



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 8SZP / pdb_00008szp
Title : Human DHX9 bound to ADP
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Deposited on : 2023-05-30
Resolution : 2.62 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

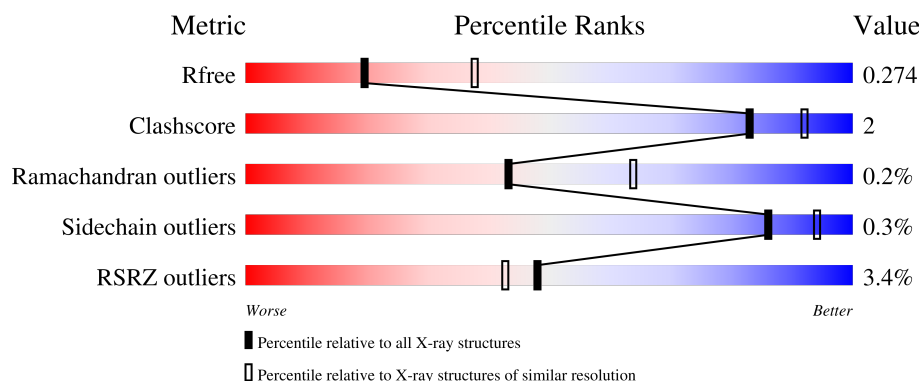
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	1010	
1	B	1010	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 13893 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 ATP-dependent RNA helicase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	855	Total	C	N	O	S	0	1	0
			6777	4325	1160	1248	44			
1	B	860	Total	C	N	O	S	0	1	0
			6817	4347	1172	1254	44			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	149	MET	-	initiating methionine	UNP Q08211
A	1151	ASP	-	expression tag	UNP Q08211
A	1152	TYR	-	expression tag	UNP Q08211
A	1153	LYS	-	expression tag	UNP Q08211
A	1154	ASP	-	expression tag	UNP Q08211
A	1155	ASP	-	expression tag	UNP Q08211
A	1156	ASP	-	expression tag	UNP Q08211
A	1157	ASP	-	expression tag	UNP Q08211
A	1158	LYS	-	expression tag	UNP Q08211
B	149	MET	-	initiating methionine	UNP Q08211
B	1151	ASP	-	expression tag	UNP Q08211
B	1152	TYR	-	expression tag	UNP Q08211
B	1153	LYS	-	expression tag	UNP Q08211
B	1154	ASP	-	expression tag	UNP Q08211
B	1155	ASP	-	expression tag	UNP Q08211
B	1156	ASP	-	expression tag	UNP Q08211
B	1157	ASP	-	expression tag	UNP Q08211
B	1158	LYS	-	expression tag	UNP Q08211

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	68	Total O 68 68	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	66	Total	O	0	0
			66	66		

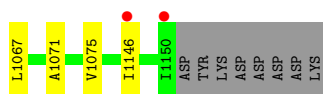
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

[illegible]

Chain B:

79% 6% 15%

Label	Value	Color
ARG	1270	Green
SER	294	Yellow
PHE	297	Green
ILE	304	Green
GLU	306	Green
GLN	307	Green
ALA	310	Yellow
THR	311	Green
LEU	314	Green
GLY	320	Green
ASP	327	Green
ASN	336	Yellow
TRP	339	Yellow
THR	340	Green
LEU	352	Green
ALA	353	Green
ASN	354	Green
ALA	355	Green
LYS	356	Green
ALA	357	Green
ARG	358	Yellow
LEU	370	Yellow
ASN	371	Green
GLN	372	Green
PHE	373	Green
GLN	374	Yellow
LYS	382	Green
ILE	389	Orange
GLN	403	Yellow
GLY	421	Yellow
TYR	422	Yellow
THR	430	Yellow
GLY	435	Yellow
LEU	453	Yellow
THR	457	Yellow
LYS	462	Green
ASP	469	Green
GLU	474	Yellow
ASP	498	Green
ASP	502	Green
LYS	525	Green
ASP	539	Green
GLU	540	Green
ASP	541	Yellow
ASP	550	Green
ASP	556	Green
GLU	573	Green
ASP	577	Green
LYS	586	Green
ASP	588	Green
ASP	593	Grey
LYS	598	Green
ASP	606	Green
ASP	626	Yellow
ASP	649	Green
GLY	658	Green
GLU	659	Green
ASP	660	Green
ASP	661	Green
ASP	674	Green
ASP	683	Green
ASP	695	Green
ASP	703	Green
ASP	709	Green
ASP	7104	Green
ASP	71045	Green
ASP	71050	Green
ASP	71051	Green
ASP	71058	Green
ASP	71061	Green



