



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 11:22 am BST

PDB ID : 5X9W
Title : Mismatch Repair Protein
Authors : Nair, D.T.; Nirwal, S.
Deposited on : 2017-03-10
Resolution : 3.30 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 : 2.11
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) : 2.11

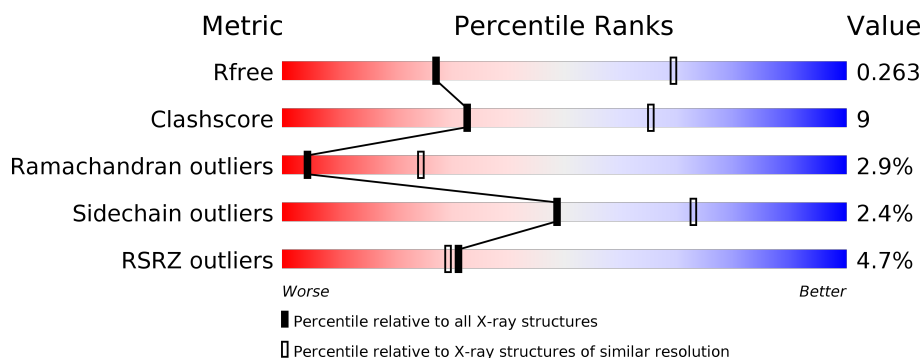
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	816	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>• 6%</div> </div> </div>
1	B	816	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>18%</div> <div>• 6%</div> </div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 11874 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.

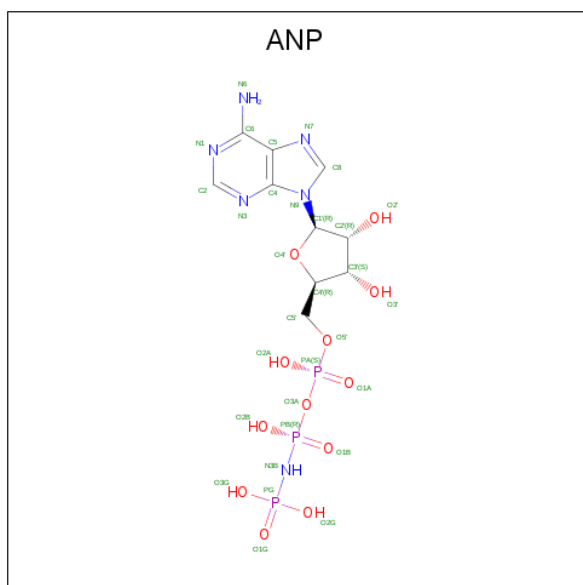
- Molecule 1 is a protein called DNA mismatch repair protein MutS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	771	Total	C	N	O	S	0	0	0
			5906	3733	1046	1107	20			
1	B	771	Total	C	N	O	S	0	0	0
			5906	3733	1046	1107	20			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLN	-	expression tag	UNP Q5F5J4
A	0	SER	-	expression tag	UNP Q5F5J4
B	-1	GLN	-	expression tag	UNP Q5F5J4
B	0	SER	-	expression tag	UNP Q5F5J4

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).

