



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2026 – 01:17 pm BST

PDB ID : 28ZS / pdb_000028zs
Title : Crystal structure of human DHX8 in complex with compound 53 and ADP
Authors : Graedler, U.; Augustin, M.; Lammens, A.; van Montfort, R.L.M.
Deposited on : 2026-03-03
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	:	1.8.4, CSD as541be (2020)
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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

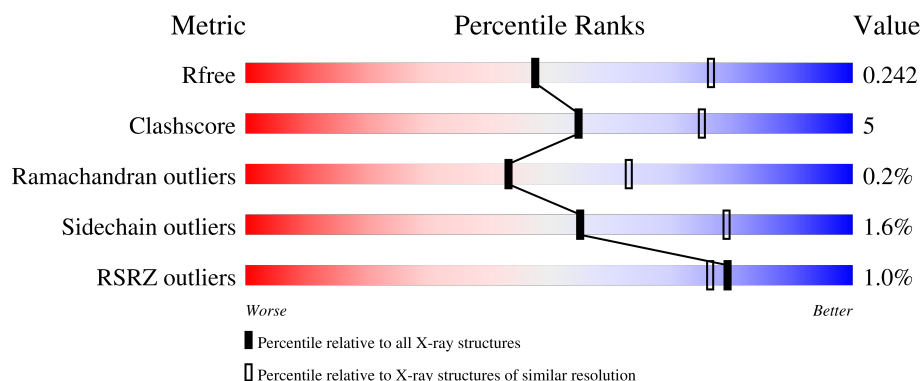
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

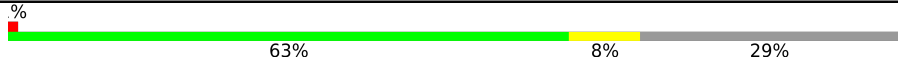
The reported resolution of this entry is 2.50 Å.

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)

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	881	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5156 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.

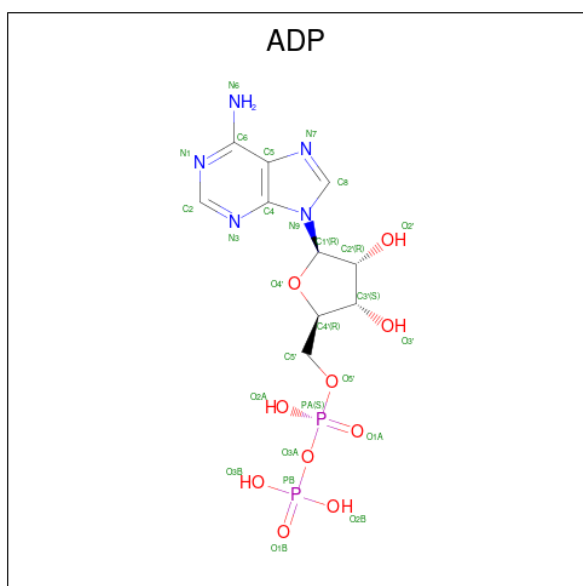
- Molecule 1 is a protein called Glutathione S-transferase class-mu 26 kDa isozyme,ATP-dependent RNA helicase DHX8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	626	Total	C	N	O	S	0	2	0
			4886	3119	805	926	36			

There are 25 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	308	MET	-	initiating methionine	UNP P08515
A	309	SER	-	expression tag	UNP P08515
A	310	SER	-	expression tag	UNP P08515
A	311	HIS	-	expression tag	UNP P08515
A	312	HIS	-	expression tag	UNP P08515
A	313	HIS	-	expression tag	UNP P08515
A	314	HIS	-	expression tag	UNP P08515
A	315	HIS	-	expression tag	UNP P08515
A	316	HIS	-	expression tag	UNP P08515
A	317	HIS	-	expression tag	UNP P08515
A	318	HIS	-	expression tag	UNP P08515
A	319	ASP	-	expression tag	UNP P08515
A	320	THR	-	expression tag	UNP P08515
A	321	GLU	-	expression tag	UNP P08515
A	322	GLU	-	expression tag	UNP P08515
A	541	SER	-	linker	UNP P08515
A	542	ASP	-	linker	UNP P08515
A	543	GLY	-	linker	UNP P08515
A	544	SER	-	linker	UNP P08515
A	545	GLU	-	linker	UNP P08515
A	546	ASN	-	linker	UNP P08515
A	547	LEU	-	linker	UNP P08515
A	548	TYR	-	linker	UNP P08515
A	549	PHE	-	linker	UNP P08515
A	550	GLN	-	linker	UNP P08515

