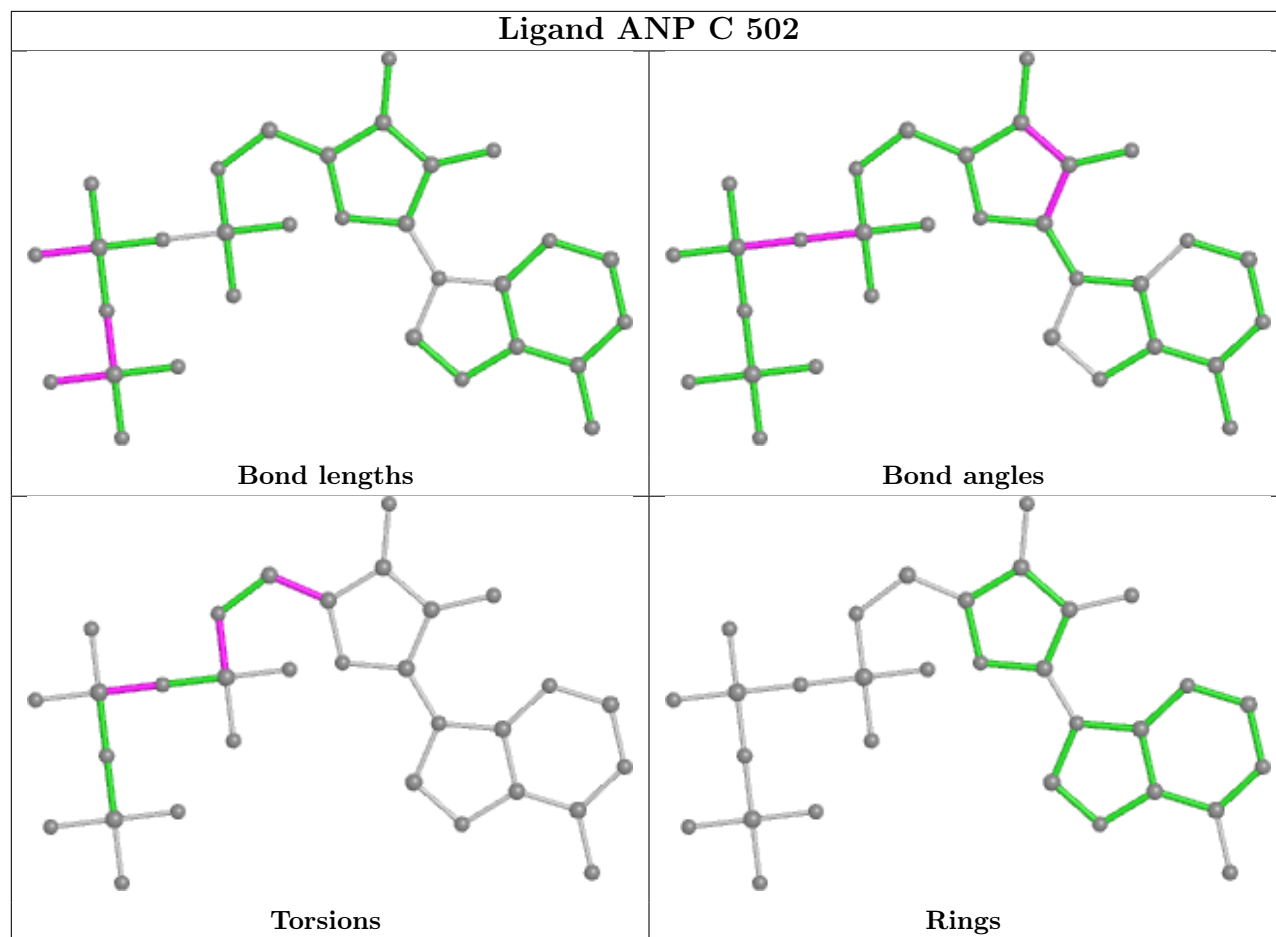
Mol	Chain	Res	Type	Atoms
3	A	502	ANP	PA-O3A-PB-O2B
3	D	502	ANP	PB-N3B-PG-O1G

