



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 11:14 AM UTC

PDB ID : 5ORK / pdb_00005ork
Title : The crystal structure of CK2alpha in complex with compound 6
Authors : Brear, P.; De Fusco, C.; Iegre, J.; Yoshida, M.; Mitchell, S.; Rossmann, M.; Carro, L.; Sore, H.; Hyvonen, M.; Spring, D.
Deposited on : 2017-08-16
Resolution : 2.14 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

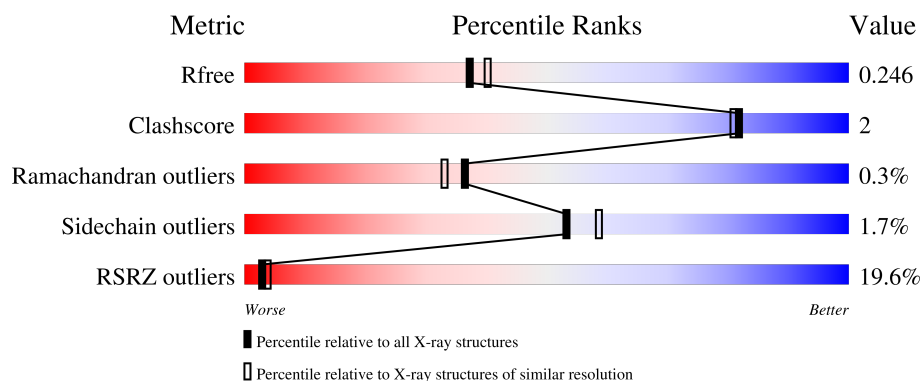
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	352	8% 81% 10% • 8%
1	B	352	28% 85% 6% • 8%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 5735 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 Casein kinase II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	323	Total	C	N	O	S	0	2	0
			2750	1762	483	494	11			
1	A	324	Total	C	N	O	S	0	2	0
			2757	1767	484	495	11			

There are 50 discrepancies between the modelled and reference sequences:

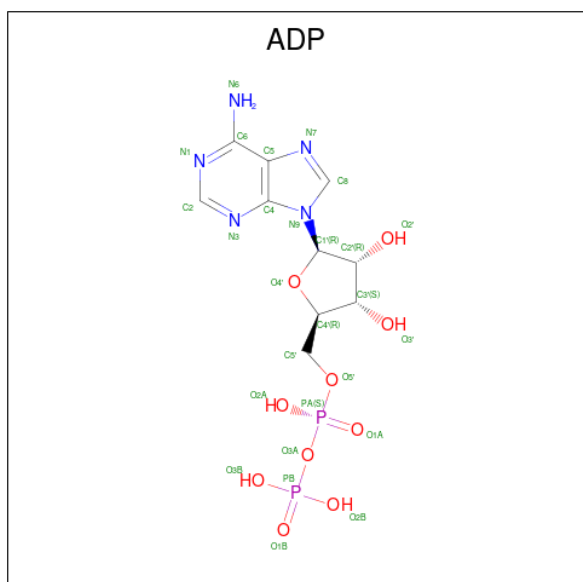
Chain	Residue	Modelled	Actual	Comment	Reference
B	-22	GLY	-	expression tag	UNP P68400
B	-21	SER	-	expression tag	UNP P68400
B	-20	MET	-	expression tag	UNP P68400
B	-19	ASP	-	expression tag	UNP P68400
B	-18	ILE	-	expression tag	UNP P68400
B	-17	GLU	-	expression tag	UNP P68400
B	-16	PHE	-	expression tag	UNP P68400
B	-15	ASP	-	expression tag	UNP P68400
B	-14	ASP	-	expression tag	UNP P68400
B	-13	ASP	-	expression tag	UNP P68400
B	-12	ALA	-	expression tag	UNP P68400
B	-11	ASP	-	expression tag	UNP P68400
B	-10	ASP	-	expression tag	UNP P68400
B	-9	ASP	-	expression tag	UNP P68400
B	-8	GLY	-	expression tag	UNP P68400
B	-7	SER	-	expression tag	UNP P68400
B	-6	GLY	-	expression tag	UNP P68400
B	-5	SER	-	expression tag	UNP P68400
B	-4	GLY	-	expression tag	UNP P68400
B	-3	SER	-	expression tag	UNP P68400
B	-2	GLY	-	expression tag	UNP P68400
B	-1	SER	-	expression tag	UNP P68400
B	0	GLY	-	expression tag	UNP P68400
B	1	SER	-	expression tag	UNP P68400
B	21	SER	ARG	engineered mutation	UNP P68400

