



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:18 PM UTC

PDB ID : 3ZD7 / pdb_00003zd7
Title : Snapshot 3 of RIG-I scanning on RNA duplex
Authors : Luo, D.; Pyle, A.M.
Deposited on : 2012-11-25
Resolution : 2.50 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

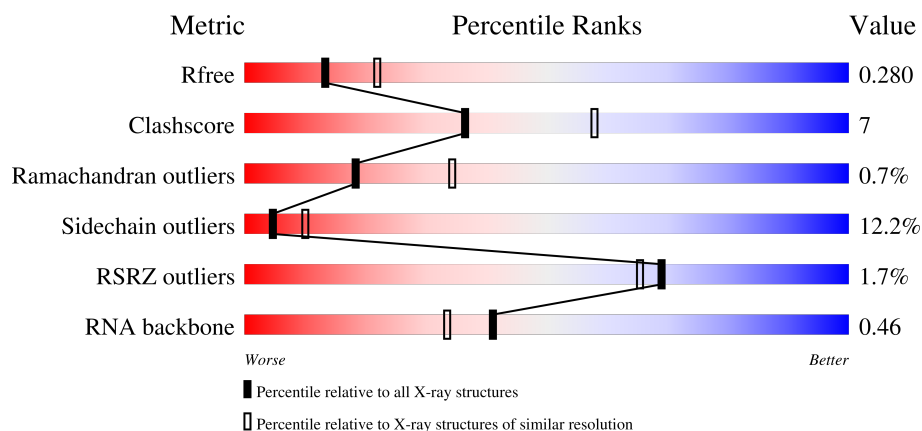
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)
RNA backbone	3983	1003 (2.78-2.22)

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	696	
2	C	10	
2	D	10	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5369 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 PROBABLE ATP-DEPENDENT RNA HELICASE DDX58.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	623	Total	C	N	O	S	4	0	0
			4856	3114	814	899	29			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	306	ASN	GLN	conflict	UNP O95786
A	499	SER	ILE	conflict	UNP O95786
A	696	LEU	ALA	conflict	UNP O95786
A	828	ASP	GLU	conflict	UNP O95786

- Molecule 2 is a RNA chain called RNA DUPLEX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	P	0	0	0
			212	95	40	68	9			
2	D	10	Total	C	N	O	P	0	0	0
			212	95	40	68	9			

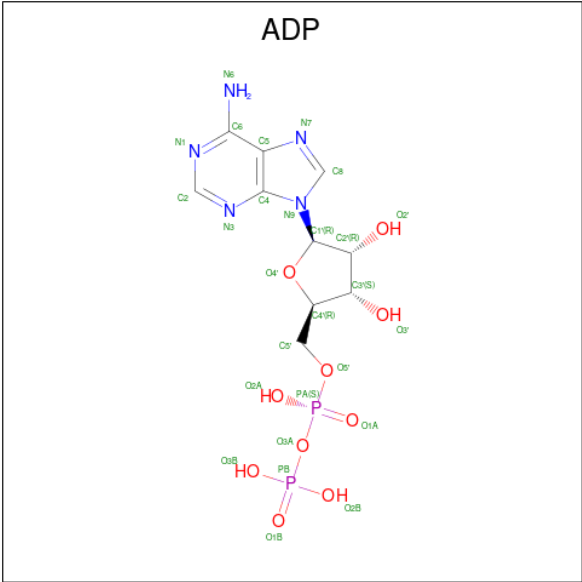
- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	56	Total	O	0	0
			56	56		
6	C	1	Total	O	0	0
			1	1		
6	D	3	Total	O	0	0
			3	3		

- Molecule 1: PROBABLE ATP-DEPENDENT RNA HELICASE DDX58





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.25Å 76.00Å 207.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 2.50 25.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (25.00-2.50) 97.9 (25.00-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.229 , 0.288 0.222 , 0.280	Depositor DCC
R_{free} test set	1343 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	52.7	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5369	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, MG, ZN

