



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2023 – 12:08 AM EST

PDB ID : 6PAN
Title : Structure of a bacterial Atm1-family ABC exporter with ATP bound
Authors : Fan, C.; Kaiser, J.T.; Rees, D.C.
Deposited on : 2019-06-11
Resolution : 3.40 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

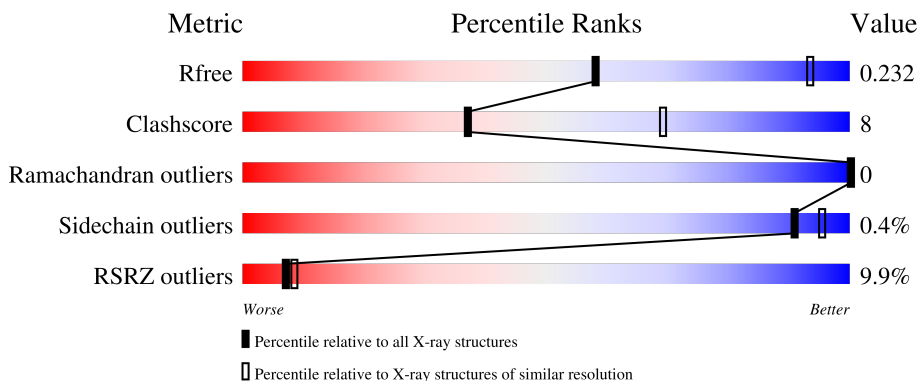
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	614	 9% 74% 19% 7%
1	B	614	 9% 77% 16% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8921 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 ATM1-type heavy metal exporter.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	572	4426	2819	786	808	1	12	0	0	0
1	B	573	4433	2824	787	809	1	12	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP Q2G506
A	526	CYS	SER	engineered mutation	UNP Q2G506
A	609	HIS	-	expression tag	UNP Q2G506
A	610	HIS	-	expression tag	UNP Q2G506
A	611	HIS	-	expression tag	UNP Q2G506
A	612	HIS	-	expression tag	UNP Q2G506
A	613	HIS	-	expression tag	UNP Q2G506
A	614	HIS	-	expression tag	UNP Q2G506
B	1	MSE	-	initiating methionine	UNP Q2G506
B	526	CYS	SER	engineered mutation	UNP Q2G506
B	609	HIS	-	expression tag	UNP Q2G506
B	610	HIS	-	expression tag	UNP Q2G506
B	611	HIS	-	expression tag	UNP Q2G506
B	612	HIS	-	expression tag	UNP Q2G506
B	613	HIS	-	expression tag	UNP Q2G506
B	614	HIS	-	expression tag	UNP Q2G506

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.50Å 134.58Å 190.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.71 – 3.40 39.71 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.7 (39.71-3.40) 98.8 (39.71-3.40)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.40Å)	Xtrriage
Refinement program	PHENIX 1.15.2_3472, REFMAC	Depositor
R, R_{free}	0.191 , 0.233 0.193 , 0.232	Depositor DCC
R_{free} test set	1697 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	140.4	Xtrriage
Anisotropy	0.363	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 135.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	8921	wwPDB-VP
Average B, all atoms (Å ²)	196.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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 [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	0.24	0/4490	0.42	0/6076
1	B	0.24	0/4497	0.41	0/6086
All	All	0.24	0/8987	0.42	0/12162

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	4426	0	4509	78	0
1	B	4433	0	4518	70	0
2	A	31	0	12	0	0
2	B	31	0	12	1	0
All	All	8921	0	9051	140	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 8.

