



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 19, 2023 – 08:09 PM JST

PDB ID : 7XF0  
Title : Crystal structure of CasDinG in complex with ATP  
Authors : Zhang, J.T.; Cui, N.; Liu, Y.R.; Huang, H.D.; Jia, N.  
Deposited on : 2022-03-31  
Resolution : 3.10 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.34  
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) : 2.34

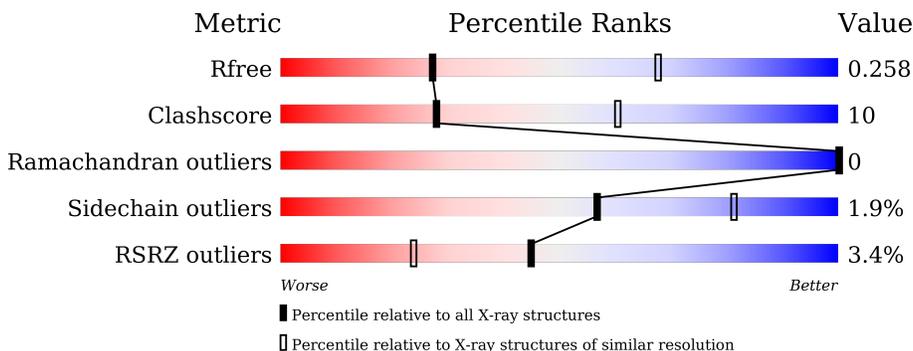
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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	626	 3% 71% 23% 6%
1	B	626	 5% 74% 20% • 5%
1	C	626	 2% 79% 17% •

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
2	ATP	A	701	-	-	-	X

## 2 Entry composition [i](#)

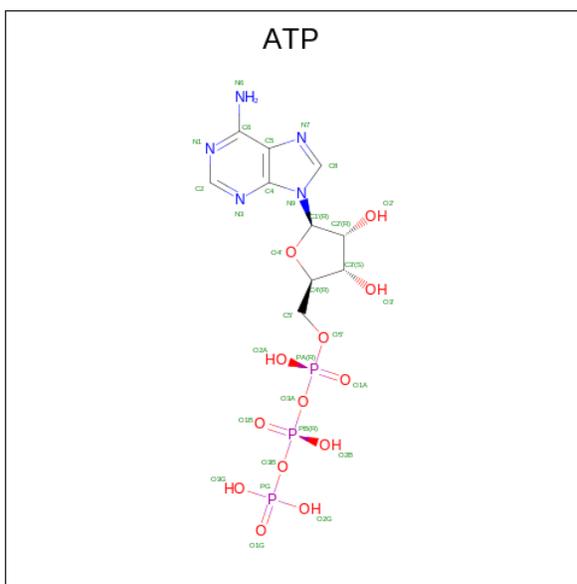
There are 2 unique types of molecules in this entry. The entry contains 13697 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CasDinG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	C	598	Total 4561	C 2883	N 824	O 836	S 18	0	0	0
1	A	591	Total 4514	C 2854	N 818	O 824	S 18	0	0	0
1	B	593	Total 4529	C 2860	N 821	O 830	S 18	0	0	0

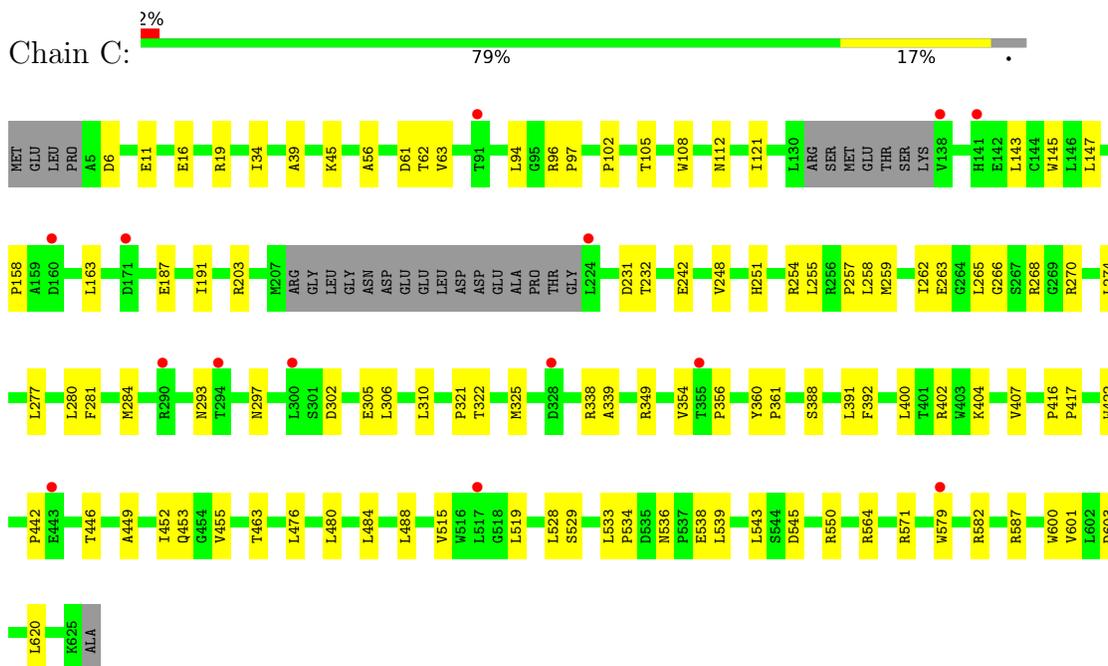
- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>13</sub>P<sub>3</sub>) (labeled as "Ligand of Interest" by depositor).



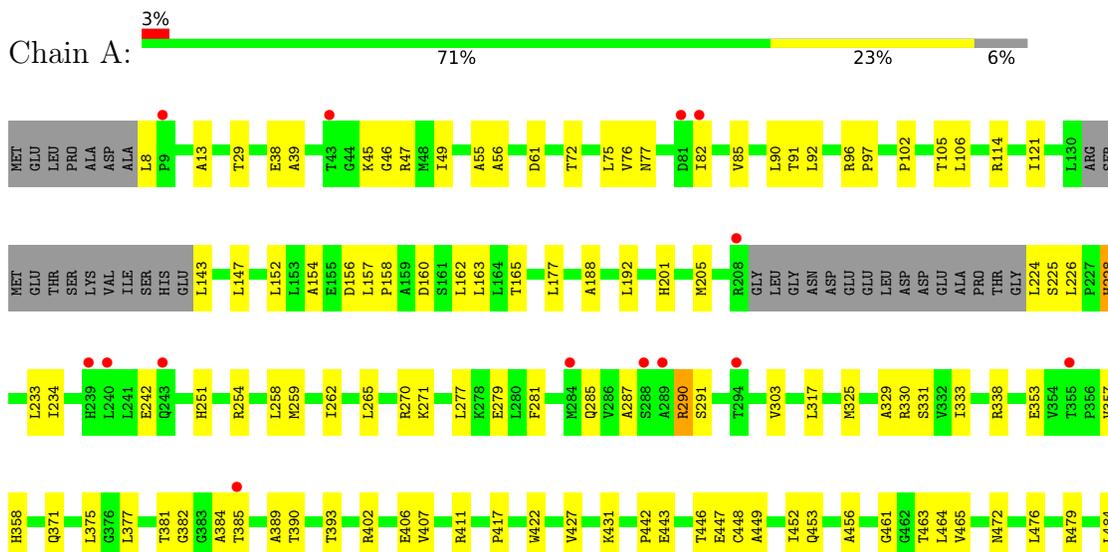
### 3 Residue-property plots i

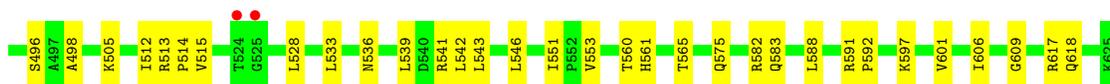
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: CasDinG



