



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 06:21 AM UTC

PDB ID : 4CGZ / pdb_00004cgz
Title : Crystal structure of the Bloom's syndrome helicase BLM in complex with DNA
Authors : Newman, J.A.; Savitsky, P.; Krojer, T.; von Delft, F.; Arrowsmith, C.H.;
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Deposited on : 2013-11-27
Resolution : 3.20 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

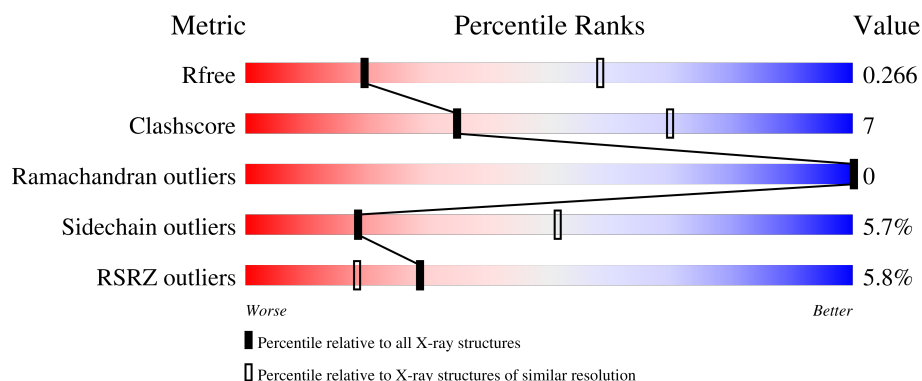
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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	665	6% 75% 17% • 5%
2	B	12	75% 25%
3	C	17	47% 53%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5591 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 BLOOM'S SYNDROME HELICASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	629	Total	C	N	O	S	0	0	0
			4981	3158	863	925	35			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	634	SER	-	expression tag	UNP P54132
A	635	MET	-	expression tag	UNP P54132

- Molecule 2 is a DNA chain called 5'-D(*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	P	0	0	0
			245	117	48	69	11			

- Molecule 3 is a DNA chain called 5'-D(*GP*AP*TP*CP*TP*CP*GP*AP*CP*GP*CP*TP*CP*DT*CP*CP*CP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	17	Total	C	N	O	P	0	0	0
			337	162	57	102	16			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	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		

4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, α , β , γ	149.53Å 149.53Å 64.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.65 – 3.20 48.65 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (48.65-3.20) 99.4 (48.65-3.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 3.19Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.229 , 0.259 0.228 , 0.266	Depositor DCC
R_{free} test set	1178 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	147.0	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 150.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.053 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5591	wwPDB-VP
Average B, all atoms (Å ²)	178.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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, 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	0.41	0/5078	0.99	17/6855 (0.2%)
2	B	0.30	0/275	0.47	0/423
3	C	0.25	0/375	0.46	0/575
All	All	0.39	0/5728	0.94	17/7853 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1163	ALA	N-CA-C	-10.40	100.54	113.02
1	A	1150	ILE	N-CA-C	-10.19	103.42	113.20
1	A	1161	ILE	N-CA-C	-9.06	96.95	109.46
1	A	1129	GLY	N-CA-C	8.68	123.15	112.73
1	A	1179	THR	N-CA-C	-7.99	102.79	112.54
1	A	1015	THR	N-CA-C	-7.01	105.34	114.04
1	A	1154	ILE	N-CA-C	-6.94	105.08	111.67
1	A	1069	THR	N-CA-C	6.82	118.36	111.07
1	A	1210	GLN	N-CA-C	6.02	117.84	111.28
1	A	873	LYS	N-CA-C	-5.66	104.12	111.71
1	A	1123	SER	N-CA-C	-5.49	105.20	112.94
1	A	1177	ALA	N-CA-C	5.49	118.02	111.71
1	A	1158	ASP	CA-C-N	-5.43	114.46	123.37
1	A	1158	ASP	C-N-CA	-5.43	114.46	123.37
1	A	1149	LEU	N-CA-C	-5.29	105.47	112.94
1	A	1160	TYR	CA-C-N	-5.26	116.64	122.27
1	A	1160	TYR	C-N-CA	-5.26	116.64	122.27