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	119.10Å 122.26Å 349.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.62 – 2.62 59.62 – 2.62	Depositor EDS
% Data completeness (in resolution range)	99.6 (59.62-2.62) 99.6 (59.62-2.62)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0405	Depositor
R, R_{free}	0.219 , 0.274 0.223 , 0.274	Depositor DCC
R_{free} test set	3769 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	78.3	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.033 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13893	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.42% 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: SO4, EDO, 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	0.45	0/6926	0.83	0/9401
1	B	0.45	0/6967	0.84	0/9458
All	All	0.45	0/13893	0.83	0/18859

There are no bond length outliers.

There are no bond angle outliers.

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	6777	0	6822	31	0
1	B	6817	0	6869	34	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	35	0	0	1	0
4	B	30	0	0	0	0
5	A	12	0	18	0	0
5	B	32	0	48	0	0
6	A	68	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	66	0	0	0	0
All	All	13893	0	13781	65	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 2.

The worst 5 of 65 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:1000:TYR:CD1	1:A:1001:PRO:HA	2.22	0.74
1:B:886:ALA:HB1	1:B:918:LEU:HD11	1.83	0.61
1:B:1000:TYR:CD1	1:B:1001:PRO:HA	2.37	0.58
1:A:1000:TYR:CG	1:A:1001:PRO:HA	2.38	0.58
1:A:457:VAL:HG12	1:A:469:CYS:SG	2.43	0.57

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	848/1010 (84%)	806 (95%)	41 (5%)	1 (0%)	48	69
1	B	855/1010 (85%)	806 (94%)	47 (6%)	2 (0%)	43	64
All	All	1703/2020 (84%)	1612 (95%)	88 (5%)	3 (0%)	43	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1151	ASP
1	B	294	ASN
1	B	658	PRO

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	756/888 (85%)	755 (100%)	1 (0%)	88	96
1	B	761/888 (86%)	757 (100%)	4 (0%)	81	91
All	All	1517/1776 (85%)	1512 (100%)	5 (0%)	86	94

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

Mol	Chain	Res	Type
1	A	799	HIS
1	B	399	GLU
1	B	550	MET
1	B	980	THR
1	B	1015	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	285	GLN
1	B	366	ASN
1	B	1006	HIS
1	B	444	GLN
1	B	904	HIS

