



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:47 PM UTC

PDB ID : 6S3H / pdb_00006s3h
Title : Crystal structure of helicase Pif1 from *Thermus oshimai* in complex with ADP-AlF₄ and (dT)₇ds11bp
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

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

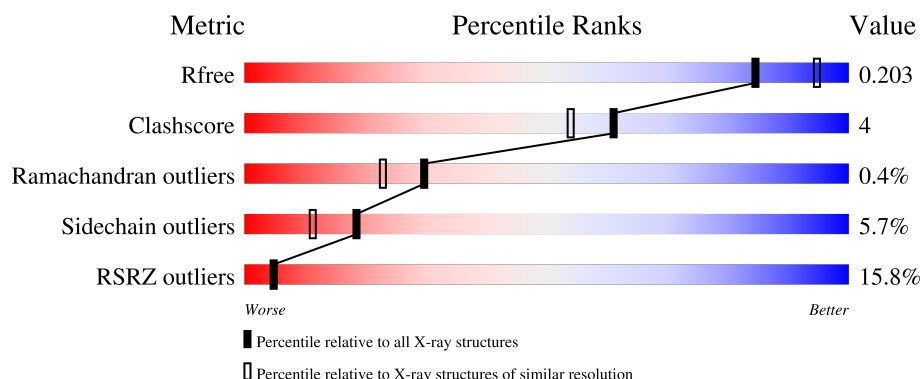
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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}	180053	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (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 ≥ 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	3% 88% 6% • 5%
1	B	444	26% 78% 15% • 5%
2	D	7	14% 43% 43% 14%
2	E	7	29% 71% 29%

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			

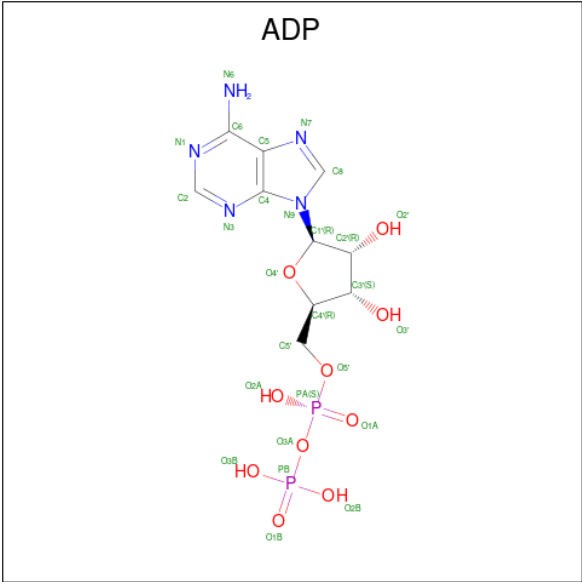
There are 6 discrepancies between the modelled and reference sequences:

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').

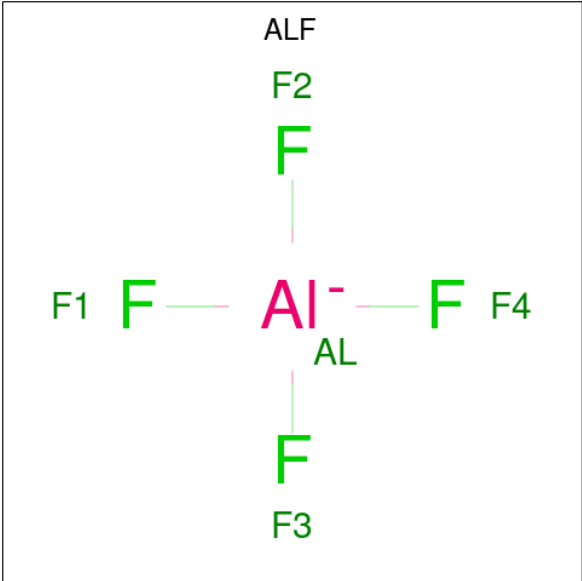
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	6	Total	C	N	O	P	0	0	0
			120	60	12	42	6			
2	E	5	Total	C	N	O	P	0	0	0
			100	50	10	35	5			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂) (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 (CCD ID: ALF) (formula: AlF_4^-) (labeled as "Ligand of Interest" by depositor).



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

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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 (CCD ID: 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		

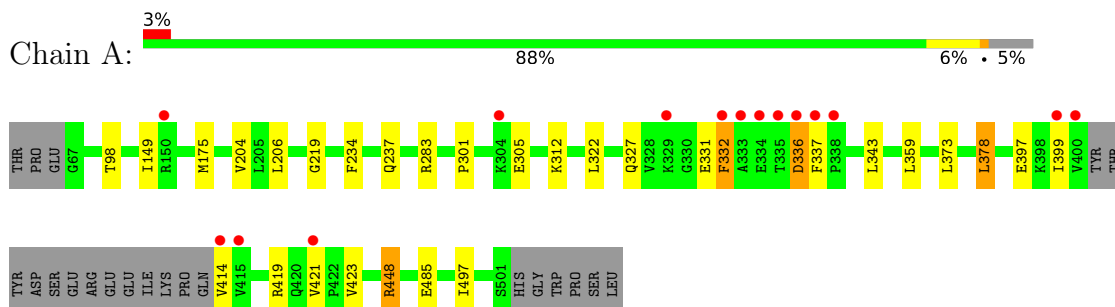
- Molecule 6 is water.

