



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:22 PM UTC

PDB ID : 4USJ / pdb_00004usj
Title : N-acetylglutamate kinase from Arabidopsis thaliana in complex with PII from Chlamydomonas reinhardtii
Authors : Chellamuthu, V.R.; Forchhammer, K.; Hartmann, M.D.
Deposited on : 2014-07-08
Resolution : 2.85 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

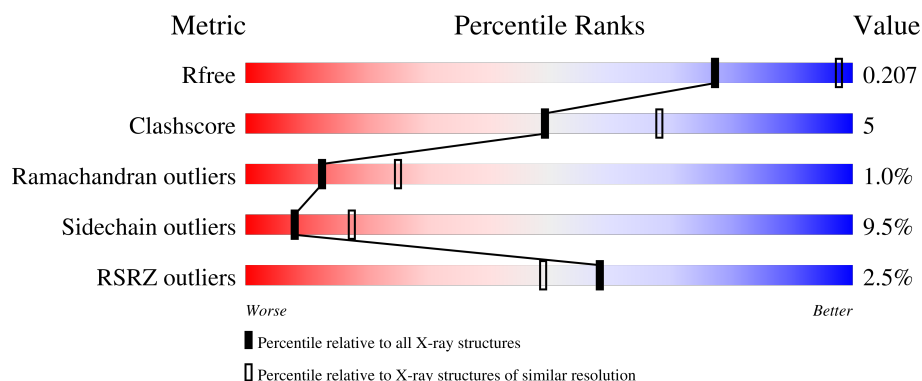
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	318	2% 69% 16% • 12%
1	B	318	3% 69% 16% • 12%
2	C	154	• 85% 5% • 8%
2	D	154	3% 82% 10% • 8%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 6567 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 ACETYLGLUTAMATE KINASE, CHLOROPLASTIC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2066	1304	359	393	10			
1	B	281	Total	C	N	O	S	0	0	0
			2058	1298	357	393	10			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP Q9SCL7
A	-19	GLY	-	expression tag	UNP Q9SCL7
A	-18	SER	-	expression tag	UNP Q9SCL7
A	-17	SER	-	expression tag	UNP Q9SCL7
A	-16	HIS	-	expression tag	UNP Q9SCL7
A	-15	HIS	-	expression tag	UNP Q9SCL7
A	-14	HIS	-	expression tag	UNP Q9SCL7
A	-13	HIS	-	expression tag	UNP Q9SCL7
A	-12	HIS	-	expression tag	UNP Q9SCL7
A	-11	HIS	-	expression tag	UNP Q9SCL7
A	-10	SER	-	expression tag	UNP Q9SCL7
A	-9	SER	-	expression tag	UNP Q9SCL7
A	-8	GLY	-	expression tag	UNP Q9SCL7
A	-7	LEU	-	expression tag	UNP Q9SCL7
A	-6	VAL	-	expression tag	UNP Q9SCL7
A	-5	PRO	-	expression tag	UNP Q9SCL7
A	-4	ARG	-	expression tag	UNP Q9SCL7
A	-3	GLY	-	expression tag	UNP Q9SCL7
A	-2	SER	-	expression tag	UNP Q9SCL7
A	-1	HIS	-	expression tag	UNP Q9SCL7
A	0	MET	-	expression tag	UNP Q9SCL7
B	-20	MET	-	expression tag	UNP Q9SCL7
B	-19	GLY	-	expression tag	UNP Q9SCL7
B	-18	SER	-	expression tag	UNP Q9SCL7
B	-17	SER	-	expression tag	UNP Q9SCL7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	expression tag	UNP Q9SCL7
B	-15	HIS	-	expression tag	UNP Q9SCL7
B	-14	HIS	-	expression tag	UNP Q9SCL7
B	-13	HIS	-	expression tag	UNP Q9SCL7
B	-12	HIS	-	expression tag	UNP Q9SCL7
B	-11	HIS	-	expression tag	UNP Q9SCL7
B	-10	SER	-	expression tag	UNP Q9SCL7
B	-9	SER	-	expression tag	UNP Q9SCL7
B	-8	GLY	-	expression tag	UNP Q9SCL7
B	-7	LEU	-	expression tag	UNP Q9SCL7
B	-6	VAL	-	expression tag	UNP Q9SCL7
B	-5	PRO	-	expression tag	UNP Q9SCL7
B	-4	ARG	-	expression tag	UNP Q9SCL7
B	-3	GLY	-	expression tag	UNP Q9SCL7
B	-2	SER	-	expression tag	UNP Q9SCL7
B	-1	HIS	-	expression tag	UNP Q9SCL7
B	0	MET	-	expression tag	UNP Q9SCL7

- Molecule 2 is a protein called NITROGEN REGULATORY PROTEIN PII.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	142	Total	C	N	O	S	0	1	0
			1087	694	188	200	5			
2	D	142	Total	C	N	O	S	0	1	0
			1086	694	187	200	5			

There are 22 discrepancies between the modelled and reference sequences:

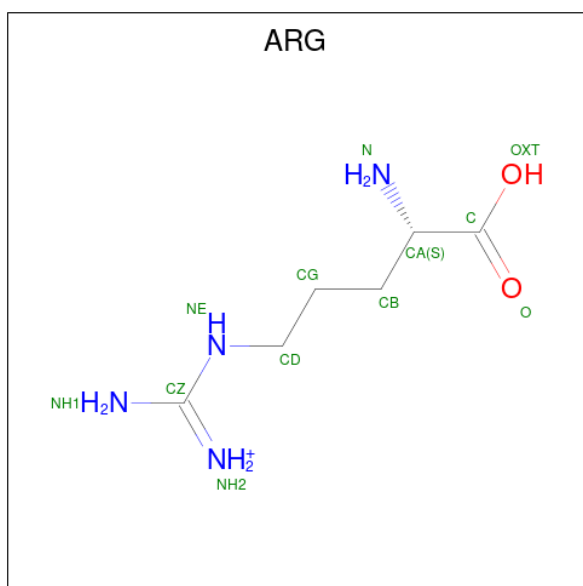
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	expression tag	UNP A8JI83
C	145	SER	-	expression tag	UNP A8JI83
C	146	ALA	-	expression tag	UNP A8JI83
C	147	TRP	-	expression tag	UNP A8JI83
C	148	SER	-	expression tag	UNP A8JI83
C	149	HIS	-	expression tag	UNP A8JI83
C	150	PRO	-	expression tag	UNP A8JI83
C	151	GLN	-	expression tag	UNP A8JI83
C	152	PHE	-	expression tag	UNP A8JI83
C	153	GLU	-	expression tag	UNP A8JI83
C	154	LYS	-	expression tag	UNP A8JI83
D	1	MET	-	expression tag	UNP A8JI83
D	145	SER	-	expression tag	UNP A8JI83

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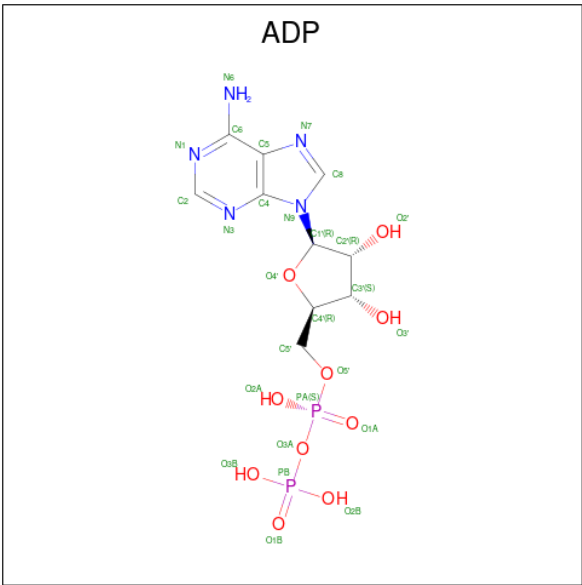
Chain	Residue	Modelled	Actual	Comment	Reference
D	146	ALA	-	expression tag	UNP A8JI83
D	147	TRP	-	expression tag	UNP A8JI83
D	148	SER	-	expression tag	UNP A8JI83
D	149	HIS	-	expression tag	UNP A8JI83
D	150	PRO	-	expression tag	UNP A8JI83
D	151	GLN	-	expression tag	UNP A8JI83
D	152	PHE	-	expression tag	UNP A8JI83
D	153	GLU	-	expression tag	UNP A8JI83
D	154	LYS	-	expression tag	UNP A8JI83

- Molecule 3 is ARGinine (CCD ID: ARG) (formula: $C_6H_{15}N_4O_2$).