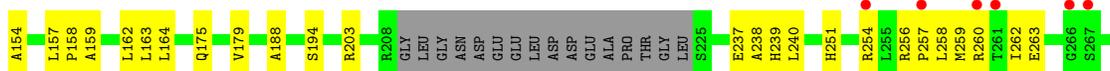
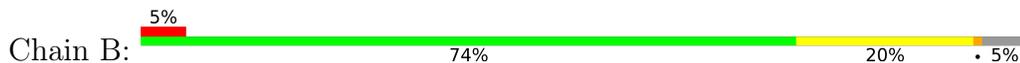
#### • Molecule 1: CasDinG





ALA

• Molecule 1: CasDinG



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.55Å 72.09Å 224.23Å 90.00° 90.84° 90.00°	Depositor
Resolution (Å)	38.91 – 3.10 38.92 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (38.91-3.10) 100.0 (38.92-3.10)	Depositor EDS
$R_{merge}$	0.17	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.99 (at 3.12Å)	Xtrriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, $R_{free}$	0.224 , 0.261 0.225 , 0.258	Depositor DCC
$R_{free}$ test set	2019 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	65.9	Xtrriage
Anisotropy	0.787	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 31.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.000 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	13697	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% 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: ATP

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	0.27	0/4604	0.55	0/6263
1	B	0.28	0/4620	0.57	0/6286
1	C	0.26	0/4652	0.53	0/6330
All	All	0.27	0/13876	0.55	0/18879

There are no bond length outliers.

There are no bond angle outliers.

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	4514	0	4613	90	0
1	B	4529	0	4609	116	0
1	C	4561	0	4652	69	0
2	A	31	0	12	1	0
2	B	31	0	12	0	0
2	C	31	0	12	1	0
All	All	13697	0	13910	273	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 10.

