



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 15, 2024 – 11:12 pm GMT

PDB ID : 6SIZ
Title : PaaK family AMP-ligase with ANP and substrate
Authors : Naismith, J.H.; Song, H.
Deposited on : 2019-08-12
Resolution : 1.77 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 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

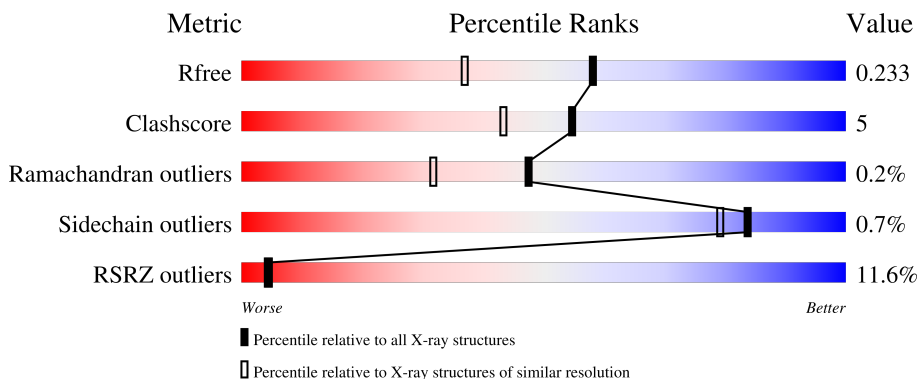
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	437	 11% 88% 1%
1	B	437	 12% 92% 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	EDO	A	505	-	-	X	-
5	EDO	A	506	-	-	X	-
5	EDO	A	507	-	-	X	-
7	PEG	B	507	-	-	X	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 7207 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 AMP-dependent synthetase and ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	433	3419	2161	606	638	14	0	6	0
1	B	437	3442	2171	613	643	15	0	5	0

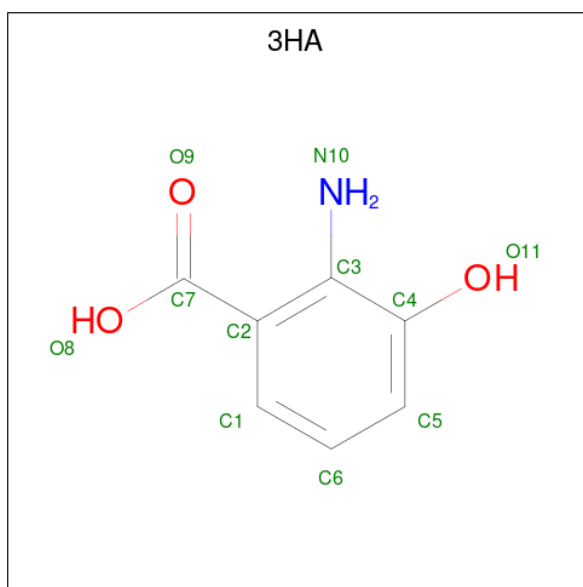
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP A0A022MRT4
B	0	ALA	-	expression tag	UNP A0A022MRT4

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

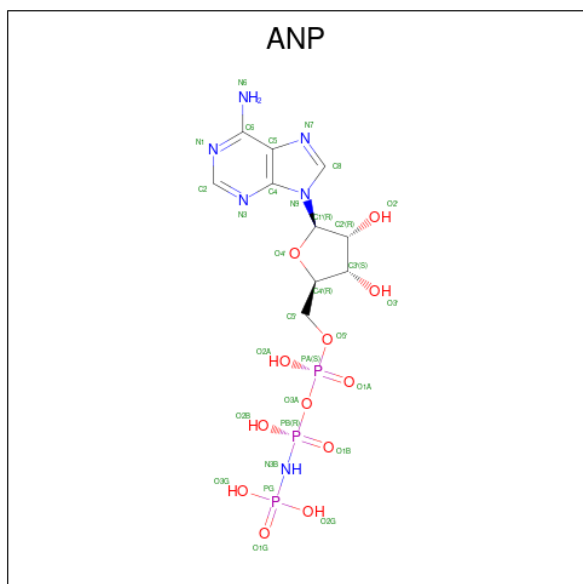
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is 3-HYDROXYANTHRANILIC ACID (three-letter code: 3HA) (formula: C₇H₇NO₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	11	7	1	3	0	0
3	B	1	11	7	1	3	0	0

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$) (labeled as "Ligand of Interest" by depositor).



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

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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	1	4	2	0	0
5	A	1	4	2	0	0
5	A	1	4	2	0	0
5	A	1	4	2	0	0
5	B	1	4	2	0	0
5	B	1	4	2	0	0
5	B	1	4	2	0	0

- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

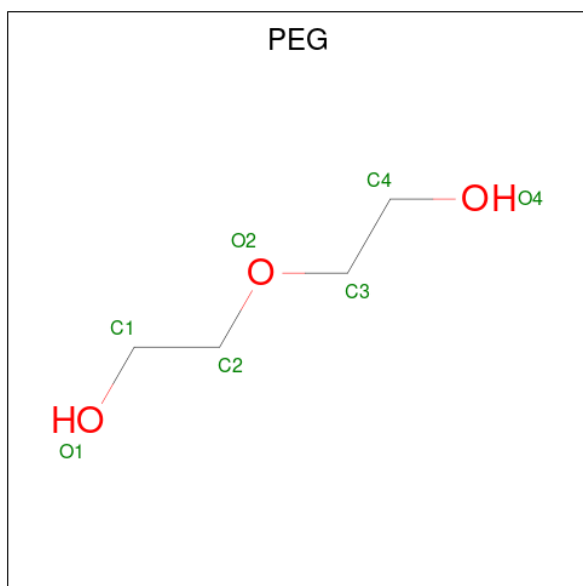
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	A	3	3	3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
6	B	1	1	1	0	0