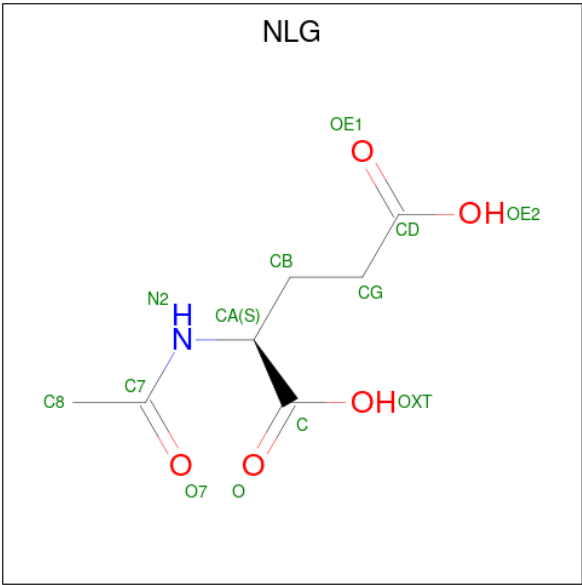
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			12	6	4	2		
3	B	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



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

- Molecule 5 is N-ACETYL-L-GLUTAMATE (CCD ID: NLG) (formula: C₇H₁₁NO₅).

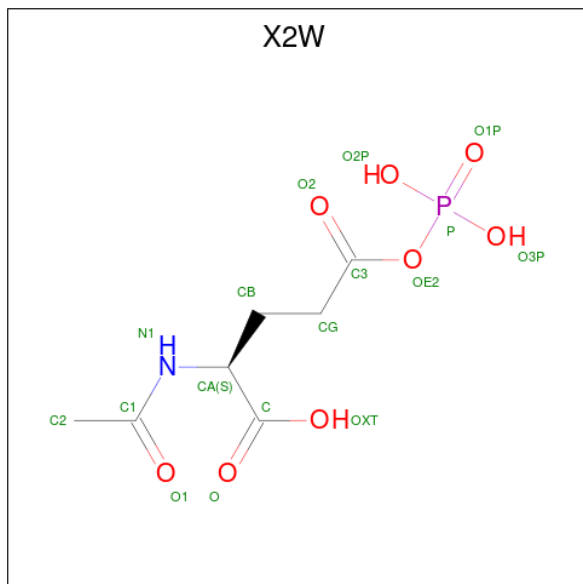


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O		0	0
			13	7	1	5			

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

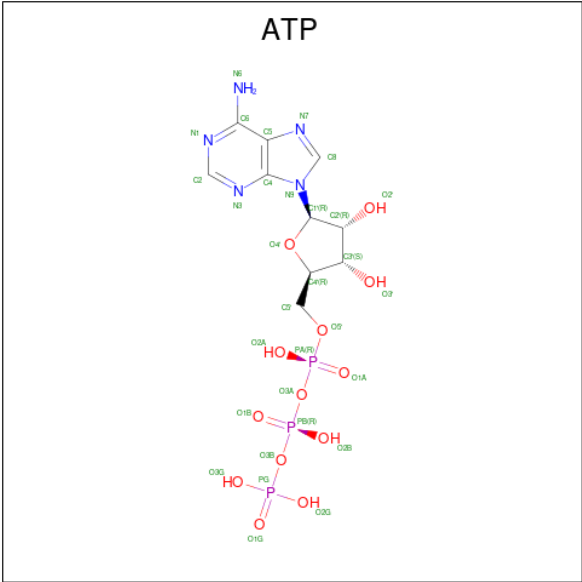
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		
6	C	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		

- Molecule 7 is N-ACETYL-L-GLUTAMYL 5-PHOSPHATE (CCD ID: X2W) (formula: $C_7H_{12}NO_8P$).



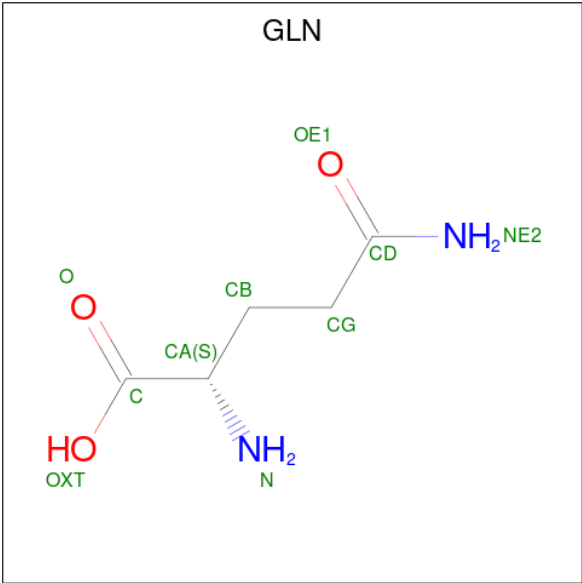
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	N	O	P	0	0
			17	7	1	8	1		

- Molecule 8 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



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

- Molecule 9 is GLUTAMINE (CCD ID: GLN) (formula: C₅H₁₀N₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total	C	N	O	0	0
			10	5	2	3		
9	D	1	Total	C	N	O	0	0
			10	5	2	3		

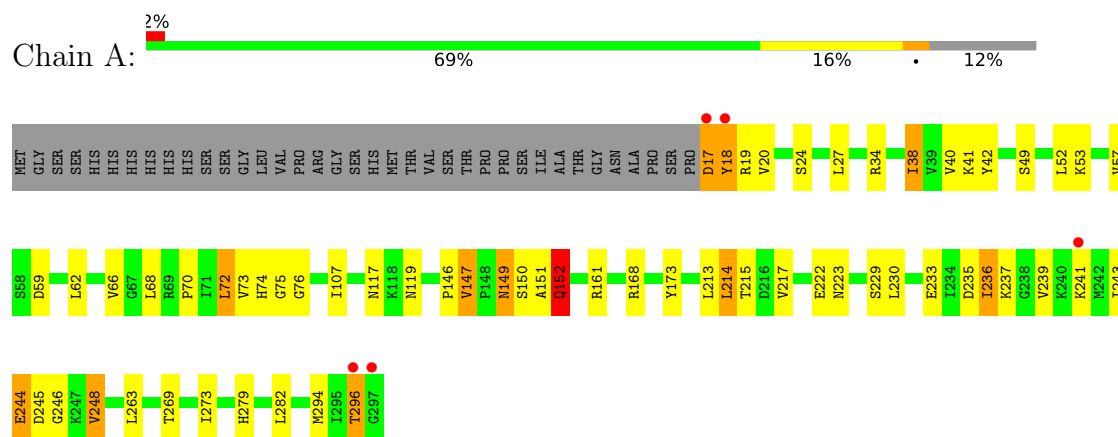
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	37	Total 37	O 37	0	0
10	B	30	Total 30	O 30	0	0
10	C	20	Total 20	O 20	0	0
10	D	17	Total 17	O 17	0	0

