



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 10:55 PM EDT

PDB ID : 6S3H  
Title : Crystal structure of helicase Pif1 from *Thermus oshimai* in complex with ADP-AlF<sub>4</sub> and (dT)<sub>7</sub>ds11bp  
Authors : Dai, Y.X.; Chen, W.F.; Teng, F.Y.; Liu, N.N.; Hou, X.M.; Dou, S.X.; Rety, S.; Xi, X.G.  
Deposited on : 2019-06-25  
Resolution : 2.06 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

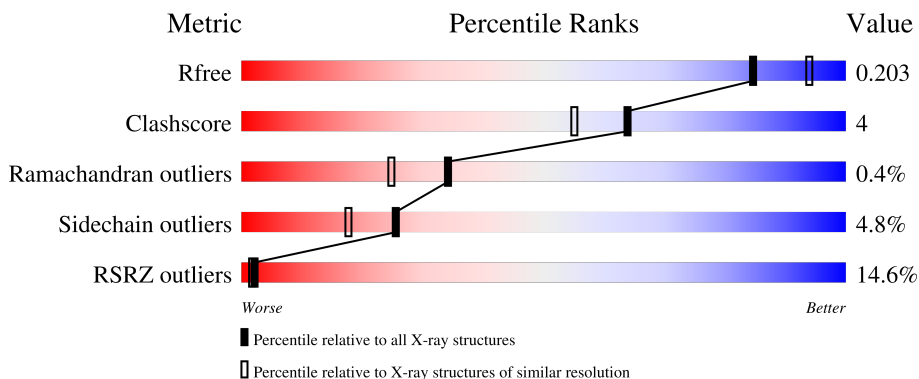
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.06 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))
$R_{free}$	130704	2684 (2.08-2.04)
Clashscore	141614	2801 (2.08-2.04)
Ramachandran outliers	138981	2768 (2.08-2.04)
Sidechain outliers	138945	2768 (2.08-2.04)
RSRZ outliers	127900	2646 (2.08-2.04)

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	444	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>5% • 5%</div> </div> </div>
1	B	444	<div> <div>25%</div> <div> <div></div> <div>80%</div> <div>13% • 5%</div> </div> </div>
2	D	7	<div> <div>14%</div> <div> <div></div> <div>43%</div> <div>14%</div> <div>29%</div> <div>14%</div> </div> </div>
2	E	7	<div> <div>29%</div> <div> <div></div> <div>57%</div> <div>14%</div> <div>29%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	MG	A	1003	-	-	-	X
5	MG	B	601	-	-	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7550 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 PIF1 helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	422	Total	C	N	O	S	0	0	0
			3378	2163	619	593	3			
1	B	423	Total	C	N	O	S	0	0	0
			3390	2171	621	595	3			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	64	THR	ALA	conflict	UNP K7RJ88
A	162	ILE	MET	conflict	UNP K7RJ88
A	456	LEU	PRO	conflict	UNP K7RJ88
B	64	THR	ALA	conflict	UNP K7RJ88
B	162	ILE	MET	conflict	UNP K7RJ88
B	456	LEU	PRO	conflict	UNP K7RJ88

- Molecule 2 is a DNA chain called DNA (5'-D(P\*TP\*TP\*TP\*TP\*TP\*T)-3').

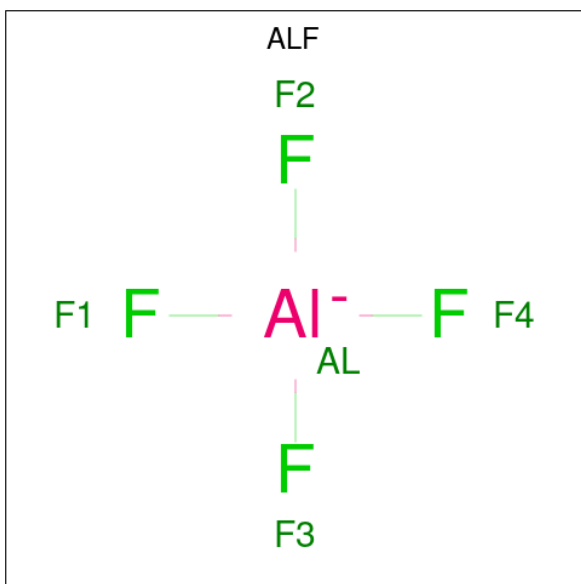
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	6	Total	C	N	O	P	0	0	0
			120	60	12	42	6			
2	E	5	Total	C	N	O	P	0	0	0
			100	50	10	35	5			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is TETRAFLUOROALUMINATE ION (three-letter code: ALF) (formula:  $\text{AlF}_4$ ) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 5	Al 1	F 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	Al	F	0	0
			5	1	4		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

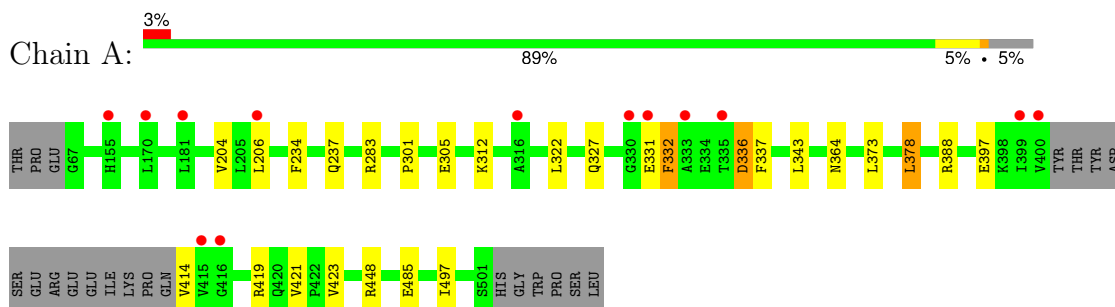
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	347	Total	O	0	0
			347	347		
6	B	127	Total	O	0	0
			127	127		
6	D	19	Total	O	0	0
			19	19		
6	E	3	Total	O	0	0
			3	3		