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 28 ligands modelled in this entry, 2 are monoatomic - leaving 26 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SO4	A	1307	-	4,4,4	0.34	0	6,6,6	0.10	0
5	EDO	A	1312	-	3,3,3	0.06	0	2,2,2	0.02	0
5	EDO	B	1309	-	3,3,3	0.10	0	2,2,2	0.25	0
5	EDO	B	1312	-	3,3,3	0.07	0	2,2,2	0.13	0
2	ADP	A	1301	3	28,29,29	0.47	0	43,45,45	0.55	0
4	SO4	B	1307	-	4,4,4	0.33	0	6,6,6	0.11	0
4	SO4	A	1303	-	4,4,4	0.34	0	6,6,6	0.16	0
5	EDO	B	1310	-	3,3,3	0.08	0	2,2,2	0.13	0
4	SO4	A	1305	-	4,4,4	0.33	0	6,6,6	0.07	0
4	SO4	A	1309	-	4,4,4	0.33	0	6,6,6	0.08	0
5	EDO	A	1311	-	3,3,3	0.10	0	2,2,2	0.15	0
4	SO4	B	1305	-	4,4,4	0.32	0	6,6,6	0.08	0
5	EDO	B	1315	-	3,3,3	0.09	0	2,2,2	0.20	0
4	SO4	A	1306	-	4,4,4	0.33	0	6,6,6	0.09	0
5	EDO	B	1316	-	3,3,3	0.09	0	2,2,2	0.17	0
5	EDO	B	1314	-	3,3,3	0.11	0	2,2,2	0.17	0
5	EDO	B	1311	-	3,3,3	0.06	0	2,2,2	0.02	0
4	SO4	B	1303	-	4,4,4	0.33	0	6,6,6	0.10	0
4	SO4	A	1308	-	4,4,4	0.33	0	6,6,6	0.08	0
2	ADP	B	1301	3	28,29,29	0.49	0	43,45,45	0.60	0
5	EDO	A	1310	-	3,3,3	0.09	0	2,2,2	0.20	0
4	SO4	B	1306	-	4,4,4	0.32	0	6,6,6	0.08	0
4	SO4	B	1308	-	4,4,4	0.33	0	6,6,6	0.08	0
5	EDO	B	1313	-	3,3,3	0.10	0	2,2,2	0.19	0
4	SO4	A	1304	-	4,4,4	0.32	0	6,6,6	0.09	0
4	SO4	B	1304	-	4,4,4	0.34	0	6,6,6	0.08	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
2	ADP	B	1301	3	-	1/16/32/32	0/3/3/3
5	EDO	A	1310	-	-	1/1/1/1	-
5	EDO	A	1312	-	-	1/1/1/1	-
5	EDO	B	1316	-	-	0/1/1/1	-
5	EDO	B	1310	-	-	1/1/1/1	-
5	EDO	B	1309	-	-	0/1/1/1	-
5	EDO	B	1314	-	-	0/1/1/1	-
5	EDO	B	1311	-	-	1/1/1/1	-
5	EDO	B	1312	-	-	0/1/1/1	-
5	EDO	A	1311	-	-	1/1/1/1	-
5	EDO	B	1313	-	-	1/1/1/1	-
2	ADP	A	1301	3	-	5/16/32/32	0/3/3/3
5	EDO	B	1315	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1301	ADP	PA-O3A-PB-O3B
2	A	1301	ADP	C3'-C4'-C5'-O5'
2	A	1301	ADP	O4'-C4'-C5'-O5'
5	B	1310	EDO	O1-C1-C2-O2
5	B	1311	EDO	O1-C1-C2-O2