All (273) 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:280:LEU:HD13	1:B:310:LEU:HD21	1.27	1.15
1:B:254:ARG:HD3	1:B:257:PRO:HG2	1.18	1.10
1:B:279:GLU:OE1	1:B:309:ALA:HB2	1.56	1.06
1:B:254:ARG:CD	1:B:257:PRO:HG2	1.95	0.95
1:A:8:LEU:HD22	1:A:55:ALA:HB2	1.49	0.93
1:B:279:GLU:OE1	1:B:309:ALA:CB	2.20	0.88
1:C:392:PHE:O	1:C:582:ARG:NH2	2.06	0.87
1:B:274:LEU:HD22	1:B:274:LEU:O	1.77	0.83
1:B:262:ILE:HD13	1:B:277:LEU:HD22	1.62	0.81
1:B:279:GLU:OE2	1:B:283:GLN:HG2	1.79	0.81
1:B:271:LYS:HB2	1:B:272:PRO:HD3	1.61	0.80
1:C:484:LEU:HD13	1:C:515:VAL:HG21	1.63	0.80
1:B:307:ILE:HG22	1:B:311:LYS:HE2	1.64	0.79
1:B:108:TRP:HB2	1:B:254:ARG:HH12	1.48	0.78
1:B:158:PRO:HG2	1:B:254:ARG:NH2	2.01	0.76
1:B:322:THR:HG22	1:B:325:MET:HE2	1.66	0.74
1:C:147:LEU:HD22	1:C:163:LEU:HD21	1.70	0.73
1:A:431:LYS:H	1:A:431:LYS:HD2	1.53	0.73
1:B:263:GLU:HG2	1:B:270:ARG:HE	1.53	0.72
1:C:39:ALA:O	1:C:45:LYS:NZ	2.22	0.72
1:B:108:TRP:CD1	1:B:254:ARG:NH1	2.58	0.71
1:B:262:ILE:CD1	1:B:277:LEU:HD22	2.20	0.70
1:B:402:ARG:NH1	1:B:407:VAL:O	2.23	0.70
1:B:528:LEU:HD12	1:B:543:LEU:HD22	1.74	0.70
1:B:108:TRP:HD1	1:B:254:ARG:NH1	1.90	0.69
1:C:484:LEU:HD12	1:C:488:LEU:HD12	1.74	0.69
1:B:354:VAL:HG13	1:B:356:PRO:HD2	1.75	0.69
1:B:254:ARG:HD3	1:B:257:PRO:CG	2.11	0.69
1:B:258:LEU:CD1	1:B:277:LEU:HD13	2.24	0.68
1:A:49:ILE:HG21	1:A:75:LEU:HD22	1.74	0.68
1:B:465:VAL:HG12	1:B:547:VAL:HB	1.75	0.68
1:A:393:THR:HG21	1:A:575:GLN:HG2	1.74	0.67
1:B:203:ARG:HH22	1:B:251:HIS:CE1	2.13	0.67
1:C:242:GLU:OE1	1:C:564:ARG:NH2	2.29	0.66
1:B:162:LEU:HD21	1:B:254:ARG:NH2	2.09	0.66
1:B:283:GLN:HG3	1:B:309:ALA:HB2	1.78	0.66
1:B:462:GLY:HA2	1:B:514:PRO:HD2	1.77	0.66
1:B:392:PHE:O	1:B:582:ARG:NH1	2.29	0.65
1:A:165:THR:HG21	1:A:331:SER:HB3	1.78	0.65
1:B:279:GLU:CD	1:B:283:GLN:HG2	2.16	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:GLY:O	1:A:49:ILE:HG22	1.95	0.65
1:B:551:ILE:HD11	1:B:606:ILE:HD11	1.78	0.65
1:B:354:VAL:HG22	1:B:355:THR:H	1.62	0.65
1:B:162:LEU:HD21	1:B:254:ARG:HH22	1.62	0.64
1:C:601:VAL:HG11	1:C:620:LEU:HD11	1.80	0.63
1:B:11:GLU:O	1:B:19:ARG:NH1	2.32	0.63
1:B:279:GLU:OE2	1:B:283:GLN:CG	2.48	0.62
1:C:297:ASN:O	1:C:349:ARG:NH2	2.32	0.62
1:C:402:ARG:NH1	1:C:407:VAL:O	2.32	0.62
1:B:270:ARG:HD2	1:B:270:ARG:O	1.99	0.62
1:A:147:LEU:HD22	1:A:163:LEU:HD21	1.82	0.62
1:A:449:ALA:O	1:A:453:GLN:HG3	1.99	0.61
1:A:233:LEU:O	1:A:384:ALA:HA	2.00	0.60
1:B:475:LEU:O	1:B:479:ARG:HD3	2.02	0.60
1:A:290:ARG:HH11	1:A:291:SER:HA	1.67	0.60
1:B:158:PRO:CG	1:B:254:ARG:NH2	2.65	0.60
1:A:90:LEU:HD11	1:A:192:LEU:HD12	1.83	0.60
1:B:279:GLU:OE1	1:B:283:GLN:CG	2.50	0.60
1:A:8:LEU:HD22	1:A:55:ALA:CB	2.26	0.60
1:C:16:GLU:HA	1:C:19:ARG:HG3	1.84	0.59
1:B:106:LEU:HB2	1:B:121:ILE:HG21	1.84	0.59
1:A:258:LEU:O	1:A:262:ILE:HG12	2.03	0.59
1:B:203:ARG:HH12	1:B:251:HIS:HE2	1.48	0.59
1:B:97:PRO:HA	1:B:163:LEU:HD13	1.83	0.59
1:B:258:LEU:HD12	1:B:277:LEU:CD1	2.32	0.59
1:B:308:PRO:HA	1:B:311:LYS:HE3	1.84	0.59
1:C:550:ARG:HA	1:C:603:ASP:HB2	1.85	0.59
1:C:259:MET:O	1:C:263:GLU:HG3	2.03	0.58
1:A:29:THR:HG21	1:A:385:THR:OG1	2.03	0.58
1:C:108:TRP:O	1:C:112:ASN:ND2	2.27	0.58
1:B:430:HIS:NE2	1:B:598:ASN:OD1	2.26	0.58
1:A:446:THR:OG1	1:A:447:GLU:OE1	2.22	0.58
1:B:158:PRO:HG2	1:B:254:ARG:HH21	1.67	0.58
1:B:540:ASP:OD2	1:B:591:ARG:NH2	2.32	0.57
1:B:325:MET:HE3	1:B:325:MET:O	2.03	0.57
1:C:11:GLU:O	1:C:19:ARG:NH1	2.37	0.57
1:C:263:GLU:HG2	1:C:274:LEU:HD11	1.87	0.57
1:B:487:ARG:NH2	1:B:513:ARG:HB2	2.20	0.57
1:B:279:GLU:OE1	1:B:283:GLN:HG3	2.05	0.57
1:B:256:ARG:O	1:B:260:ARG:HG3	2.05	0.57
1:A:8:LEU:CD2	1:A:55:ALA:HB2	2.28	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:484:LEU:HG	1:A:515:VAL:HG11	1.86	0.56
1:B:258:LEU:HD12	1:B:277:LEU:HD13	1.87	0.56
1:B:284:MET:HE3	1:B:352:ILE:HG23	1.87	0.56
1:C:94:LEU:HD13	1:C:143:LEU:HD11	1.86	0.56
1:B:321:PRO:HB2	1:B:323:LYS:HG3	1.87	0.56
1:A:102:PRO:HA	1:A:121:ILE:HD11	1.87	0.56
1:C:322:THR:HA	1:C:325:MET:HE2	1.88	0.56
1:C:254:ARG:NH1	1:C:360:TYR:OH	2.35	0.56
1:C:579:TRP:HA	1:C:582:ARG:HB2	1.88	0.56
1:C:528:LEU:HD12	1:C:543:LEU:HD22	1.88	0.56
1:B:522:ALA:HA	1:B:526:ILE:HG12	1.88	0.55
1:B:551:ILE:HG22	1:B:553:VAL:HG23	1.89	0.55
1:B:491:GLN:HG3	1:B:516:TRP:HE1	1.72	0.55
1:B:259:MET:HG2	1:B:277:LEU:HD21	1.87	0.55
1:C:442:PRO:O	1:C:446:THR:HG23	2.07	0.54
1:A:72:THR:O	1:A:76:VAL:HG23	2.07	0.54
1:A:38:GLU:OE2	1:A:582:ARG:NH2	2.36	0.54
1:B:108:TRP:CB	1:B:254:ARG:HH12	2.19	0.54
1:B:463:THR:HB	1:B:515:VAL:HG12	1.88	0.54
1:A:329:ALA:O	1:A:333:ILE:HG12	2.08	0.54
1:C:388:SER:HB3	1:C:391:LEU:HG	1.91	0.53
1:B:538:GLU:O	1:B:541:ARG:NH1	2.42	0.53
1:C:536:ASN:HB3	1:C:539:LEU:HD12	1.91	0.53
1:A:152:LEU:HD22	1:A:498:ALA:HB2	1.91	0.53
1:B:270:ARG:HD2	1:B:270:ARG:C	2.29	0.53
1:C:63:VAL:HG22	1:C:232:THR:HB	1.90	0.53
1:A:8:LEU:CD2	1:A:55:ALA:CB	2.86	0.53
1:C:255:LEU:HB2	1:C:361:PRO:HG2	1.91	0.52
1:A:143:LEU:HB3	1:A:177:LEU:HD21	1.91	0.52
1:A:242:GLU:OE2	1:A:560:THR:HG21	2.09	0.52
1:C:571:ARG:HH22	1:A:106:LEU:HD21	1.75	0.52
1:A:382:GLY:O	1:A:411:ARG:NH2	2.43	0.52
1:A:72:THR:HG21	1:A:92:LEU:HD11	1.92	0.52
1:B:262:ILE:CD1	1:B:277:LEU:CD2	2.87	0.52
1:C:268:ARG:HD3	1:C:321:PRO:HG3	1.93	0.51
1:B:259:MET:CG	1:B:277:LEU:HD21	2.40	0.51
1:A:160:ASP:OD2	1:A:251:HIS:HA	2.10	0.51
1:C:62:THR:HG23	1:C:231:ASP:H	1.75	0.51
1:A:377:LEU:O	1:A:381:THR:HG23	2.11	0.50
1:C:306:LEU:HB3	1:C:310:LEU:HD23	1.93	0.50
1:A:38:GLU:OE1	1:A:417:PRO:HB3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:LEU:HD22	1:B:274:LEU:C	2.27	0.50
1:B:279:GLU:OE1	1:B:283:GLN:HG2	2.10	0.49
1:B:157:LEU:HD13	1:B:162:LEU:HD12	1.94	0.49
1:B:523:TRP:CH2	1:B:552:PRO:HG3	2.46	0.49
1:C:533:LEU:HD13	1:C:539:LEU:HB2	1.93	0.49
1:A:422:TRP:CE2	1:A:592:PRO:HG3	2.47	0.49
1:B:527:ASP:OD1	1:B:590:ARG:NE	2.45	0.49
1:A:461:GLY:HA3	1:A:541:ARG:O	2.12	0.49
1:A:13:ALA:HB1	1:A:47:ARG:HD2	1.94	0.49
1:A:39:ALA:O	1:A:389:ALA:HA	2.12	0.49
1:A:152:LEU:O	1:A:496:SER:OG	2.20	0.49
1:C:538:GLU:HG2	1:C:539:LEU:HG	1.93	0.48
1:A:45:LYS:HG3	2:A:701:ATP:O1B	2.12	0.48
1:A:442:PRO:HB3	1:A:479:ARG:NH2	2.28	0.48
1:A:259:MET:HG2	1:A:277:LEU:HD13	1.93	0.48
1:B:14:VAL:O	1:B:19:ARG:NH1	2.47	0.48
1:A:533:LEU:HD13	1:A:539:LEU:HB2	1.96	0.48
1:A:97:PRO:HA	1:A:163:LEU:HD13	1.95	0.48
1:B:279:GLU:CD	1:B:283:GLN:CG	2.82	0.48