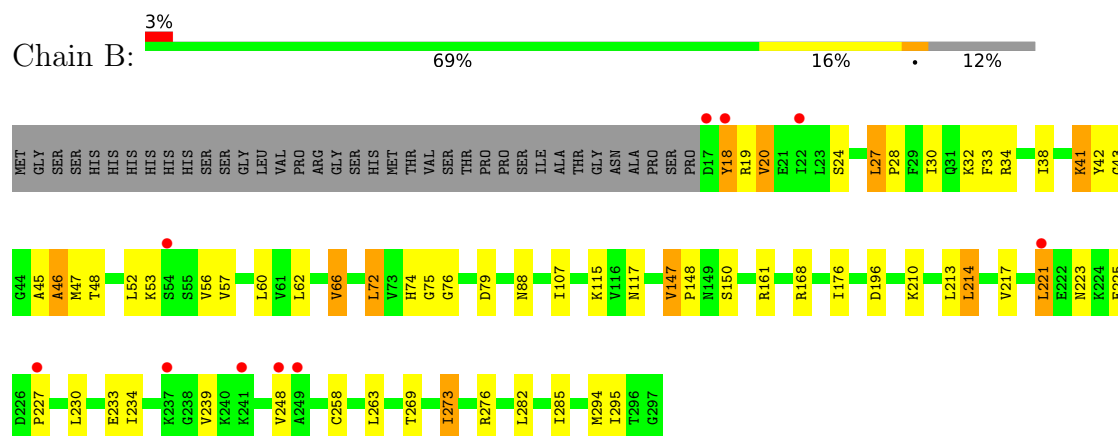
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

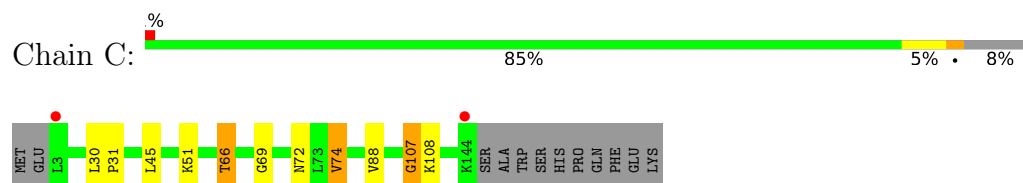
• Molecule 1: ACETYLGLUTAMATE KINASE, CHLOROPLASTIC



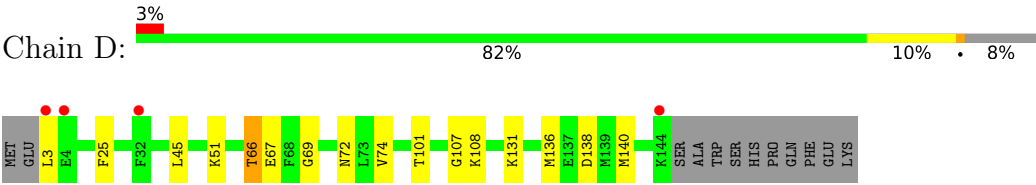
• Molecule 1: ACETYLGLUTAMATE KINASE, CHLOROPLASTIC



• Molecule 2: NITROGEN REGULATORY PROTEIN PII



• Molecule 2: NITROGEN REGULATORY PROTEIN PII



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	171.43Å 171.43Å 171.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.36 – 2.85 39.36 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.0 (39.36-2.85) 99.1 (39.36-2.85)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.189 , 0.220 0.173 , 0.207	Depositor DCC
R_{free} test set	2027 reflections (5.19%)	wwPDB-VP
Wilson B-factor (Å ²)	56.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.035 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6567	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% 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, ATP, MG, NLG, X2W

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	1.19	3/2091 (0.1%)	1.23	6/2832 (0.2%)
1	B	1.13	2/2083 (0.1%)	1.18	2/2824 (0.1%)
2	C	1.03	1/1109 (0.1%)	1.11	2/1496 (0.1%)
2	D	1.04	0/1108	1.13	3/1495 (0.2%)
All	All	1.12	6/6391 (0.1%)	1.18	13/8647 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	147	VAL	N-CA	-6.31	1.38	1.46
1	A	70	PRO	C-O	-6.09	1.17	1.23
2	C	74	VAL	C-O	-5.47	1.18	1.24
1	B	115	LYS	CA-C	5.30	1.57	1.52
1	B	273	ILE	CA-C	-5.17	1.47	1.52
1	A	146	PRO	N-CA	-5.12	1.41	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	107	GLY	N-CA-C	6.79	119.05	111.85
1	B	285	ILE	N-CA-C	6.24	117.80	111.00
1	A	152	GLN	CB-CA-C	-6.22	99.70	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	147	VAL	N-CA-CB	-6.20	102.53	111.21
2	D	25	PHE	N-CA-C	5.74	115.68	108.45
1	A	40	VAL	CB-CA-C	-5.57	102.53	110.83
1	A	68	LEU	N-CA-C	-5.46	102.67	110.59
1	A	236	ILE	N-CA-C	5.17	115.38	110.42
2	D	67	GLU	CB-CA-C	5.11	118.56	109.72
1	B	176	ILE	CB-CA-C	-5.09	105.05	110.95
2	D	101	THR	CB-CA-C	-5.07	100.33	110.42
1	A	38	ILE	N-CA-CB	-5.03	105.80	112.34
2	C	88	VAL	N-CA-C	5.03	115.18	110.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	150	SER	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	2066	0	2153	28	0
1	B	2058	0	2131	29	0
2	C	1087	0	1096	7	0
2	D	1086	0	1091	8	0
3	A	12	0	12	0	0
3	B	12	0	12	2	0
4	A	27	0	12	0	0
5	A	13	0	9	0	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	B	17	0	9	0	0
8	C	31	0	12	2	0
8	D	31	0	12	2	0
9	C	10	0	7	0	0
9	D	10	0	7	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	A	37	0	0	0	0
10	B	30	0	0	1	0
10	C	20	0	0	0	0
10	D	17	0	0	0	0
All	All	6567	0	6563	70	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 5.