All (140) 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:176:PHE:HB3	1:A:180:PHE:HE1	1.45	0.80
1:A:363:PHE:O	1:A:381:SER:HA	1.86	0.75
1:A:354:LEU:HB2	1:A:428:VAL:HG11	1.72	0.71
1:A:176:PHE:HB3	1:A:180:PHE:CE1	2.25	0.71
1:B:420:ILE:HG13	1:B:425:ILE:HD11	1.76	0.68
1:B:363:PHE:O	1:B:381:SER:HA	1.95	0.67
1:A:595:ARG:NH1	1:B:530:THR:OG1	2.29	0.66
1:A:165:THR:HG22	1:A:314:PRO:HB2	1.78	0.65
1:A:246:ARG:NH1	1:B:453:TYR:OH	2.30	0.65
1:A:575:GLU:OE2	1:A:588:LEU:N	2.26	0.64
1:B:202:ILE:HG21	1:B:268:LEU:HB2	1.79	0.64
1:A:494:ARG:O	1:A:503:LYS:NZ	2.28	0.63
1:A:531:ARG:NH1	1:B:591:GLU:OE2	2.34	0.61
1:B:438:GLY:HA3	1:B:516:PRO:HG3	1.82	0.60
1:A:165:THR:HG21	1:A:318:LEU:HG	1.83	0.60
1:B:176:PHE:HB3	1:B:185:VAL:HG12	1.82	0.60
1:A:555:ARG:HA	1:A:596:GLN:HE22	1.67	0.60
1:A:376:ILE:HG21	1:A:402:THR:HG21	1.84	0.59
1:A:384:VAL:HG13	1:A:390:VAL:HG21	1.84	0.59
1:A:35:LEU:HD22	1:A:108:VAL:HG22	1.85	0.59
1:B:320:MSE:HG3	1:B:323:ARG:HE	1.66	0.59
1:A:50:LYS:HZ3	1:A:168:GLU:HG2	1.69	0.58
1:B:362:THR:HB	1:B:419:LEU:HB2	1.85	0.58
1:A:144:ILE:HA	1:A:335:MSE:HE2	1.85	0.58
1:A:116:LEU:HD23	1:A:151:ILE:HG21	1.85	0.58
1:B:130:ARG:NH1	1:B:344:GLU:OE2	2.38	0.57
1:A:35:LEU:HD13	1:A:108:VAL:HG13	1.87	0.56
1:A:439:ILE:HG12	1:A:520:LEU:HB3	1.86	0.56
1:B:409:ARG:NH1	1:B:412:ASP:OD1	2.39	0.56
1:B:365:ASN:H	1:B:381:SER:HB3	1.71	0.56
1:A:345:VAL:HG13	1:A:409:ARG:HE	1.70	0.55
1:B:128:SER:HB3	1:B:344:GLU:H	1.70	0.55
1:A:115:HIS:O	1:A:119:ASN:ND2	2.35	0.55
1:A:506:VAL:O	1:A:510:ARG:HG3	2.05	0.55
1:A:359:PRO:O	1:A:548:THR:OG1	2.22	0.54
1:B:291:TRP:HB3	1:B:294:GLY:H	1.72	0.54
1:A:382:PHE:HB3	1:A:573:LEU:HD22	1.89	0.54
1:A:267:LEU:O	1:A:270:ILE:HG13	2.08	0.54
1:A:302:VAL:HA	1:A:305:ASN:ND2	2.22	0.54
1:A:438:GLY:HA3	1:A:516:PRO:HG3	1.90	0.54
1:B:142:LYS:HG2	1:B:221:LEU:HD23	1.89	0.53
1:B:42:ALA:HB1	1:B:160:PHE:HE1	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:437:LEU:O	1:B:514:LYS:NZ	2.39	0.53
1:B:417:ARG:HE	1:B:419:LEU:HD21	1.74	0.52
1:A:136:ARG:HG2	1:A:222:ALA:HB1	1.89	0.52
1:A:398:ALA:HB1	1:A:568:LEU:HB3	1.91	0.52
1:B:361:VAL:HB	1:B:384:VAL:HB	1.91	0.52
1:A:403:ILE:HD11	1:A:568:LEU:HD21	1.92	0.52
1:B:280:MSE:HG3	1:B:308:LEU:HD13	1.91	0.52
1:B:223:ARG:HD3	1:B:246:ARG:HB3	1.92	0.51
1:B:75:PRO:O	1:B:79:VAL:N	2.38	0.51
1:A:367:VAL:HB	1:A:415:GLU:HB2	1.92	0.51
1:A:515:ASN:OD1	1:A:547:ARG:NH2	2.44	0.51
1:B:575:GLU:OE2	1:B:588:LEU:N	2.41	0.51
1:A:320:MSE:HA	1:A:323:ARG:HG2	1.92	0.51
1:B:333:ALA:O	1:B:337:ARG:HB2	2.10	0.50
1:B:575:GLU:HB3	1:B:582:LEU:HD22	1.92	0.50
1:B:202:ILE:HB	1:B:268:LEU:HD13	1.94	0.50
1:B:367:VAL:HG22	1:B:379:GLY:H	1.76	0.50
1:B:505:ARG:HH21	1:B:532:THR:HG21	1.76	0.50
1:B:206:ARG:NH1	1:B:323:ARG:HH21	2.10	0.49
1:A:362:THR:HB	1:A:419:LEU:HB2	1.94	0.49
1:B:123:ARG:HB2	1:B:339:ILE:HD11	1.93	0.49
1:A:315:LEU:HA	1:A:318:LEU:HB2	1.94	0.49
1:B:62:LYS:HB3	1:B:79:VAL:HG13	1.95	0.49
1:B:67:MSE:HB2	1:B:298:VAL:HB	1.93	0.49
1:B:176:PHE:HA	1:B:180:PHE:CD1	2.47	0.49
1:A:370:TYR:H	1:A:376:ILE:HD13	1.77	0.49
1:B:144:ILE:HA	1:B:335:MSE:HE3	1.94	0.49
1:B:109:GLY:O	1:B:113:THR:HG23	2.13	0.49
1:B:42:ALA:HB1	1:B:160:PHE:CE1	2.47	0.48
1:A:101:ARG:HD2	1:A:160:PHE:CD2	2.49	0.47
1:A:367:VAL:HG22	1:A:379:GLY:H	1.79	0.47