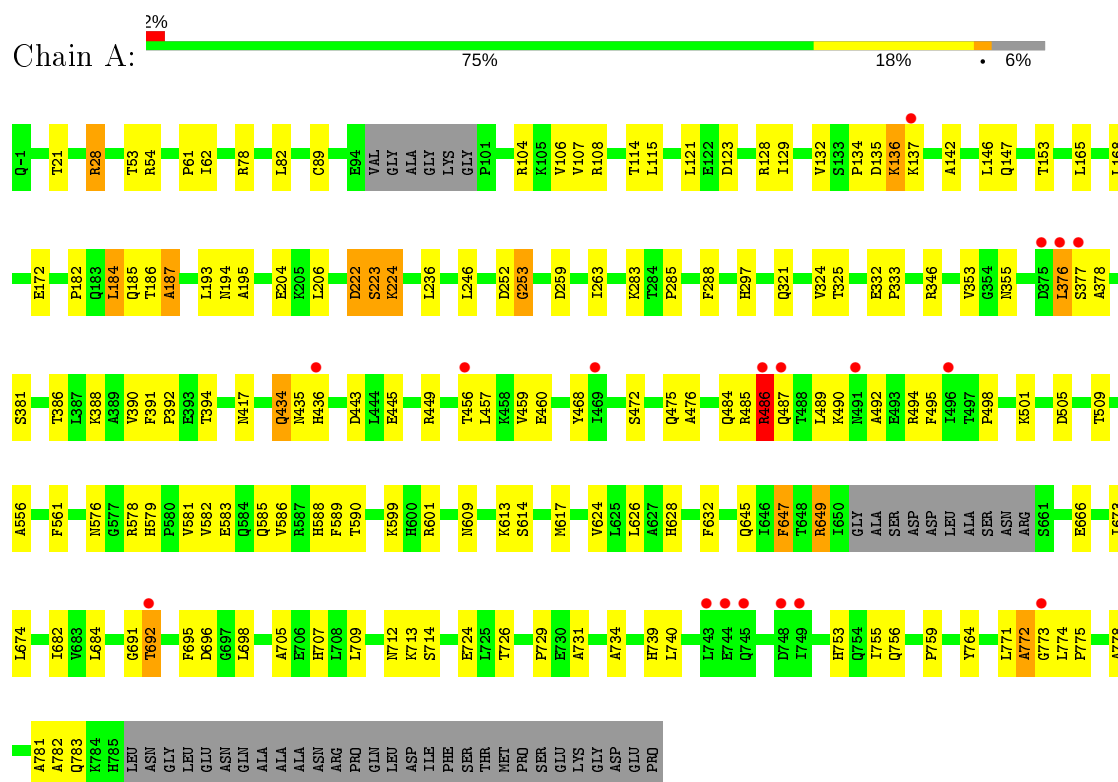


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

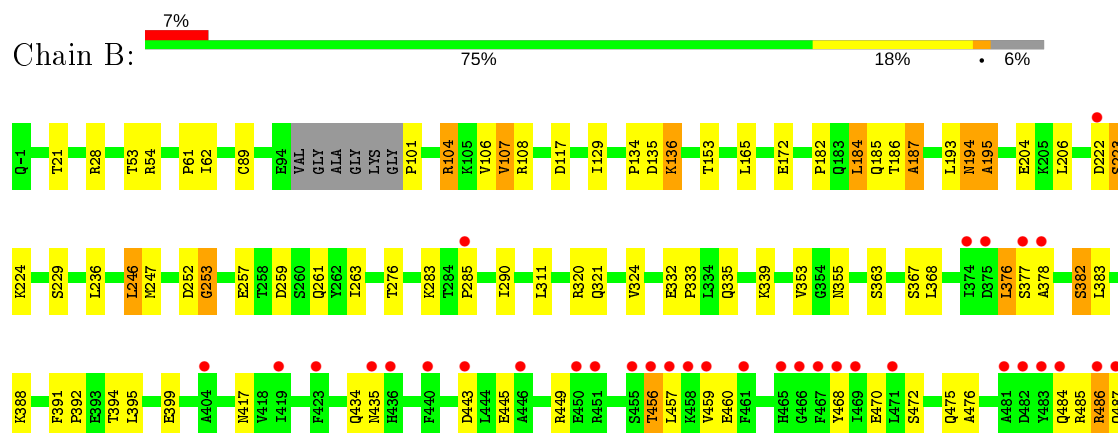
3 Residue-property plots

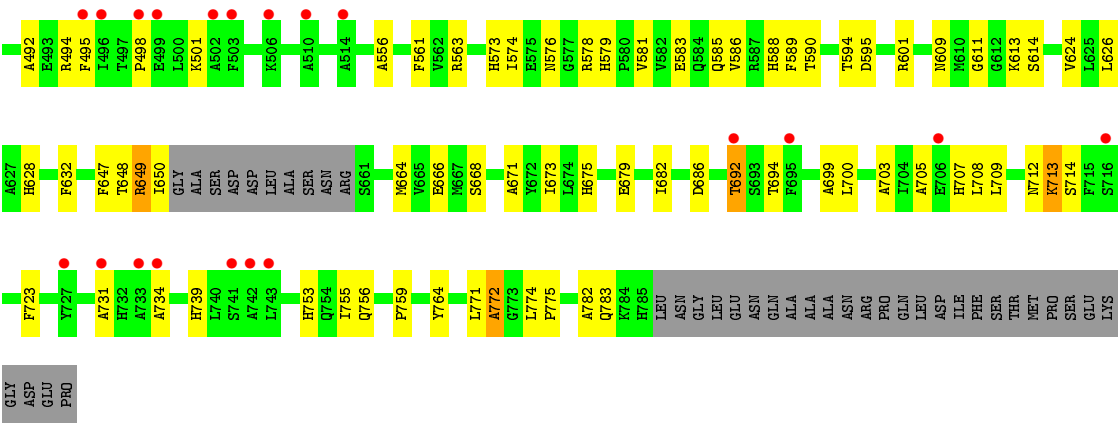
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 mismatch repair protein MutS



• Molecule 1: DNA mismatch repair protein MutS





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	89.51Å 102.07Å 235.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.93 – 3.30 49.88 – 3.30	Depositor EDS
% Data completeness (in resolution range)	97.3 (49.93-3.30) 97.4 (49.88-3.30)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 3.33Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.221 , 0.273 0.218 , 0.263	Depositor DCC
R_{free} test set	1646 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	86.5	Xtriage
Anisotropy	0.441	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 59.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11874	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.90% 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	0.61	1/6015 (0.0%)	0.71	1/8154 (0.0%)
1	B	0.46	0/6015	0.61	1/8154 (0.0%)
All	All	0.54	1/12030 (0.0%)	0.66	2/16308 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	773	GLY	CA-C	5.28	1.60	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	775	PRO	N-CA-CB	6.27	110.82	103.30
1	B	775	PRO	N-CA-CB	6.24	110.78	103.30

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	5906	0	5861	111	0
1	B	5906	0	5861	110	0
2	A	31	0	13	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	31	0	13	8	0
All	All	11874	0	11748	206	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 9.