1:C:305:GLU:CD	1:C:305:GLU:H	2.16	0.48
1:A:154:ALA:HB3	1:A:157:LEU:HD23	1.95	0.48
1:A:271:LYS:HE2	1:A:271:LYS:HA	1.95	0.48
1:A:371:GLN:O	1:A:375:LEU:HB2	2.13	0.47
1:A:251:HIS:CE1	1:A:338:ARG:HG2	2.49	0.47
1:B:68:PRO:HG2	1:B:237:GLU:OE1	2.13	0.47
1:B:271:LYS:HB2	1:B:272:PRO:CD	2.39	0.47
1:C:404:LYS:NZ	1:C:579:TRP:HZ2	2.11	0.47
1:A:390:THR:HG21	1:A:583:GLN:HG2	1.97	0.47
1:A:601:VAL:HG11	1:A:606:ILE:HD12	1.97	0.47
1:B:162:LEU:CD2	1:B:254:ARG:NH2	2.78	0.47
1:C:16:GLU:OE2	1:C:19:ARG:NH2	2.47	0.47
1:A:251:HIS:HE1	1:A:338:ARG:HG2	1.78	0.47
1:A:402:ARG:NH1	1:A:407:VAL:O	2.45	0.47
1:B:442:PRO:HA	1:B:445:ALA:HB3	1.96	0.47
1:A:561:HIS:O	1:A:565:THR:HG23	2.15	0.47
1:B:262:ILE:HD13	1:B:277:LEU:CD2	2.40	0.47
1:B:105:THR:HG22	1:B:121:ILE:HD11	1.97	0.46
1:A:533:LEU:HB3	1:A:536:ASN:HB2	1.97	0.46
1:B:470:TYR:HA	1:B:473:THR:HG22	1.97	0.46
1:B:283:GLN:HA	1:B:286:VAL:HG22	1.96	0.46
1:B:353:GLU:HB2	1:B:358:HIS:ND1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:388:SER:HB3	1:B:391:LEU:HG	1.97	0.46
1:B:293:ASN:HD21	1:B:296:LEU:HG	1.80	0.46
1:B:96:ARG:HD3	1:B:164:LEU:HG	1.98	0.46
1:C:476:LEU:O	1:C:480:LEU:HB2	2.16	0.46
1:C:102:PRO:HB3	1:C:145:TRP:CZ3	2.51	0.46
1:C:449:ALA:HB1	1:C:480:LEU:HD13	1.98	0.46
1:A:105:THR:HA	1:A:162:LEU:HD22	1.97	0.46
1:A:82:ILE:HD11	1:A:85:VAL:HG13	1.98	0.45
1:A:201:HIS:CD2	1:A:226:LEU:H	2.35	0.45
1:A:427:VAL:HA	1:A:597:LYS:O	2.16	0.45
1:B:58:ILE:HD11	1:B:84:GLU:HB3	1.98	0.45
1:A:609:GLY:HA2	1:A:617:ARG:HH22	1.81	0.45
1:B:325:MET:HG3	1:B:330:ARG:HD2	1.98	0.45
1:B:326:SER:HB3	1:B:329:ALA:HB3	1.98	0.45
1:C:187:GLU:OE1	1:C:191:ILE:HD11	2.17	0.45
1:C:422:TRP:HA	1:B:60:GLY:HA3	1.98	0.45
1:B:67:ALA:O	1:B:194:SER:HA	2.17	0.45
1:B:175:GLN:O	1:B:179:VAL:HG23	2.16	0.45
1:B:279:GLU:OE1	1:B:309:ALA:HB1	2.13	0.45
1:B:326:SER:HB3	1:B:329:ALA:CB	2.47	0.45
1:C:400:LEU:HD23	1:C:579:TRP:CZ3	2.52	0.44
1:B:325:MET:SD	1:B:325:MET:C	2.95	0.44
1:B:113:GLU:O	1:B:113:GLU:HG2	2.17	0.44
1:C:259:MET:HG3	1:C:277:LEU:HD23	2.00	0.44
1:C:452:ILE:HG21	1:C:480:LEU:HD21	2.00	0.44
1:A:114:ARG:HH12	1:A:156:ASP:CG	2.20	0.44
1:B:45:LYS:HD2	1:B:387:VAL:HG12	1.98	0.44
1:C:258:LEU:O	1:C:262:ILE:HG12	2.16	0.44
1:C:463:THR:HG23	1:C:545:ASP:HB2	1.99	0.44
1:B:487:ARG:HH21	1:B:513:ARG:HB2	1.82	0.44
1:C:254:ARG:NH1	1:C:257:PRO:HG3	2.33	0.44
1:C:258:LEU:HG	1:C:277:LEU:HD21	2.00	0.44
1:C:265:LEU:HD21	1:C:325:MET:HG2	1.99	0.44
1:B:91:THR:HG22	1:B:188:ALA:HB3	2.00	0.44
1:C:455:VAL:HG22	1:C:600:TRP:CE2	2.52	0.44
1:A:546:LEU:HD12	1:A:588:LEU:HB2	2.00	0.44
1:B:283:GLN:HB3	1:B:306:LEU:HD23	2.00	0.44
1:B:106:LEU:O	1:B:110:ILE:HG13	2.18	0.44
1:B:325:MET:HE2	1:B:325:MET:HB3	1.79	0.44
1:A:281:PHE:O	1:A:285:GLN:HG3	2.18	0.44
1:A:443:GLU:OE1	1:A:443:GLU:N	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:404:LYS:HG2	1:C:564:ARG:CZ	2.48	0.43
1:A:45:LYS:NZ	1:A:389:ALA:HB2	2.33	0.43
1:C:56:ALA:O	1:C:61:ASP:HB2	2.18	0.43
1:C:536:ASN:ND2	1:C:538:GLU:OE2	2.48	0.43
1:A:205:MET:HE1	1:A:228:HIS:CE1	2.53	0.43
1:B:159:ALA:O	1:B:163:LEU:HG	2.19	0.43
1:B:281:PHE:HE1	1:B:354:VAL:HG23	1.83	0.43
1:B:325:MET:O	1:B:325:MET:SD	2.76	0.43
1:C:404:LYS:HZ2	1:C:579:TRP:HZ2	1.66	0.43
1:A:533:LEU:O	1:A:591:ARG:NH2	2.51	0.43
1:C:354:VAL:HG23	1:C:356:PRO:HD2	1.99	0.43
1:A:234:ILE:HG23	1:A:385:THR:HB	2.00	0.43
1:A:353:GLU:HB2	1:A:358:HIS:CG	2.53	0.43
1:C:158:PRO:HG3	1:C:254:ARG:HD3	2.00	0.43
1:A:91:THR:HG23	1:A:188:ALA:HB3	2.01	0.43
1:A:290:ARG:NH1	1:A:291:SER:HA	2.31	0.43
1:A:49:ILE:HD11	1:A:234:ILE:HG22	2.01	0.43
1:A:442:PRO:O	1:A:446:THR:HG23	2.19	0.43
1:A:96:ARG:N	1:A:97:PRO:HD2	2.34	0.43
1:A:303:VAL:HG23	1:A:303:VAL:O	2.19	0.42
1:B:105:THR:HA	1:B:162:LEU:HD13	2.01	0.42
1:B:551:ILE:HA	1:B:552:PRO:HD3	1.86	0.42
1:C:105:THR:HG22	1:C:121:ILE:HD11	2.01	0.42
1:C:266:GLY:O	1:C:270:ARG:NH1	2.53	0.42
1:A:371:GLN:HG2	1:A:406:GLU:CD	2.39	0.42
1:A:464:LEU:HD12	1:A:465:VAL:H	1.84	0.42
1:A:528:LEU:HD23	1:A:543:LEU:HD13	2.01	0.42
1:C:187:GLU:OE1	1:C:187:GLU:HA	2.20	0.42
1:C:533:LEU:N	1:C:534:PRO:HD3	2.35	0.42
1:B:154:ALA:HB3	1:B:157:LEU:HD23	2.02	0.42
1:C:34:ILE:HD12	1:C:407:VAL:HG13	2.00	0.42
1:A:56:ALA:O	1:A:61:ASP:HB2	2.19	0.42
1:A:505:LYS:HG2	1:A:542:LEU:HD11	2.01	0.42
1:B:238:ALA:HB3	1:B:391:LEU:HD21	2.02	0.42
1:A:8:LEU:HD23	1:A:8:LEU:HA	1.81	0.42
1:B:293:ASN:OD1	1:B:296:LEU:HD12	2.20	0.42
1:A:287:ALA:HA	1:A:290:ARG:HB3	2.02	0.42
1:A:357:VAL:HG13	1:A:358:HIS:ND1	2.35	0.42
1:A:512:ILE:O	1:A:514:PRO:HD3	2.20	0.42
1:B:8:LEU:HD12	1:B:55:ALA:CB	2.49	0.42
1:B:466:LEU:HB3	1:B:523:TRP:CE2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:96:ARG:N	1:C:97:PRO:HD2	2.35	0.42
1:A:158:PRO:HG3	1:A:254:ARG:HD3	2.02	0.42
1:B:96:ARG:N	1:B:97:PRO:HD2	2.35	0.42
1:C:45:LYS:HE2	2:C:701:ATP:O2B	2.20	0.41
1:A:265:LEU:O	1:A:270:ARG:HD3	2.21	0.41
1:A:463:THR:HG23	1:A:515:VAL:HG23	2.02	0.41
1:B:254:ARG:CD	1:B:257:PRO:CG	2.81	0.41
1:C:16:GLU:HG3	1:C:19:ARG:HE	1.85	0.41
1:C:281:PHE:HA	1:C:284:MET:HE2	2.03	0.41
1:A:456:ALA:O	1:A:513:ARG:NH2	2.54	0.41
1:B:305:GLU:O	1:B:308:PRO:HD2	2.21	0.41
1:A:472:ASN:O	1:A:476:LEU:HG	2.21	0.41
1:B:152:LEU:HD23	1:B:152:LEU:HA	1.88	0.41
1:C:480:LEU:HG	1:C:484:LEU:CD1	2.50	0.41
1:A:224:LEU:HD12	1:A:225:SER:N	2.36	0.41
1:B:422:TRP:CE2	1:B:592:PRO:HG3	2.56	0.41
1:C:203:ARG:HD2	1:C:248:VAL:HG12	2.03	0.41
1:A:325:MET:HG2	1:A:329:ALA:HB3	2.03	0.41
1:B:239:HIS:CD2	1:B:240:LEU:HG	2.55	0.41
1:B:331:SER:O	1:B:335:ILE:HG23	2.20	0.41
1:B:487:ARG:NE	1:B:513:ARG:O	2.54	0.41
1:C:251:HIS:HB3	1:C:339:ALA:HA	2.03	0.41
1:A:448:CYS:O	1:A:452:ILE:HD12	2.21	0.41
1:C:400:LEU:O	1:C:404:LYS:HG3	2.20	0.40
1:C:416:PRO:HA	1:C:417:PRO:HD3	1.91	0.40
1:A:317:LEU:HG	1:A:333:ILE:HG23	2.04	0.40
1:A:551:ILE:HG22	1:A:553:VAL:HG23	2.04	0.40
1:C:280:LEU:O	1:C:284:MET:HG3	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	585/626 (94%)	576 (98%)	9 (2%)	0	100	100
1	B	587/626 (94%)	577 (98%)	10 (2%)	0	100	100
1	C	592/626 (95%)	581 (98%)	11 (2%)	0	100	100
All	All	1764/1878 (94%)	1734 (98%)	30 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	475/503 (94%)	469 (99%)	6 (1%)	69	87
1	B	476/503 (95%)	463 (97%)	13 (3%)	44	74
1	C	480/503 (95%)	472 (98%)	8 (2%)	60	83
All	All	1431/1509 (95%)	1404 (98%)	27 (2%)	57	81