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
7	B	1	7	4	3	0	0

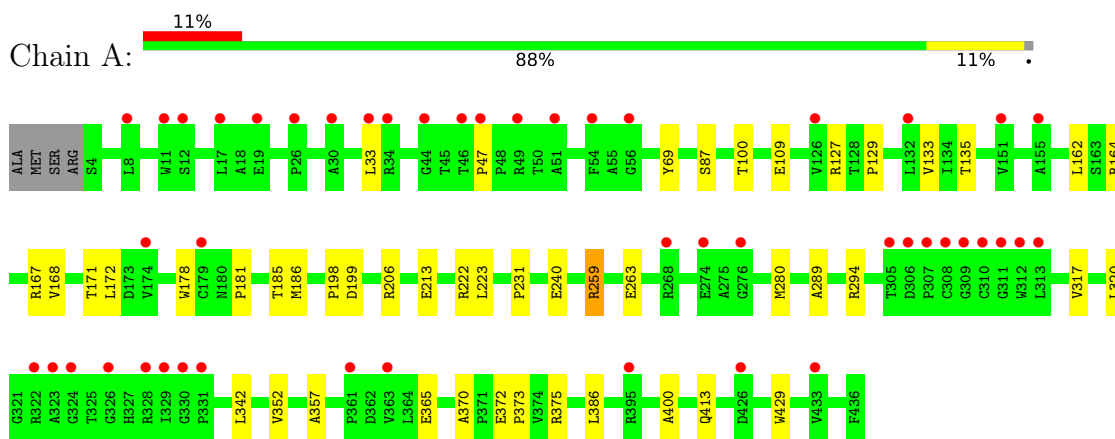
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	A	99	99	99	0	0
8	B	122	122	122	0	0

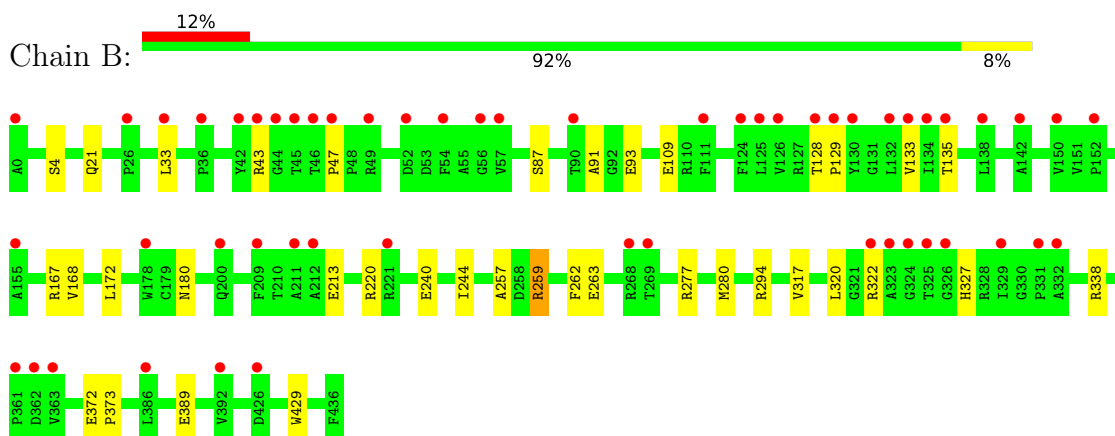
3 Residue-property plots [i](#)

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: AMP-dependent synthetase and ligase



- Molecule 1: AMP-dependent synthetase and ligase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	107.45Å 138.81Å 130.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.80 – 1.77 51.80 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.4 (51.80-1.77) 99.4 (51.80-1.77)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 1.77Å)	Xtrriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.200 , 0.228 0.208 , 0.233	Depositor DCC
R_{free} test set	4694 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	36.9	Xtrriage
Anisotropy	0.476	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.6	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	0.97	EDS
Total number of atoms	7207	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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: 3HA, MG, ZN, ANP, EDO, PEG

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	0.65	0/3503	0.77	2/4777 (0.0%)
1	B	0.67	1/3526 (0.0%)	0.78	1/4806 (0.0%)
All	All	0.66	1/7029 (0.0%)	0.77	3/9583 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	213	GLU	CD-OE1	-5.31	1.19	1.25

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	259	ARG	NE-CZ-NH2	-6.81	116.90	120.30
1	B	259	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	A	259	ARG	NE-CZ-NH1	5.01	122.80	120.30

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	3419	0	3368	37	0
1	B	3442	0	3391	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	11	0	5	0	0
3	B	11	0	5	0	0
4	A	31	0	13	0	0
4	B	31	0	13	2	0
5	A	16	0	24	15	0
5	B	12	0	18	2	0
6	A	3	0	0	0	0
6	B	1	0	0	0	0
7	B	7	0	10	11	0
8	A	99	0	0	0	0
8	B	122	0	0	7	0
All	All	7207	0	6847	72	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 5.