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		

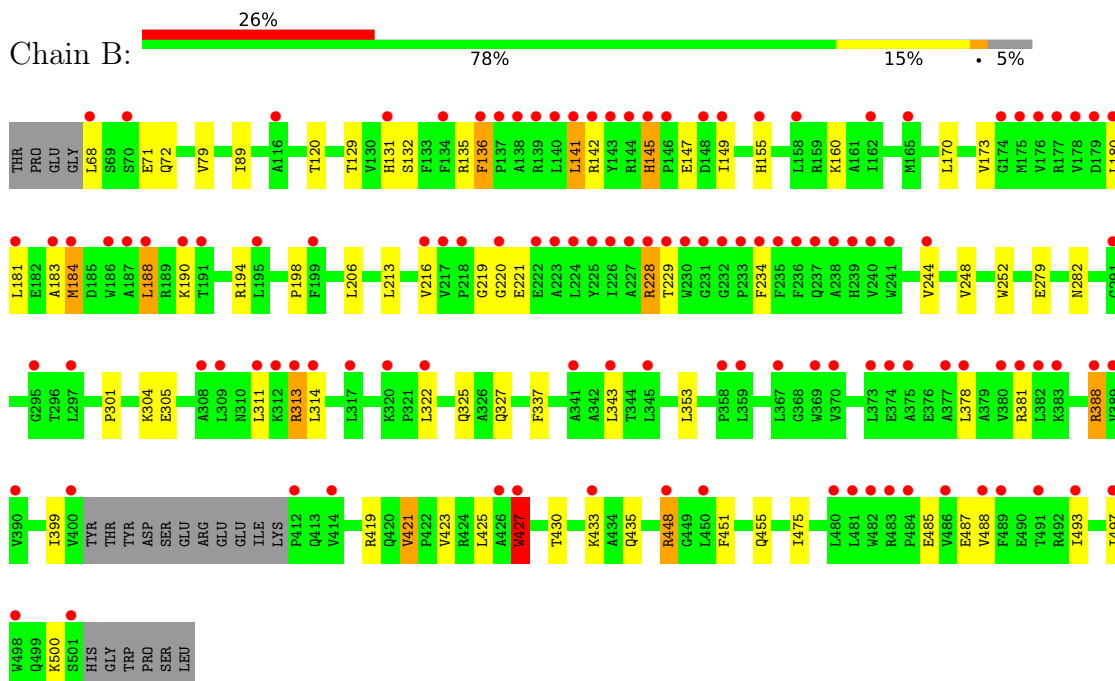
3 Residue-property plots

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.

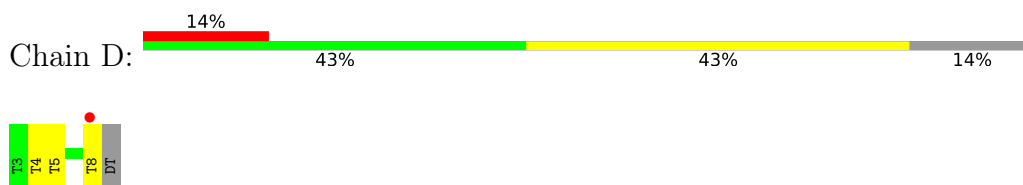
• Molecule 1: PIF1 helicase



• Molecule 1: PIF1 helicase

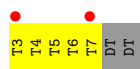


• Molecule 2: DNA (5'-D(P*TP*TP*TP*TP*TP*T)-3')



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

Chain E:  29% 71% 29%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	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) 97.1 (29.51-2.06)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	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 (2.93%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	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 ²)	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, ALF, 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	0.92	1/3456 (0.0%)	1.15	4/4689 (0.1%)
1	B	0.82	1/3469 (0.0%)	1.22	13/4707 (0.3%)
2	D	0.70	0/130	0.95	0/196
2	E	0.63	0/109	0.85	0/166
All	All	0.87	2/7164 (0.0%)	1.18	17/9758 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	175	MET	SD-CE	-11.39	1.51	1.79
1	B	184	MET	SD-CE	-6.99	1.62	1.79

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	336	ASP	CA-C-N	7.99	136.08	121.70
1	A	336	ASP	C-N-CA	7.99	136.08	121.70
1	B	194	ARG	CA-C-N	6.62	129.16	120.28
1	B	194	ARG	C-N-CA	6.62	129.16	120.28
1	B	427	TRP	N-CA-C	-6.50	104.28	111.82
1	A	219	GLY	N-CA-C	6.22	121.96	113.99
1	A	98	THR	CA-CB-OG1	-5.91	100.73	109.60
1	B	136	PHE	CA-CB-CG	5.68	119.48	113.80
1	B	219	GLY	N-CA-C	5.39	120.89	113.99
1	B	337	PHE	CA-CB-CG	5.21	119.01	113.80
1	B	311	LEU	CA-C-N	5.09	127.06	120.44
1	B	311	LEU	C-N-CA	5.09	127.06	120.44
1	B	188	LEU	CA-C-N	5.07	127.03	120.44
1	B	188	LEU	C-N-CA	5.07	127.03	120.44
1	B	72	GLN	CA-C-N	5.06	127.02	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	72	GLN	C-N-CA	5.06	127.02	120.44
1	B	421	VAL	N-CA-CB	5.03	115.76	110.17

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:LEU:HA	1:B:184:MET:HE3	1.62	0.79
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
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:141:LEU:HD13	1:B:183:ALA:HB2	1.93	0.51
1:B:448:ARG:O	1:B:448:ARG:HG3	2.10	0.50
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: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:71:GLU:CD	1:B:252:TRP:H	2.22	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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 [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	418/444 (94%)	406 (97%)	10 (2%)	2 (0%)	24	17
1	B	419/444 (94%)	404 (96%)	14 (3%)	1 (0%)	43	38
All	All	837/888 (94%)	810 (97%)	24 (3%)	3 (0%)	30	23

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%)	334 (95%)	16 (5%)	24	17
1	B	352/371 (95%)	328 (93%)	24 (7%)	14	8
All	All	702/742 (95%)	662 (94%)	40 (6%)	18	11

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	149	ILE
1	A	204	VAL
1	A	206	LEU
1	A	283	ARG
1	A	312	LYS
1	A	322	LEU
1	A	332	PHE
1	A	359	LEU
1	A	373	LEU
1	A	378	LEU
1	A	399	ILE
1	A	414	VAL
1	A	423	VAL
1	A	448	ARG
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	147	GLU
1	B	149	ILE
1	B	155	HIS
1	B	160	LYS
1	B	188	LEU
1	B	190	LYS
1	B	221	GLU

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Mol	Chain	Res	Type
1	B	228	ARG
1	B	279	GLU
1	B	313	ARG
1	B	322	LEU
1	B	325	GLN
1	B	378	LEU
1	B	388	ARG
1	B	399	ILE
1	B	427	TRP
1	B	448	ARG
1	B	487	GLU
1	B	497	ILE
1	B	500	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	155	HIS
1	A	237	GLN
1	A	255	GLN
1	A	327	GLN
1	B	131	HIS
1	B	212	GLN
1	B	282	ASN
1	B	325	GLN
1	B	327	GLN
1	B	432	HIS
1	B	435	GLN
1	B	455	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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	$\# Z > 2$
3	ADP	A	1001	4,5	28,29,29	0.83	1 (3%)	43,45,45	0.55	0
3	ADP	B	602	4,5	28,29,29	0.60	0	43,45,45	0.43	0
4	ALF	B	603	3,5	4,4,4	1.38	0	-		
4	ALF	A	1002	3,5	4,4,4	1.45	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	4,5	-	2/16/32/32	0/3/3/3
3	ADP	B	602	4,5	-	1/16/32/32	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

There are no bond angle outliers.