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	GLY	-	expression tag	UNP P68400
A	-21	SER	-	expression tag	UNP P68400
A	-20	MET	-	expression tag	UNP P68400
A	-19	ASP	-	expression tag	UNP P68400
A	-18	ILE	-	expression tag	UNP P68400
A	-17	GLU	-	expression tag	UNP P68400
A	-16	PHE	-	expression tag	UNP P68400
A	-15	ASP	-	expression tag	UNP P68400
A	-14	ASP	-	expression tag	UNP P68400
A	-13	ASP	-	expression tag	UNP P68400
A	-12	ALA	-	expression tag	UNP P68400
A	-11	ASP	-	expression tag	UNP P68400
A	-10	ASP	-	expression tag	UNP P68400
A	-9	ASP	-	expression tag	UNP P68400
A	-8	GLY	-	expression tag	UNP P68400
A	-7	SER	-	expression tag	UNP P68400
A	-6	GLY	-	expression tag	UNP P68400
A	-5	SER	-	expression tag	UNP P68400
A	-4	GLY	-	expression tag	UNP P68400
A	-3	SER	-	expression tag	UNP P68400
A	-2	GLY	-	expression tag	UNP P68400
A	-1	SER	-	expression tag	UNP P68400
A	0	GLY	-	expression tag	UNP P68400
A	1	SER	-	expression tag	UNP P68400
A	21	SER	ARG	engineered mutation	UNP P68400

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

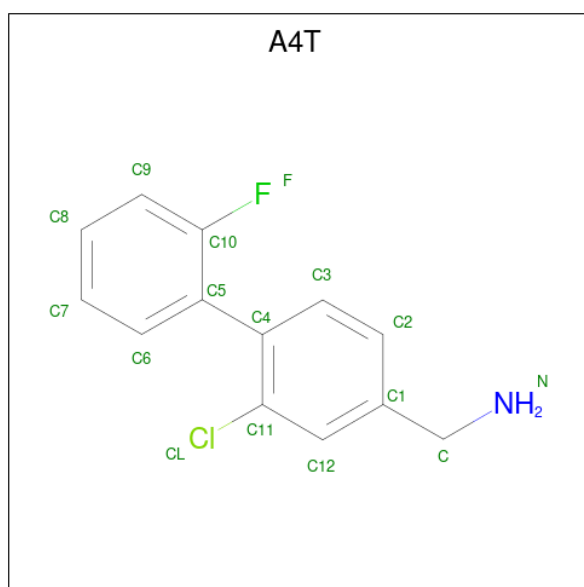


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- 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		

- Molecule 4 is [3-chloranyl-4-(2-fluorophenyl)phenyl]methanamine (CCD ID: A4T) (formula: C₁₃H₁₁ClFN) (labeled as "Ligand of Interest" by depositor).

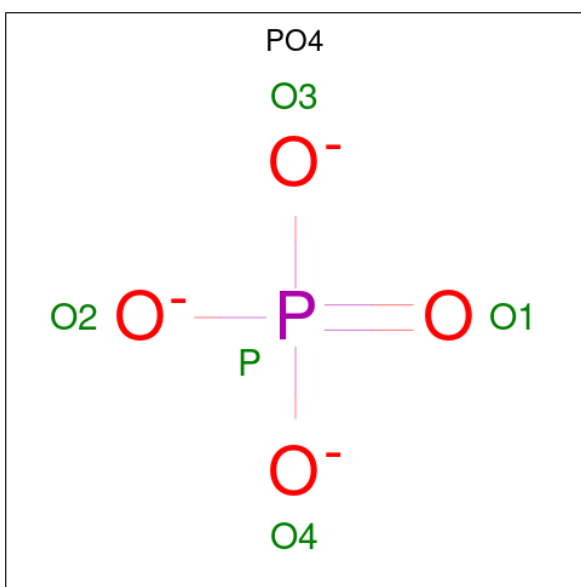


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Cl	F	N	0	0
			16	13	1	1	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	49	Total	O	0	0
			49	49		
7	A	101	Total	O	0	0
			101	101		