All (70) 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:269:THR:HB	1:A:294:MET:HE2	1.63	0.81
1:B:161:ARG:HA	2:C:66:THR:HB	1.68	0.76
2:C:69:GLY:H	2:C:72:ASN:HD22	1.31	0.76
1:A:161:ARG:HA	2:D:66:THR:HB	1.68	0.74
2:D:69:GLY:H	2:D:72:ASN:HD22	1.37	0.73
1:A:74:HIS:HE1	1:A:117:ASN:HD22	1.36	0.71
1:A:149:ASN:H	1:A:149:ASN:HD22	1.43	0.66
1:B:217:VAL:HA	1:B:276:ARG:HH21	1.63	0.64
1:B:41:LYS:HD2	1:B:196:ASP:OD1	1.97	0.64
1:B:269:THR:HB	1:B:294:MET:HE2	1.80	0.63
1:B:74:HIS:HE1	1:B:117:ASN:HD22	1.46	0.62
1:A:17:ASP:OD1	1:A:18:TYR:N	2.33	0.61
2:C:69:GLY:N	2:C:72:ASN:HD22	1.98	0.61
2:D:69:GLY:N	2:D:72:ASN:HD22	1.99	0.60
1:A:269:THR:CB	1:A:294:MET:HE2	2.32	0.58
1:A:17:ASP:OD1	1:A:17:ASP:C	2.46	0.58
1:B:74:HIS:HD2	1:B:75:GLY:O	1.88	0.56
2:C:69:GLY:H	2:C:72:ASN:ND2	2.02	0.56
1:A:214:LEU:HD22	1:A:273:ILE:HD11	1.86	0.56
1:B:234:ILE:O	1:B:295:ILE:HA	2.06	0.55
1:A:269:THR:HB	1:A:294:MET:CE	2.36	0.55
1:B:30:ILE:HG23	1:B:66:VAL:HG13	1.89	0.55
1:A:74:HIS:HD2	1:A:75:GLY:O	1.92	0.53
1:B:214:LEU:HD22	1:B:273:ILE:HD11	1.90	0.52
2:D:131:LYS:NZ	2:D:138:ASP:OD1	2.40	0.51
1:A:62:LEU:HD23	1:A:282:LEU:HD11	1.93	0.51
1:A:149:ASN:O	1:A:152:GLN:HG2	2.11	0.51
1:B:210:LYS:HE3	3:B:301:ARG:OXT	2.11	0.50
1:A:42:TYR:OH	1:A:53:LYS:HA	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:ALA:O	1:B:47:MET:N	2.45	0.50
2:C:108:LYS:HE3	8:C:301:ATP:O1B	2.11	0.50
1:B:32:LYS:HD3	10:B:2002:HOH:O	2.11	0.50
1:A:243:ILE:HG12	1:A:248:VAL:HG22	1.94	0.49
1:A:149:ASN:HB2	1:A:152:GLN:HG2	1.94	0.49
1:B:45:ALA:O	1:B:46:ALA:C	2.56	0.49
1:B:41:LYS:HB3	1:B:213:LEU:HD23	1.94	0.48
1:A:41:LYS:HA	1:A:73:VAL:O	2.13	0.48
2:D:69:GLY:H	2:D:72:ASN:ND2	2.07	0.48
2:D:108:LYS:HE3	8:D:301:ATP:O1B	2.14	0.47
1:A:42:TYR:HB2	1:A:72:LEU:HD21	1.96	0.47
1:B:60:LEU:HD11	1:B:72:LEU:HG	1.97	0.47
1:A:269:THR:CG2	1:A:294:MET:HE2	2.44	0.47
1:B:294:MET:HB2	3:B:301:ARG:NH1	2.30	0.46
1:A:53:LYS:NZ	1:A:119:ASN:HD21	2.14	0.46
2:D:107:GLY:HA2	8:D:301:ATP:H5'1	1.95	0.46
1:A:222:GLU:HB3	1:A:229:SER:HB2	1.97	0.46
1:B:52:LEU:O	1:B:56:VAL:HG23	2.16	0.46
1:B:45:ALA:C	1:B:47:MET:N	2.73	0.46
1:A:41:LYS:HB3	1:A:213:LEU:HD23	2.00	0.43
1:A:18:TYR:C	1:A:18:TYR:CD1	2.96	0.43
1:B:18:TYR:CD1	1:B:18:TYR:C	2.96	0.43
2:C:107:GLY:HA2	8:C:301:ATP:H5'1	1.99	0.43
1:B:32:LYS:HG2	1:B:33:PHE:CZ	2.54	0.43
1:B:223:ASN:HD21	1:B:225:GLU:HG2	1.84	0.42
1:B:221:LEU:CD2	1:B:227:PRO:HA	2.49	0.42
1:B:42:TYR:OH	1:B:53:LYS:HA	2.18	0.42
1:B:43:GLY:HA2	1:B:47:MET:HE2	2.02	0.42
2:D:136:MET:HG2	2:D:140:MET:HE2	2.02	0.42
1:A:59:ASP:OD2	1:A:279:HIS:HA	2.19	0.41
1:B:27:LEU:N	1:B:28:PRO:CD	2.84	0.41
1:A:236:ILE:O	1:A:237:LYS:C	2.61	0.41
1:B:62:LEU:HD23	1:B:282:LEU:HD11	2.03	0.41
1:A:244:GLU:O	1:A:246:GLY:N	2.54	0.41
1:A:215:THR:HG23	1:A:217:VAL:H	1.86	0.41
1:B:18:TYR:C	1:B:20:VAL:N	2.80	0.40
1:A:52:LEU:HD23	1:A:52:LEU:HA	1.74	0.40
1:B:147:VAL:HG22	1:B:148:PRO:HD2	2.02	0.40
1:A:282:LEU:HD23	1:A:282:LEU:HA	1.90	0.40
2:C:30:LEU:HB3	2:C:31:PRO:HD3	2.04	0.40
1:B:282:LEU:HD23	1:B:282:LEU:HA	1.93	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	279/318 (88%)	261 (94%)	13 (5%)	5 (2%)	6	15
1	B	279/318 (88%)	262 (94%)	14 (5%)	3 (1%)	11	24
2	C	141/154 (92%)	135 (96%)	6 (4%)	0	100	100
2	D	141/154 (92%)	134 (95%)	7 (5%)	0	100	100
All	All	840/944 (89%)	792 (94%)	40 (5%)	8 (1%)	12	25

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	ALA
1	B	46	ALA
1	A	245	ASP
1	B	19	ARG
1	A	76	GLY
1	A	173	TYR
1	A	296	THR
1	B	76	GLY

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	223/256 (87%)	195 (87%)	28 (13%)	4	8
1	B	221/256 (86%)	196 (89%)	25 (11%)	5	11
2	C	113/127 (89%)	109 (96%)	4 (4%)	32	57
2	D	112/127 (88%)	107 (96%)	5 (4%)	24	48
All	All	669/766 (87%)	607 (91%)	62 (9%)	8	18

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	18	TYR
1	A	19	ARG
1	A	20	VAL
1	A	24	SER
1	A	27	LEU
1	A	34	ARG
1	A	38	ILE
1	A	49	SER
1	A	57	VAL
1	A	66	VAL
1	A	72	LEU
1	A	107	ILE
1	A	147	VAL
1	A	149	ASN
1	A	152	GLN
1	A	168	ARG
1	A	214	LEU
1	A	223	ASN
1	A	230	LEU
1	A	233	GLU
1	A	235	ASP
1	A	239	VAL
1	A	241	LYS
1	A	244	GLU
1	A	248	VAL
1	A	263	LEU
1	A	296	THR
1	B	18	TYR
1	B	20	VAL
1	B	24	SER
1	B	27	LEU
1	B	34	ARG

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Mol	Chain	Res	Type
1	B	38	ILE
1	B	41	LYS
1	B	48	THR
1	B	57	VAL
1	B	66	VAL
1	B	72	LEU
1	B	79	ASP
1	B	88	ASN
1	B	107	ILE
1	B	147	VAL
1	B	150	SER
1	B	168	ARG
1	B	214	LEU
1	B	221	LEU
1	B	230	LEU
1	B	233	GLU
1	B	239	VAL
1	B	248	VAL
1	B	258	CYS
1	B	263	LEU
2	C	45	LEU
2	C	51	LYS
2	C	66	THR
2	C	74	VAL
2	D	3	LEU
2	D	45	LEU
2	D	51	LYS
2	D	66	THR
2	D	74	VAL

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	74	HIS
1	A	119	ASN
1	A	149	ASN
1	A	283	HIS
1	B	74	HIS
1	B	119	ASN
1	B	223	ASN
2	C	47	ASN
2	C	72	ASN

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Mol	Chain	Res	Type
2	C	112	HIS
2	D	47	ASN
2	D	72	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 3 are monoatomic - leaving 9 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	$\# Z > 2$
9	GLN	D	303	-	8,9,9	0.92	1 (12%)	8,11,11	1.32	1 (12%)
3	ARG	B	301	-	10,11,11	0.67	0	9,13,13	1.43	1 (11%)
4	ADP	A	302	6	28,29,29	1.61	5 (17%)	43,45,45	1.86	10 (23%)
7	X2W	B	303	-	15,16,16	2.23	2 (13%)	20,22,22	1.84	6 (30%)
9	GLN	C	303	-	8,9,9	0.90	1 (12%)	8,11,11	0.97	1 (12%)
8	ATP	D	301	6	32,33,33	1.56	6 (18%)	48,52,52	2.19	14 (29%)
3	ARG	A	301	-	10,11,11	0.87	1 (10%)	9,13,13	1.72	2 (22%)
5	NLG	A	303	-	12,12,12	0.99	0	15,15,15	1.06	1 (6%)
8	ATP	C	301	6	32,33,33	1.43	6 (18%)	48,52,52	1.88	13 (27%)

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
9	GLN	D	303	-	-	1/9/9/9	-
3	ARG	B	301	-	-	4/11/11/11	-
4	ADP	A	302	6	-	8/16/32/32	0/3/3/3
7	X2W	B	303	-	-	0/16/18/18	-
9	GLN	C	303	-	-	2/9/9/9	-
8	ATP	D	301	6	-	5/22/38/38	0/3/3/3
3	ARG	A	301	-	-	2/11/11/11	-
5	NLG	A	303	-	-	0/13/13/13	-
8	ATP	C	301	6	-	4/22/38/38	0/3/3/3

