



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:12 AM UTC

PDB ID : 9DK2 / pdb\_00009dk2  
Title : Lexapeptide dehydratase complex LxmKY, ATP bound  
Authors : Randall, G.T.; Bashiri, G.  
Deposited on : 2024-09-07  
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](mailto: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>.

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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

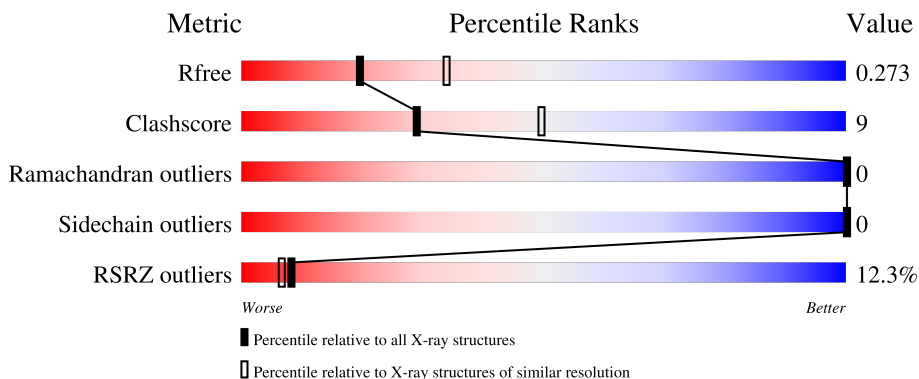
# 1 Overall quality at a glance

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)

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  $\geq 3$ , 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	403	
2	B	378	

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 4876 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 Kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	340	2522	1591	455	469	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP A0A0K1TP15
A	0	ALA	-	expression tag	UNP A0A0K1TP15

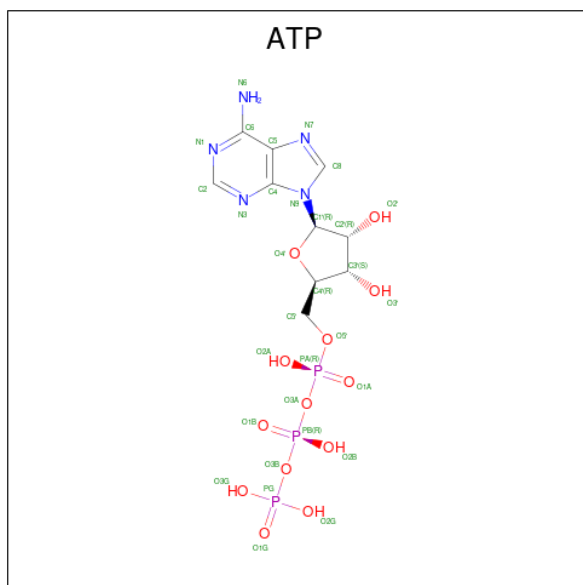
- Molecule 2 is a protein called Lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	308	2235	1400	423	409	3	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	expression tag	UNP A0A0K1TP21
B	0	ALA	-	expression tag	UNP A0A0K1TP21

- Molecule 3 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).

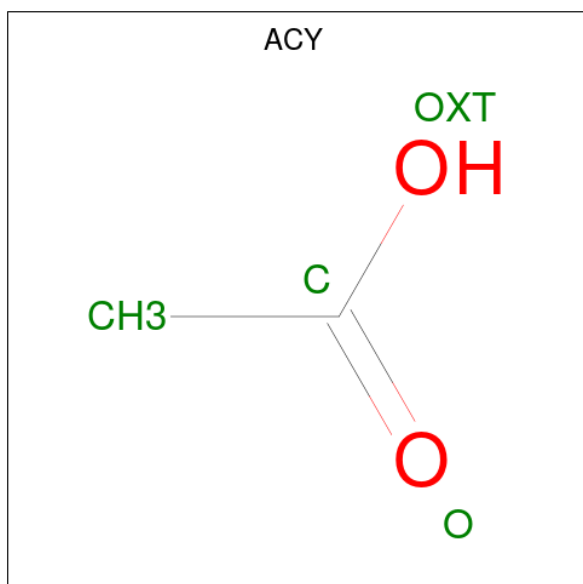


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	31	10	5	13	3	0	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

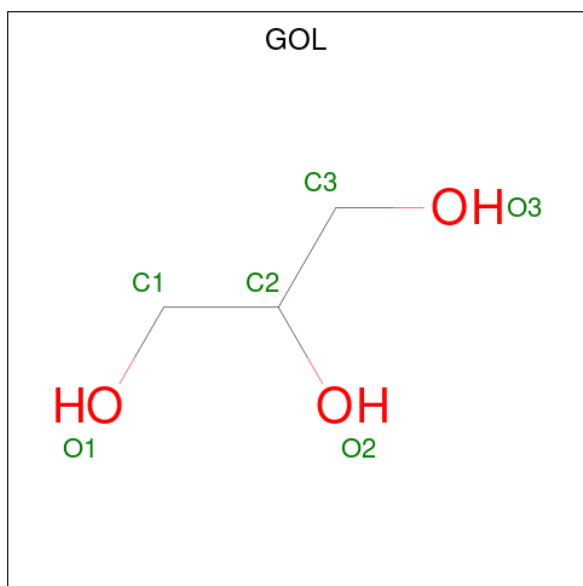
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	2	2	2	0	0