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	64.98Å 68.74Å 332.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	166.04 – 2.14 166.04 – 2.14	Depositor EDS
% Data completeness (in resolution range)	99.1 (166.04-2.14) 99.6 (166.04-2.14)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.14Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.216 , 0.243 0.214 , 0.246	Depositor DCC
R_{free} test set	2099 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtriage
Anisotropy	0.513	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5735	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.72% 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, A4T, CL, PO4, 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	0.96	0/2832	1.18	9/3831 (0.2%)
1	B	0.83	0/2825	1.18	4/3821 (0.1%)
All	All	0.90	0/5657	1.18	13/7652 (0.2%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	230	GLU	CB-CG-CD	6.62	123.85	112.60
1	B	121	PHE	CA-CB-CG	6.24	120.04	113.80
1	B	230	GLU	CB-CG-CD	6.21	123.15	112.60
1	A	121	PHE	CA-CB-CG	5.80	119.60	113.80
1	A	314	THR	N-CA-C	-5.58	103.02	110.55
1	A	55	GLU	N-CA-C	-5.48	100.75	109.96
1	B	55	GLU	N-CA-C	-5.48	100.75	109.96
1	B	314	THR	N-CA-C	-5.46	103.17	110.55
1	A	124	LEU	CA-C-N	5.44	128.32	120.38
1	A	124	LEU	C-N-CA	5.44	128.32	120.38
1	A	132	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	325	TYR	CA-C-N	5.17	127.21	120.28
1	A	325	TYR	C-N-CA	5.17	127.21	120.28

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	2757	0	2698	17	0
1	B	2750	0	2689	11	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
3	A	2	0	0	0	0
4	A	16	0	0	2	0
5	A	1	0	0	0	0
6	A	5	0	0	0	0
7	A	101	0	0	0	0
7	B	49	0	0	0	0
All	All	5735	0	5411	27	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (27) 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:224:SER:HB2	1:B:230:GLU:HG2	1.74	0.67
1:A:224:SER:HB2	1:A:230:GLU:HG2	1.76	0.67
1:A:73:VAL:HG22	1:A:74:LYS:H	1.68	0.58
1:B:258:ILE:HA	1:B:263:ILE:HD12	1.88	0.55
1:A:120:ASP:HB3	1:A:123:GLN:HB2	1.90	0.54
1:A:134:ARG:HG2	1:A:323:TYR:CZ	2.44	0.53
1:A:165:ASP:HB3	1:A:170:LYS:HB3	1.91	0.52
1:B:165:ASP:HB3	1:B:170:LYS:HB3	1.92	0.51
1:B:73:VAL:HG22	1:B:74:LYS:H	1.76	0.51
1:B:20:PRO:HG2	1:A:105:VAL:HG11	1.95	0.49
1:A:33:TRP:CH2	1:A:109:PRO:HB3	2.47	0.49
1:A:162:VAL:HG11	4:A:404:A4T:CL	2.52	0.46
1:A:221:MET:HE1	4:A:404:A4T:CL	2.52	0.46
1:B:303:LYS:HB3	1:B:313:LEU:HG	2.00	0.43
1:A:258:ILE:HA	1:A:263:ILE:HD12	2.00	0.42
1:A:128:LEU:HD12	1:A:225:MET:HE2	2.01	0.42
1:B:251:THR:O	1:B:255:TYR:HD2	2.02	0.42
1:A:303:LYS:HB3	1:A:313:LEU:HG	2.00	0.42
1:B:224:SER:CB	1:B:230:GLU:HG2	2.47	0.42
1:B:128:LEU:HD22	1:B:132:ASP:HB3	2.01	0.42
1:B:47:ARG:HG3	1:B:52:GLU:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:VAL:HG22	1:A:293:VAL:HG11	2.02	0.41
1:A:322:PRO:O	1:A:325:TYR:HD2	2.03	0.41
1:A:33:TRP:CZ3	1:A:109:PRO:HB3	2.56	0.41
1:A:47:ARG:HG3	1:A:52:GLU:HG3	2.03	0.40
1:A:31:VAL:HG11	1:A:82:ILE:HD13	2.02	0.40
1:B:246:ALA:HA	1:B:307:TYR:OH	2.21	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	324/352 (92%)	313 (97%)	10 (3%)	1 (0%)	36	33
1	B	323/352 (92%)	309 (96%)	13 (4%)	1 (0%)	36	33
All	All	647/704 (92%)	622 (96%)	23 (4%)	2 (0%)	36	33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	VAL
1	A	73	VAL

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	301/319 (94%)	296 (98%)	5 (2%)	53	58
1	B	300/319 (94%)	295 (98%)	5 (2%)	53	58
All	All	601/638 (94%)	591 (98%)	10 (2%)	53	58

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	21	SER
1	B	70	LEU
1	B	230	GLU
1	B	258	ILE
1	B	288	GLU
1	A	21	SER
1	A	230	GLU
1	A	288	GLU
1	A	296	GLU
1	A	327	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	118	ASN
1	B	186	GLN
1	B	234	HIS
1	B	270	ASN
1	A	186	GLN
1	A	234	HIS
1	A	270	ASN