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	0.81	6/4953 (0.1%)	1.05	12/6702 (0.2%)
2	C	0.68	0/236	1.23	0/367
2	D	0.62	0/236	1.19	2/367 (0.5%)
All	All	0.80	6/5425 (0.1%)	1.07	14/7436 (0.2%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	807	LYS	CE-NZ	-15.18	1.03	1.49
1	A	375	HIS	CG-ND1	-7.30	1.30	1.38
1	A	914	GLU	CG-CD	-6.92	1.34	1.52
1	A	375	HIS	CD2-NE2	-6.11	1.31	1.37
1	A	300	ILE	CA-CB	6.00	1.57	1.54
1	A	409	THR	C-O	-5.43	1.17	1.23

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	914	GLU	CB-CG-CD	14.31	136.93	112.60
1	A	914	GLU	CG-CD-OE1	-9.17	97.31	118.40
1	A	914	GLU	CG-CD-OE2	8.82	138.69	118.40
1	A	807	LYS	CD-CE-NZ	8.54	139.23	111.90
1	A	701	ASP	N-CA-C	7.67	120.52	108.79
2	D	10	C	C3'-C2'-O2'	-6.98	104.13	114.60
1	A	771	TRP	CA-CB-CG	6.68	126.29	113.60
1	A	379	LYS	N-CA-C	6.31	120.32	112.24
1	A	365	ILE	CB-CA-C	-5.81	103.15	112.16
1	A	379	LYS	CA-C-N	-5.77	116.24	126.45
1	A	379	LYS	C-N-CA	-5.77	116.24	126.45
1	A	399	SER	N-CA-C	5.44	117.96	108.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	536	LYS	N-CA-C	-5.18	105.08	111.40
2	D	10	C	C3'-C2'-C1'	5.12	106.62	101.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4856	0	4731	73	0
2	C	212	0	112	1	0
2	D	212	0	112	1	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	27	0	12	1	0
6	A	56	0	0	1	0
6	C	1	0	0	0	0
6	D	3	0	0	0	0
All	All	5369	0	4967	74	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 7.