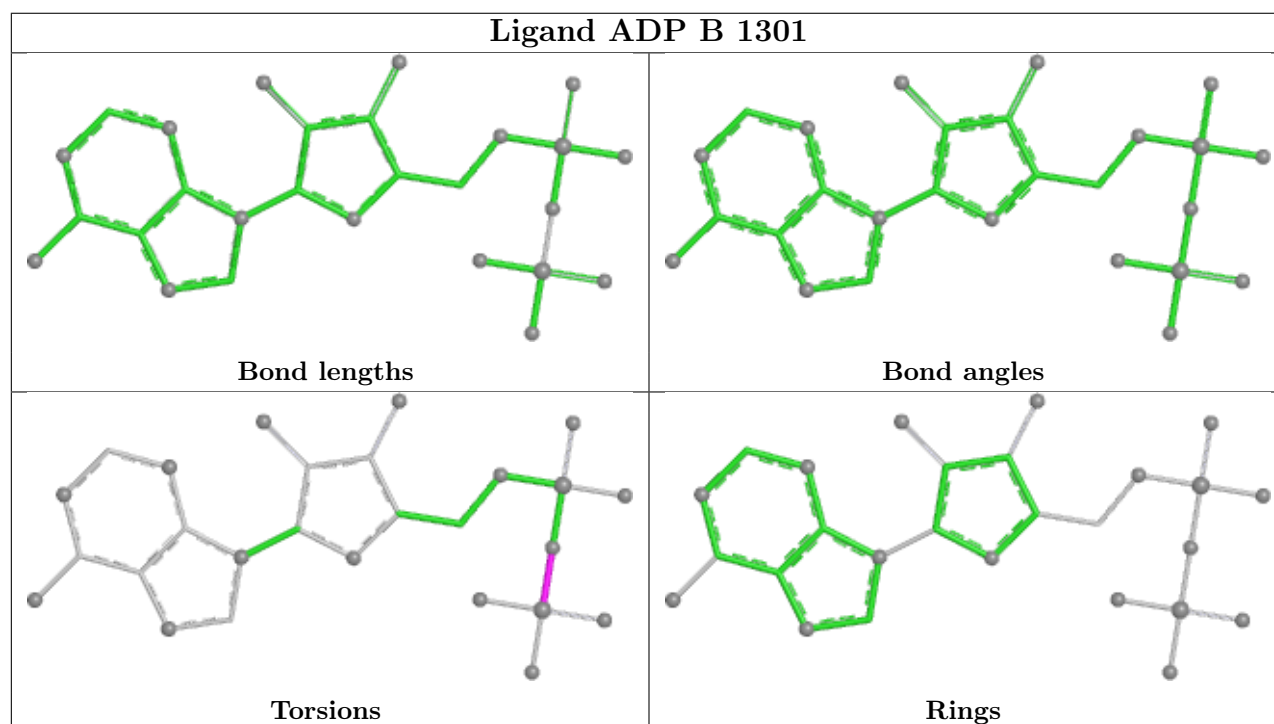
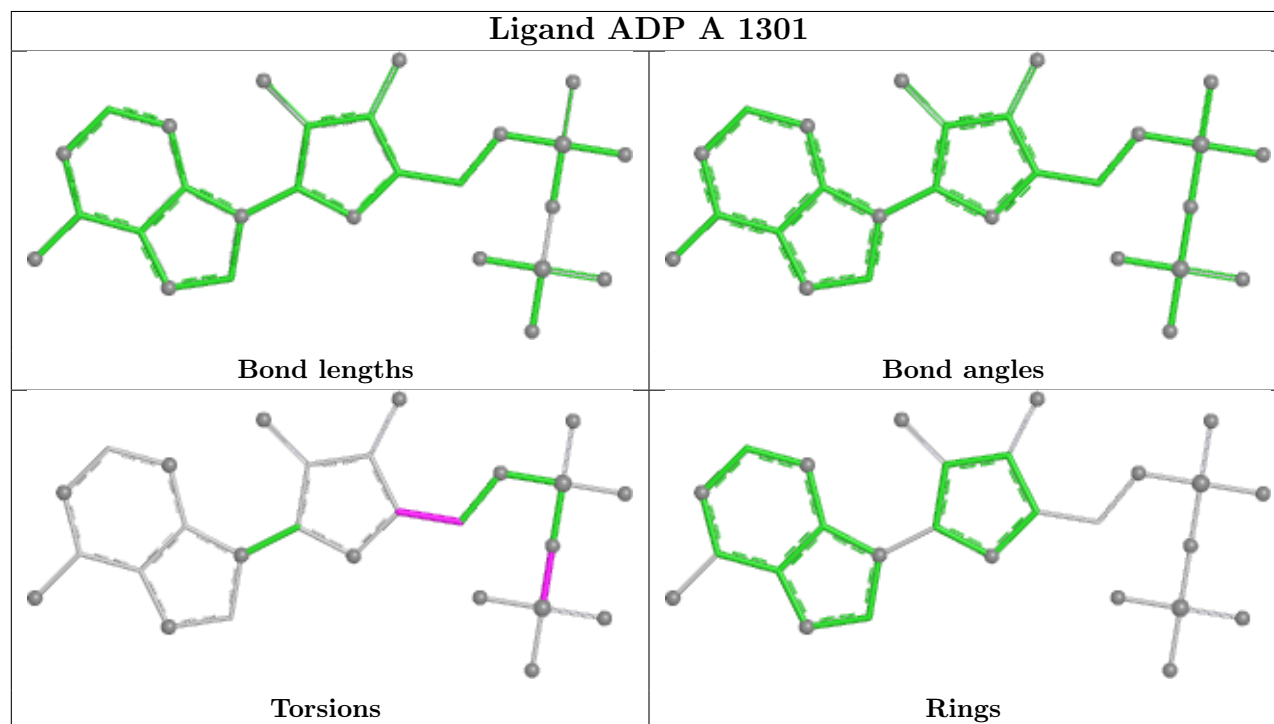
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1307	SO4	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	855/1010 (84%)	0.27	27 (3%)	50 45	51, 85, 135, 173	1 (0%)
1	B	860/1010 (85%)	0.32	32 (3%)	45 40	48, 85, 138, 190	1 (0%)
All	All	1715/2020 (84%)	0.29	59 (3%)	48 43	48, 85, 137, 190	2 (0%)