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

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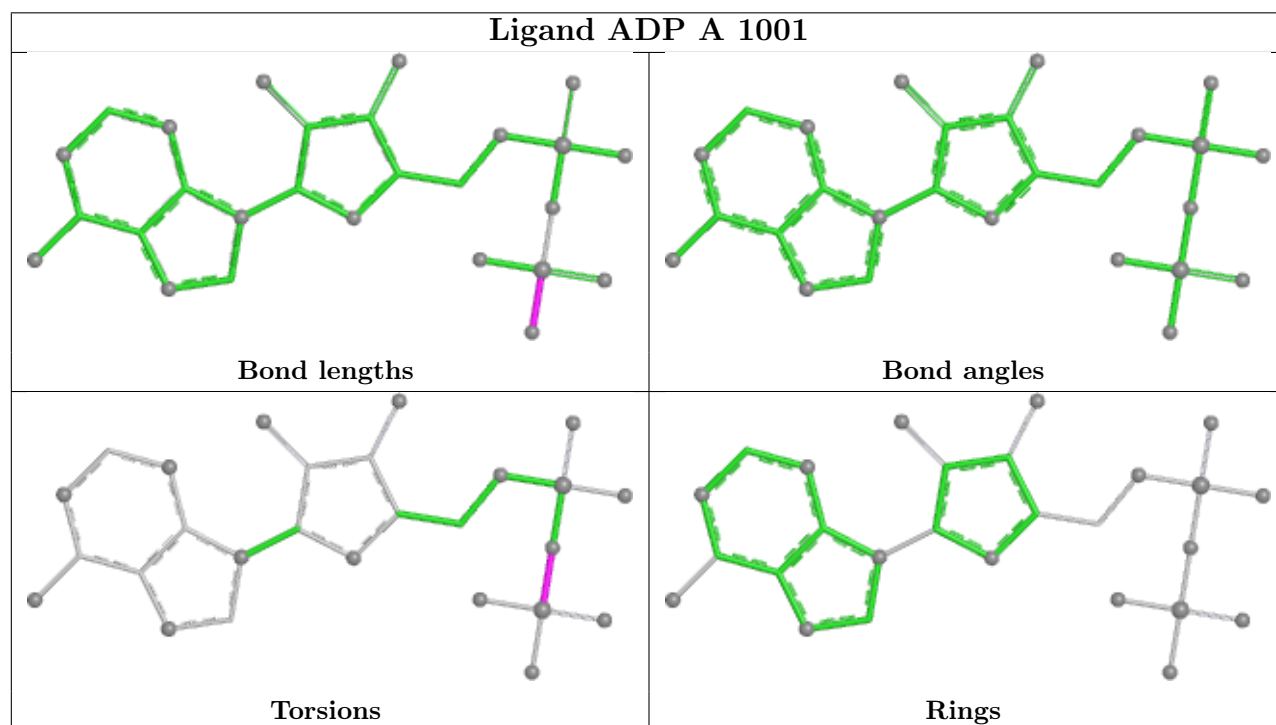
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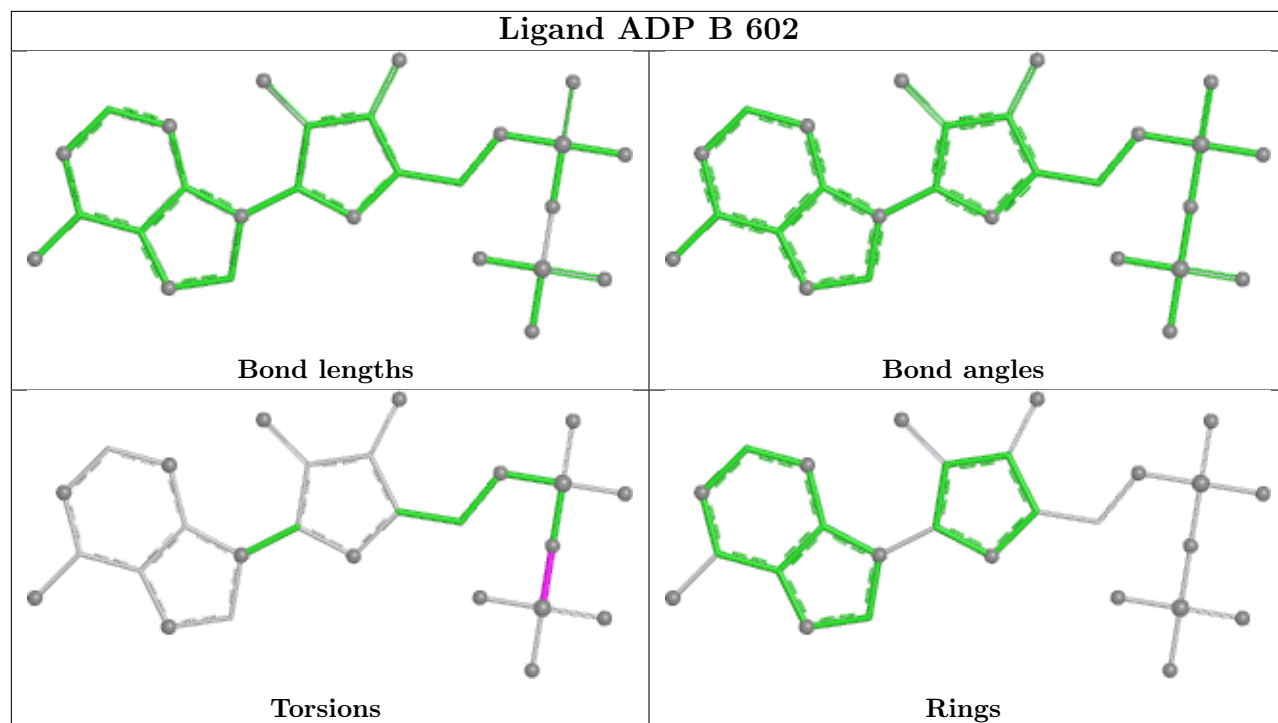
Mol	Chain	Res	Type	Atoms
3	B	602	ADP	PA-O3A-PB-O2B
3	A	1001	ADP	PA-O3A-PB-O1B