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 7 ligands modelled in this entry, 3 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	PO4	A	406	-	4,4,4	2.59	3 (75%)	6,6,6	0.70	0
2	ADP	B	401	-	28,29,29	0.33	0	43,45,45	0.65	1 (2%)
4	A4T	A	404	-	17,17,17	0.14	0	23,23,23	0.37	0
2	ADP	A	401	3	28,29,29	0.51	0	43,45,45	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	B	401	-	-	2/16/32/32	0/3/3/3
4	A4T	A	404	-	-	0/6/6/6	0/2/2/2
2	ADP	A	401	3	-	1/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	406	PO4	P-O1	4.28	1.60	1.50
6	A	406	PO4	P-O2	2.06	1.60	1.54
6	A	406	PO4	P-O4	2.02	1.60	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	ADP	O3B-PB-O3A	2.36	112.55	104.64

There are no chirality outliers.

All (3) torsion outliers are listed below:

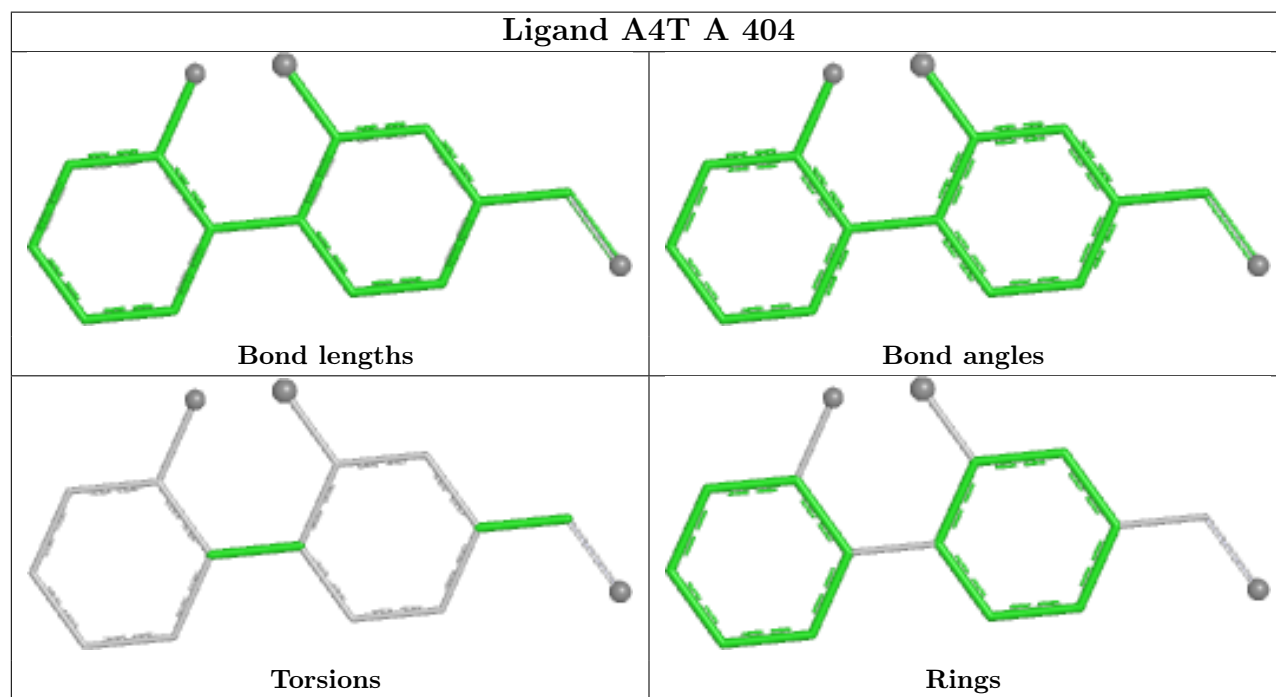
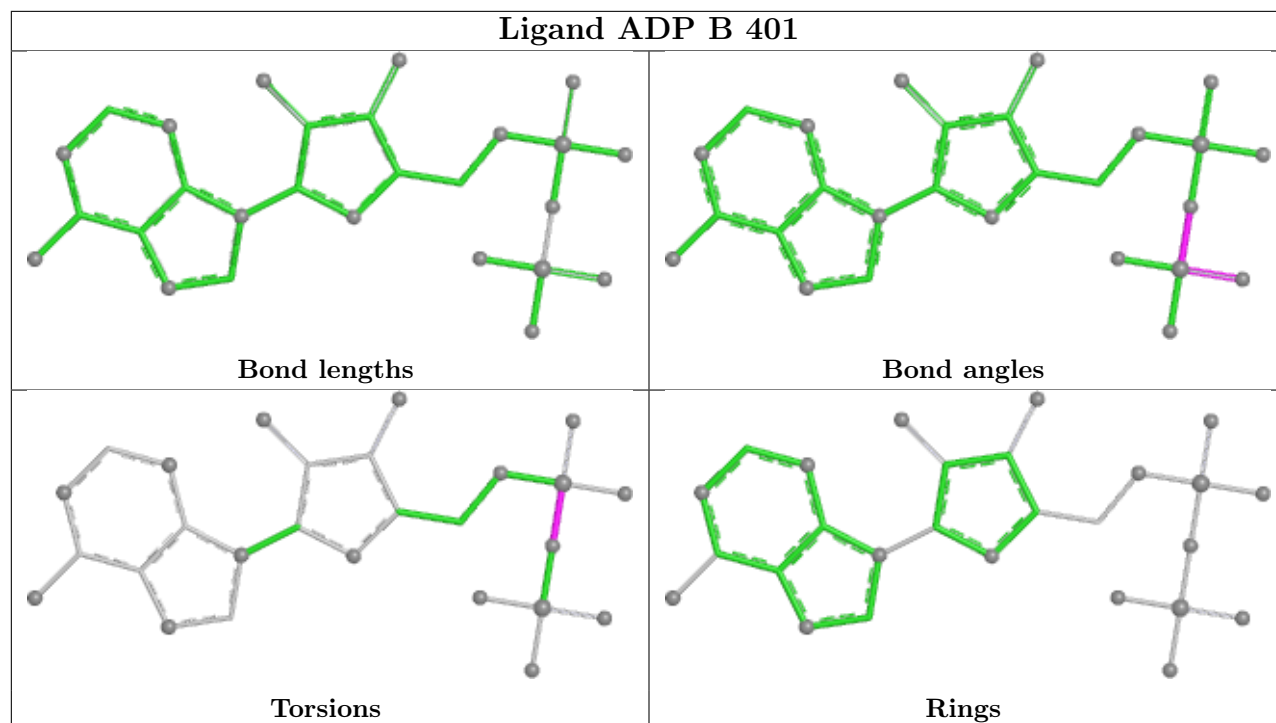
Mol	Chain	Res	Type	Atoms
2	B	401	ADP	PB-O3A-PA-O1A
2	A	401	ADP	PB-O3A-PA-O1A
2	B	401	ADP	PB-O3A-PA-O2A