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	303	X2W	P-OE2	7.62	1.73	1.59
4	A	302	ADP	C5-C4	5.51	1.48	1.39
8	D	301	ATP	C5-C4	4.52	1.47	1.39
8	C	301	ATP	C5-C4	4.06	1.46	1.39
8	C	301	ATP	C5-N7	-3.58	1.32	1.39
8	D	301	ATP	C5-N7	-3.28	1.33	1.39
4	A	302	ADP	C8-N7	3.16	1.37	1.31
4	A	302	ADP	C4-N9	-3.09	1.31	1.37
8	D	301	ATP	PB-O3B	2.69	1.62	1.59
8	C	301	ATP	C4-N9	-2.60	1.32	1.37
4	A	302	ADP	PA-O3A	2.56	1.62	1.59
8	D	301	ATP	C8-N7	2.55	1.36	1.31
8	D	301	ATP	C8-N9	-2.46	1.33	1.37
8	C	301	ATP	C8-N7	2.37	1.36	1.31
8	C	301	ATP	PB-O3B	2.30	1.62	1.59
8	D	301	ATP	C5-C6	2.28	1.47	1.41
4	A	302	ADP	C5-C6	2.22	1.47	1.41
3	A	301	ARG	OXT-C	-2.17	1.23	1.30
7	B	303	X2W	OXT-C	-2.04	1.24	1.30
9	D	303	GLN	OXT-C	-2.04	1.24	1.30
9	C	303	GLN	OXT-C	-2.03	1.24	1.30
8	C	301	ATP	C5-C6	2.01	1.46	1.41

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	D	301	ATP	O2B-PB-O3A	6.72	125.43	107.27
8	D	301	ATP	C5-C4-N3	-6.35	117.97	126.72
8	C	301	ATP	C5-C4-N3	-4.90	119.97	126.72
8	D	301	ATP	C4-C5-N7	-4.83	105.06	110.58
4	A	302	ADP	O5'-PA-O1A	4.83	128.08	108.94
4	A	302	ADP	C5-C4-N3	-4.75	120.18	126.72
8	C	301	ATP	C4-C5-N7	-4.66	105.25	110.58
4	A	302	ADP	N3-C2-N1	-4.14	122.32	128.58
8	D	301	ATP	N3-C4-N9	4.13	134.20	127.17
7	B	303	X2W	CB-CA-C	4.12	120.12	110.35
3	B	301	ARG	OXT-C-O	-3.74	115.60	124.08
3	A	301	ARG	OXT-C-O	-3.63	115.85	124.08
9	D	303	GLN	OXT-C-O	-3.53	116.07	124.08
4	A	302	ADP	C2-N3-C4	3.49	120.36	111.83
8	C	301	ATP	C5-N7-C8	3.47	108.90	103.45
4	A	302	ADP	N3-C4-N9	3.43	133.00	127.17
8	C	301	ATP	N3-C2-N1	-3.42	123.41	128.58
8	D	301	ATP	C5-N7-C8	3.32	108.67	103.45
8	C	301	ATP	C2-N1-C6	3.19	123.97	118.73
8	D	301	ATP	C2-N3-C4	3.16	119.54	111.83
8	C	301	ATP	C6-C5-N7	3.13	138.12	132.09
7	B	303	X2W	O2-C3-CG	-3.07	111.77	123.78
8	C	301	ATP	C2-N3-C4	3.07	119.33	111.83
4	A	302	ADP	C2-N1-C6	3.03	123.71	118.73
7	B	303	X2W	C-CA-N1	-2.98	103.67	110.57
8	D	301	ATP	O2B-PB-O3B	-2.95	99.30	107.27
8	C	301	ATP	O4'-C1'-N9	-2.95	102.42	108.09
8	D	301	ATP	O3G-PG-O2G	2.91	118.70	107.80
8	C	301	ATP	N3-C4-N9	2.90	132.10	127.17
8	C	301	ATP	N9-C8-N7	-2.69	110.12	113.94
7	B	303	X2W	OE2-C3-CG	2.47	122.72	111.87
4	A	302	ADP	C4-C5-N7	-2.47	107.76	110.58
9	C	303	GLN	OXT-C-O	-2.45	118.53	124.08
8	D	301	ATP	N3-C2-N1	-2.38	124.98	128.58
4	A	302	ADP	O2B-PB-O1B	2.37	120.07	110.83
7	B	303	X2W	CB-CG-C3	2.35	119.88	113.21
8	C	301	ATP	O3A-PB-O1B	-2.28	103.85	110.70
8	D	301	ATP	O3A-PA-O1A	2.25	117.46	110.70
8	C	301	ATP	O2B-PB-O3A	2.18	113.16	107.27
8	D	301	ATP	O2A-PA-O1A	2.17	122.55	112.44
8	D	301	ATP	O3A-PB-O1B	-2.17	104.17	110.70
4	A	302	ADP	C6-C5-N7	2.15	136.24	132.09
3	A	301	ARG	CG-CB-CA	2.15	120.16	113.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	301	ATP	O2A-PA-O1A	2.14	122.41	112.44
4	A	302	ADP	C4-N9-C8	2.05	107.89	105.74
8	D	301	ATP	C3'-C2'-C1'	2.05	105.33	101.46
8	D	301	ATP	C6-C5-C4	2.04	119.96	117.18
5	A	303	NLG	OE1-CD-CG	-2.01	116.71	123.09
7	B	303	X2W	OXT-C-O	-2.01	119.52	124.08

There are no chirality outliers.

All (26) torsion outliers are listed below:

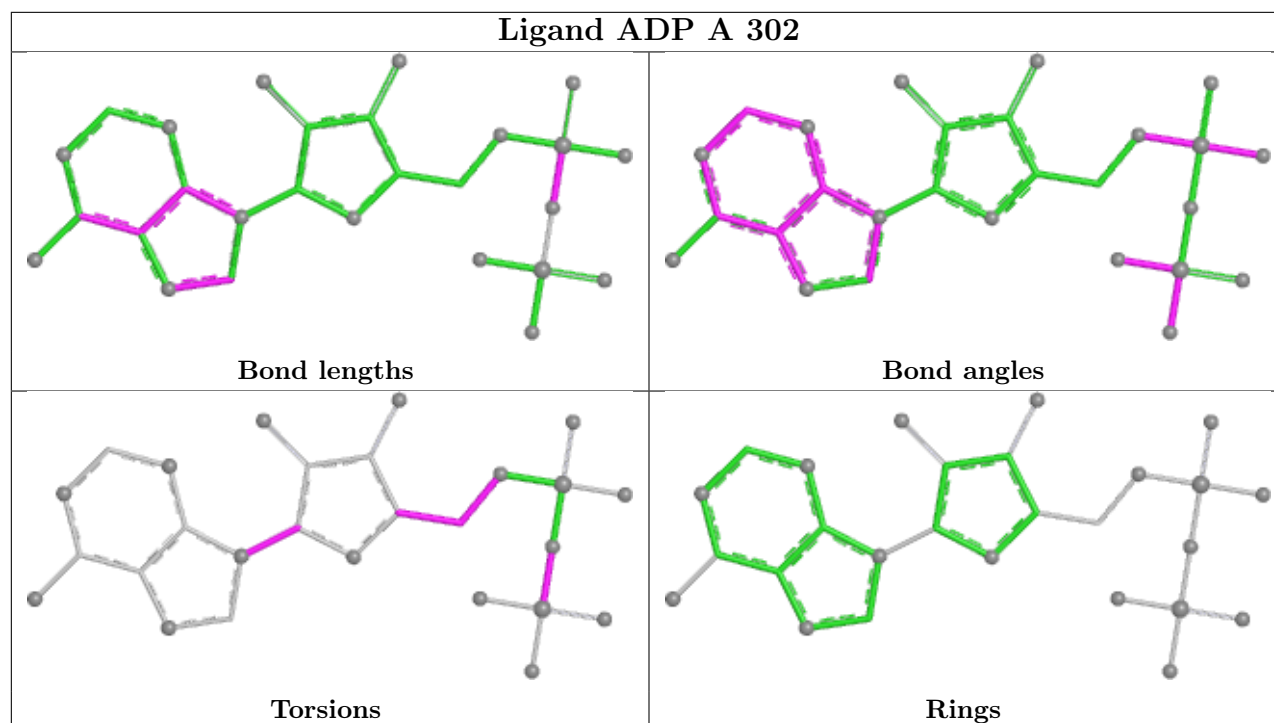
Mol	Chain	Res	Type	Atoms
3	B	301	ARG	N-CA-CB-CG
3	B	301	ARG	C-CA-CB-CG
4	A	302	ADP	PA-O3A-PB-O3B
8	C	301	ATP	C5'-O5'-PA-O2A
8	C	301	ATP	C5'-O5'-PA-O3A
8	D	301	ATP	C5'-O5'-PA-O2A
8	D	301	ATP	C5'-O5'-PA-O3A
3	A	301	ARG	NE-CD-CG-CB
3	B	301	ARG	NE-CD-CG-CB
4	A	302	ADP	C4'-C5'-O5'-PA
4	A	302	ADP	C3'-C4'-C5'-O5'
3	B	301	ARG	CA-CB-CG-CD
8	C	301	ATP	PG-O3B-PB-O1B
4	A	302	ADP	O4'-C4'-C5'-O5'
4	A	302	ADP	PA-O3A-PB-O2B
4	A	302	ADP	C2'-C1'-N9-C8
4	A	302	ADP	C2'-C1'-N9-C4
3	A	301	ARG	CA-CB-CG-CD
9	C	303	GLN	O-C-CA-N
9	D	303	GLN	OXT-C-CA-N
9	C	303	GLN	OXT-C-CA-N
8	D	301	ATP	PB-O3B-PG-O3G
4	A	302	ADP	O4'-C1'-N9-C8
8	C	301	ATP	PG-O3B-PB-O2B
8	D	301	ATP	PB-O3A-PA-O1A
8	D	301	ATP	PA-O3A-PB-O2B