All (206) 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:614:SER:OG	2:A:901:ANP:O3G	1.81	0.98
1:A:186:THR:HA	1:A:187:ALA:CB	2.06	0.85
1:B:186:THR:HA	1:B:187:ALA:CB	2.07	0.84
1:A:376:LEU:O	1:A:378:ALA:N	2.11	0.83
1:A:772:ALA:CB	1:B:675:HIS:CE1	2.62	0.83
1:A:696:ASP:HB2	1:B:764:TYR:CB	2.11	0.81
1:B:376:LEU:O	1:B:378:ALA:N	2.14	0.80
1:A:764:TYR:CB	1:B:692:THR:HG21	2.13	0.78
1:B:134:PRO:HG3	1:B:182:PRO:HD3	1.67	0.76
1:B:186:THR:HA	1:B:187:ALA:HB2	1.68	0.76
1:A:186:THR:HA	1:A:187:ALA:HB2	1.65	0.75
1:A:332:GLU:HG2	1:A:333:PRO:HD3	1.69	0.74
1:A:772:ALA:HB1	1:B:675:HIS:ND1	2.02	0.74
1:A:647:PHE:HD2	1:A:673:ILE:HG12	1.52	0.74
1:B:106:VAL:O	1:B:108:ARG:N	2.21	0.71
1:B:611:GLY:O	2:B:901:ANP:O1B	2.07	0.71
1:B:332:GLU:HG2	1:B:333:PRO:HD3	1.72	0.71
1:A:772:ALA:HB2	1:B:675:HIS:CE1	2.27	0.69
1:A:486:ARG:HG2	1:A:487:GLN:H	1.57	0.69
1:A:28:ARG:O	1:A:104:ARG:NH2	2.26	0.69
1:B:486:ARG:HG2	1:B:487:GLN:H	1.58	0.68
1:B:609:ASN:O	2:B:901:ANP:O2B	2.10	0.68
1:A:468:TYR:CE1	1:A:494:ARG:HD3	2.29	0.67
1:B:753:HIS:ND1	2:B:901:ANP:N3	2.42	0.67
1:A:772:ALA:HB1	1:B:675:HIS:CE1	2.28	0.67
1:A:134:PRO:HG3	1:A:182:PRO:HD3	1.75	0.67
1:B:712:ASN:O	1:B:714:SER:N	2.28	0.66
1:B:614:SER:OG	2:B:901:ANP:PG	2.54	0.65
1:A:391:PHE:O	1:A:394:THR:HG22	1.97	0.64
1:A:252:ASP:O	1:A:253:GLY:O	2.17	0.63
1:A:434:GLN:HG3	1:A:435:ASN:N	2.13	0.62
1:B:186:THR:CA	1:B:187:ALA:HB2	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:186:THR:CA	1:B:187:ALA:CB	2.78	0.61
1:A:106:VAL:O	1:A:108:ARG:N	2.29	0.61
1:A:186:THR:CA	1:A:187:ALA:HB2	2.31	0.61
1:B:460:GLU:HB2	1:B:468:TYR:CE1	2.37	0.60
1:A:609:ASN:O	2:A:901:ANP:O1B	2.20	0.60
1:B:89:CYS:SG	1:B:104:ARG:HG3	2.41	0.60
1:A:613:LYS:HB2	2:A:901:ANP:O2B	2.02	0.60
1:A:771:LEU:HA	1:B:671:ALA:HB2	1.83	0.59
1:A:186:THR:CA	1:A:187:ALA:CB	2.79	0.59
1:B:186:THR:HA	1:B:187:ALA:HB3	1.85	0.59
1:A:712:ASN:O	1:A:714:SER:N	2.37	0.58
1:A:647:PHE:CD2	1:A:673:ILE:HG12	2.36	0.58
1:B:185:GLN:HG2	1:B:187:ALA:HB2	1.86	0.57
1:A:724:GLU:OE1	1:B:694:THR:OG1	2.20	0.57
1:A:460:GLU:HB2	1:A:468:TYR:CE1	2.39	0.57
1:B:193:LEU:O	1:B:194:ASN:C	2.43	0.57
1:A:649:ARG:HE	1:A:666:GLU:HG2	1.70	0.57
1:A:498:PRO:HA	1:A:501:LYS:HB2	1.87	0.57
1:B:391:PHE:O	1:B:394:THR:HG22	2.04	0.57
1:B:434:GLN:HG3	1:B:435:ASN:N	2.20	0.57
1:A:617:MET:HB3	1:A:684:LEU:HD23	1.86	0.56
1:B:586:VAL:HG21	1:B:589:PHE:HB2	1.87	0.56
1:A:434:GLN:HG3	1:A:435:ASN:H	1.70	0.56
1:B:614:SER:OG	2:B:901:ANP:O2G	2.24	0.56
1:A:78:ARG:O	1:A:82:LEU:HG	2.05	0.56
1:B:614:SER:OG	2:B:901:ANP:O1G	2.23	0.56
1:A:457:LEU:HD12	1:A:457:LEU:O	2.06	0.56
1:A:472:SER:O	1:A:476:ALA:N	2.38	0.56
1:A:53:THR:HG21	1:A:61:PRO:HB3	1.87	0.56
1:B:445:GLU:O	1:B:449:ARG:HG2	2.06	0.56
1:B:556:ALA:HA	1:B:561:PHE:HB2	1.86	0.55
1:A:186:THR:HA	1:A:187:ALA:HB3	1.88	0.55
1:B:353:VAL:HG23	1:B:355:ASN:HB2	1.87	0.55
1:A:472:SER:HA	1:A:492:ALA:HA	1.89	0.55
1:A:614:SER:CB	2:A:901:ANP:O3G	2.56	0.54
1:B:579:HIS:O	1:B:583:GLU:HB2	2.07	0.54
1:A:586:VAL:HG21	1:A:589:PHE:HB2	1.89	0.54
1:A:321:GLN:HA	1:A:324:VAL:HG12	1.89	0.53
1:A:556:ALA:HA	1:A:561:PHE:HB2	1.90	0.53
1:A:486:ARG:CG	1:A:487:GLN:H	2.21	0.53
1:A:696:ASP:CB	1:B:764:TYR:CB	2.86	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:GLN:HG2	1:A:187:ALA:HB2	1.91	0.53
1:A:89:CYS:SG	1:A:104:ARG:HG3	2.49	0.53
1:B:581:VAL:HG12	1:B:585:GLN:NE2	2.24	0.52
1:B:590:THR:OG1	1:B:753:HIS:O	2.27	0.52
1:B:782:ALA:HA	1:B:783:GLN:C	2.30	0.52
1:A:445:GLU:O	1:A:449:ARG:HG2	2.11	0.51
1:B:601:ARG:HB2	1:B:734:ALA:HB1	1.93	0.51
1:A:578:ARG:NE	1:A:583:GLU:OE2	2.44	0.51
1:B:193:LEU:O	1:B:195:ALA:N	2.44	0.51
1:B:498:PRO:HA	1:B:501:LYS:HB2	1.92	0.51
1:B:28:ARG:O	1:B:104:ARG:NH2	2.42	0.51
1:B:624:VAL:HG11	1:B:682:ILE:HD12	1.93	0.50
1:A:586:VAL:O	1:A:588:HIS:N	2.44	0.50
1:B:129:ILE:HD12	1:B:172:GLU:HB3	1.93	0.50
1:B:485:ARG:HA	1:B:495:PHE:HA	1.93	0.50
1:B:204:GLU:OE2	1:B:223:SER:OG	2.29	0.49
1:A:54:ARG:O	1:A:62:ILE:HB	2.12	0.49
1:B:368:LEU:HD22	1:B:394:THR:HG21	1.95	0.49
1:A:193:LEU:O	1:A:194:ASN:C	2.50	0.49
1:B:609:ASN:O	2:B:901:ANP:PB	2.70	0.49
1:B:391:PHE:HB2	1:B:392:PRO:HD3	1.95	0.49
1:B:468:TYR:CE1	1:B:494:ARG:HD3	2.48	0.48
1:A:391:PHE:HB2	1:A:392:PRO:HD3	1.94	0.48
1:B:472:SER:HA	1:B:492:ALA:HA	1.95	0.48
1:B:573:HIS:ND1	1:B:595:ASP:OD1	2.45	0.48
1:A:581:VAL:HG12	1:A:585:GLN:NE2	2.28	0.48
1:B:434:GLN:HG3	1:B:435:ASN:H	1.77	0.48
1:A:456:THR:CG2	1:A:475:GLN:HE22	2.26	0.48
1:B:486:ARG:CG	1:B:487:GLN:H	2.24	0.48
1:B:117:ASP:OD1	1:B:355:ASN:ND2	2.47	0.48
1:A:624:VAL:HG11	1:A:682:ILE:HD12	1.95	0.47
1:B:649:ARG:HE	1:B:666:GLU:HG2	1.79	0.47
1:A:645:GLN:HB2	1:A:647:PHE:HE1	1.79	0.47