- Molecule 5 is ACETIC ACID (CCD ID: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



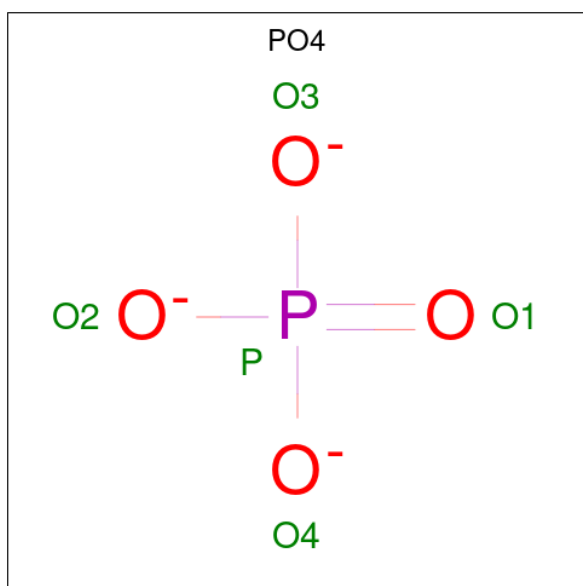
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 7 is PHOSPHATE ION (CCD ID: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	O	P	0	0
			5	4	1		

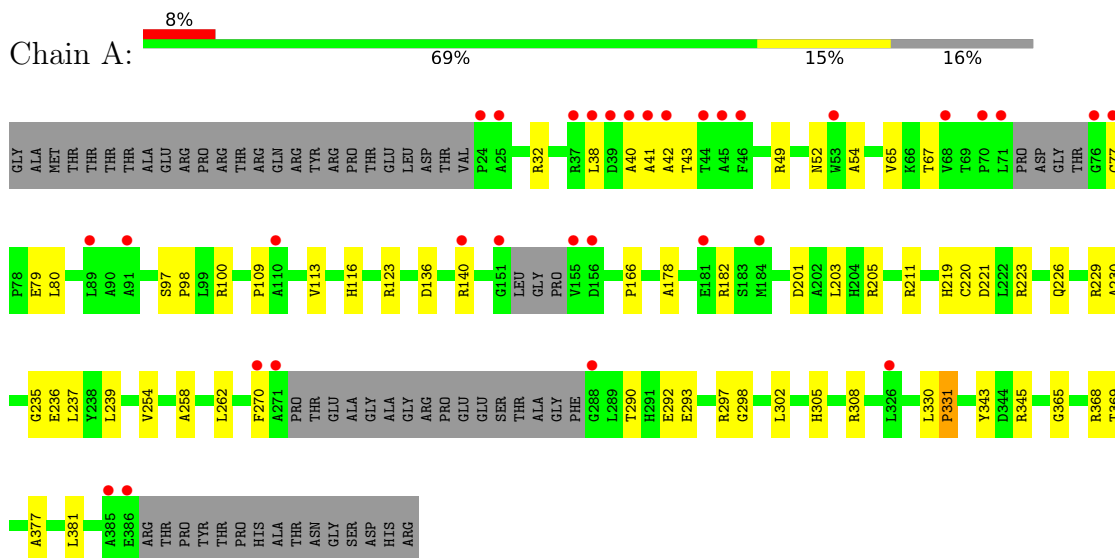
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	44	Total	O	0	0
			44	44		
8	B	27	Total	O	0	0
			27	27		