All (74) 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:703:GLY:HA2	1:A:704:ILE:CB	1.86	1.05
1:A:478:LEU:O	1:A:482:THR:HG23	1.66	0.94
1:A:540:LEU:HD21	1:A:583:GLU:HG3	1.53	0.89
1:A:428:CYS:SG	1:A:779:LYS:NZ	2.50	0.85
1:A:483:GLU:OE2	1:A:502:ARG:NH1	2.13	0.80
1:A:265:PRO:HG2	1:A:453:VAL:HG21	1.65	0.79
1:A:379:LYS:O	1:A:380:GLN:HB2	1.82	0.79
1:A:315:GLU:O	1:A:316:ARG:CB	2.35	0.74
1:A:412:VAL:HG22	1:A:430:LEU:HD23	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:GLY:HA2	5:A:1924:ADP:O1A	1.89	0.71
1:A:661:LEU:HD23	1:A:696:LEU:HD22	1.74	0.70
1:A:357:LYS:HA	1:A:357:LYS:HE2	1.74	0.69
1:A:657:LYS:O	1:A:693:ILE:HG23	1.93	0.68
1:A:379:LYS:O	2:C:5:G:OP1	2.14	0.66
1:A:864:CYS:HB3	1:A:871:HIS:H	1.62	0.65
1:A:656:LEU:HA	1:A:694:LEU:HD23	1.78	0.64
1:A:483:GLU:CD	1:A:502:ARG:HH12	2.06	0.63
1:A:580:ASP:HB2	1:A:583:GLU:HB2	1.79	0.63
1:A:630:THR:HB	1:A:695:ILE:HG13	1.81	0.62
1:A:580:ASP:HB2	1:A:583:GLU:H	1.65	0.61
1:A:701:ASP:O	1:A:702:GLU:HB2	2.05	0.57
1:A:449:LEU:C	1:A:451:GLN:H	2.13	0.57
1:A:258:LYS:HE2	1:A:773:GLU:OE1	2.06	0.56
1:A:554:ILE:HD11	1:A:638:ALA:HB1	1.88	0.56
1:A:703:GLY:CA	1:A:704:ILE:CB	2.70	0.56
1:A:379:LYS:O	1:A:380:GLN:CB	2.49	0.56
1:A:412:VAL:CG1	1:A:427:ILE:HG12	2.36	0.56
1:A:412:VAL:HG22	1:A:430:LEU:CD2	2.35	0.54
1:A:889:ILE:HB	1:A:908:TRP:CE2	2.43	0.54
1:A:482:THR:OG1	1:A:545:LEU:HD21	2.07	0.54
1:A:485:LEU:O	1:A:488:ARG:HB2	2.08	0.54
1:A:768:LEU:HD12	1:A:768:LEU:C	2.33	0.54
1:A:826:ILE:HB	1:A:830:HIS:HB2	1.90	0.53
1:A:702:GLU:HA	1:A:704:ILE:CB	2.40	0.52
1:A:325:SER:HA	1:A:350:ILE:HD11	1.93	0.51
2:D:4:C:H2'	2:D:5:G:O4'	2.09	0.51
1:A:264:ALA:O	1:A:410:ALA:HA	2.10	0.51
1:A:653:LEU:HB3	1:A:656:LEU:HD22	1.93	0.51
1:A:508:LYS:O	1:A:511:GLN:N	2.43	0.51
1:A:412:VAL:HG11	1:A:427:ILE:HG12	1.93	0.50
1:A:653:LEU:O	1:A:656:LEU:HB2	2.12	0.50
1:A:864:CYS:HB3	1:A:871:HIS:N	2.27	0.49
1:A:888:LYS:HB2	1:A:890:GLU:HG2	1.94	0.49
1:A:399:SER:HA	1:A:400:GLY:HA3	1.70	0.48
1:A:477:GLN:HA	1:A:477:GLN:OE1	2.13	0.48
1:A:587:THR:HG22	1:A:591:GLU:OE2	2.14	0.48
1:A:852:GLN:HA	1:A:857:GLU:HG3	1.94	0.48
1:A:475:ILE:HB	1:A:552:LEU:HD11	1.97	0.47
1:A:482:THR:OG1	1:A:545:LEU:CD2	2.62	0.47
1:A:824:ARG:HA	1:A:916:ILE:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:GLN:OE1	1:A:480:ARG:NE	2.36	0.46
1:A:328:THR:O	1:A:329:ALA:HB3	2.14	0.46
1:A:449:LEU:C	1:A:451:GLN:N	2.73	0.46
1:A:348:PRO:HD2	6:A:2018:HOH:O	2.16	0.46
1:A:347:THR:OG1	1:A:350:ILE:HD12	2.15	0.46
1:A:300:ILE:HB	1:A:301:PRO:HD3	1.98	0.45
1:A:514:VAL:C	1:A:516:VAL:H	2.25	0.45
1:A:418:LYS:HE3	1:A:422:GLU:OE2	2.18	0.44
1:A:252:LEU:HB3	1:A:253:PRO:HD3	1.99	0.44
1:A:656:LEU:HA	1:A:694:LEU:CD2	2.46	0.44
1:A:557:HIS:HD1	1:A:610:LYS:NZ	2.16	0.43
1:A:702:GLU:HA	1:A:703:GLY:HA2	1.76	0.43
1:A:740:LEU:HD12	1:A:748:ILE:HD13	2.01	0.43
1:A:325:SER:HA	1:A:350:ILE:CD1	2.48	0.43
1:A:323:GLY:HA2	1:A:345:ILE:O	2.20	0.42
1:A:424:LEU:HD23	1:A:424:LEU:HA	1.88	0.41
1:A:469:ASP:OD1	1:A:471:PHE:HB3	2.21	0.41
1:A:475:ILE:HG21	1:A:552:LEU:HD13	2.03	0.41
1:A:768:LEU:C	1:A:768:LEU:CD1	2.94	0.41
1:A:655:PHE:O	1:A:694:LEU:HD21	2.21	0.41
1:A:281:HIS:O	1:A:284:LYS:HG2	2.21	0.40
1:A:650:ASN:HA	1:A:651:PRO:HD2	1.79	0.40
1:A:836:ASP:OD1	1:A:836:ASP:N	2.53	0.40
1:A:773:GLU:OE2	1:A:777:ARG:NH2	2.53	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	609/696 (88%)	567 (93%)	38 (6%)	4 (1%)	18 34