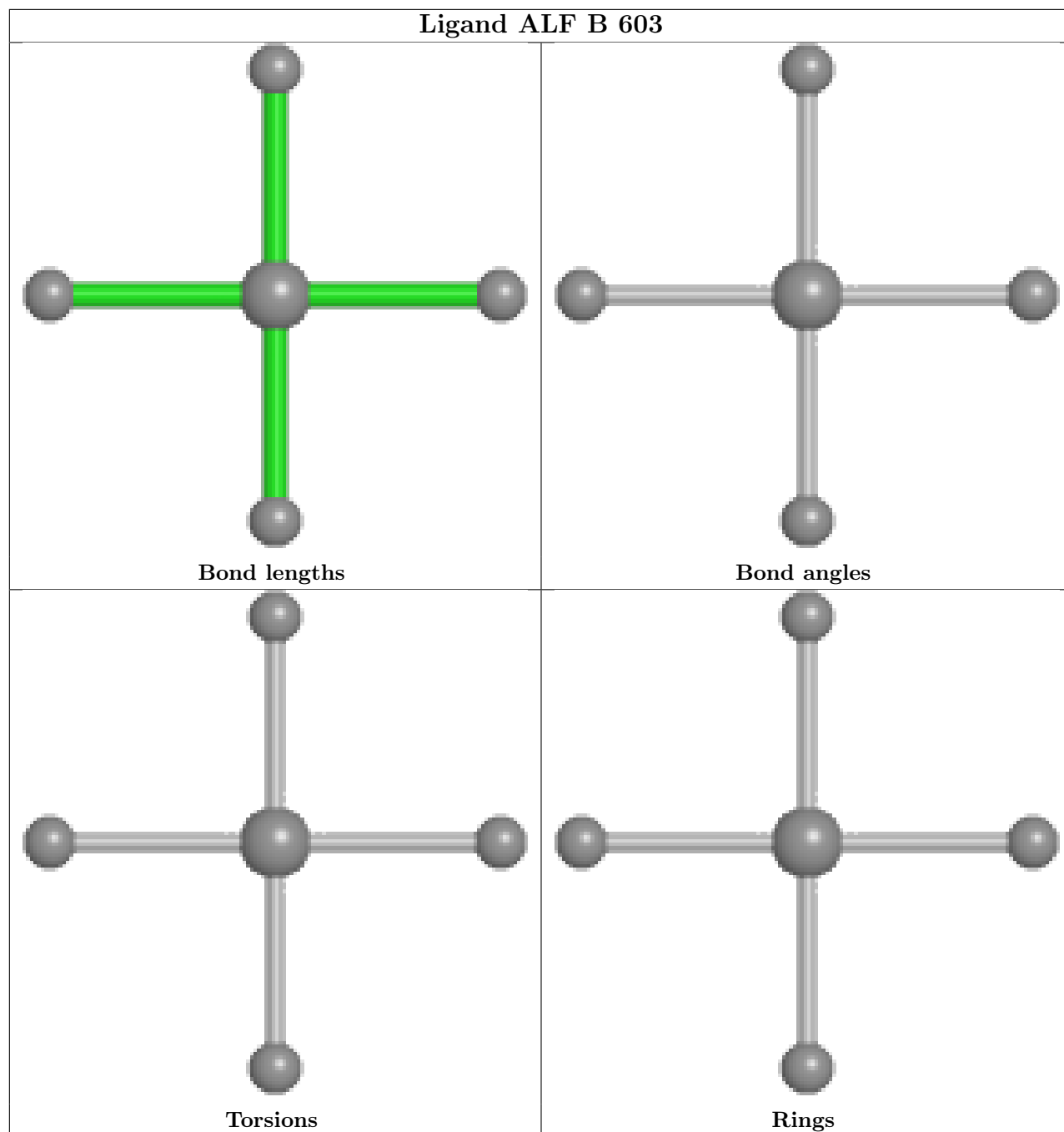
There are no ring outliers.

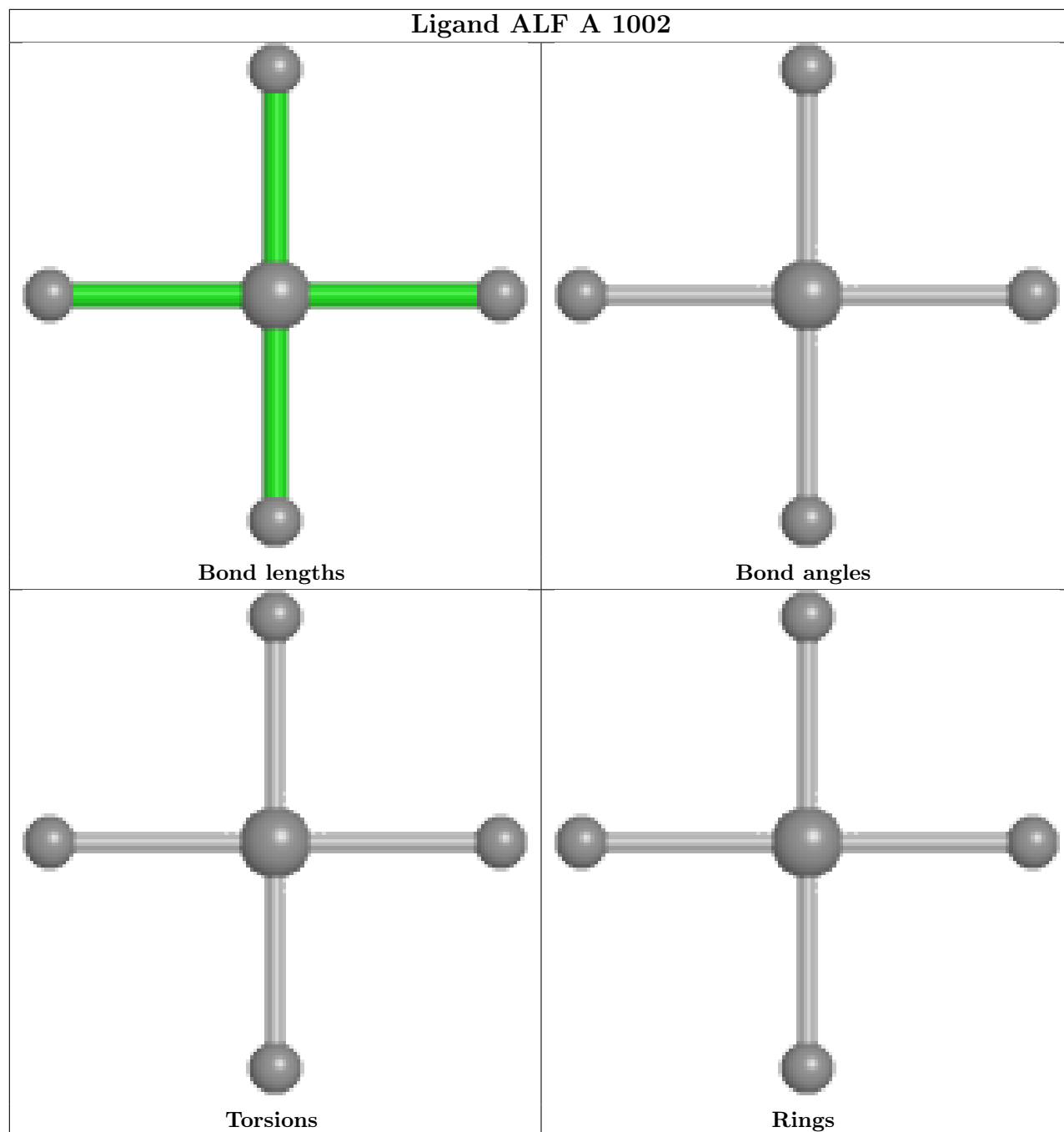
No monomer is involved in short contacts.