1:B:472:SER:O	1:B:476:ALA:N	2.48	0.47
1:B:563:ARG:HB2	1:B:632:PHE:CZ	2.49	0.47
1:B:470:GLU:HA	1:B:494:ARG:HA	1.97	0.47
1:B:263:ILE:HD11	1:B:628:HIS:CD2	2.50	0.47
1:A:485:ARG:HA	1:A:495:PHE:HA	1.97	0.47
1:B:586:VAL:O	1:B:588:HIS:N	2.45	0.46
1:B:311:LEU:HD11	1:B:320:ARG:CZ	2.46	0.46
1:A:129:ILE:HG23	1:A:236:LEU:HD11	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:ARG:HG2	1:A:487:GLN:N	2.27	0.46
1:A:778:ALA:O	1:B:699:ALA:HB1	2.15	0.46
1:B:276:THR:O	1:B:283:LYS:NZ	2.47	0.46
1:A:674:LEU:O	1:A:712:ASN:ND2	2.49	0.46
1:A:263:ILE:HD11	1:A:628:HIS:CD2	2.52	0.45
1:A:705:ALA:O	1:A:709:LEU:HD12	2.16	0.45
1:A:691:GLY:C	1:A:692:THR:HG1	2.19	0.45
1:A:698:LEU:HD22	1:A:698:LEU:O	2.16	0.45
1:B:53:THR:HG21	1:B:61:PRO:HB3	1.99	0.45
1:A:132:VAL:HG23	1:A:132:VAL:O	2.17	0.45
1:A:505:ASP:O	1:A:509:THR:OG1	2.19	0.45
1:B:153:THR:OG1	1:B:229:SER:HB2	2.16	0.45
1:B:363:SER:O	1:B:367:SER:OG	2.30	0.45
1:A:114:THR:HB	1:A:146:LEU:HD12	1.99	0.45
1:A:435:ASN:OD1	1:A:436:HIS:N	2.50	0.45
1:B:574:ILE:HB	1:B:594:THR:HB	1.98	0.44
1:B:650:ILE:HA	1:B:686:ASP:HB3	1.99	0.44
1:A:194:ASN:CG	1:A:194:ASN:O	2.55	0.44
1:A:674:LEU:HD23	1:A:674:LEU:HA	1.85	0.44
1:B:335:GLN:O	1:B:339:LYS:HB2	2.18	0.44
1:B:755:ILE:HD12	1:B:755:ILE:O	2.17	0.44
1:A:726:THR:O	1:A:729:PRO:HD2	2.17	0.44
1:B:578:ARG:NE	1:B:583:GLU:OE2	2.51	0.44
1:A:129:ILE:HD12	1:A:172:GLU:HB3	1.98	0.44
1:B:252:ASP:O	1:B:253:GLY:O	2.36	0.44
1:A:579:HIS:O	1:A:583:GLU:HB2	2.18	0.44
1:A:755:ILE:O	1:A:755:ILE:HD12	2.18	0.44
1:A:579:HIS:ND1	1:A:582:VAL:HG23	2.33	0.43
1:A:649:ARG:NE	1:A:666:GLU:HG2	2.32	0.43
1:A:781:ALA:HB3	1:B:699:ALA:HA	2.00	0.43
1:B:708:LEU:HA	1:B:712:ASN:OD1	2.18	0.43
1:A:386:THR:O	1:A:390:VAL:HG23	2.18	0.43
1:A:128:ARG:NH1	1:A:168:LEU:O	2.47	0.43
1:B:648:THR:HB	1:B:650:ILE:CD1	2.48	0.43
1:A:132:VAL:CG2	1:A:132:VAL:O	2.66	0.43
1:A:184:LEU:HD23	1:A:185:GLN:O	2.18	0.43
1:A:782:ALA:HA	1:A:783:GLN:C	2.39	0.43
1:A:115:LEU:HB2	1:A:121:LEU:HD21	2.01	0.43
1:A:445:GLU:HG3	1:A:459:VAL:HG23	2.00	0.43
1:B:321:GLN:HA	1:B:324:VAL:HG12	2.01	0.43
1:B:486:ARG:NH2	1:B:494:ARG:HD2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:764:TYR:CA	1:B:692:THR:HG21	2.48	0.43
1:B:382:SER:OG	1:B:383:LEU:N	2.50	0.43
1:B:54:ARG:O	1:B:62:ILE:HB	2.18	0.43
1:A:778:ALA:CB	1:B:700:LEU:HD23	2.48	0.43
1:A:484:GLN:O	1:A:485:ARG:HB3	2.19	0.43
1:B:129:ILE:HG23	1:B:236:LEU:HD11	2.00	0.43
1:A:147:GLN:OE1	1:A:346:ARG:NE	2.50	0.43
1:A:489:LEU:HB3	1:A:490:LYS:H	1.72	0.42
1:B:614:SER:HB2	2:B:901:ANP:N3B	2.34	0.42
1:B:290:ILE:HA	1:B:290:ILE:HD13	1.89	0.42
1:B:679:GLU:HA	1:B:713:LYS:O	2.20	0.42
1:B:184:LEU:HD23	1:B:185:GLN:O	2.19	0.42
1:B:486:ARG:HG2	1:B:487:GLN:N	2.29	0.42
1:B:648:THR:HB	1:B:650:ILE:HD11	2.01	0.42
1:A:204:GLU:OE2	1:A:223:SER:OG	2.36	0.42
1:A:695:PHE:CD1	1:B:723:PHE:HB3	2.55	0.42
1:B:611:GLY:O	1:B:613:LYS:N	2.50	0.42
1:A:590:THR:OG1	1:A:753:HIS:O	2.38	0.42
1:A:647:PHE:CD1	1:A:647:PHE:N	2.87	0.42
1:B:457:LEU:O	1:B:457:LEU:HD12	2.20	0.42
1:B:456:THR:CG2	1:B:475:GLN:HE22	2.33	0.42
1:B:771:LEU:O	1:B:772:ALA:HB2	2.20	0.42
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.95	0.41
1:A:325:THR:HG23	1:A:632:PHE:HZ	1.85	0.41
1:B:445:GLU:HG3	1:B:459:VAL:HG23	2.01	0.41
1:A:222:ASP:O	1:A:224:LYS:N	2.52	0.41
1:B:664:MET:O	1:B:668:SER:N	2.48	0.41
1:A:137:LYS:HE2	1:A:137:LYS:HB2	1.93	0.41
1:A:599:LYS:O	1:A:734:ALA:HA	2.21	0.41
1:B:388:LYS:HD3	1:B:388:LYS:HA	1.95	0.41
1:B:484:GLN:O	1:B:485:ARG:HB3	2.21	0.41
1:A:283:LYS:HE3	1:A:288:PHE:HD2	1.86	0.41
1:B:647:PHE:HB3	1:B:673:ILE:HG12	2.02	0.41
1:B:705:ALA:O	1:B:709:LEU:HD12	2.21	0.41
1:B:185:GLN:HG2	1:B:187:ALA:CB	2.50	0.41
1:B:246:LEU:HD13	1:B:247:MET:N	2.36	0.41
1:A:123:ASP:HB3	1:A:297:HIS:CE1	2.56	0.41
1:A:378:ALA:HB3	1:A:388:LYS:NZ	2.36	0.41
1:A:468:TYR:CZ	1:A:494:ARG:HD3	2.56	0.41
1:A:739:HIS:CE1	1:A:756:GLN:HB2	2.56	0.41
1:B:257:GLU:HA	1:B:261:GLN:OE1	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:739:HIS:CE1	1:B:756:GLN:HB2	2.56	0.40
1:A:142:ALA:HA	1:A:153:THR:HA	2.03	0.40
1:A:252:ASP:O	1:A:253:GLY:C	2.58	0.40
1:A:613:LYS:HG2	1:A:740:LEU:HD12	2.03	0.40
1:B:395:LEU:O	1:B:399:GLU:HG2	2.21	0.40
1:A:778:ALA:N	1:B:703:ALA:HB2	2.36	0.40
1:A:353:VAL:HG23	1:A:355:ASN:HB2	2.03	0.40
1:A:601:ARG:HB2	1:A:734:ALA:HB1	2.02	0.40
1:B:106:VAL:O	1:B:107:VAL:HG22	2.20	0.40
1:B:709:LEU:HD23	1:B:734:ALA:HB3	2.04	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	765/816 (94%)	677 (88%)	65 (8%)	23 (3%)	4	24
1	B	765/816 (94%)	677 (88%)	66 (9%)	22 (3%)	4	24
All	All	1530/1632 (94%)	1354 (88%)	131 (9%)	45 (3%)	4	24