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	4981	0	4940	70	1
2	B	245	0	136	3	0
3	C	337	0	193	12	0
4	A	1	0	0	0	0
5	A	27	0	12	0	0
All	All	5591	0	5281	79	1

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 (79) 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:1033:ILE:HD11	1:A:1192:THR:HG21	1.58	0.85
1:A:641:HIS:HB3	1:A:644:PHE:HD2	1.42	0.84
1:A:1028:HIS:CE1	1:A:1151:LEU:HG	2.16	0.80
1:A:858:ASN:HB2	1:A:1042:LEU:HD11	1.64	0.79
1:A:676:ILE:HD13	1:A:701:LEU:HD23	1.73	0.70
1:A:671:ASN:ND2	1:A:854:SER:O	2.26	0.69
1:A:733:PRO:HB2	1:A:760:ILE:HA	1.75	0.68
1:A:1153:LYS:HE2	1:A:1176:LYS:HE3	1.77	0.66
1:A:870:LYS:HD3	1:A:873:LYS:HD3	1.77	0.65
1:A:1116:ASP:OD1	1:A:1139:ARG:NH2	2.26	0.65
1:A:1028:HIS:HE1	1:A:1151:LEU:HG	1.63	0.63
1:A:1211:ARG:NH1	1:A:1288:TRP:O	2.31	0.63
1:A:641:HIS:HB3	1:A:644:PHE:CD2	2.29	0.62
1:A:1180:VAL:HG22	1:A:1185:LEU:HD23	1.82	0.62
1:A:1015:THR:O	1:A:1018:THR:OG1	2.18	0.59
1:A:670:THR:HB	1:A:855:MET:HE3	1.84	0.58
1:A:1121:SER:OG	1:A:1122:LYS:N	2.37	0.58
3:C:4:DC:H5'	3:C:4:DC:H6	1.69	0.58
1:A:1149:LEU:O	1:A:1155:LEU:N	2.34	0.57
1:A:1168:ILE:HD13	2:B:2:DG:H4'	1.86	0.57
1:A:859:ARG:NH1	1:A:978:GLY:O	2.38	0.56
1:A:954:ASP:HB2	1:A:979:ARG:NH2	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1158:ASP:O	1:A:1169:ALA:HA	2.07	0.53
3:C:9:DC:H2''	3:C:10:DG:C8	2.43	0.53
1:A:756:LYS:NZ	1:A:782:ASN:HB3	2.24	0.53
1:A:1002:LYS:HB3	1:A:1159:LEU:HD11	1.91	0.52
1:A:1161:ILE:HD13	1:A:1167:ALA:HB2	1.91	0.51
3:C:7:DG:H1'	3:C:8:DA:C8	2.45	0.51
1:A:919:HIS:HB2	3:C:17:DC:OP1	2.11	0.50
1:A:1003:ARG:HH12	3:C:14:DT:H5''	1.75	0.50
1:A:735:THR:HG21	1:A:749:ILE:HD12	1.92	0.50
1:A:1158:ASP:HB3	1:A:1170:TYR:HB2	1.93	0.50
1:A:1017:GLU:O	1:A:1020:PHE:HB2	2.12	0.49
1:A:1175:ASN:OD1	1:A:1176:LYS:N	2.46	0.49
1:A:991:LEU:HD11	1:A:1026:MET:HE2	1.95	0.48
1:A:756:LYS:HG2	1:A:786:ARG:HG2	1.95	0.48
3:C:16:DC:N4	3:C:17:DC:H42	2.12	0.48