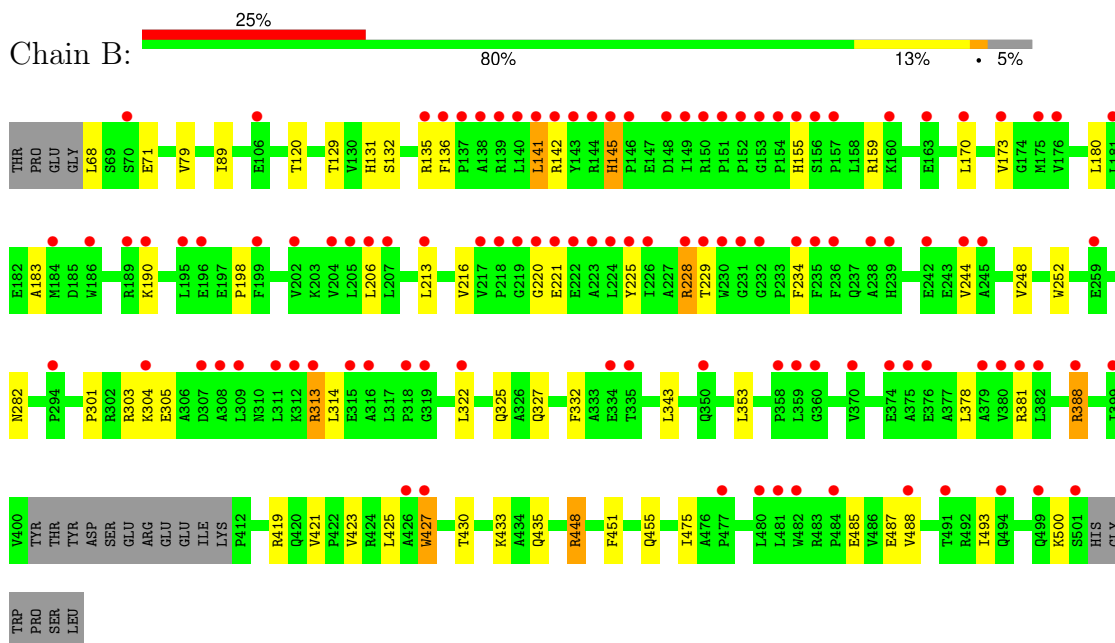
### 3 Residue-property plots

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.

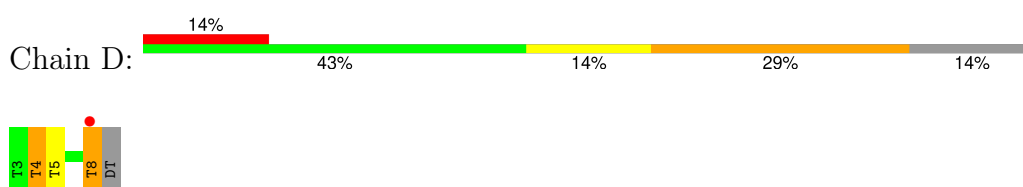
#### • Molecule 1: PIF1 helicase



#### • Molecule 1: PIF1 helicase

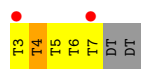


#### • Molecule 2: DNA (5'-D(P\*TP\*TP\*TP\*TP\*TP\*T)-3')



- Molecule 2: DNA (5'-D(P\*TP\*TP\*TP\*TP\*TP\*T)-3')

Chain E: 29% 57% 14% 29%





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.68Å 200.13Å 53.95Å 90.00° 93.44° 90.00°	Depositor
Resolution (Å)	29.51 – 2.06 29.51 – 2.06	Depositor EDS
% Data completeness (in resolution range)	97.0 (29.51-2.06) 97.0 (29.51-2.06)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.84 (at 2.06Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.201 , 0.227 0.205 , 0.203	Depositor DCC
$R_{free}$ test set	2020 reflections (3.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.4	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 51.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7550	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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, ALF

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	0.57	0/3456	0.67	1/4689 (0.0%)
1	B	0.47	0/3469	0.66	0/4707
2	D	1.57	1/130 (0.8%)	1.35	1/196 (0.5%)
2	E	1.55	1/109 (0.9%)	1.19	0/166
All	All	0.59	2/7164 (0.0%)	0.70	2/9758 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	4	DT	C1'-N1	6.10	1.57	1.49
2	D	4	DT	C1'-N1	5.28	1.56	1.49

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	336	ASP	C-N-CA	5.75	136.08	121.70
2	D	8	DT	O4'-C1'-N1	5.13	111.59	108.00

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	3378	0	3450	9	0
1	B	3390	0	3463	47	0
2	D	120	0	74	3	0
2	E	100	0	61	7	0
3	A	27	0	12	0	0
3	B	27	0	12	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	347	0	0	1	0
6	B	127	0	0	0	0
6	D	19	0	0	0	0
6	E	3	0	0	0	0
All	All	7550	0	7072	59	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 4.

All (59) 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:378:LEU:HD21	1:A:421:VAL:HG21	1.38	1.03
1:B:131:HIS:HD2	2:E:6:DT:H1'	1.24	1.00
1:B:313:ARG:HH21	1:B:427:TRP:HB2	1.35	0.88
1:B:129:THR:HG23	1:B:132:SER:H	1.46	0.81
1:B:131:HIS:CD2	2:E:6:DT:H1'	2.13	0.79
1:B:313:ARG:HH12	1:B:425:LEU:HD13	1.53	0.73
1:B:313:ARG:NH1	1:B:425:LEU:HD13	2.04	0.72
1:B:381:ARG:HH11	1:B:388:ARG:HE	1.41	0.66
1:B:451:PHE:H	1:B:455:GLN:HE22	1.43	0.66
1:B:421:VAL:HG23	1:B:423:VAL:HG22	1.79	0.65
1:B:120:THR:HG21	1:B:433:LYS:O	1.97	0.65
1:B:313:ARG:NH2	1:B:427:TRP:HB2	2.12	0.63
1:B:248:VAL:HG11	1:B:493:ILE:HG23	1.81	0.62
1:B:313:ARG:HH11	1:B:314:LEU:HB2	1.65	0.61
1:A:301:PRO:HD2	1:A:305:GLU:OE1	2.04	0.58
1:B:301:PRO:HD2	1:B:305:GLU:OE1	2.04	0.57
1:B:129:THR:HG21	2:E:7:DT:OP1	2.06	0.56
2:E:3:DT:H1'	2:E:4:DT:C2	2.41	0.56
2:D:4:DT:C7	2:D:5:DT:H72	2.38	0.54
1:B:213:LEU:HB2	1:B:435:GLN:HE22	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:ARG:HB2	1:B:145:HIS:CD2	2.44	0.53
1:B:430:THR:HG21	2:E:5:DT:OP1	2.09	0.52
1:B:343:LEU:HD21	1:B:423:VAL:HG23	1.91	0.52
2:D:4:DT:H72	2:D:5:DT:H72	1.91	0.52
1:A:234:PHE:H	1:A:237:GLN:HE21	1.58	0.52
1:B:448:ARG:O	1:B:448:ARG:HG3	2.10	0.51
1:B:141:LEU:HD13	1:B:183:ALA:HB2	1.93	0.51
1:B:213:LEU:H	1:B:435:GLN:HE22	1.60	0.50
1:B:430:THR:HG23	1:B:433:LYS:H	1.76	0.49
1:B:131:HIS:HD2	2:E:6:DT:C1'	2.11	0.49
1:B:131:HIS:CE1	1:B:180:LEU:HD13	2.49	0.48
1:B:304:LYS:HE3	1:B:448:ARG:NH2	2.29	0.48
1:A:336:ASP:N	1:A:337:PHE:HB2	2.29	0.47
1:B:173:VAL:HG21	1:B:206:LEU:HD13	1.96	0.47
1:A:448:ARG:O	1:A:448:ARG:HG3	2.14	0.47
1:B:170:LEU:HD23	1:B:206:LEU:HD22	1.97	0.46
1:B:228:ARG:HG2	1:B:229:THR:N	2.29	0.46
1:B:303:ARG:HE	1:B:433:LYS:HZ1	1.64	0.46
1:B:451:PHE:H	1:B:455:GLN:NE2	2.12	0.46
1:A:343:LEU:HD13	6:A:1105:HOH:O	2.14	0.46
1:B:282:ASN:HD21	1:B:475:ILE:H	1.63	0.46
1:B:131:HIS:ND1	1:B:136:PHE:HB2	2.31	0.46
1:B:353:LEU:HD23	1:B:423:VAL:HG12	1.98	0.45
1:B:170:LEU:HB3	1:B:206:LEU:HD22	1.99	0.45
1:B:485:GLU:HA	1:B:488:VAL:HG22	1.99	0.44
1:B:129:THR:HG22	1:B:132:SER:HB3	1.99	0.44
1:B:216:VAL:HG13	2:E:4:DT:O2	2.18	0.44
1:A:378:LEU:CD2	1:A:421:VAL:HG21	2.28	0.44
1:B:79:VAL:HG11	1:B:89:ILE:HD11	1.99	0.44
1:B:198:PRO:HG2	1:B:244:VAL:HB	1.99	0.43
1:B:234:PHE:CD2	1:B:485:GLU:HG3	2.55	0.42
1:A:397:GLU:O	2:D:8:DT:H1'	2.20	0.41
1:B:213:LEU:HB2	1:B:435:GLN:NE2	2.34	0.41
1:B:248:VAL:HG21	1:B:493:ILE:HD12	2.02	0.41
1:B:71:GLU:CD	1:B:252:TRP:H	2.22	0.41
1:B:327:GLN:HE22	1:B:419:ARG:HH11	1.68	0.41
1:B:304:LYS:HE3	1:B:448:ARG:HH22	1.84	0.41
1:A:327:GLN:HE22	1:A:419:ARG:HH11	1.69	0.41
1:B:381:ARG:HD2	1:B:388:ARG:HG3	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	418/444 (94%)	406 (97%)	10 (2%)	2 (0%)	29	19
1	B	419/444 (94%)	404 (96%)	14 (3%)	1 (0%)	47	39
All	All	837/888 (94%)	810 (97%)	24 (3%)	3 (0%)	34	25

