



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:36 PM UTC

PDB ID : 4UBF / pdb\_00004ubf  
Title : HsMCAK motor domain complex  
Authors : Welburn, J.P.I.; Talapatra, S.K.  
Deposited on : 2014-08-12  
Resolution : 3.00 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](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>.

---

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)  
Xtrriage (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

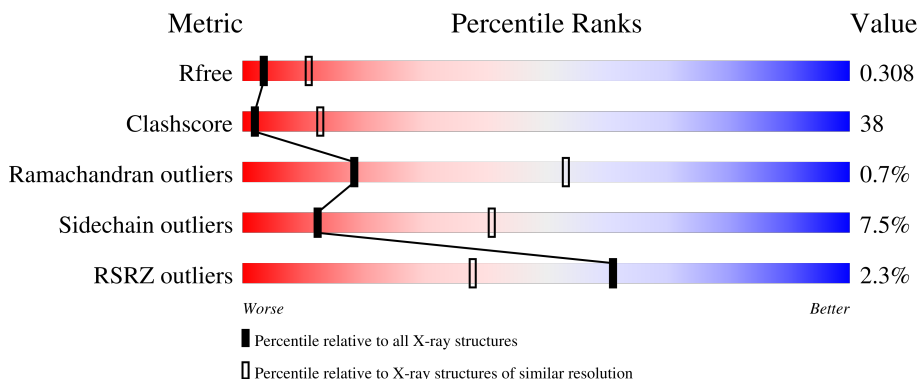
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	387	 43% 32% 20%
1	B	387	 40% 37% 18%
1	C	387	 47% 34% 17%
1	D	387	 35% 40% 17%
2	P	12	 25% 25% 42%

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 9707 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 Kinesin-like protein KIF2C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	309	2322	1490	392	419	21	0	3	0
1	B	319	2404	1537	412	434	21	0	1	0
1	C	322	2412	1546	401	444	21	0	1	0
1	D	322	2337	1501	389	428	19	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207	MET	-	expression tag	UNP Q99661
A	208	GLY	-	expression tag	UNP Q99661
A	209	SER	-	expression tag	UNP Q99661
A	210	SER	-	expression tag	UNP Q99661
A	211	HIS	-	expression tag	UNP Q99661
A	212	HIS	-	expression tag	UNP Q99661
A	213	HIS	-	expression tag	UNP Q99661
A	214	HIS	-	expression tag	UNP Q99661
A	215	HIS	-	expression tag	UNP Q99661
A	216	HIS	-	expression tag	UNP Q99661
A	217	SER	-	expression tag	UNP Q99661
A	218	SER	-	expression tag	UNP Q99661
A	219	GLY	-	expression tag	UNP Q99661
A	220	LEU	-	expression tag	UNP Q99661
A	221	VAL	-	expression tag	UNP Q99661
A	222	PRO	-	expression tag	UNP Q99661
A	223	ARG	-	expression tag	UNP Q99661
A	224	GLY	-	expression tag	UNP Q99661
B	207	MET	-	expression tag	UNP Q99661
B	208	GLY	-	expression tag	UNP Q99661
B	209	SER	-	expression tag	UNP Q99661

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
B	210	SER	-	expression tag	UNP Q99661
B	211	HIS	-	expression tag	UNP Q99661
B	212	HIS	-	expression tag	UNP Q99661
B	213	HIS	-	expression tag	UNP Q99661
B	214	HIS	-	expression tag	UNP Q99661
B	215	HIS	-	expression tag	UNP Q99661
B	216	HIS	-	expression tag	UNP Q99661
B	217	SER	-	expression tag	UNP Q99661
B	218	SER	-	expression tag	UNP Q99661
B	219	GLY	-	expression tag	UNP Q99661
B	220	LEU	-	expression tag	UNP Q99661
B	221	VAL	-	expression tag	UNP Q99661
B	222	PRO	-	expression tag	UNP Q99661
B	223	ARG	-	expression tag	UNP Q99661
B	224	GLY	-	expression tag	UNP Q99661
C	207	MET	-	expression tag	UNP Q99661
C	208	GLY	-	expression tag	UNP Q99661
C	209	SER	-	expression tag	UNP Q99661
C	210	SER	-	expression tag	UNP Q99661
C	211	HIS	-	expression tag	UNP Q99661
C	212	HIS	-	expression tag	UNP Q99661
C	213	HIS	-	expression tag	UNP Q99661
C	214	HIS	-	expression tag	UNP Q99661
C	215	HIS	-	expression tag	UNP Q99661
C	216	HIS	-	expression tag	UNP Q99661
C	217	SER	-	expression tag	UNP Q99661
C	218	SER	-	expression tag	UNP Q99661
C	219	GLY	-	expression tag	UNP Q99661
C	220	LEU	-	expression tag	UNP Q99661
C	221	VAL	-	expression tag	UNP Q99661
C	222	PRO	-	expression tag	UNP Q99661
C	223	ARG	-	expression tag	UNP Q99661
C	224	GLY	-	expression tag	UNP Q99661
D	207	MET	-	expression tag	UNP Q99661
D	208	GLY	-	expression tag	UNP Q99661
D	209	SER	-	expression tag	UNP Q99661
D	210	SER	-	expression tag	UNP Q99661
D	211	HIS	-	expression tag	UNP Q99661
D	212	HIS	-	expression tag	UNP Q99661
D	213	HIS	-	expression tag	UNP Q99661
D	214	HIS	-	expression tag	UNP Q99661
D	215	HIS	-	expression tag	UNP Q99661