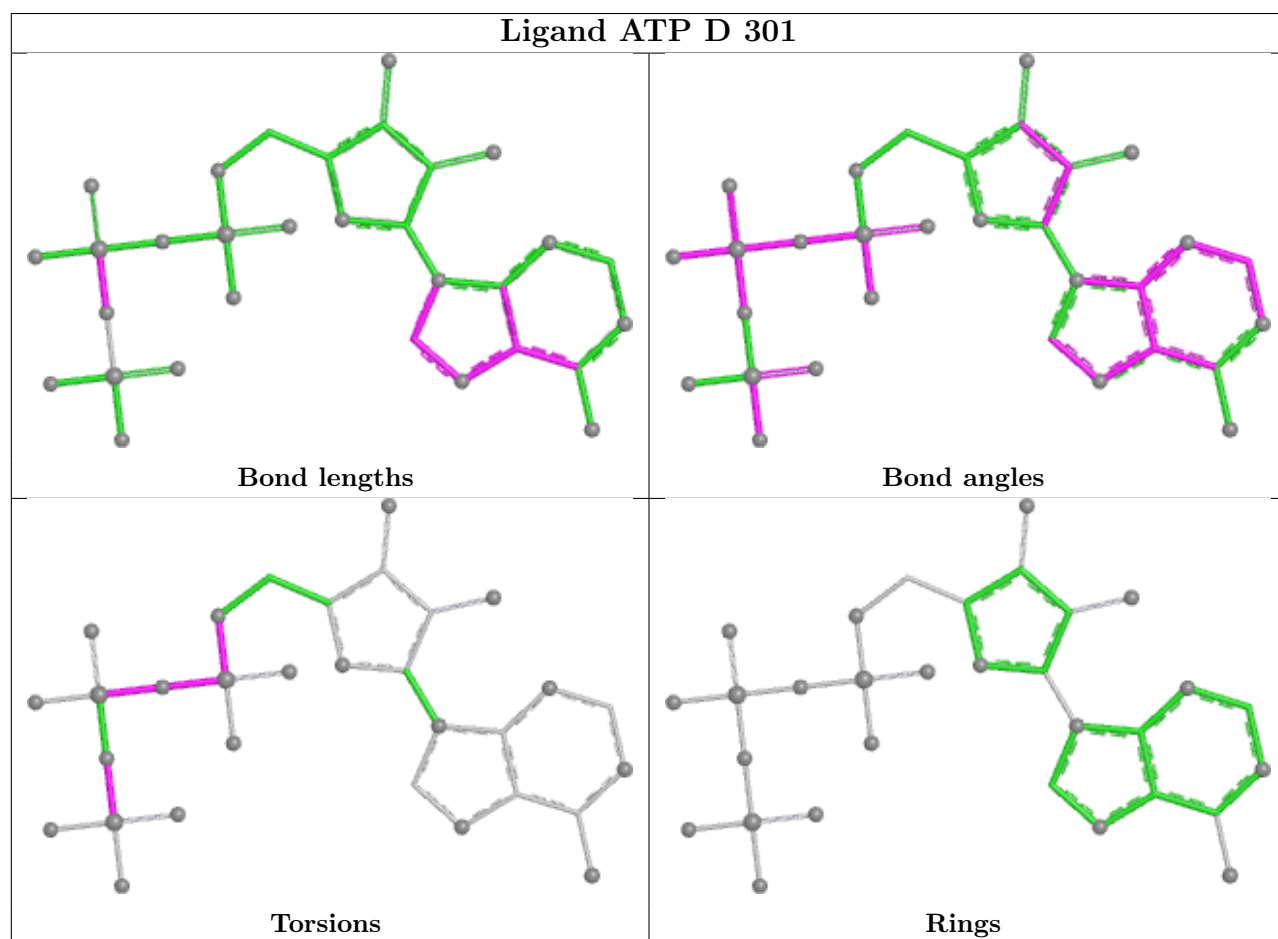
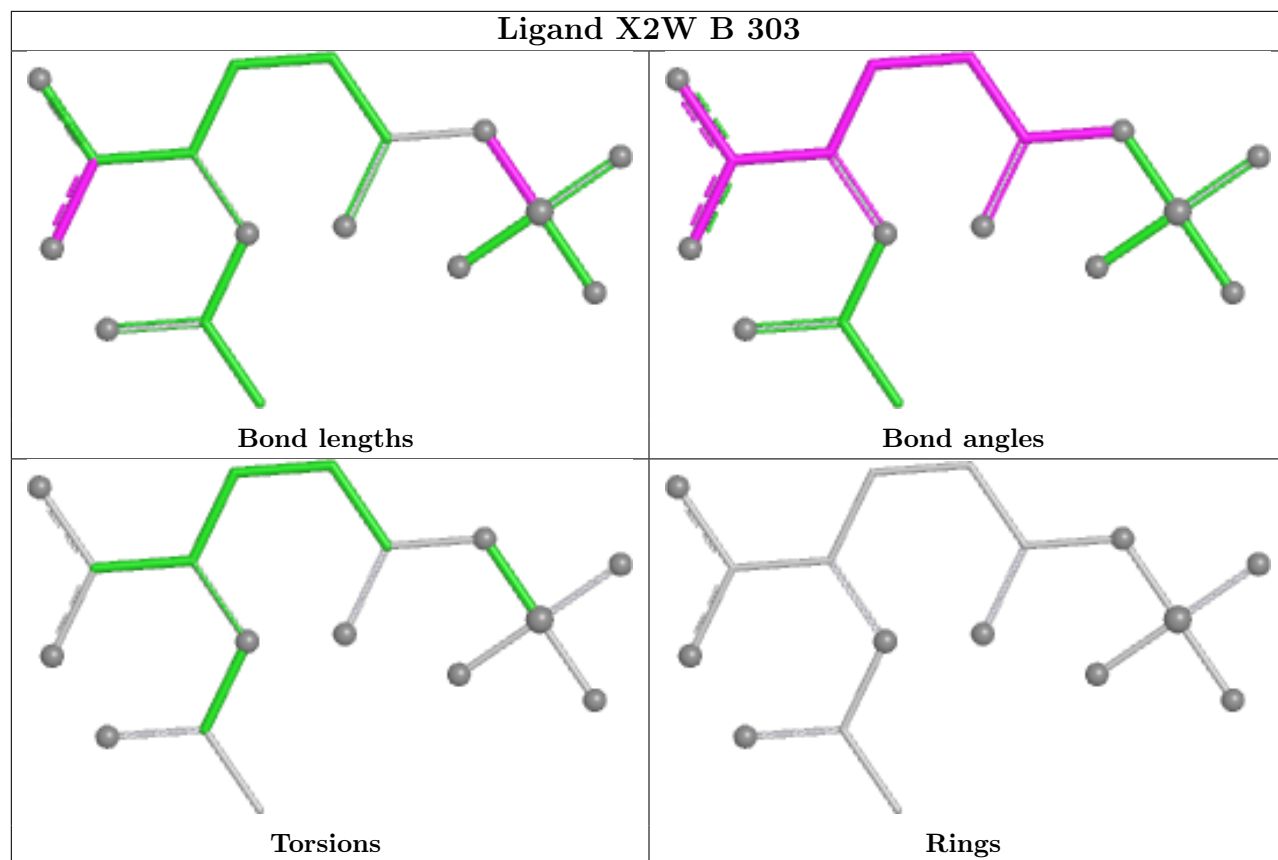
There are no ring outliers.