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	332	PHE
1	A	331	GLU
1	B	220	GLY

### 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	350/371 (94%)	336 (96%)	14 (4%)	31	24
1	B	352/371 (95%)	332 (94%)	20 (6%)	20	12
All	All	702/742 (95%)	668 (95%)	34 (5%)	25	18

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	204	VAL
1	A	206	LEU
1	A	283	ARG

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Mol	Chain	Res	Type
1	A	312	LYS
1	A	322	LEU
1	A	332	PHE
1	A	364	ASN
1	A	373	LEU
1	A	378	LEU
1	A	388	ARG
1	A	414	VAL
1	A	423	VAL
1	A	485	GLU
1	A	497	ILE
1	B	68	LEU
1	B	135	ARG
1	B	141	LEU
1	B	145	HIS
1	B	155	HIS
1	B	159	ARG
1	B	190	LYS
1	B	221	GLU
1	B	225	TYR
1	B	228	ARG
1	B	313	ARG
1	B	322	LEU
1	B	325	GLN
1	B	332	PHE
1	B	378	LEU
1	B	388	ARG
1	B	427	TRP
1	B	448	ARG
1	B	487	GLU
1	B	500	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	GLN
1	A	237	GLN
1	A	327	GLN
1	A	364	ASN
1	A	494	GLN
1	B	131	HIS
1	B	212	GLN

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Mol	Chain	Res	Type
1	B	282	ASN
1	B	327	GLN
1	B	435	GLN
1	B	455	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 monosaccharides 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	$\# Z  > 2$
3	ADP	A	1001	5,4	24,29,29	1.08	1 (4%)	29,45,45	0.84	1 (3%)
4	ALF	A	1002	5,3	4,4,4	1.45	0	-		
3	ADP	B	602	5,4	24,29,29	0.86	0	29,45,45	0.74	1 (3%)
4	ALF	B	603	5,3	4,4,4	1.38	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
3	ADP	A	1001	5,4	-	2/12/32/32	0/3/3/3
3	ADP	B	602	5,4	-	1/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	ADP	PB-O2B	-3.90	1.40	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	ADP	C5-C6-N6	2.25	123.74	120.31
3	B	602	ADP	C5-C6-N6	2.22	123.69	120.31

There are no chirality outliers.

All (3) torsion outliers are listed below:

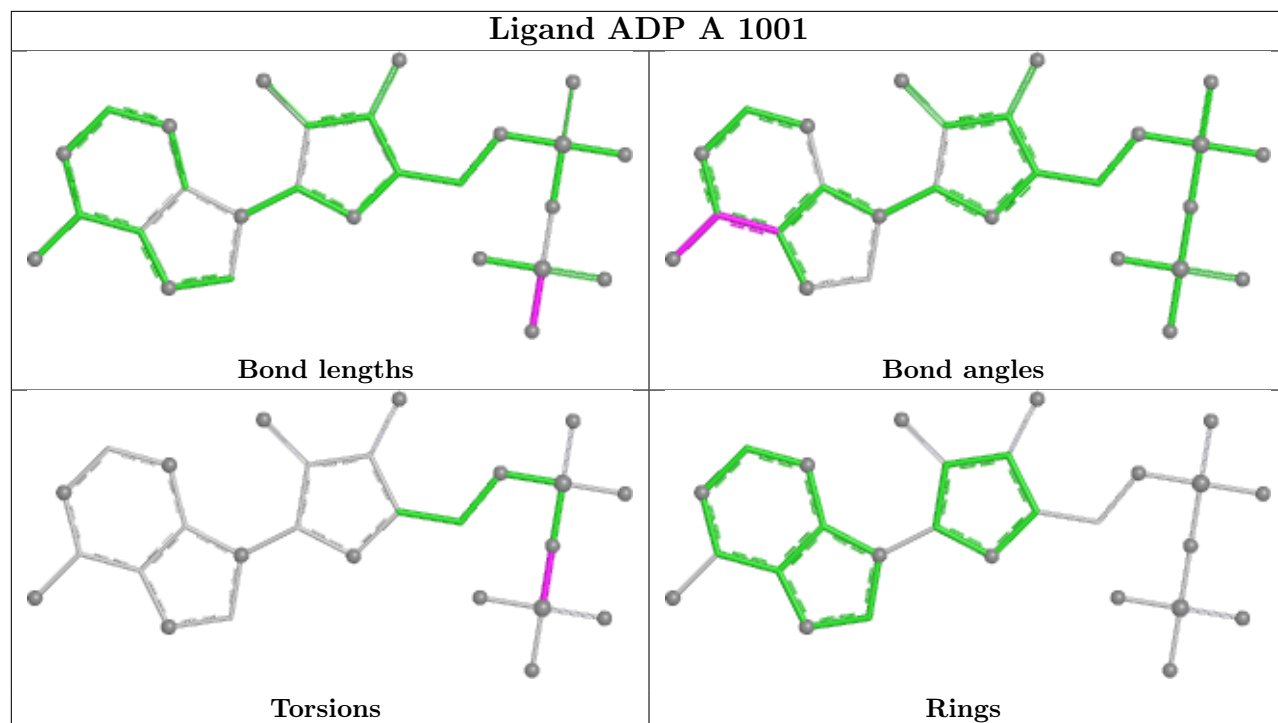
Mol	Chain	Res	Type	Atoms
3	A	1001	ADP	PA-O3A-PB-O2B
3	B	602	ADP	PA-O3A-PB-O2B
3	A	1001	ADP	PA-O3A-PB-O1B