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

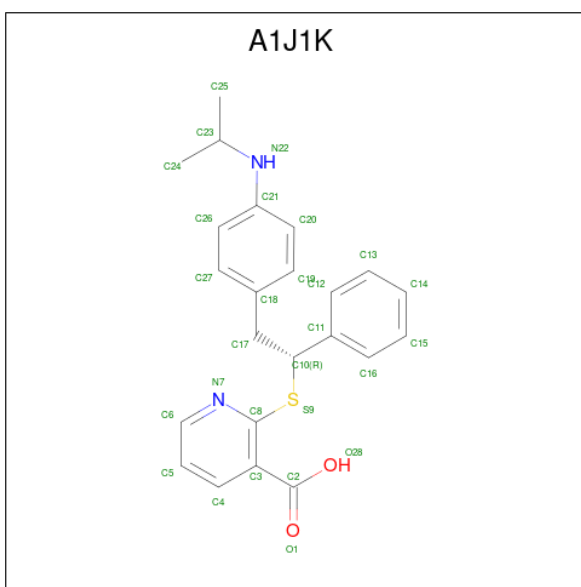


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is 2-[(1R)-1-phenyl-2-[4-(propan-2-ylamino)phenyl]ethyl]sulfanylpuridine-3-carboxylic acid (CCD ID: A1J1K) (formula: $C_{23}H_{24}N_2O_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			28	23	2	2	1		

- Molecule 5 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	200	Total 202	O 202	0	2

- Molecule 1: Glutathione S-transferase class-mu 26 kDa isozyme,ATP-dependent RNA helicase DHX8



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.68Å 71.01Å 90.34Å 90.00° 121.83° 90.00°	Depositor
Resolution (Å)	44.91 – 2.50 44.91 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.8 (44.91-2.50) 98.8 (44.91-2.50)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.10.4 (26-JUL-2023)	Depositor
R, R_{free}	0.212 , 0.252 0.205 , 0.242	Depositor DCC
R_{free} test set	1336 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	46.9	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5156	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.15% 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: DMS, A1J1K, ADP, 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	0.69	0/4983	1.06	2/6762 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	1040	GLY	N-CA-C	6.20	119.65	111.52
1	A	1087	ASP	CA-CB-CG	5.13	117.73	112.60