All (72) 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:180:ASN:ND2	7:B:507:PEG:H11	1.65	1.11
1:A:352:VAL:O	5:A:507:EDO:H21	1.62	0.98
1:B:128:THR:HG22	7:B:507:PEG:H21	1.51	0.92
1:B:180:ASN:ND2	7:B:507:PEG:C1	2.48	0.76
5:A:504:EDO:O2	5:A:507:EDO:H22	1.88	0.74
1:B:128:THR:HG22	7:B:507:PEG:C2	2.20	0.70
1:A:69:TYR:OH	1:B:167:ARG:NH1	2.24	0.70
1:B:180:ASN:HD22	7:B:507:PEG:H11	1.54	0.67
1:B:109:GLU:OE1	1:B:259:ARG:NH2	2.30	0.64
1:B:180:ASN:CG	7:B:507:PEG:H11	2.19	0.63
1:B:135[A]:THR:HG21	7:B:507:PEG:H41	1.81	0.63
1:A:109:GLU:OE1	1:A:259:ARG:NH2	2.30	0.63
1:A:186[B]:MET:HE3	8:B:610:HOH:O	1.99	0.63
1:A:413:GLN:HB3	5:A:505:EDO:H11	1.82	0.62
1:A:352:VAL:O	5:A:507:EDO:C2	2.45	0.61
1:A:198:PRO:HD2	5:A:506:EDO:C1	2.31	0.59
1:A:222:ARG:NH1	5:A:507:EDO:H22	2.17	0.59
1:A:164:ARG:HB2	5:A:505:EDO:H21	1.85	0.58
1:B:128:THR:CG2	7:B:507:PEG:H21	2.30	0.58
1:A:222:ARG:HD2	5:A:504:EDO:H12	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:222:ARG:HD2	5:A:504:EDO:C1	2.35	0.56
1:A:164:ARG:CB	5:A:505:EDO:H21	2.36	0.56
1:B:33:LEU:HD21	1:B:47:PRO:CB	2.36	0.55
5:B:505:EDO:H21	8:B:601:HOH:O	2.06	0.55
1:A:198:PRO:HD2	5:A:506:EDO:H12	1.89	0.54
7:B:507:PEG:H12	8:B:702:HOH:O	2.08	0.53
1:B:277:ARG:NH2	1:B:320:LEU:HD13	2.25	0.52
1:A:168:VAL:HG13	1:A:172:LEU:HD12	1.92	0.52
1:A:87:SER:OG	1:A:240:GLU:OE1	2.27	0.51
1:A:186[B]:MET:CE	8:B:610:HOH:O	2.55	0.51
1:A:181:PRO:HD2	1:A:213:GLU:CG	2.41	0.51
1:B:322:ARG:NH2	4:B:503:ANP:O1B	2.43	0.51
1:B:87:SER:OG	1:B:240:GLU:OE1	2.30	0.50
1:B:33:LEU:HD21	1:B:47:PRO:HB2	1.93	0.50
1:B:180:ASN:HD22	7:B:507:PEG:C1	2.18	0.49
1:A:280:MET:HE1	1:A:317:VAL:HG21	1.94	0.49
1:A:129:PRO:HB2	1:A:133:VAL:CG2	2.44	0.48
1:A:181:PRO:HD2	1:A:213:GLU:HG2	1.95	0.47
1:A:162:LEU:HD11	1:A:186[B]:MET:HG2	1.96	0.47
1:A:370:ALA:O	1:A:375:ARG:NH1	2.48	0.46
1:A:199:ASP:HB3	5:A:506:EDO:H21	1.98	0.46
1:B:372:GLU:N	1:B:373:PRO:CD	2.79	0.46
1:A:222:ARG:HH11	5:A:507:EDO:H22	1.81	0.46
1:B:220:ARG:NH1	8:B:604:HOH:O	2.49	0.45
1:A:198:PRO:CD	5:A:506:EDO:H12	2.47	0.45
1:B:135[A]:THR:HG21	7:B:507:PEG:C4	2.47	0.45
1:A:280:MET:CE	1:A:317:VAL:HG21	2.47	0.44
1:B:168:VAL:HG13	1:B:172:LEU:HD12	1.99	0.44
1:B:280:MET:CE	1:B:317:VAL:HG21	2.48	0.44
1:B:33:LEU:HD21	1:B:47:PRO:CG	2.48	0.44
1:A:375:ARG:NH1	1:A:400:ALA:HA	2.32	0.44
5:A:505:EDO:H22	1:B:91:ALA:HB1	2.00	0.43
1:A:33:LEU:HD11	1:A:47:PRO:HB2	2.01	0.43
1:A:135[A]:THR:HG22	1:A:178:TRP:HE1	1.83	0.43
1:B:129:PRO:HB2	1:B:133:VAL:CG2	2.49	0.43
1:B:280:MET:HE1	1:B:317:VAL:HG21	2.01	0.43
1:B:338:ARG:NH2	1:B:389:GLU:OE1	2.52	0.42
1:A:372:GLU:OE2	1:A:373:PRO:HA	2.18	0.42
1:B:93:GLU:HG2	8:B:714:HOH:O	2.19	0.42
1:B:257:ALA:HB1	5:B:505:EDO:H11	2.01	0.42
1:A:185:THR:HG23	1:A:223:LEU:CD2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:GLN:NE2	8:B:608:HOH:O	2.53	0.41
1:B:263:GLU:OE2	1:B:294:ARG:HD3	2.21	0.41
1:A:206:ARG:O	1:A:231:PRO:HD2	2.20	0.41
1:B:322:ARG:NH1	4:B:503:ANP:O1B	2.53	0.41
1:B:277:ARG:NH2	1:B:320:LEU:CD1	2.83	0.41
1:A:167:ARG:O	1:A:171[B]:THR:HG22	2.21	0.41
1:A:100:THR:HG23	1:A:289:ALA:HB2	2.03	0.40
1:B:244:ILE:HB	1:B:262:PHE:CE1	2.56	0.40
1:A:263:GLU:OE2	1:A:294:ARG:HD3	2.22	0.40
1:A:357:ALA:HA	1:A:365:GLU:O	2.22	0.40
1:A:342:LEU:HD13	1:A:386:LEU:HD12	2.03	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	437/437 (100%)	422 (97%)	15 (3%)	0	100	100
1	B	440/437 (101%)	421 (96%)	17 (4%)	2 (0%)	29	14
All	All	877/874 (100%)	843 (96%)	32 (4%)	2 (0%)	47	32

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	327	HIS
1	B	43	ARG

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	353/350 (101%)	350 (99%)	3 (1%)	81	76
1	B	355/350 (101%)	353 (99%)	2 (1%)	86	82
All	All	708/700 (101%)	703 (99%)	5 (1%)	84	79

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	ARG
1	A	320	LEU
1	A	429	TRP
1	B	4	SER
1	B	429	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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
4	ANP	B	503	-	29,33,33	1.27	4 (13%)	31,52,52	1.32	4 (12%)
3	3HA	B	502	-	10,11,11	1.25	1 (10%)	14,15,15	1.16	0
5	EDO	B	506	-	3,3,3	0.07	0	2,2,2	0.16	0
7	PEG	B	507	-	6,6,6	0.16	0	5,5,5	0.27	0
5	EDO	A	506	-	3,3,3	0.20	0	2,2,2	0.47	0
5	EDO	B	505	-	3,3,3	0.16	0	2,2,2	0.18	0
5	EDO	A	504	-	3,3,3	0.28	0	2,2,2	0.29	0
5	EDO	A	507	-	3,3,3	0.41	0	2,2,2	0.51	0
4	ANP	A	503	6	29,33,33	1.33	4 (13%)	31,52,52	1.30	3 (9%)
5	EDO	B	504	-	3,3,3	0.08	0	2,2,2	0.22	0
3	3HA	A	502	-	10,11,11	1.15	1 (10%)	14,15,15	1.82	2 (14%)
5	EDO	A	505	-	3,3,3	0.12	0	2,2,2	0.60	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ANP	B	503	-	-	5/14/38/38	0/3/3/3
3	3HA	B	502	-	-	0/4/4/4	0/1/1/1
5	EDO	B	506	-	-	0/1/1/1	-
7	PEG	B	507	-	-	2/4/4/4	-
5	EDO	A	506	-	-	1/1/1/1	-
5	EDO	B	505	-	-	0/1/1/1	-
5	EDO	A	504	-	-	0/1/1/1	-
5	EDO	A	507	-	-	0/1/1/1	-
4	ANP	A	503	6	-	4/14/38/38	0/3/3/3
5	EDO	B	504	-	-	1/1/1/1	-
3	3HA	A	502	-	-	1/4/4/4	0/1/1/1
5	EDO	A	505	-	-	1/1/1/1	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	503	ANP	PG-O1G	3.76	1.52	1.46
4	B	503	ANP	PG-O1G	3.72	1.52	1.46
4	A	503	ANP	PB-O1B	3.47	1.51	1.46
4	B	503	ANP	PB-O1B	3.12	1.51	1.46
3	B	502	3HA	C2-C3	2.93	1.47	1.42
3	A	502	3HA	C2-C3	2.78	1.47	1.42
4	B	503	ANP	PG-O2G	-2.30	1.50	1.56
4	A	503	ANP	PB-O3A	2.24	1.61	1.59
4	B	503	ANP	PB-O2B	-2.15	1.51	1.56
4	A	503	ANP	PB-O2B	-2.05	1.51	1.56