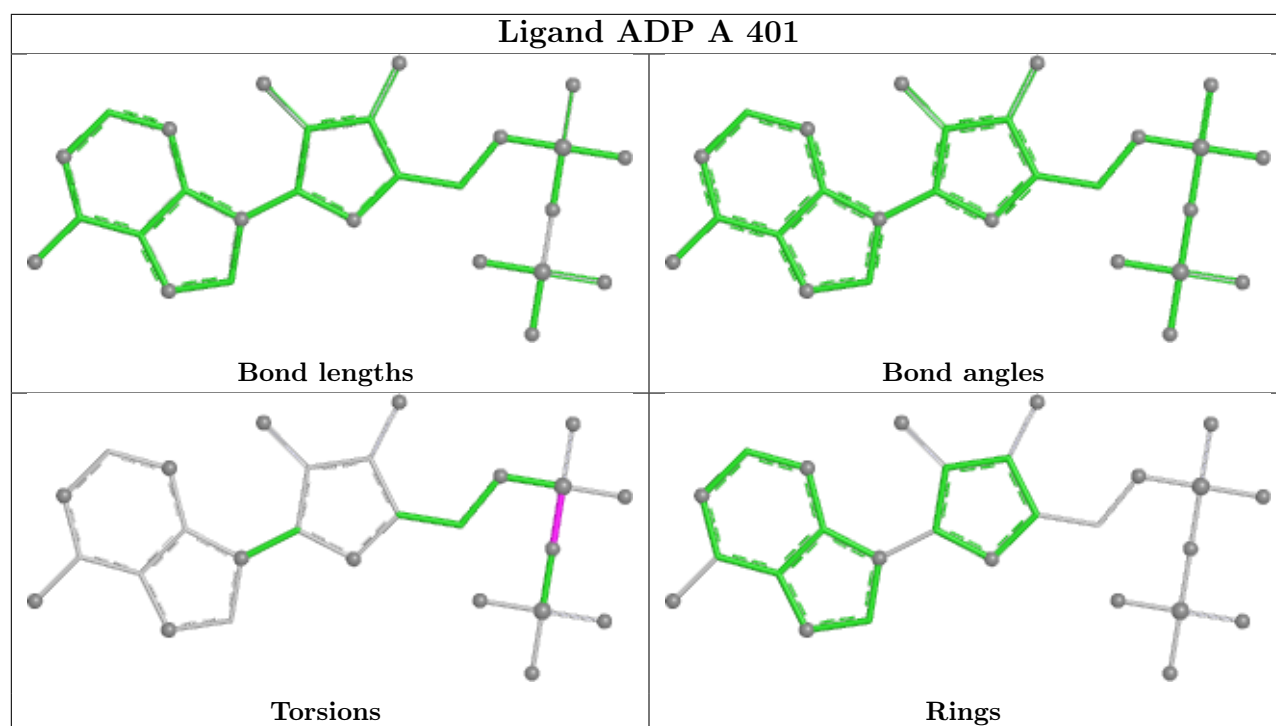
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	404	A4T	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	324/352 (92%)	0.60	28 (8%) 16 18	20, 46, 81, 101	2 (0%)
1	B	323/352 (91%)	1.60	99 (30%) 1 1	31, 71, 108, 138	2 (0%)
All	All	647/704 (91%)	1.10	127 (19%) 3 4	20, 59, 100, 138	4 (0%)