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	741	ALA	5.1
1	A	739	PHE	4.8
1	B	1150	ILE	4.7
1	B	352	LEU	4.5
1	A	320	PRO	4.3

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](#)

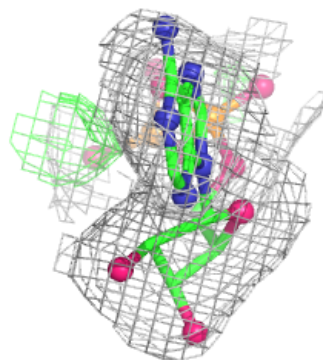
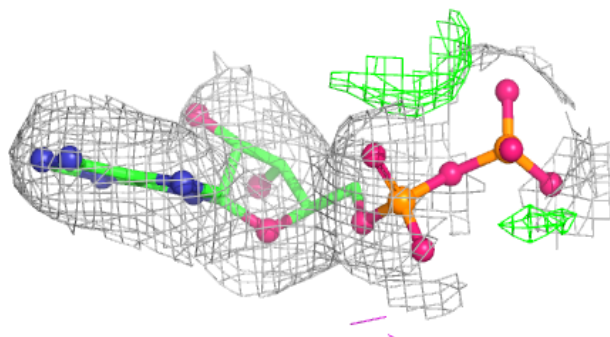
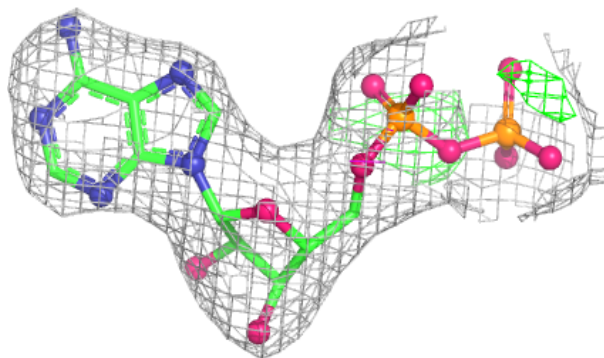
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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	EDO	B	1314	4/4	0.58	0.26	98,101,102,102	0
4	SO4	B	1307	5/5	0.62	0.09	130,141,143,144	0
4	SO4	A	1304	5/5	0.64	0.12	103,111,121,129	0
4	SO4	A	1309	5/5	0.67	0.10	152,155,163,166	0
4	SO4	A	1308	5/5	0.72	0.12	157,158,160,166	0
4	SO4	A	1305	5/5	0.73	0.11	110,120,126,130	0
4	SO4	A	1307	5/5	0.79	0.10	134,141,147,149	0
4	SO4	B	1305	5/5	0.79	0.10	87,96,103,108	0
5	EDO	B	1312	4/4	0.80	0.25	100,100,105,106	0
5	EDO	B	1315	4/4	0.81	0.17	91,91,92,94	0
4	SO4	B	1308	5/5	0.82	0.10	132,137,138,146	0
5	EDO	B	1313	4/4	0.85	0.20	78,86,88,88	0
5	EDO	A	1311	4/4	0.87	0.16	77,84,86,87	0
5	EDO	B	1310	4/4	0.87	0.12	109,114,114,114	0
4	SO4	B	1306	5/5	0.88	0.08	91,109,114,115	0
4	SO4	A	1306	5/5	0.89	0.07	126,143,144,146	0
5	EDO	B	1309	4/4	0.92	0.15	74,76,78,78	0
5	EDO	A	1310	4/4	0.92	0.18	74,76,76,77	0
4	SO4	B	1304	5/5	0.92	0.06	90,96,104,105	0
5	EDO	B	1316	4/4	0.93	0.14	81,82,84,86	0
4	SO4	A	1303	5/5	0.94	0.08	77,80,86,90	0
5	EDO	B	1311	4/4	0.95	0.09	59,60,61,62	4
2	ADP	A	1301	27/27	0.95	0.08	57,77,86,89	0
2	ADP	B	1301	27/27	0.95	0.10	63,95,123,129	0
4	SO4	B	1303	5/5	0.96	0.07	76,82,84,85	0
3	MG	B	1302	1/1	0.98	0.04	71,71,71,71	0
5	EDO	A	1312	4/4	0.98	0.08	57,58,58,59	4
3	MG	A	1302	1/1	0.99	0.04	67,67,67,67	0