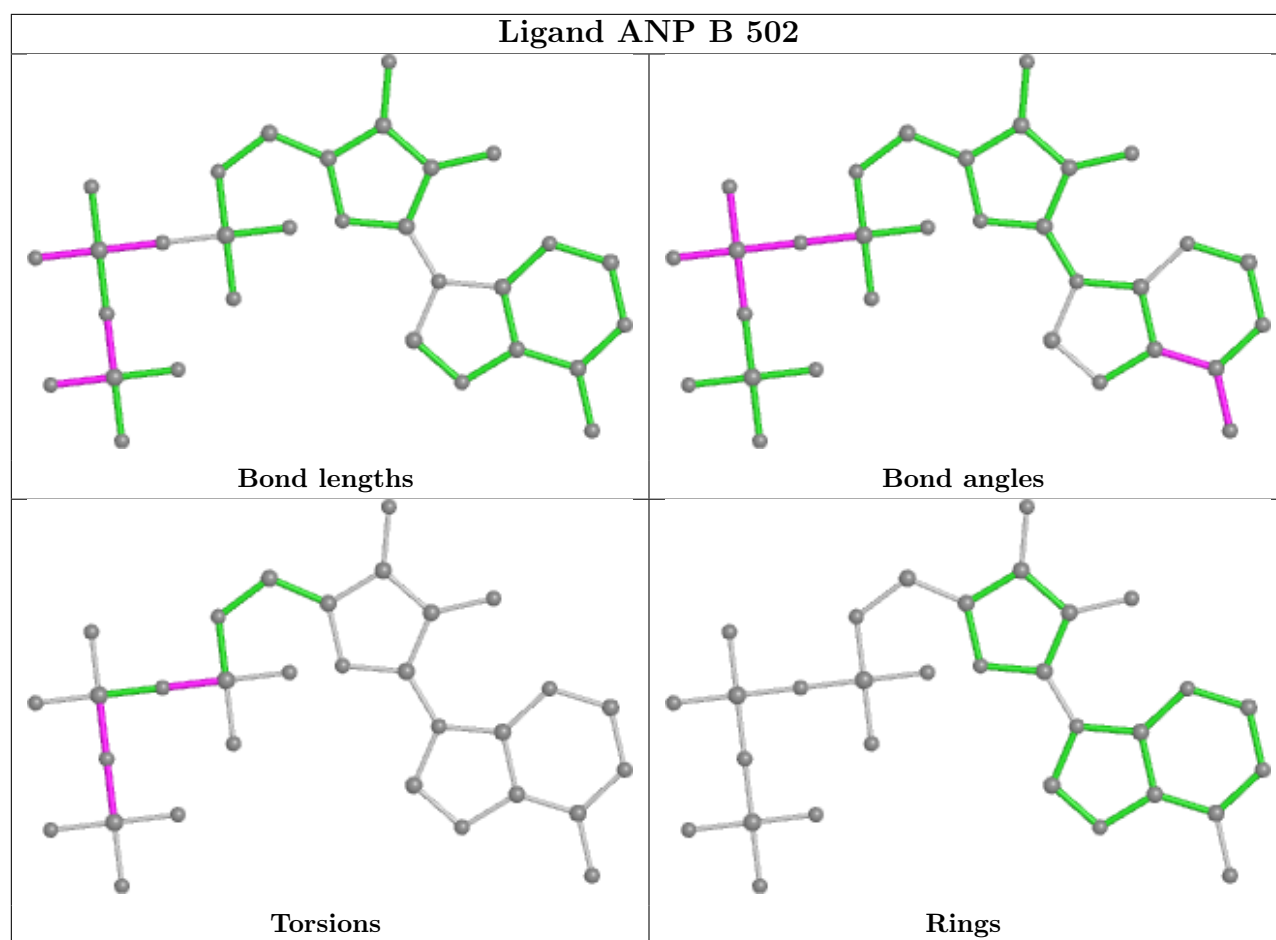
There are no ring outliers.