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	702	GLU
1	A	704	ILE
1	A	316	ARG
1	A	452	VAL

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	518/625 (83%)	455 (88%)	63 (12%)	5 10

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	239	SER
1	A	242	LYS
1	A	244	ARG
1	A	248	LEU
1	A	266	THR
1	A	270	LYS
1	A	276	LEU
1	A	283	LYS
1	A	299	GLN
1	A	322	THR
1	A	328	THR
1	A	334	VAL
1	A	339	GLU
1	A	357	LYS
1	A	398	SER
1	A	412	VAL
1	A	418	LYS
1	A	420	THR
1	A	424	LEU
1	A	449	LEU
1	A	453	VAL

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Mol	Chain	Res	Type
1	A	457	GLN
1	A	470	LYS
1	A	493	LEU
1	A	500	GLN
1	A	534	ILE
1	A	538	LEU
1	A	540	LEU
1	A	552	LEU
1	A	559	ARG
1	A	564	LEU
1	A	575	ARG
1	A	589	ARG
1	A	594	LEU
1	A	598	GLU
1	A	600	VAL
1	A	601	SER
1	A	602	ARG
1	A	612	GLU
1	A	614	LEU
1	A	617	ILE
1	A	627	GLU
1	A	629	ILE
1	A	631	ILE
1	A	643	LEU
1	A	656	LEU
1	A	694	LEU
1	A	699	VAL
1	A	710	ASN
1	A	711	LEU
1	A	716	GLU
1	A	741	LEU
1	A	750	LYS
1	A	758	GLU
1	A	768	LEU
1	A	780	ILE
1	A	787	GLU
1	A	807	LYS
1	A	811	ARG
1	A	825	VAL
1	A	856	PHE
1	A	896	ASP
1	A	906	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	336	GLN
1	A	340	ASN
1	A	451	GLN
1	A	720	ASN
1	A	762	ASN
1	A	769	GLN
1	A	876	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	9/10 (90%)	1 (11%)	0
2	D	9/10 (90%)	1 (11%)	0
All	All	18/20 (90%)	2 (11%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	C	10	C
2	D	5	G

There are no RNA pucker outliers to report.

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The

Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ADP	A	1924	4	28,29,29	1.54	4 (14%)	43,45,45	1.74	7 (16%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ADP	A	1924	4	-	5/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1924	ADP	C5-C4	5.40	1.48	1.39
5	A	1924	ADP	C5-C6	3.14	1.49	1.41
5	A	1924	ADP	PA-O3A	2.68	1.62	1.59
5	A	1924	ADP	C8-N7	2.12	1.35	1.31

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1924	ADP	C5-C4-N3	-5.61	118.99	126.72
5	A	1924	ADP	N3-C4-N9	4.43	134.70	127.17
5	A	1924	ADP	C2-N3-C4	3.88	121.30	111.83
5	A	1924	ADP	N3-C2-N1	-3.52	123.25	128.58
5	A	1924	ADP	C4-C5-N7	-3.31	106.80	110.58
5	A	1924	ADP	C6-C5-N7	2.35	136.62	132.09
5	A	1924	ADP	C5-N7-C8	2.26	107.00	103.45

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1924	ADP	PA-O3A-PB-O2B
5	A	1924	ADP	O4'-C4'-C5'-O5'
5	A	1924	ADP	C5'-O5'-PA-O1A