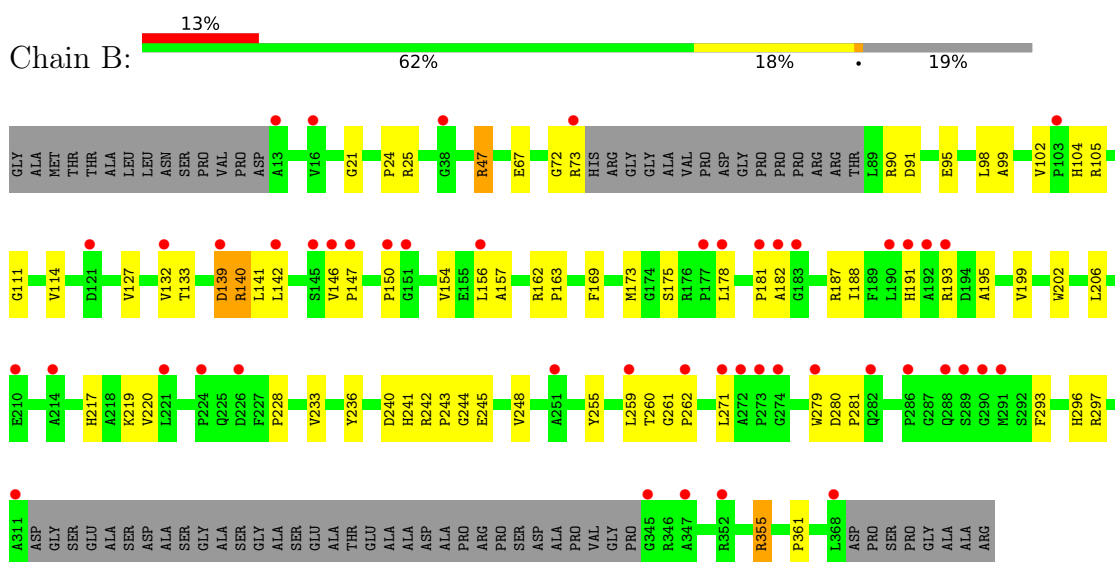
### 3 Residue-property plots [i](#)

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.

- Molecule 1: Kinase



- Molecule 2: Lyase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.72Å 120.66Å 152.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.28 – 2.50 49.28 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.28-2.50) 99.9 (49.28-2.50)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.41 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.8.0349	Depositor
R, $R_{free}$	0.224 , 0.268 0.227 , 0.273	Depositor DCC
$R_{free}$ test set	1916 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	59.7	Xtrriage
Anisotropy	0.474	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 58.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4876	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PO4, MG, GOL, ACY, ATP

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	0.78	3/2580 (0.1%)	1.08	1/3522 (0.0%)
2	B	0.79	3/2287 (0.1%)	1.16	8/3132 (0.3%)
All	All	0.79	6/4867 (0.1%)	1.12	9/6654 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
2	B	0	3
All	All	0	10

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	24	PRO	C-N	9.89	1.46	1.33
2	B	188	ILE	C-N	5.97	1.41	1.33
1	A	331	PRO	C-N	5.85	1.41	1.33
1	A	116	HIS	CE1-NE2	5.75	1.38	1.32
2	B	25	ARG	C-N	-5.58	1.25	1.33
1	A	305	HIS	CE1-NE2	5.29	1.37	1.32

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	24	PRO	O-C-N	7.43	130.20	122.18
2	B	140	ARG	N-CA-C	-7.35	102.58	112.94
2	B	271	LEU	N-CA-C	-6.58	106.20	114.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	140	ARG	CB-CA-C	6.41	121.66	110.64
2	B	163	PRO	N-CA-C	6.20	121.65	114.03
2	B	139	ASP	CA-CB-CG	5.76	118.36	112.60
2	B	25	ARG	CA-C-N	5.08	129.19	120.71
2	B	25	ARG	C-N-CA	5.08	129.19	120.71
1	A	254	VAL	N-CA-C	-5.03	105.80	110.53

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	211	ARG	Sidechain
1	A	223	ARG	Sidechain
1	A	229	ARG	Sidechain
1	A	297	ARG	Sidechain
1	A	308	ARG	Sidechain
1	A	32	ARG	Sidechain
1	A	49	ARG	Sidechain
2	B	162	ARG	Sidechain
2	B	355	ARG	Sidechain
2	B	47	ARG	Sidechain