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	ALA
1	A	253	GLY
1	A	285	PRO
1	A	377	SER
1	A	713	LYS
1	A	774	LEU
1	B	187	ALA
1	B	195	ALA

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Mol	Chain	Res	Type
1	B	285	PRO
1	B	377	SER
1	B	713	LYS
1	A	136	LYS
1	A	195	ALA
1	A	222	ASP
1	A	224	LYS
1	A	576	ASN
1	A	692	THR
1	B	136	LYS
1	B	224	LYS
1	B	253	GLY
1	B	576	ASN
1	B	692	THR
1	B	772	ALA
1	B	774	LEU
1	A	135	ASP
1	A	223	SER
1	A	376	LEU
1	A	731	ALA
1	A	759	PRO
1	B	222	ASP
1	B	376	LEU
1	B	731	ALA
1	B	759	PRO
1	A	434	GLN
1	A	707	HIS
1	A	772	ALA
1	B	107	VAL
1	B	194	ASN
1	B	382	SER
1	B	707	HIS
1	A	107	VAL
1	A	381	SER
1	B	135	ASP
1	A	486	ARG
1	B	223	SER

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	608/668 (91%)	594 (98%)	14 (2%)	50	73
1	B	608/668 (91%)	593 (98%)	15 (2%)	47	72
All	All	1216/1336 (91%)	1187 (98%)	29 (2%)	49	73

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	28	ARG
1	A	136	LYS
1	A	165	LEU
1	A	184	LEU
1	A	206	LEU
1	A	246	LEU
1	A	259	ASP
1	A	417	ASN
1	A	443	ASP
1	A	486	ARG
1	A	626	LEU
1	A	647	PHE
1	A	649	ARG
1	B	21	THR
1	B	101	PRO
1	B	104	ARG
1	B	136	LYS
1	B	165	LEU
1	B	184	LEU
1	B	206	LEU
1	B	246	LEU
1	B	259	ASP
1	B	417	ASN
1	B	443	ASP
1	B	456	THR
1	B	486	ARG
1	B	626	LEU
1	B	649	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	194	ASN
1	A	272	ASN
1	A	475	GLN
1	A	537	GLN
1	A	585	GLN
1	A	592	ASN
1	A	754	GLN
1	B	194	ASN
1	B	272	ASN
1	B	421	HIS
1	B	475	GLN
1	B	585	GLN
1	B	592	ASN
1	B	675	HIS
1	B	754	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	901	-	29,33,33	2.10	8 (27%)	31,52,52	2.18	7 (22%)
2	ANP	B	901	-	29,33,33	2.72	11 (37%)	31,52,52	1.81	9 (29%)