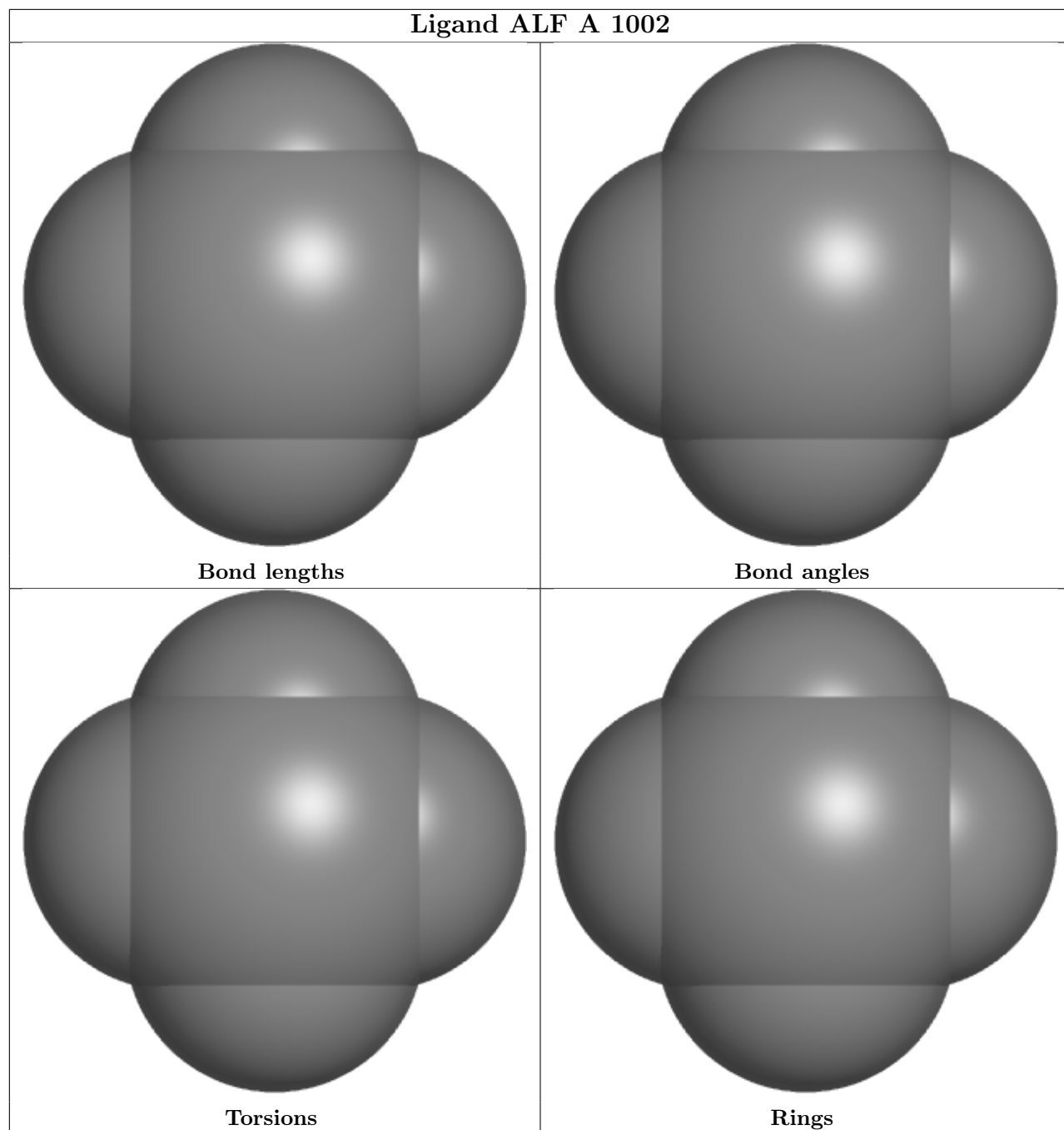
There are no ring outliers.

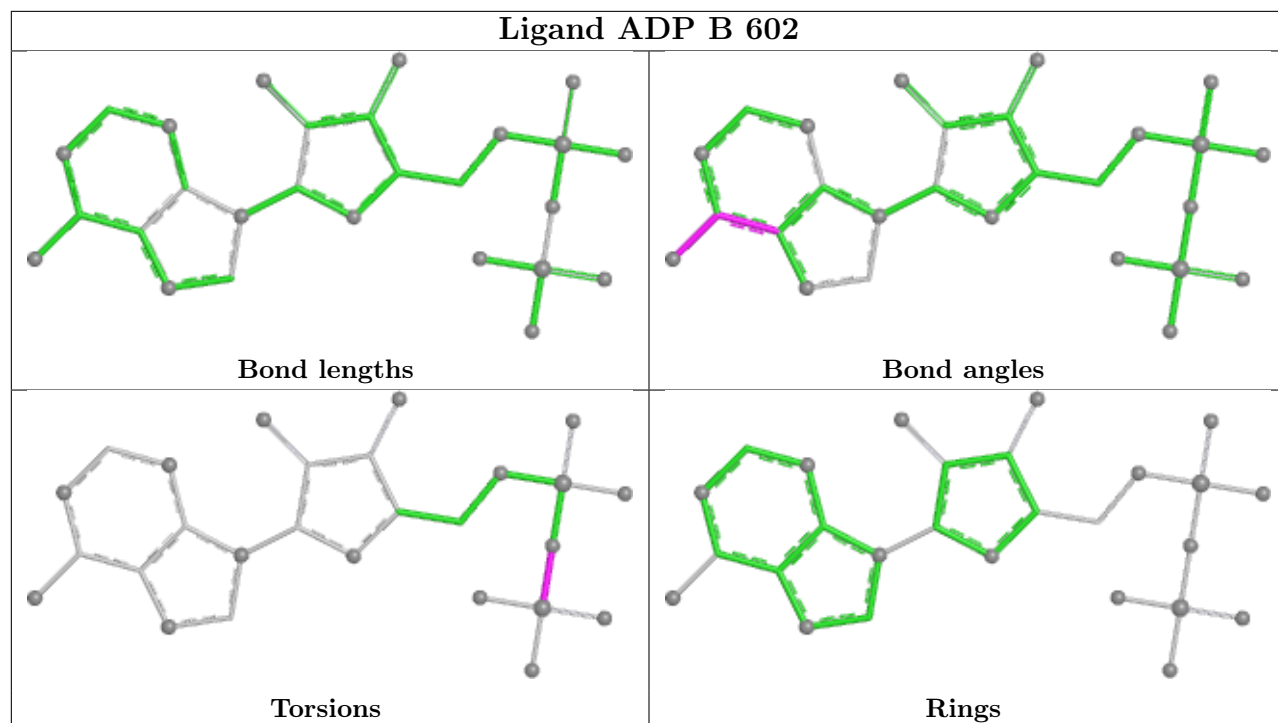
No monomer is involved in short contacts.