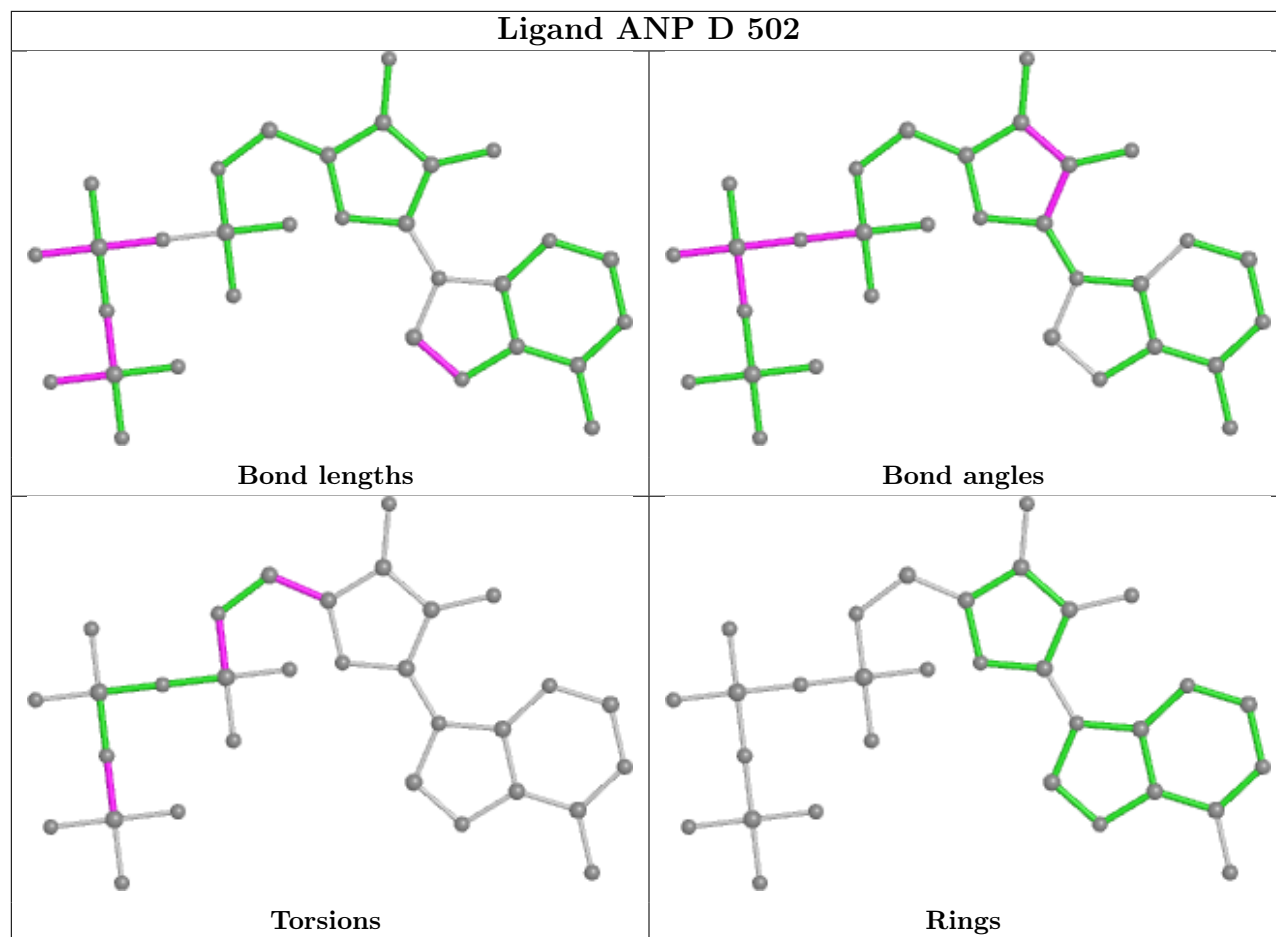
4 monomers are involved in 8 short contacts:

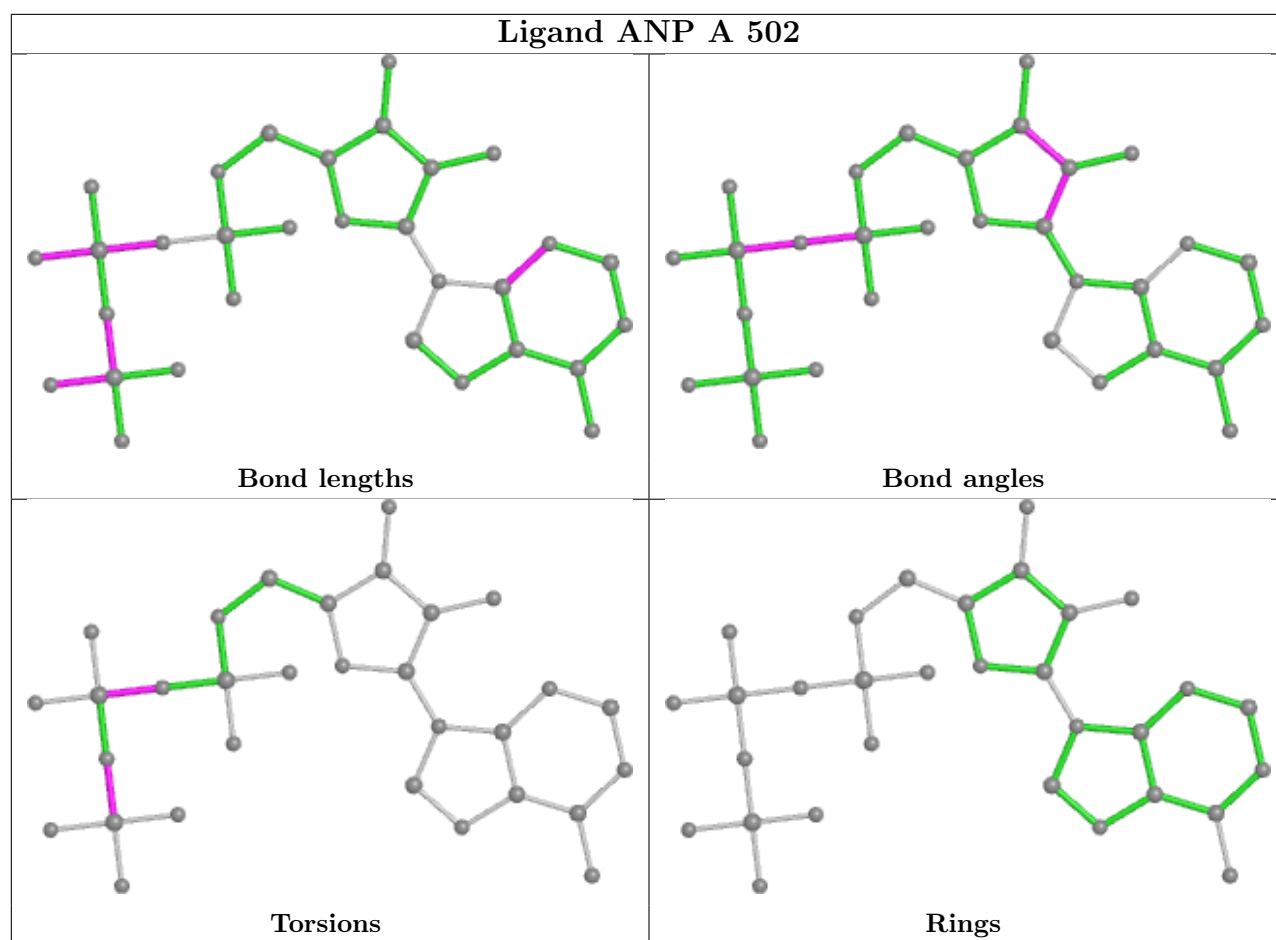
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	502	ANP	3	0
3	B	502	ANP	1	0
3	D	502	ANP	2	0
3	A	502	ANP	2	0

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.









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	374/408 (91%)	0.13	14 (3%) 41 37	29, 46, 78, 118	0
1	B	374/408 (91%)	0.05	6 (1%) 72 71	24, 50, 88, 100	0
1	C	374/408 (91%)	0.16	17 (4%) 33 29	25, 48, 92, 118	0
1	D	374/408 (91%)	0.14	14 (3%) 41 37	27, 51, 83, 119	0
All	All	1496/1632 (91%)	0.12	51 (3%) 45 40	24, 48, 87, 119	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	349	LYS	4.8
1	A	346	ARG	4.6
1	B	48	ARG	4.2
1	C	420	SER	4.0
1	D	343	LEU	3.6
1	C	348	VAL	3.6
1	A	348	VAL	3.5
1	C	48	ARG	3.5
1	A	419	ALA	3.3
1	C	346	ARG	3.3
1	C	350	LEU	3.3
1	B	349	LYS	3.1
1	C	276	MET	3.0
1	C	408	GLY	2.9
1	A	418	ARG	2.8
1	B	407	ILE	2.8
1	D	402	ASN	2.7
1	D	350	LEU	2.7
1	C	340	PHE	2.7
1	D	147	ARG	2.7
1	A	335	ARG	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	420	SER	2.6
1	C	273	GLU	2.6
1	A	415	ALA	2.6
1	D	177	GLU	2.6
1	A	420	SER	2.5
1	D	339	ASP	2.5
1	C	347	GLY	2.5
1	D	351	ALA	2.5
1	D	337	PHE	2.4
1	A	349	LYS	2.4
1	C	275	GLU	2.4
1	D	194	LEU	2.4
1	C	354	ASP	2.4
1	C	254	GLN	2.4
1	C	49	TYR	2.3
1	A	147	ARG	2.3
1	A	343	LEU	2.2
1	D	341	ARG	2.2
1	D	344	LEU	2.2
1	B	304	GLU	2.2
1	A	416	ILE	2.2
1	D	406	GLU	2.2
1	C	281	LEU	2.2
1	D	334	LEU	2.2
1	B	346	ARG	2.2
1	C	289	ASP	2.1
1	A	127	LYS	2.1
1	A	342	ASN	2.1
1	A	302	GLU	2.0
1	B	350	LEU	2.0