1:A:417:ARG:HE	1:A:419:LEU:HD21	1.79	0.47
1:B:367:VAL:HB	1:B:415:GLU:HB2	1.97	0.47
1:B:64:VAL:HG13	1:B:296:LEU:HD22	1.97	0.47
1:A:305:ASN:OD1	1:A:306:THR:N	2.48	0.47
1:B:395:PRO:HD2	1:B:568:LEU:O	2.15	0.47
1:A:180:PHE:HZ	1:A:185:VAL:H	1.62	0.47
1:B:101:ARG:NH1	1:B:156:TYR:OH	2.48	0.47
1:A:103:ILE:HG13	1:B:263:ASN:HA	1.97	0.46
1:B:376:ILE:HG21	1:B:402:THR:HG21	1.98	0.46
1:A:280:MSE:HG3	1:A:308:LEU:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:LYS:HE3	1:A:167:ILE:HG22	1.96	0.46
1:B:313:ARG:O	1:B:317:MSE:HG2	2.15	0.46
1:A:36:ARG:O	1:A:39:VAL:HG22	2.15	0.46
1:A:180:PHE:HZ	1:A:185:VAL:N	2.14	0.46
1:A:589:TYR:HA	1:A:592:MSE:HE2	1.96	0.45
1:A:346:ALA:O	1:A:409:ARG:NH2	2.49	0.45
1:B:399:GLY:O	1:B:402:THR:OG1	2.27	0.45
1:A:399:GLY:O	1:A:402:THR:OG1	2.32	0.45
1:B:287:THR:HG21	1:B:304:VAL:HG21	1.99	0.45
1:A:206:ARG:HH22	1:A:210:ARG:HE	1.63	0.45
1:A:57:PRO:HA	1:A:60:TYR:HD2	1.81	0.44
1:B:60:TYR:CD2	1:B:303:PHE:HB2	2.53	0.44
1:B:320:MSE:O	1:B:323:ARG:HG2	2.18	0.44
1:B:400:LYS:N	2:B:701:ATP:O2B	2.50	0.44
1:A:172:VAL:O	1:A:176:PHE:HB2	2.17	0.44
1:A:291:TRP:HD1	1:A:293:GLN:H	1.66	0.44
1:A:180:PHE:CZ	1:A:184:LEU:HB3	2.53	0.44
1:A:177:TRP:CZ3	1:A:182:LEU:HG	2.53	0.43
1:A:454:ASN:O	1:A:510:ARG:HG2	2.18	0.43
1:B:176:PHE:HA	1:B:180:PHE:HD1	1.82	0.43
1:B:191:ALA:HB3	1:B:279:LEU:HD22	1.99	0.43
1:A:293:GLN:HB2	1:A:298:VAL:HG13	2.00	0.43
1:B:476:ILE:HG23	1:B:505:ARG:HD2	2.00	0.43
1:B:561:ASP:OD1	1:B:561:ASP:N	2.50	0.43
1:A:122:ALA:O	1:A:126:LYS:HG2	2.18	0.43
1:B:138:GLY:HA3	1:B:222:ALA:HA	2.01	0.43
1:A:138:GLY:HA3	1:A:222:ALA:HA	2.01	0.43
1:B:100:LEU:O	1:B:103:ILE:HG13	2.19	0.43
1:B:142:LYS:HD3	1:B:142:LYS:HA	1.83	0.43
1:A:475:ALA:O	1:A:505:ARG:NH2	2.49	0.42
1:A:51:ALA:O	1:A:55:ALA:N	2.53	0.42
1:B:502:GLU:HG3	1:B:505:ARG:HH11	1.83	0.42
1:A:106:GLU:HG2	1:B:262:GLU:HB2	2.02	0.42
1:A:291:TRP:CD1	1:A:293:GLN:HG2	2.55	0.42
1:B:151:ILE:HD11	1:B:332:MSE:HB2	2.01	0.42
1:A:87:TYR:CE2	1:B:280:MSE:HE2	2.54	0.42
1:A:263:ASN:HA	1:B:103:ILE:HG22	2.00	0.42
1:B:60:TYR:O	1:B:64:VAL:HG23	2.19	0.42
1:B:541:ARG:HD3	1:B:561:ASP:OD2	2.20	0.42
1:A:142:LYS:HB2	1:A:221:LEU:HD23	2.02	0.41
1:A:437:LEU:HD23	1:A:518:ILE:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:ALA:O	1:A:79:VAL:HG22	2.19	0.41
1:B:101:ARG:HD2	1:B:160:PHE:CD1	2.55	0.41
1:A:180:PHE:CD2	1:A:180:PHE:C	2.94	0.41
1:B:370:TYR:CE1	1:B:402:THR:HG22	2.55	0.41
1:A:180:PHE:CZ	1:A:185:VAL:N	2.89	0.41
1:A:180:PHE:CE2	1:A:184:LEU:HB3	2.56	0.41
1:A:290:GLY:HA3	1:A:295:LYS:HG3	2.02	0.41
1:A:318:LEU:HD23	1:A:318:LEU:HA	1.94	0.41
1:B:54:LEU:O	1:B:57:PRO:HD2	2.20	0.41
1:A:273:ALA:HB1	1:B:95:VAL:HG21	2.03	0.41
1:A:100:LEU:O	1:A:103:ILE:HG22	2.21	0.40
1:A:147:GLY:HA3	1:A:335:MSE:HE3	2.03	0.40
1:B:296:LEU:N	1:B:300:ASP:OD2	2.44	0.40
1:A:287:THR:HG21	1:A:304:VAL:HG11	2.03	0.40
1:B:56:LEU:HB2	1:B:57:PRO:HD3	2.02	0.40
1:B:136:ARG:HB2	1:B:139:GLU:HG2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	570/614 (93%)	564 (99%)	6 (1%)	0	100	100
1	B	571/614 (93%)	563 (99%)	8 (1%)	0	100	100
All	All	1141/1228 (93%)	1127 (99%)	14 (1%)	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	455/478 (95%)	453 (100%)	2 (0%)	91	95
1	B	456/478 (95%)	454 (100%)	2 (0%)	91	95
All	All	911/956 (95%)	907 (100%)	4 (0%)	91	95