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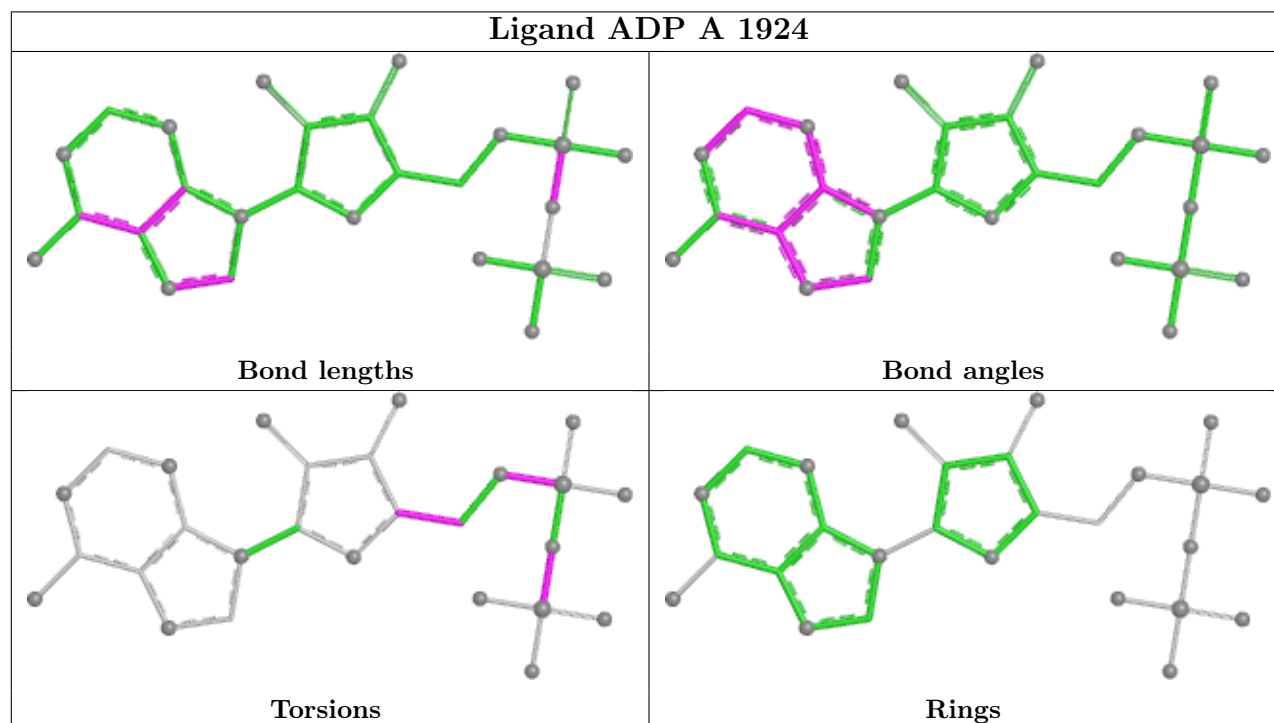
Mol	Chain	Res	Type	Atoms
5	A	1924	ADP	C3'-C4'-C5'-O5'
5	A	1924	ADP	PA-O3A-PB-O1B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1924	ADP	1	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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

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

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	623/696 (89%)	0.07	11 (1%) 67 64	23, 60, 111, 140	2 (0%)
2	C	10/10 (100%)	0.13	0 100 100	62, 97, 124, 126	0
2	D	10/10 (100%)	-0.06	0 100 100	75, 106, 118, 123	0
All	All	643/716 (89%)	0.07	11 (1%) 69 65	23, 61, 113, 140	2 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	856	PHE	3.4
1	A	830	HIS	2.5
1	A	517	GLN	2.4
1	A	577	ALA	2.3
1	A	865	ALA	2.3
1	A	519	ALA	2.2
1	A	906	SER	2.2
1	A	866	ARG	2.2
1	A	700	ALA	2.2
1	A	541	TYR	2.1
1	A	693	ILE	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](#)