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	3HA	C3-C2-C7	-5.93	116.89	120.90
4	A	503	ANP	O2B-PB-O1B	4.44	119.23	109.92
4	B	503	ANP	O2B-PB-O1B	4.26	118.86	109.92
4	B	503	ANP	O3G-PG-O1G	-2.85	106.29	113.45
4	B	503	ANP	C5-C6-N6	2.74	124.52	120.35
4	A	503	ANP	C5-C6-N6	2.66	124.39	120.35
4	A	503	ANP	O1G-PG-N3B	-2.63	107.89	111.77
4	B	503	ANP	O1B-PB-N3B	-2.46	108.15	111.77
3	A	502	3HA	C1-C2-C7	2.08	123.41	118.63

There are no chirality outliers.

All (15) torsion outliers are listed below:

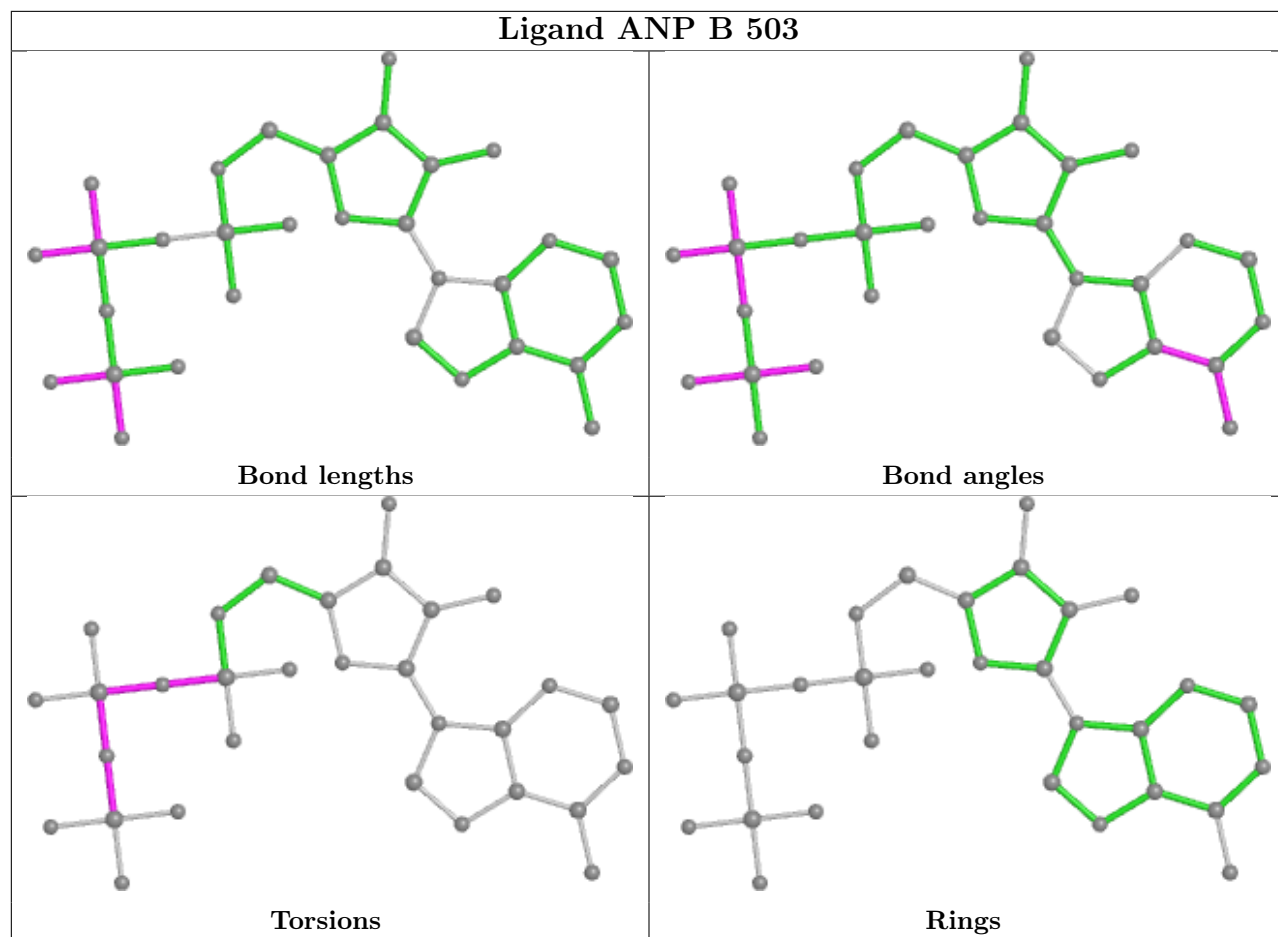
Mol	Chain	Res	Type	Atoms
4	A	503	ANP	PB-N3B-PG-O1G
4	A	503	ANP	PA-O3A-PB-O1B
4	A	503	ANP	PA-O3A-PB-O2B
4	A	503	ANP	PB-O3A-PA-O5'
4	B	503	ANP	PB-N3B-PG-O1G
4	B	503	ANP	PA-O3A-PB-O1B
4	B	503	ANP	PA-O3A-PB-O2B
5	A	506	EDO	O1-C1-C2-O2
5	B	504	EDO	O1-C1-C2-O2
7	B	507	PEG	O1-C1-C2-O2
4	B	503	ANP	PB-O3A-PA-O5'
7	B	507	PEG	C1-C2-O2-C3
4	B	503	ANP	PG-N3B-PB-O3A
5	A	505	EDO	O1-C1-C2-O2
3	A	502	3HA	C3-C2-C7-O9