*Continued on next page...*

*Continued from previous page...*

Chain	Residue	Modelled	Actual	Comment	Reference
D	216	HIS	-	expression tag	UNP Q99661
D	217	SER	-	expression tag	UNP Q99661
D	218	SER	-	expression tag	UNP Q99661
D	219	GLY	-	expression tag	UNP Q99661
D	220	LEU	-	expression tag	UNP Q99661
D	221	VAL	-	expression tag	UNP Q99661
D	222	PRO	-	expression tag	UNP Q99661
D	223	ARG	-	expression tag	UNP Q99661
D	224	GLY	-	expression tag	UNP Q99661

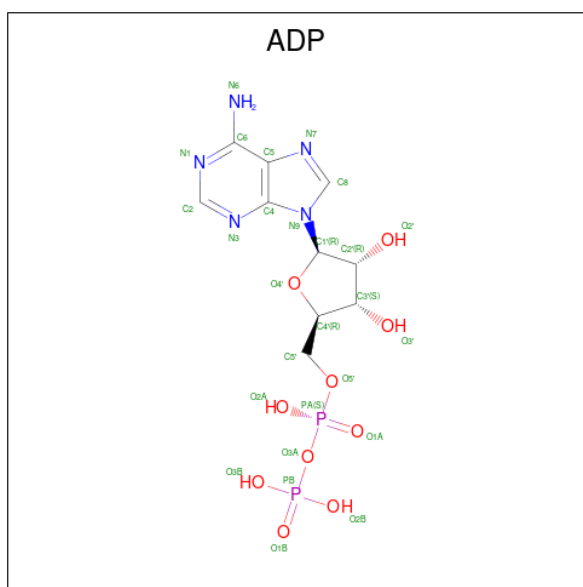
- Molecule 2 is a protein called Kinesin-like protein KIF2C.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace	
			Total	C	N				O
2	P	7	48	27	8	13	0	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	2	Total	Mg	0	0
			2	2		
3	C	2	Total	Mg	0	0
			2	2		
3	D	1	Total	Mg	0	0
			1	1		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>).

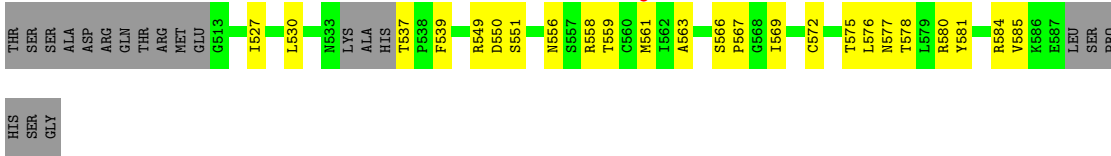


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	C	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

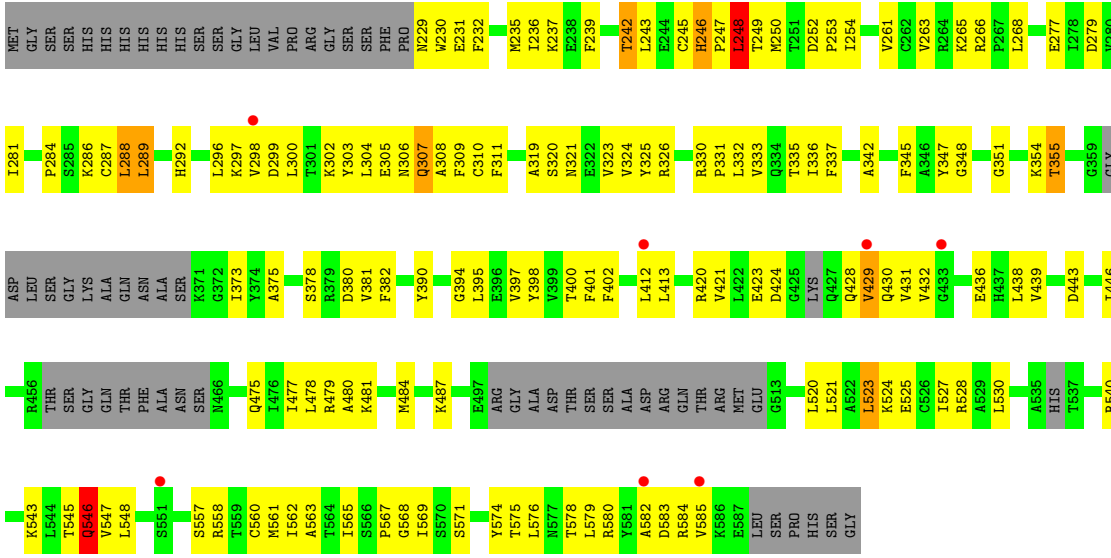
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total	O	0	0
			14	14		
5	B	20	Total	O	0	0
			20	20		
5	C	17	Total	O	0	0
			17	17		
5	D	16	Total	O	0	0
			16	16		
5	P	2	Total	O	0	0
			2	2		