## 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	2522	0	2437	38	0
2	B	2235	0	2181	44	0
3	A	31	0	12	0	0
4	A	2	0	0	0	0
5	A	4	0	3	0	0
6	A	6	0	8	0	0
7	B	5	0	0	0	0
8	A	44	0	0	1	0
8	B	27	0	0	0	0
All	All	4876	0	4641	82	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 (82) 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)
2:B:127:VAL:HG21	2:B:156:LEU:HD11	1.61	0.81
2:B:142:LEU:HD11	2:B:157:ALA:HB2	1.65	0.76
1:A:77:CYS:SG	1:A:79:GLU:OE1	2.45	0.74
2:B:220:VAL:HG23	2:B:233:VAL:HG22	1.74	0.69
2:B:242:ARG:HB2	2:B:243:PRO:HD3	1.76	0.67
2:B:193:ARG:NH2	2:B:262:PRO:HD3	2.10	0.65
2:B:244:GLY:O	2:B:248:VAL:HG23	1.95	0.65
1:A:38:LEU:HD12	1:A:38:LEU:O	1.96	0.64
2:B:187:ARG:HD2	2:B:280:ASP:OD1	1.96	0.64
2:B:255:TYR:CD1	2:B:259:LEU:HD22	2.34	0.62
1:A:345:ARG:HD2	8:A:611:HOH:O	2.00	0.62
2:B:102:VAL:HB	2:B:105:ARG:HH12	1.65	0.61
1:A:77:CYS:SG	1:A:79:GLU:HB2	2.40	0.61
1:A:290:THR:HB	1:A:293:GLU:HG3	1.85	0.58
1:A:136:ASP:HB3	1:A:140:ARG:HH12	1.71	0.56
2:B:178:LEU:HD11	2:B:217:HIS:CD2	2.42	0.55
2:B:193:ARG:HH22	2:B:262:PRO:HD3	1.72	0.55
1:A:40:ALA:O	1:A:43:THR:HG22	2.07	0.54
2:B:293:PHE:CE1	2:B:297:ARG:NE	2.76	0.54
2:B:72:GLY:O	2:B:73:ARG:CB	2.57	0.53
1:A:38:LEU:HD12	1:A:38:LEU:C	2.35	0.52
1:A:80:LEU:HD21	1:A:109:PRO:HA	1.92	0.51
1:A:100:ARG:NH1	1:A:237:LEU:O	2.44	0.51
1:A:136:ASP:HB3	1:A:140:ARG:NH1	2.25	0.51
1:A:41:ALA:O	1:A:42:ALA:HB3	2.11	0.51
1:A:226:GLN:O	1:A:239:LEU:HD12	2.11	0.50
2:B:195:ALA:O	2:B:199:VAL:HG23	2.12	0.50
2:B:191:HIS:HE1	2:B:228:PRO:HB2	1.76	0.50
2:B:104:HIS:O	2:B:105:ARG:NH1	2.45	0.49
2:B:104:HIS:CD2	2:B:175:SER:HB3	2.48	0.48
2:B:95:GLU:O	2:B:99:ALA:N	2.43	0.48
2:B:220:VAL:O	2:B:220:VAL:HG13	2.13	0.47
2:B:141:LEU:HA	2:B:156:LEU:HD23	1.96	0.47
2:B:241:HIS:HD2	2:B:245:GLU:OE2	1.97	0.47
1:A:201:ASP:O	1:A:205:ARG:HG3	2.15	0.47
1:A:38:LEU:HD13	1:A:43:THR:HG21	1.97	0.47
2:B:47:ARG:HH11	2:B:47:ARG:HB3	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:THR:HG23	1:A:43:THR:O	2.14	0.47
2:B:98:LEU:HD22	2:B:220:VAL:HG11	1.97	0.46
1:A:136:ASP:CB	1:A:140:ARG:HH12	2.28	0.46
1:A:52:ASN:HA	1:A:65:VAL:O	2.16	0.46
1:A:262:LEU:CD2	1:A:302:LEU:HD11	2.45	0.46
1:A:365:GLY:O	1:A:369:THR:HG23	2.16	0.46
2:B:90:ARG:O	2:B:91:ASP:C	2.58	0.46
1:A:41:ALA:C	1:A:43:THR:H	2.24	0.45
1:A:330:LEU:HB3	1:A:331:PRO:HD3	1.97	0.45
2:B:139:ASP:OD1	2:B:140:ARG:HG3	2.16	0.45
2:B:67:GLU:O	2:B:72:GLY:N	2.49	0.45
2:B:355:ARG:NH2	2:B:361:PRO:HG2	2.32	0.45
2:B:191:HIS:O	2:B:260:THR:HG22	2.17	0.44
1:A:290:THR:HG22	1:A:292:GLU:H	1.82	0.44
2:B:202:TRP:CE2	2:B:206:LEU:HD11	2.52	0.44
1:A:343:TYR:OH	1:A:368:ARG:HB2	2.18	0.43
1:A:123:ARG:HG3	1:A:123:ARG:HH21	1.82	0.43
1:A:67:THR:HG22	1:A:113:VAL:HG22	2.01	0.43
2:B:173:MET:HG2	2:B:217:HIS:CE1	2.54	0.43
2:B:202:TRP:CZ2	2:B:206:LEU:HD11	2.53	0.43
1:A:270:PHE:HE2	1:A:298:GLY:HA2	1.84	0.43
2:B:21:GLY:O	2:B:361:PRO:HB2	2.19	0.42
1:A:43:THR:HA	1:A:54:ALA:O	2.20	0.42
2:B:146:VAL:O	2:B:147:PRO:C	2.63	0.42
1:A:221:ASP:O	1:A:226:GLN:HG3	2.19	0.42
1:A:258:ALA:O	1:A:262:LEU:HG	2.19	0.42
1:A:166:PRO:HG3	1:A:203:LEU:HD22	2.02	0.42
2:B:240:ASP:OD1	2:B:242:ARG:HD2	2.20	0.42
1:A:236:GLU:H	1:A:236:GLU:CD	2.28	0.41
2:B:241:HIS:CE1	2:B:279:TRP:CZ2	3.08	0.41
2:B:255:TYR:HB3	2:B:259:LEU:HB2	2.02	0.41
2:B:219:LYS:HD3	2:B:236:TYR:OH	2.21	0.41
2:B:181:PRO:O	2:B:182:ALA:HB3	2.21	0.41
2:B:281:PRO:HB3	2:B:296:HIS:ND1	2.35	0.41
1:A:290:THR:HB	1:A:293:GLU:CG	2.48	0.41
2:B:111:GLY:O	2:B:154:VAL:HG22	2.20	0.41
2:B:132:VAL:HG22	2:B:133:THR:N	2.35	0.41
2:B:191:HIS:HB3	2:B:261:GLY:H	1.86	0.41
1:A:97:SER:HA	1:A:98:PRO:HD3	1.95	0.41
1:A:219:HIS:O	1:A:220:CYS:HB2	2.20	0.41
2:B:169:PHE:CG	2:B:219:LYS:HE3	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ALA:O	1:A:182:ARG:HG2	2.22	0.40
1:A:230:ALA:O	1:A:235:GLY:N	2.52	0.40
1:A:377:ALA:O	1:A:381:LEU:HG	2.20	0.40
2:B:114:VAL:O	2:B:150:PRO:HB3	2.22	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	332/403 (82%)	321 (97%)	11 (3%)	0	100	100
2	B	302/378 (80%)	281 (93%)	21 (7%)	0	100	100
All	All	634/781 (81%)	602 (95%)	32 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	242/302 (80%)	242 (100%)	0	100	100
2	B	213/277 (77%)	213 (100%)	0	100	100
All	All	455/579 (79%)	455 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	HIS
1	A	180	GLN
2	B	363	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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z  > 2$
6	GOL	A	505	-	5,5,5	0.19	0	5,5,5	0.42	0
7	PO4	B	401	-	4,4,4	0.69	0	6,6,6	0.50	0
5	ACY	A	504	-	3,3,3	1.04	0	3,3,3	0.77	0
3	ATP	A	501	4	32,33,33	0.77	2 (6%)	48,52,52	0.81	1 (2%)