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	VAL
1	A	408	PHE
1	B	161	ASN
1	B	408	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

2 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	1.03	1 (3%)	31,52,52	1.45	5 (16%)
2	ATP	A	701	-	26,33,33	1.05	1 (3%)	31,52,52	1.43	5 (16%)

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	-	-	5/18/38/38	0/3/3/3
2	ATP	A	701	-	-	6/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	ATP	C5-C4	2.83	1.48	1.40
2	B	701	ATP	C5-C4	2.80	1.48	1.40

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	701	ATP	C4-C5-N7	-3.61	105.64	109.40
2	A	701	ATP	C4-C5-N7	-3.34	105.92	109.40
2	B	701	ATP	N3-C2-N1	-3.18	123.71	128.68
2	A	701	ATP	PB-O3B-PG	-2.91	122.83	132.83
2	B	701	ATP	PA-O3A-PB	-2.85	123.03	132.83
2	A	701	ATP	N3-C2-N1	-2.80	124.30	128.68
2	B	701	ATP	PB-O3B-PG	-2.62	123.83	132.83
2	A	701	ATP	PA-O3A-PB	-2.51	124.23	132.83
2	A	701	ATP	C3'-C2'-C1'	2.27	104.40	100.98
2	B	701	ATP	O2A-PA-O1A	2.11	122.70	112.24

There are no chirality outliers.