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	6	ASP
1	C	293	ASN
1	C	302	ASP
1	C	338	ARG
1	C	453	GLN
1	C	519	LEU
1	C	529	SER
1	C	587	ARG
1	A	77	ASN
1	A	228	HIS
1	A	279	GLU
1	A	290	ARG
1	A	330	ARG
1	A	618	GLN
1	B	15	ARG

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Mol	Chain	Res	Type
1	B	270	ARG
1	B	274	LEU
1	B	315	LYS
1	B	322	THR
1	B	323	LYS
1	B	325	MET
1	B	328	ASP
1	B	334	ARG
1	B	434	CYS
1	B	545	ASP
1	B	580	HIS
1	B	605	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	103	GLN
1	C	430	HIS
1	C	583	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](#)

3 ligands are modelled in this entry.

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
2	ATP	B	701	-	26,33,33	0.60	0	31,52,52	0.72	2 (6%)
2	ATP	A	701	-	26,33,33	0.59	0	31,52,52	0.78	1 (3%)
2	ATP	C	701	-	26,33,33	0.59	0	31,52,52	0.76	2 (6%)

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	ATP	B	701	-	-	6/18/38/38	0/3/3/3
2	ATP	A	701	-	-	6/18/38/38	0/3/3/3
2	ATP	C	701	-	-	3/18/38/38	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	ATP	C5-C6-N6	2.31	123.86	120.35
2	C	701	ATP	C5-C6-N6	2.31	123.86	120.35
2	B	701	ATP	C5-C6-N6	2.27	123.81	120.35
2	C	701	ATP	PB-O3B-PG	2.09	139.98	132.83
2	B	701	ATP	PB-O3B-PG	2.08	139.96	132.83

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	ATP	C5'-O5'-PA-O1A
2	A	701	ATP	C5'-O5'-PA-O2A
2	A	701	ATP	O4'-C4'-C5'-O5'
2	A	701	ATP	C3'-C4'-C5'-O5'
2	C	701	ATP	O4'-C4'-C5'-O5'
2	B	701	ATP	PA-O3A-PB-O3B
2	B	701	ATP	PB-O3B-PG-O1G