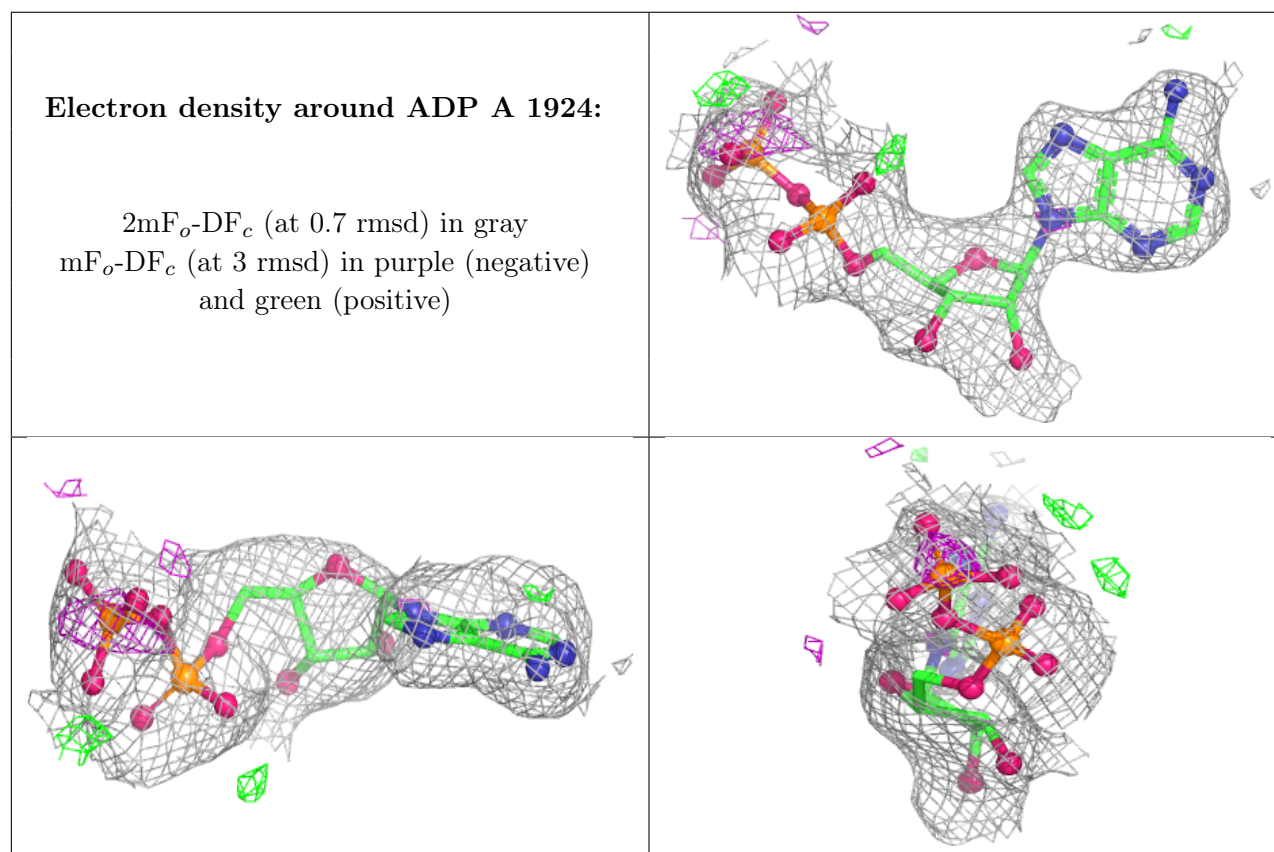
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
4	MG	A	1923	1/1	0.79	0.20	75,75,75,75	0
5	ADP	A	1924	27/27	0.81	0.10	60,69,75,77	0
3	ZN	A	927	1/1	0.98	0.09	82,82,82,82	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.