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	4886	0	4788	46	0
2	A	27	0	12	1	0
3	A	1	0	0	0	0
4	A	28	0	0	0	0
5	A	12	0	18	0	0
6	A	202	0	0	1	0
All	All	5156	0	4818	47	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 (47) 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:890:ARG:NH2	1:A:893:ARG:HH11	1.52	1.06
1:A:1055:ASN:HD22	1:A:1061:TRP:CD1	1.86	0.94
1:A:890:ARG:HH21	1:A:893:ARG:NH1	1.71	0.87
1:A:890:ARG:HH21	1:A:893:ARG:HH11	0.86	0.84
1:A:890:ARG:NH2	1:A:893:ARG:NH1	2.25	0.83
1:A:1055:ASN:ND2	1:A:1061:TRP:CD1	2.48	0.81
1:A:688:HIS:NE2	1:A:844:THR:HG21	2.05	0.71
1:A:1000:GLY:HA2	1:A:1094:VAL:HG21	1.76	0.66
1:A:1000:GLY:HA2	1:A:1094:VAL:CG2	2.25	0.66
1:A:1039:GLU:HB2	1:A:1043:LEU:HD12	1.80	0.63
1:A:1116:ALA:HB1	1:A:1124:TYR:HB3	1.81	0.63
1:A:753:GLU:HG2	1:A:754:THR:N	2.17	0.60
1:A:1040:GLY:HA2	1:A:1141:LEU:HG	1.84	0.58
1:A:570:LEU:HD11	1:A:738:PRO:HD2	1.84	0.57
1:A:1086:MET:HE3	1:A:1093:VAL:HG22	1.86	0.57
1:A:963:THR:HG23	1:A:1179:ALA:HB3	1.86	0.56
1:A:890:ARG:HH21	1:A:893:ARG:HD2	1.73	0.54
1:A:854:VAL:HG23	1:A:891:ALA:HB2	1.88	0.54
1:A:999:LEU:O	1:A:1102:ARG:HD2	2.09	0.53
1:A:646:ILE:HG22	1:A:662:THR:HG23	1.92	0.52
1:A:765:MET:HE3	1:A:796:ARG:HB3	1.91	0.51
1:A:669:GLU:OE1	1:A:678:GLN:NE2	2.43	0.50
1:A:589:GLU:HG3	1:A:739:GLY:O	2.12	0.50
1:A:681:ILE:HG12	1:A:712:LYS:HB2	1.93	0.50
1:A:812:VAL:HG22	1:A:824:ILE:HG21	1.93	0.50
2:A:1201:ADP:H2	6:A:1308:HOH:O	1.95	0.49
1:A:602:LEU:HD13	1:A:681:ILE:HD13	1.96	0.48
1:A:683:MET:HE3	1:A:716:THR:HG21	1.96	0.48
1:A:1005:MET:HE1	1:A:1107:ILE:HG13	1.95	0.47
1:A:1055:ASN:ND2	1:A:1061:TRP:NE1	2.61	0.47
1:A:667:LEU:CD2	1:A:693:HIS:HD2	2.28	0.47
1:A:753:GLU:CG	1:A:754:THR:N	2.78	0.47
1:A:574:LEU:HD21	1:A:598:ILE:HG12	1.97	0.47
1:A:824:ILE:HD12	1:A:848:ILE:HD11	1.96	0.47
1:A:1000:GLY:HA2	1:A:1094:VAL:HG23	1.98	0.46
1:A:595:THR:HG22	1:A:626:VAL:HG11	1.99	0.45
1:A:667:LEU:HD22	1:A:693:HIS:HD2	1.82	0.44
1:A:645:THR:OG1	1:A:659:LYS:HE3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1114:ASN:O	1:A:1150:VAL:HA	2.17	0.44
1:A:964:LEU:HD22	1:A:991:LYS:HG2	2.00	0.43
1:A:1021:PRO:HB2	1:A:1023:ASP:OD1	2.19	0.43
1:A:753:GLU:HG2	1:A:754:THR:H	1.84	0.42
1:A:820[A]:MET:HA	1:A:823:ARG:HD2	2.01	0.41
1:A:765:MET:HE3	1:A:796:ARG:CB	2.51	0.41
1:A:756:TYR:HB2	1:A:857:PRO:HB3	2.03	0.40
1:A:687:ALA:HB1	1:A:698:PHE:HZ	1.86	0.40
1:A:753:GLU:CG	1:A:754:THR:H	2.35	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	626/881 (71%)	611 (98%)	14 (2%)	1 (0%)	43 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	640	GLN

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	514/782 (66%)	506 (98%)	8 (2%)	55 79