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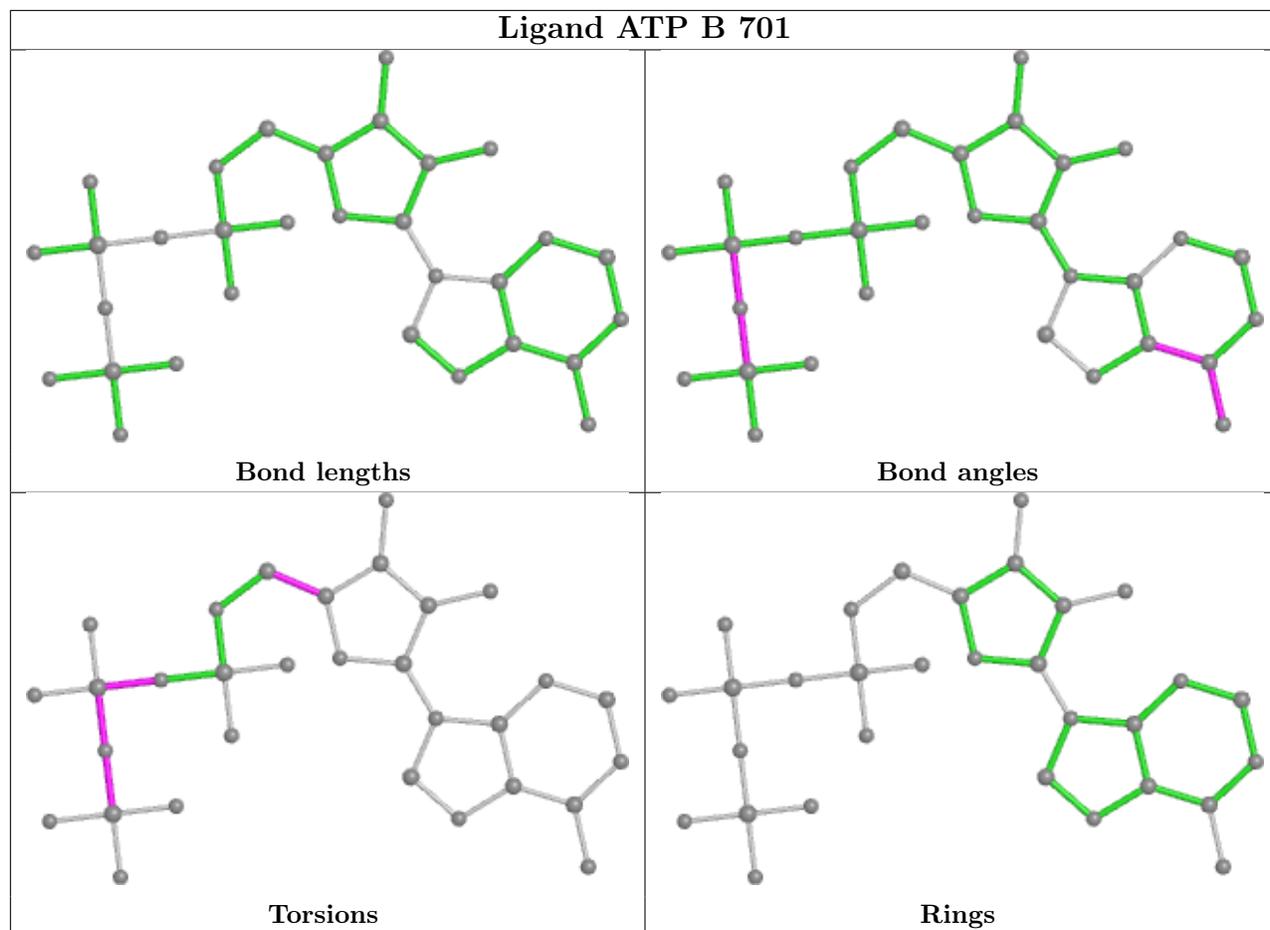
Mol	Chain	Res	Type	Atoms
2	B	701	ATP	PG-O3B-PB-O1B
2	C	701	ATP	C3'-C4'-C5'-O5'
2	A	701	ATP	C4'-C5'-O5'-PA
2	B	701	ATP	O4'-C4'-C5'-O5'
2	B	701	ATP	PB-O3B-PG-O2G
2	B	701	ATP	PB-O3B-PG-O3G
2	A	701	ATP	C5'-O5'-PA-O3A
2	C	701	ATP	PA-O3A-PB-O2B

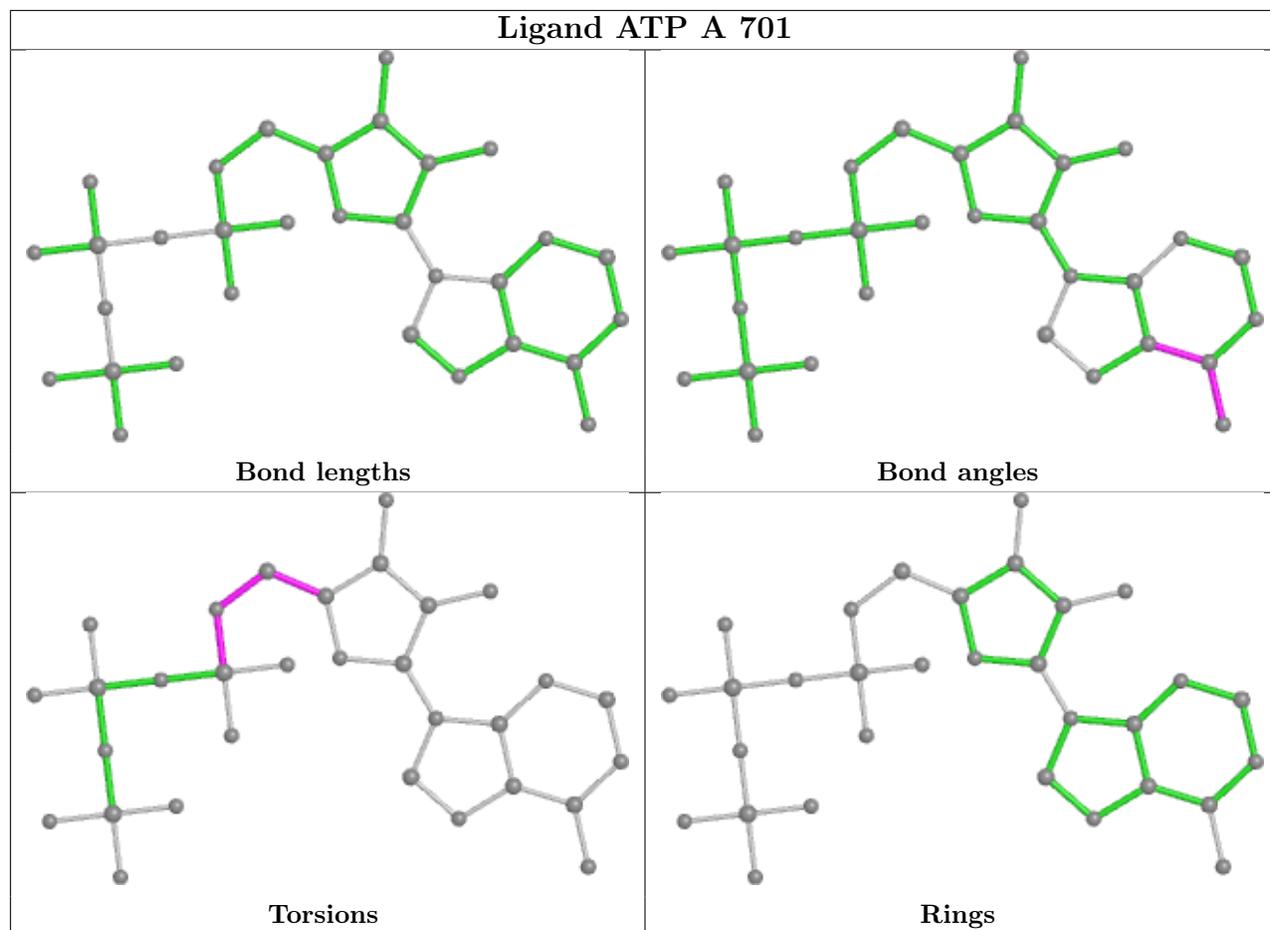
There are no ring outliers.