1:A:1162:ASN:C	1:A:1164:ASN:H	2.18	0.47
1:A:679:ALA:O	1:A:791:ARG:NH1	2.48	0.47
1:A:1064:ASP:HA	1:A:1067:CYS:HB2	1.98	0.46
1:A:893:ILE:HG21	1:A:904:MET:HE2	1.96	0.46
1:A:1162:ASN:OD1	1:A:1163:ALA:N	2.48	0.46
1:A:998:VAL:HG12	1:A:1002:LYS:HE3	1.97	0.46
1:A:1064:ASP:OD1	1:A:1065:ASN:N	2.48	0.46
3:C:4:DC:H5'	3:C:4:DC:C6	2.50	0.45
1:A:1179:THR:O	1:A:1184:ASN:HB2	2.15	0.45
1:A:1014:HIS:C	1:A:1017:GLU:HG2	2.41	0.45
1:A:1081:VAL:HG21	1:A:1187:VAL:HG21	1.98	0.45
1:A:1162:ASN:CG	1:A:1163:ALA:H	2.22	0.45
1:A:1178:GLN:HA	1:A:1181:LEU:HB2	1.98	0.45
1:A:1002:LYS:HG2	1:A:1020:PHE:CE1	2.52	0.44
1:A:1014:HIS:HB3	1:A:1017:GLU:OE2	2.17	0.44
1:A:654:GLU:O	1:A:658:ILE:HG13	2.17	0.44
1:A:701:LEU:HB3	1:A:702:PRO:HD3	2.00	0.44
1:A:1133:LYS:C	1:A:1135:SER:H	2.26	0.43
3:C:13:DC:H6	3:C:13:DC:O5'	2.01	0.43
1:A:1178:GLN:O	1:A:1182:ASN:N	2.52	0.43
1:A:747:THR:HA	1:A:750:TYR:HD2	1.83	0.43
1:A:1003:ARG:NH1	3:C:14:DT:OP1	2.52	0.42
1:A:1211:ARG:HH12	1:A:1289:THR:HA	1.84	0.42
1:A:1140:HIS:HD2	1:A:1144:ARG:HD2	1.85	0.42
1:A:658:ILE:HD12	1:A:705:VAL:HB	2.01	0.42
1:A:1154:ILE:O	1:A:1174:GLY:N	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1161:ILE:HD13	1:A:1161:ILE:HA	1.97	0.42
1:A:871:PRO:O	2:B:5:DT:OP1	2.38	0.41
2:B:4:DG:H2'	2:B:5:DT:H72	2.03	0.41
3:C:9:DC:H2''	3:C:10:DG:H8	1.84	0.41
1:A:893:ILE:HD13	1:A:904:MET:HE2	2.01	0.41
1:A:971:GLU:HG2	1:A:972:GLY:H	1.85	0.41
1:A:1033:ILE:HB	1:A:1068:LYS:HE3	2.02	0.41
1:A:735:THR:OG1	1:A:736:TYR:N	2.54	0.41
3:C:17:DC:H6	3:C:17:DC:H2'	1.64	0.41
1:A:1004:LEU:HD13	1:A:1004:LEU:HA	1.90	0.41
1:A:784:TYR:OH	1:A:823:SER:HB3	2.21	0.40
1:A:657:LYS:HG3	1:A:661:LYS:NZ	2.37	0.40
1:A:1081:VAL:O	1:A:1085:VAL:HG23	2.22	0.40
1:A:1178:GLN:HG3	1:A:1182:ASN:OD1	2.22	0.40
1:A:1214:MET:HE3	1:A:1288:TRP:CZ2	2.56	0.40
1:A:1166:GLN:NE2	3:C:13:DC:OP1	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:744:SER:OG	1:A:1162:ASN:O[3_554]	1.91	0.29