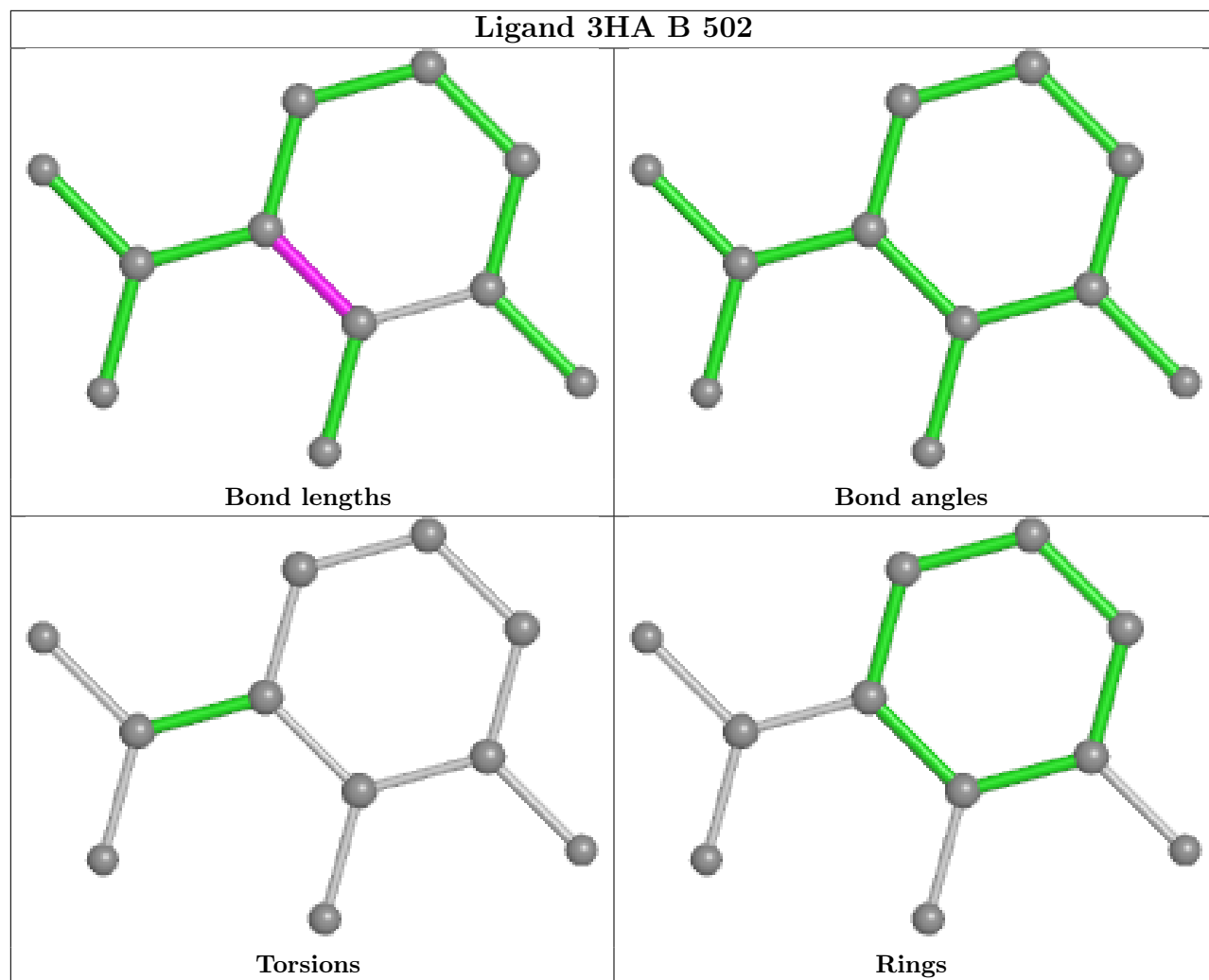
There are no ring outliers.

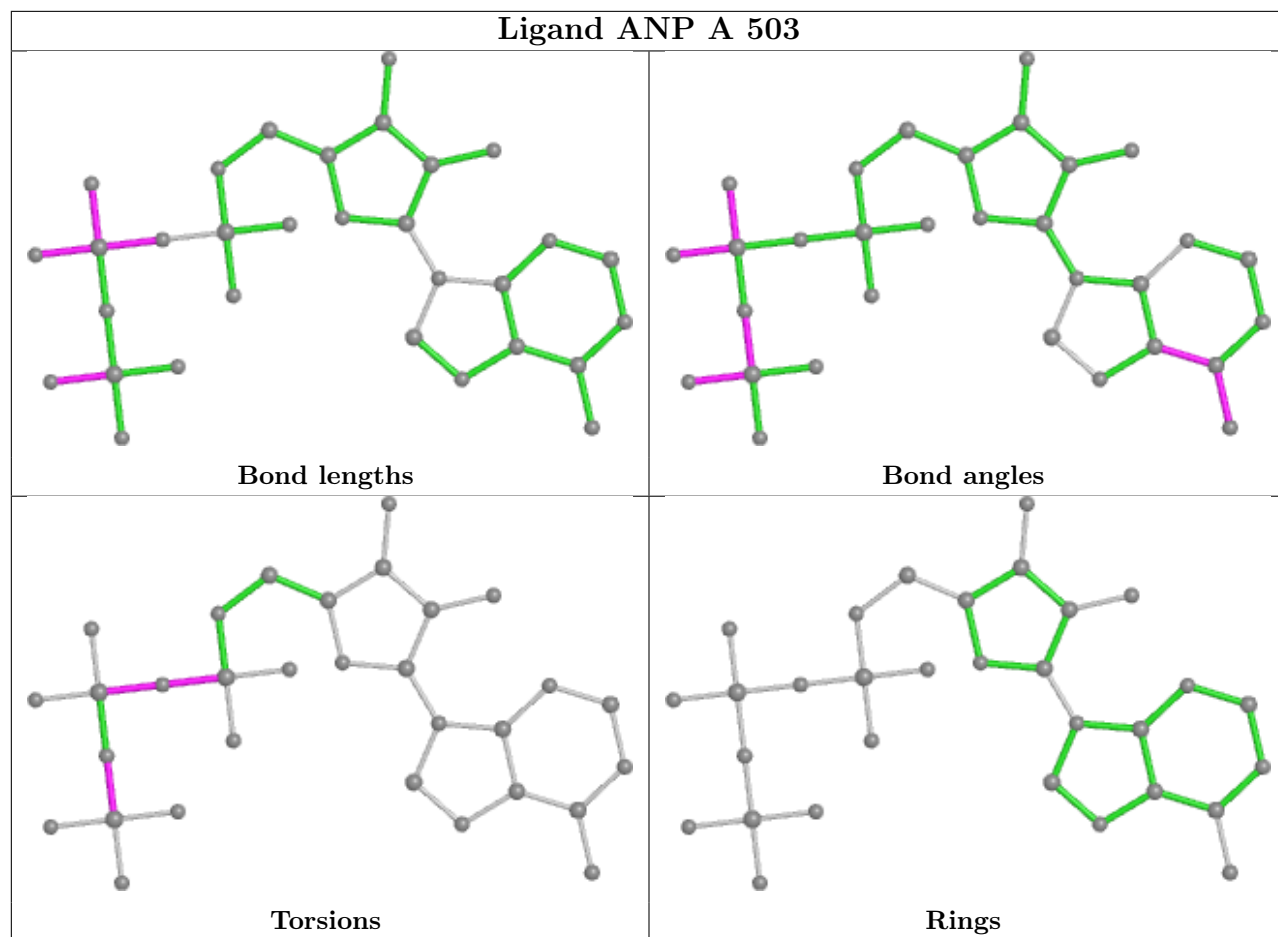
7 monomers are involved in 30 short contacts:

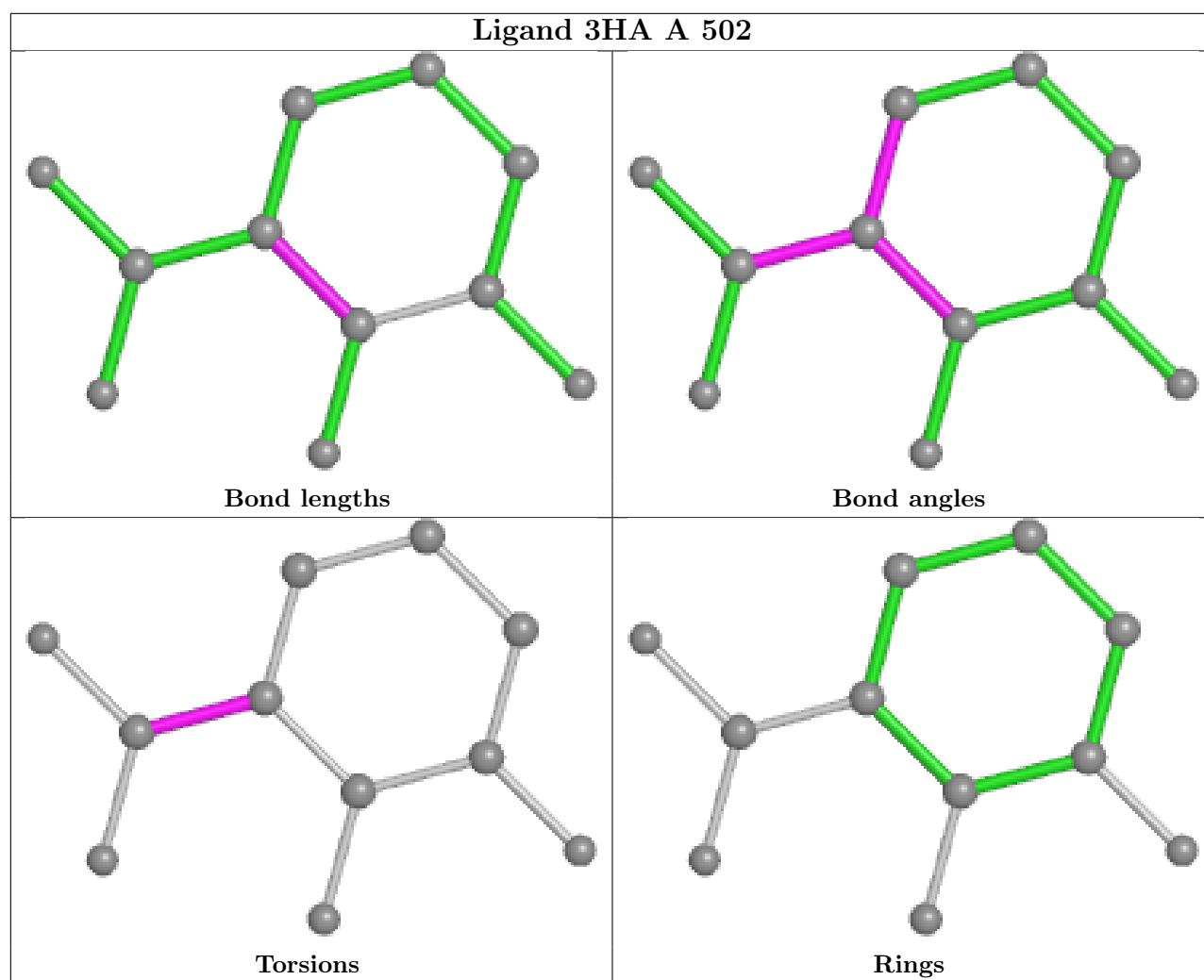
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	503	ANP	2	0
7	B	507	PEG	11	0
5	A	506	EDO	4	0
5	B	505	EDO	2	0
5	A	504	EDO	3	0
5	A	507	EDO	5	0
5	A	505	EDO	4	0