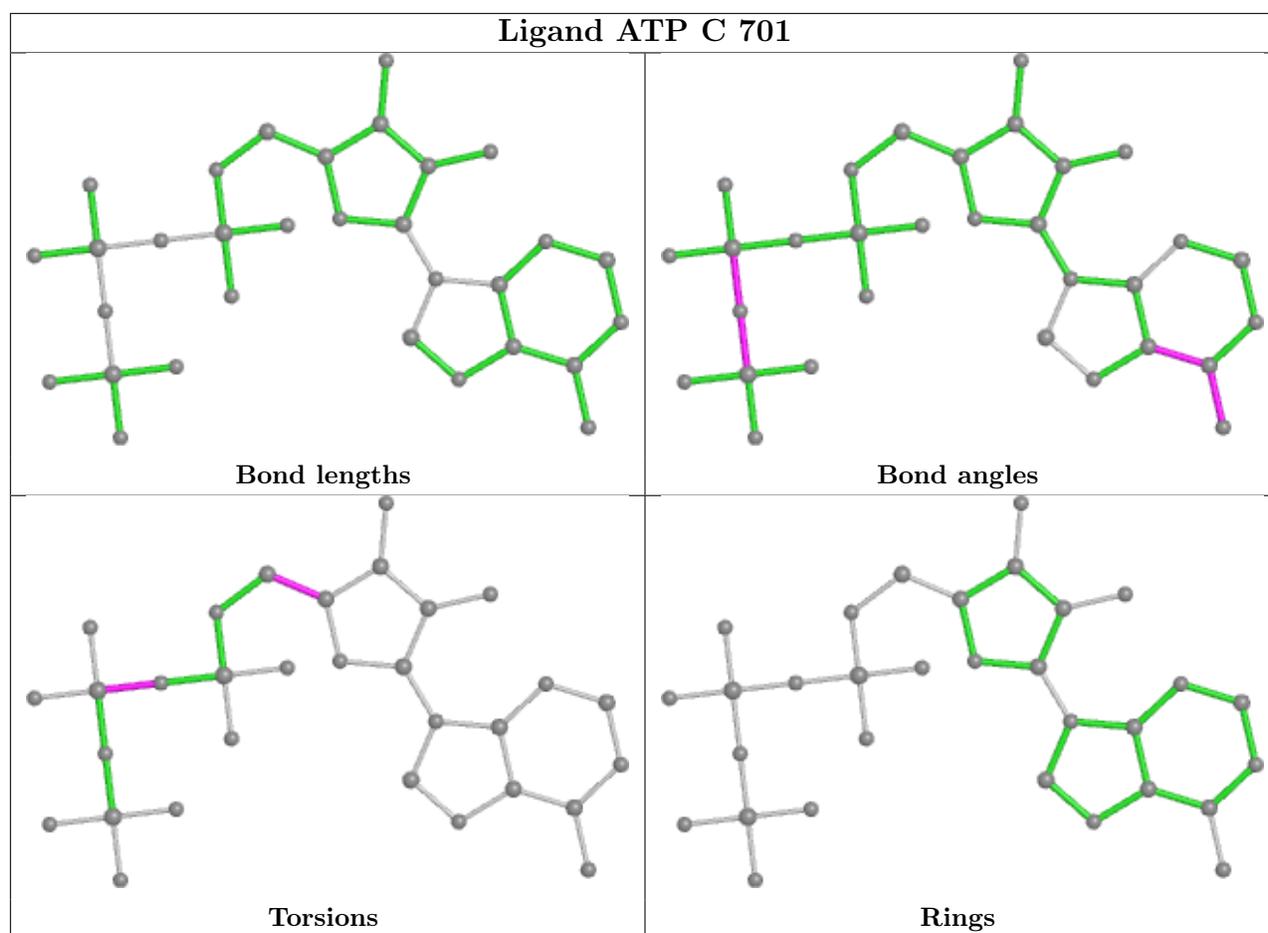
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	ATP	1	0
2	C	701	ATP	1	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, 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	591/626 (94%)	0.18	16 (2%) 54 31	39, 80, 110, 128	0
1	B	593/626 (94%)	0.32	31 (5%) 27 12	36, 76, 143, 165	0
1	C	598/626 (95%)	0.03	14 (2%) 60 39	36, 57, 94, 110	0
All	All	1782/1878 (94%)	0.18	61 (3%) 45 24	36, 70, 117, 165	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	275	ASP	5.2
1	B	306	LEU	4.7
1	B	277	LEU	4.2
1	A	289	ALA	4.1
1	B	261	THR	3.9
1	B	271	LYS	3.8
1	B	272	PRO	3.8
1	A	81	ASP	3.5
1	B	480	LEU	3.3
1	A	524	THR	3.2
1	B	310	LEU	3.1
1	B	267	SER	3.1
1	B	266	GLY	3.1
1	B	254	ARG	3.1
1	B	270	ARG	3.1
1	A	243	GLN	3.1
1	A	9	PRO	3.0
1	A	525	GLY	2.9
1	A	284	MET	2.8
1	B	363	LEU	2.8
1	B	347	HIS	2.8
1	B	324	GLY	2.8
1	B	280	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	43	THR	2.7
1	A	385	THR	2.7
1	B	274	LEU	2.6
1	A	294	THR	2.6
1	C	300	LEU	2.6
1	C	443	GLU	2.6
1	B	284	MET	2.6
1	A	288	SER	2.6
1	C	328	ASP	2.5
1	B	517	LEU	2.5
1	C	355	THR	2.5
1	B	257	PRO	2.5
1	B	343	ALA	2.5
1	C	138	VAL	2.5
1	A	82	ILE	2.4
1	C	224	LEU	2.4
1	A	239	HIS	2.4
1	C	91	THR	2.4
1	B	309	ALA	2.3
1	B	326	SER	2.3
1	C	579	TRP	2.3
1	B	260	ARG	2.2
1	C	290	ARG	2.2
1	B	532	SER	2.2
1	A	240	LEU	2.2
1	B	481	GLY	2.1
1	C	141	HIS	2.1
1	B	300	LEU	2.1
1	B	313	THR	2.1
1	B	434	CYS	2.1
1	C	517	LEU	2.1
1	A	355	THR	2.1
1	B	524	THR	2.1
1	C	160	ASP	2.1
1	C	171	ASP	2.1
1	A	208	ARG	2.0
1	C	294	THR	2.0
1	B	273	ALA	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](#)