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
6	GOL	A	505	-	-	0/4/4/4	-
3	ATP	A	501	4	-	3/22/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	ATP	PA-O3A	2.61	1.62	1.59
3	A	501	ATP	PB-O3A	2.12	1.61	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	ATP	O3G-PG-O1G	2.53	120.68	110.83

There are no chirality outliers.

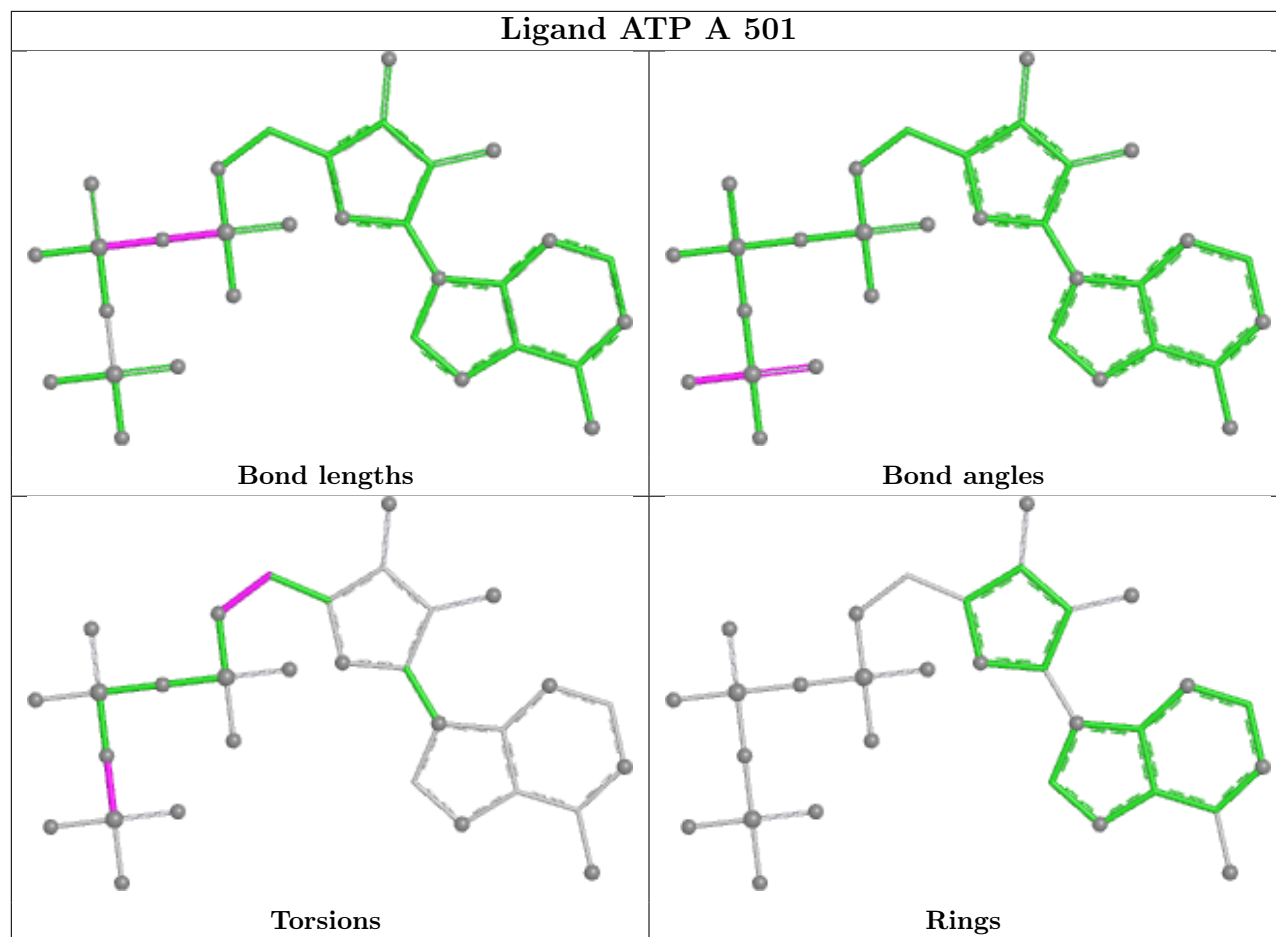
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	ATP	PB-O3B-PG-O2G
3	A	501	ATP	C4'-C5'-O5'-PA
3	A	501	ATP	PB-O3B-PG-O1G