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	901	-	-	1/14/38/38	0/3/3/3
2	ANP	B	901	-	-	9/14/38/38	0/3/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	ANP	C2-N1	-6.21	1.22	1.33
2	B	901	ANP	PB-N3B	6.09	1.79	1.63
2	A	901	ANP	PB-N3B	6.03	1.79	1.63
2	B	901	ANP	PG-N3B	5.82	1.78	1.63
2	A	901	ANP	PG-N3B	5.31	1.77	1.63
2	B	901	ANP	C4-N3	-5.20	1.28	1.35
2	B	901	ANP	PG-O1G	4.38	1.53	1.46
2	A	901	ANP	PG-O1G	3.28	1.51	1.46
2	B	901	ANP	PB-O1B	3.26	1.51	1.46
2	A	901	ANP	PB-O2B	-2.93	1.48	1.56
2	B	901	ANP	C8-N7	-2.83	1.29	1.34
2	A	901	ANP	C5-C4	2.81	1.48	1.40
2	B	901	ANP	C5-N7	-2.44	1.30	1.39
2	A	901	ANP	C2-N3	2.26	1.35	1.32
2	A	901	ANP	PB-O3A	2.24	1.61	1.59
2	A	901	ANP	PG-O3G	-2.14	1.51	1.56
2	B	901	ANP	PB-O3A	2.11	1.61	1.59
2	B	901	ANP	PB-O2B	-2.03	1.51	1.56
2	B	901	ANP	C2'-C1'	-2.03	1.50	1.53

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	ANP	O1G-PG-N3B	-7.93	100.10	111.77
2	B	901	ANP	O2B-PB-O1B	4.76	119.91	109.92
2	A	901	ANP	PA-O3A-PB	-4.07	118.30	132.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	901	ANP	C3'-C2'-C1'	3.98	106.98	100.98
2	B	901	ANP	PA-O3A-PB	-3.40	120.65	132.62
2	A	901	ANP	C3'-C2'-C1'	3.29	105.94	100.98
2	A	901	ANP	N3-C2-N1	-3.08	123.86	128.68
2	A	901	ANP	O1B-PB-N3B	-2.98	107.39	111.77
2	B	901	ANP	N3-C2-N1	-2.96	124.05	128.68
2	B	901	ANP	C4-C5-N7	-2.90	106.38	109.40
2	B	901	ANP	O2B-PB-O3A	2.36	112.51	104.64
2	B	901	ANP	C5-C6-N6	-2.32	116.82	120.35
2	A	901	ANP	C4-C5-N7	-2.32	106.98	109.40
2	B	901	ANP	O3G-PG-O2G	2.30	113.76	107.64
2	B	901	ANP	O1G-PG-N3B	-2.06	108.74	111.77
2	A	901	ANP	O2A-PA-O1A	2.04	122.31	112.24

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	ANP	PG-N3B-PB-O1B
2	B	901	ANP	PB-N3B-PG-O1G
2	B	901	ANP	PG-N3B-PB-O1B
2	B	901	ANP	PA-O3A-PB-O2B
2	B	901	ANP	C5'-O5'-PA-O1A
2	B	901	ANP	C5'-O5'-PA-O2A
2	B	901	ANP	O4'-C4'-C5'-O5'
2	B	901	ANP	C3'-C4'-C5'-O5'
2	B	901	ANP	C5'-O5'-PA-O3A
2	B	901	ANP	PG-N3B-PB-O3A

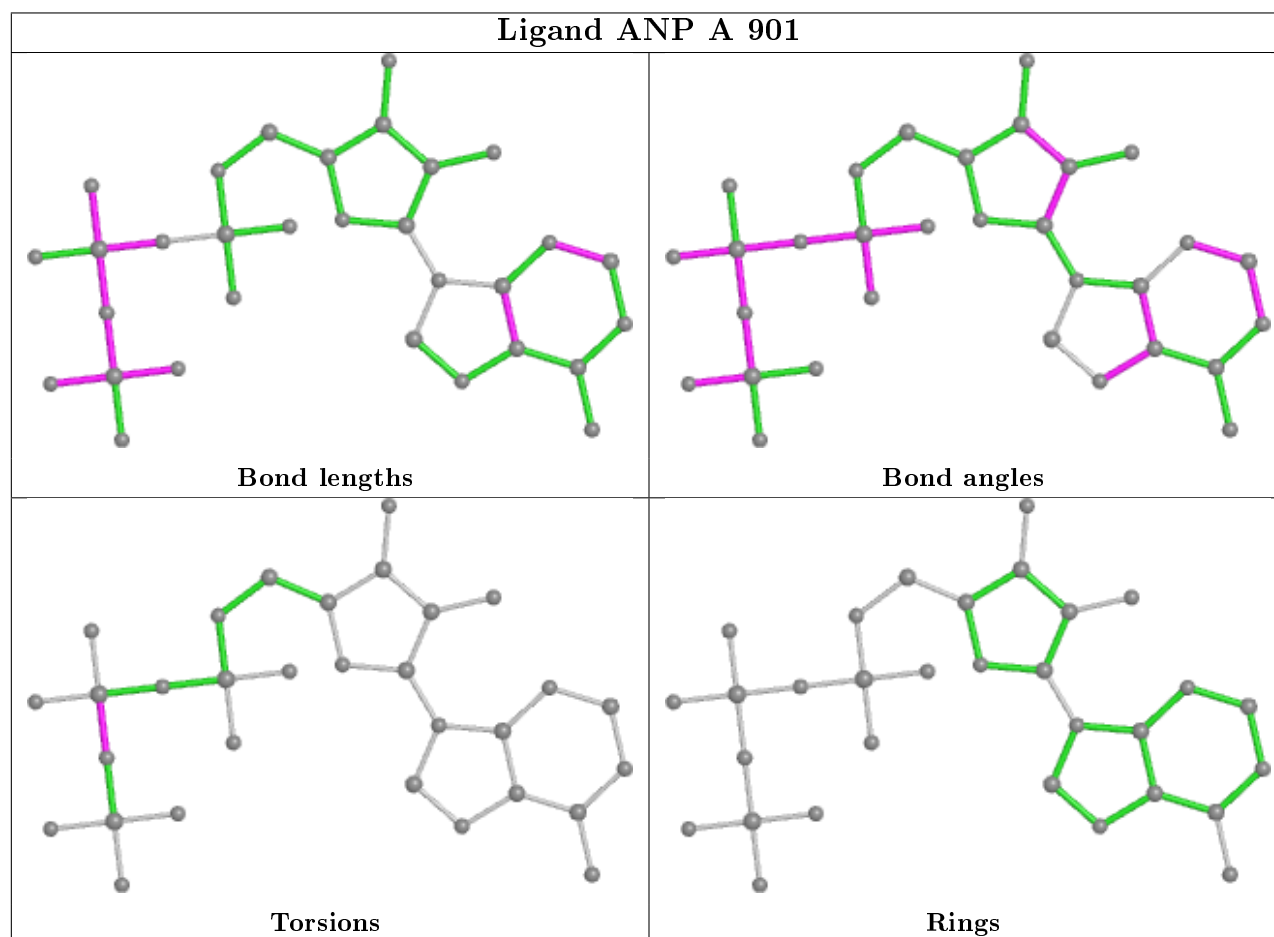
There are no ring outliers.