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	661	MET
1	A	731	GLU
1	A	741	THR
1	A	784	GLU
1	A	873	GLN
1	A	969	ASP
1	A	1074	ARG
1	A	1180	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	693	HIS
1	A	706	GLN
1	A	1068	GLN
1	A	1104	GLN
1	A	1131	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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
2	ADP	A	1201	3	27,29,29	0.72	0	42,45,45	0.55	0
5	DMS	A	1204	-	3,3,3	0.71	0	3,3,3	0.32	0
4	A1J1K	A	1203	-	29,30,30	0.43	0	36,40,40	0.47	0
5	DMS	A	1205	-	3,3,3	0.63	0	3,3,3	0.50	0
5	DMS	A	1206	-	3,3,3	0.69	0	3,3,3	0.32	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	A1J1K	A	1203	-	-	7/19/20/20	0/3/3/3
2	ADP	A	1201	3	-	5/16/32/32	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

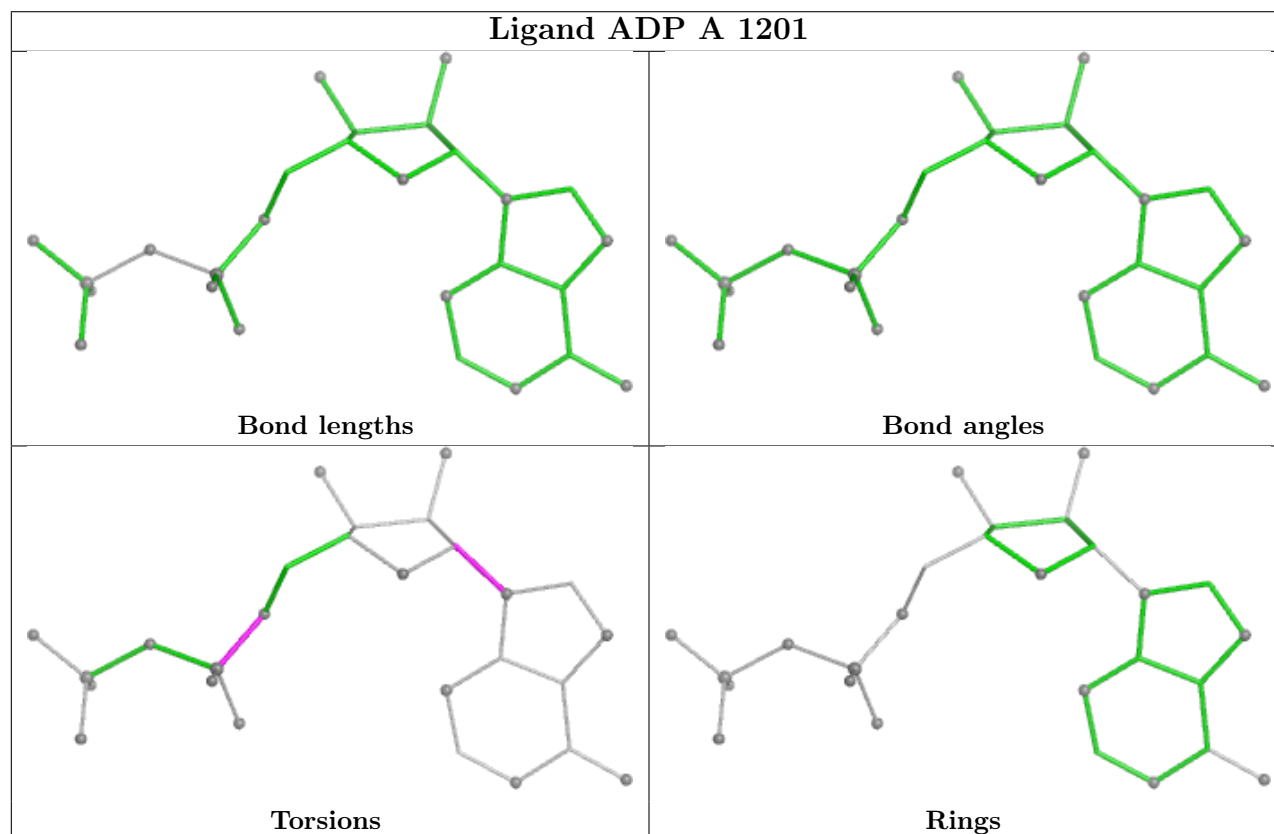
Mol	Chain	Res	Type	Atoms
2	A	1201	ADP	C5'-O5'-PA-O1A
4	A	1203	A1J1K	N7-C8-S9-C10
4	A	1203	A1J1K	O1-C2-C3-C8
4	A	1203	A1J1K	O28-C2-C3-C8
2	A	1201	ADP	C5'-O5'-PA-O3A
2	A	1201	ADP	C5'-O5'-PA-O2A
4	A	1203	A1J1K	S9-C10-C11-C12
4	A	1203	A1J1K	S9-C10-C11-C16
2	A	1201	ADP	O4'-C1'-N9-C4
2	A	1201	ADP	O4'-C1'-N9-C8
4	A	1203	A1J1K	O1-C2-C3-C4
4	A	1203	A1J1K	O28-C2-C3-C4