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	340/403 (84%)	0.62	32 (9%) 14 12	36, 63, 112, 145	0
2	B	308/378 (81%)	1.16	48 (15%) 5 4	48, 85, 115, 147	0
All	All	648/781 (82%)	0.88	80 (12%) 8 7	36, 76, 115, 147	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	24	PRO	7.4
1	A	71	LEU	7.4
1	A	386	GLU	6.4
2	B	13	ALA	5.0
1	A	155	VAL	4.9
2	B	311	ALA	4.6
1	A	39	ASP	4.5
2	B	288	GLN	4.4
2	B	368	LEU	4.2
2	B	290	GLY	3.9
1	A	46	PHE	3.8
1	A	156	ASP	3.8
1	A	38	LEU	3.7
2	B	73	ARG	3.7
1	A	45	ALA	3.6
1	A	270	PHE	3.6
2	B	345	GLY	3.6
2	B	156	LEU	3.3
1	A	76	GLY	3.3
2	B	286	PRO	3.3
2	B	181	PRO	3.2
1	A	271	ALA	3.2
2	B	182	ALA	3.1
2	B	16	VAL	3.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	288	GLY	3.1
2	B	214	ALA	3.0
2	B	190	LEU	3.0
1	A	151	GLY	3.0
2	B	183	GLY	3.0
1	A	77	CYS	2.8
1	A	385	ALA	2.8
2	B	145	SER	2.8
1	A	44	THR	2.8
1	A	140	ARG	2.8
2	B	226	ASP	2.8
2	B	259	LEU	2.7
1	A	41	ALA	2.7
2	B	191	HIS	2.7
1	A	53	TRP	2.7
1	A	70	PRO	2.6
2	B	352	ARG	2.6
1	A	110	ALA	2.6
2	B	347	ALA	2.5
2	B	279	TRP	2.5
2	B	103	PRO	2.5
2	B	224	PRO	2.5
2	B	273	PRO	2.5
2	B	193	ARG	2.4
2	B	151	GLY	2.3
1	A	37	ARG	2.3
1	A	326	LEU	2.3
1	A	184	MET	2.3
2	B	177	PRO	2.3
2	B	142	LEU	2.3
2	B	150	PRO	2.3
2	B	289	SER	2.3
2	B	178	LEU	2.3
2	B	121	ASP	2.3
2	B	221	LEU	2.2
2	B	271	LEU	2.2
1	A	40	ALA	2.2
2	B	291	MET	2.2
1	A	42	ALA	2.2
2	B	282	GLN	2.2
2	B	251	ALA	2.2
1	A	91	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	192	ALA	2.1
1	A	181	GLU	2.1
1	A	68	VAL	2.1
2	B	132	VAL	2.1
2	B	146	VAL	2.1
2	B	272	ALA	2.1
2	B	147	PRO	2.1
2	B	262	PRO	2.1
2	B	274	GLY	2.1
2	B	210	GLU	2.1
1	A	25	ALA	2.0
1	A	89	LEU	2.0
2	B	38	GLY	2.0
2	B	139	ASP	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.