All (11) torsion outliers are listed below:

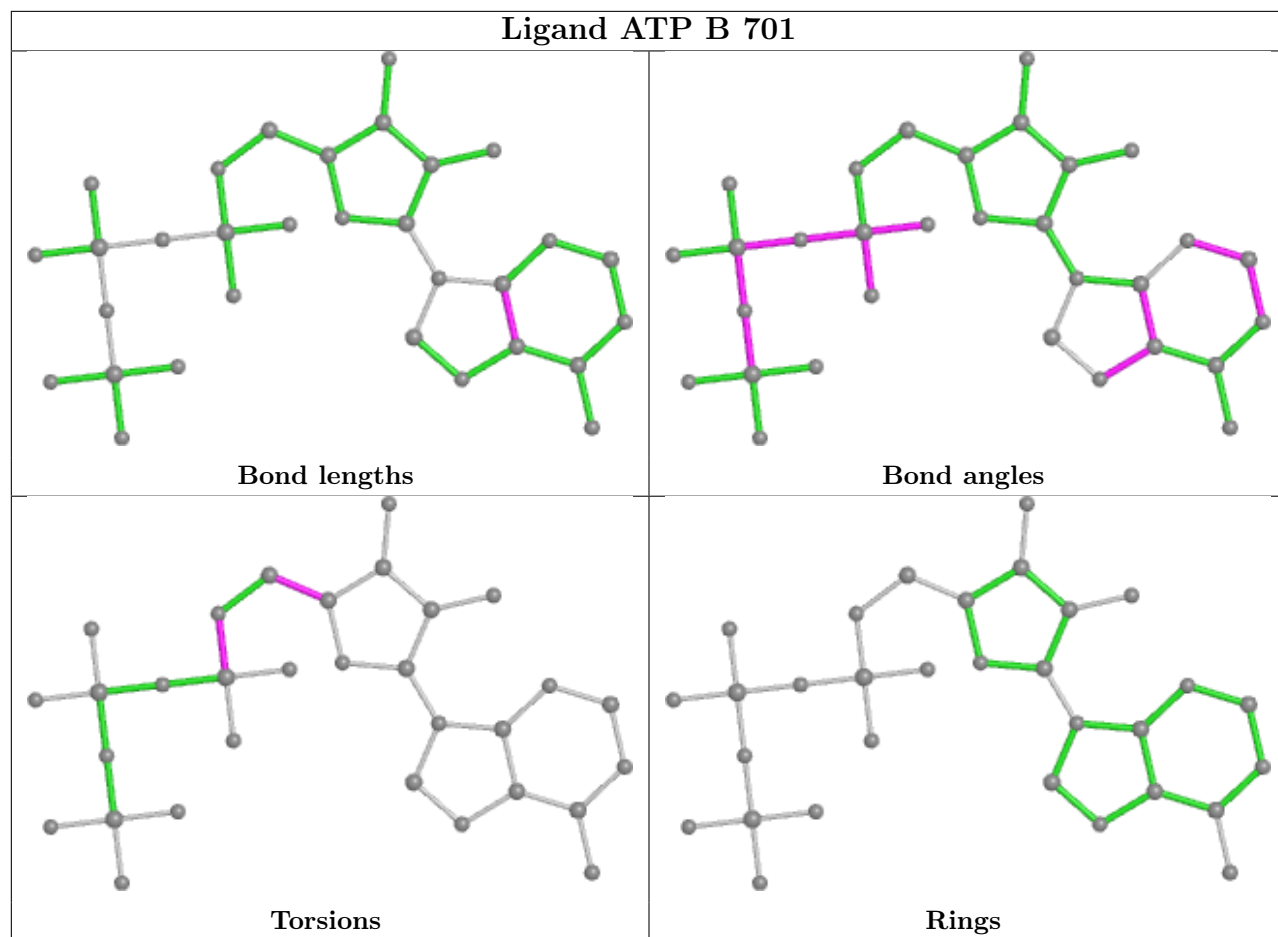
Mol	Chain	Res	Type	Atoms
2	A	701	ATP	O4'-C4'-C5'-O5'
2	B	701	ATP	C5'-O5'-PA-O2A
2	A	701	ATP	PB-O3A-PA-O5'
2	A	701	ATP	C5'-O5'-PA-O3A
2	B	701	ATP	C5'-O5'-PA-O3A
2	A	701	ATP	C5'-O5'-PA-O2A
2	B	701	ATP	C5'-O5'-PA-O1A
2	B	701	ATP	O4'-C4'-C5'-O5'
2	A	701	ATP	PB-O3B-PG-O1G
2	B	701	ATP	C3'-C4'-C5'-O5'
2	A	701	ATP	PB-O3B-PG-O2G