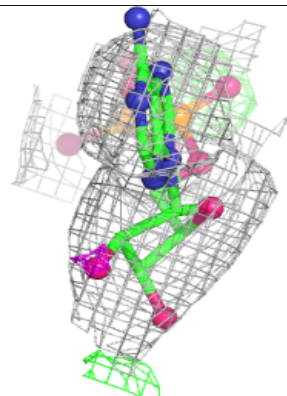
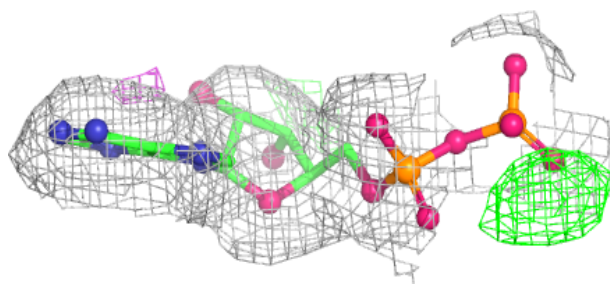
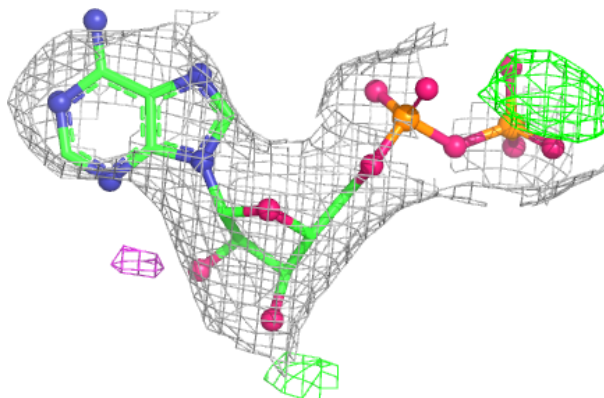
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP A 1301:

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

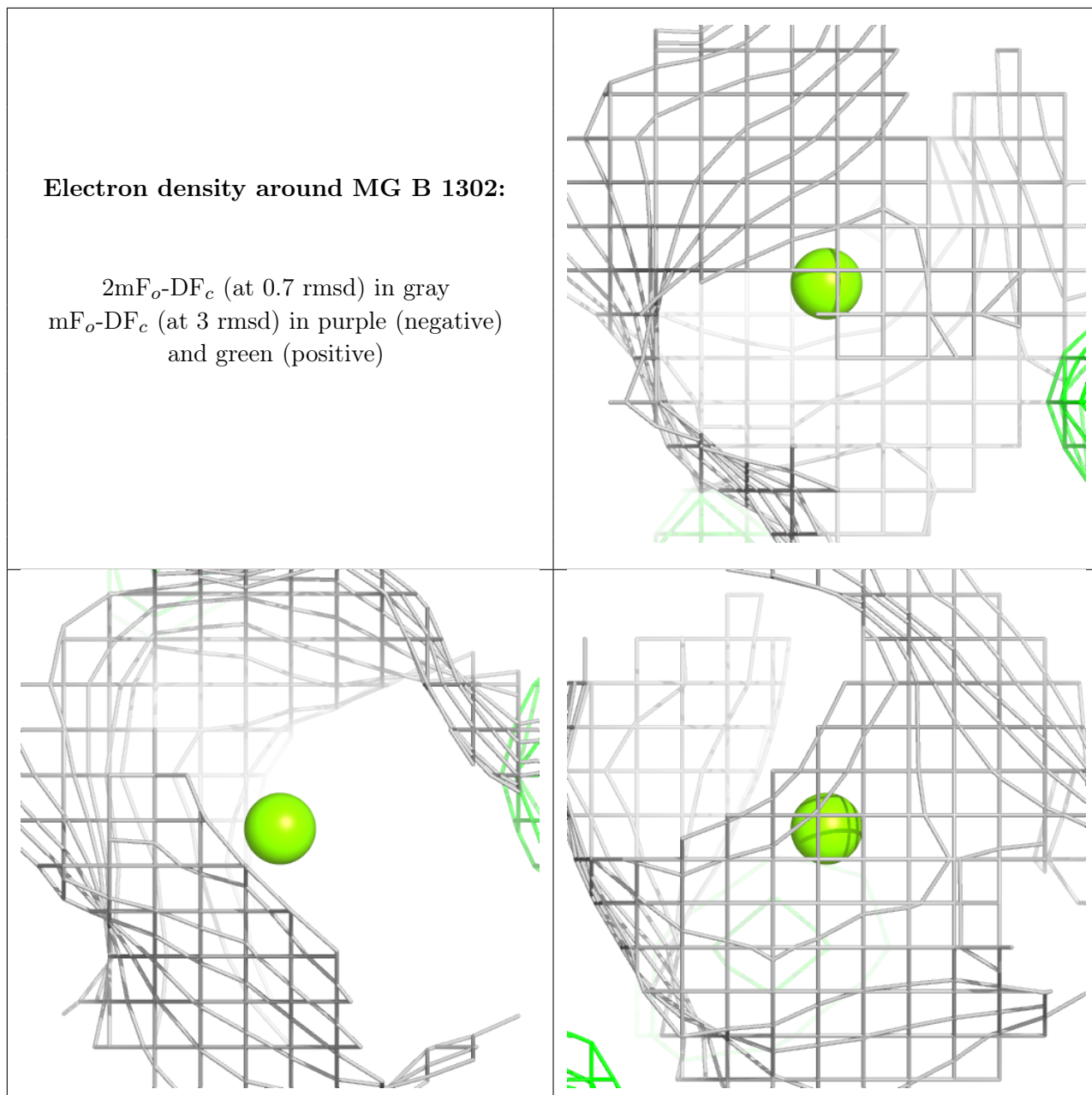
**Electron density around ADP B 1301:**