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	433/437 (99%)	0.86	47 (10%) 5 5	28, 51, 82, 113	0
1	B	437/437 (100%)	0.84	54 (12%) 4 3	30, 48, 80, 117	0
All	All	870/874 (99%)	0.85	101 (11%) 4 4	28, 49, 82, 117	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	331	PRO	9.9
1	B	326	GLY	9.8
1	B	325	THR	6.2
1	B	323	ALA	5.8
1	A	44	GLY	5.0
1	B	268	ARG	5.0
1	B	45	THR	4.7
1	B	46	THR	4.7
1	B	361	PRO	4.4
1	B	54	PHE	4.4
1	B	324	GLY	4.3
1	A	310	CYS	4.2
1	A	268	ARG	4.1
1	A	11	TRP	3.9
1	A	330	GLY	3.9
1	A	324	GLY	3.9
1	A	33	LEU	3.8
1	A	274	GLU	3.7
1	A	34	ARG	3.6
1	A	311	GLY	3.6
1	B	155	ALA	3.6
1	A	329	ILE	3.6
1	A	328	ARG	3.5
1	B	426	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	362	ASP	3.4
1	B	43	ARG	3.4
1	B	132	LEU	3.3
1	B	134	ILE	3.3
1	A	46	THR	3.3
1	A	426	ASP	3.3
1	A	312	TRP	3.2
1	A	331	PRO	3.2
1	A	308	CYS	3.2
1	A	322	ARG	3.2
1	A	56	GLY	3.2
1	B	56	GLY	3.2
1	A	49	ARG	3.1
1	B	126	VAL	3.1
1	B	332	ALA	3.0
1	A	47	PRO	3.0
1	B	329	ILE	2.9
1	A	323	ALA	2.9
1	B	386	LEU	2.9
1	B	269	THR	2.9
1	B	212	ALA	2.8
1	B	44	GLY	2.8
1	B	125	LEU	2.8
1	A	326	GLY	2.8
1	B	42	TYR	2.7
1	B	130	TYR	2.7
1	A	12	SER	2.7
1	A	276	GLY	2.7
1	B	49	ARG	2.7
1	A	132	LEU	2.7
1	A	305	THR	2.6
1	B	124	PHE	2.6
1	B	135[A]	THR	2.5
1	A	26	PRO	2.5
1	B	47	PRO	2.5
1	B	150	VAL	2.5
1	A	54	PHE	2.4
1	A	361	PRO	2.4
1	A	363	VAL	2.4
1	B	0	ALA	2.4
1	A	30	ALA	2.4
1	B	52	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	155	ALA	2.4
1	B	26	PRO	2.4
1	A	19	GLU	2.4
1	B	322	ARG	2.3
1	A	8	LEU	2.3
1	A	309	GLY	2.3
1	B	133	VAL	2.3
1	B	111	PHE	2.3
1	B	142	ALA	2.3
1	A	126	VAL	2.3
1	A	17	LEU	2.3
1	A	151	VAL	2.3
1	B	178	TRP	2.3
1	A	395	ARG	2.3
1	B	152	PRO	2.3
1	A	307	PRO	2.2
1	B	392	VAL	2.2
1	B	200	GLN	2.2
1	A	433[A]	VAL	2.2
1	A	51	ALA	2.2
1	B	129	PRO	2.2
1	B	138	LEU	2.1
1	B	128	THR	2.1
1	B	211	ALA	2.1
1	A	306	ASP	2.1
1	B	363	VAL	2.1
1	B	90	THR	2.1
1	B	57	VAL	2.1
1	A	179	CYS	2.1
1	B	36	PRO	2.0
1	B	209	PHE	2.0
1	A	313	LEU	2.0
1	B	221	ARG	2.0
1	A	174	VAL	2.0
1	B	33	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 [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

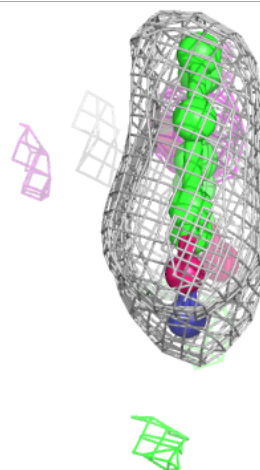
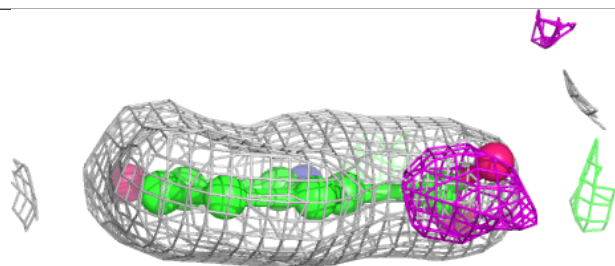
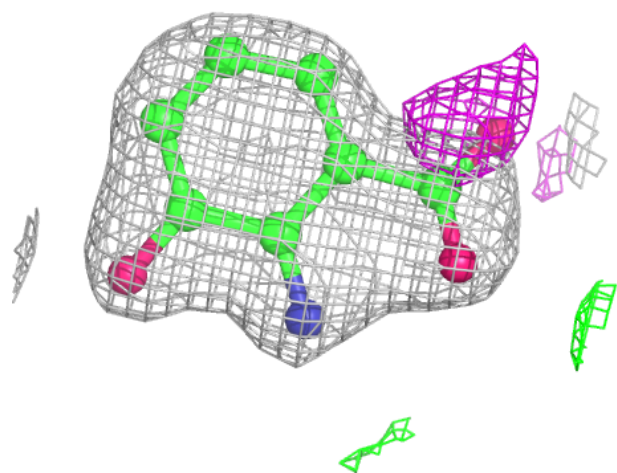
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	B	506	4/4	0.82	0.26	77,79,79,81	0
6	MG	A	510	1/1	0.83	0.19	73,73,73,73	0
6	MG	A	509	1/1	0.86	0.23	40,40,40,40	0
3	3HA	A	502	11/11	0.87	0.15	54,56,59,68	0
6	MG	B	508	1/1	0.89	0.14	61,61,61,61	0
3	3HA	B	502	11/11	0.91	0.16	41,44,48,51	0
4	ANP	A	503	31/31	0.91	0.11	43,48,71,73	0
5	EDO	A	505	4/4	0.91	0.27	43,64,66,81	0
5	EDO	B	504	4/4	0.91	0.41	57,58,59,60	0
7	PEG	B	507	7/7	0.91	0.15	37,41,54,60	0
6	MG	A	508	1/1	0.93	0.18	48,48,48,48	0
4	ANP	B	503	31/31	0.95	0.11	31,36,60,66	0
5	EDO	A	504	4/4	0.96	0.38	41,44,46,46	0
5	EDO	B	505	4/4	0.96	0.29	51,52,53,54	0
5	EDO	A	506	4/4	0.97	0.22	37,42,44,46	0
5	EDO	A	507	4/4	0.97	0.24	40,44,46,46	0
2	ZN	A	501	1/1	0.98	0.03	59,59,59,59	0
2	ZN	B	501	1/1	0.99	0.07	49,49,49,49	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.