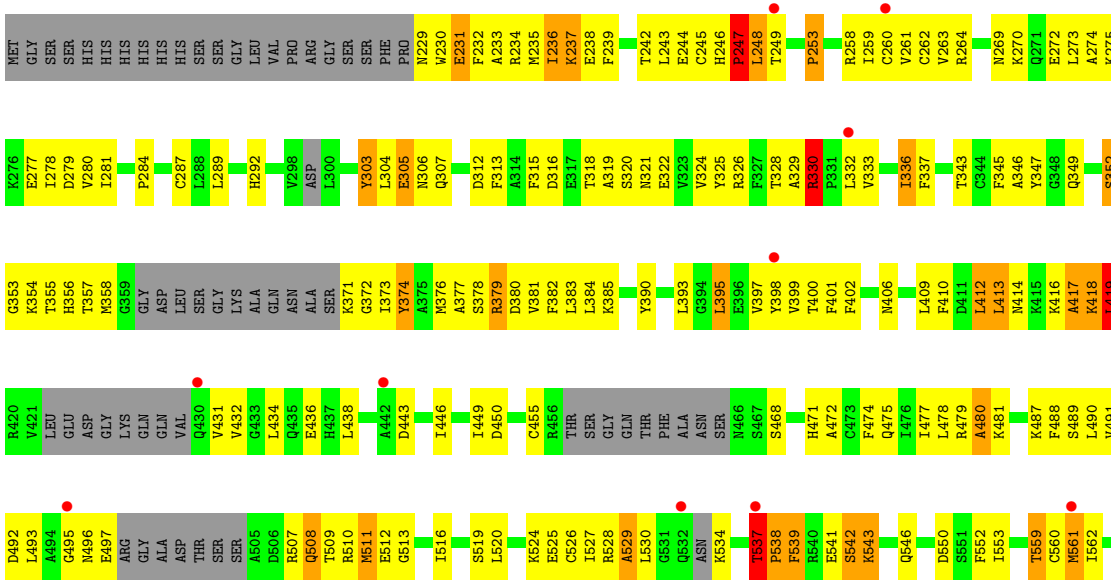




● Molecule 1: Kinesin-like protein KIF2C

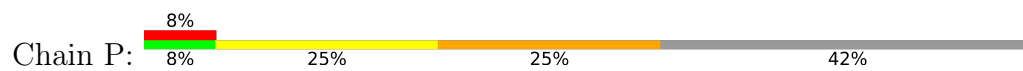


● Molecule 1: Kinesin-like protein KIF2C





- Molecule 2: Kinesin-like protein KIF2C



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.31Å 245.64Å 79.40Å 90.00° 95.84° 90.00°	Depositor
Resolution (Å)	29.49 – 3.00 29.49 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.49-3.00) 99.1 (29.49-3.00)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.33 (at 3.00Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, $R_{free}$	0.264 , 0.286 (Not available) , 0.308	Depositor DCC
$R_{free}$ test set	1761 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	77.5	Xtrriage
Anisotropy	0.294	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 61.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	9707	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	71.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% 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: MG, ADP

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	0.56	2/2368 (0.1%)	1.06	14/3198 (0.4%)
1	B	0.66	3/2443 (0.1%)	1.25	18/3295 (0.5%)
1	C	0.39	3/2451 (0.1%)	1.01	17/3307 (0.5%)
1	D	0.47	2/2372 (0.1%)	1.20	30/3208 (0.9%)
2	P	0.47	0/47	1.91	4/62 (6.5%)
All	All	0.53	10/9681 (0.1%)	1.14	83/13070 (0.6%)

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	B	0	2
1	C	0	1
1	D	0	2
All	All	0	5

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	229	ASN	C-N	-24.10	0.99	1.33
1	A	455[A]	CYS	CA-C	9.62	1.65	1.52
1	A	455[B]	CYS	CA-C	9.62	1.65	1.52
1	B	356	HIS	CA-C	-7.16	1.44	1.52
1	C	246	HIS	C-N	5.42	1.40	1.33

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	229	ASN	CA-C-N	24.46	168.25	121.54
1	B	229	ASN	C-N-CA	24.46	168.25	121.54
1	A	585	VAL	N-CA-C	-20.26	92.92	112.17
1	B	229	ASN	O-C-N	-19.85	91.24	123.00
1	D	491	VAL	N-CA-C	16.64	131.47	108.17

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	229	ASN	Mainchain,Peptide
1	C	560[A]	CYS	Mainchain
1	D	330	ARG	Peptide
1	D	510	ARG	Peptide

## 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	2322	0	2270	122	0
1	B	2404	0	2346	228	0
1	C	2412	0	2331	139	0
1	D	2337	0	2214	235	0
2	P	48	0	33	5	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	1	0	0	0	0
4	A	27	0	12	5	0
4	B	27	0	12	1	0
4	C	27	0	12	3	0
4	D	27	0	12	7	0
5	A	14	0	0	1	0
5	B	20	0	0	3	0
5	C	17	0	0	6	0
5	D	16	0	0	7	0
5	P	2	0	0	1	0
All	All	9707	0	9242	719	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 38.