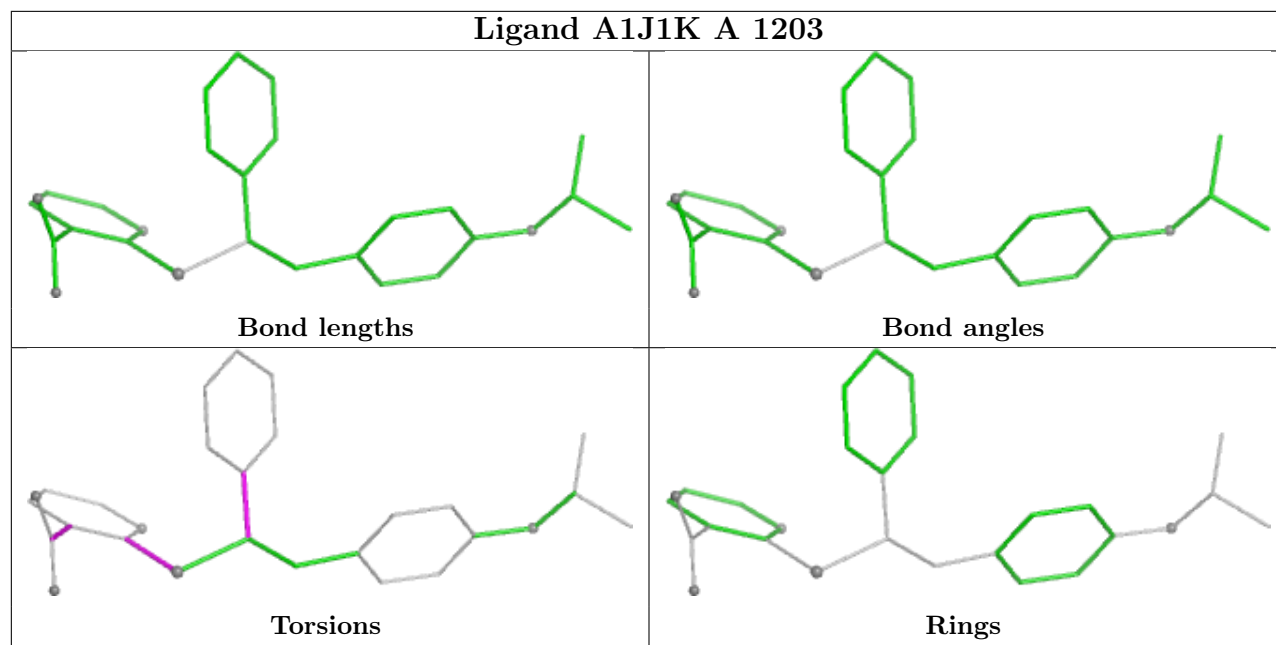
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	626/881 (71%)	-0.02	6 (0%) 79 76	27, 53, 74, 91	2 (0%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1180	PHE	2.7
1	A	752	PRO	2.6
1	A	717	SER	2.6
1	A	740	ARG	2.3
1	A	937	ILE	2.2
1	A	739	GLY	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(Å ²)	Q<0.9
5	DMS	A	1204	4/4	0.72	0.22	91,91,91,91	0