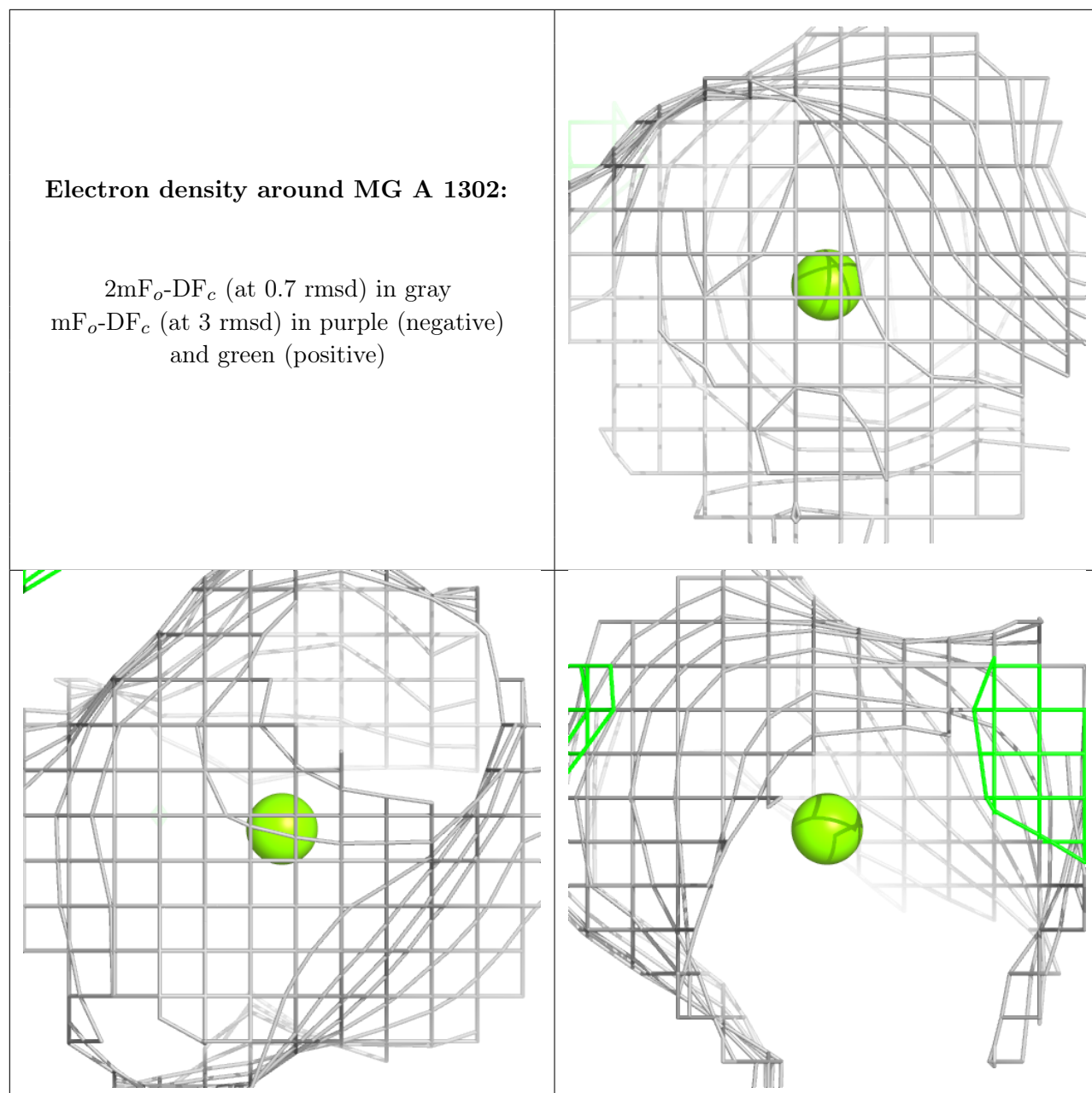
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around MG B 1302:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.