The worst 5 of 719 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:B:413:LEU:HD12	1:B:437:HIS:CD2	1.14	1.61
1:B:413:LEU:CD1	1:B:437:HIS:HD2	1.02	1.59
1:D:395:LEU:HD12	1:D:480:ALA:CA	1.25	1.55
1:D:395:LEU:CD1	1:D:480:ALA:HA	1.36	1.51
1:D:384:LEU:HD21	1:D:390:TYR:CE2	1.48	1.47

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	300/387 (78%)	261 (87%)	36 (12%)	3 (1%)	12	45
1	B	306/387 (79%)	265 (87%)	40 (13%)	1 (0%)	36	70
1	C	309/387 (80%)	278 (90%)	30 (10%)	1 (0%)	36	70
1	D	308/387 (80%)	266 (86%)	38 (12%)	4 (1%)	9	38
2	P	5/12 (42%)	4 (80%)	1 (20%)	0	100	100
All	All	1228/1560 (79%)	1074 (88%)	145 (12%)	9 (1%)	18	53

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	230	TRP
1	A	353	GLY
1	A	455[A]	CYS
1	A	455[B]	CYS
1	D	330	ARG

### 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	238/332 (72%)	222 (93%)	16 (7%)	15	46
1	B	244/332 (74%)	227 (93%)	17 (7%)	14	44
1	C	244/332 (74%)	232 (95%)	12 (5%)	22	56
1	D	225/332 (68%)	201 (89%)	24 (11%)	6	26
2	P	4/11 (36%)	2 (50%)	2 (50%)	0	0
All	All	955/1339 (71%)	884 (93%)	71 (7%)	12	42

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	378	SER
1	D	395	LEU
1	D	497	GLU
1	B	391	ARG
1	B	358	MET

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	C	257	HIS
1	C	306	ASN
1	D	546	GLN
1	D	356	HIS
1	D	475	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 11 ligands modelled in this entry, 7 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
4	ADP	D	602	3	28,29,29	1.46	5 (17%)	43,45,45	1.83	8 (18%)
4	ADP	B	601	3	28,29,29	1.46	5 (17%)	43,45,45	1.84	8 (18%)
4	ADP	A	602	3	28,29,29	1.41	3 (10%)	43,45,45	1.97	10 (23%)
4	ADP	C	602	-	28,29,29	1.44	5 (17%)	43,45,45	1.78	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
4	ADP	D	602	3	-	2/16/32/32	0/3/3/3
4	ADP	B	601	3	-	1/16/32/32	0/3/3/3
4	ADP	A	602	3	-	7/16/32/32	0/3/3/3
4	ADP	C	602	-	-	4/16/32/32	0/3/3/3

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	602	ADP	C5-C4	4.85	1.47	1.39

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	601	ADP	C5-C4	4.84	1.47	1.39
4	D	602	ADP	C5-C4	4.81	1.47	1.39
4	C	602	ADP	C5-C4	4.80	1.47	1.39
4	C	602	ADP	C5-C6	2.81	1.48	1.41

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	602	ADP	C5-C4-N3	-6.14	118.26	126.72
4	B	601	ADP	C5-C4-N3	-6.07	118.36	126.72
4	D	602	ADP	C5-C4-N3	-6.03	118.41	126.72
4	C	602	ADP	C5-C4-N3	-5.87	118.64	126.72
4	A	602	ADP	N3-C4-N9	5.22	136.04	127.17

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	602	ADP	PA-O3A-PB-O2B
4	A	602	ADP	PA-O3A-PB-O3B
4	A	602	ADP	O4'-C4'-C5'-O5'
4	A	602	ADP	C3'-C4'-C5'-O5'
4	A	602	ADP	C2'-C1'-N9-C8