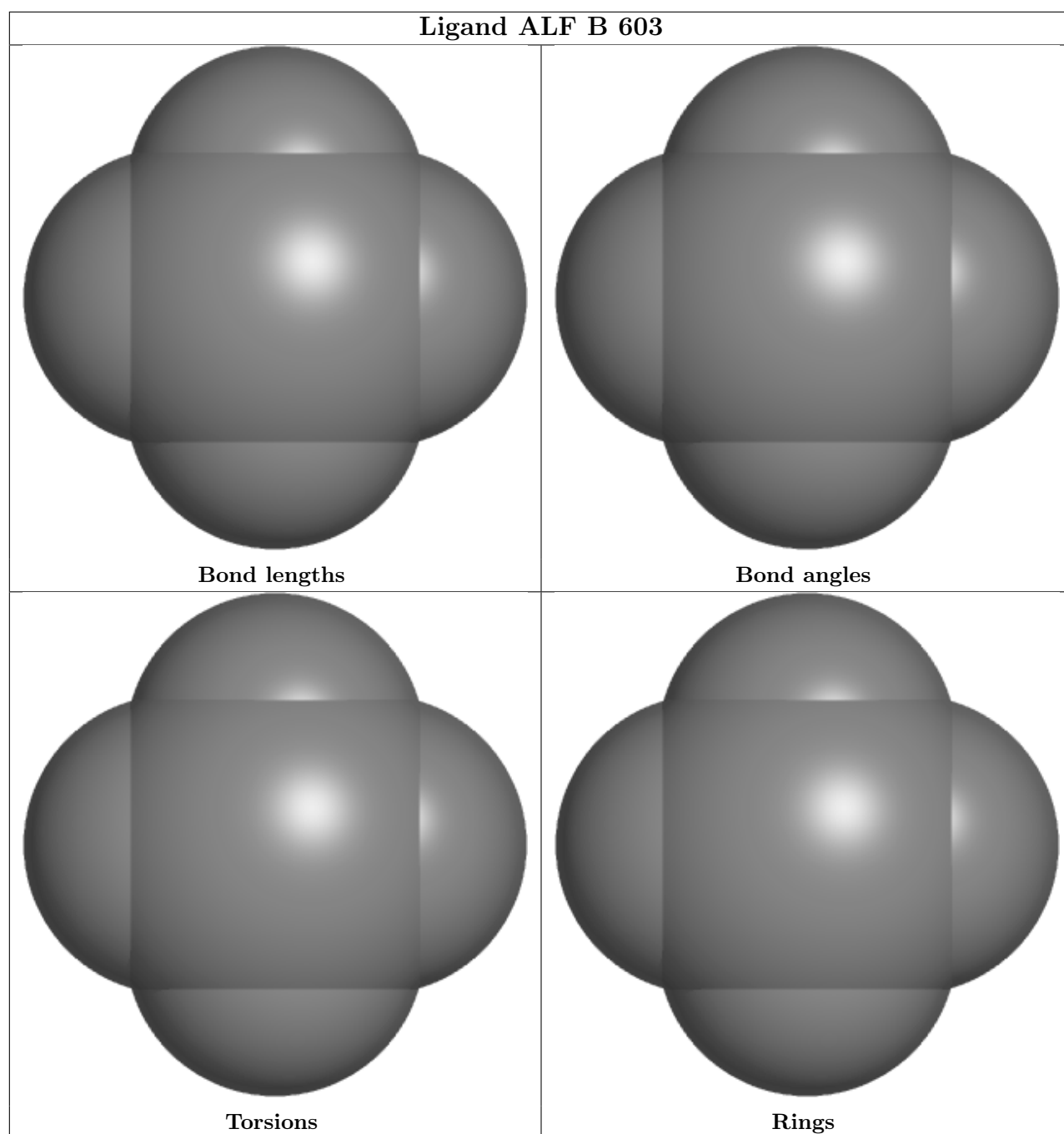
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	7:DT	O3'	8:DT	P	4.48

## 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	422/444 (95%)	0.18	13 (3%) 49 52	18, 34, 68, 106	0
1	B	423/444 (95%)	1.36	109 (25%) 0 0	33, 71, 109, 132	0
2	D	6/7 (85%)	1.56	1 (16%) 1 1	34, 37, 54, 227	0
2	E	5/7 (71%)	1.58	2 (40%) 0 0	75, 76, 80, 89	0
All	All	856/902 (94%)	0.78	125 (14%) 2 2	18, 51, 103, 227	0