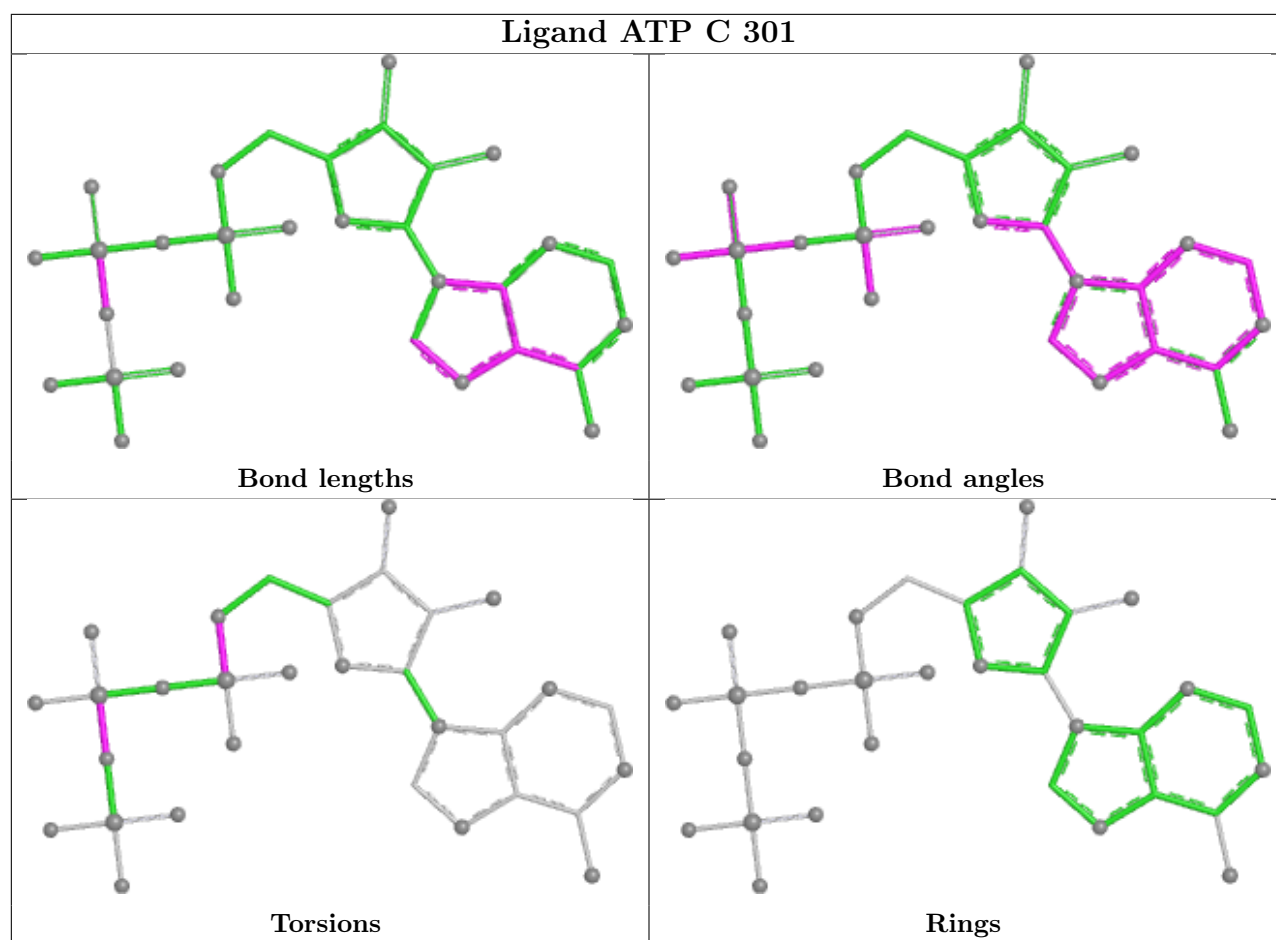
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	ARG	2	0
8	D	301	ATP	2	0
8	C	301	ATP	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 [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, 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	281/318 (88%)	-0.38	5 (1%) 67 61	36, 53, 89, 132	0
1	B	281/318 (88%)	-0.25	10 (3%) 46 36	38, 56, 110, 143	0
2	C	142/154 (92%)	-0.48	2 (1%) 73 67	29, 58, 80, 102	1 (0%)
2	D	142/154 (92%)	-0.51	4 (2%) 55 46	30, 56, 76, 115	1 (0%)
All	All	846/944 (89%)	-0.37	21 (2%) 58 49	29, 56, 98, 143	2 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	248	VAL	5.1
2	D	3	LEU	4.9
1	B	227	PRO	3.9
1	A	297	GLY	3.6
2	C	3	LEU	3.3
1	B	18	TYR	3.2
1	B	249	ALA	2.7
1	B	237	LYS	2.6
1	A	17	ASP	2.5
1	B	54	SER	2.5
2	D	4	GLU	2.5
1	B	22	ILE	2.4
1	A	241	LYS	2.3
1	A	18	TYR	2.2
2	C	144	LYS	2.2
2	D	144	LYS	2.2
2	D	32[A]	PHE	2.2
1	B	17	ASP	2.1
1	B	221	LEU	2.1
1	A	296	THR	2.0
1	B	241	LYS	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](#)

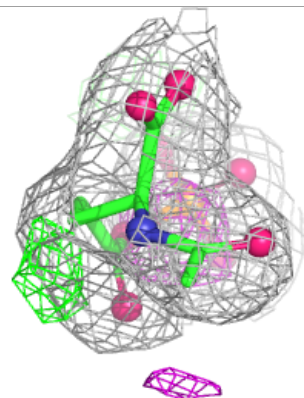
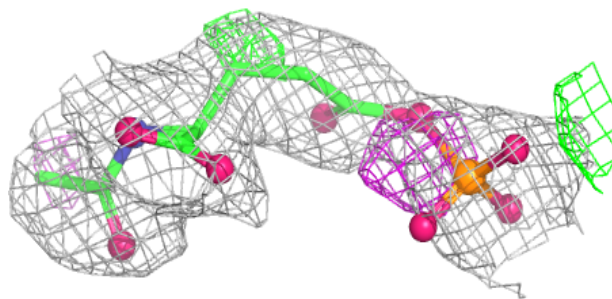
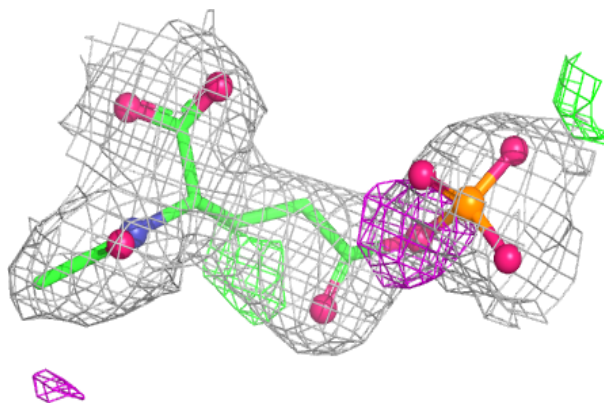
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
9	GLN	C	303	10/10	0.92	0.12	54,62,76,82	0
7	X2W	B	303	17/17	0.93	0.10	47,51,102,105	0
3	ARG	B	301	12/12	0.94	0.10	69,75,86,86	0
9	GLN	D	303	10/10	0.95	0.10	44,59,71,80	0
3	ARG	A	301	12/12	0.96	0.09	66,68,71,77	0
5	NLG	A	303	13/13	0.97	0.08	40,45,49,50	0
4	ADP	A	302	27/27	0.98	0.06	45,59,63,64	0
8	ATP	D	301	31/31	0.99	0.04	41,48,52,54	0
6	MG	A	304	1/1	0.99	0.04	41,41,41,41	0
8	ATP	C	301	31/31	0.99	0.04	42,48,52,56	0
6	MG	D	302	1/1	1.00	0.02	53,53,53,53	0
6	MG	C	302	1/1	1.00	0.01	58,58,58,58	0