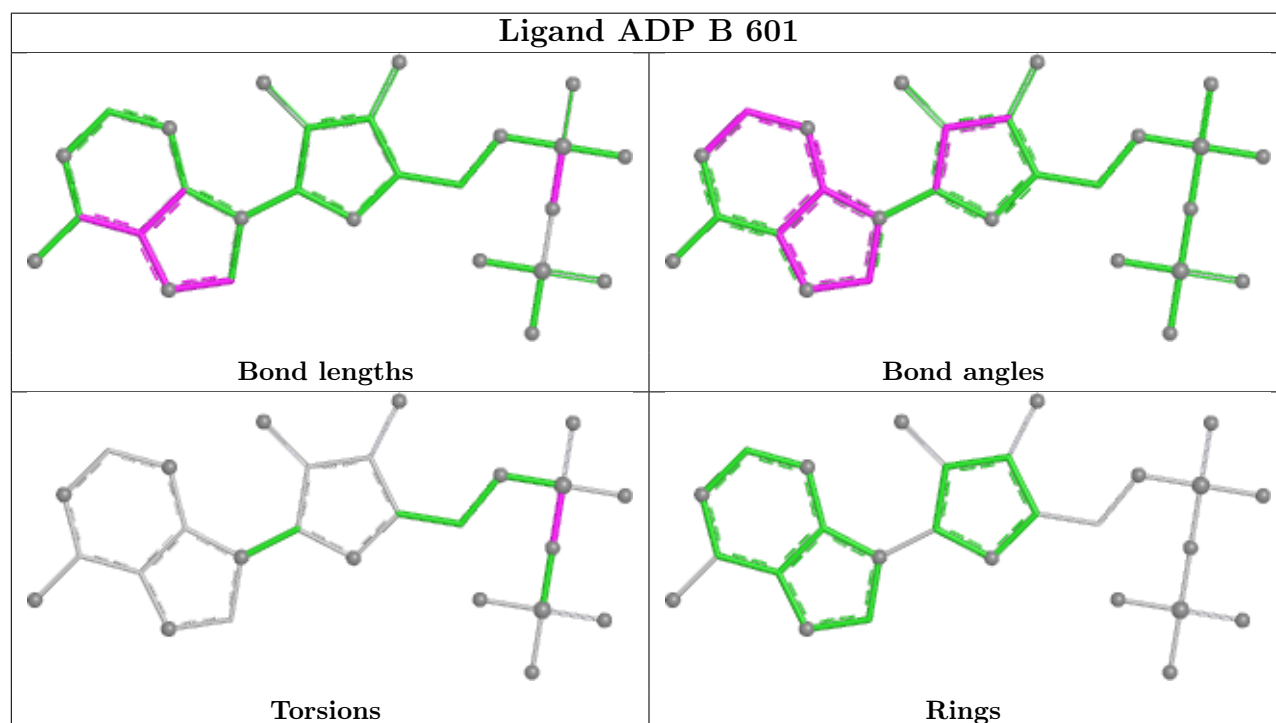
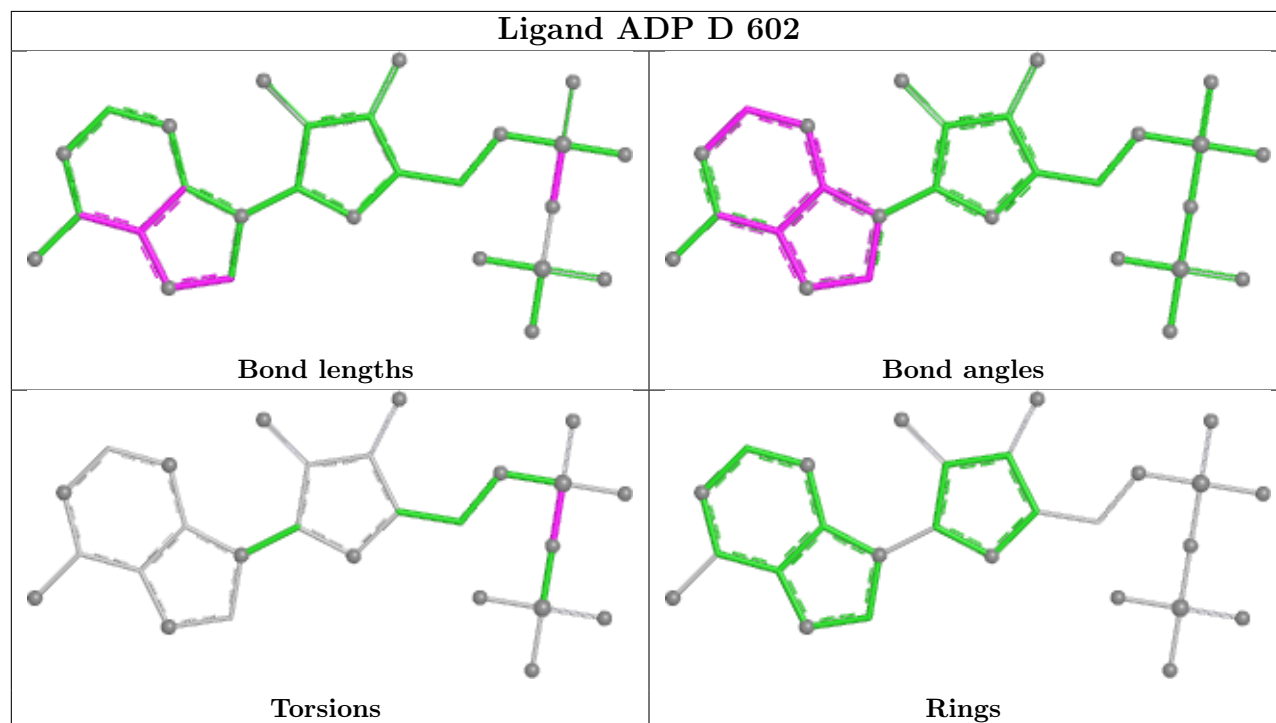
There are no ring outliers.