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	8	DT	8.7
1	B	225	TYR	8.4
1	B	231	GLY	7.2
1	B	186	TRP	7.2
1	B	138	ALA	7.0
1	B	482	TRP	6.7
1	B	491	THR	6.1
1	B	388	ARG	6.1
1	B	235	PHE	5.9
1	B	154	PRO	5.8
1	B	144	ARG	5.6
1	B	218	PRO	5.6
1	B	150	ARG	5.5
1	B	195	LEU	5.5
1	B	153	GLY	5.5
1	B	221	GLU	5.5
1	B	228	ARG	5.3
1	B	142	ARG	5.2
1	B	381	ARG	5.2
1	B	156	SER	5.2
1	B	181	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	157	PRO	5.1
1	B	145	HIS	5.0
1	B	217	VAL	4.9
1	B	155	HIS	4.9
1	B	219	GLY	4.9
1	A	415	VAL	4.8
1	B	140	LEU	4.8
1	B	501	SER	4.7
1	B	173	VAL	4.7
1	B	481	LEU	4.6
1	B	137	PRO	4.6
1	B	141	LEU	4.4
1	B	238	ALA	4.3
1	B	220	GLY	4.3
1	B	143	TYR	4.3
1	B	232	GLY	4.2
1	B	335	THR	4.1
1	B	375	ALA	4.1
1	B	234	PHE	4.0
1	B	245	ALA	4.0
1	B	226	ILE	3.9
1	A	331	GLU	3.9
1	B	427	TRP	3.7
1	B	229	THR	3.6
1	B	239	HIS	3.6
1	A	399	ILE	3.5
2	E	3	DT	3.5
1	B	206	LEU	3.4
1	B	360	GLY	3.4
1	B	136	PHE	3.3
1	B	230	TRP	3.3
1	B	196	GLU	3.3
1	B	149	ILE	3.2
1	B	304	LYS	3.2
1	B	318	PRO	3.2
1	B	135	ARG	3.2
1	B	190	LYS	3.2
1	B	146	PRO	3.1
1	B	151	PRO	3.1
1	B	480	LEU	3.1
1	B	223	ALA	3.1
1	B	207	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	334	GLU	3.0
1	B	311	LEU	3.0
1	B	236	PHE	3.0
1	B	315	GLU	3.0
1	B	222	GLU	2.9
1	A	181	LEU	2.9
1	B	484	PRO	2.8
1	B	316	ALA	2.8
1	B	494	GLN	2.8
1	A	330	GLY	2.7
1	B	426	ALA	2.7
1	B	202	VAL	2.7
1	B	170	LEU	2.7
2	E	7	DT	2.6
1	A	400	VAL	2.6
1	B	382	LEU	2.6
1	B	379	ALA	2.6
1	B	199	PHE	2.6
1	B	370	VAL	2.6
1	B	380	VAL	2.6
1	B	160	LYS	2.6
1	B	399	ILE	2.6
1	B	374	GLU	2.5
1	B	488	VAL	2.5
1	A	335	THR	2.5
1	B	213	LEU	2.5
1	B	244	VAL	2.5
1	B	309	LEU	2.5
1	B	106	GLU	2.5
1	B	359	LEU	2.5
1	B	358	PRO	2.5
1	B	294	PRO	2.4
1	A	416	GLY	2.4
1	A	316	ALA	2.4
1	B	224	LEU	2.4
1	B	307	ASP	2.4
1	B	70	SER	2.4
1	B	319	GLY	2.4
1	B	259	GLU	2.4
1	B	148	ASP	2.4
1	B	152	PRO	2.3
1	B	499	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	350	GLN	2.3
1	B	322	LEU	2.3
1	B	176	VAL	2.3
1	B	242	GLU	2.3
1	B	308	ALA	2.2
1	B	204	VAL	2.2
1	B	184	MET	2.2
1	A	155	HIS	2.2
1	A	170	LEU	2.2
1	B	163	GLU	2.2
1	B	175	MET	2.2
1	B	477	PRO	2.1
1	B	376	GLU	2.1
1	B	313	ARG	2.1
1	B	139	ARG	2.1
1	B	312	LYS	2.1
1	B	205	LEU	2.1
1	A	333	ALA	2.1
1	A	206	LEU	2.0
1	B	189	ARG	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 monosaccharides 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.

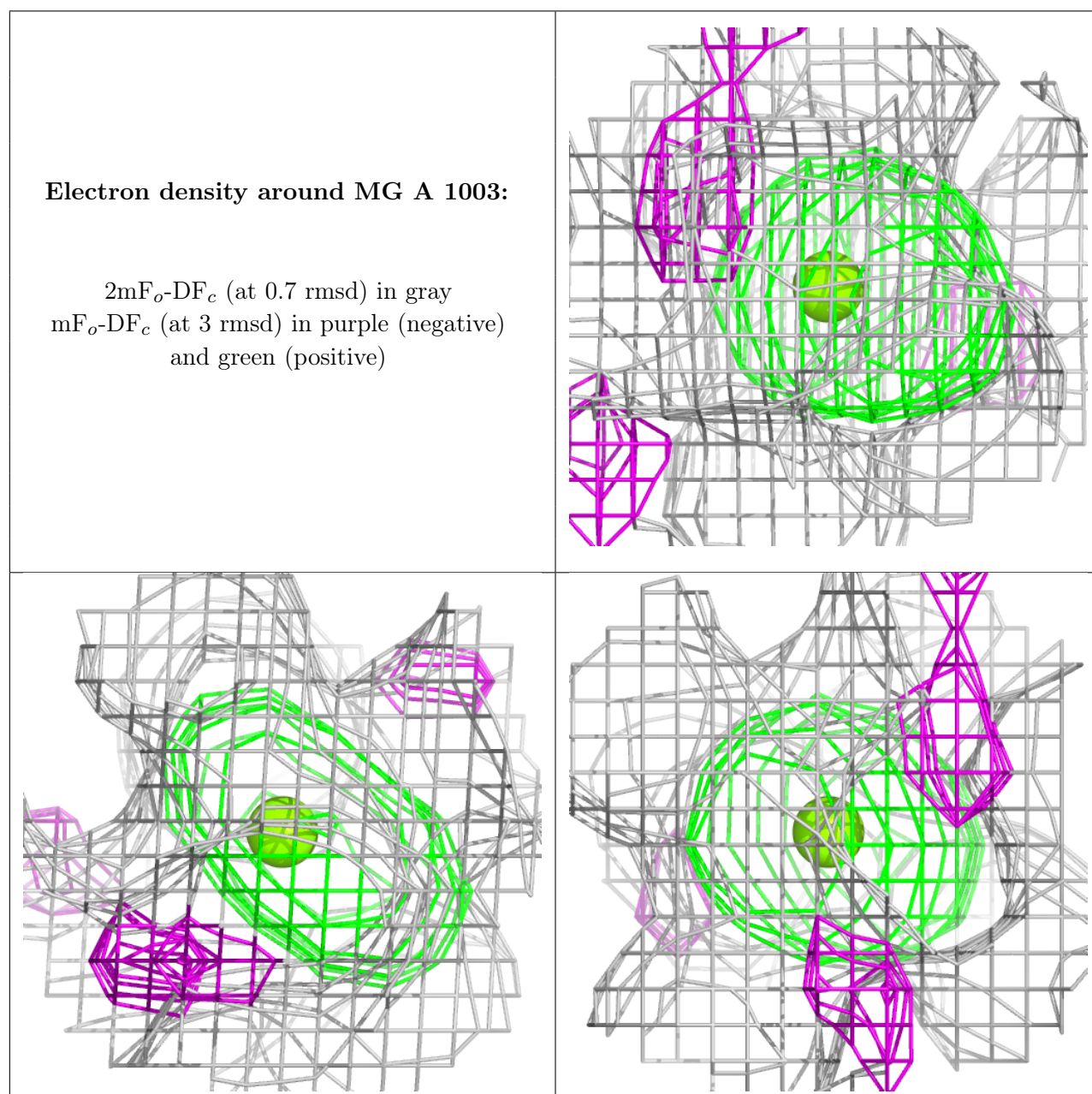
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	MG	A	1003	1/1	0.64	0.51	93,93,93,93	0
5	MG	B	601	1/1	0.70	0.45	121,121,121,121	0
3	ADP	B	602	27/27	0.95	0.12	36,42,55,55	0