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands

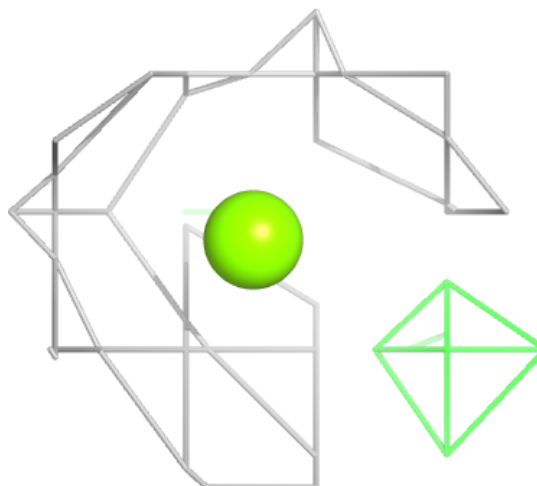
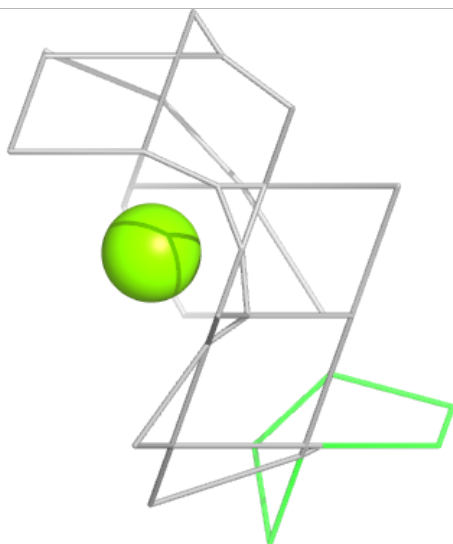
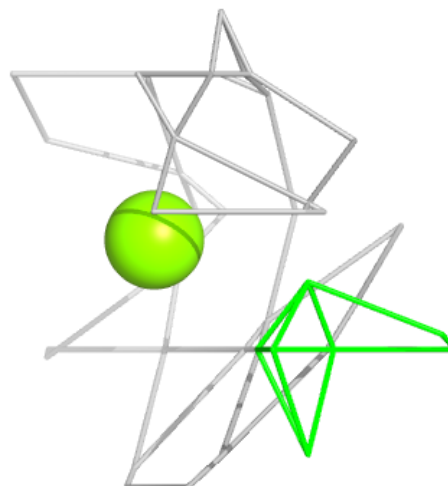
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MG	C	501	1/1	0.94	0.11	40,40,40,40	0
2	MG	B	501	1/1	0.95	0.20	37,37,37,37	0
3	ANP	D	502	31/31	0.95	0.18	32,44,53,56	0
3	ANP	A	502	31/31	0.96	0.17	27,40,48,50	0
2	MG	A	501	1/1	0.96	0.09	27,27,27,27	0
3	ANP	C	502	31/31	0.97	0.18	27,33,41,42	0
3	ANP	B	502	31/31	0.97	0.17	29,34,43,45	0
2	MG	D	501	1/1	0.98	0.13	44,44,44,44	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.

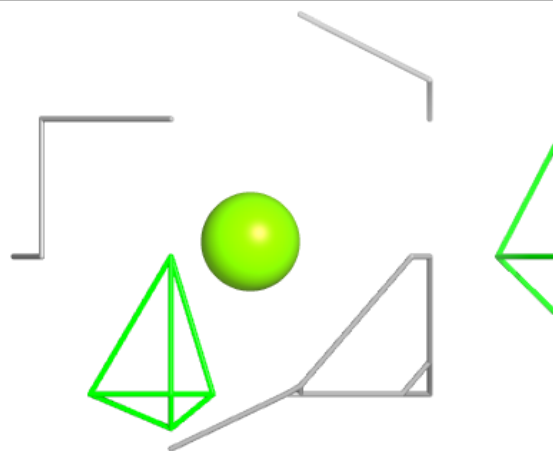
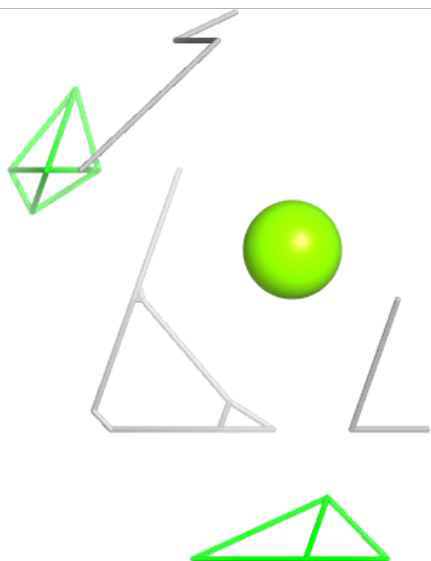
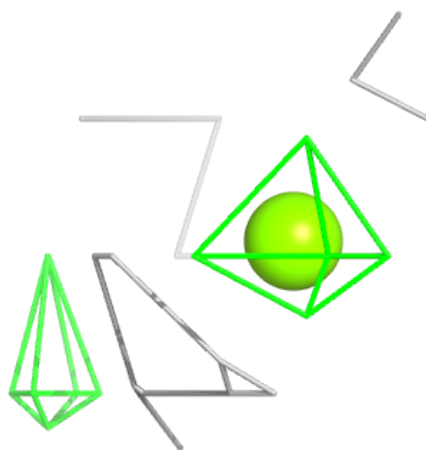
Electron density around MG C 501:

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



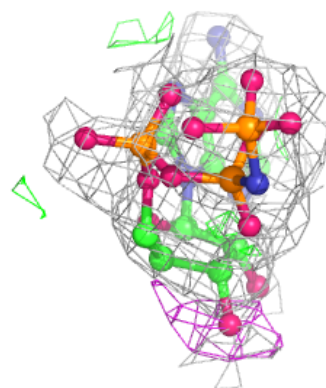
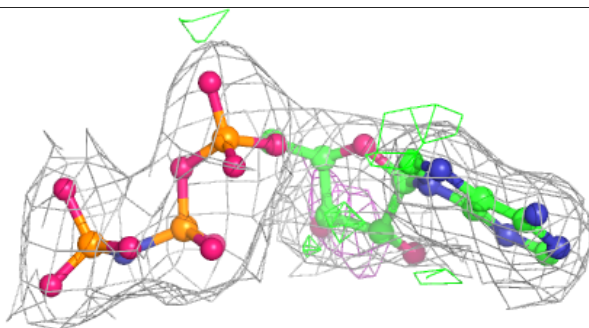
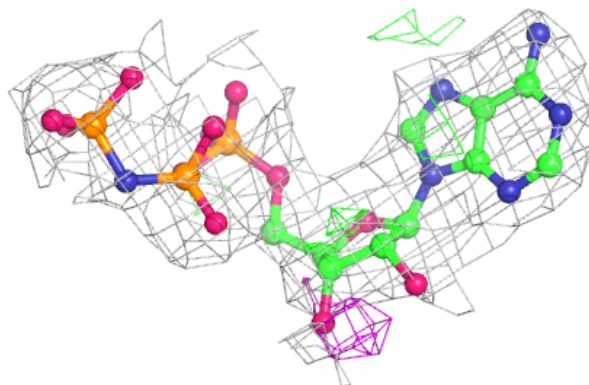
Electron density around MG B 501:

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

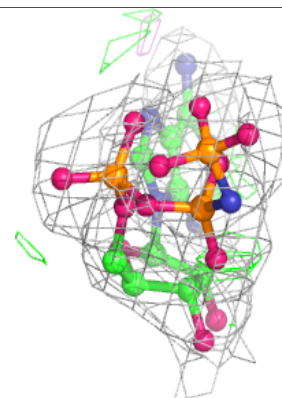
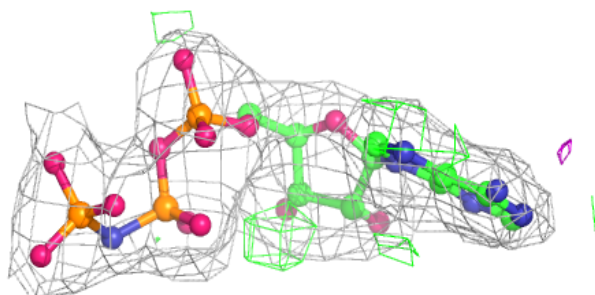
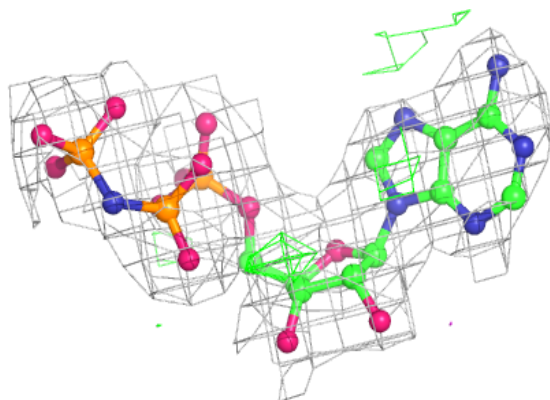


Electron density around ANP D 502:

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

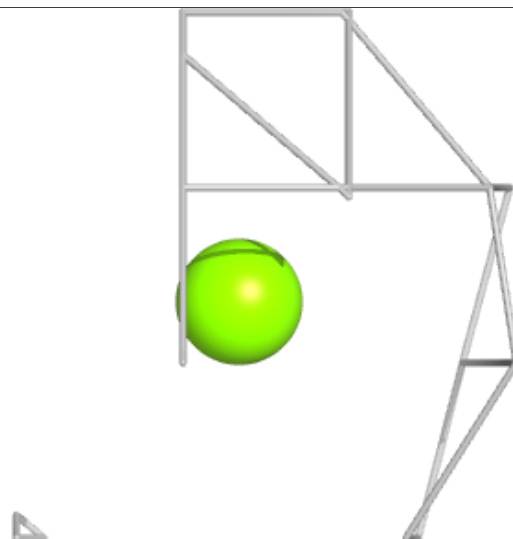
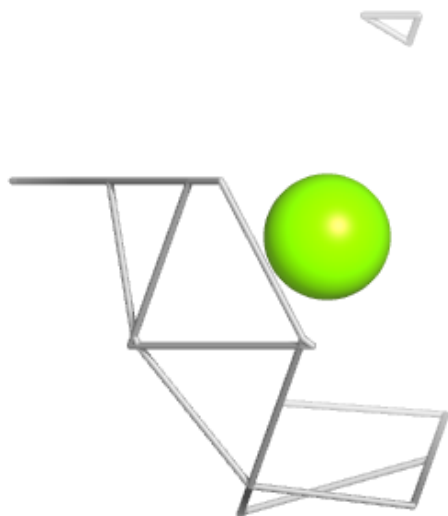
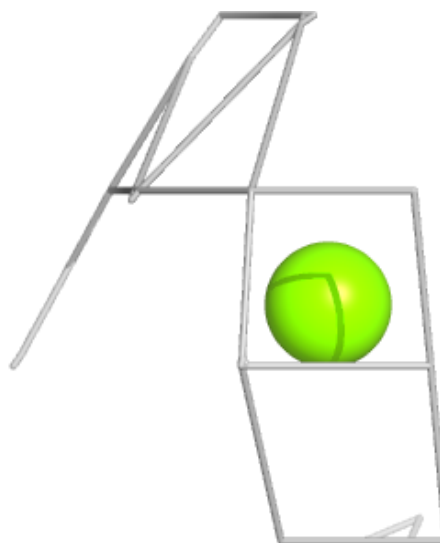
**Electron density around ANP A 502:**

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



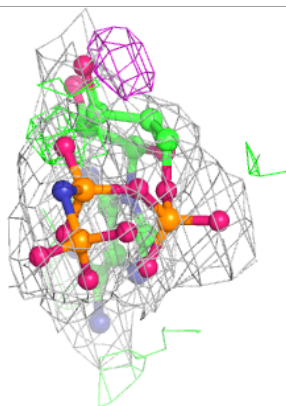
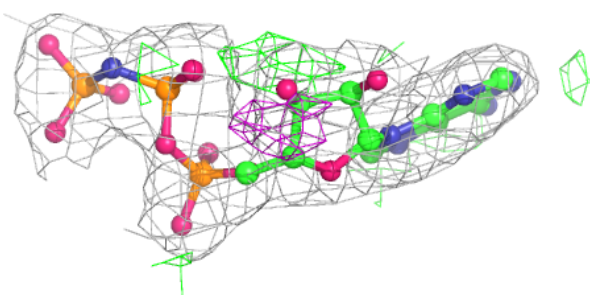
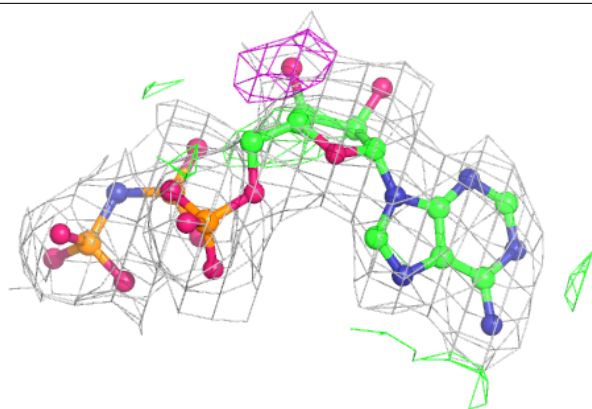
Electron density around MG A 501:

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

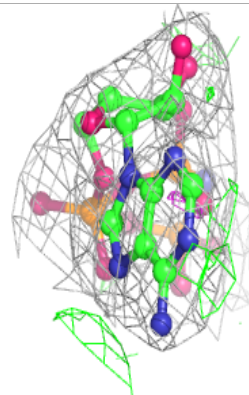
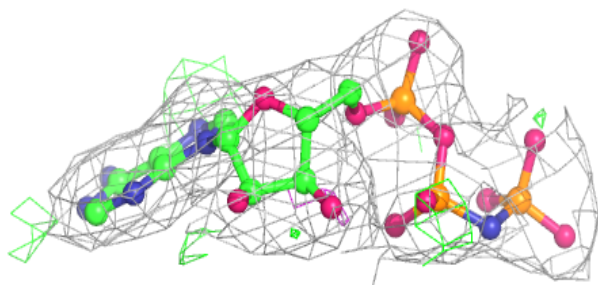
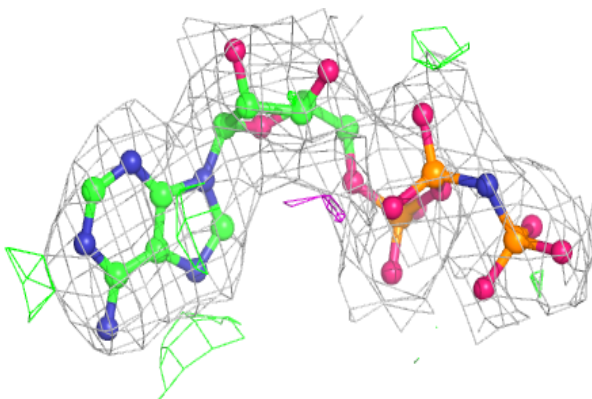


Electron density around ANP C 502:

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

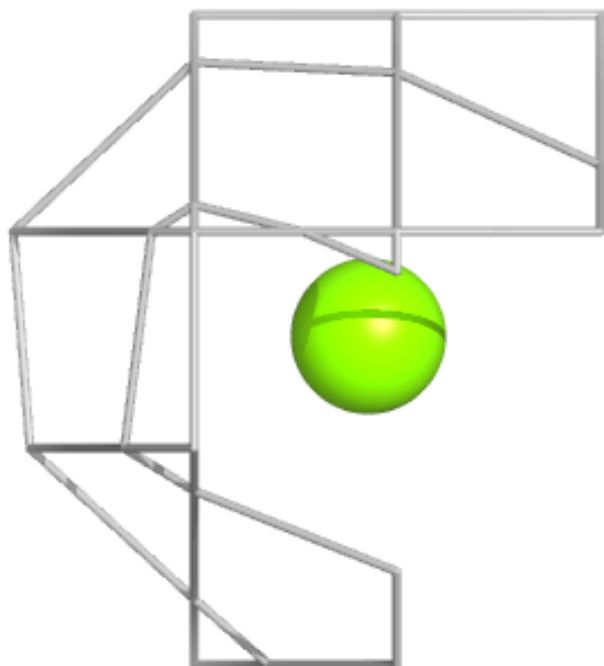
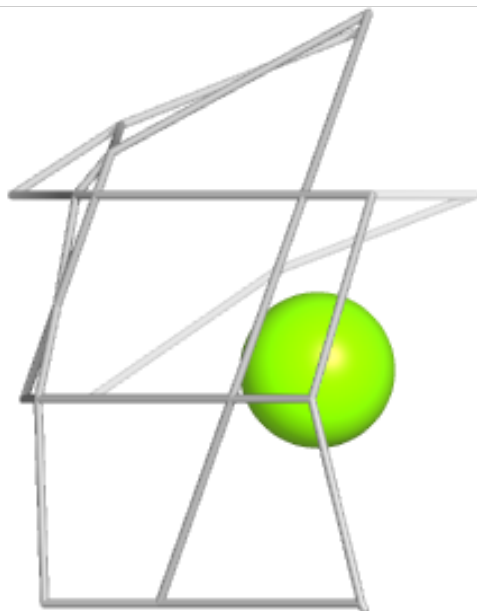
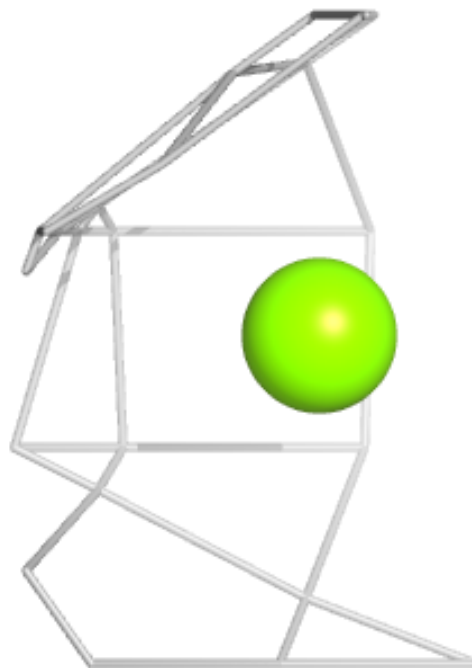
**Electron density around ANP B 502:**

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



Electron density around MG 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.