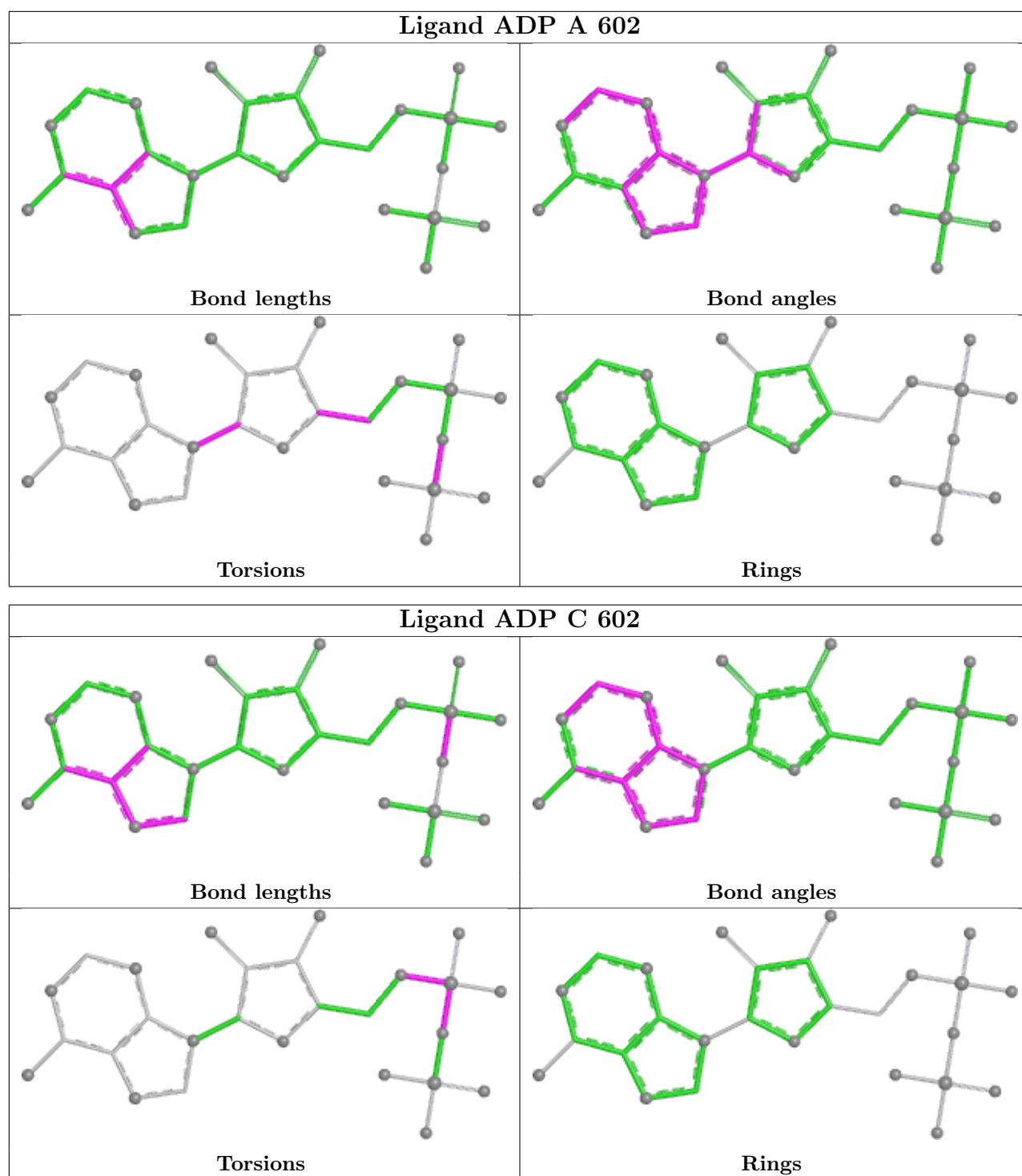
4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	602	ADP	7	0
4	B	601	ADP	1	0
4	A	602	ADP	5	0
4	C	602	ADP	3	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	229:ASN	C	230:TRP	N	1.00

## 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, 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	309/387 (79%)	0.08	3 (0%) 79 59	28, 65, 100, 114	3 (0%)
1	B	319/387 (82%)	0.32	9 (2%) 55 32	29, 64, 93, 113	1 (0%)
1	C	322/387 (83%)	0.28	7 (2%) 62 39	25, 74, 118, 149	1 (0%)
1	D	322/387 (83%)	0.41	10 (3%) 51 30	30, 77, 117, 129	0
2	P	7/12 (58%)	0.40	1 (14%) 6 3	43, 54, 66, 67	0
All	All	1279/1560 (81%)	0.28	30 (2%) 61 38	25, 70, 111, 149	5 (0%)

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	585	VAL	5.1
1	C	433	GLY	4.5
1	B	399	VAL	4.2
1	C	298	VAL	4.0
1	B	397	VAL	3.8