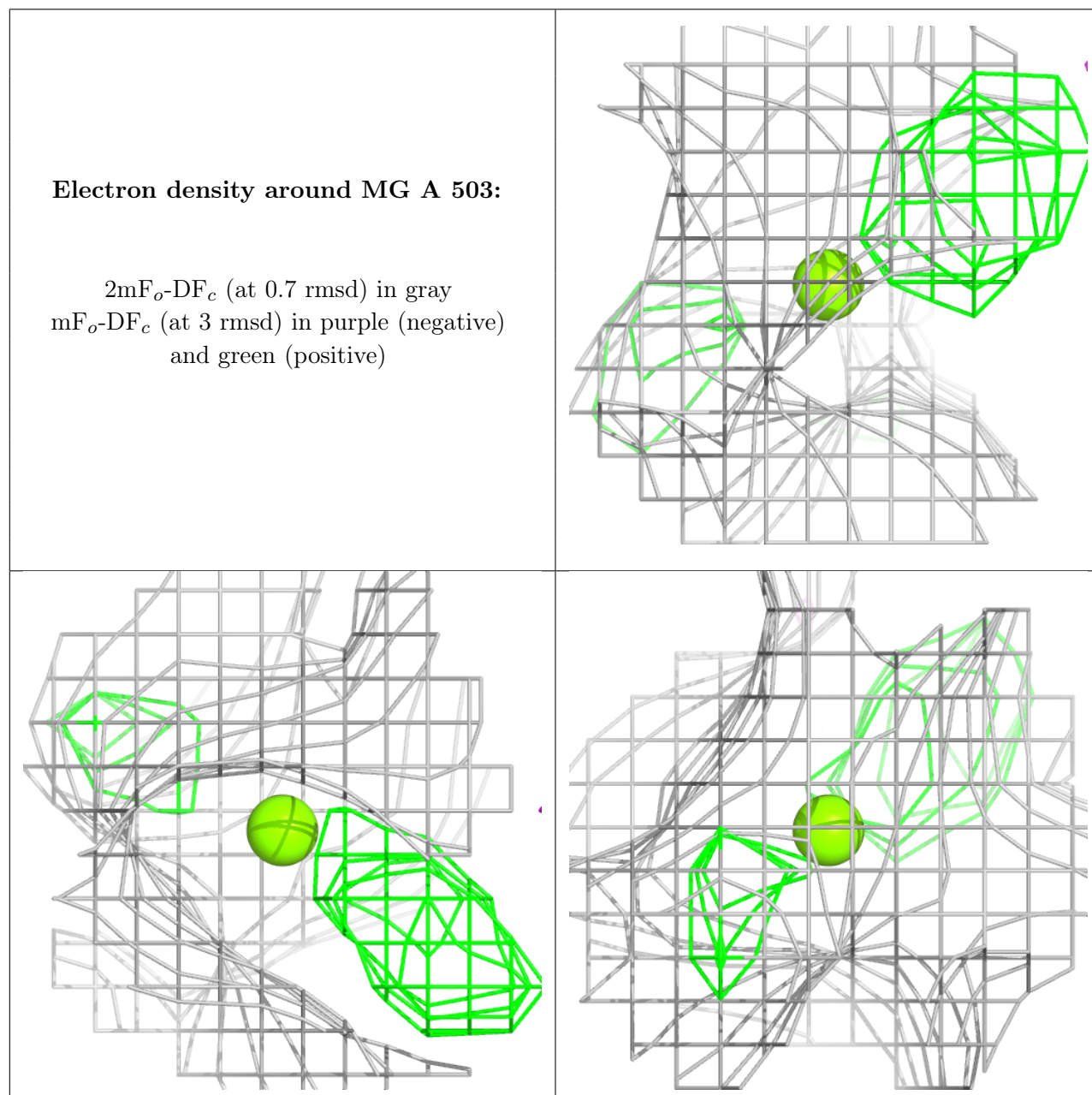
## 6.4 Ligands [i](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	ACY	A	504	4/4	0.79	0.25	62,63,72,78	0
4	MG	A	503	1/1	0.85	0.18	101,101,101,101	0
6	GOL	A	505	6/6	0.87	0.21	66,81,87,87	0
7	PO4	B	401	5/5	0.87	0.14	121,123,131,133	0
3	ATP	A	501	31/31	0.97	0.06	51,63,70,70	0
4	MG	A	502	1/1	0.98	0.06	59,59,59,59	0

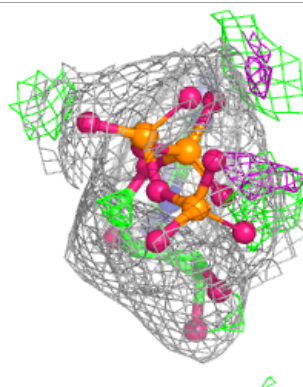
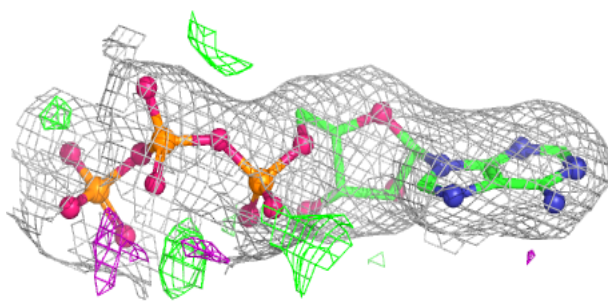
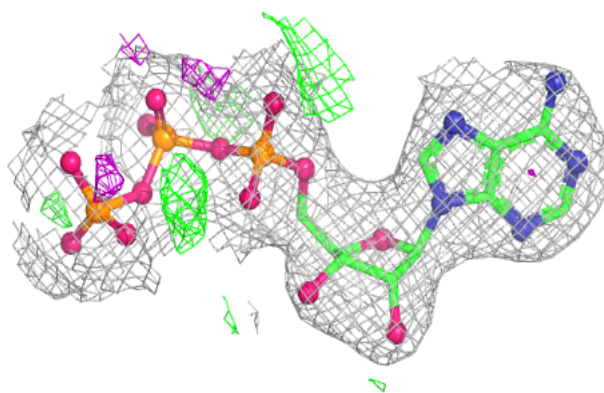
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