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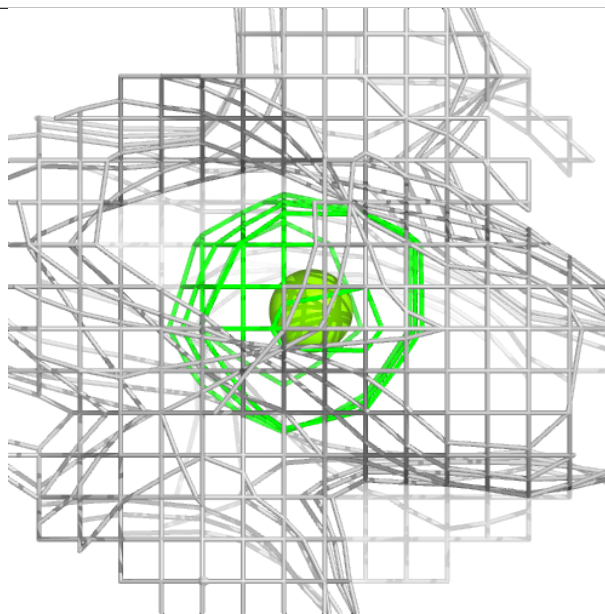
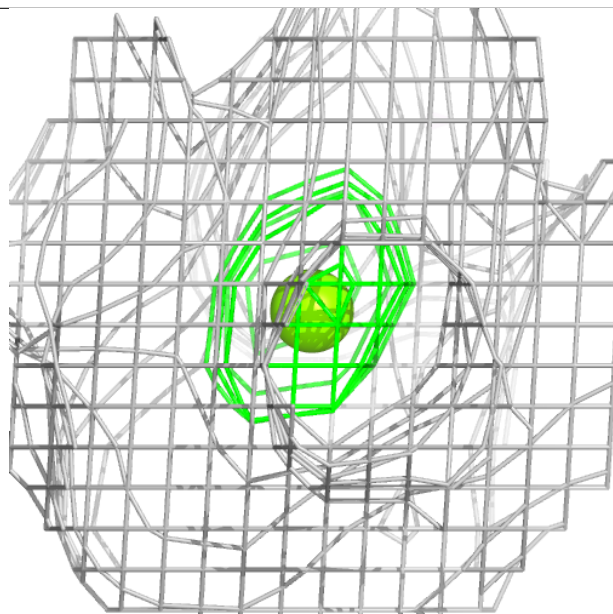
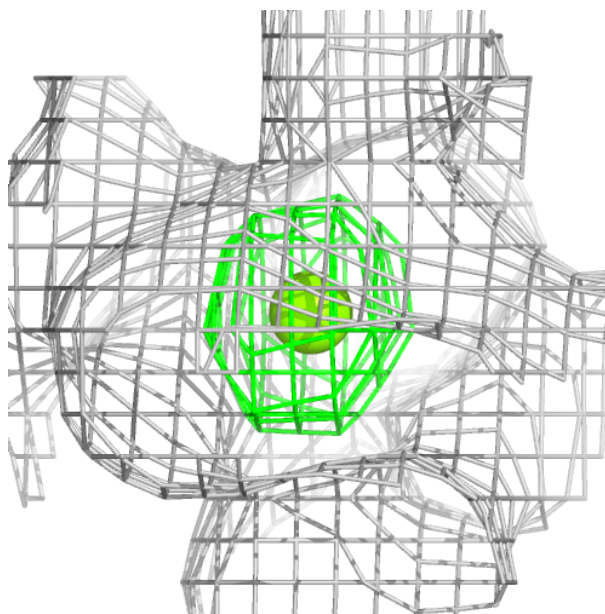
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	ALF	A	1002	5/5	0.96	0.13	20,21,25,28	0
3	ADP	A	1001	27/27	0.97	0.11	18,25,37,41	0
4	ALF	B	603	5/5	0.97	0.14	38,41,41,46	0

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.



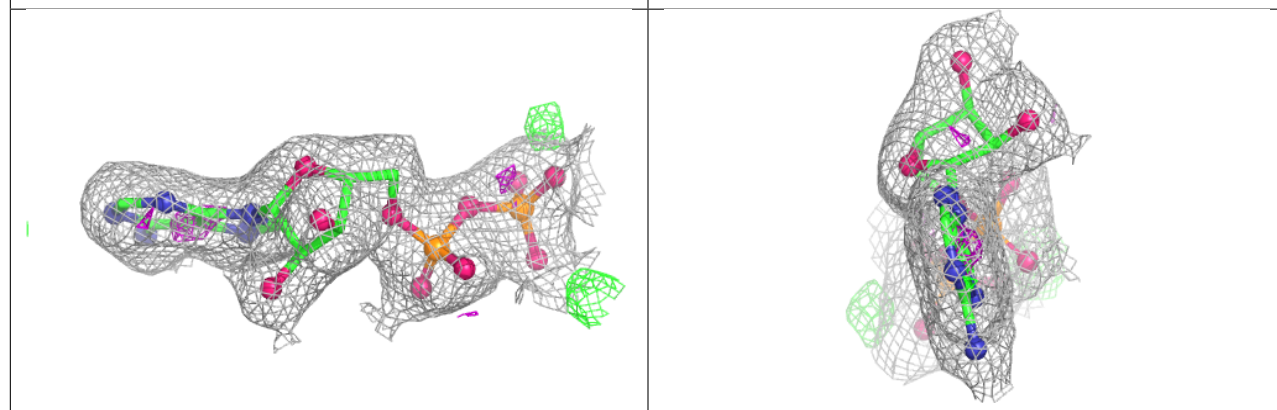
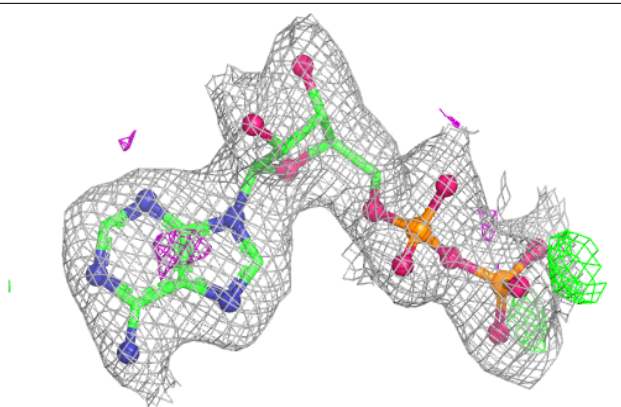
**Electron density around MG B 601:**