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	50	TYR	8.2
1	A	33	TRP	6.8
1	A	70	LEU	5.1
1	B	227	PHE	4.9
1	A	73	VAL	4.9
1	B	50	TYR	4.8
1	A	325	TYR	4.8
1	B	305	LEU	4.8
1	A	72	PRO	4.6
1	B	326	THR	4.6
1	A	327	VAL	4.5
1	B	73	VAL	4.4
1	B	265	LEU	4.3
1	A	104	PRO	4.3
1	B	33	TRP	4.3
1	B	307	TYR	4.2
1	B	254	LEU	4.1
1	B	269	PHE	4.0
1	B	258	ILE	3.9
1	B	281	TRP	3.9
1	B	45	LEU	3.9
1	A	326	THR	3.8
1	B	272	ILE	3.7
1	B	292	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	125	TYR	3.6
1	B	77	LYS	3.6
1	B	273	LEU	3.6
1	B	298	LEU	3.5
1	B	74	LYS	3.5
1	B	233	PHE	3.5
1	B	263	ILE	3.5
1	B	72	PRO	3.4
1	B	249	LEU	3.4
1	A	71	LYS	3.4
1	B	223	ALA	3.4
1	B	257	TYR	3.3
1	A	121	PHE	3.3
1	B	46	GLY	3.3
1	B	267	PRO	3.3
1	B	206	TYR	3.3
1	B	5	VAL	3.2
1	B	105	VAL	3.2
1	B	293	VAL	3.1
1	B	128	LEU	3.1
1	B	251	THR	3.0
1	B	248	VAL	2.9
1	B	285	VAL	2.9
1	B	26	TYR	2.9
1	B	216	TRP	2.9
1	A	76	LYS	2.9
1	A	271	ASP	2.9
1	B	70	LEU	2.8
1	A	128	LEU	2.8
1	B	64	LYS	2.8
1	B	255	TYR	2.8
1	B	325	TYR	2.8
1	A	125	TYR	2.8
1	A	124	LEU	2.8
1	B	297	ALA	2.7
1	B	108	THR	2.7
1	B	284	PHE	2.7
1	A	122	LYS	2.7
1	B	17	THR	2.7
1	B	117	ASN	2.7
1	B	276	HIS	2.6
1	B	76	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	124	LEU	2.6
1	B	324	PHE	2.6
1	B	204	VAL	2.6
1	B	48	GLY	2.6
1	B	261	TYR	2.5
1	B	308	ASP	2.5
1	B	4	PRO	2.5
1	B	6	PRO	2.5
1	B	300	PHE	2.5
1	B	42	VAL	2.5
1	B	286	HIS	2.5
1	B	302	ASP	2.5
1	B	247	LYS	2.5
1	B	57	ILE	2.5
1	B	271	ASP	2.5
1	B	29	HIS	2.5
1	B	226	ILE	2.5
1	B	21	SER	2.4
1	A	107	ARG	2.4
1	B	266	ASP	2.4
1	A	75	LYS	2.4
1	B	166	HIS	2.4
1	B	232	PHE	2.4
1	A	103	ASP	2.4
1	B	121	PHE	2.4
1	B	268	ARG	2.4
1	B	144	LEU	2.3
1	B	270	ASN	2.3
1	A	4	PRO	2.3
1	B	228	ARG	2.3
1	A	49	LYS	2.3
1	B	301	LEU	2.3
1	B	24	TRP	2.3
1	B	311[A]	SER	2.2
1	A	269	PHE	2.2
1	B	245	ILE	2.2
1	A	267	PRO	2.2
1	B	102	LYS	2.2
1	B	182	TYR	2.2
1	B	31	VAL	2.2
1	B	123	GLN	2.2
1	B	135	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	168	HIS	2.2
1	B	203	LEU	2.2
1	B	225	MET	2.2
1	A	266	ASP	2.2
1	B	30	VAL	2.1
1	B	250	GLY	2.1
1	A	278	ARG	2.1
1	B	44	LYS	2.1
1	B	116	VAL	2.1
1	B	49	LYS	2.1
1	B	51	SER	2.1
1	B	295	PRO	2.1
1	A	268	ARG	2.1
1	B	75	LYS	2.1
1	A	265	LEU	2.0
1	B	19[A]	ARG	2.0
1	B	239	TYR	2.0
1	B	169	ARG	2.0
1	B	323	TYR	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, 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.