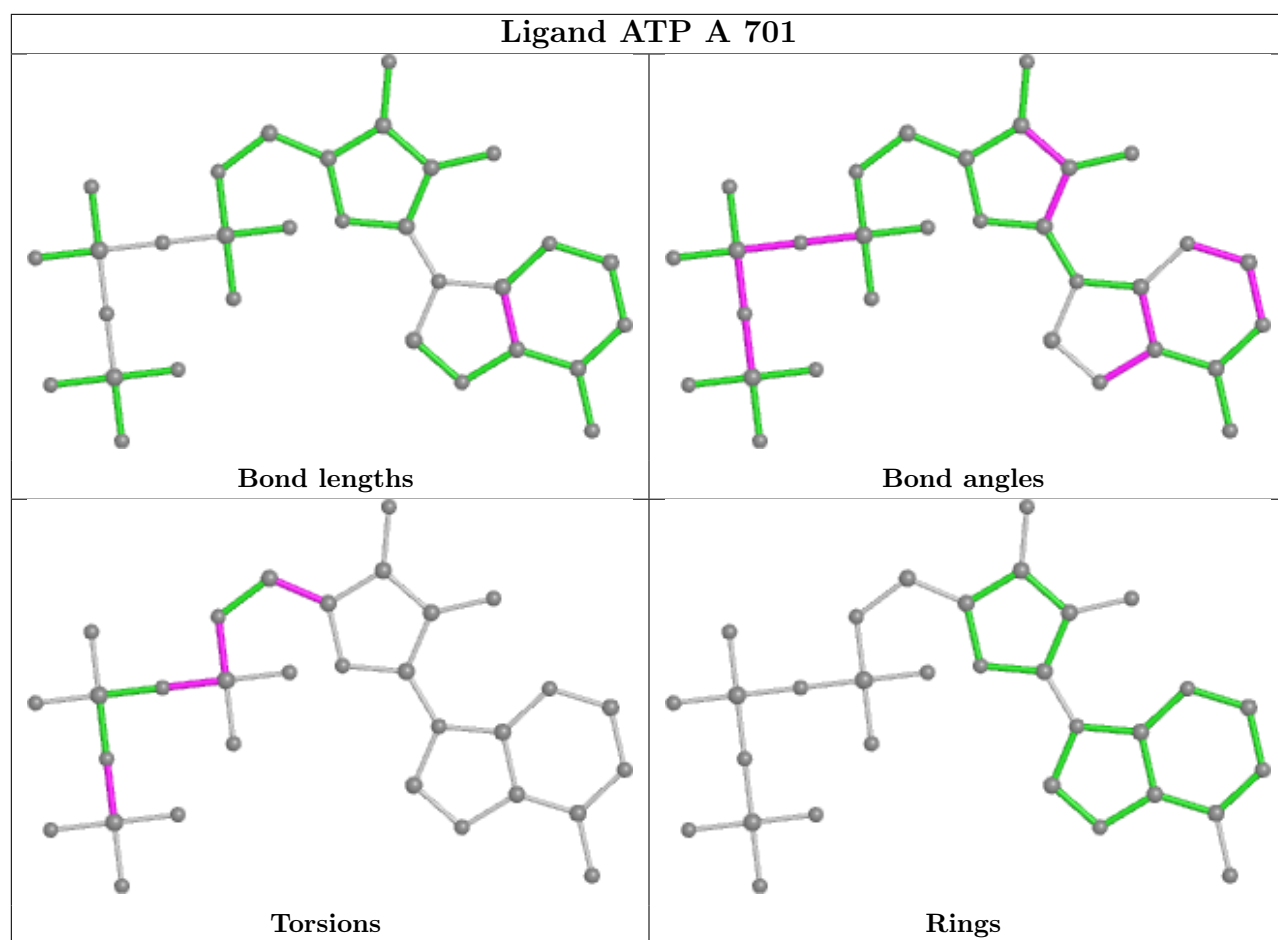
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	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 [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	560/614 (91%)	0.45	53 (9%) 8 10	84, 171, 307, 371	41 (7%)
1	B	561/614 (91%)	0.56	58 (10%) 6 8	100, 178, 314, 368	41 (7%)
All	All	1121/1228 (91%)	0.51	111 (9%) 7 8	84, 176, 309, 371	82 (7%)