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	623/665 (94%)	593 (95%)	30 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	548/593 (92%)	517 (94%)	31 (6%)	18 51

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	662	LYS
1	A	688	LEU
1	A	709	VAL
1	A	714	SER
1	A	722	ASP
1	A	756	LYS
1	A	762	LEU
1	A	765	VAL
1	A	769	LYS
1	A	786	ARG
1	A	789	LEU
1	A	818	ARG
1	A	819	GLN
1	A	848	LEU
1	A	872	LYS
1	A	874	VAL
1	A	910	ARG
1	A	955	LYS
1	A	971	GLU
1	A	994	THR
1	A	1004	LEU
1	A	1010	ASP
1	A	1012	ASN
1	A	1056	LYS
1	A	1133	LYS
1	A	1151	LEU
1	A	1156	ASP
1	A	1173	LEU
1	A	1176	LYS
1	A	1181	LEU

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Mol	Chain	Res	Type
1	A	1208	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	782	ASN
1	A	819	GLN
1	A	860	HIS
1	A	1028	HIS
1	A	1089	GLN
1	A	1140	HIS
1	A	1166	GLN
1	A	1210	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 2 ligands modelled in this entry, 1 is 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	2292	-	28,29,29	1.36	4 (14%)	43,45,45	1.82	8 (18%)

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
5	ADP	A	2292	-	-	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	2292	ADP	C5-C4	4.36	1.46	1.39
5	A	2292	ADP	C5-N7	-2.50	1.34	1.39
5	A	2292	ADP	C5-C6	2.37	1.47	1.41
5	A	2292	ADP	C8-N7	2.34	1.36	1.31

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2292	ADP	C5-C4-N3	-5.91	118.58	126.72
5	A	2292	ADP	N3-C4-N9	4.76	135.27	127.17
5	A	2292	ADP	C2-N3-C4	3.83	121.19	111.83
5	A	2292	ADP	N3-C2-N1	-3.45	123.36	128.58
5	A	2292	ADP	C4-C5-N7	-2.95	107.21	110.58
5	A	2292	ADP	C4-N9-C8	2.46	108.32	105.74
5	A	2292	ADP	C5-N7-C8	2.30	107.06	103.45
5	A	2292	ADP	C3'-C2'-C1'	2.03	105.31	101.46

There are no chirality outliers.

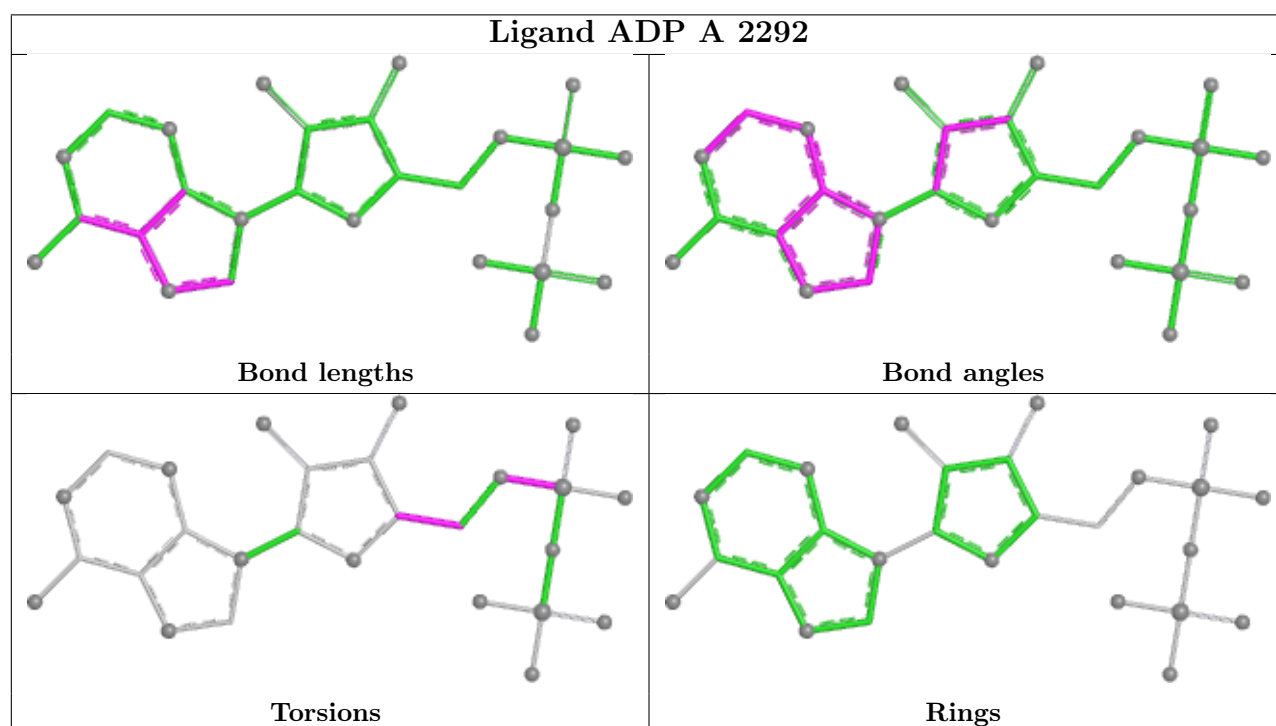
All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	2292	ADP	C5'-O5'-PA-O1A
5	A	2292	ADP	C5'-O5'-PA-O3A
5	A	2292	ADP	O4'-C4'-C5'-O5'
5	A	2292	ADP	C5'-O5'-PA-O2A
5	A	2292	ADP	C3'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