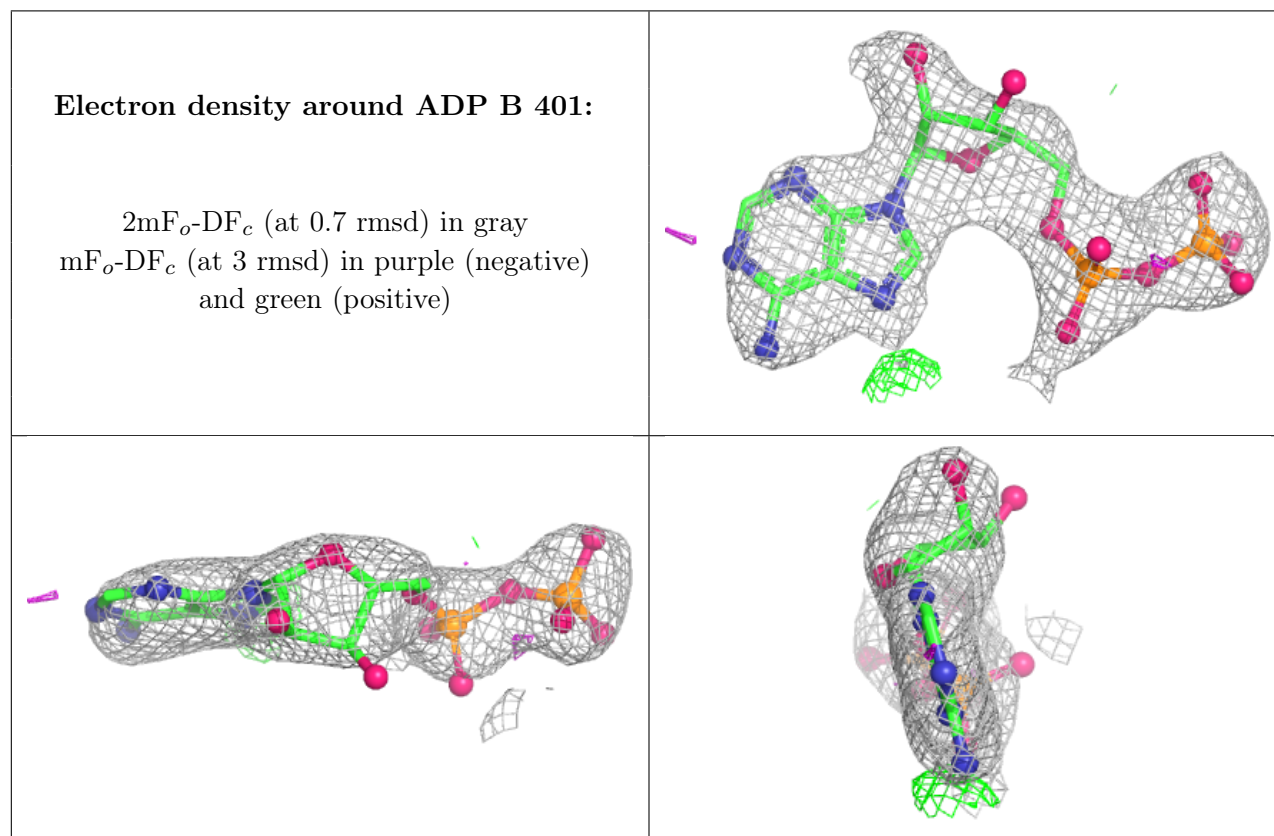
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ADP	B	401	27/27	0.81	0.13	75,94,103,104	0
4	A4T	A	404	16/16	0.83	0.18	51,63,71,72	0
6	PO4	A	406	5/5	0.86	0.11	72,74,81,82	0
2	ADP	A	401	27/27	0.88	0.11	41,55,72,74	0