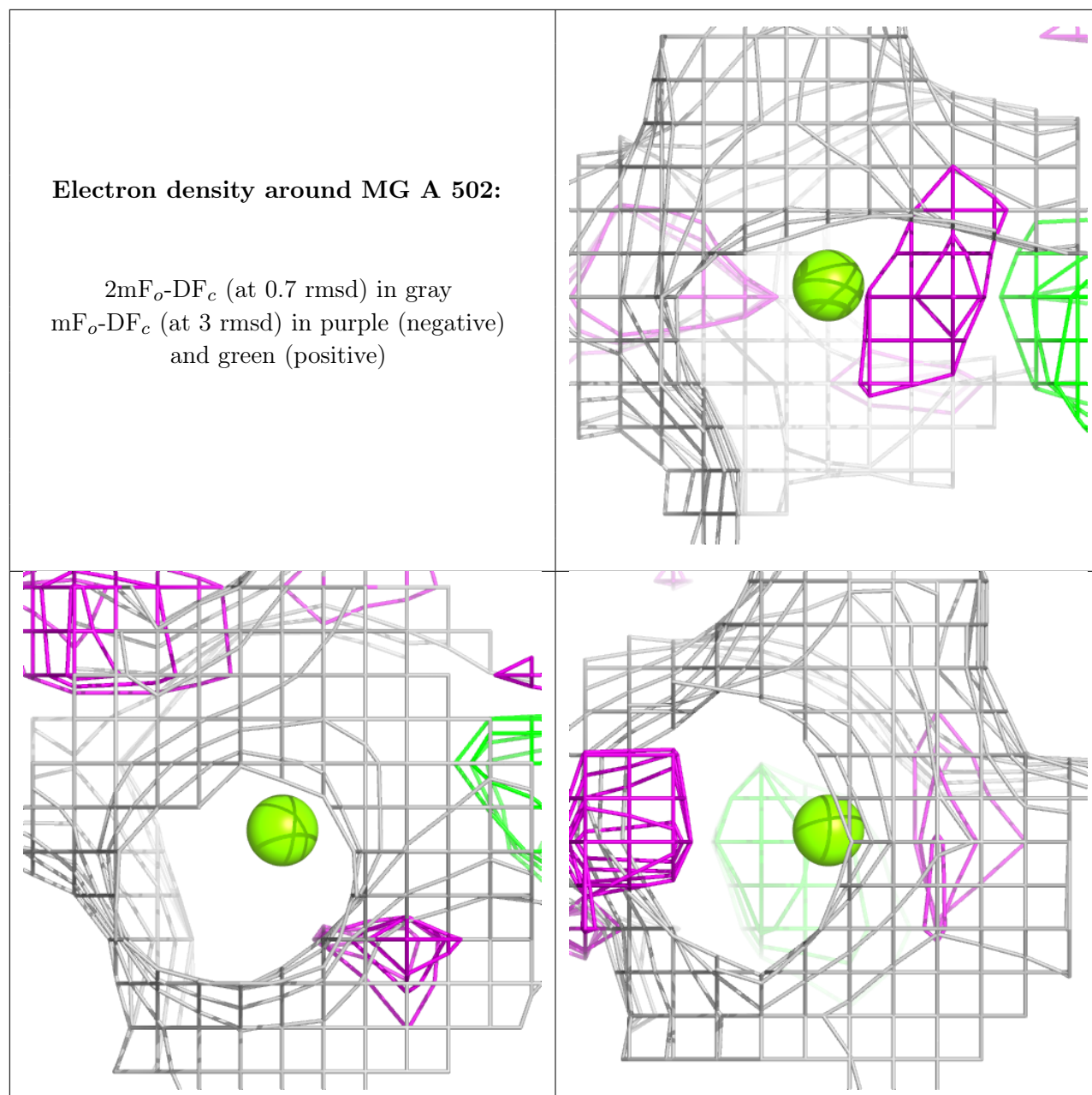
as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



**Electron density around ATP A 501:**

$2mF_o-DF_c$  (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.