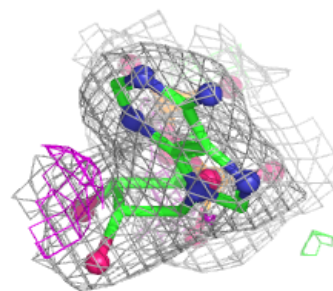
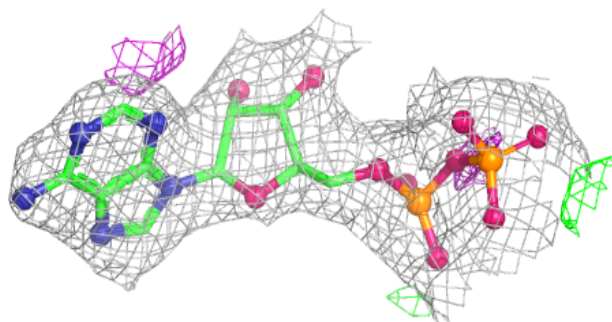
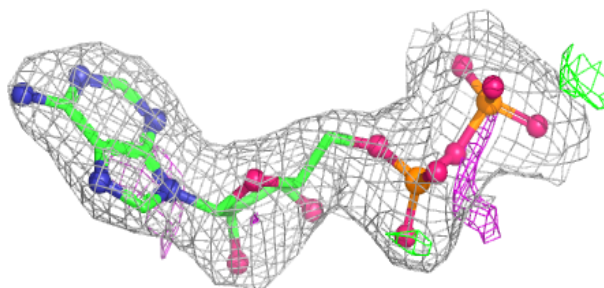
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around X2W B 303:

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

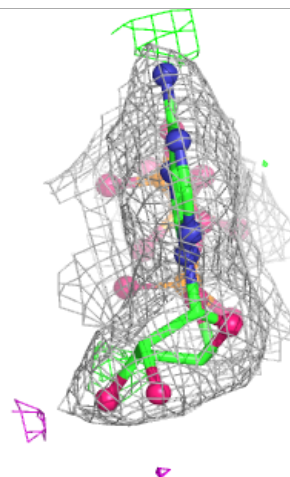
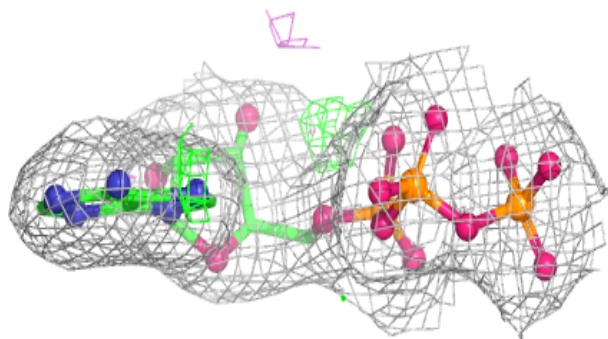
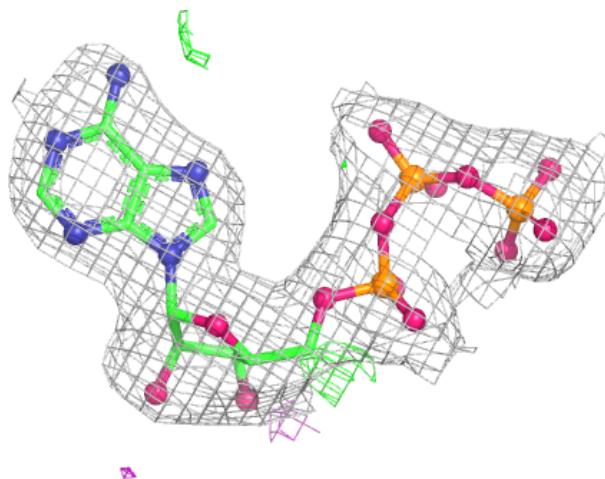
**Electron density around ADP A 302:**

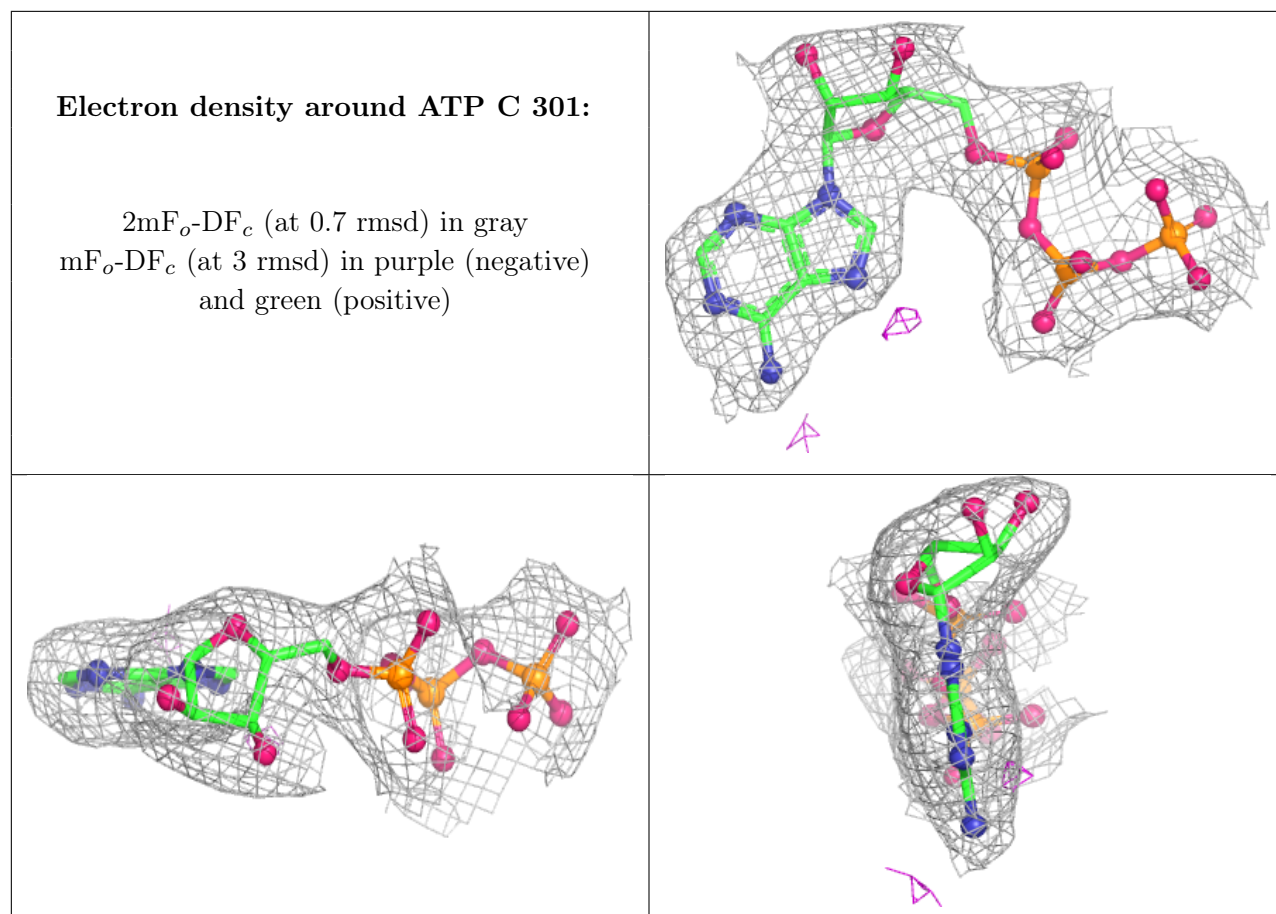
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ATP D 301:

$2mF_o-DF_c$ (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.