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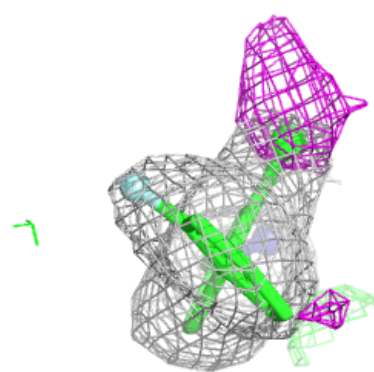
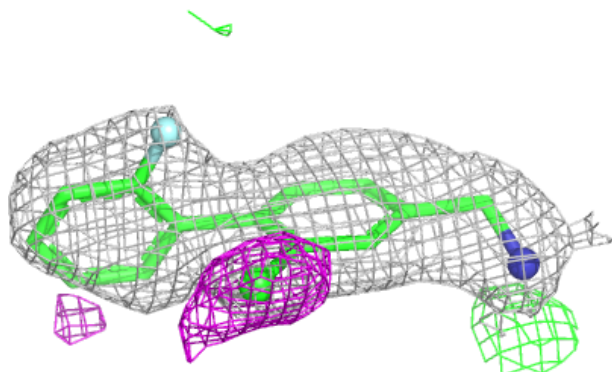
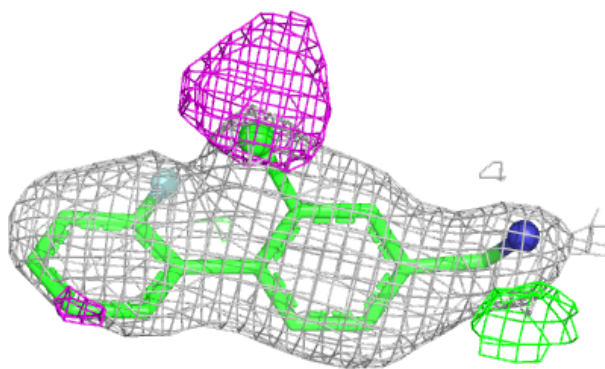
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	402	1/1	0.90	0.09	49,49,49,49	0
5	CL	A	405	1/1	0.93	0.18	69,69,69,69	0
3	MG	A	403	1/1	0.93	0.11	52,52,52,52	0

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.

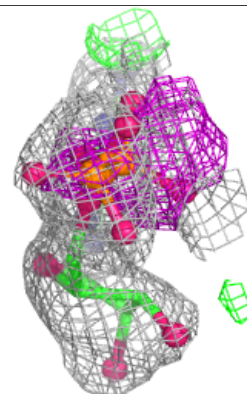
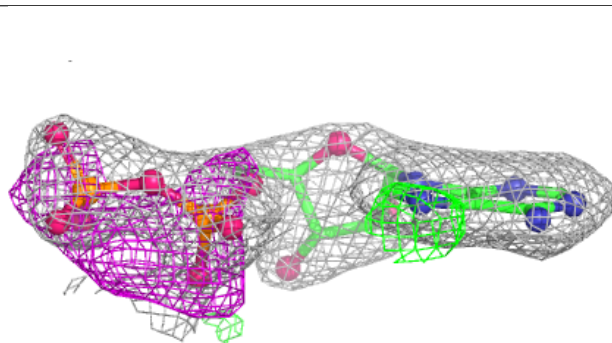
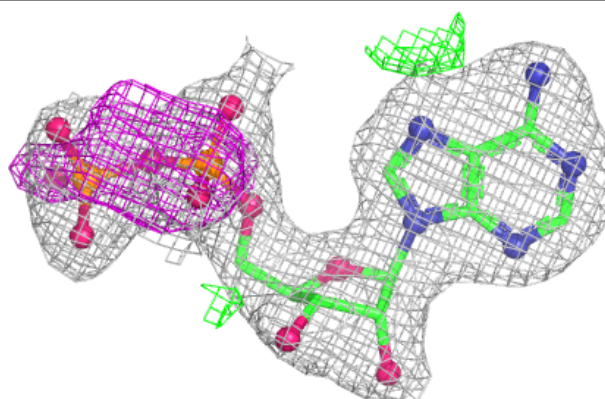


Electron density around A4T A 404:

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

**Electron density around ADP A 401:**

$2mF_o-DF_c$ (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.