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



**Electron density around ADP B 602:**

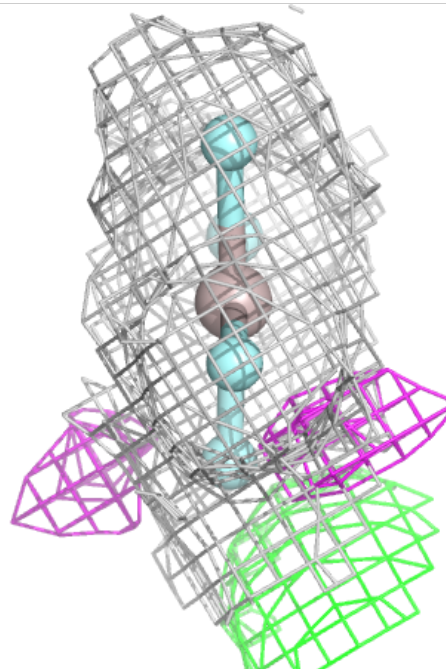
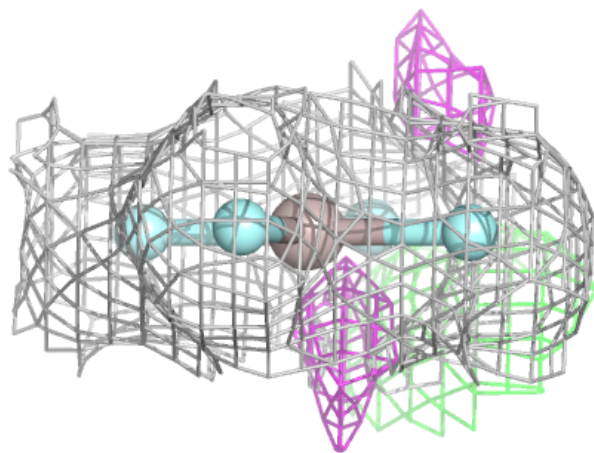
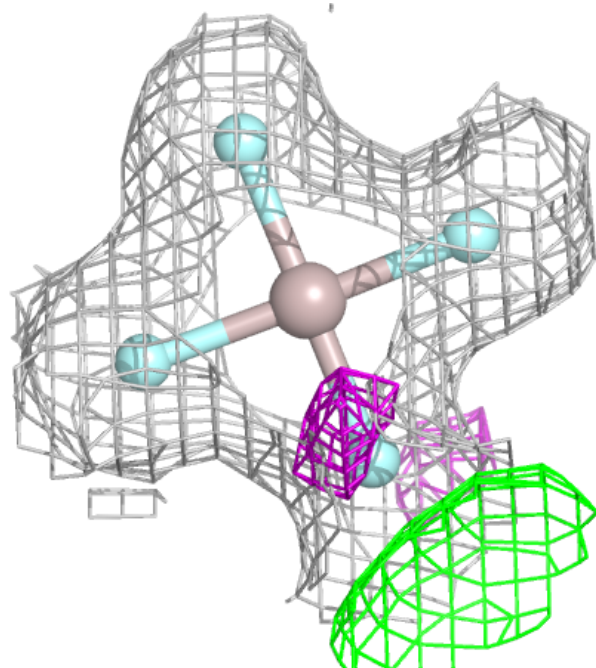
$2mF_o - DF_c$  (at 0.7 rmsd) in gray  
 $mF_o - DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





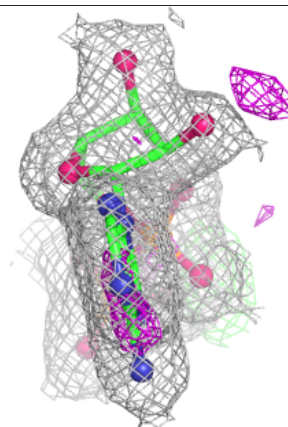
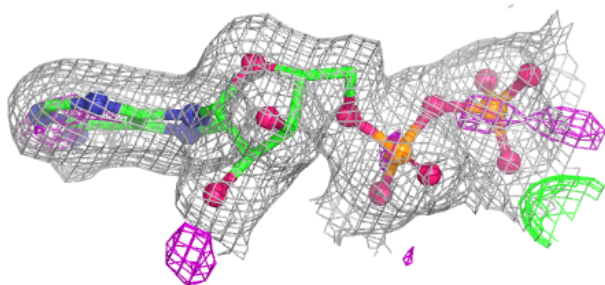
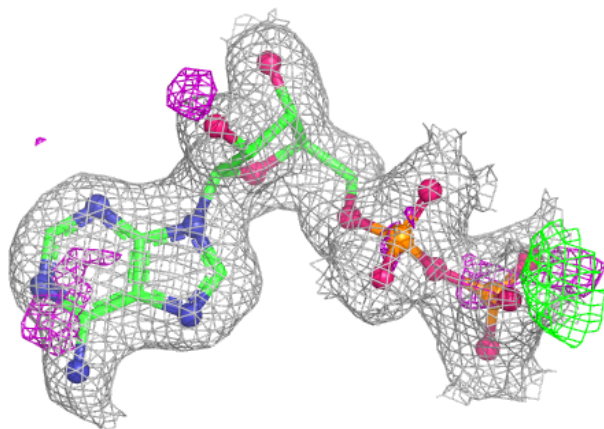
**Electron density around ALF A 1002:**

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



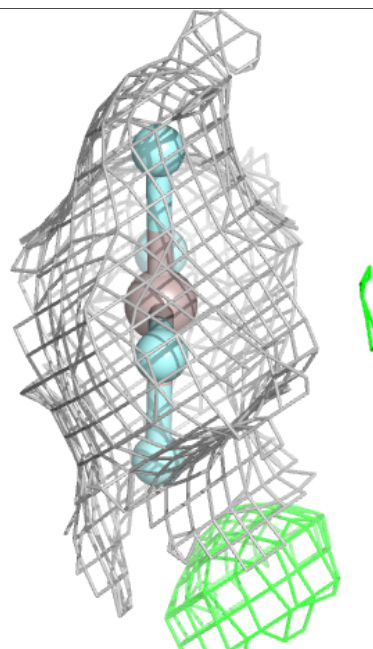
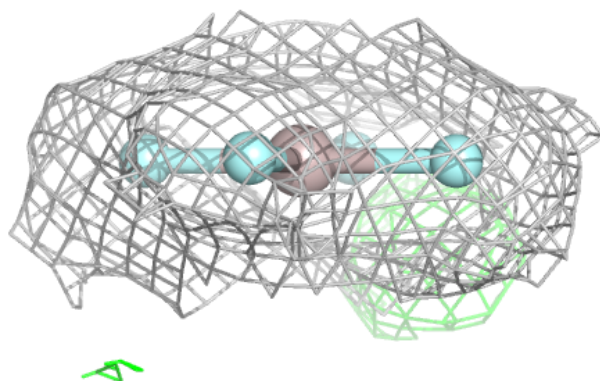
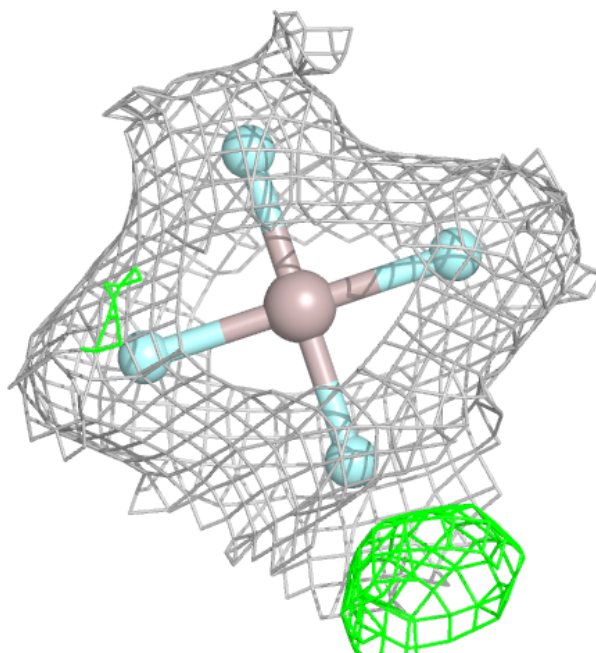
**Electron density around ADP A 1001:**

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



**Electron density around ALF B 603:**

$2mF_o-DF_c$  (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.