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	73	ALA	37.8
1	B	78	THR	27.8
1	A	72	GLY	25.6
1	A	74	GLN	24.8
1	B	72	GLY	23.4
1	B	69	LEU	23.3
1	B	71	GLY	21.4
1	B	68	THR	21.0
1	B	65	ASP	20.4
1	A	78	THR	20.3
1	B	73	ALA	20.2
1	B	77	LEU	18.1
1	B	70	GLY	17.3
1	B	76	ALA	13.4
1	B	79	VAL	12.1
1	B	75	PRO	10.7
1	A	289	TYR	10.0
1	A	290	GLY	8.6
1	B	62	LYS	8.4
1	A	64	VAL	8.3
1	B	64	VAL	8.2
1	B	289	TYR	8.2
1	B	66	ALA	7.9
1	A	291	TRP	7.4

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Mol	Chain	Res	Type	RSRZ
1	B	82	ALA	7.1
1	B	74	GLN	6.8
1	B	81	LEU	6.7
1	A	32	ASN	6.4
1	B	58	PHE	6.4
1	A	299	GLY	6.1
1	A	79	VAL	5.9
1	A	75	PRO	5.3
1	A	462	ALA	5.3
1	A	77	LEU	5.0
1	B	285	ALA	4.9
1	B	286	TRP	4.8
1	A	297	THR	4.5
1	A	81	LEU	4.4
1	A	298	VAL	4.3
1	A	334	GLU	4.3
1	B	160	PHE	4.3
1	A	33	ALA	4.1
1	A	296	LEU	4.0
1	A	331	ASP	4.0
1	B	327	GLN	4.0
1	B	334	GLU	3.9
1	B	326	ARG	3.9
1	B	158	LEU	3.9
1	B	150	SER	3.9
1	A	285	ALA	3.7
1	A	350	ASN	3.6
1	A	526	CYS	3.6
1	B	526	CYS	3.5
1	B	80	ALA	3.4
1	A	63	ALA	3.4
1	B	293	GLN	3.4
1	B	85	LEU	3.3
1	B	462	ALA	3.3
1	A	443	ASP	3.3
1	A	292	SER	3.3
1	B	297	THR	3.3
1	A	160	PHE	3.3
1	A	337	ARG	3.3
1	B	157	PHE	3.3
1	A	40	VAL	3.3
1	B	61	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	292	SER	3.2
1	B	153	THR	3.2
1	A	294	GLY	3.2
1	A	71	GLY	3.2
1	A	328	GLY	3.2
1	B	63	ALA	3.1
1	B	32	ASN	3.0
1	A	352	PRO	3.0
1	A	286	TRP	3.0
1	A	338	LEU	3.0
1	B	291	TRP	2.9
1	B	162	ILE	2.8
1	B	180	PHE	2.8
1	A	463	SER	2.8
1	B	330	ILE	2.8
1	A	444	SER	2.8
1	A	44	LEU	2.7
1	A	159	LEU	2.7
1	B	156	TYR	2.7
1	B	296	LEU	2.7
1	A	330	ILE	2.7
1	B	298	VAL	2.7
1	A	61	LYS	2.6
1	A	351	ALA	2.6
1	A	427	HIS	2.6
1	A	461	GLY	2.6
1	B	155	LEU	2.5
1	B	83	PHE	2.5
1	A	293	GLN	2.5
1	B	305	ASN	2.4
1	A	428	VAL	2.4
1	B	325	ILE	2.4
1	B	525	THR	2.4
1	B	323	ARG	2.4
1	A	442	GLN	2.4
1	A	288	VAL	2.3
1	B	299	GLY	2.3
1	B	161	ASN	2.2
1	B	54	LEU	2.1
1	A	43	ILE	2.1
1	B	179	ASN	2.1
1	A	158	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	331	ASP	2.0
1	A	146	ARG	2.0
1	A	295	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 monosaccharides in this entry.