### 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.

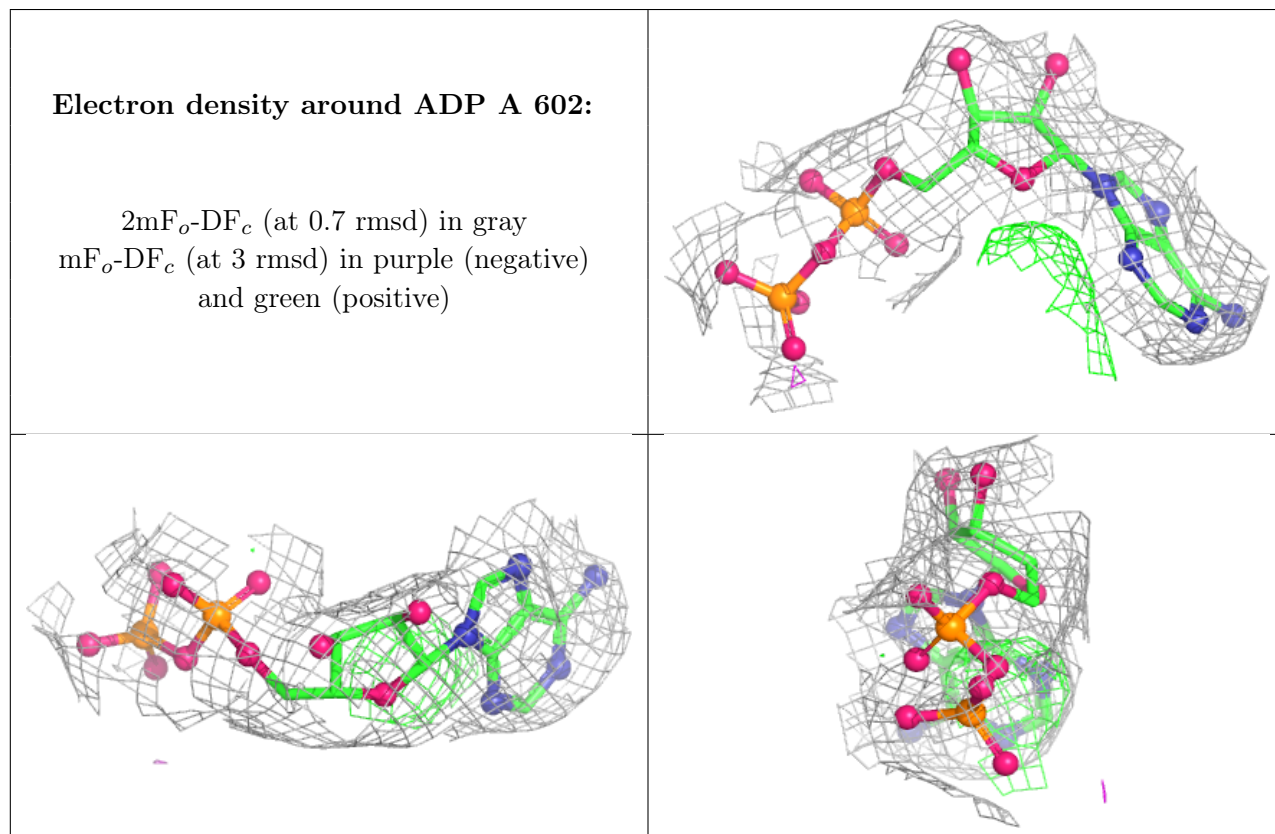
### 6.4 Ligands [i](#)

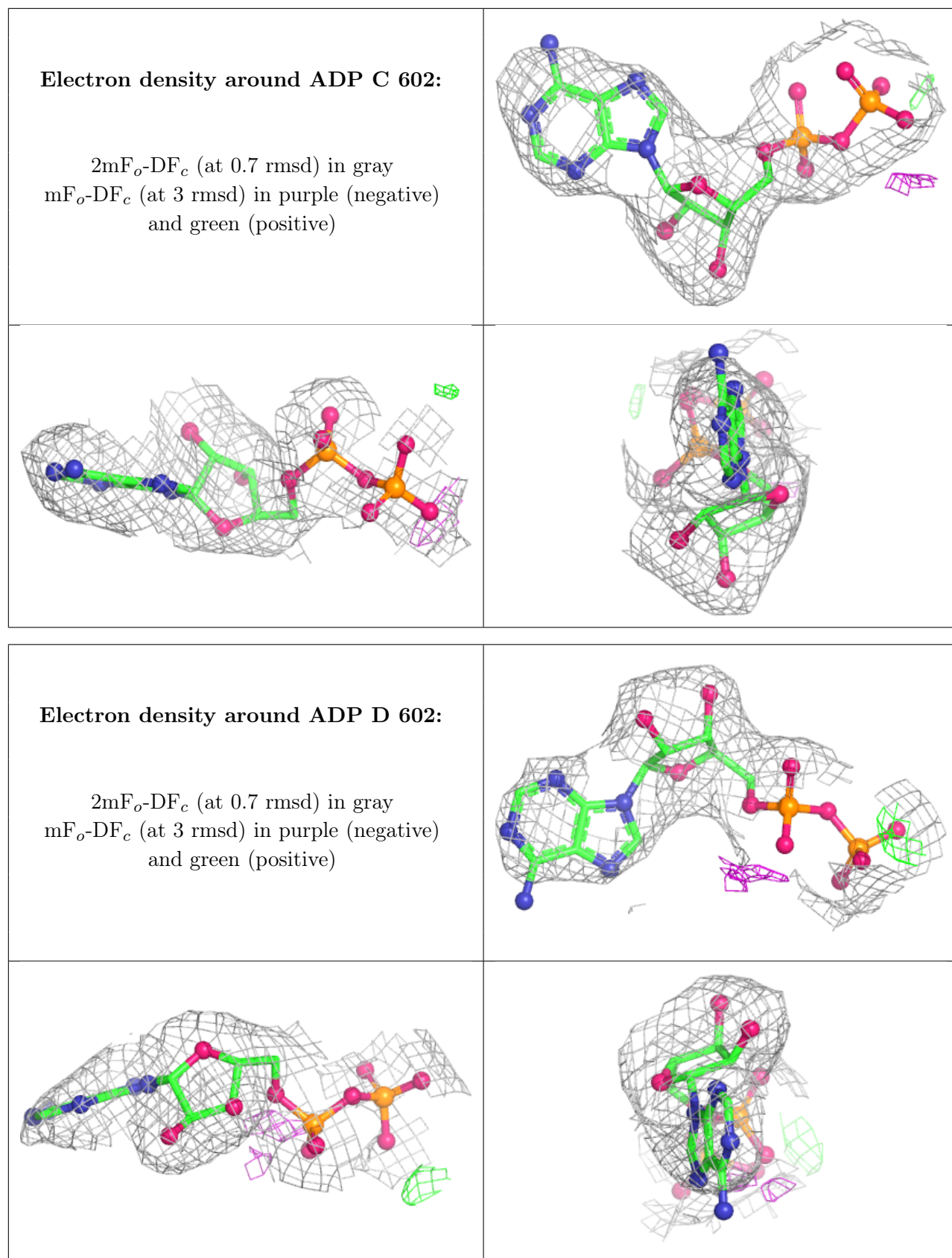
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