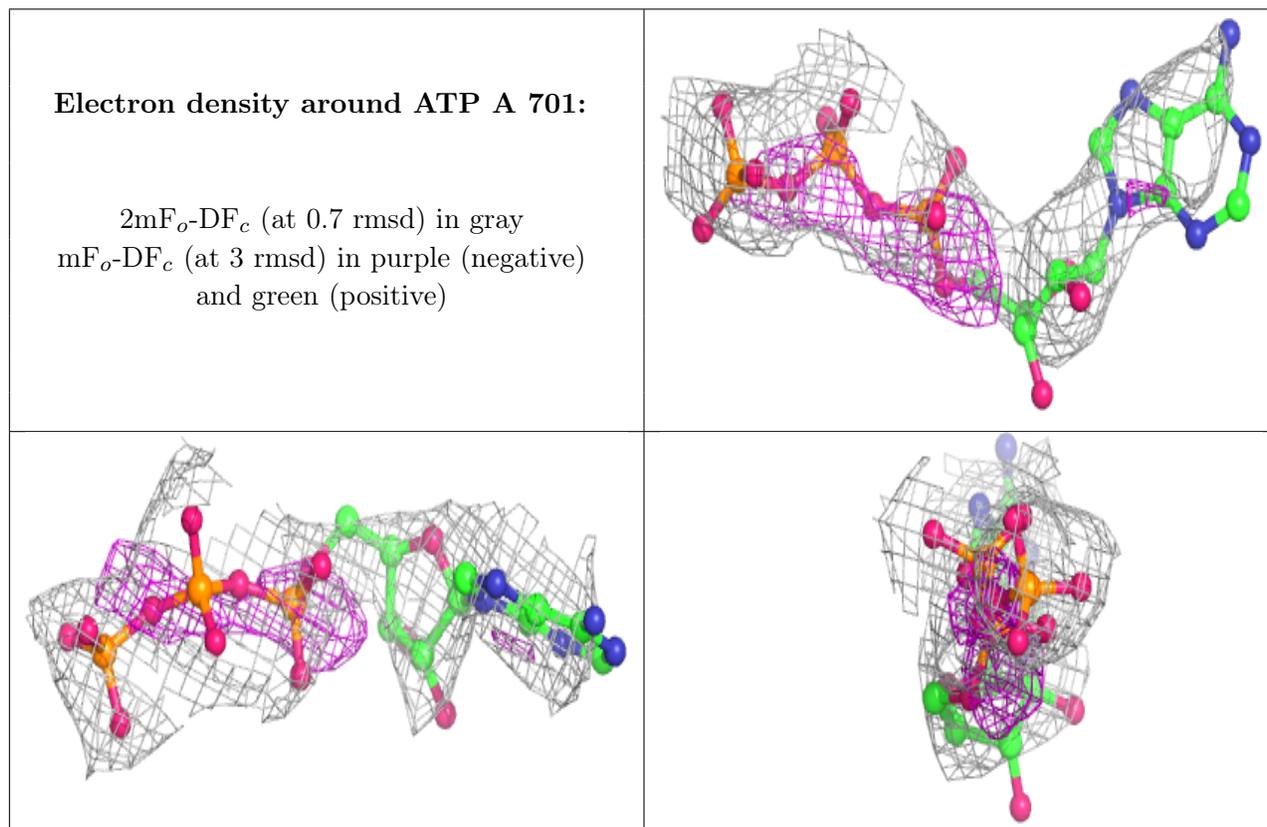
There are no monosaccharides in this entry.

### 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.

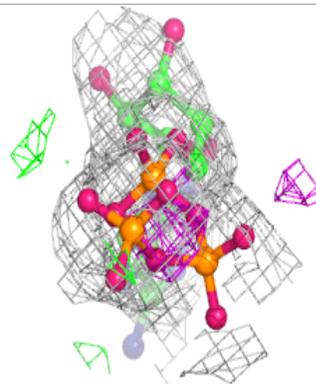
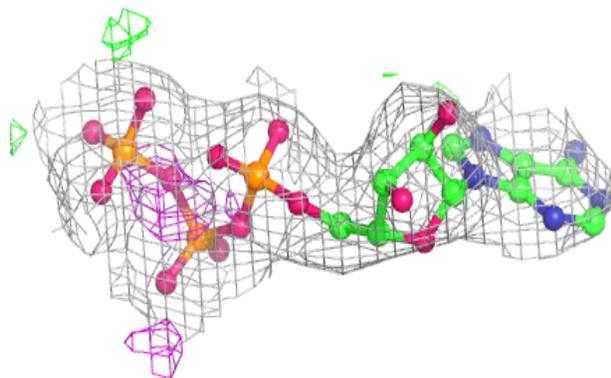
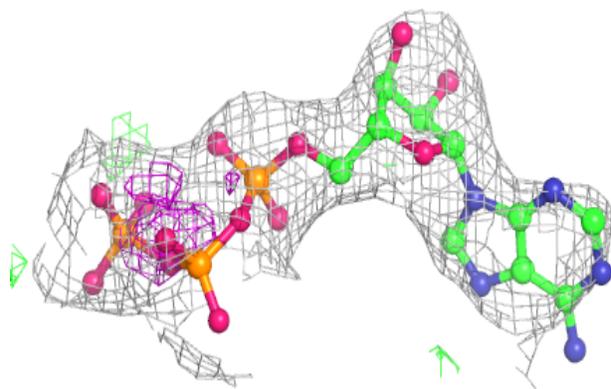
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	ATP	A	701	31/31	0.67	0.41	92,115,127,130	0
2	ATP	B	701	31/31	0.80	0.23	78,97,103,103	0
2	ATP	C	701	31/31	0.91	0.17	53,74,79,79	0

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.

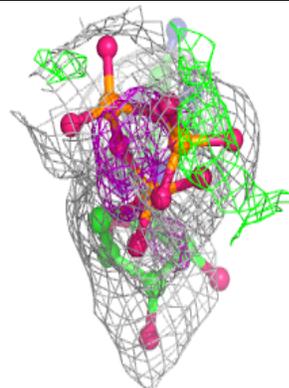
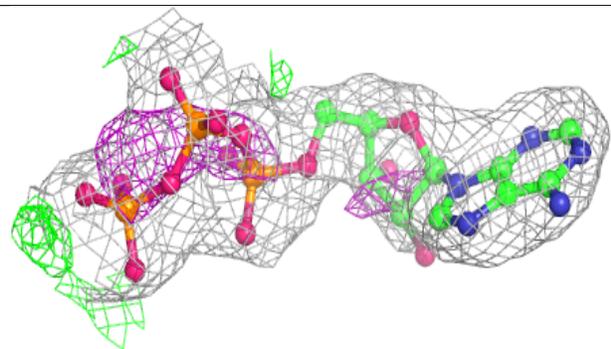
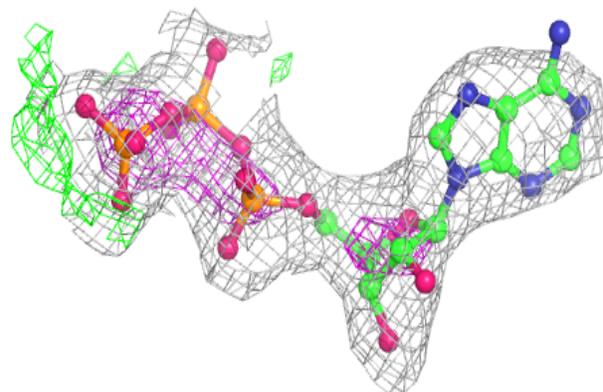


**Electron density around ATP B 701:**

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

**Electron density around ATP C 701:**

$2mF_o-DF_c$  (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.