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, 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	422/444 (95%)	-0.10	15 (3%) 46 47	18, 34, 68, 106	0
1	B	423/444 (95%)	1.30	117 (27%) 1 1	33, 71, 109, 132	0
2	D	6/7 (85%)	0.69	1 (16%) 4 4	34, 37, 54, 227	0
2	E	5/7 (71%)	2.01	2 (40%) 1 0	75, 76, 80, 89	0
All	All	856/902 (94%)	0.61	135 (15%) 5 5	18, 51, 103, 227	0

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	138	ALA	5.1
1	B	400	VAL	4.9
1	B	375	ALA	4.9
1	B	225	TYR	4.8
1	B	186	TRP	4.7
1	B	141	LEU	4.6
1	B	234	PHE	4.4
1	B	238	ALA	4.4
1	B	232	GLY	4.3
1	A	400	VAL	4.3
1	B	231	GLY	4.3
2	D	8	DT	4.2
1	B	230	TRP	4.1
1	B	481	LEU	4.0
1	B	226	ILE	3.8
1	B	136	PHE	3.8
1	B	486	VAL	3.7
1	B	427	TRP	3.7
1	A	414	VAL	3.7
1	B	149	ILE	3.6
1	B	146	PRO	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	482	TRP	3.5
1	A	415	VAL	3.5
1	B	217	VAL	3.5
1	B	380	VAL	3.5
1	B	497	ILE	3.4
1	B	235	PHE	3.4
1	B	297	LEU	3.4
1	B	140	LEU	3.4
1	B	381	ARG	3.4
1	B	493	ILE	3.4
1	B	359	LEU	3.3
2	E	3	DT	3.3
1	B	224	LEU	3.3
1	B	233	PRO	3.2
1	A	337	PHE	3.2
1	B	199	PHE	3.2
1	B	314	LEU	3.2
1	B	383	LYS	3.1
1	B	313	ARG	3.1
1	B	181	LEU	3.1
1	B	143	TYR	3.1
1	B	145	HIS	3.1
1	B	236	PHE	3.0
1	B	195	LEU	3.0
1	B	322	LEU	3.0
1	B	414	VAL	3.0
1	B	68	LEU	3.0
1	B	498	TRP	2.9
1	B	228	ARG	2.8
1	B	373	LEU	2.8
1	B	382	LEU	2.8
1	B	369	TRP	2.8
1	B	308	ALA	2.8
1	B	412	PRO	2.8
1	B	137	PRO	2.8
1	B	244	VAL	2.8
1	B	370	VAL	2.8
1	B	239	HIS	2.7
1	A	332	PHE	2.7
1	B	227	ALA	2.7
1	B	180	LEU	2.7
1	B	148	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	175	MET	2.7
1	B	144	ARG	2.7
1	B	388	ARG	2.7
1	B	480	LEU	2.7
1	B	116	ALA	2.6
1	B	312	LYS	2.6
1	B	142	ARG	2.6
1	B	216	VAL	2.6
2	E	7	DT	2.6
1	B	131	HIS	2.6
1	B	229	THR	2.6
1	B	158	LEU	2.6
1	B	378	LEU	2.6
1	A	333	ALA	2.5
1	B	309	LEU	2.5
1	B	311	LEU	2.5
1	B	317	LEU	2.5
1	B	178	VAL	2.5
1	A	338	PRO	2.5
1	B	70	SER	2.5
1	B	489	PHE	2.5
1	A	304	LYS	2.5
1	B	291	GLY	2.5
1	B	176	VAL	2.4
1	B	218	PRO	2.4
1	B	358	PRO	2.4
1	B	377	ALA	2.4
1	B	426	ALA	2.4
1	B	374	GLU	2.4
1	B	483	ARG	2.4
1	A	336	ASP	2.4
1	B	501	SER	2.4
1	B	488	VAL	2.3
1	B	179	ASP	2.3
1	A	150	ARG	2.3
1	B	345	LEU	2.3
1	A	334	GLU	2.3
1	B	222	GLU	2.3
1	B	240	VAL	2.3
1	B	433	LYS	2.3
1	B	191	THR	2.2
1	B	177	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	190	LYS	2.2
1	A	335	THR	2.2
1	B	220	GLY	2.2
1	B	237	GLN	2.2
1	B	491	THR	2.2
1	B	389	VAL	2.2
1	B	390	VAL	2.2
1	B	367	LEU	2.2
1	A	399	ILE	2.1
1	B	295	GLY	2.1
1	B	183	ALA	2.1
1	B	187	ALA	2.1
1	B	450	LEU	2.1
1	B	165	MET	2.1
1	B	241	TRP	2.1
1	B	162	ILE	2.1
1	B	174	GLY	2.1
1	B	484	PRO	2.1
1	B	155	HIS	2.1
1	B	188	LEU	2.1
1	B	320	LYS	2.1
1	A	421	VAL	2.1
1	B	223	ALA	2.1
1	B	184	MET	2.0
1	B	343	LEU	2.0
1	B	134	PHE	2.0
1	B	341	ALA	2.0
1	B	139	ARG	2.0
1	B	448	ARG	2.0
1	A	329	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands