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	629/665 (94%)	0.16	38 (6%) 27 17	129, 176, 221, 240	0
2	B	12/12 (100%)	-0.82	0 100 100	160, 182, 205, 205	0
3	C	17/17 (100%)	-0.17	0 100 100	182, 192, 206, 218	0
All	All	658/694 (94%)	0.14	38 (5%) 29 18	129, 178, 220, 240	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	663	PHE	4.6
1	A	828	ALA	4.2
1	A	1223	THR	3.7
1	A	975	GLN	3.6
1	A	847	ILE	3.4
1	A	968	LYS	3.3
1	A	698	CYS	3.2
1	A	647	LEU	3.2
1	A	1146	PHE	3.2
1	A	1147	LYS	3.1
1	A	762	LEU	3.0
1	A	954	ASP	3.0
1	A	992	PHE	3.0
1	A	792	PHE	2.9
1	A	764	TYR	2.9
1	A	1165	ASP	2.8
1	A	1111	MET	2.8
1	A	711	VAL	2.7
1	A	842	LEU	2.6
1	A	966	LEU	2.6
1	A	1001	LEU	2.5
1	A	1023	LEU	2.5
1	A	1244	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	852	VAL	2.3
1	A	870	LYS	2.3
1	A	996	HIS	2.3
1	A	960	PHE	2.3
1	A	760	ILE	2.3
1	A	1219	LEU	2.3
1	A	1164	ASN	2.3
1	A	723	GLN	2.2
1	A	1084	ILE	2.2
1	A	753	LEU	2.2
1	A	763	LEU	2.2
1	A	709	VAL	2.1
1	A	1222	LEU	2.1
1	A	1243	THR	2.0
1	A	1126	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](#)

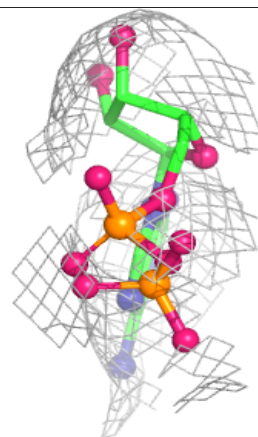
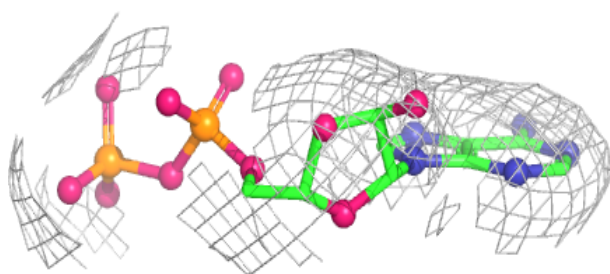
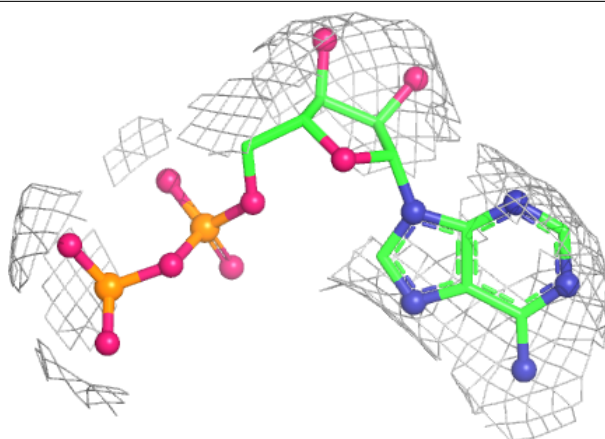
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
5	ADP	A	2292	27/27	0.95	0.06	136,163,170,173	0
4	ZN	A	2291	1/1	0.99	0.08	155,155,155,155	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 ADP A 2292:

$2mF_o - DF_c$ (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.