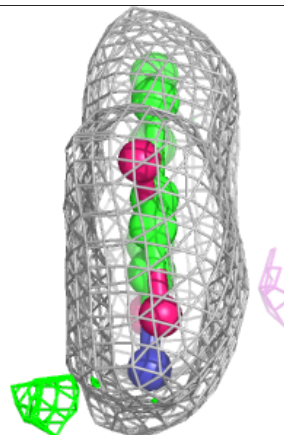
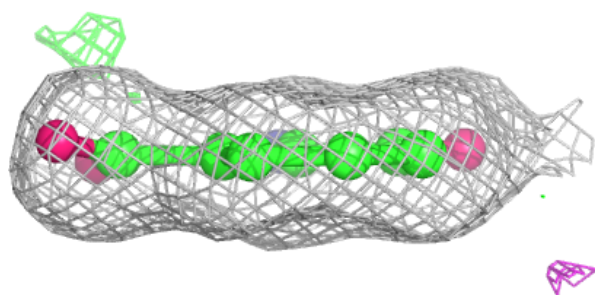
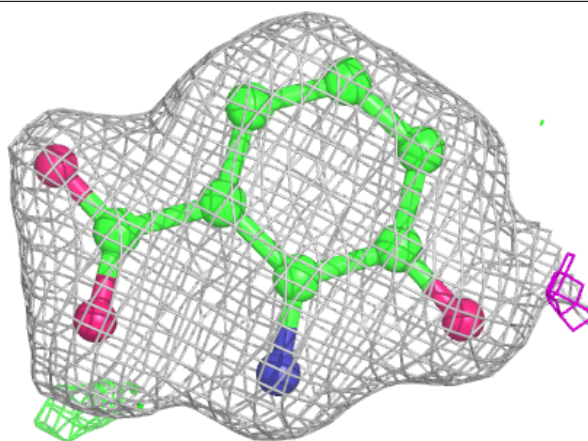
Electron density around 3HA A 502:

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

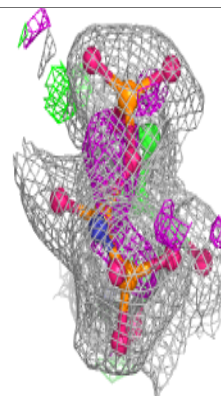
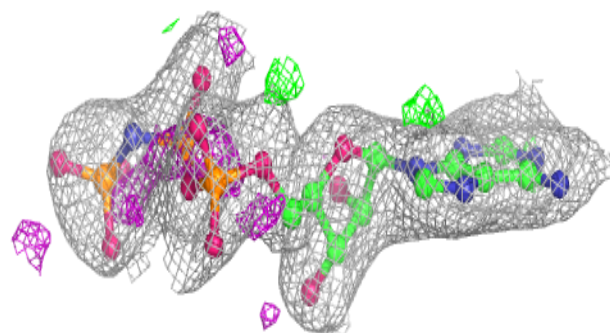
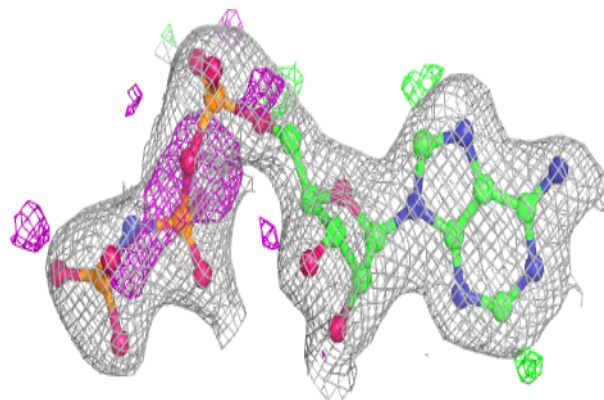


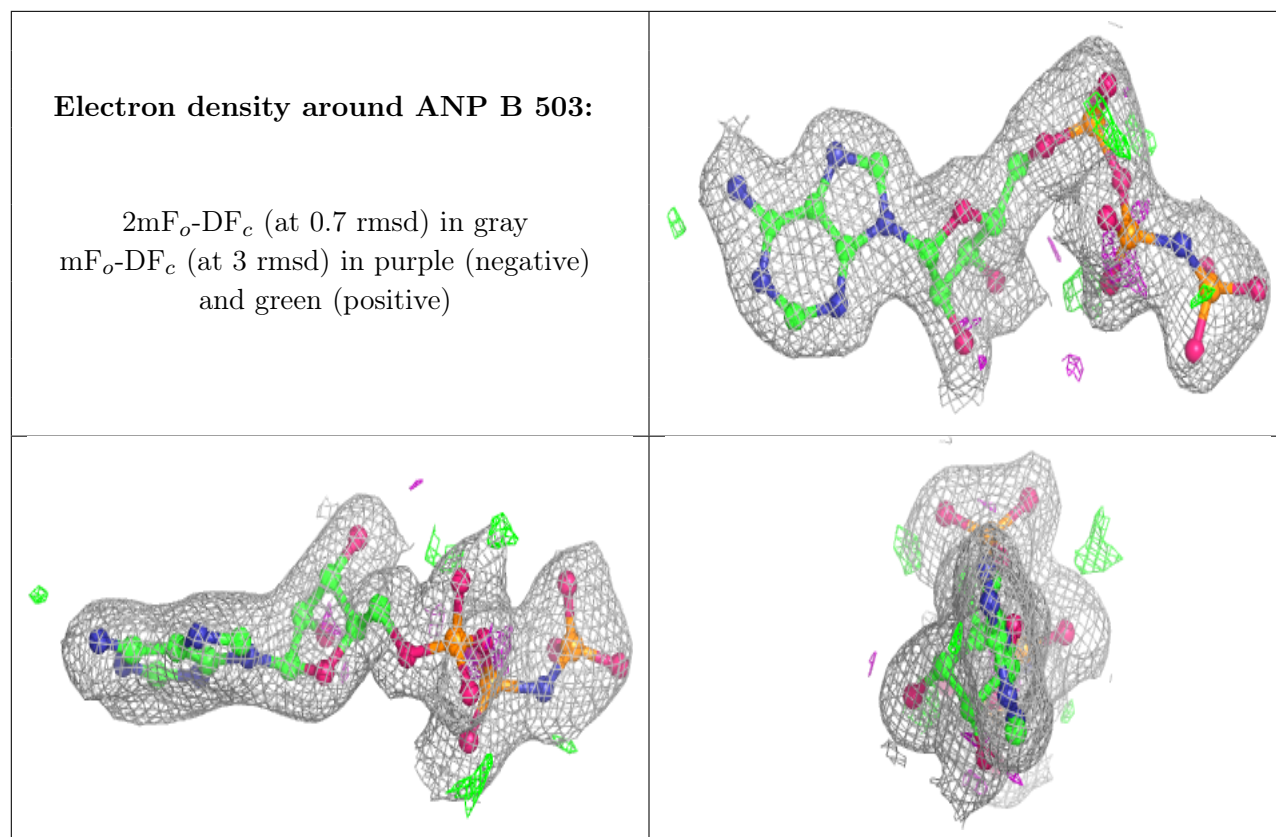
Electron density around 3HA B 502:

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

**Electron density around ANP A 503:**

$2mF_o-DF_c$ (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.