6.4 Ligands [i](#)

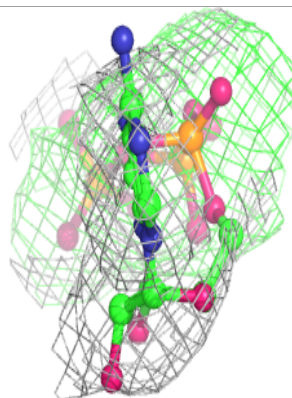
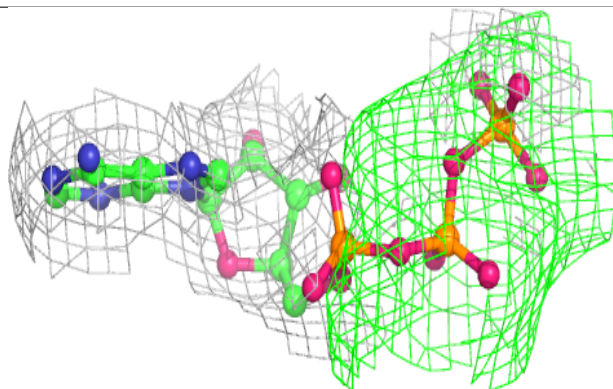
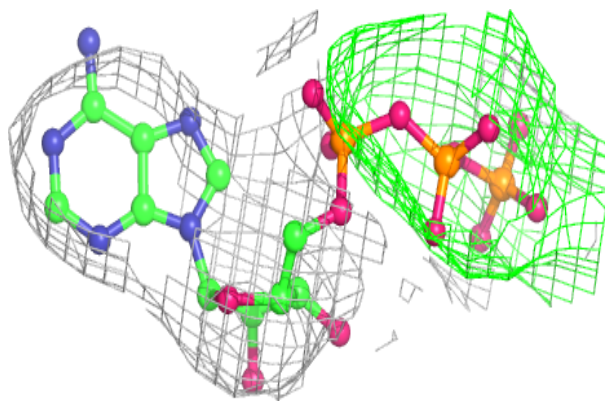
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ATP	A	701	31/31	0.86	0.38	162,195,254,260	0
2	ATP	B	701	31/31	0.92	0.37	154,198,218,228	0

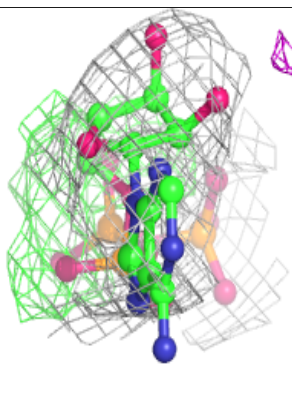
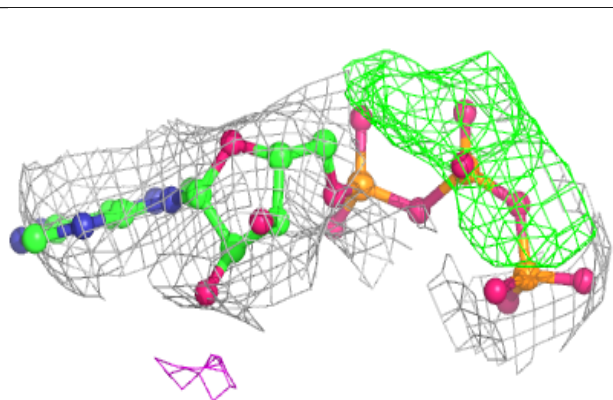
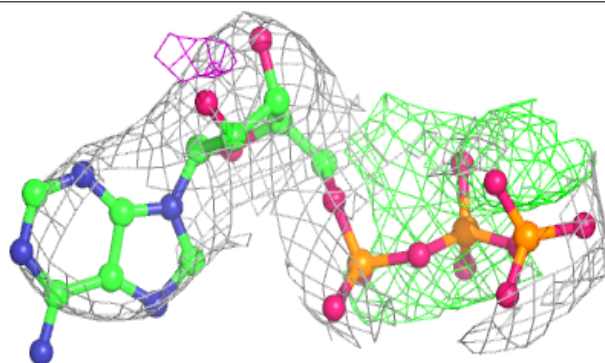
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ATP A 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 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.