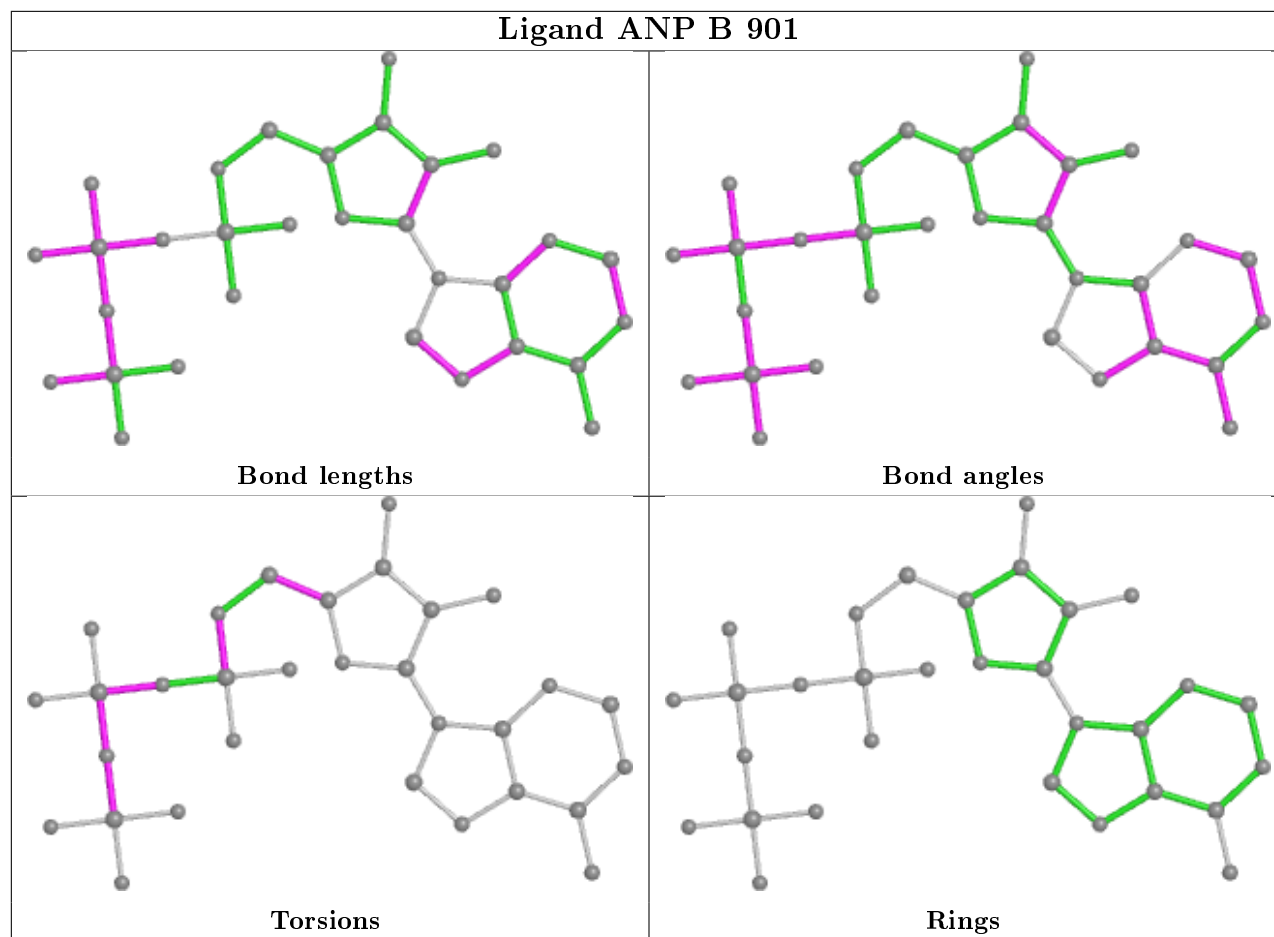
2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	ANP	4	0
2	B	901	ANP	8	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	771/816 (94%)	-0.07	18 (2%) 60 59	50, 84, 147, 212	0
1	B	771/816 (94%)	0.34	54 (7%) 16 16	75, 121, 210, 281	0
All	All	1542/1632 (94%)	0.14	72 (4%) 31 29	50, 103, 182, 281	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	459	VAL	9.4
1	B	377	SER	7.3
1	B	502	ALA	6.9
1	B	457	LEU	6.1
1	B	486	ARG	6.0
1	B	743	LEU	5.6
1	B	496	ILE	5.0
1	B	375	ASP	4.9
1	B	436	HIS	4.8
1	A	745	GLN	4.7
1	B	469	ILE	4.6
1	B	510	ALA	4.6
1	B	483	TYR	4.5
1	B	503	PHE	4.4
1	B	456	THR	4.4
1	B	467	PHE	4.3
1	B	455	SER	4.2
1	B	443	ASP	4.2
1	A	743	LEU	4.1
1	B	484	GLN	3.9
1	B	471	LEU	3.8
1	B	482	ASP	3.8
1	B	435	ASN	3.6
1	B	498	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	446	ALA	3.5
1	B	499	GLU	3.5
1	B	506	LYS	3.4
1	B	451	ARG	3.4
1	A	486	ARG	3.3
1	B	458	LYS	3.3
1	B	450	GLU	3.2
1	A	456	THR	3.2
1	A	436	HIS	3.1
1	A	744	GLU	3.1
1	B	468	TYR	3.0
1	B	741	SER	2.9
1	B	727	TYR	2.9
1	B	733	ALA	2.9
1	A	137	LYS	2.9
1	B	378	ALA	2.8
1	B	423	PHE	2.8
1	B	465	HIS	2.8
1	B	374	ILE	2.8
1	B	487	GLN	2.7
1	B	461	PHE	2.6
1	A	469	ILE	2.6
1	B	514	ALA	2.5
1	B	481	ALA	2.5
1	B	466	GLY	2.5
1	A	748	ASP	2.5
1	B	419	ILE	2.5
1	B	440	PHE	2.4
1	A	749	ILE	2.4
1	B	716	SER	2.4
1	A	376	LEU	2.4
1	B	222	ASP	2.4
1	A	491	ASN	2.4
1	B	706	GLU	2.4
1	B	495	PHE	2.3
1	B	742	ALA	2.3
1	B	692	THR	2.3
1	B	285	PRO	2.3
1	B	731	ALA	2.2
1	A	692	THR	2.2
1	A	496	ILE	2.2
1	A	377	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	695	PHE	2.1
1	A	375	ASP	2.1
1	B	404	ALA	2.1
1	B	734	ALA	2.1
1	A	773	GLY	2.0
1	A	487	GLN	2.0