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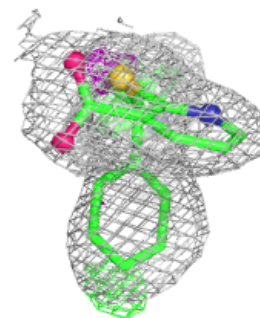
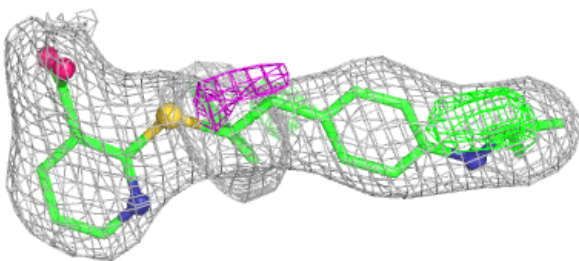
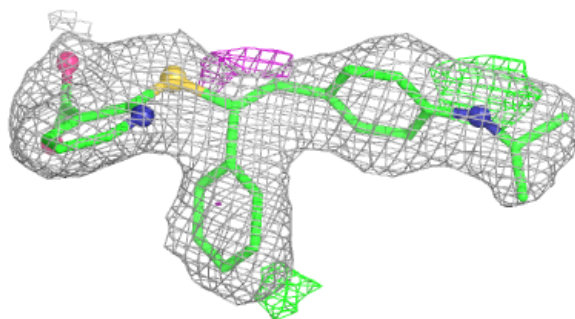
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	DMS	A	1206	4/4	0.81	0.24	89,89,89,89	0
4	A1J1K	A	1203	28/28	0.90	0.12	44,47,48,48	0
5	DMS	A	1205	4/4	0.91	0.15	71,71,71,71	4
2	ADP	A	1201	27/27	0.93	0.10	58,63,64,64	27
3	MG	A	1202	1/1	0.94	0.06	42,42,42,42	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.

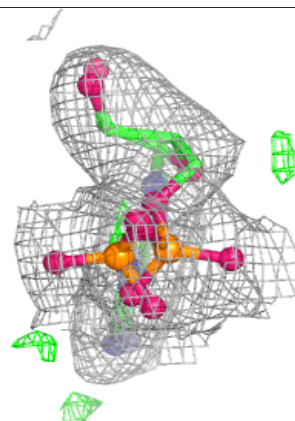
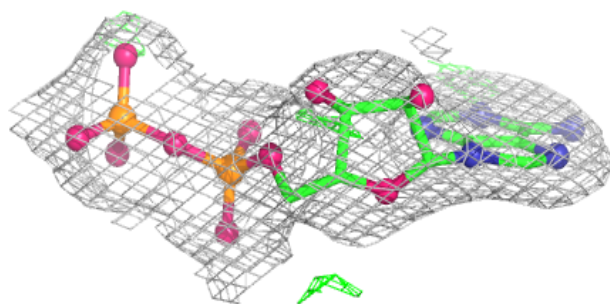
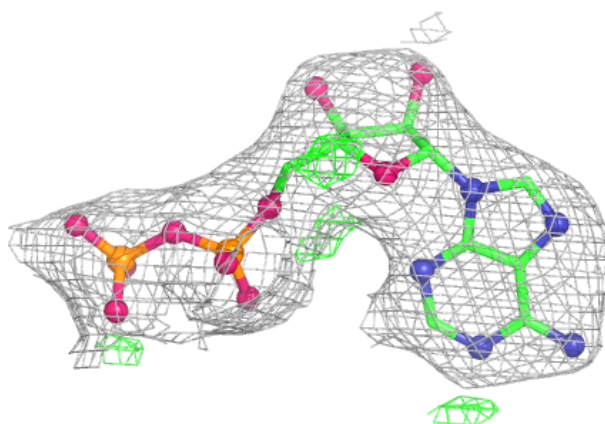
Electron density around A1J1K A 1203:

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 ADP A 1201:

$2mF_o-DF_c$ (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.