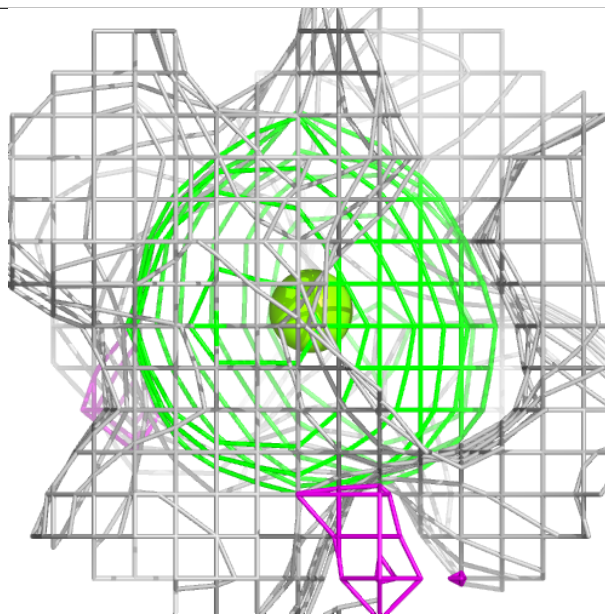
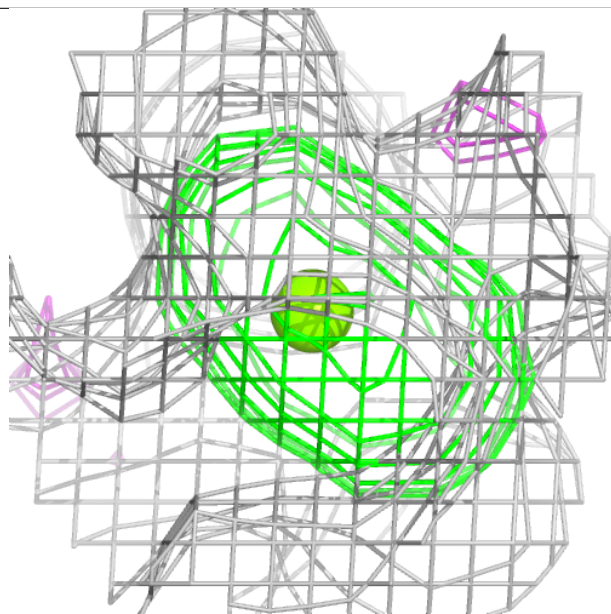
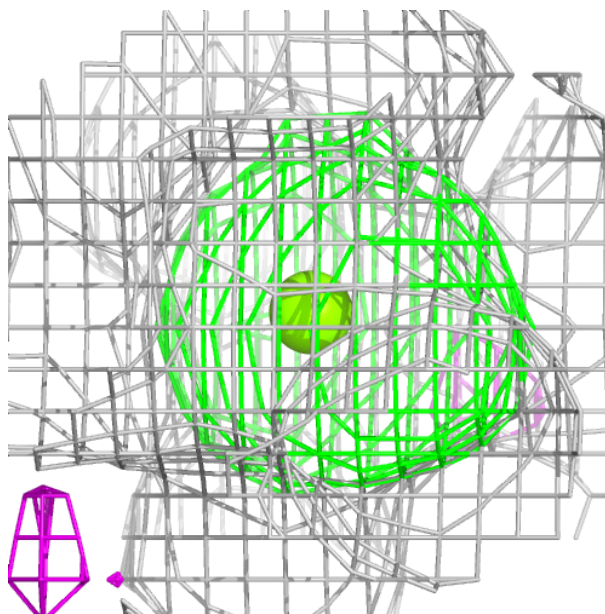
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	MG	A	1003	1/1	0.63	0.35	93,93,93,93	0
5	MG	B	601	1/1	0.81	0.29	121,121,121,121	0
4	ALF	B	603	5/5	0.98	0.05	38,41,41,46	0
3	ADP	B	602	27/27	0.98	0.06	36,42,55,55	0
4	ALF	A	1002	5/5	0.98	0.04	20,21,25,28	0
3	ADP	A	1001	27/27	0.99	0.04	18,25,37,41	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.

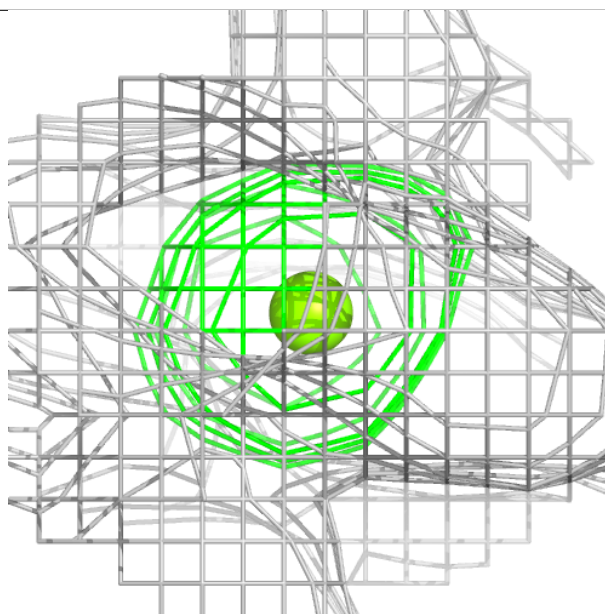
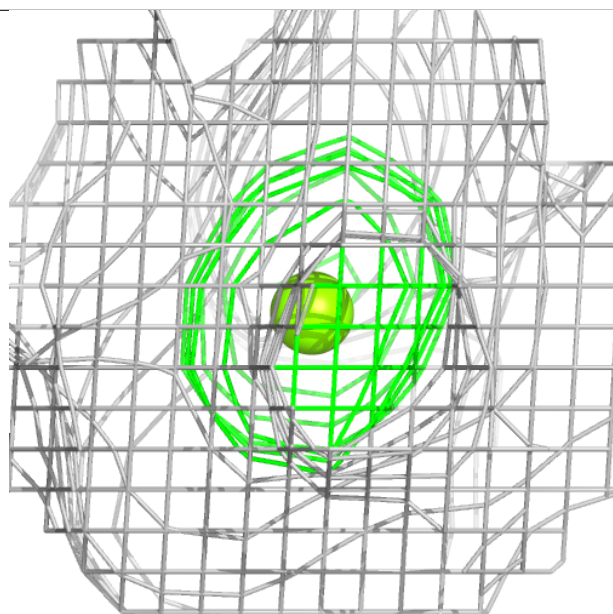
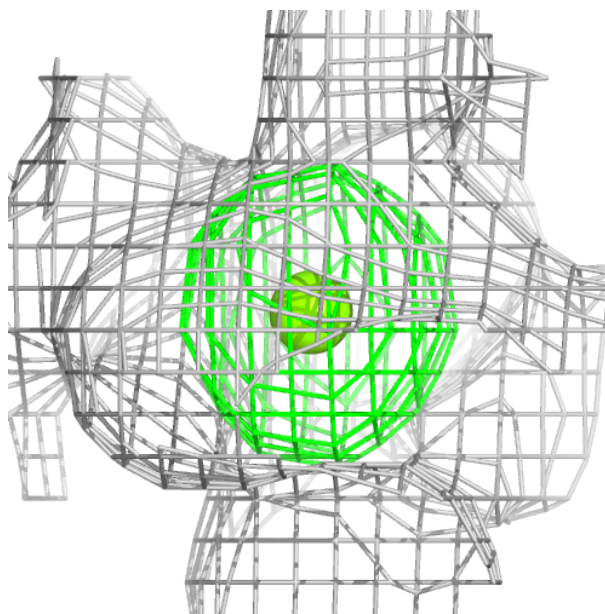
Electron density around MG A 1003:

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



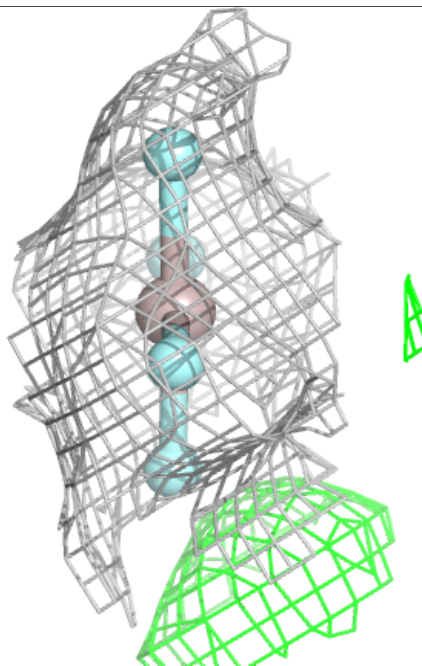
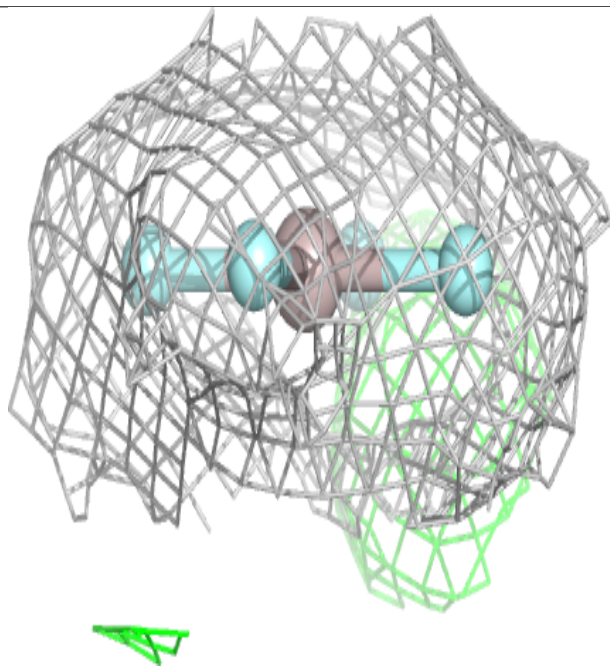
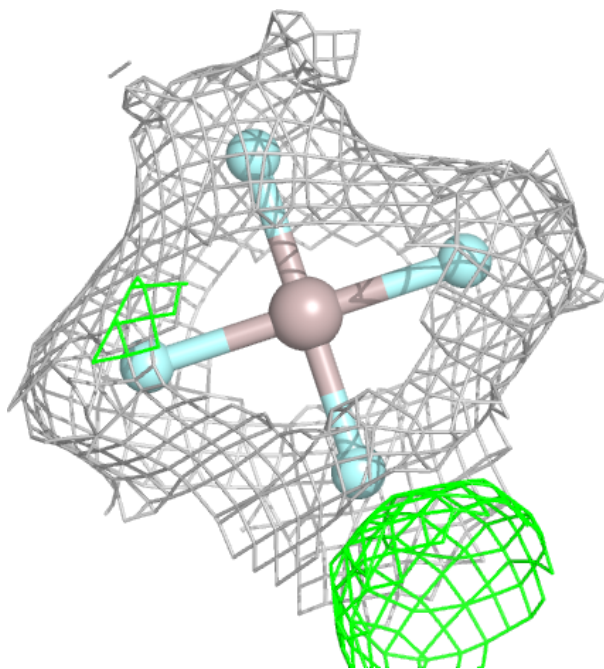
Electron density around MG B 601:

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



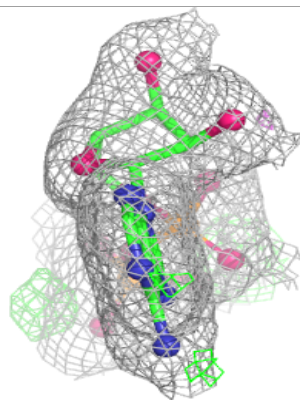
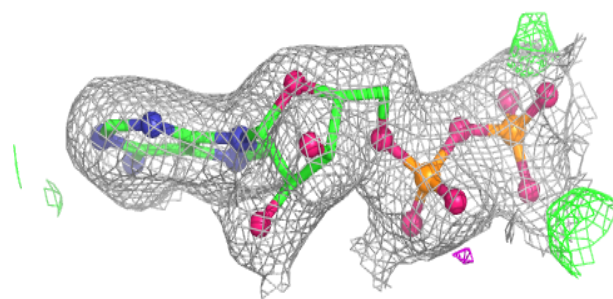
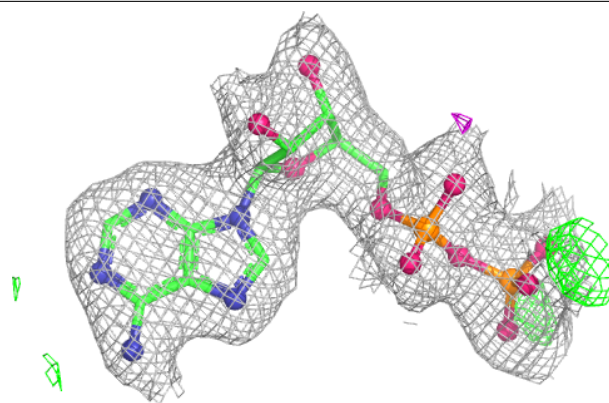
Electron density around ALF B 603:

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



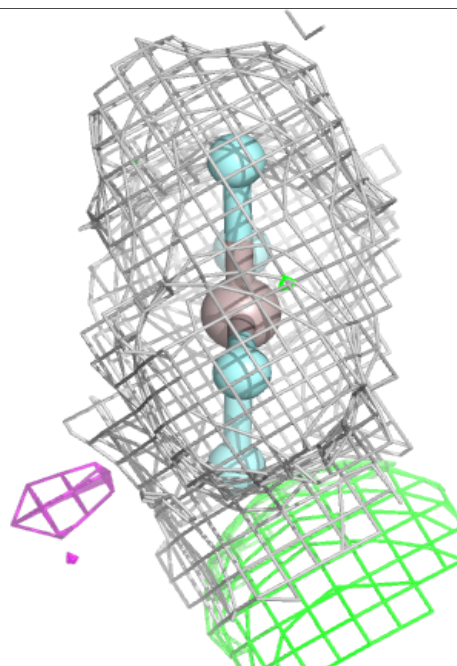
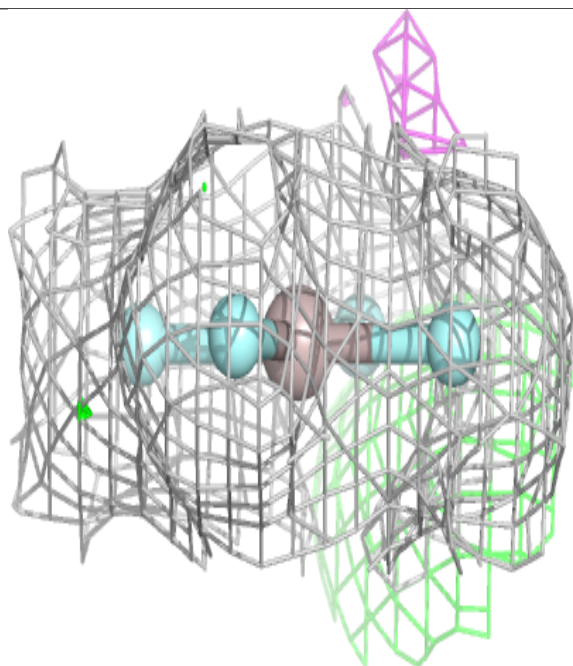
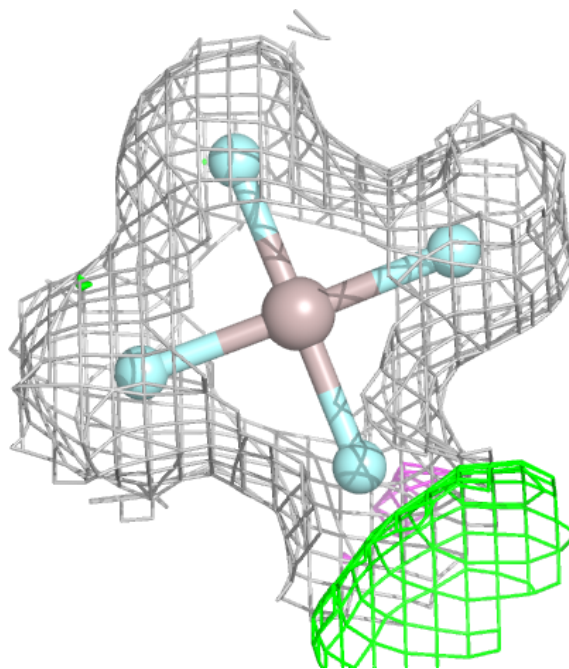
Electron density around ADP B 602:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



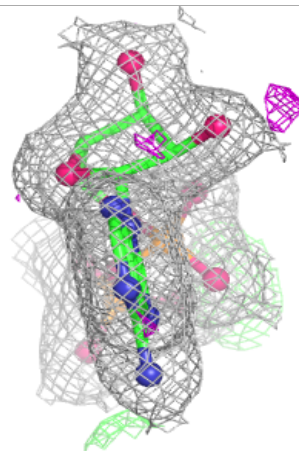
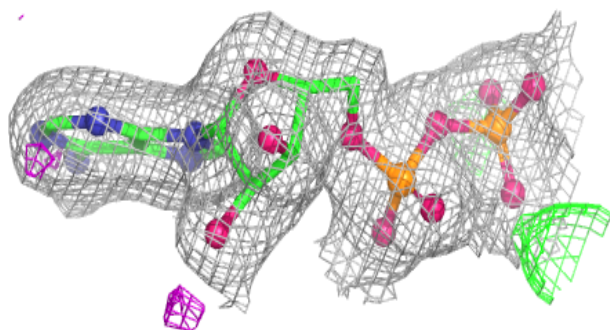
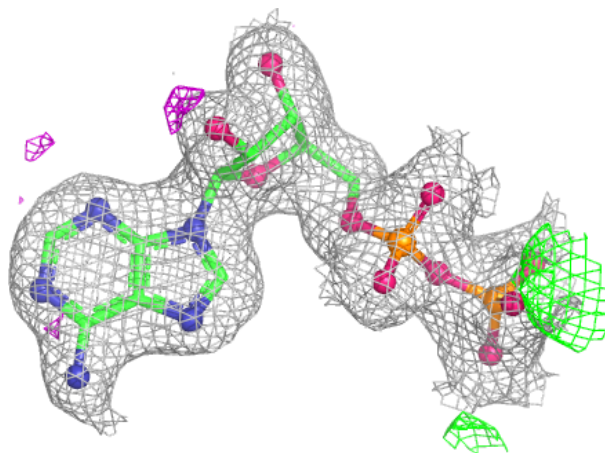
Electron density around ALF A 1002:

$2mF_o-DF_c$ (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)



6.5 Other polymers [i](#)

There are no such residues in this entry.