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 carbohydrates in this entry.

6.4 Ligands [i](#)

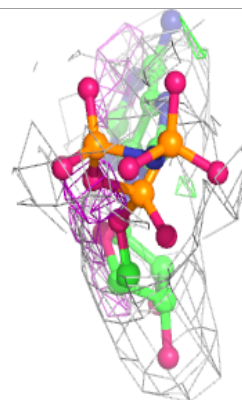
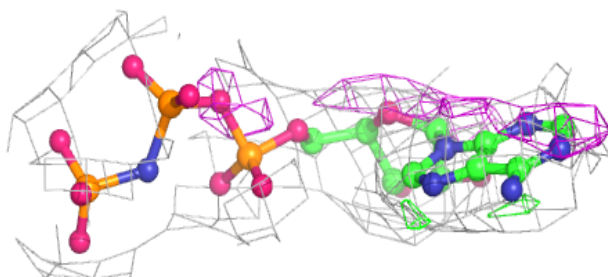
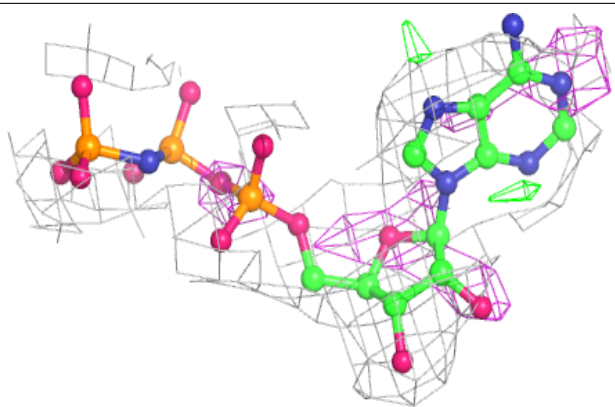
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	B	901	31/31	0.91	0.17	73,96,131,139	0
2	ANP	A	901	31/31	0.93	0.22	63,77,98,107	0

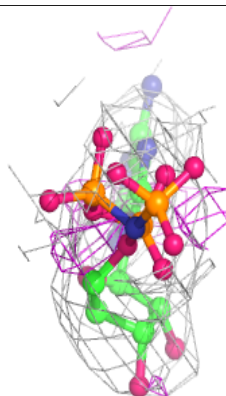
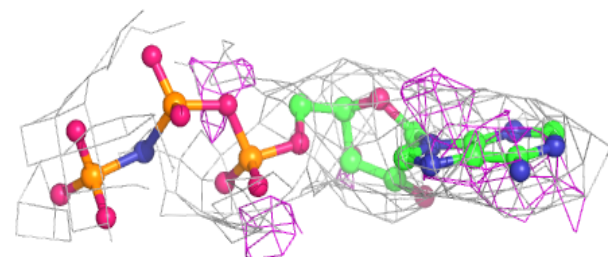
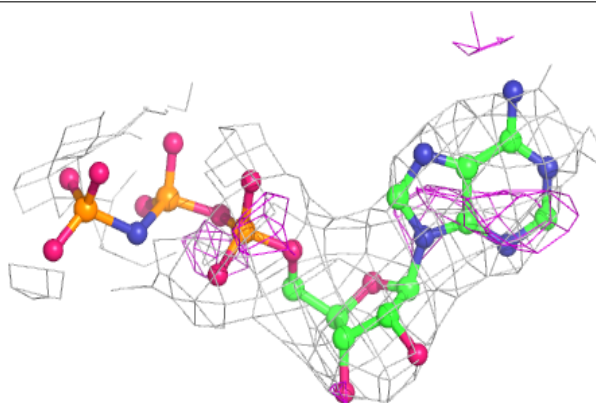
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ANP B 901:

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

**Electron density around ANP A 901:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.