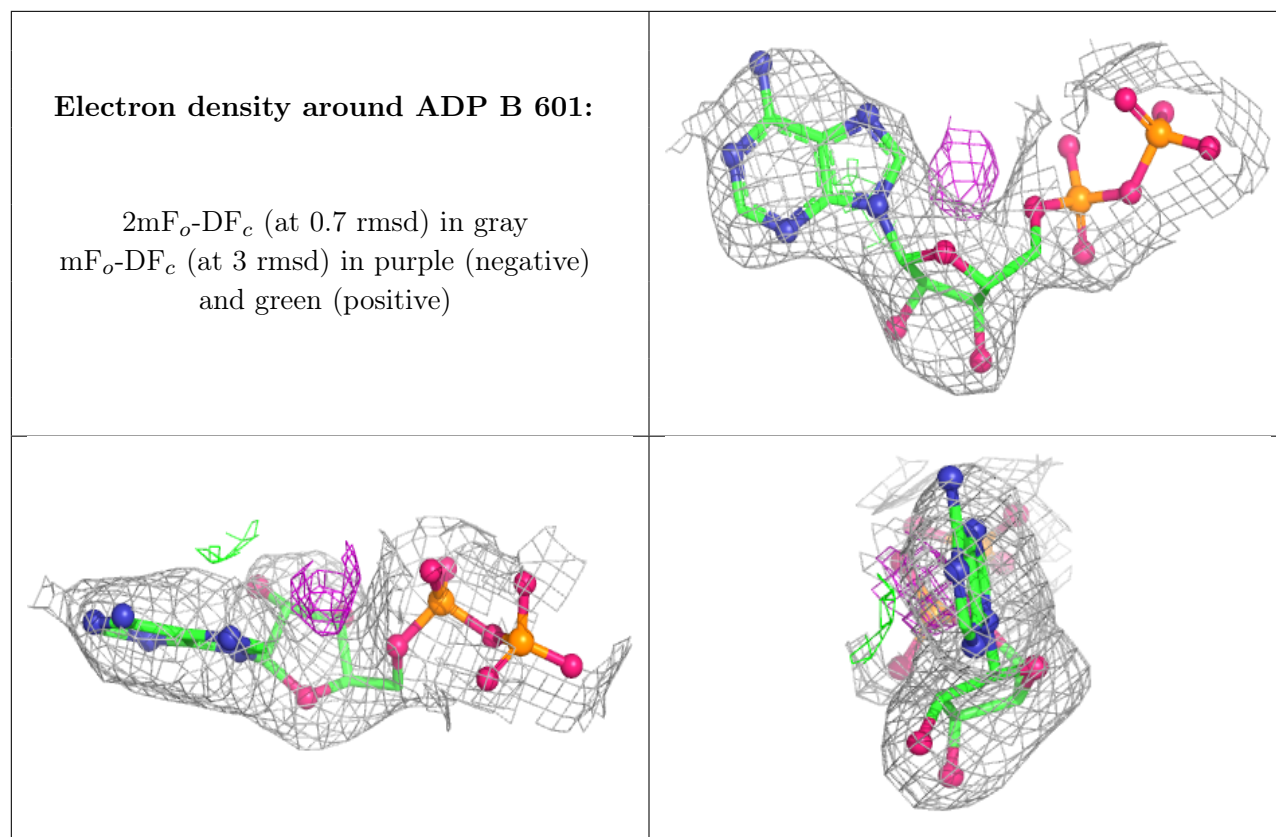
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	C	603	1/1	0.64	0.28	78,78,78,78	0
3	MG	D	601	1/1	0.79	0.12	49,49,49,49	0
4	ADP	A	602	27/27	0.87	0.09	54,79,94,105	0
3	MG	A	601	1/1	0.89	0.06	54,54,54,54	0
4	ADP	C	602	27/27	0.90	0.08	48,66,75,81	0
3	MG	C	601	1/1	0.92	0.16	53,53,53,53	0
4	ADP	D	602	27/27	0.94	0.08	49,74,85,92	0
4	ADP	B	601	27/27	0.95	0.08	38,50,57,59	0
3	MG	A	603	1/1	0.95	0.12	42,42,42,42	0
3	MG	B	603	1/1	0.95	0.04	30,30,30,30	0
3	MG	B	602	1/1	0.96	0.20	41,41,41,41	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.